2023 Veterinary Scholars Symposium
San Juan Puerto Rico
August 3rd—5th

AAVMC
American Association of Veterinary Medical Colleges

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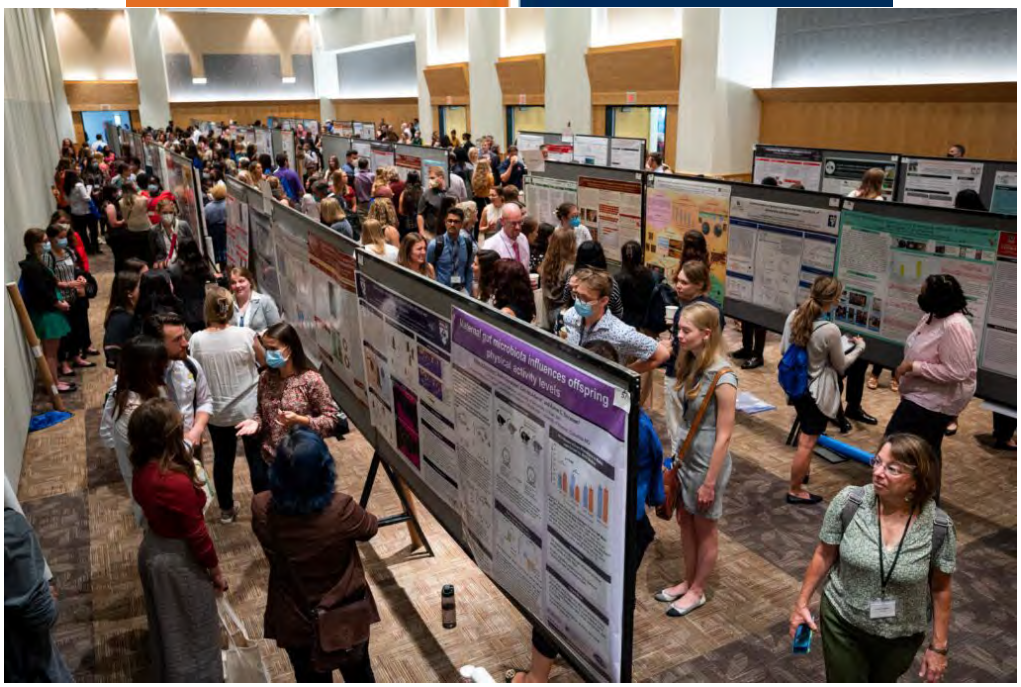
Veterinary Scholars Symposium



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Welcome

The variety of research areas in which this year's participants in the Veterinary Scholars Program worked is remarkable, and it speaks to the many ways that veterinarians and veterinary science contribute to both public and animal health. Boehringer Ingelheim is proud to join forces with our esteemed co-sponsors and leading veterinary schools to provide veterinary students with a preview of where they might choose to apply their many talents and skills, and impact One Health for generations to come.

Caroline Belmont, Head of Animal Health Global Innovation, Boehringer

The AAVMC is proud to support the presentation of the 2023 Veterinary Scholars Symposium. Scientific explorations and advancements in the body of knowledge are more important than ever before as we face the impending disease and food security threats of the future, and veterinary medicine must play a role at the heart of that effort. This program encourages our students to gain experience, develop their skills and consider careers in this vital area of our profession. It also celebrates and illuminates the success of the important work they have accomplished. The AAVMC is honored to be a part of it.

Andy Maccabe, CEO, American Association of Veterinary Medical Colleges

Thank you to the Veterinary Scholars Symposium Advisory Committee and Programming Committee!

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ADDITIONAL SUPPORT PROVIDED BY:

Abstract Title	Prevalence of cutaneous autoimmune and immune-mediated diseases at a tertiary hospital in the United States
Authors	Mikayla R. Adams, Jason B. Pieper, and Darren J. Berger
Affiliations	Department of Veterinary Clinical Sciences, College of Veterinary Medicine, Iowa State University, Ames, IA.
Abstract	The most recent reviews of the prevalence of cutaneous autoimmune and immune-mediated diseases in dogs and cats were published in 1975 and 1987. Since that time, newer diseases have been identified which are believed to be more common than other diseases and could significantly alter the prevalence rates compared to the previous data. The goal of this study is to evaluate the prevalence of all cutaneous autoimmune and immune-mediated diseases. Data was collected from electronic medical records at the Iowa State University Lloyd Veterinary Medical Center between January 1, 2010 and December 31, 2022. Search terms consisted of all cutaneous autoimmune and immune-mediated diseases and various general descriptive terms. There were 430 cases of canine autoimmune and immune-mediated diseases with 0.57% (430/75,580) of all the hospital medical records and 11.2% (430/3,826) of specific dermatology canine visits over that time period. Pemphigus foliaceus was the most common and accounted for 20.69% (89/430) of the diagnosed autoimmune diseases. This was followed by symmetrical lupoid onychomadesis (11.16%; 48/430), sebaceous adenitis (10%; 43/430), discoid lupus erythematosus (9.76%; 42/430), immune-mediated blepharitis (9.30%; 40/430), sterile nodular panniculitis (8.60%; 37/430), and juvenile cellulitis (6.51%; 28/430). The remaining diseases each occurred at less than 6%. Our data indicate that the prevalence of pemphigus foliaceus is the most common cutaneous autoimmune/immune-mediated disease, similar to previous reports. The second and third most common diseases are newer described conditions that were not included in prior reports. There may be some regional differences identified in the United States.
Research Grant	Self-funded
Field of Research	Dermatology

Abstract Title	Determining the ability of MALDI-TOF to properly categorize Staphylococcus chromogenes MLST clonal complexes
Authors	Ridwan O. Adesola, and Pamela R. F. Adkins
Affiliations	Department of Veterinary Medicine and Surgery, College of Veterinary Medicine, University of Missouri, Columbia, Missouri, USA
Abstract	Mastitis is one of the most common and costly diseases impacting dairy cattle globally. Non-aureus staphylococci (NAS) have become the most frequently identified bacteria isolated from milk samples collected from dairy cows globally and among the NAS species, Staphylococcus chromogenes is most frequently identified. In some studies, S. chromogenes has been associated with persistent intramammary infections and elevated somatic cell counts, while others have identified this species to have minimal impact on the gland or potentially protective effects. It is likely that strain differences contribute to these conflicting results. Identifying simple ways to differentiate S. chromogenes strains is important to understanding the molecular epidemiology of this organism. Therefore, the goal of this study is to determine if MALDI-TOF mass spectrometry can be used to determine the MLST clonal complex subtypes of S. chromogenes isolates collected from dairy farms in the United States. A collection of S. chromogenes isolates (n = 46) with known MLST clonal complex determinations was used. To date, a total of 15 S. chromogenes isolates were selected as representatives of each clonal complex and were added to the MALDI-TOF (Bruker Daltonics, Billerica, MA, USA) database following the manufacturer's guidelines. Next, we plan to test 31 isolates with known MLST clonal complex identifications to determine if the MALDI-TOF matching algorithm will correctly match the test isolates with the database isolates of the same clonal complex. The goal is to identify a method of strain typing that will be simple, fast, and inexpensive.
Research Grant	USDA-NIFA Award #2022-67015-37123
Field of Research	Production Animal Medicine

Abstract Title	Comparison of variation in the probing duration of Aedes aegypti on humans and mice using electropenetrography
Authors	Favour Akinfemi Ajibade, Anastasia M. W. Cooper, Babatunde Olowu, Vivienne Velic, Dana Mitzel, Kathryn Reif, and Kristopher Silver
Affiliations	University of Ibadan, Nigeria (Ajibade, Olowu), Kansas State University, Manhattan, KS, USA (Cooper, Silver, Reif), University of Veterinary Sciences, Brno, Czech Republic (Velic), National Bio and Agro-defense Facility, USDA, Manhattan, KS, USA (Mitzel)
Abstract	Blood-feeding arthropods such as ticks, black flies, mosquitoes, and sandflies are vectors of infectious diseases of both veterinary and medical importance. Aedes aegypti mosquitoes are known to transmit pathogens of deadly diseases such as yellow fever virus, dengue fever virus, and Zika virus via their saliva while blood-feeding on a suitable host (animals) as they obtain nutrients needed for egg production. Therefore, the transmission of pathogens by these insects requires an in-depth understanding of how the feeding behaviors of these blood-sucking insects, such as probing, salivation, and ingestion, are related to the inoculation of pathogens into new hosts which will aid the development of effective strategies to block pathogen transmission. Accordingly, we used electropenetrography (EPG) to compare the average probing duration of laboratory-reared (pathogen-free) Ae. aegypti on humans and mice during blood-feeding to better understand host differences influence probing duration. EPG is a technique that allows real-time monitoring and visualization of the probing behaviors of Ae. aegypti while the proboscis (i.e., mouthparts) is concealed in the animal's opaque tissues during probing. In EPG, Ae. aegypti and the host (i.e., human, mouse) are part of an electrical circuit that is complete when the mosquito makes contact with the host, producing electrical signals (waveforms) that correlate with feeding behaviors such as probing and ingestion. Future work will include evaluating how frequency and duration of probing and salivation events determine the pathogen load inoculated into the susceptible host to test the hypothesis that longer probing time enhances pathogen transmission by Ae. aegypti.
Research Grant	USDA Research, Education, and Economics Workforce Development Agreement (#58-3022-0-002) and the Hatch Multistate Project (NE1943).
Field of Research	Parasitology

Abstract Title	Pharmacodynamics of low-dose and label-dose desoxycorticosterone pivalate in dogs with hypoadrenocorticism
Authors	Camille E. Akin, Jean M. Brudvig, Daniel K. Langlois
Affiliations	Michigan State University, College of Veterinary Medicine, East Lansing, MI
Abstract	Monthly injections of desoxycorticosterone pivalate (DOCP) are used to treat the mineralocorticoid deficiency associated with hypoadrenocorticism in dogs. High drug costs have prompted investigations of alternatives to manufacturer-recommended protocols, with some clinicians utilizing lower dosages whereas others prolong dosing intervals. No studies have directly compared the physiologic appropriateness or cost benefits of these alternative approaches. The objectives of this study were to evaluate single dose pharmacodynamics of low-dose (1.1 mg/kg) and label-dose (2.2 mg/kg) DOCP. Dogs with newly diagnosed hypoadrenocorticism and concurrent hyponatremia or hyperkalemia were enrolled and treated with either 1.1 or 2.2 mg/kg DOCP in randomized fashion. Serum electrolyte concentrations and plasma renin activities (PRA) were measured at set time-points until recurrence of either hyperkalemia or hyponatremia. Pharmacodynamics variables were compared between groups. Seven dogs have completed this study, including 4 dogs treated with label-dose DOCP and 3 dogs treated with low-dose DOCP. The median duration of action as determined by recurrence of electrolyte abnormalities was 57 days in label-dose dogs and 42 days in low-dose dogs. Assessments of drug potency, which will be defined as the inverse of the area under the PRA curve, and duration of over-treatment, which will be defined as the time period in which PRA values are abnormally low, are pending PRA measurements. Continued enrollment of additional dogs and integration of PRA data will allow more detailed analyses. Preliminary results suggest that low-dose protocols might be more cost-effective and physiologically appropriate than interval prolongation protocols.
Research Grant	The Stanton Foundation
Field of Research	Pharmacology and Toxicology

Abstract Title	Establishing a reference database for Arrdc5 exon variation in domestic bulls
Authors	Ammasie Allred and Michela Ciccarelli
Affiliations	Department of Veterinary Clinical Sciences (Allred, Ciccarelli) and School of Molecular Biosciences (Ciccarelli), College of Veterinary Medicine, Washington State University, Pullman, WA
Abstract	Selective breeding in food animal production is key to trait improvement and addressing challenges in food security. Assisted reproductive technologies, especially artificial insemination, have bolstered the impact of selective breeding through increased access to sperm from bulls with desirable genomes. Conventionally, bulls are selected after they have reached puberty based on their pedigree and breeding soundness. However, new screening methods are needed to streamline the selection process for which bull calves are kept and raised as breeding stock. Recently, the gene arrestin-domain containing 5 (Arrdc5) was discovered as a potential evolutionarily conserved core regulator of mammalian spermatogenesis with a profound impact on sperm quality. Arrdc5 knockout mice exhibit male-specific sterility due to oligoasthenoteratospermia, which is the production of a low number of immotile sperm with morphological abnormalities. The genotypic data from Arrdc5 exons of bulls correlated to their phenotypic sperm quality will create a reference database to be used as a screening tool for selecting young bulls as future elite sires. To achieve this, frozen-thawed semen quality from 95 bulls was analyzed using computer-assisted sperm analysis (CASA) and bright-field microscopy. DNA was then extracted from the sperm of each bull and amplified by PCR to isolate each of the three coding exons of Arrdc5. Sequencing data from these amplicons paired with the sperm parameters of each bull will result in a reference database for identifying bulls carrying mutations in Arrdc5. The outcomes of this study represent key steps in developing a tool to screen bulls of any age for functional Arrdc5 gene, which could predict their future fertility.
Research Grant	WSU College of Veterinary Medicine
Field of Research	Theriogenology

Abstract Title	Pannexin as a pain biosensor for dogs
Authors	Dina Alter, Erik Henze, Kie Kawate, Jordyn Boesch, & Toshi Kawate
Affiliations	Department of Molecular Medicine, College of Veterinary Medicine (Alter, Henze, Kawate), Department of Clinical Sciences, College of Veterinary Medicine (Boesch) Cornell University, Ithaca, NY
Abstract	No objective measures of pain currently exist in companion animals, resulting in often arduous and ineffective treatment plans. Given that the ATP-release channel pannexin-1 is known to mediate chronic pain signaling, we hypothesize that pannexin activation can be used as an objective measure of pain in dogs. Our preliminary studies found a positive correlation between pannexin-1 activation and pain severity in dogs with joint disease. This current study aims to elevate our understanding of pannexin as a potential pain biosensor by testing a variety of sample types. These include synovial fluid, cerebral spinal fluid, effusion, and wound exudates. The samples are analyzed with robust metadata that includes not only a pain score, but age, sex, breed, diagnosis, and medication history. Analyzing pannexin activation in these contexts enhances the specificity and therefore the utility of pannexin as a biosensor. In addition to pannexin-1, we also investigate pannexin-2, which is known to be activated by similar signaling molecules although its physiological function remains elusive. Preliminary data from samples drawn from 97 dog patients showed a diverse array of activation, some of which are pannexin subtype specific. We expect that the thorough analysis will reveal the utility of pannexin as a novel “painometer.” Once established as such, this work will not only aid clinicians in analgesia choice but open the door for developing novel, pannexin-specific therapeutic approaches for alleviating chronic pain.
Research Grant	Cornell Richard P. Riney Canine Health Center Research Grants Program
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Characterizing immunosuppression in canine sarcomas
Authors	Zynia Alvarez, Davis Seelig, Jessica Lawrence, Kim Demos-Davis
Affiliations	Department of Veterinary Clinical Sciences (Alvarez, Seelig, Lawrence, Demos-Davis), College of Veterinary Medicine, University of Minnesota, Saint Paul, MN; Masonic Cancer Center (Seelig, Lawrence), University of Minnesota, Minneapolis, MN, USA
Abstract	The checkpoint protein B7-H3 is expressed in human sarcoma cells and is associated with progression and metastasis. B7-H3 can also be induced on immune cells to promote immunosuppression. Peripheral immune cell B7-H3 expression has not been described in canine sarcomas and will aid design of novel B7-H3 targeted therapies. The aim of this study is to characterize B7-H3 expression in peripheral immunosuppressive cells from dogs diagnosed with sarcomas. To investigate this aim, peripheral blood mononuclear cells (PBMCs) were collected at diagnosis in dogs with osteosarcoma (OSA), soft tissue sarcoma (STS) or primary bone hemangiosarcoma (HSA). Myeloid-derived suppressor cells (MDSCs), regulatory T cells (Tregs), and B7-H3-expressing cells were quantified by flow cytometry. In a subset of dogs administered radiation therapy (RT), PBMCs were serially analyzed after treatment. Spearman's correlation test, one-way ANOVA, or t-test were used to analyze cell subsets. B7-H3 expression in sarcoma tissue was assessed by immunohistochemistry in a pilot group of dogs undergoing RT. The finding showed that B7-H3 expression was detected on PBMCs in dogs with OSA (N=4), STS (N=5) and HSA (N=1). B7-H3+ monocytes and B7-H3+ T cells were detected in 8 and 6 dogs, respectively. There was no correlation between B7-H3+ cells and MDSCs or Tregs. Dogs with OSA had increased B7-H3+ cell subsets, polymorphonuclear (PMN)-MDSCs and Tregs compared to dogs with STS. In dogs (N=3) serially assessed after RT, B7-H3+ cell subsets and PMN-MDSCs increased after RT. B7-H3 expression was strongly positive before and after RT in 4 dogs. Additional study is warranted to define B7-H3 expression and its contribution to immunosuppression.
Research Grant	D23CA-506 Morris Animal Foundation DCORC2021-002 V Foundation
Field of Research	Immunology

Abstract Title	Contrast-enhanced and quantitative MRI of femoral head repair in a piglet model of Legg-Calvé-Perthes disease
Authors	Ashton A. Amann [1], Erick O. Buko [1], Alexandra R. Armstrong [1], Ferenc Toth [1], Jennifer C. Laine [2,5], Susan A. Novotny [3,5], Reza Talaie [4], Casey P. Johnson [1]
Affiliations	[1] Department of Veterinary Clinical Sciences, College of Veterinary Medicine, University of Minnesota, St. Paul, MN; [2] Department of Orthopedic Surgery, [3] Department of Rehabilitation Medicine, [4] Department of Radiology, Medical School, Minneapolis, MN; [5] Gillette Children's Specialty Healthcare, St. Paul, MN
Abstract	Legg-Calvé-Perthes Disease (LCPD) is an idiopathic, pediatric hip disorder caused by reduced blood flow (ischemia) to the femoral head. Ischemia affecting the femoral head leads to osteonecrosis of bone trabeculae, reduced marrow cellularity, and eventual collapse of the femoral head. While gadolinium contrast-enhanced MRI (CE-MRI) is the clinical standard in diagnosing femoral head ischemia, there is no diagnostic method available for early detection of bone injury and subsequent repair. Previous studies have shown that quantitative T2, adiabatic T1rho (aT1ρ), and adiabatic T2rho (aT2ρ) relaxation time mappings are sensitive to acute injury in a piglet model of LCPD following surgical induction of global femoral head ischemia. However, the sensitivities of these techniques have not been assessed in cases of partial femoral head ischemia or during the subsequent repair processes. In this study, using a minimally-invasive piglet model, partial femoral head ischemia was induced bilaterally in three piglets (n=6 femoral heads) by intravascular administration of embolic particles under fluoroscopic guidance. Femoral heads were imaged in vivo one-week post-operatively at 3T MRI utilizing: (i) morphological 3D DESS; (ii) quantitative maps (i.e., 3D T2, aT1ρ, and aT2ρ); and (iii) 3D CE-MRI. Femoral heads were processed for histology, and H&E-stained photomicrographs were subsequently spatially co-registered to the 3D DESS images. Sensitivities analyses were then performed to compare the quantitative maps to H&E sections and CE-MRI. Results from this work will help inform whether quantitative maps may be an alternative or complementary technique to CE-MRI to assess early-stage LCPD.
Research Grant	Pediatric Orthopaedic Society of North America; Gillette Children's Foundation; and National Institutes of Health (R56AR078315)
Field of Research	Orthopedics

Abstract Title	Can Florfenicol be a Substitute for Chloramphenicol in Resistant Canine UTIs?
Authors	Elayna Anderson, Kate KuKanich, Astrid Carcamo Tzic, Butch KuKanich
Affiliations	Departments of Clinical Sciences (Anderson, K KuKanich) and Anatomy and Physiology (Carcamo Tzic, B KuKanich), College of Veterinary Medicine, Kansas State University, Manhattan, KS
Abstract	The urinary excretion profile of florfenicol was evaluated in dogs to explore its potential usefulness for treating resistant canine urinary tract infections. Nine healthy male intact purpose-bred Beagles and four healthy client-owned dogs (Standard Poodle, Greyhound, Pug, and English Setter) each received a single oral dose of florfenicol 20mg/kg (300mg/ml parenteral solution) mixed with ½ can maintenance food. Adverse effects were recorded. All voluntary urinations were collected at baseline and for 12 hours after dosing, with target intervals of 6-, 8-, and 12-hrs after drug administration. Urine was measured for volume and florfenicol concentration using high performance liquid chromatography. Seven (of 9) Beagles and 4/4 client-owned dogs completely ingested the florfenicol and were enrolled in the study; salivation (n=1) and head-shaking (n=3) were observed. The last measurable urine florfenicol concentration was within similar range for Beagles (n=7) and the Pug (0.23-3.19 mcg/mL), whereas the English Setter, Greyhound, and Standard Poodle had a range of 13.0-32.7 mcg/mL. The urine half-life was within similar range for Beagles and the Pug (0.76-1.39 h), whereas the English Setter, Greyhound, and Standard Poodle had a urine half-life range of 1.70-1.82 h. The three larger breed dogs had >8 mcg/mL florfenicol in their urine at 12 h, whereas the Beagles and Pug had <8 mcg/mL; it is unclear if this is a breed or size difference. Due to the variability in urine excretion, oral florfenicol does not appear to be ideal for resistant canine UTIs unless drug monitoring is available.
Research Grant	Kansas State University Department of Clinical Science Research Grant
Field of Research	Pharmacology and Toxicology

Abstract Title	Effects of BCAA metabolism on inflammasome priming and activation in macrophages
Authors	Elena Anderson, Mikel Haggadone, Sunny Shin
Affiliations	School of Veterinary Medicine (Anderson) and Department of Microbiology, Perelman School of Medicine (Haggadone, Shin), University of Pennsylvania, Philadelphia, PA
Abstract	The innate immune system acts through a suite of pattern recognition receptors (PRRs) to serve as the host's first line of defense against pathogens. Inflammasomes comprise an important class of cytosolic PRRs triggered during infection. Oligomerization of these multiprotein complexes in response to pathogen sensing and/or cellular damage drives an inflammatory form of cell death called pyroptosis that is coupled to interleukin (IL)-1 cytokine release. Our lab is interested in the functions of two major inflammasomes, the canonical NLRP3 inflammasome and the noncanonical caspase-11 inflammasome. NLRP3 and caspase-11 both require a priming signal driven by Toll-like receptor (TLR) signaling. A secondary activation signal, either potassium efflux for NLRP3 or cytosolic LPS for caspase-11, promotes inflammasome assembly and proteolytic cleavage of the pore-forming protein gasdermin D to drive pyroptosis and IL-1 release. It is known that macrophages undergo metabolic rewiring after PRR activation to promote their proinflammatory functions. However, much remains unknown about the metabolic drivers of inflammasome priming and activation. Here, we have studied the role of branched-chain amino acids (BCAAs) in regulating NLRP3 and caspase-11 inflammasome biology in macrophages. Our data suggest that metabolic stress invoked by restricting BCAAs dampens pyroptotic cell death driven by both the NLRP3 and caspase-11 inflammasomes. Mechanistically, BCAA restriction post-translationally blunts NLRP3 inflammasome activation and post-transcriptionally abrogates caspase-11 priming in response to various TLR ligands. Here, we have unveiled a new role for BCAAs in metabolically licensing NLRP3- and caspase-11-driven pyroptosis.
Research Grant	R01AI118861
Field of Research	Immunology

Abstract Title	Investigating the circulation and maintenance of SARS-CoV-2 in free ranging white-tailed deer
Authors	Gayatri Anil, Lina M. Covaleda, Leonardo C. Caserta, Krysten L. Schuler, and Diego G. Diel
Affiliations	Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine (Anil, Covaleda, Caserta, Diel); Animal Health Diagnostic Center (Covaleda, Caserta, Schuler, Diel); Department of Public & Ecosystem Health, College of Veterinary Medicine (Schuler), Cornell University, Ithaca, New York
Abstract	A high prevalence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in free-ranging white-tailed deer (WTD) has been detected across North America. The angiotensin-converting enzyme 2 (ACE2), the main host cellular receptor for SARS-CoV-2, of WTD shares a high sequence homology with the human ACE2 receptor. Moreover, animal studies have found that intranasal inoculation resulted in infection and shedding in WTD, and infected animals can transmit the virus to non-inoculated deer. A previous study from our laboratory found that in New York State (NY), the incidence of SARS-CoV-2 in WTD increased from 0.6% in 2020 to 21.1% in 2021 as detected by real-time PCR (rtPCR). Sequence analysis of positive samples identified three variants of concern, Alpha, Gamma, and Delta, with the first two being detected in WTD after their broad circulation in humans. Based on these findings, we sought to determine whether SARS-CoV-2 is maintained over time in free-ranging WTD. A total of 2700 retropharyngeal lymph node samples were collected from hunter-harvested free-ranging WTD in 2022. These samples are being homogenized and tested via rtPCR for SARS-CoV-2 RNA. Samples with cycle threshold (Ct) < 30 will then be confirmed via virus isolation and sequencing. Geospatial and phylogenetic analyses will later be conducted to evaluate the distribution and epidemiological links between SARS-CoV-2 viruses circulating in WTD in NY. Frequent interactions between WTD and humans make a better understanding of the prevalence and epidemiology of SARS-CoV-2 in WTD important to prevent the occurrence of spillback events into humans or spillover into wildlife reservoirs.
Research Grant	USDA-NIFA-2023-70432-39463
Field of Research	One Health

Abstract Title	Comparison of effects of intestinal normothermic machine perfusion and cold storage on CD3+ cell populations
Authors	Ariana Antezana, Caroline McKinney, Elsa Ludwig, John Freund, Liara Gonzalez
Affiliations	North Carolina State University CVM
Abstract	Intestinal transplantation (IT) is the only life saving option for intestinal failure patients when parenteral nutrition has failed. Unfortunately, the rates of graft success are hindered due to ischemia-reperfusion injury (IRI)-associated damage from procurement and storage. The gold standard method for intestinal allograft preservation is cold storage (CS). However, a new method of liver preservation utilizing normothermic machine perfusion (NMP), has been found to reduce inflammation and hepatocellular damage. The method of NMP sustains an organ in a normal environment complete with oxygen and nutrition. We, therefore, aimed to evaluate intestinal allografts treated by either CS or NMP and to specifically compare immune cell population dynamics between these methods. It is known that some T cell populations influence graft rejection and viability why others, such as γδ T cell, can have protective effects. We hypothesized that NMP reduces IRI via the reduction of immune cell infiltration after transplantation compared to CS. We evaluated the presence of CD3+ T cells in the transplanted intestine stored using NMP or CS via immunofluorescence. T-cell number was quantified in samples obtained from allografts collected at the time of procurement and 1 hour after transplantation. Preliminary results of NMP jejunal samples show a trend of increasing CD3+ T cells to DAPI cells infiltrating the crypts and villus epithelium compared to CS samples. Further results are pending. Understanding what factors augment the viability of intestines in NMP may provide useful information on how to better improve the outcome of intestinal allograft transplant patients.
Research Grant	Veterinary Scholars Program NC State University Office of the Associate Dean for Research and Graduate Studies and U.S. Department of Defense PR181265
Field of Research	Immunology

Abstract Title	Hookworms and roundworms in dogs: a retrospective study of comorbidities, awareness, and prevention
Authors	Briana Arceneaux, Athema Etzioni
Affiliations	Tuskegee CVM
Abstract	Hookworms and roundworms are two helminths commonly affecting many dogs around the world. These intestinal worms can cause inflammation in the dog's gastrointestinal system and hookworms can cause life-threatening anemia. When co-infection occurs with either of these helminths or with other parasites; treatment may need to be more aggressive, and recovery may take longer. Performing diagnostic testing is important to ensure the proper diagnosis is elucidated and the appropriate treatment is administered. The age range of dogs infected can vary, but helminth infections are more commonly seen in puppies. Over the years, pet owners have minimized the importance of intestinal worms, and many are not aware of methods of prevention or that zoonoses can occur. This study analyses the current knowledge of ascarids and ancylostomatids, focusing on the awareness, importance of diagnostics, control methods and to prevent infection by owner education to enhance compliance.
Research Grant	TUCVM Veterinary Scholars Program & Mississippi State CVM
Field of Research	Parasitology

Abstract Title	Megasphaera elsdenii: effect on blood/fecal pH and lactate in horses transitioned to high grain low fiber diet
Authors	C Arias, S Mordoh, H Banse, A Chapman, M Keowen, F Garza, Jr., A Ferdonnet, F Andrews, M Mitchell
Affiliations	Equine Health and Sports Performance (EHSP), Veterinary Clinical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA (Arias, Mordoh, Banse, Chapman, Keowen, Garza, Ferdonnet, Andrews), Pathobiological Sciences (Mitchell)
Abstract	Current feeding practices in competition horses include increased amounts of grain/starch and lower amounts of forage/fiber. This change in diet has been shown to shift the microbial community to lactic acid producing bacteria and can lead to colonic acidosis. Many probiotics fed to horses do not address lactic acidosis in the hindgut of horses on high grain diets. Megasphaera elsdenii (Mega e) is a lactate utilizer and native inhabitant of the equine gut (Biddle et al. 2013; Douthit et al. 2019). There are few reports in the literature on the effects of feeding Mega e to horses. The purpose of this study is to measure fecal and blood pH, fecal and blood lactic acid, and evaluate the microbiome in horses transitioned to a high grain, low roughage diet. We hypothesize that daily oral administration of Mega e reduces fecal lactic acid, maintains fecal and blood pH in horses transitioned to a high grain, low roughage diet. Blood and manure samples were collected from 6 horses from the LSU EHSP herd. Horses were randomized into 2 groups (treatment and control) and housed in stalls. Group 1 received 2 Mega e boluses (Lactipro) mixed with feed on Days 0-14, then 1 bolus on Days 15-42. Group 2 received no treatment Days 0-42. Days 0-14 both groups were fed a normal diet then transitioned to a high grain/low roughage diet during Days 15-42. Preliminary results show decreased blood pH in Group 2 from days 0-35. The pH did not decrease in the treated group during this time, suggesting Mega e might be utilizing lactic acid. Data collection is ongoing, and results are expected to show normal blood pH for Group 1 and decreased pH for Group 2.
Research Grant	MS Biotec LLC, Wamego, KS
Field of Research	Equine Medicine and Surgery

Abstract Title	Early gut microbiota colonization and its relationship to lung hyperresponsiveness and increased inflammatory
Authors	Yahawa Z. Ashaqua, Ivon Moya-Uribe, and Linda S. Mansfield
Affiliations	Michigan State University College of Veterinary Medicine, East Lansing MI
Abstract	Asthma is a chronic respiratory disease that affects approximately 1 in 13 people in the United States. The pathogenesis of this disease is not well understood, but we know there is a correlation between the formation and composition of the neonatal gut microbiota and an individual's susceptibility to asthma. Our focus is to understand the relationship between the mouse neonatal gut microbiota development and the emergence of allergies and asthma later in life. We hypothesized that there will be more inflammatory cells in the bronchoalveolar lavage fluid from mice with humanized gut microbiota with known allergy agonists when compared to the group with the conventional mouse microbiota. During the mouse neonatal stage, mice in the experimental treatment group were exposed to a human derived gut microbiota (HU) while the control group was exposed to conventional mouse microbiota (MO). HU mice used were split into two groups; One group received a house dust mite allergen intranasally while the other received intranasal saline. Control (MO) mice were split in a similar fashion. For allergen sensitization each group was repeatedly exposed to either saline or house dust mites for two weeks. A bronchoalveolar lavage was performed on day 15 post euthanasia to measure pulmonary inflammation. Cytology was performed on the sample and the immune cell composition was observed. Our aim was to understand how exposure to a certain gut composition early in life can influence lung hyperresponsiveness to allergens and the quantity of inflammatory cells in the airways. Understanding the mechanisms may lead to future development of new therapies against asthma and allergies that can benefit both the human and animal world.
Research Grant	NHLBI grant
Field of Research	Microbiomes

Abstract Title	Characterizing triatomine bloodmeal hosts and the effects of insecticides in kennel environments, Texas, USA
Authors	Olivia Ashbaugh, Rachel Busselman, Ashley Saunders, and Sarah Hamer
Affiliations	Department of Veterinary Integrative Biosciences (Ashbaugh, Busselman, Hamer) and Department of Small Animal Clinical Sciences (Saunders), School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA
Abstract	Trypanosoma cruzi is a zoonotic, protozoan parasite causing Chagas disease in humans, dogs, and other mammals, with clinical disease ranging from chronic heart disease to sudden death. In previous controlled laboratory experiments, we showed that some commercially available flea/tick preventives for dogs rapidly induce mortality in triatomines ("kissing bugs", the vector of T. cruzi) that fed on treated dogs. Our overall goal is to suppress the local vector population through kennel-wide application of systemic insecticides, leading to a reduced risk of T. cruzi infections in dogs. Our objective was to characterize variation in vector infection prevalence, bloodmeal hosts, and insect mortality in relation to the differential use of insecticides at kennels. At 6 kennels in Texas, we performed systematic surveillance and counted insects found dead vs. alive. A subset of bugs was dissected, underwent hindgut DNA extraction, quantitative polymerase chain reaction (qPCR), amplification of T. cruzi, and amplification and sequencing of the vertebrate cytB gene from insect gut contents. Of the insects dissected (n=99), 16% were alive, 84% were dead upon collection, and more alive insects were found by kennels using fluralaner. T. cruzi prevalence was 31.3% with no significant difference between kennels ($p<0.05$). Sanger sequencing was successful for 23 samples (23%), and 4 distinct host species were identified including dog and cricket in insects found alive (n=3) vs. dog, cricket, toad, and porcupine in insects found dead (n=20). Initial data suggests that systemic insecticide use in canines may be useful in decreasing triatomine populations in and around kennels and may be used to guide further research.
Research Grant	American Kennel Club Canine Health Foundation Grant No. 02980
Field of Research	Epidemiology

Abstract Title	Metabolic biology of the White-Bellied Pangolin (Phantaginus tricuspus)
Authors	Lauren Ayres Martinez, David Kersey, Copper Aitken-Palmer
Affiliations	College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA (Ayres Martinez & Kersey). Brookfield Zoo, Chicago Zoological Society, Brookfield, IL (Aitken-Palmer).
Abstract	The white-bellied pangolin (Manis tricuspis) is one of eight pangolin species within a family of mammals that have gained notoriety as the most illegally trafficked animals in the wildlife trade. Due to their value, illegal poaching operations have decimated wild populations of pangolins, with six of eight species listed as endangered. As part of a comprehensive study of pangolin biology, we are investigating thyroid physiology to establish normative metabolic activity and the relationship with reproductive function. The results of this study will enhance understanding of basic pangolin biology, which are necessary for captive conservation efforts. We will establish a baseline knowledge of the thyroid biology of the white-bellied pangolin by assessing patterns of thyroid gland hormone metabolites from fecal samples of fifteen captive individuals at the Brookfield Zoo. Animal care and management were reviewed and approved by Brookfield Zoo's Institutional Care and Use Committee. This study is a necessary component of a biomedical survey of this rare population and utilizes non-invasively collected fecal samples. In a preliminary study, we validated the use of feces in thyroid hormone assessments. In this study, we will track circannual patterns of triiodothyronine (T3) and thyroxin (T4), coupled with environmental and behavioral data, to establish a baseline of thyroid activity. Additionally, we will compare male and female thyroid hormone patterns to previous assessments of reproductive activity to determine the relationship between metabolic and reproductive expenditure. Results of this study will contribute to conservation efforts, inform captive management, and guide future research for all 8 pangolin species.
Research Grant	Chicago Board of Trade.
Field of Research	Wildlife Conservation

Abstract Title	Mycobacterium isolates from dogs and cats-speciation and antimicrobial susceptibility testing
Authors	Jaclyn Azelby, Porsha Reed, Rebekah Jones, Brian Johnson, Rajeev V. Nair and Sreekumari Rajeev
Affiliations	Department of Biomedical and Diagnostic Sciences, and the Department of Small Animal Clinical Sciences, College of Veterinary Medicine, University of Tennessee, Knoxville,TN, USA.
Abstract	Nontuberculous Mycobacterium spp. are an increasing cause of morbidity in humans and animals. These infections are often challenging to diagnose and treat due to the diversity of species causing these infections, and hence the variation in antimicrobial susceptibility patterns. In this study, we characterized mycobacterial isolates obtained from dogs and cats representing both in house and referral cases submitted between 2016 and 2022 at the University of Tennessee Veterinary Medical Center. We performed a variety of tests, including Gram staining, Acid-fast staining, Matrix-Assisted Laser Desorption/Ionization Time-of-flight mass spectrometry (MALDI-TOF MS), 16s rRNA amplification and sequencing with two different sets of primers for the identification of these isolates and antimicrobial susceptibility testing on all the isolates. We observed a discrepancy in identifications made by MALDI-TOF and those made by DNA sequencing. Of the 25 samples with an identification by both MALDI-TOF and sequencing using the primer pair-1, only 9 samples (36%) had a correct match. Of the 24 samples with an identification by both MALDI-TOF and sequencing using primer pair 2, 15 samples (62.5%) had a correct match. Antimicrobial susceptibility testing using a commercially available broth dilution test did not show consistent susceptibility patterns between isolates. While all of the isolates tested were susceptible to amikacin, 44% of isolates were resistant to doxycycline. Characterization of genotypic and phenotypic attributes of mycobacterial isolates in combination with their antimicrobial susceptibility pattern may benefit diagnostic care and more effective treatment.
Research Grant	None
Field of Research	Bacteriology

Abstract Title	Mycoplasma species isolated from dogs and cats from non-respiratory clinical presentations
Authors	Jaclyn Azelby, Porsha Reed, Rebekah Jones, Brian Johnson, Rajeev V. Nair and Sreekumari Rajeev
Affiliations	Department of Biomedical and Diagnostic Sciences, and the Department of Small Animal Clinical Sciences, College of Veterinary Medicine, University of Tennessee, Knoxville,TN, USA.
Abstract	Mycoplasma spp. are cell wall-deficient bacteria that have been classified as commensal organisms of mucosal surfaces and opportunistic pathogens that can cause a broad spectrum of disease in both humans and animals. Although most commonly associated with respiratory illness, Mycoplasma have been reported in association with cases of urogenital tract disease, keratoconjunctivitis, polyarthritis, and soft tissue infections in dogs and cats. Mycoplasma species' specific growth requirements for culture often allows them to go undetected and are commonly isolated from patients who fail to respond to standard beta-lactam antibiotic therapy. Given their commensal nature, their characteristics and significance as a causative pathogen in many non-respiratory infections is not fully understood. In this study, we isolated and speciated 33 Mycoplasma isolates obtained from dogs and cats representing both in house and referral cases submitted between 2021 and 2023 at the University of Tennessee Veterinary Bacteriology and Mycology Laboratory. The isolates included were from vaginal samples (5), urine (5), ears (2), wounds (7), cornea (3), conjunctiva (1), semen (1), joints (4), abscess (1), skin (3) and lymph nodes (1). We performed 16s rRNA amplification and sequencing for the identification of these isolates. The species identifications so far made were Mycoplasma canis (n=2), Mycoplasma arginini (n=1), Metamycoplasma gaetae (n=1), Mycoplasma felis (n=2), Mycoplasmopsis canis (n=3), and Mycoplasma edwardii (n=1). Our study suggests that multiple Mycoplasma spp. can infect dogs and cats. We are continuing to identify the rest of the isolates.
Research Grant	None
Field of Research	Bacteriology

Abstract Title	Histologic and genomic quantification of ovarian follicular dysplasia in Florida beef cattle
Authors	Cydney Babione, John F. Roberts, Christopher J. Martyniuk, Fernando H Biase, Christopher Vulpe
Affiliations	(Babione, Roberts) Department of Comparative, Diagnostic & Population Medicine, (Martyniuk, Vulpe) Department of Physiological Sciences, College of Veterinary Medicine University of Florida, Gainesville, FL (Biase) College of Agriculture and Life Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA
Abstract	Bovine ovarian follicular dysplasia (OFD) is a slowly progressive ovary disease associated with primary follicle loss, decreased fertility, and development of Sertoli-form sex cord tumors in Florida beef herds. A quantitative digital pathology artificial intelligence (AI) platform was used to classify 18 microscopic characteristics in ascending order of priority with lowest value given to general ovary tissue, then stromal components, followed by follicle structures and finally areas (mm^2) of OFD. The percent of OFD area per cross section was used to generate a grading system as follows: grade 0= <0.09%, grade 1= 0.10-0.5%, grade 2= 0.50-0.99%, grade 3= 1.00-4.99%, grade 4= >5.00%. Arterial smooth muscle area was negatively correlated with OFD area (r= -0.30, p= 0.04). RNAseq was performed on the ovarian cortex to identify differentially expressed genes from approximately 13,000 sequences. Genes with the most deviated expression included paraspeckle component 1 (PSPC1) (r= 0.84, p= 0.02), K-(lysine)-acetyltransferase 2A (KAT2A) (r= 0.90, p= 0.01), anoctamin 3 (ANO3) (r= 0.96, p= 0.00060), family with sequence similarity 184A (FAM184A) (r= 0.94, p= 0.0014), endomucin (EMCN) (r= -0.77, p= 0.04), and transcription Factor 4 (TCF4) (r= -0.78, p= 0.04). These six genes whose protein products have functions in sex cord cell tumors, gamete production, and tissue adhesions may be used to explain OFD pathophysiology, with PSPC1 protein as primary candidate as a prognostic OFD biomarker due to its upregulation in Sertoli cells.
Research Grant	Florida Beef Enhancement Board – UFLOR P0298199
Field of Research	Anatomic Pathology

Abstract Title	Investigation of a Drug Interaction Between Omeprazole and Vinblastine in an In Vitro Canine Model
Authors	Dominic A. Baechler, Luke A. Wittenburg
Affiliations	Department of Surgical and Radiological Sciences, School of Veterinary Medicine, University of California-Davis, Davis, CA
Abstract	Preliminary data from the Wittenburg lab has shown that canine patients with mast cell tumors that received co-administration of omeprazole with vinblastine had lower serum vinblastine concentrations compared to dogs without omeprazole administration. Previous human studies have shown that omeprazole can activate the Pregnane X Receptor (PXR) transcription factor, which increases expression of the CYP3A metabolizing enzyme and P-glycoprotein drug efflux protein, causing increased drug metabolism and elimination. We hypothesized that omeprazole will activate PXR, leading to increased mRNA and protein expression of cytochrome P450 proteins and resulting in faster in vitro metabolism of vinblastine. A luminescence-based canine assay was used to measure PXR activity when exposed to varying concentrations of omeprazole. The results of this assay demonstrated a 5-fold increase in total PXR transcription factor activity supporting the molecular basis for canine CYP activation. CYP and P-gp gene expression changes were evaluated by exposing canine hepatocytes to 0, 25, and 50uM doses of omeprazole for 24, 48, and 72hrs. Quantitative real-time PCR was performed for Cyp1A1, CYP1A2, CYP3A12, Cyp3A26, CYP2B11 and ABCB1 and the results showed a marked 11-fold increase in Cyp1A1 mRNA expression compared to a mild 1-fold increase in Cyp3A26 and P-gp in the 72hr treatment group. Hepatocytes exposed to 50uM of omeprazole prior to vinblastine exposure also showed greater loss of vinblastine relative to the 25uM and control groups as measured via LC-MS/MS. As we gather more qPCR and western blot data, we anticipate that PXR-mediated CYP induction will provide a molecular basis for the increased rate of vinblastine metabolism observed.
Research Grant	None
Field of Research	Oncology

Abstract Title	Neuropathologic findings in dogs with partial seizures
Authors	Kristin Baert, Sue Osting, Paul Buckmaster, and Starr Cameron
Affiliations	Department of Medical Sciences, SVM, University of Wisconsin (UW)-Madison, Madison, WI (Baert, Cameron) Department of Neurology, School of Medicine and Public Health, UW-Madison, Madison, WI (Osting) Departments of Comparative Medicine and Neurology & Neurosurgical Sciences, Stanford University, Stanford, CA (Buckmaster)
Abstract	Epilepsy is the most common chronic neurological condition in dogs, and anti-epileptic drugs (AEDs) are currently the mainstay of treatment for canine idiopathic epilepsy. However, 20-30% of patients remain poorly controlled despite proper treatment with AEDs. In humans, the most common form of epilepsy is temporal lobe epilepsy (TLE) and people with TLE have a greater tendency to become pharmacoresistant compared to other epilepsy disorders. The most common seizure semiology of people with TLE is partial seizures, and therefore, our study included dogs with a history of partial seizures. We hypothesized that dogs with TLE-like seizures would exhibit similar neuropathological changes as humans with TLE, including hippocampal sclerosis. For analysis, Timm's stain was used to visualize mossy fiber sprouting. Nissl stain was used to analyze architecture and assess the number of hilar neurons within the dentate gyrus region of the hippocampus. Immunohistochemistry, specifically parvalbumin, was used to evaluate the loss of inhibitory neurons. We expect to see an increase in mossy fiber sprouting and a decrease in the number of hilar neurons and inhibitory neurons (parvalbumin-immunoreactive) within the dentate gyrus region of the hippocampus. Preliminary data shows an asymmetry between hippocampi in the number of hilar neurons, which is consistent with previous findings of volumetric hippocampal asymmetry in 80% of people with TLE. If the neuropathology of dogs with TLE-like seizures is similar to the features seen in humans and other species, then advanced treatment options currently used for people, such as laser ablation and surgical resection, may be viable options for dogs affected with pharmacoresistant epilepsy.
Research Grant	American Kennel Club Companion Health Fund 02792
Field of Research	One Health

Abstract Title	Elk isolates of Mycobacterium tuberculosis variant bovis containing polymorphisms
Authors	Khelsea Bahr, Muhammad Yasir Zahoor, Suelee Robbe-Austermann, Tyler Thacker, Evan Brenner, Joe Darish, Srinand Sreevatsan
Affiliations	College of Veterinary Medicine, Department of Pathobiology and diagnostic investigation, Michigan State University, East Lansing, MI(Bahr, Zahoor, Brenner, Darish, Sreevatsan) USDA National Veterinary Services Laboratory, Ames, IA (Robbe-Austermann)and USDA the Department of Animal and Plant Health Inspection Services (Thacker)
Abstract	Tuberculosis is a disease of multiple host species, caused by members of the Mycobacterium tuberculosis Complex (MTBC). Previous research on a known set of single nucleotide polymorphisms (SNPs) using MassArrayTM technology showed that all elk isolates from different geographic locations in the US, phylogenetically clustered into a unique clade separated from related M. bovis isolates. A genome wide analysis for comprehensive single nucleotide polymorphisms and/or insertion-deletion events was undertaken to better define host adaptation, host range, and zoonotic potential of these strains. MBO genomic DNA from elk obtained from USDA and sequenced with Illumina (NovaSeq) technology. Whole genomic DNA from MBO isolates were quality checked and analyzed using BV-BRC (bacterial and viral bioinformatics resource) and snippy (a program that is used for rapid haploid variant calling and core genome alignment). Genomes were assembled de novo and phylogenetic analysis revealed the elk genomes clustered, as expected, in a separate clade within MTBC. Using Snippy, SNPs extracted using the cattle strain AF2122/97 as a reference to define the evolutionary trajectory of elk isolates. We then compared our samples against Mycobacterium bovis strains 99-0440, 95-1315, 61-09 and10-7428 to emphasize the uniqueness of the elk SNPs. A total of 95 SNPs were identified on the elk MBO genomes, of these 54 were nonsynonymous SNPs located on specialty genes and likely indicate risk factors for developing disease. The genomic analysis of the elk isolates provides a snapshot of how MBO is phylogenetically different in some hosts and raises the idea that within host evolution as a major driver of host adaptation.
Research Grant	NIH grant R25HL103156; Sreevatsan lab is funded by USDA and Ag Experiment Station
Field of Research	Bacteriology

Abstract Title	Presence of bald eagle hepacivirus (BeHV) in a sample population of Michigan bald eagles
Authors	Shayla Bajric, Nicole Grosjean, Julie Melotti, Megan Moriarty, Mayra Tsoi, Steven Bolin
Affiliations	Michigan State University College of Veterinary Medicine (Bajric), Michigan State University Veterinary Diagnostic Laboratory (Grosjean), Michigan Department of Natural Resources (Melotti, Moriarty), Michigan State University Pathobiology and Diagnostic Investigation (Tsoi, Bolin)
Abstract	Bald eagles, a culturally significant symbol in the United States and to North American Indigenous peoples, were listed as threatened and endangered in the twentieth century due to illegal shooting, habitat destruction, and environmental contamination. Conservation efforts and regulatory changes since then have facilitated bald eagle recovery and their de-listing under the Endangered Species Act. Currently, the effect of infectious diseases on bald eagle population health has become a concern. As an example, a 2019 Wisconsin study associated a mortality event with novel hepacivirus detected in bald eagles. The virus was termed Bald Eagle Hepacivirus (BeHV) and analysis of the viral genome identified similarities with the pathogen, hepatitis C virus, which causes cirrhosis in humans. The goal of our study was to determine if BeHV was present in tissue samples from n = 37 dead bald eagles submitted to the Michigan Department of Natural Resources in 2023 for postmortem examination. An additional n = 3 samples of blood from live bald eagles were available. Two PCR assays targeting genomic regions encoding BeHV structural proteins were used in testing fresh liver n = 37, fresh brain n = 24, formalin-fixed paraffin-embedded tissues n = 4, and blood samples n = 3. BeHV viral RNA was detected in both fresh liver and brain from 16 bald eagles and brain only in 1 bald eagle. Histopathologic examination of bald eagle tissues was performed to identify the presence of microscopic lesions. A moderate degree of autolysis postmortem made microscopic examination challenging. Five of the BeHV-positive livers had evidence of moderate to severe mononuclear inflammation. There were no significant findings in the 24 brains examined.
Research Grant	-
Field of Research	Wildlife Conservation

Abstract Title	Validation of the MIZAR® Rheometer for Detection of Inflammation in Veterinary Species
Authors	Marta Bakaj and Erica Behling-Kelly
Affiliations	College of Veterinary Medicine (Bakaj), Department of Population Medicine and Diagnostic Sciences (Behling-Kelly), Cornell University, Ithaca, NY
Abstract	Early detection of inflammation aids in diagnosis and accelerates therapeutic intervention in veterinary medicine, but current methods are expensive and can lack sensitivity. In this study, we sought to validate the MIZAR® rheometer, a point-of-care analyzer that uses syllectometry to detect changes in mechanical properties of patient red blood cells (RBC) as potential biomarkers for inflammation. Parameters including distribution index (Di), aggregation index (Ai), and base point low (BPL) were compared between dogs with anemia, overt inflammation, immune-mediated hemolytic anemia (IMHA), and healthy dogs. The impact of common interfering substances (lipid, bilirubin, IgG, and hemoglobin) was also evaluated. Bilirubin and canine IgG caused no significant difference in tested parameters. Lipoproteins caused a decrease in BPL and hemoglobin was associated with lower Di and higher BPL values. Addition of a lipid emulsion resulted in variable readings in multiple parameters. Fibrinogen tended to increase Di and Ai. High intra-assay variation, determined by evaluating ten replicative runs in healthy patient samples (Di CV=11.4; Ai CV=0.77; BPL CV=18.9), could underlie the nonlinear responses. Di was not different across patient samples. Ai was significantly lower in anemic patients compared to dogs with inflammation and healthy dogs and low in dogs with IMHA compared to dogs with inflammation. BPL was significantly higher in anemic vs inflammatory patients. These results indicate that the MIZAR® rheometer holds potential as an easy and inexpensive method for detecting changes in RBC rheology that might predict inflammation, but changes in anemic patients and common interfering substances may confound clinical use.
Research Grant	ALCOR® Scientific
Field of Research	Clinical Pathology

Abstract Title	Determining the Role of Non-Coding RNAs in Malignant Testicular Germ Cell Tumors
Authors	Kimaya M. Bakhle, Michelle Liu, Alexandria J. Shumway, Praveen Sethupathy, Robert S. Weiss
Affiliations	Department of Biomedical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY
Abstract	Testicular germ cell tumors (TGCTs) are the most common cancer in young men, with rising incidence. Non-seminoma, a subtype of TGCT, is often a mix of pluripotent, malignant embryonal carcinoma (EC) cells and differentiated, benign teratoma cells. MicroRNAs (miRNAs, miRs) are short, non-coding transcripts that are aberrantly expressed in diseases, including TGCTs. They modulate gene expression and can be effective biomarkers. The pluripotency-associated miR-371-373 cluster is established as a circulating biomarker of TGCTs. Recently, the homologous cluster in mice, miR-290-295, has been shown to be expressed and secreted by pluripotent EC cells, and its expression is lost in EC cells that have been differentiated by thioridazine treatment (TR cells). Here, we seek to determine the function of this miRNA cluster in EC cells through miRNA inhibition using locked nucleic acidic (LNA) antisense oligonucleotide inhibitors. After treating EC cells with an anti-miR-291a-3p LNA inhibitor, we assessed changes in cell morphology, proliferation, and expression of pluripotency markers. We also used fluorescent in situ hybridization to test the localization of miR-291a-3p within TGCT tissues. Another species of non-coding RNAs, long intergenic non-coding RNAs (lincRNAs) have been shown to exhibit more tissue-specific expression in the testis than in any other tissue. We used the results of an RNA sequencing experiment comparing expression in EC and TR cells to identify lincRNAs associated with TGCTs. We will analyze these lincRNAs further by transcription factor and miRNA binding site enrichment analysis to define critical upstream regulators. Together, these studies will shed light on the role of non-coding RNAs in TGCT malignancy.
Research Grant	None
Field of Research	Oncology

Abstract Title	Changes in the blood biochemical parameters in cattle experimentally infected by Ostertagia ostertagi
Authors	Maya Ballout, Mariam Bakshi, Eliseo Miramontes, and Wenbin Tuo
Affiliations	Western University of Health Sciences CVM, Pomona, CA (Ballout) USDA/ARS, Beltsville, MD (Bakshi, Miramontes, Tuo)
Abstract	Although the gastric pathologies of ruminant stomach worms are well-defined, the systemic consequences of infection remain unclear. Parasitic nematodes, most belonging to the family Trichostrongylidae, are prevalent in ruminants in temperate regions. In cattle, Ostertagia ostertagi (OO) is the most pathogenic nematode, causing ostertagiasis entailing gastric pathologies; clinical symptoms include reduced appetite, diarrhea, and weight loss. Nematodes in small ruminants can also cause changes in blood biochemistry, implicating extra-gastric pathologies. To investigate this further, with OO specifically, we infected 4 helminth-free, 4-5 months old, Holstein calves with 200k OO L3 and collected blood weekly for 5 weeks. Pre and post infection plasma samples were submitted to the Immunodiagnostic laboratory for a Comprehensive Chemistry analysis aimed at possible indications of extra-gastric disease. Additionally, pre and post infection plasma was tested by ELISA for OO-specific antibodies (Ab) using OO adult/L4 antigens. All data was analyzed using the Prism software. Our results showed an increase ($P<0.05$) in Ab levels by week 5. Albumin, total protein, potassium, sodium, chloride, creatinine, and lactate dehydrogenase increased at week 4 ($P<0.05$) and returned to normal levels by week 5 post infection. Interestingly, none of the parameters relating to hepatic function changed. Thus, we found no evidence for hepatic pathology, but changes in blood chemistry indicate that infection may cause subclinical dehydration, tissue damage and muscle wasting. Given substantial economic losses to cattle production, further research investigating the systemic effects of O. ostertagi may suggest best practices to manage systemic disease.
Research Grant	USDA/ARS in-house funds
Field of Research	Parasitology

Abstract Title	The unseen threat: esbls & carbapenem-resistant bacteria in eastern Mississippi
Authors	Talia Barnes, John Webb, Joo Youn Park, Keun Seok Seo, Cooper Brookshire
Affiliations	Department of Clinical Sciences (Barnes, Webb, Brookshire) and Department of Comparative Biomedical Sciences (Park, Seo) Mississippi State University College of Veterinary Medicine, Mississippi State, MS
Abstract	Concern exists about humans and animals sharing antibiotic resistant pathogens with each other, which justifies One Health focused antibiotic resistance studies. Carbapenem-resistant Enterobacterales (CRE) have recently emerged in companion animal veterinary medicine, especially in tertiary referral hospitals. Extended spectrum betalactamase producing Enterobacterales (ESBLs) have been common in veterinary medicine for many years. In Mississippi, carbapenemase producing ST307 Klebsiella pneumoniae with blaNDM-5 was recently reported in hospitalized dogs. The objective of this study was to estimate the detection rate of CRE and ESBLs in the East Mississippi general dog population. We hypothesized that the detection rate of CRE would be very low and the detection rate of ESBLs would be high. To test our hypothesis, we collected 274 fecal samples through pooled sampling from residential areas, dog parks, and veterinary hospitals across seven cities in Eastern Mississippi. Using selective media containing ceftiofur (for ESBL isolation) and meropenem (for CRE isolation), we detected 57 ESBLs and 0 CRE. Each isolate was further characterized with chromogenic media, and antibiotic susceptibility testing was used to confirm ESBL and CRE phenotypes. Prevalence was estimated using a pooled sample calculation, with an ESBL prevalence estimate of 22.6% (95% CI 0.17-0.29) and CRE prevalence estimate of 0% (95% CI 0.0-0.01). These data suggest that ESBLs continue to be common in the general dog population, while CRE are very uncommon and may be a localized issue in tertiary referral hospitals.
Research Grant	NIH 2U54GM115428-06
Field of Research	One Health

Abstract Title	Analysis of proliferation of genetically modified spotted fever group Rickettsia species in mammalian cells
Authors	Lucy Barré, Ibrahim Ogunleti, Juan Martinez
Affiliations	Department of Pathobiological Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA (Barré, Ogunleti, Martinez) McNeese State University, Lake Charles, LA (Ogunleti)
Abstract	Spotted fever group rickettsioses are spread by ticks to mammals. Patients can suffer lesions, fever and malaise. Severe cases may lead to vascular necrosis, systems failure and death. Etiologic agents include obligate intracellular bacteria R. rickettsii and R. parkeri. SFG Rickettsia primarily target endothelial cells in vasculature, but studies linked strains of strong virulence with infection of phagocytic cells. To infect, Rickettsia must elicit entry, avoid lysis, inhibit apoptosis and seize nutrients. We investigated this using single transposon mutants of R. parkeri strain "Portsmouth". A pilot study in the Martinez laboratory determined that mutant SP39 (insertion in gene for protein RARP-1) is able to infect and proliferate within mammalian endothelial (EAhy926) and epithelial (Vero) cells but not within human macrophages (THP-1). Similar mutants were not impaired for growth in THP-1 cells. Thus, we investigated if SP39 and other defined mutants exhibit growth differences within immortalized murine bone marrow derived macrophages (iBMDMs) as compared to wild type R. parkeri. Growth characteristics were noted via immunofluorescence microscopy and real-time qPCR-based assays. R. parkeri WT, R. parkeri SP9 and R. parkeri SP39 demonstrated similar growth patterns within EAhy926 cells. Despite impaired growth in THP-1 cells, mutant SP39 grew like the wild type within iBMDM cells. Also, mutant SP64 (insertion in gene for protein RARP-2) exhibited delayed growth within EAhy926 and iBMDMs despite normal growth in THP-1. Results suggest that species differences in cell lines may account for the disparities in growth outcomes for the mutants. Mechanisms governing these phenotypes are currently under active investigation.
Research Grant	None
Field of Research	Bacteriology

Abstract Title	Characterization of maternal care in dogs in a small-scale breeding facility
Authors	Kyle Barron, Aynsley Romaniuk, Shanis Barnard, and Candace Croney
Affiliations	Purdue University College of Veterinary Medicine; Departments of Comparative Pathobiology and Animal Science, Purdue University; Center for Animal Welfare Science, Purdue University
Abstract	The postnatal period of mammals is essential for the emergence of social behaviors and responses to stress. Maternal care (e.g., contact with offspring and nursing styles) during this period plays a crucial role in the behavioral development of offspring later in life. Studies conducted on rodents, for example, demonstrated that maternal care has lasting effects on the physiology of their offspring throughout life as it can modulate the activation of the hypothalamic-pituitary-adrenal axis, which is involved in the stress responses of animals. Maternal care in dogs remains understudied with current literature showing conflicting results. A study conducted in a working dog population indicated that high levels of maternal care (e.g., increased contact with offspring, increased time spent in the whelping box, and nursing) are associated with lower levels of stress and anxiety in offspring as adults. Conversely, a study conducted in a guide dog population showed a positive association between high levels of maternal care and stress and anxiety in offspring later in life. This discrepancy could be due to the differences in populations as a result of factors such as genetic selection. It is crucial to better understand maternal care in different dog populations. In this study, we conducted behavioral observations of 2 dams and their litters from a small-scale commercial dog breeding facility during the first 3 weeks post-parturition. Characterization of maternal care in dams in diverse breeding populations may inform future investigations of the relationship between maternal care and stress in puppies, which in turn, may help support best management practices and standards of care for improved welfare.
Research Grant	Dr Candace Croney Discretionary Funds
Field of Research	Animal Welfare

Abstract Title	Vitamin D binding protein and vitamin D and their association with disease severity in hospitalized foals
Authors	Celine Bartish, Ahmed Kamr, William Gilsenan, Amanda Samuels, Bryson Jacobs, Payton Kelly, Ramiro Toribio
Affiliations	College of Veterinary Medicine, The Ohio State University, Columbus, OH (Bartish, Kamr, Samuels, Jacobs, Kelly, Toribio) Rood and Riddle Equine Hospital, Lexington, KY (Gilsenan)
Abstract	Vitamin D is a steroid that plays a vital role in skeletal development, calcium and phosphorus regulation, and immune modulation. Biological metabolites of vitamin D include 25-hydroxyvitamin D (25[OH]D) and 1,25-dihydroxyvitamin D. Due to their steroid properties, in blood these metabolites are bound to vitamin D-binding protein (DBP). DBP is a small protein that also neutralizes actin released during cell injury. Previous studies in our lab showed that critically ill foals frequently have low vitamin D concentrations. Due to its small size, DBP may decrease during intestinal and renal diseases, which could contribute to hypovitaminosis D in critically ill foals. This study aimed to measure DBP in healthy and hospitalized foals. We hypothesized that DBP concentrations would be low and associated with disease severity and mortality in hospitalized foals. We measured 25[OH]D and DBP using validated ELISAs in 9 healthy and 37 hospitalized foals (29 septic and 8 sick non-septic). Preliminary findings showed significantly lower 25[OH]D and DBP concentrations in hospitalized and septic compared to healthy foals. Our findings indicate that low DBP could contribute to hypovitaminosis D in sick foals. This study provided additional insight on the pathogenesis of hypovitaminosis D and likely hypocalcemia in critically ill foals.
Research Grant	Dynamics of Vitamin D in Foals (Grayson-Jockey Club Research Foundation)
Field of Research	Equine Medicine and Surgery

Abstract Title	The effect of priming on extracellular vesicles derived from equine bone marrow-derived mesenchymal stem cells
Authors	Jillian Bastidas, Lauren Olenick, Alexandra Usimaki, and Kyla Ortved
Affiliations	PennVet Ortved Orthopedic Regenerative Medicine Lab, Clinical Studies-New Bolton Center, University of Pennsylvania, Kennett Square, PA
Abstract	Despite its high prevalence in the equine industry, osteoarthritis (OA) currently lacks an effective treatment. OA is a complex disease driven by intra-articular inflammation, making the development of an intra-articular biotherapeutic that targets and suppresses inflammatory cascades highly beneficial. This proposal investigates the effects of priming on the production of extracellular vesicles (EVs) derived from equine bone marrow-derived mesenchymal stem cells (BM-MSCs). Studies have shown that MSCs can inhibit inflammation and show promising biotherapeutic potential in OA treatment. Priming stem cells has emerged as a recent strategy to enhance their immunomodulatory potential by exposing them to various microenvironments. Priming has the potential to increase the production of an anti-inflammatory secretome, including modification of EV biocargo. We hypothesize that priming MSCs with interferon gamma (IFN-γ), tumor necrosis factor alpha (TNF-α), or a combination of both will result in an increased yield and immunodulatory signature of EVs. The aim of this study is to optimize an in vitro priming protocol for BM-MSCs using IFN-γ, TNF-α, or a combination, while maintaining cell proliferation and enhancing EV production. Cell proliferation will be quantified and cell culture supernatants will be collected for cytokine analysis using a multiplex immunoassay. Additionally, EV isolation will be conducted through stepwise ultracentrifugation, and nanoparticle tracking analysis and Western blot analysis will be employed to confirm the presence of EVs. By investigating these factors, we hope to contribute to the development of novel therapies for the treatment of OA in horses with potential for translation to human patients.
Research Grant	Raymond Firestone Trust and Raker/Tulleners Fund
Field of Research	Orthopedics

Abstract Title	The influence of xenobiotic metabolism on the developmental neurotoxicity of PCB 11 in CYP-humanized mice
Authors	Ashley Batra*, Rebecca J Wilson*, Rosalia Mendieta*, Pamela J Lein*
Affiliations	University of California, Davis, School of Veterinary Medicine, Davis, CA*
Abstract	Polychlorinated biphenyls (PCBs) are ubiquitous environmental pollutants that pose a risk to the developing human brain. While higher chlorinated (HC)-PCBs, are known to cause developmental neurotoxicity (DNT), little is known about the DNT potential of lower chlorinated (LC)-PCBs. This is a critical data gap because LC-PCBs predominate in contemporary human brain samples, and PCB 11, a prevalent LC-PCB, and its metabolites generated by cytochrome P450 (CYP)-mediated metabolism, significantly increased dendritic and axonal growth in vitro in cortical and hippocampal neurons. While altered neuronal morphogenesis is associated with behavioral deficits in humans with neurodevelopmental disorders, whether developmental exposure to LC-PCBs causes behavioral deficits is unknown. Additionally, the impact of PCB metabolism on LC-PCB DNT is not clear. We are conducting in vivo studies using CYP-humanized mouse models that express human CYP2A6 and CYP2B6 but lack the murine isoforms of these enzymes to test the isoform-specific effects of human CYPs on LC-PCB DNT. Wild type, Cyp2abfgs null, and CYP-humanized mice were exposed throughout gestation and lactation to vehicle, 0.1, 1, or 6 mg/kg of PCB 11 in the maternal diet. Our preliminary findings suggest that PCB 11 disrupts social communication, as seen with dose- and genotype-dependent changes in ultrasonic vocalizations in P7 pups. We are also measuring Y-maze performance at P24 to assess learning and memory. CYP2B6 and CYP null males and females potentially display poorer cognitive performance relative to sex-matched wildtype mice. Results from these studies will inform risk assessments of LC-PCB DNT, and determine whether human CYP polymorphisms modify individual risk.
Research Grant	NIEHS R01 ES014901
Field of Research	Pharmacology and Toxicology

Abstract Title	Immune responses to radiation therapy and immunomodulation in an oral squamous cell carcinoma mouse model
Authors	Amber Beeney, Braden Burdekin, Nolan Sweeting, Ber-In Lee, Mary-Keara Boss
Affiliations	Department of Clinical Sciences, College of Veterinary Biomedical Science, Colorado state University, Fort Collins, Colorado (Beeney, Burdekin, Lee, Boss) Animal, Poultry and Veterinary Science, College of Agriculture, Environment and Nutritional Sciences, Tuskegee University, Tuskegee, Alabama (Sweeting)
Abstract	Purpose: New therapies are needed for advanced oral squamous cell carcinoma (SCC). Propranolol (P) and Losartan (L) are repurposed immunomodulatory drugs which decrease immunosuppressive myeloid cells. L also improves tumor oxygenation. Our overall hypothesis is that P+L and radiation (RT) will improve survival in a syngeneic, orthotopic oral SCC mouse model compared to RT alone due to immunomodulatory and vascular effects. Methods: Murine LY2 SCC was injected into the buccal mucosa of BALB/c mice. Two days later, mice were randomized to treatment (n=6/group) with daily intraperitoneal (IP) injections of either saline control (C), L, or P, and two groups received radiation therapy (RT) (4Gy x 3; L+RT, P+RT) when tumor volumes reached 150 mm3. Body weight and tumor volumes were monitored until morbidity endpoint. Kaplan-Meier survival curves were generated and compared via log-rank test. Results: There was a statistically significant difference in survival times across the treatment groups. Neither L nor P alone improved survival compared to C, but mice treated with either L+RT or P+RT lived significantly longer than C, L, and P groups. There was no survival difference between L+RT or P+RT. Conclusion: RT improved survival when combined with P or L compared to other groups. These results will be integrated into a larger mouse study investigating C, PL, RT, RT+PL. Serum cytokine analysis and pathologic review and immunohistochemical quantification of immune and endothelial cells from tissue samples are underway.
Research Grant	NIH, K01OD031809
Field of Research	Oncology

Abstract Title	Investigating the association of Giardia sp. infection with respiratory signs in domestic animals.
Authors	Niv Beili, Holly White, Manigandan Lejeune
Affiliations	Animal Health and Diagnostics Center (AHDC), Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY, USA 14853
Abstract	Giardia sp. is a cosmopolitan protozoan parasite of domestic animals and humans. This parasite has a predilection for the small intestine and causes diarrhea. Recently, we have been noticing a trend indicating the association of Giardia sp. with extraintestinal signs of chronic cough in some animals. Our aim was to retrospectively analyze cases of giardiasis (diagnostically confirmed at AHDC) associated with chronic cough and determine epidemiological trends pointing to risk factors for exposed populations. We retrieved data from the AHDC's Laboratory Information Management System (VetView) for all fecal-positive Giardia cases confirmed between January 2021 to July 2023. Altogether, 885 positive Giardia cases were analyzed which include cats(n=71), dogs(n=234), cattle(n=230), goats(n=118), and sheep(n=137). Of the 885 cases, 23 had chronic coughs as indicated by clients. Six additional cases (no history provided) that were submitted for lungworm testing but tested positive for Giardia were also analyzed. Interestingly, none of the 29 cases had a confirmed respiratory etiology except for one with a lungworm (Muellerius capillaris). In total, 1 cat, 4 dogs, 5 cows, 11 goats, and 8 sheep had respiratory signs associated with the fecal detection of Giardia sp. Furthermore, 76% of the Giardia-associated respiratory cases were in animals aged ≤ 1 year and 60% were in females. There was no breed specificity and no correlation with parasite intensity as determined by fecal cyst counts. Our findings indicate a strong association between intestinal infection of Giardia sp. with respiratory signs of chronic cough. To conclude, giardiasis should be on the differential list while examining cases of chronic cough in domestic animals.
Research Grant	none
Field of Research	Parasitology

Abstract Title	Identifying Veterinary Care Deserts: Piloting the Definition
Authors	Hailey Bernal, Laura Bunke, Gillian Angliss, and Rhea Hanselmann
Affiliations	College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA (Bernal, Hanselmann), San Diego Humane Society (Bunke), College of Veterinary Medicine, Long Island University, Brookville, NY (Angliss)
Abstract	Uneven distribution of access to veterinary care is one of the most significant issues facing the veterinary profession and is influenced by social and geographical factors. A definition for veterinary care desert was recently developed based on accessibility, affordability, and availability of veterinary care in a given area. Here, we aimed 1) to pilot the definition of veterinary care desert in diverse communities in the San Diego Humane Society's service area to determine its utility in identifying veterinary care deserts, and 2) to generate a user-friendly checklist of its application. We selected 5 communities representative of rural, suburban, and urban cities. Using publicly available data, we applied the definition's criteria to determine if census tracts in these communities had accessible, affordable, and available veterinary care. Specifically, we examined the location of veterinary services and their distance from the center of each census tract, median household income and the percent of households living in poverty at the census tract level, and the ratio of veterinary professionals to the population. Because confirming the number of veterinary professionals was a limiting factor in determining availability, we created a median number of employees per type of veterinary clinic as an alternative. While the definition proved effective in finding areas lacking access to veterinary care, the results challenged our hypotheses around the interactions of the definitions themes in rural and urban areas. Applying the veterinary care desert definition can aid veterinary care providers and organizations to determine areas of need in their communities and allocate resources to address the access to care gap.
Research Grant	San Diego Humane Society- John R Peterson Foundation Residency Program in Shelter Medicine resident research funds to Bunke
Field of Research	Animal Welfare

Abstract Title	Literature Review: Comparing diagnostic methods for detection of Toxoplasma gondii exposure in sea lions
Authors	Jumanah Bilal, Justin Sanders, Wendy Black, Shea Steingass, Julia Burco, Brianna Beechler
Affiliations	Department of Biomedical Sciences, Carlson College of Veterinary Medicine (Bilal, Sanders, Black, Beechler) and Department of Fisheries, Wildlife, and Conservation Science (Steingass), Oregon State University, Corvallis, OR, Oregon Department of Fish and Wildlife (Burco)
Abstract	Toxoplasma gondii is a widespread zoonotic parasite that is commonly diagnosed in numerous marine mammal species and can result in a clinical disease called toxoplasmosis. The exact mechanism of transmission of T. gondii in marine animals is unknown, but the presence of the definitive hosts near coastal communities can result in contamination of coastal habitats. Many marine animals live in close proximity to humans, and can also serve as a food source for certain communities. As a result, T. gondii infections in wild marine animals and marine animals under human care are of clinical and public health importance. However, diagnostics can be a challenge in non-traditional species such as pinnipeds and other marine mammals. In this study we will evaluate known diagnostic methods for detection of Toxoplasma in marine mammals, then compare several diagnostics for Toxoplasma exposure in sea lions including an IFA, two ELISA's and a modified agglutination test (MAT). Initial results from our literature review suggested ELISAs to be most popular in detecting exposure to T. gondii due to its better performance and utility across multiple species, as well as the possibility of testing different types of samples. However, MAT has been evaluated to be useful because it is species independent, sensitive and specific. With this information in mind, we will then use the most accurate method to measure the seroprevalence of T. gondii in both Stellar and California sea lions in Oregon.
Research Grant	Carlson College of Veterinary Medicine, Department of Biomedical Sciences Intramural Fund
Field of Research	One Health

Abstract Title	Identification of candidate variants for lone atrial fibrillation in horses
Authors	Laurine Bini, Freya Stein, Joy Stock, Molly McCue and Sian A. Durward-Akhurst
Affiliations	Oniris (Bini), National Veterinary School, Nantes, France; Veterinary Clinical Sciences Department (Stein, Stock, Durward-Akhurst) and Veterinary Population Medicine Department (McCue), University of Minneapolis, Saint Paul, Minnesota
Abstract	Lone atrial fibrillation (LAF) is an important cause of poor performance in racehorses. These ones have no underlying structural heart disease, making it virtually impossible to identify horses that will go on to develop LAF. LAF is an important cause of morbidity and mortality in humans with several similarities to horses. Variants in ion channel gene are known to cause LAF in human families. The purpose of this study is to identify variants that could be causing LAF in a population of apparently healthy Standardbred racehorses. We are performing cardiac examinations including electrocardiography and echocardiography on and collecting whole blood from 500 Standardbred racehorses. DNA isolation will be performed using the Qiagen whole blood isolation protocol. We performed whole genome sequence at a target depth of 12 X on 14 Standardbred racehorses with LAF. Variants were identified with modified version of the genome analysis toolkit best practices. Ensembl-VEP was used for variant annotation. The results showed 10 high, 252 moderate, and 534 low impact variants identified. Additional variant effect prediction programs (SNPs&GO and SIFT) were used to identify high or moderate impact variants predicted to be deleterious. 22 out of 262 variants were predicted by SNPs&GO and 31 out of 262 variants were predicted by SIFT to be deleterious. These variants will be genotyped in an independent population of Standardbred racehorses with and without LAF to identify LAF-causing variants. Identification of LAF-causing variants will allow for improved diagnosis of horses with LAF that has resolved prior to examination and will allow breeders to make educated breeding decisions to reduce the risk of LAF in future generations.
Research Grant	CVM Resident and Graduate Student Research Award, AAEP Young Investigator Award, MAF (D20EQ-013)
Field of Research	Equine Medicine and Surgery

Abstract Title	Do dogs increase their owner's exposure to ticks and mosquitoes?
Authors	Holly E. Black, Rebecca L. Smith
Affiliations	Department of Pathobiology, College of Veterinary Medicine, University of Illinois, Urbana IL Midwest Center of Excellence for Vector-Borne Disease, Madison WI
Abstract	Tick and mosquito borne illnesses continue to threaten the health of people and their pets in Illinois. The purpose of this study is to determine risk factors associated with exposure to ticks, mosquitoes, and vector-borne disease in adults, with a focus on dog owners. We hypothesize that there is a relationship between human exposure to ticks and dog ownership, and a relationship between dog exposure to ticks and movement, activities, and home environment type. We created a survey to collect information about tick and mosquito exposure, time spent outside, dog ownership, and prevention use. Survey participants were recruited from online social media posts and in-person outreach events. Outreach events included festivals, markets, and educational events at nature centers throughout different regions of Illinois. Survey recruitment is ongoing, but preliminary analysis includes logistic regression to identify factors associated with exposure to ticks or mosquitoes or having been diagnosed with a tick-borne disease. The incidence of vector-borne diseases has been increasing rapidly in Illinois, and we believe that this study will help to provide a systematic and scientifically sound assessment of the risks and potentially effective prevention and communication methods.
Research Grant	Cooperative Agreement Number U01CK000651 from the Centers for Disease Control and Prevention
Field of Research	Epidemiology

Abstract Title	Influence of Muscle Attachments on Osteoderm Development in the American Alligator: Implications for HO
Authors	Katie Black, Brooke Dubansky
Affiliations	Department of Comparative Biomedical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	Heterotopic ossification is characterized by bone formation in areas normally comprised of soft tissue, usually caused by trauma or inflammation. The morphology of HO lesions shares similarities to that of osteoderms, naturally occurring discs of ectopic bone in the skin of American alligators (Alligator mississippiensis). Some aspects of HO pathogenesis and osteoderm development have been characterized, but the initiation of either process is not well understood. Some HO studies suggest that this type of bone formation is initiated by mechanical stress on soft tissue. Given the morphological similarities between HO lesions and osteoderms, we hypothesized that mechanotransduction may play a role in the initiation of osteoderm formation. We used dissection to characterize tendinous attachments to osteoderms in the head, neck, and shoulder regions of ten juvenile alligators. Three layers of muscle and fascia were found to adhere to the cervical osteoderms. The superficial cervical fascia is directly beneath the skin and attaches to small tuberculate scales lateral to the large nuchal and cervical osteoderms. Deep to this, the trapezius and teres major muscles attach to the dermis of the large cervical osteoderms. The deep cervical fascia is comprised of a superficial and deep leaf. The superficial leaf covers the lateral surface of the neck muscles and adheres to the dermis of the nuchal shield osteoderms. Both left and right superficial leaves combine at the dorsal midline to create the deep leaf that extends from the medial edge of the nuchal and cervical osteoderms to the spinous processes of the cervical vertebrae. These attachments from the body musculature to osteoderms redistribute forces and trigger bone formation.
Research Grant	Kenneth Burns Foundation
Field of Research	Anatomy

Abstract Title	Induction/recovery time and immunity in mice repeatably anesthetized with ketamine-xylazine or tribromoethanol
Authors	Catherine Black, Stephen Harvey, Steven Holladay, Robert M. Gogal Jr.
Affiliations	Department of Population Health (Black, Harvey), Department of Biomedical Sciences (Black, Holladay, Gogal), College of Veterinary Medicine, University of Georgia, 501 DW Brooks Drive, Athens, GA 30602.
Abstract	Mus musculus, the house mouse, is the most widely used mammalian model in biomedical research. Mice frequently undergo injectable anesthesia for numerous research procedures, with the most common anesthetic protocol being ketamine-xylazine (K/X). 2,2,2-Tribromoethanol (TBE), a non-pharmaceutical chemical, is also used, but has been linked to peritonitis. The focus of this study was to directly compare these two anesthetic protocols by evaluating induction rates, recovery times, weight data, and immune endpoints. Thirty CD-1 female (8-10-week-old) mice were divided into two experiments. Two anesthetic events were performed two weeks apart. For each experiment, mice received an intraperitoneal (IP) injection of phosphate buffered saline (n= 3 mice), an IP injection of K/X (n=6 mice), and an IP injection of sterile TBE (n=6 mice). Baseline, 2-week, and 4-week peripheral blood was collected for serum cytokines. Mice were euthanized 2 weeks post last anesthetic event. Spleen, liver, kidney, and peritoneal tissue samples were weighed, sectioned, and submitted for histopathology. A splenic section/mouse was re-weighed, dissociated for cell counting, cytology, and flow cytometry. Induction rates were comparable across the two anesthetic groups (2-4 min) however, TBE mice had quicker recovery time (~25 min) compared to K/X (~50 min), which also had 50% anesthetic mortalities. Kidney weight ratio for K/X was significantly higher than the saline and TBE ratios. Weight data, liver or spleen organ weight ratios, immune phenotype, cytology and histopathology were unremarkable. Preliminary findings indicate TBE performed better as an injectable murine anesthetic compared to K/X with no overt evidence of local or systemic inflammation.
Research Grant	UGA Foundation, Veterinary Medical Experiment Station, UGA College of Veterinary Medicine
Field of Research	Immunology

Abstract Title	Identifying functional variants associated with equine myotonia
Authors	Kendall R. Blanchard, Lauren Hughes, Jillian Marlowe, Sian Durward-Akhurst*, and Molly McCue* (*shared attribution)
Affiliations	Department of Veterinary Population Medicine, University of Minnesota College of Veterinary Medicine, Saint Paul, MN (Blanchard, Hughes, McCue) Department of Veterinary Clinical Sciences, University of Minnesota College of Veterinary Medicine, Saint Paul, MN (Marlowe, Durward-Akhurst)
Abstract	Myotonia is characterized by prolonged muscle contraction after stimulation due to cellular ion channel overexcitability. Expansive research in human myotonias has identified specific genetic variants responsible for a range of clinical severities. In people, genetic testing is routinely used for carrier screening, diagnosis, and management. Horses also suffer from myotonic disease, however, the genetic basis of equine myotonia and the correlations between specific variants and clinical presentations is poorly understood. Here we use candidate gene prioritization to identify genes for further investigation in equine myotonia. Sixty-eight candidate genes were identified using a literature search, Phenolyzer, the Online Mendelian Inheritance of Man database, the Online Mendelian Inheritance of Animal database, and Open Targets. Whole genome sequencing from 5 Quarter Horses with myotonia was processed by a computational pipeline using modified Genome Analysis Toolkit best practices. Variants identified with this pipeline were annotated using Ensembl Variant Effect Predictor (VEP) and SnpEff. A total of 14 high- and 149 moderate-impact variants were identified by VEP within the 68 candidate genes while SnpEff identified 41 high- and 325 moderate-impact variants. These high- and moderate-impact variants will undergo further analyses using SNPS&GO and SIFT programs to predict protein effects. Our results will elucidate genes and putative functional variants for equine myotonia that will be investigated as candidates for future genetic test development.
Research Grant	None
Field of Research	Equine Medicine and Surgery

Abstract Title	The effect of N-Nitrosodimethylamine and L. reuteri on DNA mutagenesis and cancer development
Authors	Megan Blawas, Lindsay B. Volk, Monet Norales, Bevin P. Engelward
Affiliations	North Carolina State University College of Veterinary Medicine, Raleigh, NC (Blawas) Department of Biological Engineering, Massachusetts Institute of Technology, Cambridge, MA (Volk, Norales, Engelward)
Abstract	N-Nitrosodimethylamine (NDMA) is a Class 2A carcinogen that humans and animals are exposed to in contaminated water, medication, and food. After activation by the CYP2E1 enzyme, NDMA causes DNA damage through creation of 3-methyladenine and O6-methylguanine lesions. Transgenic mouse strains lacking DNA repair proteins 3-alkyladenine DNA glycosylase (AAG) or O6-methylguanine-DNA methyltransferase (MGMT) experience a higher incidence of unrepaired DNA lesions, leading to more frequent carcinogenesis. We hypothesize that the AAG/MGMT double knockout mice exposed to NDMA will exhibit increased mutations, cell death, and inflammatory pathway activation. To quantify the mutagenic effects in this model, RaDR imaging is used to visualize large scale mutations caused by homologous recombination. Liver tissue appears particularly susceptible, possibly due to high levels of CYP2E1 converting NDMA into a DNA-reactive molecule. To learn how the liver responds to NDMA, we are performing Western Blots to understand which inflammatory, cell signaling, and tissue repair proteins are altered in NDMA-treated mice. Importantly, epidemiologic evidence suggests children may be more susceptible to NDMA and we are therefore investigating if age influences susceptibility. Finally, accessible interventions that suppress the consequences of NDMA are needed. We are currently studying the impact of L. reuteri, a widely-available probiotic shown to be beneficial for wound repair and immune proficiency, as an intervention to NDMA-induced damage. Overall, this work will shed light on gene-environment interactions that shape disease risk, and how age and beneficial microbes modulate the risk of NDMA-induced pathological responses.
Research Grant	NIH T35 OD033655
Field of Research	Pharmacology and Toxicology

Abstract Title	Investigation of the effect of pre-visit gabapentin on blood pressure outcomes in cats
Authors	Taylor Bobst, Emily Wheeler, Joyce Carnevale, Laura Van Vertloo
Affiliations	Department of Veterinary Clinical Sciences, Iowa State University College of Veterinary Medicine, Ames, IA
Abstract	Systemic hypertension is common in aging cats and can lead to serious complications such as blindness and organ damage if untreated; however, completing blood pressure (BP) measurements poses multiple challenges in this species. Taking BP measurements is technically challenging and time consuming, which is exacerbated by stress behaviors exhibited by cats during the procedure. Furthermore, stress behaviors during BP measurement have been associated with higher BPs and may result in misdiagnosing cats with hypertension (situational hypertension). Identifying a solution to minimize these challenges may result in veterinarians performing more BP monitoring and, ultimately, earlier detection and more effective monitoring of feline hypertension. Gabapentin, an anticonvulsant that has been shown to decrease stress related to veterinary visits in cats, could be a solution to optimize feline BP monitoring. We hypothesized that pre-treatment with gabapentin will reduce the difficulty of BP measurement and lower stress scores. In our double-blinded placebo-controlled crossover study, we performed two separate research visits with healthy cats: one pre-treated with gabapentin and one with placebo. The data collection for each visit was by the same research personnel in the same manner each visit. Fear-Free Certified investigators assigned the fear, anxiety and stress pre- and post-BP measurement. Six BP measurements were taken using the coccygeal artery by the same investigator for every participant. Additional data collected included the time needed to complete all BP measurements, compliance score, and sedation score. At this time, our research is ongoing and data analysis will begin upon completion of data collection.
Research Grant	VCS Research Incentive Grant
Field of Research	Behavior

Abstract Title	Development of a chronic pulmonary Mycobacterium abscessus infection model in Cystic Fibrosis (CF) ferret
Authors	John Wesley Bold Jr., Tuhina Gupta, Naveen Gokanapudi, Frederick Quinn, and Balázs Rada
Affiliations	Department of Infectious Diseases, College of Veterinary Medicine, University of Georgia, Athens, GA
Abstract	Cystic fibrosis (CF) results from autosomal recessive genetic mutations of the Cystic Fibrosis Conductance Regulator (CFTR) gene that impairs the movement of chloride and bicarbonate ions causing mucus thickness to increase in the lungs. Increased mucus in CF lungs leads to bronchiectasis and infections. Nontuberculous mycobacterial (NTM) infections especially with Mycobacterium abscessus (M. abs) is a common yet serious NTM within CF Centers. In this project, both wild-type (WT) as well as CF ferrets that harbor an Ivacaftor (VX-770)-responsive CFTR G551D mutation were infected with two morphotypes ZN55 (smooth) and ZN58 (rough) of M. abs. The study with WT ferrets last year showed no overt disease symptoms. Serum samples from both uninfected and M. abs infected WT ferrets recognized whole cell lysates, heat-killed, and gamma-irradiated ZN55 and ZN58 cells by ELISA. In the current study, the CFTR potentiator VX-770 was given twice daily to the CF ferrets until 2 weeks before intratracheal infection with 10 million CFU of M. abs ZN55 or ZN58 strains. Blood and nasal wash samples were collected pre-infection and every 2 weeks post infection (p.i.). The weight and temperature of the animals are monitored as health indicators. After the withdrawal of VX-770 drug, most CF ferrets experienced weight loss initially. Oxbow was supplemented to maintain weight. Currently, it is week 5 p.i, and a lung computerized tomography scan will be performed at week 8 p.i. with euthanasia by week 12 p.i. Through examining the disease symptoms in ferrets, comparisons can be made to M. abs infections in human CF patients. This animal model can be used for future treatment formations related to M. abs in our efforts to stop CF.
Research Grant	Cystic Fibrosis Foundation
Field of Research	Bacteriology

Abstract Title	Seroprevalence and epidemiology of influenza A viruses in rehabilitation raptors
Authors	Kate A. Bouchard, Kathryn P. Huyvaert, Katherine H. Haman, Jennifer Mannas and Justin D. Brown
Affiliations	Washington State University College of Veterinary Medicine, Pullman, WA (Bouchard, Huyvaert) Washington Department of Fish and Wildlife (Haman, Mannas) Pennsylvania State University Department of Veterinary and Biomedical Sciences, University Park, PA (Brown)
Abstract	An emerging, highly pathogenic influenza A virus (IAV) affecting birds (subtype H5N1, 2.3.4.4b) is associated with high rates of morbidity and mortality in previously unaffected wild birds and mammals. . Reports of mortality in bald eagles fom this emergent subtype motivated our study of IAVs in wild raptors at rehabilitation facilities. We hypothesized that recently admitted raptors were more likely to be exposed than education birds because the latter will have been protected from recent exposure. We also anticipate that older birds foraging in habitats with waterfowl are more likely to be seropositive for IAVs. We collected whole blood samples from wild raptors upon admission to rehabilitation clinics in Washington State from July to September 2023. Serum was processed and antibodies against IAVs were quantified using a blocking ELISA from IDEXX. Using logistic regression, we evaluated associations between the binary serostatus response and variables describing individual hosts (age, sex, species), their ecology (habitat, diet), rehabilitation circumstance (timing and reason foradmission, time at facility). We used an information-theoretic approach to model selection and to draw inferences from our model set about the epidemiology of IAVs in raptors. Better understanding the characteristics of raptors that are exposed to IAVs will allow us to predict which wild populations may be most vulnerable to the effects of IAVs. Sampling rehabilitation raptors gives us a broader geographic and temporal sample than would be possible sampling wild raptors in the same timeframe. These raptors could also serve as sentinels of IAVs in habitats and prey species such as small mammals that do not get regularly sampled for IAVs.
Research Grant	Washington State Department of Fish and Wildlife
Field of Research	Wildlife Conservation

Abstract Title	Immunomodulatory effects of articular chondroprogenitor cells
Authors	Taryn Boxleitner, Lynn Pezzanite, Lyndah Chow, Parvathy Thampi, Steve Dow, Laurie Goodrich, and Brian Johnstone
Affiliations	Department of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO Department of Orthopaedics and Rehabilitation, School of Medicine, Oregon Health & Science University, Portland, OR (Johnstone)
Abstract	Osteoarthritis (OA) is a degenerative disease that results in destruction of articular cartilage in joints of many species. OA has an inflammatory component that provides a potential therapeutic target for slowing OA progression. Bone marrow-derived mesenchymal stromal cells (MSCs) may be beneficial in the context of OA due to their immunomodulatory activity. However, they do not appear to stimulate new cartilage growth when injected into joints and present challenges in clinical use due to variability in donors and preparations. Articular chondroprogenitors (ACPs), isolated from healthy articular cartilage, pose advantages as an alternative therapy. Unlike MSCs, they have the ability to divide and expand in culture long-term without loss of chondrogenic capability. The goal of this study was to compare functional activity of equine ACPs and MSCs in vitro. We hypothesized that ACPs have comparable immunomodulatory properties to MSCs. Equine ACP clones and MSCs from three donors were grown to generate conditioned medium (CM) which was then used to determine the effects of ACP and MSC secretory products on macrophages. The macrophages were activated using a combination of IL-1β and TNF-α, and cultured in 1:1 media to CM. Their secretome profile was then analyzed with an equine multiplex cytokine assay. The macrophages exposed to ACP or MSC CM produced significantly less inflammatory cytokines (IL-1β ($p<0.0001$) and TNF-α ($p=0.01$, $p=0.03$)) compared with positive controls. The macrophages cultured with ACP CM produced significantly more anti-inflammatory IL-10 versus untreated controls ($p<0.01$). We concluded that ACPs exhibit immunomodulatory functions and further investigation of ACPs as a therapy for OA is warranted.
Research Grant	Honk Kong Jockey Club Equine Welfare Research Foundation
Field of Research	Orthopedics

Abstract Title	Comparative brain morphology among Musteloids
Authors	Angela Boyer, Christopher P. Heesy, Dominik Valdez, Leigha M. Lynch
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ (Boyer); College of Graduate Studies, Midwestern University, Glendale, AZ (Heesy, Valdez, Lynch)
Abstract	Brain morphology of relatively large-brained mammals has been linked to variation in diet, environment, sociality, and body size. This data, however, is biased toward primates with little data on the comparative anatomy of other large-brained clades, such as carnivorans. The purpose of this study is to identify and compare endocast morphology among musteloids, providing a foundation to further explore the evolutionary relationship between these species and to interpret their complex behaviors. We studied the following species: Procyon lotor (raccoon), Neovison vison (mink), Mustela erminea (ermine), Pekania pennanti (fisher), Martes americana (North American pin marten), Taxidea taxus (North American badger). We generated endocast models from micro-CT scans of skulls of each species using Avizo, a software application for data visualization and analysis. We then labeled 3D anatomical images and published them onto Sketchfab, which is an open-access 3D modeling platform. We identified gyri and sulci by following previously published brain atlases from Mustela putorius furo (ferret). We found that the larger the species, the more profound gyri and sulci they have compared to smaller species. We also found that some species, such as the Pekania pennanti and Procyon lotor have an additional gyrus, the post cruciate gyrus. The post cruciate gyrus was not evident in the Mustela erminea, Martes americana, or Neovison vision. Asymmetry of the ectosylvian gyrus was noted in Neovison vison. This data now enables future studies analyzing per- and polyfluroalkyl substances (PFAS) and heavy metals in the areas where these species inhabit and how it affects brain development.
Research Grant	Oklahoma State University Center for Health Sciences, Midwestern University
Field of Research	Anatomy

Abstract Title	Exploring the Mechanisms Behind Embryonic Wound Healing
Authors	Maya Boyle, Ryan R. Driskell, Iwona M. Driskell, Miranda Bernhardt
Affiliations	School of Molecular Biosciences, Washington State University, Pullman, WA College of Veterinary Medicine, Washington State University, Pullman, WA
Abstract	Skin is the largest organ of the human body and a critical barrier against disease and injury. Interestingly, embryonic skin is thought to have the ability to completely regenerate after wounding. However, the degree of regeneration is currently unquantified and the mechanisms behind embryonic regeneration are unknown. As this regenerative ability is lost post-partum, there is significant potential in understanding how embryonic skin undergoes wound healing and how this can be translated to improve adult wound healing. To explore the mechanisms behind wound healing in embryos, a surgical protocol was established in wildtype mice where embryos are wounded on their dorsum at both the E14.5 and E16.5 timepoints. Using H&E analysis, we quantified the level of regeneration by counting the number of regenerated hair follicles in the ~1mm dorsal regenerated wound bed. Our analyses explore whether hair follicles fully regenerate and the amount of fibrotic scar tissue generated. Using this established surgical protocol, we are able to explore how loss of Lef1, a gene heavily involved in hair development and regeneration, impacts embryonic wound healing.
Research Grant	NIH (NIAMS) RO1 AR078743 Washington State University College of Veterinary Medicine
Field of Research	Dermatology

Abstract Title	Immune modulating effects of feeding a synbiotic supplement to cats
Authors	Krista Bratlien, Lyndah Chow, Jennifer Hawley, Kara Maslyn, Steven Dow, Michael Lappin
Affiliations	Center for Companion Animal Studies and Center for Immunology, Department of Clinical Sciences, Colorado State University, Fort Collins, CO
Abstract	Understanding the immunologic effects of probiotics in cats is important to possibly aid in the management of feline diseases, including viruses. The probiotic Enterococcus faecium strain SF68 has been shown to have immune modulating properties, including studies showing supplemented cats have less recurrent signs of feline herpesvirus-1 and increased CD4+ lymphocytes over time. We are now able to analyze the immune system of cats more completely by combining total RNA sequencing with select cytokine/chemokine production to assess specific cellular changes. E. faecium strain SF68 has been combined with the prebiotic, psyllium which is commercially available as a synbiotic (Fortiflora SA, Purina PetCare). The primary objectives of this study were to further define the immune modulating effects of the synbiotic in healthy cats using total RNA sequencing (Novogene) of peripheral blood mononuclear cells (PBMC) and a feline cytokine/chemokine panel (Milliplex MAP). In addition, a feline infectious peritonitis virus in vitro inhibition test using the Fcwf-4 macrophage cell line was used to assess for antiviral activity in the serum of supplemented cats. Compared to controls, the cats fed the synbiotic had 45 up regulated genes and 33 down regulated genes in PBMC collected on Day 28. A KEGG pathway analysis was completed and revealed a significant up regulation in the TNF-alpha pathway and down regulation in the IFN-gamma and IFN-alpha pathways. The cytokine/chemokine analysis showed increases in IL-12 in supplemented cats. Serum from supplemented cats induced numerical decreases in FIPV mediated cytotoxicity. These results provide more information documenting that this probiotic is an immune modulator in cats.
Research Grant	Nestlé Purina PetCare
Field of Research	Immunology

Abstract Title	Cancer progression is impacted by modulating a feature of glycolytic metabolism
Authors	Nicholas Britt, Anna Barbeau, and Matthew Vander Heiden
Affiliations	(Britt) University of Tennessee College of Veterinary Medicine, Knoxville, TN and the Department of Biology (Barbeau and Vander Heiden), Koch Institute for Integrative Cancer Research, Massachusetts Institute of Technology, Cambridge, MA.
Abstract	Pyruvate kinase (PK) is the key enzyme involved in the conversion of phosphoenolpyruvate to pyruvate during the final step of glycolysis. The PK isoforms PKM1 and PKM2 have both been shown to support tumor growth in a context and tumor-specific manner. PKM1, the high activity isoform, supports the energetic needs of the cell, while PKM2, the low activity isoform, contributes to cell growth through diversion of glycolytic pathway intermediates towards biosynthesis of nucleotides and amino acids. Pancreatic ductal adenocarcinoma (PDAC) is one tumor type out of numerous that highly expresses PKM2. However, previous work has shown that pancreas-specific knockout of Pkm2 in the KP-/-C mouse model of PDAC (KrasG12D;Tp53fl/fl;Pdx1-Cre;Pkm2fl/fl) does not slow tumor growth and leads to an upregulation of Pkm1. Here, we aim to assess how loss of both Pkm1 and Pkm2 influences PDAC progression and survival in the KP-/-C mouse model. We demonstrate that Pkm1 and Pkm2 knockout in PDAC cells significantly extends survival of KP-/-C mice. Although there are no differences in tumor size at their humane endpoint, there is a significant reduction of tumor size in Pkmfl/fl mice assessed at an earlier timepoint. These data lend insight into the metabolic dependencies of PDAC tumors and may indicate a potential avenue in targeting metabolic pathways to potentiate tumor therapy success.
Research Grant	Lustgarten Foundation for Pancreatic Cancer Research
Field of Research	Oncology

Abstract Title	Effects of non-native plant invasions on tick-borne disease risk in Illinois
Authors	Jessica L. Brooks, Maria G. Muñoz, Brian F. Allan
Affiliations	College of Veterinary Medicine (Brooks) and School of Integrative Biology (Muñoz, Allan), University of Illinois at Urbana-Champaign, Urbana, IL
Abstract	Non-native plant species can greatly alter the ecological areas they invade by affecting a variety of both biotic and abiotic factors in an ecosystem. While this can have a negative impact on some species, recent research suggests that some non-native plants may provide a more conducive environment for ticks. This may occur by multiple ecological mechanisms, including altering habitat suitability for ticks or their wildlife hosts. This is a concern for both humans and animals as ticks are important vectors for multiple emerging pathogens. This study aimed to gauge the effects of multiple invasive plant species on tick populations compared to their native counterparts in natural areas located in Northern, Southern, and Central Illinois. Ticks were collected through “drag sampling” (i.e. dragging a 1m2 white cloth over vegetation) in paired plots either dominated by non-native plant species or control plots dominated by native plant species. After collection, ticks were preserved in ethanol and identified to species and life stage. Preliminary results suggest that some species of non-native plants appear to be more conducive to ticks than others. Continued research is planned to quantify the effects of different non-native plant species on the microclimates experienced by ticks, resulting differences in tick survival, and the prevalence of tick-borne pathogens in invaded and uninvaded habitats.
Research Grant	Illinois Department of Public Health
Field of Research	Parasitology

Abstract Title	Characterization of bovine extracellular vesicles and microRNA immunoregulation
Authors	Audrey Brown, Rafaela Santos, Ulrich Bickel, Fernanda Rosa
Affiliations	School of Veterinary Medicine, Texas Tech University (Brown, Santos, Rosa), Texas Tech University Health Sciences Center School of Pharmacy, Amarillo, TX (Bickel)
Abstract	Immunologically active compounds such as extracellular vesicles (EVs) containing microRNA (miRNA) can be found in bovine colostrum. Thus, this study aimed to characterize the morphology of EVs via super resolution stimulated emission depletion (STED) microscopy and to determine whether miRNA regulates the NF-Kβ signal transduction pathway. To test this, colostrum from fresh Holstein cows were collected and stored at -80°C until further analysis. Extracellular vesicles from colostrum samples were isolated using ExoQuick® ULTRA EV isolation kit and then incubated with a primary polyclonal antibody (anti-CD63) and with a secondary antibody (Alexa Fluor 594). To characterize EV morphology, STED microscopy was used to visualize labeled EV-antibody complexes. Subsequently, EVs pellets were subjected to microRNA isolation and purification using ExoQuick® RNA kit. To evaluate the immunological effect of miRNA over time, a colorimetric enzyme assay (QUANTI-Blue™, Invivogen) was used to measure the activation of the NF-Kβ pathway upon incubation with RAW-Blue™ Cells, a mouse macrophage reporter cell line known to express toll-like receptors (TLR) including TLR7 and TLR8. On day one, treatment group [RAW-Blue™ Cells + miRNA] and control group [RAW-Blue™ Cells alone] were incubated in a 96-well-plate overnight at 37°C with 5% CO2. On day two, all groups received QUANTI-Blue™ solution, and absorbance readings were taken at 620 and 655 nm over 24-hour period. The NF-Kβ activation was detected in the cells treated with bovine miRNA which led us to conclude that miRNAs can regulate immunological pathways via endosomal TLR binding independently of onset infections.
Research Grant	Agriculture and Food Research Initiative Competitive Grant no. 2023-67015-39081 from the United States Department of Agriculture (USDA) – National Institute of Food and Agriculture.
Field of Research	Immunology

Abstract Title	Virtual mechanical testing for condylar stress fracture risk assessment in Thoroughbred racehorses using CT
Authors	Nicola L. Brown(1), Soroush Irandoust(1,2), Corinne R. Henak(2), and Peter Muir(1)
Affiliations	(1)Department of Surgical Sciences, School of Veterinary Medicine (2)Department of Mechanical Engineering University of Wisconsin-Madison, Madison, WI
Abstract	Catastrophic musculoskeletal injuries (CMI) are a common fatality in Thoroughbred racehorses, and condylar stress fracture of the third metacarpal/tarsal bone (MC3/MT3) is a prevalent cause. Previous studies have demonstrated subchondral bone injury (SBI) in the parasagittal grooves (PSG) of the distal end of nonfractured MC3/MT3 with a contralateral condylar stress fracture. SBI in the PSG develops with microdamage accumulation due to repetitive high cyclic loads while galloping when the rate of microdamage exceeds that of the repair response. We hypothesized that standing computed tomography (sCT) detected structural changes due to PSG SBI correlates with increased levels of PSG stress and strain, which could indicate high risk of stress fracture. A sCT-based finite element (FE) model of each Thoroughbred's MC3/MT3 was built capturing the unique heterogenous bone mineral density and bone morphology. The FE models simulated a virtual mechanical test in which loads were applied to each condyle, mimicking those applied to the bone during galloping. Stress and strain levels were obtained and compared against experimental mechanical testing results. Elevated strain levels in the PSG were found in all condyles under load. Condyles with PSG SBI showed significantly higher levels of PSG tensile strain compared to condyles with no SBI. The sCT-based virtual mechanical testing provides a valuable non-invasive diagnostic tool for objective assessment of mechanical compromise to the distal end of the MC3/MT3 and associated risk of stress fracture. This pipeline enables interpretation of sCT imaging clinically, enabling personalized care that could reduce the incidence of condylar stress fracture in racing Thoroughbreds.
Research Grant	Grayson-Jockey Club Research Foundation
Field of Research	Orthopedics

Abstract Title	Construction of a tagged Porcine Reproductive and Respiratory Syndrome Virus with DsRed fluorescent protein
Authors	Chloe Brown, Seth Bockes, Abby Patterson
Affiliations	College of Veterinary Medicine, Iowa State University, Ames, IA(Brown), Boehringer Ingelheim (Bockes, Patterson)
Abstract	Porcine reproductive and respiratory syndrome virus (PRRSV) is an enveloped RNA virus that causes reproductive failures in sows and respiratory disease among all ages of pigs. This disease has a large economic impact on the swine industry and protection against it is strongly desired. Vaccination is important for host acquisition of immunity and the overall control of the disease. In vitro assays are heavily used in the development of effective vaccines and the construction of recombinant viruses can increase the efficiency of performing and reading those assays. A recombinant PRRSV expressing DsRed, a fluorescent protein, was constructed by inserting the DsRed protein sequence between open reading frame 7 (ORF7) and the 3' untranslated region (3'UTR) of the PRRSV genome. Successful construction of the recombinant PRRSV is characterized by the presence of red fluorescence in infected cells, confirming viral infection and spread. DsRed was chosen for ease of multiplexing with other fluorescent proteins, such as GFP, which is green. Use of this recombinant PRRSV will create the ability to track and monitor infections in various in vitro assays quickly.
Research Grant	Boehringer Ingelheim
Field of Research	Virology

Abstract Title	Construction of a tagged Porcine Reproductive and Respiratory Syndrome Virus with DsRed fluorescent protein
Authors	Chloe Brown, Seth Bockes, Abby Patterson
Affiliations	College of Veterinary Medicine, Iowa State University, Ames, IA(Brown), Boehringer Ingelheim (Bockes, Patterson)
Abstract	Porcine reproductive and respiratory syndrome virus (PRRSV) is an enveloped RNA virus that causes reproductive failures in sows and respiratory disease among all ages of pigs. This disease has a large economic impact on the swine industry and protection against it is strongly desired. Vaccination is important for host acquisition of immunity and the overall control of the disease. In vitro assays are heavily used in the development of effective vaccines and the construction of recombinant viruses can increase the efficiency of performing and reading those assays. A recombinant PRRSV expressing DsRed, a fluorescent protein, was constructed by inserting the DsRed protein sequence between open reading frame 7 (ORF7) and the 3' untranslated region (3'UTR) of the PRRSV genome. Successful construction of the recombinant PRRSV is characterized by the presence of red fluorescence in infected cells, confirming viral infection and spread. DsRed was chosen for ease of multiplexing with other fluorescent proteins, such as GFP, which is green. Use of this recombinant PRRSV will create the ability to track and monitor infections in various in vitro assays quickly.
Research Grant	Boehringer Ingelheim
Field of Research	Virology

Abstract Title	A novel approach for antemortem small intestinal microbiota sampling
Authors	Caroline Bruer, Bret Ulery, Aaron Ericsson, Samantha Huddleston, Drona Madugula, Farnoushsadat Rezaei, Craig Franklin, James Amos-Landgraf
Affiliations	Department of Veterinary Pathobiology, University of Missouri, Columbia, MO, Department of Chemical Engineering, University of Missouri, Columbia, MO
Abstract	Distinct microbial compositions between the upper and lower gastrointestinal tract (GIT) have significant implications for metabolism and disease, emphasizing the need for comprehensive analysis of the entire gut microbiota. However, no commercially available system enables sampling upper GIT contents of laboratory rodents without invasive procedures or post-mortem sampling. This project aims to contribute to the development of a non-invasive method for collecting upper GIT microorganisms in both animal models and humans. This study focuses on investigating the binding of bacteria to a novel poly(amino acid) at a pH range similar to that of the small intestine and maintain binding at a pH relevant to the colon. The proprietary polymer is designed to attach to a magnetic nanoparticle, which can capture the small intestinal microbiota, retain the contents throughout the large intestine, and be recovered from fecal samples via magnetic separation. A transgenic strain of Lactococcus lactis (L. lactis) expressing an inducible green fluorescent protein (GFP) and the TAMRA-labeled polymer were combined and observed through high-powered fluorescence microscopy. Limited positive association between the two was observed and future studies ongoing to confirm selective binding. The development of a device for capturing small intestinal microbiota has promising market potential and could revolutionize research on the human gut microbiome, enabling longitudinal studies and advancing diagnostic and therapeutic applications in gastrointestinal medicine.
Research Grant	NIH U42 OD010918-24, The Mutant Mouse Resource and Research Center at the University of Missouri
Field of Research	Microbiomes

Abstract Title	Acute effect of latanoprost on the morphology of iridocorneal angle and anterior chamber in dogs with ADAMTS10
Authors	Phillip Buckman; Christine D. Harman, BS; Amanda L. Jacobson, LVT; Lydia E. Kapeller, BS; Sichao Wang, PhD; András M. Komáromy, DrMedVet, PhD, DACVO, DECVO, FARVO
Affiliations	Department of Small Animal Clinical Sciences, College of Veterinary Medicine, Michigan State University, East Lansing, MI, USA; Center for Statistical Training and Consulting, Michigan State University, East Lansing, MI, USA
Abstract	Latanoprost is a prostaglandin F2α analog used to treat glaucoma in humans. In humans latanoprost applied over time activates matrix metalloproteinases within the trabecular meshwork increasing uveoscleral outflow of the aqueous humor. In dogs latanoprost is used to rapidly reduce IOP in emergency situations. The goal of this study is to examine the effects of topical latanoprost on the morphology of the ciliary cleft region and anterior chamber of the eye using ultrasound bio microscopy (UBM) and A-scan in ADAMTS10 open angle glaucoma dogs. This study included 16 eyes of 9 glaucomatous beagles. Subjects were sedated prior to their first series of examinations. UBM scans, IOP, This study included 16 eyes of 9 glaucomatous beagles. Subjects were sedated prior to their first series of examinations. UBM scans, IOP, pupil diameter, Pachymetry, tonography and A-scans will be performed. The same series of exams will be performed before and after topical application. The subjects will then be treated with latanoprost 0.005% ophthalmic solution once every 30 minutes for 2 hours. Totaling 5 eyedrops per eye. After topical treatment, subjects will then receive their second series of examinations. The Images of the ciliary cleft region taken using UBM will be analyzed based on the angle opening distance (AOD), ciliary cleft length (CCL), ciliary cleft width (CCW) and, depth of the anterior chamber (AC). We hypothesize that there will be a measurable difference in morphology between the anterior segment and anterior chamber of the eye before and after latanoprost treatment. Data collection is ongoing. We anticipate that the results will expand our knowledge on the hypotensive mechanism of topical latanoprost in glaucomatous dog
Research Grant	MSU Office of Undergraduate Research
Field of Research	Ophthalmology

Abstract Title	Cytokine concentration response to furosemide application in six Thoroughbred horses
Authors	Welf F. Buecken, Mallory L. Lehman, Marisa K. Ames, Jessica M. Morgan
Affiliations	Department of Veterinary Medicine and Epidemiology, School of Veterinary Medicine, University of California, Davis, CA (Buecken, Lehman, Ames, Morgan) and University of Veterinary Medicine Hannover, Foundation (Buecken)
Abstract	Furosemide is commonly administered in horses prior to racing to reduce the incidence of exercise induced pulmonary hemorrhage (EIPH) during the race through lowering of systemic blood pressure. Studies have demonstrated that furosemide has an immunomodulatory effect in humans and laboratory animals and there is recent data that it alters the mRNA expression of certain cytokines in racehorses. In the current study, our objective was to investigate the immunomodulatory effect of furosemide in the horse. We hypothesized that cytokine concentrations would be altered after furosemide application. A crossover study design with a 14-day washout period between trials was used. Serum samples from six healthy Thoroughbred horses were collected through a catheter prior to intravenous furosemide application (1.0 mg/kg) or an equivalent amount of saline solution (0.02 ml/kg), as well as 4 and 24 hours after treatment. The serum samples were stored at –80°C and analyzed with a Luminex assay for 23 different cytokines. The data showed significant effect of the horse in all 23 cytokines ($P < 0.01$). No significant concentration changes on cytokines over time were seen in a mixed effects model ($p < 0.05$). The lack of concentration changes during the 24 hour timeframe post treatment can be due to delayed mRNA translation or mRNA degradation, which warrants analysis of cytokine concentrations beyond the 24 hour mark.
Research Grant	This project was supported by UC Davis Center for Equine Health
Field of Research	Equine Medicine and Surgery

Abstract Title	Quantifying tick abundance in urban natural areas across the San Gabriel Valley
Authors	Hannah Burger, Caleb Sandoval, Janel Ortiz, and Rhea Hanselmann
Affiliations	College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA (Burger, Hanselmann); Biological Sciences Department, College of Science, Cal Poly Pomona, Pomona, CA (Sandoval, Ortiz)
Abstract	Ticks and tickborne diseases are increasing worldwide and have potentially devastating consequences for human and animal health. Human population growth and urbanization increase the potential for exposure of humans and domestic animals to ticks and the pathogens they carry. Habitat type, tick species and prevalence, the presence and abundance of wildlife, and how humans interact with their environment are factors that drive exposure risk. Just under 50% of the 9.83 million people living in Los Angeles County reside within less than 1／2 mile of a park, and many residents spend time outdoors visiting the almost 200 county parks and recreating in natural areas in their cities and neighborhoods. To explore the potential magnitude of tick and tickborne disease exposure risk in LA County residents, we are describing and comparing the presence and abundance of ticks in public parks and natural areas across the San Gabriel Valley (SGV), an expansive area that makes up most of southeastern LA county. Ticks are being collected from the environment at 11 sites along a 25-km transect spanning 3 habitat types of differing vegetation and disturbance levels. All sites were sampled in February, March, May, and June of 2023 and sampling is ongoing. To date, adult Dermacentor sp. and Ixodes pacificus have been collected from some but not all habitat types. In spring, both sexes of ticks were found, whereas only female Dermacentor sp have been collected during summer months. In the next phase of the project, ticks will be screened for pathogens. The importance of the temporal and spatial distribution of ticks and tickborne diseases in natural areas across the SGV will be discussed in the context of human and animal health.
Research Grant	College of Veterinary Medicine, Western University of Health Sciences, Small Grant for Projects Involving Students (SGIS)
Field of Research	One Health

Abstract Title	Synthetic mRNA-induced expression of H2 relaxin by bovine reproductive tissue
Authors	Caitlyn Burke1, Merrilee Thoresen1, Daryll Vanover3, Kevin Walters1, Heath King1, David Christiansen1, Jean Feugang2, Amelia Woolums1, Philip Santangelo3, Peter1,2
Affiliations	1Department of Pathobiology/Population Medicine, College of Veterinary Medicine, MS State Univ. 2Department of Animal/Dairy Sciences, College of Agriculture, MS State Univ. 3Department of Biomedical Engineering, Georgia Institute of Technology and Emory Univ.
Abstract	Relaxin (RLN) is a reproductive hormone that enhances connective tissue remodeling during pregnancy and parturition and deficiencies have led to prolonged delivery, increased rate of stillbirths, and incomplete softening of connective tissues in some species (i.e. pigs and rodents). In cattle, attempts using purified porcine or recombinant human RLN to reduce the incidence of dystocia in heifers presented variable results. However, Human 2 (H2) RLN has a high affinity for the bovine RLN receptor (RXFP1) and in combination with mRNA therapeutics, H2 RLN mRNA therapy may prove to be a more efficacious treatment for dystocia. To investigate our hypothesis, bovine kidney (BK) and primary bovine epithelial cells (BVEC) were transfected with a synthetic H2 RLN- mRNA construct with a secretion signal. Cell culture supernatants and lysates were harvested and H2 relaxin was detected via ELISA, confirming expression and secretion in vitro. We then investigated the transfection of the bovine female reproductive tract in vivo. Nonpregnant cull dairy cows (n = 2) were examined and confirmed to be in normal general and reproductive health prior to intravaginal treatment with mRNA encoding H2 RLN at time 0 and 48 hours. Vaginal secretions were collected over the course of 120 hrs post-transfection. Reproductive tissues were harvested at 120 hours for detection of H2 RLN directly via western blot. Detectable concentrations of H2 RLN were present in samples of vaginal, cervical, and uterine tissues from both treated animals. These data support further investigation of H2 relaxin mRNA therapy, and studies with larger sample size are warranted.
Research Grant	USDA-ARS Biophotonics Initiative Grant (#6066-31000-015-00D)
Field of Research	Theriogenology

Abstract Title	Qualitative and quantitative assay of Salmonella serovars of poultry product using Genovar and Nano biosensors
Authors	Kierney Burks1; Rawah Faraj1; Rejoice Nyarku1, Kingsley Bentum1, Alocilja Evangelyn2; Woubit Abebe1
Affiliations	1Center for Food Animal Health, Food Safety, and Food Defense, Department of Pathobiology, College of Veterinary Medicine, Tuskegee University, Tuskegee, Alabama 2Department of Biosystems and Agricultural Engineering, Michigan State University, East Lancing, Michigan
Abstract	Salmonella outbreaks have not declined; even worse, different Salmonella serotypes have emerged as the causative agents of foodborne illnesses. This study used Magnetic Nanoparticles (MNPs) and Gold Nanoparticles (GNPs) for early detection of Salmonella. Genovar PCR assay was also used to qualitatively and quantitively determine the level of Salmonella burden. Out of a total of 24 poultry products tested, 12 samples comprising chicken necks (5), turkey necks (5), and ground turkeys (2) were selected for further analysis. Briefly, 10gm of each sample was enriched in Tryptic Soy Broth, incubated overnight at 37oC, and then serially diluted 10-1-10-8 for MNPs capture and direct plating (DP). Total DNA from the RV broth was used Genovar assay. Results showed that MNPs efficiently captured Salmonella when the level of Salmonella was higher than the overall bacteria contamination. Observed by 18/13, 5/0, 20/45, 1/0, MNP CFU versus DP CFUs, respectively, reflecting the non-specific binding of MNPs to the overcrowded bacteria population. Despite this, GNPs specifically detected Salmonella in the abundance of other organisms. DP has recorded Salmonella abundance between 2X107-4.24X109/10 gm of the sample. Chicken neck carried the most variable Salmonella serovars, 13 followed by turkey neck carrying 7 serovars. Overall, the Genovar analysis revealed that serovars Montevideo, Infantis, Newport, Typhimurium, Saintpaul, and Hadar are the most abundant serovar from high to low ranging 3.5 X105-2.36 GE/µl. A combination of MNP and GNPs allows early detection of Salmonella. Assay like Genovar will cut the time needed to know the serovar involved in the outbreak.
Research Grant	Research Support: USDA/NIFA/CBG 2021-38821-34710, MSU/USDA/NIFA RC113747TU,
Field of Research	Microbiomes

Abstract Title	Ischemic stroke increases levels of one carbon enzymes and the folate receptor in male and female brain tissue
Authors	Petter Burrows, Himmat Dhillon, Amanda Covaleski, Lilah Manfredi, Thomas G Beach, Geidy E Serrano, and Nafisa M. Jadavji
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ; College of Osteopathic Medicine, Midwestern University, Glendale, AZ; Department of Biomedical Sciences, Midwestern University, Glendale, AZ; Banner Sun Health Research Institute Brain and Body Donation Program
Abstract	Stroke is the second most common cause of death worldwide and predominantly affects individuals over 65 years old. Its prevalence is projected to increase in parallel with the aging global population. Nutrition is a modifiable risk factor for ischemic stroke. Folates, B-vitamins and choline play a central role in one-carbon metabolism (1C), which is a key metabolic network that integrates nutritional signals with biosynthesis, redox homeostasis, epigenetics, regulation of cell proliferation, and stress resistance. Our research group has previously shown that deficiencies in 1C lead to worsened stroke outcomes using preclinical models. However, the impact of ischemic stroke on 1C enzymes remains unknown. The objective of this study is to investigate whether ischemic stroke contributes to a change in the levels of 1C enzymes after ischemic stroke in male and female patients. Brain tissue sections from ischemic stroke patients and controls were stained, all tissue was co-stained with neuronal nuclei (NeuN) and DAPI (4',6-diamidino-2-phenylindole). The colocalization of all three markers was evaluated by two individuals who were blinded to the experimental groups. Ischemic stroke increased neuronal levels of the folate receptor and 1C enzymes, methylenetetrahydrofolate reductase (MTHFR), thymidylate synthase (TS) and serine hydroxymethyltransferase (SHMT). In male stroke brain tissue was observed to have increased levels of MTHFR, TS, and SHMT. Female brain tissue had increases in the folate receptor and TS. The results suggest that ischemic stroke leads to increased demand on 1C and that there are some small differences between males and females.
Research Grant	Research Grant: American Heart Association 20AIREA35050015.We are grateful to the Banner Sun Health Research Institute Brain and Body Donation Program of Sun City, Arizona
Field of Research	Biochemistry

Abstract Title	Validation of commercial electroejaculation equipment in the domestic feline
Authors	Kristyn D Burton, Aime K Johnson, Chloe Hume
Affiliations	Oklahoma State University College of Veterinary Medicine, Stillwater, OK (Burton, Hume) Auburn University College of Veterinary Medicine, Scott Ritchey Research Center, Auburn, AL (Johnson)
Abstract	Obtaining a representative sperm sample in the cat can be necessary for a variety of reasons. The domestic cat can serve as a valuable model when developing techniques for the conservation of wild felids and serve a vital role in human medical and veterinary research. The most reliable method of collection is electroejaculation (EEJ), a technique utilized in many species. However, access to the necessary equipment has long been restricted to academia, thereby limiting the procedure's application in a clinical setting. Lane Manufacturing Inc., a manufacturer of EEJ in cattle, has recently developed a feline probe and program based on existing research equipments and protocols. Their product will allow a private practitioner working alone to perform EEJ using a specially programmed Lane Pulsator V (LPV). Interchangeable probes and the capacity to store multiple programs lends a wide range of utility to the machine, which is most commonly used in ruminants. To evaluate its performance, 10 healthy, sexually mature males were collected using both the LPV and standard EEJ machine (SDM), and semen characteristics compared. Anesthesia protocols were the same for both trials. Ejaculate volume and concentration, total sperm number (TSN), and progressive motility were compared. Upon evaluation there were no significant differences observed. These results indicate that the Lane electroejaculation equipment is an effective means of performing EEJ in the field and comparable to those validated in a research setting.
Research Grant	None
Field of Research	Theriogenology

Abstract Title	Range of motion between adjacent cervical vertebrae in horses with cervical vertebral compressive myelopathy
Authors	Dylan Burton and Yvette Nout-Lomas
Affiliations	Colorado State University CVMBS, Fort Collins, CO
Abstract	Cervical vertebral compressive myelopathy (CVCM) occurs when portions of the cervical spinal canal become stenotic, resulting in spinal cord compression. CVCM is the most common noninfectious neurologic disease in horses, and ultimately leads to unusable horses which directly impacts the equine industry. Our aim is to evaluate if range of cervical vertebrae joint movement is different between CVCM and control, unaffected, horses. We hypothesize that horses with CVCM have increased range of motion which contributes to vertebral instability. Medical records and imaging reports of 19 CVCM and 10 control horses between 2015 and 2023 were reviewed. Measurements of joint angles between adjacent vertebral bodies on survey radiographs and neutral, flexed, and extended myelographic radiographs were determined. Evaluation of survey radiographs showed no differences in joint angles between the two groups. 6 CVCM horses were compressed at 1 site, 8 at 2 sites and 5 at 3 sites. In CVCM horses, 9 were compressed at C3-4, 8 at C4-5, 9 at C5-6, 9 at C6-7, and 2 at C7-T1. The average range of motion between adjacent cervical vertebral bodies based on myelography for controls and CVCM cases, respectively, are: C3-4: 24□vs28□; C4-5: 28□vs31□; C5-6: 27□vs28□; C6-7: 27□vs30□. Evaluation of controls compared to compressed sites only shows range of motion at C3-4: 24□vs31□(n= 8); C4-5: 28□vs33□ (n=8); C5-6: 27□vs26□ (n=8); C6-7, 27□vs28□ (n=6). In reviewing this preliminary data, we conclude there does not appear to be a substantial difference in range of motion of cervical joints between control and CVCM horses. This data contributes to our further understanding of the relevance of biomechanics of the neck in the pathogenesis of CVCM.
Research Grant	Dr. Yvette Nout-Lomas, Equine Neurology Fund
Field of Research	Anatomic Pathology

Abstract Title	Radiation Therapy as a Treatment for Urinary Obstruction Secondary to Urothelial Carcinoma in Dogs
Authors	Madelyn Burtz, Mary-Keara Boss, Susan M. LaRue, Tiffany Martin
Affiliations	Flint Animal Cancer Center, Department of Clinical Science, and Department of Environmental and Radiological Health Sciences, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO.
Abstract	Transitional Cell Carcinoma (TCC) is the most common urinary tumor in dogs, often invading the bladder wall, trigone, urethra, and prostate and can lead to obstruction of the outflow of urine at the level of the ureters or urethra. Urinary obstruction indicates advanced disease and is considered a medical emergency. Radiotherapy (RT) with or without adjunct chemotherapy and non-steroidal anti-inflammatory drugs is often used for treating acute obstructions as well as loco-regional control of these tumors, but ideal treatment of urinary obstruction is still being investigated. The objective of this study was to evaluate the efficacy of multiple RT protocols in relieving symptoms of urinary obstruction secondary to tumor growth. Data was collected retrospectively from records from dogs with BRAF testing, biopsy, or cytology confirmed TCC, that showed evidence of either partial or complete urinary obstruction that were treated with RT at Colorado State University. Percent of patients experiencing relief of obstruction and time it took to experience relief of symptoms associated with obstruction was recorded. Number of dogs that required surgical intervention was recorded. Overall survival time and progression free survival time were analyzed in comparison to location of outflow obstruction and radiotherapy protocol. Various RT protocols included 2.7-8 (median 5.4) Gy per fraction for a total of 6-57 (median 34) Gy in 1-20 (median 6) fractions. Out of 38 patients included, 29 patients unobstructed from RT (66%), the remaining were either euthanized prior to completion of treatment or had surgical intervention. RT may be a successful salvage option for dogs presenting with urinary obstruction caused by urothelial carcinoma.
Research Grant	none
Field of Research	Oncology

Abstract Title	Optimizing an in vitro model of equine articular cartilage degeneration
Authors	Rosalie Bus, Brad B. Nelson
Affiliations	Orthopaedic Research Center, Colorado State University, Fort Collins, CO
Abstract	Osteoarthritis is a prevalent disease in horses and humans and is characterized by articular cartilage degeneration. Healing and regeneration of articular cartilage is extremely limited in adults. For that reason, prevention and early detection of osteoarthritis is crucial. With the current diagnostic methods, unfortunately osteoarthritis can only be detected in more progressed stages. To address this knowledge gap, in vitro models can be used to investigate the detection of early-stage osteoarthritis and treatment options, eliminating the unnecessary sacrifice of horses. Collagenase and trypsin are proteases used to degenerate cartilage in vitro. There is, however, a lack of understanding in how these enzymes degrade specific extracellular matrix components in equine articular cartilage and the duration of exposure needed. The study objective is to determine the degree equine articular cartilage degeneration following exposure to solutions of collagenase type II, trypsin and a mixture of both and to determine the temporal effects of exposure. Distal interphalangeal joint cartilage of equine cadavers were exposed to solutions of collagenase, trypsin and a mixture of both. Temporally, cartilage biopsies were collected (before digestion and after 1,2,4,8 and 24 hours of exposure). The amount of collagen and glycosaminoglycans was determined using hydroxyproline and dimethyl-methylene blue assays, respectively. Future studies can use these data to choose the optimal digestive compound and exposure time to imitate early-stage osteoarthritis without requirement of living animals.
Research Grant	College Research Council Grant at Colorado State University
Field of Research	Orthopedics

Abstract Title	Chlamydia trachomatis and the role of its inclusion membrane protein CT226 in inflammation and infection
Authors	Morgan Busby, Hollis C. Holcomb, Madison Tryzbiak, Jennifer Shaw, and Erika Lutter
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Abstract	Chlamydia trachomatis is the most frequently reported sexually transmitted bacterial infection and previous infection can result in pelvic inflammatory disease, infertility, chronic pelvic pain, and ectopic pregnancy. C. trachomatis, an obligate intracellular pathogen, forms an inclusion inside the host cell and secretes inclusion membrane proteins (Incs) into the inclusion membrane. Recent work in our lab suggests that Inc CT226 modulates the host immune response through interactions with inflammasome-regulating proteins. Two sets of mice were intravaginally infected with wildtype C. trachomatis (L2) or a deletion mutant (L2ΔCT226). Following infection of the first set of mice, intravaginal swabs were collected weekly. These samples were diluted, cultured in McCoy or HeLa cells, stained with immunofluorescent Chlamydia-specific antibodies, and viewed via immunofluorescent microscopy to quantify the number of infectious forming units (IFUs). Reproductive tracts were harvested for histopathology to compare inflammation responses. The second set of mice was sacrificed for reproductive tract collection, and the number of immune cells recruited was determined using flow cytometry. Comparing L2 to L2ΔCT226, there was a noticeable increase in markers of inflammation in the reproductive tracts of mice infected with L2ΔCT226. Similar numbers of recoverable IFUs suggest that the deletion of CT226 has no observable impact on C. trachomatis infectivity. The flow cytometry results show a non-cell-specific increase in immune cell recruitment to the reproductive tract during both infections; however, a noticeable trend emerged of higher recruitment of M1 macrophages than M2 during L2ΔCT226 infection.
Research Grant	National Institutes of Health 1R15AI149439-03
Field of Research	Bacteriology

Abstract Title	Development and Validation of an OSATS and GRS for Evaluation of Surgical Castration in a Live Equid Model
Authors	Tommy Butler, Ashley Whitehead*, James Brown, Luis Morales, Babafela Aswosile, Clint Roof, Marcelo Schmidt and Carolyn Arnold
Affiliations	Texas Tech University, School of Veterinary Medicine, Amarillo, Texas, USA *University of Calgary Veterinary Medicine, Calgary, Alberta, Canada
Abstract	Castration is the most common surgical procedure performed by equine practitioners and is a significant source of liability due to potential complications. There is a paucity of data regarding the assessment of surgical competency or best teaching practices of this skill in veterinary curricula. The purpose of this study was to develop and validate an objective structured assessment of technical skills (OSATS) and global rating scale (GRS) for use in a live model of equine castration. A cognitive task analysis (CTA) was developed using narrated video recordings of three experts performing castrations in donkeys. From the CTA, a 3-point Likert scale OSATS/GRS was created. Eleven experts in veterinary education and surgery evaluated each item of the OSATS/GRS as “not useful”, “useful”, or “necessary”. Using this data, the content validity ratio (CVR) of each item on the scale was calculated. Seventeen items met the threshold of 0.667 and were included in the validated OSATS/GRS. The content validity index relevance (S-CVIR) and content validity index average (S-CVIA), assessments of the complete scale, were calculated at 0.985 and 0.824. Finally, the validated OSATS/GRS was used by three experienced veterinary educators to assess video recordings of second-year veterinary students performing castrations (IACUC 2022-1232, IRB 2023-259). The intra-class correlation coefficient (ICC) of the OSATS/GRS between evaluators was 0.952 with 95% CI [0.88, 0.985]. The OSATS/GRS was found to effectively rank surgical skill level as not competent, competent, or proficient. Therefore this rubric can be applied in veterinary school curricula to assess surgical skills and competency.
Research Grant	We would like to thank the financial support of Boehringer Ingelheim, Inc. The content is solely the responsibility of the authors and does not represent the views of the Boehringer Ingelheim, Inc.
Field of Research	Equine Medicine and Surgery

Abstract Title	Identifying diffusible signal factor-producing enteric bacteria and evaluating the inhibitory effects on Salmo
Authors	Ava Cabble, Paulina D. Pavinski Bitar, Rimi Chowdhury, and Craig Altier
Affiliations	Department of Population Medicine & Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY
Abstract	Bacterial pathogens acquire remarkable adaptations that enable survival within their host organism. Salmonella utilizes long-chain fatty acids as signals to strictly regulate its virulence genes, thus improving its pathogenesis. These fatty acids are produced as quorum-sensing signals by intestinal microbiota, termed diffusible signaling factors (DSFs), affecting the virulence of Salmonella through inter-species signaling. We sought to determine which intestinal bacteria produce these signals and the mechanism by which they impact the virulence of Salmonella. Prior studies have shown the involvement of rpfF in the biosynthesis of DSFs. We cultured bacteria from the colonic mucosa of mice on selective media and identified the isolates. For bacterial species predicted to carry an rpfF homolog, we plan to use a functional assay to screen for Salmonella virulence inhibition. To accomplish this, we will employ a Salmonella strain containing a lacZY fusion to a known virulence gene. Screening is to be followed up by a lux-based reporter assay, which will quantitatively evaluate Salmonella virulence gene expression when co-cultured with our isolate, and when grown in the presence of long-chain fatty acids produced by the isolate. We expect fatty acids to repress virulence genes, and we plan to identify them using gas chromatography. The acquisition of this knowledge is expected to significantly contribute to the comprehension of Salmonella pathogenesis and pave the way for subsequent investigations into preventive strategies targeting Salmonella virulence expression.
Research Grant	National Institute of Allergy and Infectious Diseases
Field of Research	Bacteriology

Abstract Title	Prenatal phthalate exposure alters the development of sex-specific vocalization calls in neonatal mice
Authors	Joseph Caffarini, Jacob Maxon, Howard Gritton, Megan Mahoney
Affiliations	Department of Comparative Biology, College of Veterinary Medicine, University of Illinois at Urbana-Champaign
Abstract	In many species, social interactions can be characterized by vocalizations, including calls for maternal care, courtship, and play, that often differ across sexes due to changes in hormone signaling during neural development. Estradiol notably organizes changes in the fetal brain to promote sexual differentiation. Some environmental chemicals, including phthalates, resemble estrogen and can alter hormone signaling resulting in unspecified effects on social-sexual development. Therefore, we tested the hypothesis that in utero phthalate exposure alters hormone signaling in the developing brain, leading to reduced male-specific social behaviors after birth. We dosed pregnant CD1 mice with oil (control) or phthalates from gestation day 10.5- birth (20 ug/kg/day. 200 ug/kg/day and 200 mg/kg/day). Pups (male and female) were isolated for 5 min from their litter briefly at postnatal day (PND) 3 (n=32), 6 (n=33), 9 (n=37), and 12 (n=35) to elicit calls for maternal care that were captured at each time point. We utilized machine learning tools to identify syllables that we sorted by shape, resulting in eight syllables: Short, Slope Up, Concave, Flat, Tilde, Complex, Slope Down, and Harmonic. Using statistical analysis, we compared syllable occurrences across dosage and age groups. We discovered that in control mice, sex specific vocalizations are divergent beginning at PND 12, with female animals showing more complex, uniformly distributed syllables. In contrast, male mice show a reduced vocabulary with highly repeated syllables. Our results suggest that exposed mice are born with feminized call repertoires, and that in utero phthalate treatment changes neural circuits important for producing sex-specific social communication.
Research Grant	NIH R01ES032163
Field of Research	Pharmacology and Toxicology

Abstract Title	Developing cellular models to Understand the Roles of CDK1 and TRIM24 in Early Embryonic Development.
Authors	Matthew A. Caldwell, Bechara Saykali, Sergio Ruiz
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Abstract	Early embryonic development begins with the totipotent zygote, which differentiates into extra-embryonic tissues and all three germ layers. Studies from our lab found that Tripartite motif-containing 24 (TRIM24) and Cyclin dependent kinase 1 (CDK1) play important roles in early development both in vivo and in vitro. Our aim is to understand this regulatory role using genetic tools and cellular models, which include CRISPR-Cas9 and murine embryonic stem cells (mESCs), respectively. We previously observed that TRIM24 is recruited to nuclear foci and co-localized with the protein DUXBL upon induction of a totipotent-like-stage. We showed this co-localization to be essential in the exit from this stage. To examine the process and timing of this recruitment and co-localization, we generated an mESC reporter line by performing an endogenous tagging of the TRIM24 locus with a fluorescent protein by using a CRISPR-based method in a cell line that already has a fluorescent tag in DUXBL. This will allow us to better understand the physical interactions of TRIM24 and DUXBL and how they relate to totipotency. CDK1 is a cell cycle regulator that is essential for mitosis, and its differential activity through development may be involved in cell fate commitment during early development. Results from our lab suggested that inhibition of CDK1 activity could facilitate differentiation into trophectoderm. Using the CRISPR-Cas9 system, we generated mESC cell lines with a tagging of the FKBP domain into endogenous CDK1 loci, allowing for the immediate degradation of CDK1 upon addition of dTAG compounds. Generating a degron system enables us to explore CDK1's regulatory role during trophectoderm differentiation.
Research Grant	National Cancer Institute, Intramural Research Program
Field of Research	Physiology

Abstract Title	Testing for Chronic Wasting Disease in Elk on the Western Slope of RMNP by using PMCA and RT-QUIC
Authors	Jessi Campbell, Kirsten Marshall, Kendall O'Brien, Analeis Cofield, Mark Zabel
Affiliations	Prion Research Center, Department of Microbiology, Immunology, and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO USA 80521
Abstract	Chronic Wasting Disease (CWD) is a transmissible prion disease that causes spongiform encephalopathy in cervids such as elk, deer, and moose. This study looks at the transmission of CWD in Elk on the Western Slope of Rocky Mountain National Park (RMNP), which has not been reviewed. Elk have previously tested positive on the Eastern Slope, and any positive samples on the Western Slope indicate the spread of CWD, continuing the surveillance of the disease. It is suspected that CWD is throughout RMNP and due to the migration patterns of elk, has spread to the Western Slope. Based on previous studies, CWD has spread from Colorado (discovered in the 1960's) to over 30 states and 6 Canadian provinces. Western Blotted samples from Protein Misfolding Cyclic Amplification (PMCA) and Real-Time Quaking-Induced Conversion (RT-QUIC) were utilized to test fecal, water, and plant samples on the Western Slope of RMNP in Onahu Creek. For both the Western Blotted samples and RT-QUIC, the data showed inconclusive results. The importance of this study includes disease surveillance with faster diagnostic testing. Through these measures, this study aims to help control this disease via monitoring trends while a cure is under development.
Research Grant	NIH T35 OD015130
Field of Research	One Health

Abstract Title	Nanopore multiplex amplicon sequencing and drug resistance in asymptomatic Giardia intestinalis infections
Authors	Daniel Capasso, Oluwaremilekun Ajakaye, Mabel Tettey, Juan David Ramirez, Erick Tijhin, Michael Grigg
Affiliations	Laboratory of Parasitic Diseases, NIAID, NIH, Bethesda, MD (Capasso, Ajakaye, Tettey, Tijhin, Ramirez, Grigg), Comparative Biomedical Scientist Training Program, NIH, Bethesda, MD (Capasso), Carlson College of Veterinary Medicine, Oregon State University, Corvallis, Oregon (Capasso)
Abstract	The enteric protist Giardia intestinalis is largely thought to be a pathogen that divides by asexual reproduction. Giardia is classified into zoonotic or host specific assemblages based on multi-locus sequence typing (MLST) using 4 genes. To assess genetic diversity, we developed 10 additional markers across all chromosomes for MLST. 32 isolates that belong to 4 assemblage sub-types possessed 24 distinct sequence types using the expanded 14 gene MLST. Inheritance patterns across the isolates showed a high frequency of inter- and intra-assemblage genetic exchange, challenging the currently accepted theory that Giardia reproduces exclusively asexually. To investigate the extent of genetic diversity in an endemic focus of infection, we examined 985 stool samples in children under 10 years of age collected across 10 states in Nigeria. Real-time PCR detected a prevalence of 77.4%. Most of the cases were in asymptomatic children, which suggests that Giardia is more commensal than pathogenic. We used Nanopore Multiplex Amplicon Sequencing (NMAS-Seq) to perform MLST. Amplicon pooling and dual barcoding allowed for a high depth of coverage per dual barcode to resolve the MLST genotype, and these results will be presented. In addition to the 14 MLST markers, beta-tubulin is also a gene of interest because it is the target for benzimidazoles, a class of drugs used to treat Giardia infections. Previous studies have shown that a single nucleotide polymorphism, E198K, in this gene is associated with resistance. We will investigate whether the E198K polymorphism is present among recombinant Giardia infections to determine the role of recombination in the spread of drug resistance across assemblages.
Research Grant	NIAID, Intramural Research Program
Field of Research	Parasitology

Abstract Title	Correlation of antinociceptive and hypothermic effects of opioids in dogs
Authors	Astrid Carcamo Tzic, Butch KuKanich, Kate KuKanich, Elayna Anderson
Affiliations	Department of Anatomy and Physiology (Carcamo Tzic, KuKanich), Kansas State University College of Veterinary Medicine, Manhattan, KS, USA Department of Clinical Sciences (KuKanich, Anderson), Kansas State University College of Veterinary Medicine, Manhattan, KS, USA
Abstract	The purpose of this study was to evaluate the analgesic effects of butorphanol and methadone using a thermal pad model, and to assess the correlation of analgesia and hypothermia caused by opioids in dogs. Nine male beagles were enrolled and randomly allocated to receive intravenous methadone (0.5mg/kg), butorphanol (0.4mg/kg), or saline/placebo in an IACUC-approved three-way cross-over study. Rectal temperature and thermal withdrawals were measured prior to drug administration and through 6 hours post administration. Thermal withdrawals were obtained randomly from each hind foot, placed on thermal plates heated to a maximum of 134F (equivalent to 20 seconds) for each time point (3 per foot, 6 per dog). A positive withdrawal occurred if the dog actively removed the foot. One dog was excluded from analysis due to lack of withdrawals at maximum temperatures/times. No injuries were noted to the dogs' feet. Thermal withdrawals were significantly decreased ($P<0.5$), compared to saline, from 0.5-5h in methadone and 0.5-4h for butorphanol. Rectal temperatures were significantly decreased, compared to saline, from 0.5-5 hours for both methadone and butorphanol. The magnitude of the hypothermia was greater for methadone compared to butorphanol. There was significant ($P=0.0005$), and moderate correlation ($r2=0.43$) between the analgesic and hypothermic effects of the opioids. The dogs administered butorphanol and methadone exhibited sedation, but sedation was not specifically quantified. Based on these data, the hypothermic and analgesic effects of butorphanol and methadone were correlated. Monitoring opioid hypothermic effects is an easy, inexpensive, and humane manner for preclinical predictor of opioid analgesic effects in dogs.
Research Grant	KuKanich Clinical Pharmacology Laboratory
Field of Research	Pharmacology and Toxicology

Abstract Title	Mechanism of gut microbiome-induced obesity in the BTBR mouse strain
Authors	Sydney Cardoza, Zach McAdams, Aaron Ericsson
Affiliations	College of Veterinary Medicine, MU Metagenomics Center (McAdams, Ericsson) , Department of Veterinary Pathobiology (McAdams, Ericsson), University of Missouri, Columbia, MO
Abstract	Autism Spectrum Disorder (ASD) is a developmental disability, multifactorial in origin, resulting in social interaction deficits, communicative impairments, and repetitive behaviors, and frequently associated with obesity. While the specific factors contributing to ASD and obesity are unclear, there is a correlation between gut microbiome (GM) and severity of disease characteristics. The BTBR mouse strain demonstrates behaviors aligning with the diagnostic features of ASD and obesity, providing a model to analyze factors contributing to disease development. Studies of mice colonized with a low or high richness GM (GMlow and GMhigh) suggest subtle sex-dependent effects of the microbiome on autistic behaviors, and significant effects of the microbiome on obesity. Weight gain is determined by food intake, activity level, and fecal energy loss, among other factors. This study aims to determine whether intake, activity level, and fecal energy loss differ between BTBR mice colonized with GMlow and GMhigh. We hypothesize that the GMlow mice will have higher feed intake, measured by weighing the food hopper each morning, and lower activity levels, measured based on distance traveled on the running wheel, with no differences in fecal energy loss. These results would suggest that the decreased BW of GMlow pups at birth is due to decreased fetal growth, and that the relationship reverses with time as they maintain high intake and low activity levels throughout post-natal development.
Research Grant	Research support provided by the University of Missouri Metagenomics Center (MUMC)
Field of Research	Microbiomes

Abstract Title	Binding profiles of H5 influenza A viruses on avian and mammalian respiratory and gastrointestinal tissues
Authors	Sarah M. Carlisle, Brittany A. Seibert, L. Claire Gay, C. Joaquin Caceres, Chloe Goodwin, Nicole M. Nemeth, Daniel R. Perez and Silvia Carnaccini
Affiliations	Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, Georgia
Abstract	The current global avian influenza virus (AIV) epidemic caused by the highly pathogenic Eurasian-origin H5N1 virus subtype is devastating the poultry industry, wildlife, economy, and agriculture worldwide. AIVs continue to pose a significant threat to public health due to their zoonotic potential. The surface glycoprotein hemagglutinin (HA) is vital for the virus binding to the host cell receptors, the sialic acids, and mediating entry, thus determining virus host range and tissue tropism. Particularly for recent H5N1 AIV infections, a broader host tropism has been seen with affected species not commonly associated with AIV infections, such as waterfowl and raptors. With these observations, we hypothesized that the HAs of the circulating Eurasian H5 AIV evolved to a broader and stronger binding profile to respiratory and gastrointestinal tissues than historical H5 HA viruses. Therefore, the HA of different H5 AIVs representing recent and historical strains was generated over a laboratory-adapted isogenic backbone. Immunofluorescence assays on respiratory and gastrointestinal tissues of selected domestic gallinaceous birds, wild birds, mammals, and human differentiated airway epithelial cells were conducted to assess the binding profiles of each H5 HA selected. Sequential confocal microscopy correlated the results of the binding of the recent H5 HA with historical H5 HA and with the distribution of α2,3 and α2,6 N-linked sialic acid cell receptors and the binding profiles of the pandemic A/California/04/2009 (pdmH1N1) to the same tissue types. These findings provide insights into genetic changes in the H5 HA that modulate the binding properties of AIV and advance our understanding of the pathogenesis and ecology of AIV.
Research Grant	UGA College of Veterinary Medicine
Field of Research	Virology

Abstract Title	RNA-interference: role of Ig-like receptor B in chicken macrophage response to AIV and Salmonella typhimurium
Authors	Anaid A. Carlo-Allende, Brandi Sparling, and Yvonne Drechsler
Affiliations	Department of Immunology and Immunogenetics (Drechsler, Sparling), College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA.
Abstract	Members of the immunoglobulin-like receptor family interact with the major histocompatibility class 1 (MHC-I) molecules on immune cells to recognize antigenic peptides. Our lab characterized a new subset called Cluster Homolog of Immunoglobulin-like Receptor-B (CHIR-B) in chicken that may suppress the innate immune response. We conducted a phylogenetic analysis to explore the interrelationships of CHIRs with other Ig-like receptors in other species. Investigating CHIRs in breeding programs aims to enhance food security and poultry health during disease outbreaks. Based on data from mammalian studies, we hypothesized that using small interfering RNAs (siRNAs) to silence CHIR-B expression will improve macrophage defense against infectious agents. Our previous research demonstrated that CHIR-B silencing increased nitrate production and enhanced redox cascades in chicken macrophages after viral infection. To further understand the response in different MHC-I types and reduce biological variability, we cultured an HD11 chicken macrophage cell line and transfected them with siRNAs. We stimulated them with Salmonella typhimurium lipopolysaccharides (LPS) or infected them with Influenza A virus. We measured nitrate production at 24 and 48 hours after siRNA transfection. We detected the highest amount of nitric oxide 48 hours post-transfection with non-targeting siRNAs and stimulated with LPS. The macrophages exposed to the Influenza A virus with CHIR-B siRNAs showed no production of nitric oxide at any time point, and the possible reasons for this absent response are to be determined. Future research will explore the impact of blocking immunoglobulin-like receptor B and MHC-I, deepening our understanding of CHIR's immune role.
Research Grant	College of Veterinary Medicine small grants program
Field of Research	Immunology

Abstract Title	Evaluating firocoxib, bupivacaine liposome suspension, and/or a CO2 surgical laser to improve piglet welfare
Authors	Jessica C. Carnal, Maria E. Lou, Robin Schroeder, Kelly Lechtenberg, Michael D. Kleinhenz, Johann F. Coetzee, Kushan Kompalage, Ryan Tucker, and Abbie V. Viscardi
Affiliations	Anatomy and Physiology (Carnal, Lou, Coetzee, Kompalage, Tucker, Viscardi), Clinical Sciences (Kleinhenz), College of Veterinary Medicine, Kansas State University, Manhattan, KS; Midwest Veterinary Services, Inc. (Schroeder, Lechtenberg), Oakland, NE
Abstract	This study aimed to evaluate the effectiveness of a CO2 surgical laser and bupivacaine liposome suspension (BUP), used alone or with firocoxib (FIRO), on reducing piglet pain and improving wound healing after castration and tail docking. We hypothesized that the combined use of FIRO, BUP, and surgical laser would significantly reduce pain and improve wound healing when compared to current industry standards. 3 sows, 5 male and 5 female piglets per sow, were randomly assigned to 1 of 2 treatment groups: 3.0mg/kg FIRO oral (n=1 sow), or oral placebo (n=2 sows); therefore, piglets received either FIRO (n=10) or placebo (n=20) via the sow through transmammary delivery. Additionally, the piglets of the placebo sows were either provided 3.0mg/kg FIRO oral (n=10 piglets), or oral placebo (n=10 piglets). All piglets received BUP intratesticularly and/or at the base of the tail 30min pre-processing. Piglets were processed using 1 of 3 options: surgical laser (n=12), scalpel and pliers (conventional; n=12), or sham (handled only; n=6). Wound healing and inflammation were assessed at baseline and up to 168h post-processing. Tail and scrotal wound scores were lower in piglets that received FIRO transmammary compared to placebo ($p \leq 0.05$). Scrotal wound scores were also lower in piglets castrated using the laser ($p=0.004$), while tail wound scores were lower in piglets docked conventionally ($p=0.003$). Inflammation of the tail tissue was higher in piglets docked using the laser ($p=0.02$). Preliminary results suggest that a surgical laser may improve wound healing when used for castration, but not for tail docking, and there may be benefits to providing FIRO to piglets transmammary. Further analysis will be done to confirm these findings.
Research Grant	Agriculture and Food Research Initiative Competitive Grant no. 2020-67015-31540 from the USDA National Institute of Food and Agriculture
Field of Research	Animal Welfare

Abstract Title	The role of microRNA-145 in TGFβ-induced myofibroblastic transition in canine valvular interstitial cells
Authors	Sally Carnevale, Dawn Meola, Vicky Yang
Affiliations	Tufts University Cummings School of Veterinary Medicine, Grafton, MA
Abstract	Myxomatous mitral valve disease (MMVD) is the most commonly acquired heart disease in dogs. MMVD is characterized by prolapse of the mitral valve driven by the transition of normal fibroblastic valvular interstitial cells (VICs) with low alpha-smooth muscle actin (αSMA) expression to myofibroblasts with high αSMA expression. The cause of MMVD is unknown; however, previous studies have shown increased expression of TGFβ and microRNA-145 (miR-145) in VICs harvested from diseased valves. Furthermore, miR-145 overexpression in VICs can initiate the transition from fibroblasts to myofibroblasts. In human MMVD, increased numbers of macrophages have been found in affected valves, but their exact role in MMVD development remains unknown. As TGFβ and cytokines IL-1, IL-6, IL-10, and TNFα are secreted by macrophages, we hypothesized that these macrophage-associated factors can induce VIC myofibroblastic transition and increased miRNA-145 expression. To study the effects of macrophage-associated cytokines on VICs, VICs harvested from normal valves (n=3) were cultured with TGFβ1 (30 ng/ml), IL-10 (50 ng/ml), TNFα (50 ng/ml), IL-6 (20 ng/ml), or IL-1β (10 ng/ml) in serum free media for 24 hours. Non-cytokine treated cells acted as controls. Total RNA was isolated with the miRVana RNA isolation kit, and protein was extracted with M-Per. Western blot analysis demonstrated that αSMA expression increased only in the presence of TGFβ. Gene expression of miR-145, αSMA, TGFβ, IL-10, TNFα, IL-6, IL-1, collagen, elastin, fibronectin, and glycosaminoglycan will be analyzed with real-time PCR, and miR-145 expression will also be analyzed using drop-digital PCR. We expect that culture with TGFβ will increase VIC miR-145 expression.
Research Grant	NIH K01OD028205
Field of Research	Cardiology

Abstract Title	Seroprevalence of Cytauxzoon felis in free-ranging domestic cats from central Oklahoma
Authors	Ryan D. Carson, Pabasara Weerarathne, Julie E. Hyatt, Shannon R. Cowan, Jennifer E. Thomas, Ruth Scimeca, Mason V. Reichard, Craig A. Miller
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Abstract	Cytauxzoon felis is a blood apicomplexan responsible for causing the tick-borne disease cytauxzoonosis in domestic and wild felines. C. felis infections in the natural wildlife vertebrate reservoir, the bobcat (Lynx rufus), are considered subclinical and chronic, whereas infections in domestic cats are considered severe and life threatening. In enzootic areas, infections of C. felis in wild feline hosts can be 80% or higher, however the seroprevalence of C. felis in free-ranging domestic cat populations is unknown. The goal of this study is to determine the seroprevalence of IgG antibodies to C. felis in free-ranging domestic cats from central Oklahoma, an area considered highly enzootic for the apicomplexan. Blood samples were collected from over 800 free-ranging cats originating from 11 cities throughout central Oklahoma from 2014–2016. An optimized indirect ELISA assay from a previously published study was utilized to detect IgG antibodies from serum-based samples. Absorbance values were analyzed and converted to Percent Positive (PP) based on positive and negative control samples to limit intra-plate variation. Preliminary results indicate 76% (95% CI, 70.9%–81.3%) of free-ranging domestic cats throughout central Oklahoma had detectable IgG antibodies to C. felis. Testing of additional samples is ongoing and further analysis is planned to investigate seroprevalence relationships among different sexes, ages, and geographic regions. Results of this study demonstrate the utility of using the validated C. felis ELISA assay to estimate the risk of exposure to domestic cats. Domestic cats from other areas should be tested which would allow for comparison of C. felis exposure risk among different populations.
Research Grant	Oklahoma State University
Field of Research	Parasitology

Abstract Title	Use of real-time PCR to detect bacterial DNA in spiked equine blood as compared to lab grown cultures
Authors	Mikayla Casolari, Lauren Bookbinder, Elizabeth Carr, and Rinosh Mani
Affiliations	Department of Large Animal Clinical Sciences, CVM, Michigan State University, East Lansing, Michigan (Bookbinder and Carr) Veterinary Diagnostic Laboratory, CVM, Michigan State University, East Lansing, Michigan (Mani) CVM, Michigan State University, East Lansing, Michigan (Casolari)
Abstract	Sepsis is a serious concern in the equine field as it is major cause of death in neonatal foals that is usually accompanied by bacteremia. The current method to determine the cause of sepsis is a blood culture. However, it takes at least 24 hours to provide a result and is not always accurate. The development of a Real-Time PCR (RT-PCR) test could provide a quicker diagnosis, in one to two hours, that could be used to prescribe suitable antibiotics. This study aims to analyze a newly developed RT-PCR to determine if it can accurately detect pathogenic DNA extracted from spiked equine blood which is used to simulate blood from septic neonatal foals. We hypothesized that a Real-Time PCR could detect the presence of bacterial DNA extracted from equine blood the same as it can from DNA extracted from pure, lab grown bacterial cultures. A diagnostic analysis study was performed on a newly developed RT-PCR created to detect seven bacterial species, an equine DNA control, and a 16S control. The bacterial species included in the study were selected based off prior research on sepsis in neonatal foals. Healthy horse blood was spiked with 1-2 bacterial species. Then DNA was extracted, and a Real-Time PCR was run. The data was analyzed by determining the sensitivity (Se), specificity (Sp), positive predictive value (PPV), negative predictive value (NPV), and accuracy (ACC) of the RT-PCR to detect the DNA. The ability of the test to detect DNA from spiked horse blood was not the same as DNA extracted from lab grown cultures. However, it could detect gram-negative and gram-positive bacterial DNA alone or in combination from spiked horse blood. The results indicate its potential for use in sepsis cases involving neonatal foals.
Research Grant	Research Grant: Endowed Research Funds Project Grant College of Veterinary Medicine-Michigan State University
Field of Research	Equine Medicine and Surgery

Abstract Title	Modeling Traumatic Brain Injury
Authors	Christine E. Cassen, Shirley X. Guo-Ross, Angela K. Ross, Kendall N. McKinnon, Layne K. Jourdan, Noah A. Martin, and Russell L. Carr
Affiliations	Center for Environmental Health Sciences, Department of Comparative Biomedical Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS
Abstract	Traumatic brain injury (TBI) occurs when a violent external assault causes brain damage. Commonly occurring in sports, the battlefield, and car accidents, TBI results in the hospitalization of around 250,000 individuals and 69,000 deaths in the United States annually. Following injury, the timing and availability of treatment can determine the extent of physical, cognitive, and socioeconomic costs. The purpose of this research is to develop novel therapeutics to treat TBI that can be administered as a nasal spray formulation, allowing rapid administration post-concussion. The first step is the development of a TBI model that can serve as a template for further research; we utilized a user-friendly platform weight-drop device that can induce TBI in a rat without surgical or pre-injury manipulations, allowing a true TBI to be more accurately mimicked. Following anesthesia, 54 adult male rats were administered impact levels of either 2.5J, 2.0J, 1.5J, 1.0J, 0.5J, or Sham (no impact), with 9 rats per group. After impact, anti-sedative and pain medications were administered. At 3, 7, and 14 days, 3 rats per impact level were sampled and the hippocampus was collected. Western blot analysis was used to quantify the levels of glial fibrillary acidic protein (GFAP), a marker for astrocyte activation, and neuron-specific enolase (NSE), a marker for neuronal damage. Maximum NSE levels occurred 3 days post-impact, whereas maximum GFAP levels occurred at 7 days. The levels of both markers increased with the impact levels but plateaued at higher levels. An impact level of 2.0J was determined to be the optimum level to use in future experiments to test the effectiveness of novel nasal spray formulations to treat TBI-induced damage.
Research Grant	Funding provided by Halberd Corporation, Jackson Center, PA.
Field of Research	Pharmacology and Toxicology

Abstract Title	Metabolic and lipid profiling of captive cheetahs (Acinonyx jubatus)
Authors	Hannah Cavanaugh, Emily Nunan, Hayley Rejcek, Margaret Marsh, Hugo González-Jassí, Benjamin Alcantar, Carlos Sanchez, João Brandão, Joshua T. Butcher
Affiliations	Department of Physiological Sciences (Cavanaugh, Nunan, Marsh, Butcher) and Department of Veterinary Clinical Sciences (Rejcek, González-Jassí, Brandão), College of Veterinary Medicine, Oklahoma State University, Stillwater, OK, Wildlife Safari (Alcantar), Winston, OR, Oregon Zoo (Sanchez), Portland, OR
Abstract	Cheetahs are known for their phenomenal fitness, being one of the fastest animals on earth. However, little is known regarding their overall lipid and metabolic profiles, and the effects of a sedentary lifestyle occurring with captivity. This knowledge may have clinical relevance as the major cause of mortality in captive cheetahs is due to glomerulonephropathies, with currently available detection methods having well-characterized limitations (e.g. SDMA, BUN). The goal of this project is to assess adiposity in correlation with novel biomarkers to inform on the overall risk for development of renal disease. Eight captive cheetahs at the Wildlife Safari (Winston, Oregon) were assessed via a noninvasive bioelectrical impedance analysis instrument, along with body condition scores, glucose, with plasma also being opportunistically collected. IDEXX and plasma lipid profiles were obtained for each cheetah, along with brain natriuretic peptide, irisin, 8-isoprostane and myostatin by ELISA. Cheetahs were statistically organized into three bins based on their average ventral BMI and then correlations to biomarkers of interest were examined. Analysis is ongoing but currently there are significant correlations ($R2 > 0.90$) between ventral adiposity and plasma markers including glucose (assessed by AlphaTrak), creatinine, total protein, chloride, anion gap, and AST. SDMA was negatively correlated with ventral adiposity. Taken together, this project serves to build a more comprehensive metabolic and lipid profile in captive cheetahs. It also identifies several novel biomarkers of renal function that correlate with ventral adiposity and that could inform on the early development and progression of renal disease in captive cheetahs.
Research Grant	NIA K01 AG064121, OCAST HR21-045-1, and the Debbie and Wayne Bell Professorship
Field of Research	Exotic Pets and Zoo Animal Medicine

Abstract Title	MULTI-YEAR HEALTH ASSESSMENT OF BLUE-FOOTED BOOBIES (SULA NEBOUXII EXCISA) IN THE GALÁPAGOS ISLANDS
Authors	Ashley E. Cave, Jacqueline R. Dillard, Catalina Ulloa, Juan-Pablo Muñoz-Pérez, Alice Skehel, Diane Deresienski, Ronald K. Passingham, Jason Castaneda, Gregory A. Lewbart, Carlos A. Valle.
Affiliations	NC State University, Raleigh, NC, USA (Dillard, Passingham, Lewbart, Deresienski), Universidad San Francisco de Quito (USFQ) and UNC at Chapel Hill (Ulloa, Muñoz-Pérez, Skehel, Valle), Universidad San Francisco de Quito USFQ, Quito, Ecuador (Ulloa, Valle), University of the Sunshine Coast, Sippy Downs, Australia (Muñoz-Pérez)
Abstract	The Galápagos blue-footed booby (Sula nebouxii excisa) is a sulid subspecies native to the Galápagos archipelago. Here we present physical examination, hematology, and blood chemistry results from 60 Galápagos blue-footed boobies that were captured by hand from their nests on North Seymour Island in June 2017 and July 2022. A portable blood analyzer (iSTAT) was used to obtain values in the field for hematocrit, hemoglobin, sodium, potassium, chloride, ionized calcium, total CO2, glucose, blood urea nitrogen, creatinine and anion gap for each bird. Blood lactate, total solids, PCV and blood smears were evaluated manually on site. A white blood cell differential was performed in 2017. The breeding status of each bird and the number of chicks in the nests were also recorded. Total CO2, blood urea nitrogen, ionized calcium, potassium, anion gap, hematocrit, and hemoglobin were all higher in 2022 than 2017. There were also more nests with chicks in them in 2022 than in 2017. Lactate, ionized calcium, hematocrit, and hemoglobin were all higher in females than in males, while blood urea nitrogen was higher in males than in females. These results provide a multi-year reference to the baseline health parameters in a free-living population of Galápagos blue-footed boobies that can be used to compare and monitor the health status of this species.
Research Grant	Authorized by the Galápagos National Park Service and with support of the Heska Corporation, the Galápagos Academic Institute for the Arts and Sciences (GAIAS)-USFQ and the Galapagos Science Center
Field of Research	Wildlife Conservation

Abstract Title	A literature review of Peromyscus californicus
Authors	Jiayi Cen, Tobias Riede
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ (Cen); College of Graduate Studies, Midwestern University, Glendale, AZ (Riede)
Abstract	Peromyscus is a mouse model used in genetics, endocrinology, and renal physiology. To optimize housing, handling, and reproduction, the aim of this project was to (1) review existing knowledge about the life history of the California deer mouse (Peromyscus californicus) and (2) to review available data of a small colony that was maintained for three years. A freely accessible web search engine (Google Scholar) was used to identify relevant peer-reviewed articles. Six keywords were employed including P. californicus', habitat, reproduction, laboratory, animal model, and diseases. A retrospective analysis of colony-derived data (daily humidity, temperature, and number of pups born) was conducted on a small colony (between 10 and 15 pairs) maintained at Midwestern University between 2019 and 2022. The species' distribution in California appears to be related to the presence of dusky-footed woodrats (Neotoma fuscipes), accessibility of crevices in their surroundings, food availability, and water access. Both the review concerning laboratory housing and reproduction, as well as the assembly of colony-derived data, are ongoing. We hope to identify relevant aspects concerning the handling of deer mice under laboratory conditions and their reproduction. Additionally, we intend to explore whether there is a relationship between daily humidity, temperature, and number of live pups born into a small colony.
Research Grant	None
Field of Research	Laboratory Animal Medicine

Abstract Title	Anticoagulation assessment of rivaroxaban treatment in cats using viscoelastic coagulation monitor (VCM-Vet)
Authors	Calvin Cha, Avalene Tan, Rebecca Owen, Luke Wittenburg, Dallas Hollis, Joonbum Seo, Karl Jandrey
Affiliations	Department of Surgical and Radiological Sciences, School of Veterinary Medicine, University of California Davis, Davis, CA (Cha, Wittenburg, Hollis, Jandrey); School of Veterinary Medicine, Massey University, Palmerston North, New Zealand (Tan, Owen, Seo)
Abstract	Thromboembolism in cats can be a fatal sequela in several diseases. Point-of-care viscoelastic coagulation monitoring (VCM) could provide fast, reliable assessment of a cat's response to antithrombotic therapies. A randomized, double-blinded, placebo-controlled crossover trial was completed using healthy cats (n=12) in the Massey University Centre for Feline Nutrition. VCM was compared to standard coagulation tests in cats treated with rivaroxaban (RIV, 2.5mg) or placebo (control) orally every 24 hours for 3 days. Whole blood was collected at baseline (T0) and 3 hours after each treatment. Each cat acted as its own control after a 3-day wash-out period. At each timepoint, the following were measured: packed cell volume/total protein (PCV/TP), manual platelet count, and viscoelastic coagulation (using the VCM). Citrated plasma was frozen at -80°C for subsequent batch analysis of anti-Xa activity, prothrombin time (PT), activated partial thromboplastin time (aPTT), fibrinogen, and RIV plasma levels using ultra performance liquid chromatography-mass spectrometry (UPLC-MS). We hypothesized that RIV-treated cats will result in detectable hypocoagulable changes, indicated by an increased clot time (CT), as well as correlate with increased anti-Xa activity. Statistical analysis is ongoing. Visual trends are noted: anti-Xa activity and RIV plasma levels are increased in RIV-treated cats at T3, T27, and at T51 compared to T0. Multiple viscoelastic parameters will be evaluated at each timepoint and compared to the data above. It is the hope that these study results may be used to establish VCM as a fast, reliable, and accessible monitor for cats on anticoagulant therapy as well as prompt future studies using dual-therapy models.
Research Grant	Center for Companion Animal Health, UC Davis School of Veterinary Medicine; Emergency and Critical Care Endowment, UC Davis School of Veterinary Medicine
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Identification of apicomplexan target of triazine antiprotozoals and mechanism of drug-resistant coccidiosis
Authors	Xinyue Chai, Nicholas S. Nieto, Josh R. Beck
Affiliations	Department of Biomedical Sciences, College of Veterinary Medicine, Iowa State University, Ames, IA
Abstract	Triazines are antiprotozoal drugs used in veterinarian medicine primarily for treating coccidiosis and equine protozoal myeloencephalitis, both caused by obligate parasites in the phylum Apicomplexa. Anticoccidial use of triazines is often complicated by drug resistance within parasites, and the lack of knowledge on the mechanisms of action impairs stewardship of these important therapeutics as well as the development of more effective drugs. Triazines are also effective against other apicomplexans, including the human malarial parasite Plasmodium falciparum. Making use of the genetic tractability of P. falciparum, we aim to evolve triazine resistance in this apicomplexan model and identify resistance-conferring mutations by whole genome sequencing to identify putative targets or resistance mechanisms. Before starting the in vitro directed evolution of triazine-resistant parasites using sublethal drug concentrations, we employed a cell-based parasite killing assay that utilizes a fluorescent DNA/RNA binding dye and flow cytometry to measure IC50 values for the triazines used in this project, including diclazuril and toltrazuril. We report IC50 values in the low micromolar range for the triazines tested. Whole genome sequencing will be performed on the triazine-resistant parasites to identify the mutations of interest. Further, reverse genetic approaches will verify that candidate mutations are resistance-conferring in an isogenic parasite background, prioritizing mutations within genes that are conserved between Plasmodium and relevant coccidial species. Ongoing work results will be discussed.
Research Grant	Iowa Livestock Health Advisory Council Seed Grant Program
Field of Research	Parasitology

Abstract Title	Comparing Immune Responses of Young and Old Horses Infected with EHV-1 in Peripheral Blood Mononuclear Cells
Authors	Danielle L. Chorba, Kim Giessler, and Gisela Soboll Hussey
Affiliations	Department of Pathology and Diagnostic Investigation, College of Veterinary Medicine, Michigan State University, East Lansing, MI
Abstract	Equine herpesvirus-1 (EHV-1) myeloencephalopathy (EHM) is a significant disease affecting horses of all ages. Interestingly EHM occurs in only up to 10% of infected young horses. In contrast neurological disease can occur in up to 70% of infected horses older > 15 years. We hypothesize that this may be due to the fact, that older horses display a proinflammatory bias in their immune response to EHV-1. Because a viremia is critical in EHM pathogenesis, our objective was to compare the immune response in peripheral blood mononuclear cells (PBMCs) of old and young horses infected with EHV-1. Nine old horses (>20 years) and nine young horses (2 years) were infected with a neuropathogenic strain of EHV-1 and observed for 21 days post infection. Nasal viral shedding and cell-associated viremia were quantified by qPCR. In addition, cytokine and chemokine responses were assessed in PBMCs by real-time PCR and in nasal secretions by Luminex assay . All nine young horses developed respiratory symptoms, but only one horse displayed ataxia. In contrast, all older horses developed EHM, but no old horse showed respiratory disease. Protection from EHM was associated with an early upregulation of IFN-α (nasal secretion), IRF7/IRF9, IL-1β, CXCL10, and Tbet (PBMCs) and an IFN-γ upregulation during viremia (PBMCs). In contrast, horses affected by EHM showed a delayed interferon response, and significantly higher IL-10 levels. Determining how to shift these immune responses in “at risk” horses by vaccination will be critical to protect horses from this devastating disease in the future.
Research Grant	USDA
Field of Research	Immunology

Abstract Title	Investigating the presence of canine distemper virus in free-ranging skunks in Prince Edward Island, Canada
Authors	Savannah M. Christmas, Amanda Clark, Laura Bourque, Megan E.B. Jones, and Russell S. Fraser
Affiliations	Department of Pathology & Microbiology, Atlantic Veterinary College, University of Prince Edward Island, Prince Edward Island, Canada (SMC, AC, LB, MEBJ, RSF) Canadian Wildlife Health Cooperative, Atlantic Region, Atlantic Veterinary College, University of Prince Edward Island, Prince Edward Island, Canada (AC, LB, MEBJ)
Abstract	Canine distemper virus (CDV), also known as canine morbillivirus, is an RNA virus that affects various canid species and carnivores worldwide, with a mortality rate of ~50 % in unvaccinated dogs. Free-ranging skunks with CDV typically present with a history of neurologic or respiratory signs, weakness/lethargy, or sudden death. These clinical signs overlap with those seen in other diseases, including skunk adenovirus-1 (SkAdv-1), an emerging pathogen in Canadian skunks. Skunk adenovirus-1 is a DNA virus that infects numerous wildlife species, sometimes causing necrotizing bronchointerstitial pneumonia and tracheitis. In a previous study, skunk samples were screened for SkAdv-1, which was not detected in skunks with pulmonary lesions (n = 5). This study aims to screen spleen and lung samples from free-ranging, SkAdv-1 negative skunks in Prince Edward Island (PEI), Canada, for CDV. The hypothesis is that skunks with respiratory lesions negative for SkAdv-1 will be positive for CDV. A complete postmortem examination was performed on free-ranging skunks submitted to the Canadian Wildlife Health Cooperative, Atlantic Region, between 2020 and 2022, with duplicate tissue samples collected in formalin and stored at -80 ℃. Lung and spleen from 49 skunks from PEI will be screened for CDV using RT-PCR. First, raw RNA is extracted from the tissues and DNase-treated to remove genomic DNA contamination. Next, DNase-treated RNA is reverse-transcribed into complementary DNA and then undergoes PCR. The results of the PCR are visualized using gel electrophoresis. The results of this study will help further define the range of pathogens present in the free-ranging skunk population of PEI.
Research Grant	Discretionary funds (Dr. Russell S. Fraser), AVC Internal Research Grant, & PEI Wildlife Conservation Fund
Field of Research	Virology

Abstract Title	Expression of Adhesion Proteins in Low-Grade and High-Grade Canine Soft Tissue Sarcomas
Authors	Emma Christopher, Cambri Moeller, Lauren Guarneri, Emi Sasaki, Sita Withers
Affiliations	Department of Veterinary Clinical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	Soft tissue sarcomas (STS) are cancers of mesenchymal origin that can be divided into low-grade or high-grade tumors. High-grade tumors are more likely to metastasize and recur after incomplete surgical excision. Due to STS being more common in dogs than humans, dogs can serve as an excellent model for studying STS. One strategy utilized by cancer cells in metastasis is epithelial-to-mesenchymal transition (EMT) and its reverse process, mesenchymal-to-epithelial transition (MET). We hypothesized that high-grade canine STS would downregulate transcripts and proteins involved in cell adhesion and epithelial differentiation, and upregulate markers of mesenchymal differentiation. We identified 11 low-grade (grade 1 or 2) STS, and 11 high-grade (grade 3) STS from the tissue archives at the Louisiana Animal Disease Diagnostic Laboratory (LADDL). Transcriptomic analysis was performed using the nCounter Canine IO panel on the SPRINT profiler (Nanostring). Immunohistochemistry was performed to detect expression of adhesion proteins (epithelial cellular adhesion molecule (EpCAM) and E-cadherin), markers of epithelial differentiation (cytokeratin 7 and 14 (CK7 and CK14)), and a marker of mesenchymal differentiation (vimentin). Whole-slide imaging was performed using NanoZoomer imaging technology, and images were analyzed with QuPath software. Preliminarily, mRNA expression of EpCAM, E-Cadherin, CK7, and CK14 appears downregulated in high-grade STS when compared to low-grade STS. Analysis of protein expression via immunohistochemistry is ongoing. These data may further our understanding of the mechanisms that potentiate the aggressive clinical course of high-grade canine STS.
Research Grant	American Kennel Club Canine Health Foundation
Field of Research	Oncology

Abstract Title	Isolation and culture of equine glandular stomach for model development
Authors	Faith Church, Anthony Blikslager, Amy Stieler Stewart
Affiliations	Department of Molecular Biomedical Sciences (Church, Stewart) and Department of Clinical Sciences (Blikslager), College of Veterinary Medicine, North Carolina State University, Raleigh, North Carolina
Abstract	Equine Gastric Ulcer Syndrome is classified into Equine Squamous Gastric Disease (EGSD) and Equine Glandular Gastric Disease (EGGD). Diagnosis of EGGD is increasing with a prevalence of up to 65%. Despite this, the exact pathophysiology of EGGD remains unknown and the therapeutics available for ESGD are often less effective. Development of an in vitro model of the equine glandular stomach would be invaluable to investigate EGGD mechanisms and test novel therapeutics. Glandular stomach was collected from horses without gastrointestinal disease via endoscopic biopsy (n=1) or immediately following euthanasia (n=5). Epithelial cells (glands) were isolated, plated into a 3D matrix, and supplemented with growth factors. Resultant gastric organoids were cultured for a total of 5-10 days. Mature gastric organoids were exposed to control or acidic media (pH ~3.5) for 15 minutes, 3 times daily for 3 days, totaling 9 exposures. Culture media was collected and frozen for analysis of the proinflammatory cytokines TNF-α and IL-8. Gastric glands were successfully isolated and cultured from both endoscopic biopsies and full thickness tissue samples. Following acid exposures, the gastric organoids subjectively appeared normal, however the surrounding matrigel was visibly disrupted. Preliminary data did not indicate production of TNF-α or IL-8 via ELISA. Equine glandular stomach can be cultured in vitro, however the current model failed to demonstrate production of proinflammatory cytokines following acid exposure. Future investigation is needed to optimize the protocol, including the use of a 2D-monolayer and additional caustic agents (bile salts and/or NSAIDs).
Research Grant	NC State University Office of the Associate Dean for Research and Graduate Studies Fund for Discovery
Field of Research	Equine Medicine and Surgery

Abstract Title	Development of a FACS panel to monitor lymphocyte responses to SARS-CoV-2 MA10 infection during vaccination.
Authors	Ethan Ciannamea, Victoria Primavera, Jonathon Stone, Dan. H. Barouch, & Amanda J. Martinot
Affiliations	Dept of Infectious Diseases and Global Health (Ciannamea, Primavera, Stone, Martinot), Tufts University Cummings School of Veterinary Medicine, North Grafton, MA and Center for Virology and Vaccine Research (Barouch), Beth Israel Deaconess Medical Center, Harvard Medical School, Boston, MA
Abstract	COVID-19 mortality is linked to SARS-CoV-2-mediated cytokine storm. Cytokine storms are defined by extensive secretion of pro-inflammatory cytokines by immune cells in response to viral replication. In studies evaluating the outcomes of COVID-19 cases, researchers found that IL-6 and IL-10 play a significant role in the development of cytokine storms. Recent studies describe a new type of humoral immune cell that may impact the development of cytokine storms, the regulatory B-cell (Breg). Although Bregs are traditionally thought to play an immunosuppressive role due to secretion of IL-10, they can also secrete the pro-inflammatory cytokine IL-6 which may impact down-stream expansion of Th17 cells and T regulatory cells (Tregs) and influence the magnitude of the immune response during infections. We wanted to profile B cell development during vaccination versus natural infection with the mouse-adapted SARS-CoV-2 virus (MA10) to better understand the phenotypes of B cells during COVID-19 infection. We hypothesized that vaccinated mice would have more Bregs expressing IL-10 while B cells induced during natural infection secrete more IL-6. To test this hypothesis, we developed a targeted flow cytometry panel to profile B cells in mice vaccinated with a rhesus adenoviral (RhAd52) Spike construct as compared to unvaccinated challenged with SARS-CoV-2 MA10. We examined B cells from the spleens of naïve, vaccinated, and boosted C57BL/6 and BALB/c mice using a FACS panel to measure CD3, CD93, IgM, and IgD and intracellular cytokine staining for IL-10 and IL-6 to characterize B-cell expansion during vaccination and COVID infection in mice.
Research Grant	K08 135098-01A1
Field of Research	Immunology

Abstract Title	Neuronal Patterns May Mediate Stress-Related Opioid Dependency
Authors	Bridget Cincotta, Emma Tyner, Julie Blendy
Affiliations	Department of Pharmacology, Perelman School of Medicine University of Pennsylvania, Philadelphia, PA
Abstract	While humans experience various forms of stress each day, how individuals respond to such stress differs greatly. Recent research suggests individuals can be categorized into those who demonstrate a resilient phenotype as they adapt well to stress and those who display a susceptible phenotype as they develop maladaptive coping behaviors (Cathomas et al., 2019). Limited research has explored the underlying mechanisms for such a distinction, yet many harmful disorders, such as affective and substance abuse disorders, can result from maladaptive stress responses. In the present study, we used a murine model to examine if differences in neuronal circuitry can help account for differences in the phenotypes displayed in response to stress. Sixteen male C57BL6 mice were subjected to chronic social defeat stress for 10 days to mimic chronic stress. At the end of the paradigm, the mice underwent a social interaction test with video analysis to determine which stress response phenotype each mouse displayed. Two mice died throughout the paradigm; 6 mice displayed a resilient phenotype whereas 7 demonstrated a susceptible phenotype; 1 outlier was removed. All mice were then injected with morphine then anesthetized and perfused 90 minutes later to allow time for protein expression of c-FOS, a marker of neuronal activity. The mouse brains were then extracted, frozen, and sliced into 30-micron sections on a cryostat. Immunohistochemistry staining and image analysis will be conducted on the mounted brain slices to detect c-FOS. It is expected that c-FOS expression patterns will vary between mice displaying a resilient versus susceptible phenotype, indicating neurocircuitry differences underpinning these stress response phenotypes.
Research Grant	R01 DA-047743 (J.A.B) R01 DA-054374 (J.A.B)
Field of Research	Pharmacology and Toxicology

Abstract Title	Identifying the role of GATA6 in human adrenocortical development using a human iPSC-derived organoid system
Authors	Robert Z. Cochran, Michinori Mayama, and Kotaro Sasaki
Affiliations	Department of Biomedical Sciences, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA
Abstract	In humans, organogenesis of the embryonic adrenal cortex results in the establishment of two distinct steroidogenic (NR5A1+) zones: the peripheral definitive zone (DZ) and the central fetal zone (FZ). Previous studies of fetal adrenals (FAds) using rodent models showed reduced translatability. To overcome this, the Sasaki lab has developed a novel human fetal adrenal organoid (hFAO) system generated via stepwise induction of human-induced pluripotent stem cells. Despite reduced translatability, several murine studies have revealed data that can be applied to the hFAO model. Murine studies show that the GATA family of transcription factors play a key role in specification of steroidogenic lineages. One member of this family, GATA4, has been shown to work synergistically with NR5A1 to confer gonadal specific steroidogenic gene expression. However, studies show that GATA6, but not GATA4, is expressed in the developing adrenal cortex in humans and mice, and Gata6 mutant mice developed hypoplastic adrenals. In humans, homozygous GATA6 mutation has not been reported, likely due to embryonic lethality. We hypothesize that homozygous knockout (KO) mutations of GATA6 in hFAOs will markedly decrease the level of steroidogenesis and subsequently downregulate GATA6 targeted genes. Using GATA6 mutant hiPSC lines and their isogenic control lines, we induced hFAOs, measured steroid synthesis, and completed qPCR at various stages of development to identify target genes of GATA6. Results show GATA6 KO hFAOs have reduced steroid production. Moreover, steroidogenic enzyme gene expression is reduced in GATA6 KO compared to controls, while expression of NR5A1 shows no difference between GATA6 KO and control.
Research Grant	Open Philanthropy/Good Ventures Foundation (# 10080664)
Field of Research	Physiology

Abstract Title	Engineering chimeric antigen receptor (CAR) lymphocytes to target feline infectious peritonitis virus
Authors	James R. Cockey, Emily Kulp, Natalia Lopez-Barbosa, Christian Urbina, Gary R. Whittaker, Matthew P. DeLisa, and Cynthia A. Leifer
Affiliations	Department of Microbiology & Immunology, College of Veterinary Medicine (Cockey, Urbina, Whittaker, and Leifer), Robert Frederick Smith School of Chemical and Biomolecular Engineering (Lopez-Barbosa and DeLisa), Cornell University, Ithaca, NY
Abstract	Feline infectious peritonitis (FIP) is caused by infection of an internally mutated form of feline coronavirus that disseminates systemically and is invariably fatal. Although antivirals such as protease inhibitors and nucleoside analogs have been investigated, currently none are FDA approved treatments for veterinary use. Thus, there is an urgent need for an alternative treatment modality. One such alternative is chimeric antigen receptor (CAR) T cell therapy. CAR T cell immunotherapy has been remarkably successful in treating certain human cancers, but has not yet been developed for acute viral infections like FIPV, nor used at all in cats to date. The goal of this study is to design a novel immunotherapy targeting cells infected with FIP virus (FIPV) and thus expressing surface spike protein that can be detected by CAR-engineered immune cells. Here we have designed a CAR specific for FIPV spike protein, and confirmed both specificity and efficacy as seen by CD69 upregulation in transduced Jurkat T cells when cocultured with spike+ target cells. We also optimized the enrichment strategy and growth conditions of primary feline T cells for ex vivo expansion. We successfully transfected plasmid DNA into primary feline T cells, and successfully enriched feline NK cells from peripheral blood using a similar strategy as T cells. Completion of this study will provide proof-of-principle data using an FIPV model to support the development of FIPV CAR-cell therapy for this devastating disease in cats, and will also determine the feasibility of developing a CAR-based immunotherapy for the potential treatment of acute viral infections in humans or other diseases in cats for which there are few treatment options, such as lymphoma.
Research Grant	Cornell Feline Health Center
Field of Research	Immunology

Abstract Title	Determining the pharmacokinetic properties of two different doses of hydromorphone in barred owls (S. varia)
Authors	Maryella Cohn, Mark Mitchell, Kimberly Boykin, Haerin Rhim, Laken Russell
Affiliations	Veterinary Clinical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	Currently, avian medicine lacks research based species specific analgesic protocols, and to date there are no published pharmacokinetic studies on barred owls (Strix varia). This study seeks to determine the pharmacokinetic properties (harmonic means, times to maximum concentration, and elimination half-lives) for single intramuscular doses of 0.5 mg/kg and 1.0 mg/kg hydromorphone in 12 fledged barred owls. We hypothesize that both will provide appropriate concentrations for 12 hours and that there will be significant differences in the pharmacokinetic properties between both doses of hydromorphone in barred owls. Each owl must be >500g and will be prescreened to ensure they have a PCV >30% and a WBC estimate <30,000 cell/mL. Owls were randomly assigned to Group 1 (0.5mg/kg) or Group 2 (1.0mg/kg) doses and baseline bloodwork was drawn before hydromorphone was injected IM into the left pectoral muscle. After the injection, subsequent blood samples were collected 5 minutes, 30 minutes, 1.5 hours, 3 hours, 6 hours, 9 hours, and 12 hours later. Once all 12 owls undergo this process, an additional 10 mL of blank plasma will be collected from 5 barred owls (2 mL/bird) not participating in the trial to establish the column for the high-pressure liquid chromatography. All samples will be mailed on ice to the North Carolina State University College of Veterinary Medicine Clinical Pharmacology Lab to measure the plasma hydromorphone concentrations using high-performance liquid chromatography. At this time, samples have been collected from 10 owls and we are expecting to see maximum concentrations around 1.5-3 hours post injection of hydromorphone.
Research Grant	Morris Animal Foundation Veterinary Student Scholar fund
Field of Research	Wildlife Conservation

Abstract Title	Effects of Clodronate on equine monocyte-derived macrophages
Authors	Zoey Cole, Abigail Loucks, and Aimee Colbath
Affiliations	Cornell University College of Veterinary Medicine
Abstract	Clodronate disodium (CLO) (Osphos®, Dechra, KS, USA), is labelled for the treatment of equine navicular syndrome, the leading cause of chronic forelimb lameness in performance horses. Further, CLO has been shown to reduce lameness and pain in other equine musculoskeletal conditions. Despite its widespread use, it is unclear whether CLO has a direct anti-inflammatory effect in the joint. A recent study in horses found no measurable anti-inflammatory effect of CLO on synoviocytes or chondrocytes stimulated with recombinant equine interleukin-1β (reqIL-1β) while studies in humans have suggested that bisphosphonates, such as CLO, may cause immune cell modulation. Macrophages play a critical role in joint inflammation and homeostasis. Therefore, the objective of this study is to determine the effect of CLO on equine monocyte-derived macrophages in vitro. We hypothesized that exposure of macrophages to CLO would result in an anti-inflammatory phenotype. Monocytes were isolated from equine peripheral blood mononuclear cells and cultured in media with M-CSF in PermaLife cell culture bags for 6 days. Monocyte derived macrophages were then subjected to increasing concentrations of CLO alone and in combination with reqIL-1β; a media control and reqIL-1β control were also performed. The cell culture media was assessed for chemokine production using a multiplex assay. Cells were harvested and stored using RNA Later for qPCR. By investigating the effects of clodronate on equine monocyte-derived macrophages, this study aims to provide a better understanding of the underlying anti-inflammatory mechanisms of clodronate within the joint and its potential applications in veterinary medicine. Results currently need further analyzation.
Research Grant	USDA NIFA (#2020-05281)
Field of Research	Equine Medicine and Surgery

Abstract Title	Are blood serum-derived extracellular vesicles a viable Chronic Wasting Disease peripheralization mechanism?
Authors	Jesse Cole1, Erin McNulty, Audrey Sandoval, Amy Nalls, Joseph Westrich, Candace Mathiason
Affiliations	Dept. of Microbiology, Immunology, and Pathology, Colorado State University
Abstract	Chronic Wasting Disease (CWD) is a rapidly spreading, fatal neurodegenerative or prion disease of cervid species (deer, elk, moose and reindeer). CWD is the most efficiently transmitted of all the prion diseases and is currently detected in captive and free-ranging cervid populations in 30 U.S. States, 4 Canadian Provinces, Europe, and Asia. The effective transfer of CWD among cervids has been largely attributed to horizontal transmission by direct animal-to-animal contact via exchange of bodily secretions (saliva, blood, urine and feces), and by indirect contact with the infectious agent shed in these products to the environment. Prions have been detected in blood, as well as within the pregnancy microenvironment and fetal tissues harvested from CWD-infected cervids. To further investigate CWD peripheralization mechanisms and how prions traffic across the placental barrier, we are assessing the role blood serum-derived extracellular vesicles may play in these processes. Here, EVs were isolated from blood serum collected from experimentally CWD-infected white-tailed deer. Nanoparticle tracking analysis (NTA) was performed to quantify the size distribution and concentration of EV isolates. We are further assessing EV isolates for the presence of prions by western blot (PrPSc) and real-time quaking induced conversion (RT-QuIC) (amyloid seeding activity). These studies will provide the basis for continued studies determining CWD peripheralization in the host, and permit further investigation of EVs as a potential biomarker for CWD diagnostic testing.
Research Grant	NIH Medical Scientist Training Program (MSTP) T32 Fellowship and NIH–NIAD 2R01AI112956-06
Field of Research	Clinical Pathology

Abstract Title	Initial investigation into the effects of tissue plasminogen activator on intrasynovial tenocytes in vitro
Authors	Caitlyn V Coleman, Shannon S Connard, Drew W Koch, Anna M Froneberger, Lauren V Schnabel
Affiliations	Department of Clinical Sciences, North Carolina State University CVM , Raleigh, NC.
Abstract	In horses, tenosynovitis most commonly affects the digital flexor tendon sheath (DFTS). Injury to the deep and superficial digital flexor tendons (DDFT, SDFT) within the DFTS can result in the formation of intrasynovial adhesions, which carry a poor prognosis. Tissue plasminogen activator (TPA) is a commonly used anti-adhesive agent; however, its impact on tendon healing has yet to be investigated. The objectives of this study were to examine the effects of TPA, on equine DDFT- and SDFT-derived tenocyte 1) viability and proliferation, 2) gene and protein expression, and 3) migration in vitro. We hypothesized that TPA would not demonstrate cytotoxic effects on tenocytes or impair their proliferation capacity, migration ability, or gene expression. Briefly, DDFT- and SDFT-derived tenocytes were cultured in tenocyte media or tenocyte media containing clinically relevant doses of TPA. Cytotoxicity and proliferation were assessed using viability, population doubling, and proliferation assays. Gene expression will be evaluated using a multiplex immunoassay to quantify supernatant protein concentrations and NanoString nCounter Analysis System for transcriptional analysis. There were no significant effects of TPA on tenocyte viability or population doubling. Assays to evaluate tenocyte proliferation, gene expression, and migration are currently underway. Our initial findings suggest that TPA does not elicit any cytotoxic effects on tenocytes in vitro. The main limitation is that this study was performed in vitro. These findings will elucidate the effects of TPA on tenocytes in vitro and lay the groundwork to assess tendon healing, efficacy in adhesion prevention, and administration dose and frequency in vivo.
Research Grant	Fund for Orthopedic Research in honor of Gus and Equine athletes “F.O.R.G.E”
Field of Research	Equine Medicine and Surgery

Abstract Title	Biomarkers of brain injury in Foals with Neonatal Maladjustment Syndrome
Authors	Kinnidy Coley, Javier Perez Quesada, Jenna Schirmer, Katarzyna Dembek
Affiliations	North Carolina State University, Department of Clinical Sciences, College of Veterinary Medicine, Raleigh, North Carolina
Abstract	Neonatal maladjustment syndrome (NMS) is a common disease of neonatal foals resulting in neurological dysfunction and increased mortality. Historically, the central nervous system (CNS) damage was attributed to peripartum hypoxia and ischemia. However, post-mortem evaluation of these foals does not consistently show characteristic histological changes associated with hypoxia. Furthermore, foals with uncomplicated births can show similar behavioral changes which they spontaneously recover. Although several studies have investigated mechanisms involved in neuronal pathology in neonatal foals, the exact pathogenesis of NMS and diagnostic options are not well described. Therefore, the goal of this study is to measure blood biomarkers associated with neuronal damage in foals with NMS, healthy foals, and foals with other disorders to evaluate their association with the clinical signs of NMS and survival. We hypothesize that the blood biomarkers of neuronal damage will be altered in foals with NMS and associated with disease severity and poor outcome. Blood samples were collected from 37 hospitalized foals and 6 healthy foals <7 days old on admission. Additional blood samples were collected on day 1, 2 and 5 of hospitalization. Blood concentration of brain-derived neurotrophic factor (BDNF), glial fibrillary acidic protein (GFAP), neuropeptide Y (NPY), and pigmented epithelium-derived factor (PEDF) were measured with ELISAs. Preliminary analysis revealed that PEDF and GFAP concentrations were lower in hospitalized foals with NMS and sepsis compared to healthy foals. This is clinically relevant since the pathogenesis of NMS is unknown and may aid in its diagnosis and provide novel therapeutic options in the future.
Research Grant	North Carolina State College of Veterinary Medicine Intramural Seed Grant and The Morris Animal Foundation
Field of Research	Equine Medicine and Surgery

Abstract Title	Evaluating host pathogen interactions of Bordetella bronchiseptica and Bordetella pertussis using ALI
Authors	Amelia Collins, Amanda D. Caufield, Dr. Eric T. Harvill, Dr. Tom Krunkosky
Affiliations	Department of Infectious Diseases (Harvill, Caulfield), Department of Biomedical Sciences (Krunkosky), College of Veterinary Medicine, University of Georgia CVM, Athens, GA
Abstract	The genus Bordetella contains many common respiratory disease-causing pathogen species in both humans and animals. Bordetella pertussis (Bp) and Bordetella bronchiseptica (Bb) cause Whooping cough in humans and Kennel cough in dogs, respectively. Bp and Bb reside in the respiratory tract and tightly adhere to epithelial cells during infection. Previous in vitro model systems used to evaluate the host-pathogen interactions occurring at this critical interface have not use polarized epithelial cells that simulate the human natural respiratory tract. This study utilizes an Air-Liquid-Interface culture system (ALI) using human broncho-tracheal (NHBE) cell cultures replete with cilia, goblet cells, mucus, and sol layers to evaluate how these pathogens interact with their niche: the ciliated epithelium that lines the mammalian airways. This study utilizes a highly virulent circulating strain of Bp (D420) and two isogenic mutant strains lacking key virulence factors (btrS and pertussis toxin) to evaluate tight junction integrity via trans-epithelial electrical resistance, bacterial growth on the apical surface, migration through the epithelium to the basal media, bacterial attachment & localization, and pro-inflammatory cytokine responses to infection. The data generated from these studies will reveal the roles of specific Bordetella virulence factors in various measurable aspects of their interactions with ciliated respiratory epithelia.
Research Grant	National Institute of Allergy and Infectious Disease:1R21AI171346-01A1
Field of Research	Bacteriology

Abstract Title	Physiologic and behavioral effects following long-acting transdermal and subcutaneous buprenorphine in rats
Authors	Elijah J. Collins, Tracy L. Baker, and Rebecca A. Johnson
Affiliations	Department of Surgical Sciences (Collins, Johnson) and Comparative Biosciences (Baker), School of Veterinary Medicine, University of WI-Madison, Madison, WI
Abstract	Effective analgesia for rats frequently includes standard buprenorphine, a partial mu-opioid agonist lasting 6-8 hrs. Novel, longer-acting buprenorphine preparations are available; however, investigations concerning physiologic (ventilatory, thermoregulatory, etc.) and behavioral (food intake, pica behavior, etc.) effects in rats are sparse. The objective was to investigate physiology and behavior associated with new buprenorphine formulations in rats. Ethiqa XR (0.65 mg/kg SC; n=6), Zorbium (10 mg/kg transdermal; n=7), and appropriate controls (n=7) were given to male rats in a randomized, cross over design. Ventilation, body temperature, thermal antinociception, food/kaolin intake, and fecal output were measured 1-72 hrs post-treatment. We hypothesized that both preparations would produce antinociception, hyperthermia, reduced food intake/fecal output, and ventilatory depression for 48 hrs, returning to pre-treatment levels by 72 hrs. Overall antinociception in both buprenorphine groups differed from the control group (all $p<0.05$). Body temperatures were elevated in both buprenorphine groups from 4-24 hrs (all $p<0.05$). Food intake in the dark period was decreased from 24-72 hrs and fecal output reduced in both light/dark periods for 24 hrs following both preparations (all $p<0.05$); kaolin intake did not differ between any group (all $p>0.05$). Self-aggression was higher in both buprenorphine groups from 4-12 hrs and sedation was associated with Zorbium at 12 and 24 hrs (all $p<0.05$). Ventilation remains to be analyzed. This study provides evidence that newer, long-acting buprenorphine preparations may provide analgesia for both client owned and laboratory rats, but untoward physiologic effects need to be considered.
Research Grant	UW Veterinary Medicine Companion Animal Fund and laboratory funds from Dr. Tracy L. Baker and Jyoti J. Watters
Field of Research	Laboratory Animal Medicine

Abstract Title	Use of Gallium Nitrate as an Alternative to Antimicrobial Treatment of Equine Endometritis
Authors	Allison Conchiglia, Kaushalya Jayathilake, Samantha Frontz, Marie Montelongo, Jennifer Rudd, and Dale Kelley
Affiliations	Department of Veterinary Clinical Sciences (Conchiglia, Jayathilake, Kelley) and Department of Veterinary Pathobiology (Frontz, Montelongo, Rudd), College of Veterinary Medicine, Oklahoma State University, Stillwater, OK
Abstract	Infectious equine endometritis is a leading cause of infertility in mares. The resulting infertility is caused by dysbiosis between commensal and pathogenic bacteria which leads to inflammation of the uterine lining and localized infection. Unfortunately, rates of antimicrobial resistance are rising in common equine uterine pathogens such as Escherichia coli, Streptococcus equi zooepidemicus, Pseudomonas aeruginosa, and Klebsiella pneumoniae, emphasizing the need to identify other compounds with antibacterial properties, such as Gallium. Structural similarities to iron make gallium indistinguishable to bacteria, allowing gallium to exhibit antimicrobial properties by inhibiting iron uptake. We hypothesize that gallium nitrate, a highly soluble crystalline form of gallium, reduces the bacterial concentration of common equine uterine pathogens in a dose-dependent manner. To investigate, equine uterine samples were cultured for bacterial isolation and identification of each isolate was confirmed via matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF). Only isolated pathogens identified as the four listed previously were utilized for testing the minimum inhibitory concentration (MIC) of gallium (n=4). In a 96-well plate, we set up 2-fold serial dilutions of gallium nitrate solution before adding each bacterial isolate that was suspended in a cation balanced iron-depleted Mueller-Hinton (ID-CAMH) broth at 10^5 CFU/mL. Three replicates per isolate were performed and the results were averaged to determine an in vitro MIC for gallium nitrate. This data allows for future studies testing the safety and efficacy of the solution as an antimicrobial compound for treatment of equine endometritis.
Research Grant	Grayson Jockey Club Foundation
Field of Research	Antimicrobial Resistance

Abstract Title	Non-invasive fur follicle collection and tail biopsy provide reliable, accurate genotyping for transgenic mice
Authors	Megan Conley, Mandy McGeachy, Meryem Outouil, and Elizabeth Lavin
Affiliations	Department of Microbiology and Immunology (Conley, McGeachy) and Center for Animal Resources and Education (Outouil, Lavin), Cornell University College of Veterinary Medicine, Ithaca, NY.
Abstract	Distal tail biopsy ("tail snipping") is a common method of tissue collection used to genotype transgenic mice, and its accuracy is well established in many laboratories that use transgenic mouse models. However, despite being performed before tail vertebrae ossification, tail snipping is associated with pain, distress, and hemorrhage in mice. This study investigated two less-invasive methods of tissue collection (fur follicle and buccal swab) and compared their genotyping accuracy to that of tail snipping. Sixty-three mice less than twenty-one days old from six transgenic strains were sampled using all three methods at the time of ear tagging. The samples were digested using alkaline and thermal lysis, and a Nanodrop machine was used for DNA quantification (ng/µl) to determine if sufficient DNA was present for PCR. PCR was performed using the appropriate protocol for each mouse strain. The samples were processed via gel electrophoresis with wild type and strain-positive controls, and the specificity and sensitivity of each method was compared. Preliminary results indicate that fur follicle genotyping accuracy is comparable to that of tail snipping, despite lower DNA concentrations (90.91% correct genotyping). We were unable to obtain consistent data for buccal swabs in this study. Fecal sampling was originally planned, but practical considerations ruled this out due to wait times of 30 minutes per mouse. Future research should examine the genotyping potential of other samples, such as feces, and should investigate stress behaviors induced by sample collection to understand their impacts on animal welfare. In doing so, we can establish a genotyping collection method that optimizes genotyping accuracy and animal welfare.
Research Grant	None
Field of Research	Immunology

Abstract Title	Assessment of teleneurology and its accuracy in neurolocalization during a veterinary neurologic exam
Authors	Brett Connolly, Richard Shinn
Affiliations	Virginia Maryland College of Veterinary Medicine, Blacksburg, VA
Abstract	Telemedicine is becoming increasingly prevalent within veterinary medicine practices. Radiologists, cardiologists, and pathologists have successfully implemented telecommunication practices for consultations for decades. The advancement of telehealth in other specialty branches of veterinary medicine promises a better overall standard of care to patients. To appropriately incorporate different telecommunication modalities into routine practice an assessment of the overall accuracy must be performed in specific veterinary fields. The accuracy of telemedicine in veterinary neurology consultations, specifically, the neurologic exam and neurolocalization, has yet to be pursued. Our study consists of two groups both simulating two different modalities within telemedicine. Group 1 consists of a prerecorded video that a veterinary neurologist (VN) will review and attempt to localize a lesion if present. Group 2 consists of a live video feed where the VN will have the ability to interact with the person performing the examination. The prerecorded videos show a Kappa coefficient of (0.84) supporting a significant correlation with in-person exams. To further support this evidence, a Chi-squared analysis was performed and resulting in a $p < 0.0001$ suggesting the results were not random. Our study concluded that telecommunication is highly accurate for basic neurological examinations and lesion localization. Further data in this study will be examined to include our live video group. Our current results suggest the accuracy of telemedicine is sufficient in its use in veterinary neurology consultations and neurologic examinations.
Research Grant	NIH 2T350D011887-16
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Exploring the prevalence of infectious disease among newly purchased beef and dairy cattle in Ontario, Canada
Authors	Lilly Conteh, David Renaud, Cynthia Miltenburg, and Jessica Gordon
Affiliations	Large Animal Clinical Sciences, College of Veterinary Medicine, Michigan State University, East Lansing, MI (Conteh, Gordon); Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario (Renaud); Ontario Ministry of Agriculture, Food, and Rural Affairs, Guelph, Ontario (Miltenburg)
Abstract	The implementation of herd health management and biosecurity practices such as pre-purchase disease testing are crucial in preventing the introduction and spread of infectious disease among an operation when newly purchased cattle are brought into a herd from different geographical areas. This study aims to assess the prevalence of infectious disease among newly purchased beef and dairy cattle in the Ontario area and determine the level of pre-purchase testing carried out by producers to mitigate further spread of disease. The surveillance project was carried out from 2020-2021 on a total of 46 dairy farms and 3 cow-calf operations across Ontario, where blood samples were collected from a total of 355 animals by private veterinary practitioners. Samples were submitted to the Animal Health Laboratory in Guelph, Ontario where an ELISA antibody test was conducted to test for the presence of Anaplasma, Salmonella Dublin, Bovine leukemia virus (BLV), and Myobacterium avium susp. paratuberculosis (MAP) antibodies. Because these pathogens can often go undetected without appropriate testing and can lead to significant economic loss to an operation, their prevalence was investigated for this project. Data was also collected on whether the facility had purchased cattle within the last 5 years and whether testing was regularly conducted on newly purchased animals. Out of the 355 animals tested, 147 (41.4%) tested positive for at least one disease on the ELISA. The prevalence of Anaplasma, S. Dublin, MAP, and BLV among those infected was 0%, 2.7%, 4.8%, and 94%. Only 14.8% of farms tested cattle for disease prior to purchase, suggesting that farmers may not be aware of the infection risk to their herd and economic impacts involved.
Research Grant	Ontario Animal Health Network
Field of Research	Epidemiology

Abstract Title	Metabolic support to peripheral nerve regeneration
Authors	Aaron J. Cooper and John Svaren
Affiliations	Department of Comparative Biosciences (Svaren), University of Wisconsin-Madison School of Veterinary Medicine, Madison, WI (Cooper) Waisman Center, University of Wisconsin-Madison, Madison, WI (Svaren)
Abstract	Myelination plays a key role in the homeostasis of axons and their ability to conduct nerve impulses. Remyelination after injury is possible in peripheral nerves, but myelin sheaths generated are thinner. One reason may be metabolic since ketone bodies are abundant in the postnatal period of myelination, but their levels subside in adults. This project is focused on Schwann cell (SC) metabolism and the role of the lipogenic precursor acetyl CoA in the formation of myelin lipids and control of gene expression. SC's synthesize the bulk of myelin lipids, but the process for supplying acetyl CoA as a building block of myelin lipids remains undefined. Our overall model is that ketone bodies play a major role in myelin formation during development and their lack in adult nerves may impair regeneration after injury. Published studies have shown that ketogenic diets show beneficial effects in rodent models of myelin disorders and nerve injury. To examine if ketone bodies sustain myelin formation during development, we tested if they could provide sufficient acetyl CoA without mitochondrial produced acetyl CoA by generating a SC-specific deletion of ATP citrate lyase (ACLY), a core component of the citrate shuttle that generates cytosolic acetyl CoA for lipid synthesis. We find ACLY is not required for myelin formation in the first 2 weeks of life, but instead deficits become apparent by 5 weeks of age. We hypothesized that including supplemental ketones to the normal diet in a mouse after a SC-specific deletion of ACLY or nerve injury will rescue the loss of myelin lipid. Using a novel approach to supplement a normal diet with butanediol to generate ketone bodies, we observed substantially improved myelination in the ACLY cKO.
Research Grant	Vilas Associate Grant
Field of Research	Physiology

Abstract Title	Evaluating impacts of Culicoides sonorensis larval density on adult size and blue tongue virus susceptibility
Authors	Olivia Coppola, Bethany McGregor
Affiliations	St. George's University School of Veterinary Medicine, West Indies, Grenada. Arthropod-Borne Animal Diseases Research Unit, Center for Grain and Animal Health Research, ARS, USDA, Manhattan KS, USA
Abstract	Culicoides biting midges are known vectors for carrying arboviruses that crucially impact livestock and wildlife on a global scale, such as blue tongue virus (BTV). Larval midges often develop in semi-aquatic habitats on outskirts of water bodies; however, the impact of larval density on adult characteristics, such as body size and infection susceptibility, in these habitats are poorly understood. In understanding the effects of larval density has on the midges, we can bridge the knowledge gaps of C. Sonorensis and improve our understanding of how BTV affects C. sonorensis, a major North American BTV vector. We hypothesized that insects reared at higher densities will be smaller due to resource competition and have higher rates of infection and viral titers due to stressors in the larval stage. In this study, larval densities were evaluated: low (~5000 larvae), mid (~10,000 larvae), and high (~20,000 larvae). Wing measurements were conducted on adult male and female midges from all three treatments to evaluate effects on size. BTV infection variations were evaluated in midges from each density by providing an artificial blood meal with BTV and incubated for 10 days. Midge bodies and head were collected and tested by qRT-PCR to determine infection and dissemination, respectively, and to evaluate comparative virus titers. Results have shown larger wing lengths among lower densities and smaller wing length among the higher densities, possibly due to lack of resources causing physical stress in larvae. Data collection for virus infection study is ongoing. These studies will provide valuable data on the relationship between midges and BTV and may have implications for management of arboviruses in the field.
Research Grant	USDA-ARS NP103 CRIS Project 3020-32000-010-00D and NP104 CRIS Project 3020-32000-018-00D
Field of Research	One Health

Abstract Title	Evaluation of test-retest reliability of olfactory habituation-dishabituation tests in companion dogs
Authors	Amelia Corona, Callie Rogers, Ryan Hopper, Michele Salzman, Nathaniel Hall, Freya Mowat
Affiliations	University of Wisconsin-Madison Dept. Surgical Sciences, School of Veterinary Medicine, Texas Tech University Dept. Animal and Food Sciences
Abstract	Olfaction is an important canine sense. Dogs trained for olfactory detection can be accurately assessed for olfactory capability, but the olfactory capabilities of untrained companion dogs are poorly understood and novel methods must be developed for testing of untrained companion dogs. We hypothesized that our novel olfactory discrimination tests would be reproducible in companion dogs. Using an untrained habituation-dishabituation paradigm, n=13 client-owned dogs engaged with biologically relevant odors in 6 testing pairs. Oil based odors were diluted 100-fold in mineral oil, non-oil odors were used undiluted (meat stock) or diluted 1000-fold in buffered saline (urine). Dogs were presented with a fixed volume of habituant odor soaked on a cotton round in a steel tea-ball for 30 seconds with a 30 second inter-presentation interval. Habituation odors were presented in 4 consecutive trials. Subsequently, a novel odor was presented for 30 seconds. Interactions were video recorded and interaction times measured post-hoc. We defined a dog's pass/fail dishabituation threshold as 2 times the standard deviation of habituation trials 2-4. Dogs underwent repeated testing at a mean of 46 ? SD 30 days after the first testing. We evaluated test-retest reliability using Cohen's kappa coefficient (κ). Preliminary analysis showed 2 odorant pairs had fair agreement (κ = 0.29, 0.36), 1 had moderate agreement (κ = 0.50), and 3 had substantial agreement (κ = 0.67, 0.73, 0.74). Additional animals will be tested to confirm our findings. We plan to combine well-performing tests into a test battery to establish if dishabituation to novel odors is altered by aging in dogs.
Research Grant	Morris Animal Foundation D23CA-510, UW-Madison Companion Animal Funds
Field of Research	Ophthalmology

Abstract Title	Role of Entresto in Doxorubicin-induced cardiotoxicity
Authors	Alanna Costas, Abhishek Pandit, Biplov Sapkota, Henry Green, and Joseph Francis
Affiliations	Department of Comparative Biomedical Sciences (Costas, Pandit, Sapkota, Francis) and Department of Veterinary Clinical Sciences (Green), School of Veterinary Medicine, Louisiana State University SVM, Baton Rouge, LA
Abstract	The aim of this study was to assess the efficiency of Sacubitril/Valsartan (Entresto) in minimizing chronic side effects of doxorubicin-induced cardiotoxicity (DIC). Doxorubicin (DOX) is a chemotherapeutic agent commonly used to treat soft tissue and bone sarcomas. It is known to cause dose-dependent cardiotoxic side effects, such as hypotension, arrythmia, and congestive heart failure. These side effects limit the dosage that can be administered, consequently, restricting the capability to aggressively combat malignant neoplastic diseases. Considering decreased cardiac output due to DIC, the heart works harder to make up for the cardiotoxicity, and the kidneys react via vasoconstriction attempting to increase venous return. Entresto works to preserve renal function and prevent further damage to the heart. Thus, we hypothesized that chronic effects from DIC could be minimized using Entresto, which induces early antiproliferation and antihypertrophic effects on cardiomyocytes. The study used a mouse model injected with 4T1 cells, a triple-negative breast cancer cell line, to treat with different combinations of DOX and Entresto. Cardiac function was assessed using echocardiography and histopathological tests were performed on cardiac tissue. Atrial and B-type natriuretic peptide concentrations were measured in order to evaluate the impact of Entresto. Western blotting, immunohistochemistry, and RT-PCR assays were conducted to detect the presence of apoptosis-specific proteins, oxidative stress, and mRNA expression in cardiomyocytes, respectively. Pending results of this study, we expect to demonstrate Entresto is able to minimize chronic cardiotoxic effects of DOX, potentially improving breast cancer treatment outcomes.
Research Grant	1P20 GM135000 for Francis
Field of Research	Cardiology

Abstract Title	iDISCO highlights postnatal changes in enteric glial network development in a comparative pig model
Authors	Sara J Erwin-Craig, Sophia P Jodka, Jack Odle, Laurianne Van Landeghem, Anthony T Blikslager, Amanda L Ziegler
Affiliations	Department of Clinical Sciences (Erwin-Craig, Jodka, Blikslager, Ziegler) and Department of Molecular Biomedical Sciences (Van Landeghem), College of Veterinary Medicine, NC State University, Raleigh, NC. Department of Animal Science (Odle), College of Agriculture and Life Sciences, NC State University, Raleigh, NC.
Abstract	The glial network of the enteric nervous system is instrumental in intestinal repair, but is immature at birth. In mouse models, enteric glia are restricted to the submucosal and myenteric plexuses, and are driven to populate the lamina propria in response to microbial colonization of the gut after birth. Early postnatal development of the enteric glial network has not yet been described and measured in the pig. We hypothesized the density and distribution of glial cell subtypes would change within the early postnatal period in our comparative pig model. We aimed to measure the enteric glial network in the pig from birth to 21-days-of-age. The immunolabeling-enabled three-dimensional imaging of solvent-cleared organs (iDISCO) technique was used to triple-stain full-thickness jejunum of 1-, 7-, 14-, and 21-day-old pigs against glial markers S100β, Sox10, and glial fibrillary acidic protein (GFAP). Samples were imaged with a light-sheet microscope and glial volumes were calculated in Imaris software. In the lamina propria, density by volume of GFAP+ glia decreases (P=0.1133) while S100β+ glia density increases (P=0.5326). The number of Sox10+ nuclei increases from 1 to 21 days of age (P=0.0147). We believe this indicates GFAP is expressed in more mature glial cells and that S100β, a known inflammatory mediator, is participating in immune responses to colonizing bacteria while Sox10 marks the nuclei of progenitor glia. Understanding this early postnatal development will allow its modulation to accelerate maturation of repair mechanisms.
Research Grant	NCSU CMI TPP 2017 Seed Grant, Large Animal Models Core CGIBD P30 DK034987, USDA NIFA 1007263 and 07985, NIH P30 DK034987, NIH T32 5T32DK007737-22
Field of Research	Physiology

Abstract Title	Understanding how mutations to progesterone receptor gene impacts ligand binding
Authors	Erika Cromwell, Kelley Salem, and Amy Fowler
Affiliations	University of Wisconsin-Madison, School of Veterinary Medicine (Cromwell), Department of Radiology (Salem, Fowler), Carbone Cancer Center (Fowler), Madison, WI
Abstract	Breast cancer is one of the most diagnosed diseases amongst women in the United States. The treatment for estrogen receptor (ER) positive breast cancer involves surgical removal of the tumor in adjunct with 5 to 10 years of endocrine therapy, but recurrence and subsequent resistance to endocrine therapy is common. ER and progesterone receptor (PR) mutations have been discovered in patients with metastatic breast cancer. One of the mutations to PR has been previously shown to decrease PR activation, however, the impact these mutations have on PR function and therapy resistance is unknown. Therefore, the goal of this study is to determine how the Y890C mutation impacts PR binding to ligand. We hypothesize that tumors expressing the PR with the Y890C mutation will have decreased ligand uptake in comparison to tumors with the wild type (WT) PR due to its location being in the ligand binding domain. Ten female, athymic nude mice were bilaterally injected with WT and Y890C PR tumor cells in their thoracic mammary fat pad. As a negative control, the PR negative 231 cells were injected into the inguinal fat pad. Mice were injected with 18F-fluorofuranylnorprogesterone (FFNP), a radiotracer specific to PR, and then underwent positron emission tomography and computed tomography (PET/CT) and tissue biodistribution assay. Results showed a significant decrease in FFNP uptake in Y890C PR tumor xenografts compared to WT PR tumors (3.1± 0.6 vs. 16.6 ± 10.6, $p = 0.04$). Imaging data was correlated with PR expression via Western blot and immunohistochemistry (IHC). Mutation status was confirmed using digital droplet.
Research Grant	American Cancer Society
Field of Research	Oncology

Abstract Title	The behavioral effects following application of a long-acting transdermal buprenorphine solution in swine
Authors	Lauren Cromwell, Elizabeth Pollack, Rebecca Johnson, Adrianna Sage
Affiliations	University of Wisconsin-Madison, School of Veterinary Medicine, Madison, WI
Abstract	Pain management is often overlooked in the swine industry due to a lack of approved analgesic options and difficulty administering medications. A topical buprenorphine solution approved in cats to provide up to 4 days of analgesia may be a potential option for long lasting pain control in pigs. We hypothesized that negligible behavioral effects will be associated with both high-dose and low-dose transdermal buprenorphine. Seven healthy, 10-month-old Wisconsin mini-swine were randomly sorted into one of three groups: transdermal buprenorphine low-dose (1 mg/kg), high-dose (5 mg/kg), or anhydrous alcohol administered transdermally at equal volume to the high dose (control). Jugular catheters were surgically placed to act as both a pain stimulus and blood collection method. The assigned treatment was applied post-operatively on the dorsum, and blood draws, pain scores, and behavioral assessments were taken at regular time intervals up to 96 hours post-treatment by a blinded investigator. High-dose and low-dose treated pigs had lower pain scores compared to the control pig at 4 hours post-treatment. No difference in pain scores was found between high-dose and low-dose at any time point. The buprenorphine-treated pigs had lower behavior scores compared to control at 6 and 18 hours. The high-dose group had higher behavior scores compared to the low-dose group at 6 hours and lower scores compared to control at 24 hours. Inferences gained from this study may greatly impact the clinical management of swine in companion, production, and research settings since this could be the first easily applied opioid analgesic to show long term efficacy, allowing for substantial advancement in pig welfare and patient care.
Research Grant	University of Wisconsin-Madison SVM Companion Animal Fund
Field of Research	Pharmacology and Toxicology

Abstract Title	Increasing the efficiency of avian reovirus detection and characterization using MinION sequencing
Authors	Morgan Cunningham, Kelsey Young, Holly Sellers, Erich Linnemann, James Stanton
Affiliations	Department of Pathology (Cunningham, Young, Stanton) and Poultry Diagnostic and Research Center (Sellers, Linnemann), College of Veterinary Medicine, University of Georgia, Athens, GA
Abstract	Avian reovirus (ARV), a major cause of tenosynovitis and arthritis, is an economically significant virus in the poultry industry. ARV is a segmented RNA virus that undergoes rapid mutation and infections frequently consist of multiple viral genotypes, leading to reassortment and increased genetic changes. This complicates accurate diagnosis and decreases effectiveness of vaccination. Thus, it is imperative to have comprehensive genetic typing of ARV. MinION sequencing is a cutting-edge resource for rapid, reliable, and low-cost whole-genome sequencing. Current methods of viral diagnosis, consisting of targeted RT-PCR and cloning for Sanger sequencing are relatively inefficient. This study determined the efficiency of combining MinION sequencing with a random, strand-switching method to detect and characterize ARV, including coinfections. Samples obtained through viral culture were sequenced using MinION sequencing, starting with randomly primed strand-switching, coupled with PCR-based barcoding. This protocol identified ARV coinfections in several samples, previously unidentified by the former, targeted diagnostic methods. Reference-based and de novo assembly methods detected all 10 segments of the predominant ARV in each sample with a minimum of 15× coverage. In coinfected samples, the predominant variant was characterized and up to 3 minority variants were detected, including isolates belonging to a putative new genotype. These results demonstrate that random whole genome sequencing with the MinION platform is a useful tool in the detection of ARV, including coinfections, and will improve the monitoring of viral reassortment events.
Research Grant	US Poultry & Egg Association, Project Number RUSPA000141710A
Field of Research	Anatomic Pathology

Abstract Title	The impact of environmental stress on calves' responses to respiratory disease
Authors	Cassidy Czaykowsky, Sha Tao, and Brent Credille
Affiliations	Department of Animal and Dairy Science (Tao), Department of Population Health (Credille), Food Animal Health and Management Program (Credille), College of Veterinary Medicine (Czaykowsky, Credille), University of Georgia, Athens, Ga
Abstract	Bovine respiratory disease (BRD) is the most common, costly disease of the modern beef and dairy cattle industry. It is known to be induced by a combination of stress and/or a bacterial or viral infection. Although a few research studies highlight heat stress as a critical challenge in the animal husbandry, there is limited information investigating a correlation between heat stress and the progression of BRD in calves. Thus, it is proposed that prolonged heat stress in the southeast will increase the severity of BRD. To support this hypothesis, eighteen 6-day old, preweaned bull calves were collected from a commercial farm and transported to UGA CVM's Riverbend Farm. After an adaptation period, these calves were randomly placed into two experimental groups: one providing heat abatement through shade and forced ventilation and one in which no heat abatement was provided. Around 21 days after the adaptation period, BRD was induced through Mannheimia haemolytica. It was suspected that heat stress would compromise the immunity of the calves and increase the severity of BRD by exaggerating the inflammatory responses to the induced bacterial infection. Before and during the induction, parameters such as rectal temperature, respiration rate, and health scores (nasal, eye, ear, cough, fecal) were recorded twice a day to assess the health of the calves. Immune function parameters such as neutrophil chemotaxis, inflammatory cytokine production, and lymphocyte proliferation were also measured. Stress and inflammation were assessed through circulating cortisol and haptoglobin concentrations, respectively. Finally, lesions of the respiratory and gastrointestinal tract were investigated through necropsy.
Research Grant	Georgia Agricultural Commodity Commission for Beef
Field of Research	Production Animal Medicine

Abstract Title	The Effects of Cigarettes and Vaping on Lung Structure and Immune Function
Authors	Ariana Daldemian, Krista Thongphanh, Diwash Shrestha, Xiaohan Li, Lisa Miller, and Dr. Kent E. Pinkerton
Affiliations	School of Veterinary Medicine (Daldemian), California National Primate Center (Thongphanh, Shrestha, Miller), and Center for Health and the Environment (Li, Pinkerton), University of California, Davis, CA.
Abstract	Over recent years, vaping has become increasingly more common, including cigarette smokers switching to vaping as a perceptively less harmful alternative. However young people who have never smoked are picking up vaping as a habit. The long-term effects of exposure to e-cigarette aerosols are still unclear. Our laboratory has conducted several exposure studies to find out the extent of e-cigarette damage in the lungs, both in structure and in function. Previous studies in our lab have shown that the lungs with tobacco cigarette exposure have less Club Cell Secretory Protein, which makes mice more susceptible to viral infections as a result. In this study, we aim to see if e-cigarette aerosols impact lung immune function in a similar manner. We hypothesize that smoking may exacerbate the effects of e-cigarette vaping. Our study includes four groups of C57BL/6 mice: 1) exposure to filtered air only, 2) exposure to cigarette smoke only, 3) exposure to only to e-cigarette aerosol, and 4) exposure to tobacco smoke, followed by exposure to e-cigarette aerosol. This last group reflects the population of humans who wean off of cigarettes through vaping. Our goal is to see if vaping by itself, or switching to vaping, has any changes on the extent of lung damage. We exposed mice to tobacco smoke and/or e-cigarette aerosols in whole-body exposure chambers. Lungs were embedded, sectioned, and stained for microscopic analysis. Using H&E staining and immunohistochemistry, we will observe the physical extent of the lung damage and the exposures' impact on lung immune function, respectively.
Research Grant	None
Field of Research	Anatomic Pathology

Abstract Title	Measuring the effect of an antimicrobial stewardship program on antimicrobial use at a vet teaching hospital
Authors	Alexandra Damren, Ian DeStefano, Manlik Kwong, Emma Price, Kirthana Beaulac, Shira Doron, Claire Fellman
Affiliations	Affiliations: Department of Clinical Sciences (Fellman, DeStefano), Cummings School of Veterinary Medicine (Damren), Tufts University, North Grafton, MA; Tufts Medical Center (Kwong, Doron), Tufts University, Boston, MA; Emerson Hospital (Beaulac), Concord, MA
Abstract	Antimicrobial stewardship is the collaborative effort across health professionals to optimize the use of antimicrobials, especially in the face of growing concerns for multidrug-resistant organisms. An important component of antimicrobial stewardship is measuring antimicrobial use and the effect of interventions. The Foster Hospital for Small Animals at Tufts University launched an antimicrobial stewardship program in August 2021 consisting of educational seminars for veterinary prescribers, nurses, and students and initiatives including diarrhea packs to reduce metronidazole use for acute diarrhea and a hospital antimicrobial guideline to support empiric prescribing. To determine program effects on antimicrobial use, a veterinary-adapted observational medical outcomes partnership common data model was used to extract antimicrobial prescription data from the electronic medical record system in this descriptive observational study. Antimicrobial prescriptions for dogs and cats admitted from 2018-2022 will be assessed using days of therapy per 1000 patient days. Use rates will be compared by year and by pre- and post-stewardship program launch. Antimicrobials will be categorized by drug class and by World Health Organization importance designation and Access/Watch/Reserve grouping. Study results will establish the effectiveness of interventions and will clarify goals and priorities for future antimicrobial stewardship efforts.
Research Grant	None
Field of Research	Antimicrobial Resistance

Abstract Title	Novel surgical spoon for urocystolith removal during canine cystotomy
Authors	Davina C. D'Angelo, F.A. (Tony) Mann
Affiliations	Department of Veterinary Medicine and Surgery, College of Veterinary Medicine, University of Missouri, Columbia, Missouri
Abstract	Urolithiasis is common in dogs. Cystotomy is a standard surgical procedure to remove urocystoliths from the urinary bladder, but retrieval of urocystoliths is limited to improvised use of available surgical instruments or off-label devices. Furthermore, there is an unacceptable incidence of incomplete urocystolith extraction, which can necessitate additional surgery and exacerbate morbidity. To improve urocystolith extraction, three novel 3D-printed surgical spoons underwent a pilot proof-of-concept trial in Northwest Arkansas veterinary clinics. Postoperative questionnaires provided to those veterinarians recorded favorable experiences using one or more of the surgical spoons in two dogs weighing 23 to 34 kg. The most favored surgical spoon from the trial underwent strategic design modification to evaluate in dogs weighing less than 23 kg. The cystotomy spoon is a 12.5 cm shaft with a spoon on each end, one spoon narrower (1.4 cm at widest dimension) than the other (2.0 cm at widest dimension). The cystotomy spoon was 3D printed using Dental Surgical Guide resin and entered a proof-of-concept trial at the University of Missouri Veterinary Health Center. Faculty surgeons and residents will use the spoon during canine cystotomies and complete a postoperative questionnaire to record expert opinion on the efficacy and usefulness of the spoon. We hypothesize that these surgeons will view the spoon as effective and user-friendly for urocystolith extraction. We anticipate that these surgeons may have constructive input for design improvement. Once perfected, this surgical spoon will provide a specific device for canine urocystolith removal and positively impact the standard of healthcare for dogs requiring a cystotomy.
Research Grant	None
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Development of an Immunohistochemical Multiplex to Elucidate the Immune Landscape of Influenza A Virus
Authors	Nina Davis, Adrienne Shircliff, Bailey Arruda
Affiliations	Tuskegee University, College of Veterinary Medicine, Tuskegee, Alabama (Davis) USDA-Agriculture Research Service, National Animal Disease Center, Ames, Iowa (Arruda, Shircliff)
Abstract	Swine are an increasingly important biomedical model including for influenza A virus (IAV) infection. IAV is a significant pathogen of humans and swine. Infection of either host results in a necrotizing bronchiolitis with infiltration of leukocytes. Flow cytometry is commonly used to investigate the immune response; however, the spatial context of leukocytes is lost. Immunohistochemistry (IHC) provides this spatial context as well as providing the response of native cells. Yet, IHC is hindered in swine due to limited swine-specific antibodies and challenges of multiplexing due to species-restricted secondary antibodies. We posited that the use of a commercial platform and reagents that are primary antibody-species independent would facilitate the simultaneous detection of multiple markers using IAV infection in swine as a model. Antibody targets were evaluated via manual protocols that included four antigen retrievals and various primary antibody concentrations, incubation times and temperatures. Antibody targets included PAX5, CD79α, CD163, SLA Class II DQ, HLA Class I, HLA-DR + HLA-DP, Ki67, CD3, CD4, CD8 and IAV nucleoprotein. Antibodies were then evaluated using a commercial platform across multiple protocols. We successfully developed a manual protocol for six of the eleven antibodies; a subset was incorporated into a semi-automated multiplex that required four to 40 times more primary antibody. In conclusion, we developed a novel IHC multiplex that provides spatial context of a complex microenvironment at high resolution. Further optimization to increase the robustness of the multiplex is needed. However, our multiplex can be refined to generate similar immune landscapes across physiologic states in swine
Research Grant	Funding for this project was provided by CRIS 5030-32000-231-000D
Field of Research	Virology

Abstract Title	Social attention and behavior in a nonhuman primate model of neurodevelopmental disorders
Authors	Brittany Davis, Felisa Carbajal, Casey Phi, and Melissa Bauman
Affiliations	School of Veterinary Medicine, UC Davis, Davis, CA (Davis) California National Primate Research Center, UC Davis, Davis, CA (Carbajal, Phi, Bauman) Department of Psychiatry and Behavioral Sciences, UC Davis School of Medicine, Sacramento, CA (Bauman) The MIND Institute, UC Davis School of Medicine, Sacramento, CA (Bauman)
Abstract	Accumulating evidence from human epidemiological studies suggests that maternal infection during pregnancy may predispose children to neurodevelopmental disorders such as autism spectrum disorder and schizophrenia. Rodent and nonhuman primate animal models of maternal immune activation (MIA) have found that maternal cytokines impact fetal brain development and that animals exposed to MIA in utero have altered brain and behavioral development. People with autism spectrum disorder and schizophrenia exhibit changes in sociality and visual attention to facial expressions. Rhesus monkey (Macaca mulatta) offspring born to MIA-treated dams exhibit atypical interactions with novel social partners early in development and a decrease in affiliative interactions with familiar partners in late adolescence. Here, we use an eye tracking paradigm to assess differences in social attention between rhesus macaques exposed to MIA in utero and animals born from a healthy pregnancy. We also discuss results of a pilot study to evaluate feasibility of collecting eye tracking data in the home cage environment. Finally, we develop and pilot a new social valuation test which will be used in the future to further probe differences in social attention between MIA exposed and unexposed offspring. The data and behavioral tests presented here further support the development of the nonhuman primate model of MIA and its relevance to better understanding human neurodevelopmental disorders.
Research Grant	UC Davis Conte Center (NIMH); California National Primate Center; MIND Institute Intellectual and Developmental Disabilities Research (NIH)
Field of Research	Behavior

Abstract Title	Short-chain fatty acids acetate and butyrate inhibit Coxiella burnetii replicative vacuole expansion
Authors	Ashley Davis, Dhritiman Samanta
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ (Davis); Department of Microbiology and Immunology, College of Graduate Studies. Midwestern, University, Glendale, AZ (Samanta)
Abstract	Coxiella burnetii is a gram-negative obligate intracellular bacterium and is the causative agent of human Q fever and Coxiellosis in animals. Coxiella infects numerous animal hosts including domestic ruminants causing spontaneous abortions. Humans acquire Q fever through the aerosolization of ruminant reproductive materials. Q fever manifests as an upper respiratory infection causing flu-like symptoms and can develop into life-threatening endocarditis. Chronic infections require an 18-month antibiotic therapy. Currently, no approved vaccines are available in the United States for humans or veterinary species. Therefore, there is an urgent need to identify novel therapeutics and vaccines for Coxiella infections. Upon host cell infection, Coxiella resides in a vacuole that expands and fuses with host lysosomes to form a large, acidic vacuole termed Coxiella-containing vacuole (CCV). The CCV is central to Coxiella intracellular survival and pathogenesis. We examined the effect of short-chain fatty acids (SCFA) acetate and butyrate on CCV expansion. HeLa cells, infected with Coxiella burnetii NMII were treated with either PBS or with acetate and butyrate. At 72 h post-infection, cells were fixed and subjected to an immunofluorescent assay. Images were analyzed in ImageJ to measure CCV area. Our data revealed that treatment with 80 mM acetate and 5 and 10 mM of butyrate resulted in significantly smaller CCVs than PBS-treated cells, suggesting that SCFAs negatively affect CCV expansion. Our data for the first time show an anti-Coxiella effect of SCFAs. In the future, we plan to quantitate Coxiella growth in the SCFA-treated cells to directly assess the bactericidal effects of SCFA.
Research Grant	Midwestern University Startup Grant
Field of Research	Microbiomes

Abstract Title	The effects of different housing types for dry cows on the incidence of metritis and mastitis
Authors	Heleen de Wit, Anne-Marieke C. Smid, Gerrit Koop, and Herman W. Barkema
Affiliations	Department of Population Health Sciences, Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands (De Wit, Koop) and Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada (Smid, Barkema)
Abstract	Worldwide, public interest in animal welfare is increasing, which includes a concern about the lack of pasture access for dairy cows. Although dairy cows are highly motivated to access pasture, most research on transition diseases in dairy cows has been conducted in indoor housing systems. Therefore, the objectives of this study were to understand the effects of pasture access for dry cows on the prevalence of metritis and mastitis in the following lactation. Data were collected between July and September 2021 using a survey of the Canadian Dairy Network of Antimicrobial Stewardship and Resistance, on 18 and 22 dairy farms in Alberta and British Columbia, respectively. A non-parametric test (Mann-Whitney U Test) was used to examine the association of the provision of pasture during the dry period with the incidence of metritis and mastitis in the following lactation. Incidence of metritis and mastitis did not differ between cows that had pasture access during their dry period, and those that did not. However, the distribution of incidence differed, with dry cows that had pasture access having a wider distribution in incidence than indoor housed cows for both metritis ($P = 0.001$) and mastitis ($P = 0.002$). In conclusion, the incidence of metritis and mastitis did not differ with the provision of pasture access for dry cows. However, the incidence of these diseases was more widespread in outdoor housed dry cows.
Research Grant	Results Driven Agriculture Research (RDAR), and a Mitacs Elevate grant, with industry contributions from Alberta Milk, Dairy Farmers of Canada, Dairy Farmers of Manitoba and SaskMilk
Field of Research	Production Animal Medicine

Abstract Title	Nitric oxide buffers against excessive NPY-induced vasoconstriction in the cerebral circulation of swine
Authors	Gabriela Delgado(1), Cameron J. Morse(1), Breanna J. Barlage(1), Jordan T. Wall(1), Laura E. Shaw(1), Kendra R.C. DuRussel(1), Corey R. Tomczak, M. Harold Laughlin, Jaume Padilla, Erika M. Boerman, T. Dylan Olver(1)
Affiliations	Department of Biomedical Sciences, Western College of Veterinary Medicine (1) and College of Kinesiology (Tomczak), University of Saskatchewan, SK, Canada; Dalton Cardiovascular Research Center (Padilla, Laughlin) and Department of Medical Physiology and Pharmacology (Boerman), University of Missouri, Columbia, Missouri
Abstract	Neuropeptide Y (NPY) is a sympathetic co-transmitter that mediates vasoconstriction. However, there is evidence that it may also mediate dilation through a nitric oxide (NO)-dependent mechanism. Using swine as an experimental model, the aim of this study was to examine how NPY influences cerebral vascular regulation. It was hypothesized that NPY would elicit both constrictor and dilatory effects, and that such effects would be modulated partially by NO signaling. Briefly, cerebral perfusion (LDF), and blood pressure (arterial catheter) were monitored during intracarotid NPY infusions (0.1 ug/kg) both in presence and in absence of NO synthase (NOS) inhibition (L-NAME;0.35 mg/kg/min). Separate, in vitro experiments were conducted on isolated pial arteries to examine Y1 receptor distribution (immunohistochemistry) and vasomotor responses to intra-and extraluminal NPY under control and NOS inhibition conditions (pressure myography). Intracarotid infusions of NPY alone did not elicit robust constriction. In contrast, infusion of NPY under NOS inhibition conditions promoted constriction. Peak dilatory responses to NPY were blunted, and peak constrictor responses to NPY were augmented in NOS inhibition vs. control conditions. In isolated pial arteries, populations of NPY-Y1R were observed on both the vascular smooth muscle (VSM) and endothelium. Extraluminal application of NPY, targeting the VSM, elicited constriction. In contrast, intraluminal delivery of NPY, targeting the endothelium, elicited dilation. The magnitude of constriction was augmented, and dilation in isolated pial arteries was abolished with NOS inhibition. These data suggests NO may buffer against excessive NPY- induced constriction in cerebral circulation.
Research Grant	NSERC discovery grant and Saskatchewan Agricultural Development Fund
Field of Research	Physiology

Abstract Title	Alterations of Surface Roughness Changes Osteoblastic Cell Proliferation on Manufactured Zinc Implants
Authors	Jean-Aloïs U. Delpla, Matthew Fainor, Sarah E. Gullbrand, Guha Manogharan, and Michael W. Hast
Affiliations	Ecole Nationale Vétérinaire de Toulouse ENVT , Toulouse, France (Delpla) ; Department of Orthopaedic Research Laboratory McKay (Fainor, Gullbrand, Hast), Penn University of Medicine and Department of Materials Science and Engineering (Manogharan), Penn State College of Earth and Mineral Sciences, Philadelphia, Pennsylvania
Abstract	Advances in biomaterials and additive manufacturing (3-D printing) are rapidly changing the way orthopaedic implants are designed and implemented. Our lab has recently developed a method to 3-D print zinc, a biocompatible and biodegradable material, and a key micronutrient involved in human health. Zinc is a promising orthopaedic biomaterial because it has been shown to stimulate the expression of a transcription factor related to the differentiation of stem cells to pre-osteoblast cells (precursor cells that become osteoblasts). Recent studies have shown that Zn promotes osteoblast proliferation and increases mineralized matrix deposition via the cAMP-PKA-CREB signaling pathway. Positive effects of Zinc on osteoblast activity occur over a defined dose ranges. We believe rates of zinc elution are related to the surface texture of an implant. However, we still do not fully understand the relationships between Zinc implant surface morphology and mesenchymal stem cell behavior. In this bovine cell culture experiment, we sought to quantify collagen matrix development, mineral deposition, and survival of MSCs exposed to substrates of different roughness. We hypothesized that smoother surfaces would lead to increases in bone callus development.
Research Grant	NIH K25AR078383 and NIH/NIAMS P30AR069619 from the national institute of Arthritis and Musculoskeleton nd Skin Diseases, Perelman School of Medicine at the University of Pennsylvania
Field of Research	Orthopedics

Abstract Title	Host-derived PDCD6 mediates proliferation and egress of intracellular Toxoplasma gondii in rat macrophages.
Authors	Jordan Demanty, Shahbaz Khan, William H. Witola
Affiliations	Department of Pathobiology, College of Veterinary Medicine, University of Illinois Urbana-Champaign
Abstract	Toxoplasma gondii is an important zoonotic parasite capable of causing profound disease in almost any mammalian host. Toxoplasmosis can manifest as miscarriages, encephalitis, and blindness in humans, and it is a main cause of abortions in small ruminants. It is well documented that this parasite utilizes a plethora of mechanisms to manipulate host machinery at the molecular level, but novel interactions continue to be elucidated. Several recent studies have demonstrated that Toxoplasma exploits the host endosomal sorting complex required for transport (ESCRT) machinery for scavenging nutrients and organelles from the host. In this study, we investigated the role of programmed cell death protein 6 (PDCD6), an adaptor ESCRT protein, in mediating T. gondii survival within rat macrophages. Using PDCD6-KO- and wild-type-NR8383 rat macrophage cell lines, we found that the genetic disruption of host PDCD6 restricts the in vitro growth and multiplication of the parasite within macrophages. Furthermore, we observed a “delayed-egress” phenotype in T. gondii tachyzoites growing within PDCD6-deficient cells as compared to those infecting wild-type cells, indicating that PDCD6 is required for egress of the parasite from host cells. Overall, our results provide additional evidence for the idea that Toxoplasma utilizes components of the host ESCRT machinery to carry out important functions for its survival and proliferation. Future in-depth studies elucidating this novel relationship between T. gondii and host PDCD6 will be crucial in understanding this important host-parasite interaction.
Research Grant	None
Field of Research	Parasitology

Abstract Title	Investigating the role of IFN-γ-activated macrophages in controlling Staphylococcus aureus infection
Authors	Erin K. DeNardo, Victoria M. Lovins, Elizabeth A. Grice, Phillip Scott
Affiliations	Department of Pathobiology (DeNardo, Scott), University of Pennsylvania School of Veterinary Medicine (DeNardo, Scott); Department of Dermatology (Lovins, Grice), Perelman School of Medicine (Lovins, Grice), Philadelphia, PA.
Abstract	Cutaneous leishmaniasis is a parasitic infection that causes a wide spectrum of clinical presentations ranging from single, self-healing lesions to chronic, non-healing infections despite treatment. We found that lesions from leishmaniasis patients exhibit an altered skin microbiome, and higher levels of Staphylococcus aureus promote increased IL-1β-dependent immunopathology and healing time. Similarly, skin colonization with S. aureus enhanced disease in Leishmania braziliensis-infected mice. Since IFN-γ plays a role in clearing S. aureus in macrophages, we expected to find an inverse relationship between IFN-γ levels and S. aureus burden. In contrast, we found that high levels of IFN-γ were associated with an increased S. aureus burden in the skin and invasion of the draining lymph nodes in L. braziliensis-infected mice. Therefore, we tested if IFN-γ-activated macrophages could limit S. aureus in vitro. We infected macrophages with a S. aureus isolate from L. braziliensis lesions and compared the growth of S. aureus in control and IFN-γ-activated cells. Surprisingly, we found that instead of killing the bacteria, S. aureus grew better in IFN-γ-activated macrophages. We are currently investigating the mechanisms involved in the enhanced growth of S. aureus. Additionally, we have a panel of S. aureus isolates from L. braziliensis patients that we will test to determine if the enhanced bacteria replication in activated macrophages is a common property of S. aureus isolated from patients. These results suggest that IFN-γ has a dual role in leishmaniasis: killing parasites while also promoting increased S. aureus levels that contribute to heightened immunopathology.
Research Grant	NIH R01 AI43790
Field of Research	Immunology

Abstract Title	The bovine mammary stem cell secretome inhibits the growth of Methicillin-resistant Staphylococcus aureus
Authors	Emilie A. Dewever, Nikola Danev, and Gerlinde R. Van de Walle
Affiliations	Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Ithaca, NY (Dewever, Danev, Van de Walle) ; VetAgro Sup, Campus vétérinaire, Marcy L'Etoile, France (Dewever) ; ENS de Lyon, Lyon, France (Dewever)
Abstract	Mastitis is the most common disease and the leading cause of morbidity in the dairy industry. Often caused by bacteria, antibiotics are the standard treatment. However, the use of antibiotics raises public health concerns due to antimicrobial resistance and antibiotic residues in milk, as well as economic concerns due to necessary milk withdrawal. Therefore, alternative treatments are warranted. The secretome, collected as conditioned medium (CM), of bovine mammary stem cells (BMSCs) is one such option. Previous work from our group showed that factors secreted by BMSCs exhibit antimicrobial properties. Here, the CM of BMSCs was used to understand the consequences of CM on the growth of Methicillin-resistant Staphylococcus aureus (MRSA), a bacteria often involved in mastitis. Phase-ring microscopy, flow cytometry, immunofluorescence and antimicrobial functional assays were used to test the hypotheses that (1) the CM of BMSCs can reduce MRSA growth in vitro and (2) MRSA can become resistant to CM. Preliminary results show that bacterial growth is reduced when bacteria are cultured in the presence of CM compared to control medium. We also found that MRSA became resistant to CM after 4 serial subcultures. This work focused on analyzing the characteristics of BMSC CM in relation to its effects on bacterial growth. In order to tackle the issue of antimicrobial resistance, CM could serve as an adjunct and/or potentially replacement therapy for antibiotics.
Research Grant	Elanco Animal Health, Foundation for Food and Agriculture Research, New York Farm Viability Institute
Field of Research	Antimicrobial Resistance

Abstract Title	Determining the origins of the piglet gut microbiome using strain-resolved longitudinal metagenomics
Authors	Jessica F. DiStefano, Lisa Mattei, Clara Malekshahi, Erin DeNardo, Jalisa D. Zimmerman, Andrew Shulman, Alexander Berry, Meghann K. Pierdon, and Daniel P. Beiting
Affiliations	Department of Pathobiology, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA. Swine Teaching and Research Center, New Bolton Center, Department of Clinical Studies, School of Veterinary Medicine, University of Pennsylvania, Kennett Square, PA. (Zimmerman, Shulman, Pierson)
Abstract	The piglet gut microbiome has been linked to numerous aspects of swine health and productivity, including growth and development, fat content of tissues important in meat quality, diarrhea in neonates, and even swine welfare. Despite this association, little is known about the factors that contribute to the initial colonization of the neonatal gut. The goal of this study was to chart the assembly of the piglet gut microbiome in the three weeks following birth, while simultaneously sampling maternal and environmental microbes and using strain-tracking to identify potential sources of early life colonization. Ten farrowing units, each consisting of one sow and at least 6 piglets were housed in individual farrowing stalls in the same room. Sow feces and piglet rectal swabs were collected on days 2, 4, 7, 14, and 21 post- gestation, and sow vaginal swabs were collected pre- and post-gestation. Environmental samples, including sow feed, piglet feed from a creep-feeder, and floor swabs, were used to monitor the farrowing environment for microbes. To profile the microbiome in these samples, we extracted DNA using the Qiagen PowerSoil Pro kit, used this DNA to prepare sequence-ready libraries, and carried out shotgun metagenomic sequencing. Analysis of these data is currently underway and may provide valuable insight into the seeding and assembly of the neonate gut microbiome. This data may help identify 'keystone' bacteria that are beneficial for promoting healthy, fast-growing piglets, thus potentially setting the stage to develop probiotics that can improve animal health and production in swine farming.
Research Grant	Pennsylvania Department of Agriculture and the University of Pennsylvania
Field of Research	Microbiomes

Abstract Title	Validation of hoof accelerometer monitoring interpreted by a threshold analysis to detect horses limb motion
Authors	Giovanna DiStefano, Andrew van Eps, Darko Stefanovski
Affiliations	Department of Clinical Studies, New Bolton Center at University of Pennsylvania School of Veterinary Medicine
Abstract	Supporting Limb Laminitis (SLL) occurs in horses with persistent severe unilateral lameness and causes serious complications during recovery from conditions like fractures. SLL develops primarily in the limb contralateral to the injury, partially due to increased load but also due to an altered weight bearing pattern. Our preliminary data suggests that clinical cases have characteristic limb motion patterns, including reduced frequency of ambulatory steps (1) and static offloads (2) preceding onset of SLL. A method to quantitate these movements is needed to facilitate identification of SLL risk. The current study objective was to develop and test a threshold analysis method using hoof accelerometer data to identify steps and offloads in sound horses. Simultaneous video and hoof accelerometer data was recorded for 1 hour in 11 sound horses and 1 severely lame horse. An accelerometer was mounted midline on the dorsal hoof using a standardized technique. The video was synchronized to accelerometer data and visually coded for (1) and (2) using software (Elan). Forelimb and hindlimb data collected from each sound horse was used to generate separate threshold values using STATA 17MP. Data from the other 5 sound horses will be used as test files. Pearson's correlation and Bland Altman plots will be used to demonstrate correlation and agreement between visual counts and those generated by threshold analysis. These methods will be repeated using data from clinical cases to validate the model's application for horses with severe unilateral lameness. Results for the study are currently pending and data collection for lame horses is ongoing as cases are admitted to the hospital.
Research Grant	None
Field of Research	Equine Medicine and Surgery

Abstract Title	How Two Cannabinoids Affect the Potency of Dexamethasone: An Investigation into a Potential Adjunct Therapy
Authors	Sabrina Dixon, Todd Archer, and Barbara Kaplan
Affiliations	Mississippi State University, College of Veterinary Medicine, Starkville, MS
Abstract	The objective of this study was to examine immune effects of Dexamethasone (dex) in combination with other immune-suppressive agents to determine if dex dosing could be reduced by using adjunct immune suppressive therapies. Our hope is that an adjunct therapy will allow for reduction in the dosage of dex needed to achieve therapeutically relevant immune suppression, which will enhance the comfort of the patient during treatment and improve owner compliance and satisfaction. Two possible adjuncts are the marijuana compounds, cannabidiol (CBD), and delta-9-tetrahydrocannabidiol (THC). We utilized a pre-clinical in vitro model in which interferon-γ (IFN-γ) was stimulated within cell cultures to determine whether either cannabinoid (or the combination) had the potential to serve as an adjunct therapy to achieve the same levels of immune suppression. We hypothesized that dex, CBD, THC, and the CBD/THC combination would all suppress IFN-γ, but that the combination of dex with any of the cannabinoids would exhibit more suppression than any treatment alone. Our results showed that both CBD and THC enhanced immune suppression compared to dex alone. Mice responded variably but overall the addition of cannabinoids increased immune suppression. We also observed that the CBD/THC combination treatment suppressed more than either of the individual treatments. In canine PBMCs, immune suppression increased in a concentration-dependent manner with increasing concentrations of dex, and there was enhanced suppression of the cannabinoid treatments with dex as compared to dex alone. This suggests that these cannabinoids have the potential to serve as adjunct immune suppressive therapies for dex with the goal of decreasing the dex dose needed.
Research Grant	Mississippi State University CVM
Field of Research	Immunology

Abstract Title	Polygenic risk scoring of healthy US adults in a cross-sectional metabolic phenotyping study
Authors	Catherine Dombroski, Kristen L James, Brian J Bennett
Affiliations	UC Davis School of Veterinary Medicine, Davis, CA (Dombroski), Department of Biomedical Informatics, University of Colorado Anschutz Medical Campus, Aurora, CO (James), USDA ARS Western Human Nutrition Research Center, Davis, CA (James, Bennett), Department of Nutrition, UC Davis, Davis, CA (Bennett)
Abstract	Metabolic marker abnormalities following a meal challenge are important predictors of risk of chronic disease such as diabetes or cardiovascular disease. To comprehensively understand the environmental and physiological factors determining metabolic health, the USDA Western Human Nutrition Research Center conducted a cross-sectional metabolic phenotyping study on 393 healthy human adults in the Davis, CA region. A wide range of data regarding individual's typical diet, hormonal profile, gut microbiome and metabolic markers were collected prior to and at multiple timepoints following a high-fat challenge meal. This study design allows for tracking of the dynamic response to a meal challenge which contrasts the static measurements typical of most metabolic phenotyping studies. Additionally, genotyping data was collected for 238 of these participants, allowing for us to investigate how genetic risk can influence the dynamic metabolic phenotypes observed. Genetic risk can be assessed using polygenic risk scores (PRS), which are calculated values representing the cumulative risk of all single nucleotide polymorphisms (SNPs) predisposing to a particular phenotype weighted by their effect size. Using PRS scores generated for our cohort, we will look at associations between genetic risk and post-prandial lipid metabolism over time. Our findings will help elucidate how cumulative genetic risk influences post-prandial metabolism which can help inform our interpretation of future metabolic phenotyping studies and potentially identify targets for nutritional interventions.
Research Grant	USDA-ARS 2032–51530–025-00D; 2032-51530-026-00D
Field of Research	Physiology

Abstract Title	The impact of social groupings and conspecific interaction on salivary cortisol levels in bonobos
Authors	Bryan J. Donohue, Rebecca L. Parsons, Jared P. Taglialatela, Suzanne T. Millman, Dipak K. Sahoo, June E. Olds
Affiliations	Veterinary Clinical Sciences (Donohue, Sahoo, Olds), Veterinary Diagnostic & Production Animal Medicine (Parsons, Millman), Biomedical Sciences (Millman), College of Veterinary Medicine, Iowa State University, Ames, IA Ecology, Evolution, & Organismal Biology, Kennesaw State University, Kennesaw, GA (Taglialatela)
Abstract	Free ranging bonobos live within a fission-fusion society where an individual's social structure is characterized by frequent changes in social group size and composition. For bonobos in human care, management strategies focus on regularly changing group structure to mimic the social experiences of bonobos in nature. Changes in social factors may increase or decrease stress experienced by individual animals. Social partners may mitigate impacts of environmental stressors, as well as serve as stressors themselves. The goal of this study was to evaluate the relationship between individual behavior, social factors, and salivary cortisol levels of bonobos within an AZA certified facility. Seven bonobos in human care, four males and three females, were evaluated. Bonobo social interactions and individual social behavior, as well as behaviors associated with stress, were recorded. Eighty-three individual behavioral observations were collected over six weeks in 10-minute continuous focal animal scans. Saliva was collected three hours after completion of each observation. Data collection is ongoing and will be analyzed to test two hypotheses: 1) Individual social context will impact salivary cortisol levels: a negative correlation between cortisol levels and pro-social behaviors and a positive correlation between stress-related behaviors and aggressive interactions; 2) social group composition and context will impact both pro-social behaviors and stress-related behaviors. The findings of this study may help give direction for management strategies to positively impact welfare for bonobos in human care.
Research Grant	Mapes Wildlife Care, Education and Research Endowment
Field of Research	Animal Welfare

Abstract Title	Can tail wag in response to a novel object predict success in candidate service dog puppies?
Authors	Samantha Dunn, Margaret E. Gruen
Affiliations	North Carolina State University College of Veterinary Medicine, Raleigh, NC (Dunn) Department of Clinical Sciences, North Carolina State University College of Veterinary Medicine, Raleigh, NC (Gruen)
Abstract	Currently, there is a 50% success rate for candidate service dog puppies. As such, there is a loss of time and money when dogs fail as adolescents. One potential refinement in the selection of dogs for service work may be their emotional arousal in response to a novel object. There is limited longitudinal scientific research on cognitive and emotional development of dogs across the period from 8 - 20 weeks of age. Further, surprisingly little research has been done on tail wag, and what it indicates in regard to canine cognition and emotional reactivity. The aim of this study was to evaluate tail wag as a predictive measure of emotional arousal. Every two weeks, puppies were presented with an unfamiliar mechanical, motion-activated toy animal for a 90-second trial. Their response was coded from video for frequency of tail wag, vocalizations, play bows and a subjective score ranging from 0-5 where the two ends of the scale indicate high positive and negative arousal, respectively. A total of 332 videos from 79 puppies ranging from 8-20 weeks of age were analyzed. We found a significant relationship between tail wag frequency and subjective score, with subjective score explaining 29.9% of variability in tail wag even when controlling for puppy age ($F = 8.95$; $p < 0.0001$). Puppies with a subjective score of 0, 1, or 5 wagged significantly more than puppies with scores of 2, 3, or 4 ($F = 26.6$; $p < 0.0001$). Overall, these results indicate that tail wag is significantly associated with high emotional arousal. These findings will be further evaluated for their predictive value in success or failure in training.
Research Grant	National Institutes of Health
Field of Research	Behavior

Abstract Title	Gene expression post organophosphate poisoning: tight junction, inflammatory, mitochondrial, apoptotic markers
Authors	Raegan Dunwoodie, Janice Chambers
Affiliations	Department of Comparative Biomedical Sciences, Center for Environmental Health Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS
Abstract	Organophosphate (OP) anticholinesterases are some of the most neurotoxic synthetic chemicals known. The primary neurotoxic mechanism of OP poisoning is acetylcholinesterase (AChE) inhibition. This leads to excessive synaptic acetylcholine causing hypercholinergic activity, and non-lethal, seizures that can lead to brain damage. This brain damage could result from OP-induced inflammation, blood brain barrier (BBB) leakage, and increased apoptosis from mitochondrial damage. The objective of this project was to examine the impact of OP poisoning on tight junction (TJ), inflammatory, mitochondrial, and apoptotic expression in the piriform cortex, a location involved in the generation of seizures. The genes chosen were Occludin (OCLN), Claudin 5 (CLN5), Nucleoside Diphosphate Kinase A (NME1), FOS Proto-oncogene (FOS), and Serine/Threonine Kinase 1(AKT1). Adult male rats were injected with 0.6 mg/kg NIMP (a surrogate of the nerve agent sarin) or the vehicle. Samples were taken at early (1-2hr) or late (4-day) time points. The piriform cortex was harvested, mRNA purified, and expression levels determined by QRT-RPCR. NIMP caused a short-term decrease in mRNA expression of the TJ structural gene OCLN. Additionally, NIMP caused an increase in mRNA expression at both 1-2 hours and 4-days for CLN5, an intracellular trafficking protein related to neuronal degeneration, and FOS, a genetic marker for neurologic inflammation and increased apoptosis. These results suggest that OP poisoning may have a short-term negative impact on the BBB's structural integrity and may also increase neurological inflammation, degeneration, and apoptosis starting shortly after exposure and persisting for several days and could contribute to brain damage.
Research Grant	NIH CounterACT U01NS123255
Field of Research	Pharmacology and Toxicology

Abstract Title	Evaluating the sex-dependent effects of manipulating osteocytic HIF-α expression on skeletal development
Authors	Madelyn Dupre, Sarah Mendoza, and Clare Yellowley
Affiliations	Department of Anatomy Physiology and Cell Biology (Mendoza, Yellowley), School of Veterinary Medicine (Dupre), University of California Davis, Davis, CA.
Abstract	Osteoporosis, a low bone mass disorder, is a prevalent issue that adversely affects the aging population. Current osteoporotic therapies are suboptimal, thus investigation of novel bone preserving therapies are necessary. Hypoxia inducible factor (HIF) signaling is required for skeletal health and maintenance. HIFs are transcription factors composed of an oxygen-dependent HIF-α subunit (transcriptionally active isoforms: Hif1a, Hif2a) and a constitutively stable nuclear HIF-ß subunit. Under normoxic conditions, HIF-α subunits are hydroxylated and targeted for degradation by an E3 ligase complex Von Hippel-Lindau (VHL). Under hypoxic conditions, HIF-α subunits avoid VHL-mediated degradation and induce osteoanabolic transcriptional changes. Our lab has shown that in female mice: 1) deletion of osteocytic (OCY) Vhl generates strikingly high bone mass, 2) deletion of OCY Hif1a or Hif2a did not affect skeletal microarchitecture, 3) expressing a degradation-resistant OCY HIF-2α, not HIF-1α, generated a high bone mass phenotype. To determine sex-dependent effects of HIF signaling, we evaluated skeletal microarchitecture of 16-week-old male mice with OCY deletion of Hif1a (n=3), Hif2a cKO (n=4); or accumulation of degradation-resistant HIF-1α (n =3) or HIF-2α (n = 4) via micro-computed tomography. HIF-2α accumulation increased cortical porosity and increased trabecular bone volume fraction and trabecular number. HIF-1α accumulation and deletion of Hif2a did not affect skeletal phenotype, however, deletion of Hif1a decreased trabecular number with no effect on the cortical compartment. Our data suggests that manipulation of HIF signaling in males results in a similar skeletal phenotype to which we have described in females.
Research Grant	NIH R01 AR073772
Field of Research	Orthopedics

Abstract Title	Characterizing monocyte-dependent gene expression in metastatic canine osteosarcoma
Authors	Noah Dwyer, Alaina Ryan, Amanda Martinot, Cheryl A. London, Heather L. Gardner
Affiliations	Cummings School of Veterinary Medicine, Tufts University, North Grafton, MA
Abstract	While metastasis of canine osteosarcoma (OS) predominantly occurs in the lungs, it also develops in subcutaneous tissue, kidneys, and other bones. A role for CCR2 and IL-8 in OS pulmonary metastasis has been identified, but it is unknown whether monocytes play an equally important role in driving the metastatic behavior of OS to alternate metastatic sites. NanoString nCounter analysis of gene expression was performed in primary and multiple matched metastatic lesions (lung, kidney, subcutaneous, bone) and identified a predominance of monocyte-associated gene signatures in lung and renal sites when compared to subcutaneous and bone sites. It is therefore hypothesized that monocyte infiltrates are present in renal metastases and that monocyte-associated immunosuppressive gene expression signatures are conserved across patient-matched pulmonary and renal metastatic samples. It is further hypothesized that robust monocyte infiltrates are not present in subcutaneous or bone metastases. The NanoString GeoMX Digital Spatial Profiler will be used to analyze and compare the transcriptomes of patient-matched OS metastatic samples collected from dogs and prepared on TMAs. Fluorescent conjugated morphologic antibodies targeting nuclei, vimentin, CD3 T-cells and macrophages will be used to guide region of interest selection and to separate monocyte infiltrates from surrounding cell populations. The GeoMx Canine Cancer Panel will be hybridized to each slide allowing for analysis of differential expression of genes within selected regions of varying monocyte density at each metastatic site. These findings will help characterize the role of monocytes in driving OS metastatic behavior in alternate metastatic sites.
Research Grant	U01CA224182
Field of Research	Oncology

Abstract Title	The social network: a model of white-tail deer group structure and SARS-CoV-2 dynamics
Authors	Kortney Dziedzic, Matthew Michalska-Smith, Steven Hogg, John Moriarty, James Forester, Tiffany Wolf, and Meggan Craft
Affiliations	Ecology Evolution and Behavior (Dziedzic, Michalska-Smith, Craft), Fisheries Wildlife and Conservation Biology (Forester), and Veterinary Population Medicine (Wolf), University of Minnesota, St. Paul, MN; Three Rivers Park District (Hogg, Moriarty), Plymouth, MN
Abstract	A growing body of evidence supports interspecies transmission of SARS-CoV-2 (SCV2) in a range of domestic and wild species. North American white-tail deer (WTD) populations are of particular interest due to their abundance and proximity to humans, especially in the Midwest and East Coast. Ongoing studies have indicated that WTD are particularly susceptible to SCV2 with a suspected infection rate of 30-40%. WTD are a very social species with a complex group-living structure. We have constructed a simple stochastic model to elucidate the relationship between this structure and disease dynamics in a simulated WTD herd infected with SCV2. To better reflect reality, we have modeled our WTD population as a contact network that splits the population into social groups of two defined types, either 1) family, representing a doe and her fawns, or 2) buck, representing a male "bachelor" cluster. Our model assumes all individuals within a social group are identical and disease-causing interactions between any two individuals are determined by group association (i.e. between individuals of the same group, or between individuals of different groups). To model realistic patterns of inter-sex contact, every male in a buck group has two links to (randomly chosen) individuals in family groups. This approach allows for calculating how social structure might affect pathogen dynamics. We analyzed several hypothetical SARS-CoV-2 transmission probabilities to calculate the effects of varying group size on epidemic intensity. Preliminary results indicate that varying group size has an influence on transmission dynamics and is dependent upon both between group and within group transmission rates.
Research Grant	Van Sloun Foundation
Field of Research	Epidemiology

Abstract Title	A Novel Non-surgical Method for Sterilization in Cats
Authors	May Lynn Einfalt, Sandra Ayres
Affiliations	Department of Comparative Pathobiology (Ayres), Cummings School of Veterinary Medicine, Tufts University, Grafton, Massachusetts
Abstract	Shelter, feral, and intact cats contribute to the increasing worldwide cat population. Surgical sterilization to remove the gonads is an effective method of population control, but poses its own set of problems. We proposed a more humane approach to sterilization using a non-surgical procedure that reduces or eliminates the cells in the gonads that support development of the ova/sperm. We have designed an injectable complex consisting of a lipid nanoparticle containing a toxin that induces apoptosis. This complex is guided by an anti-Mullerian hormone II receptor antibody (AMH2) for receptors that are unique to the gonadal support cells. Preliminary work has shown that there are AMH2 receptors in the support cells in the testes and ovaries of cats and dogs and that this nanocomplex should reduce/eliminate the support cells in the gonads. We hypothesize that the treated cats can be non-surgically spayed through use of the injectable complex and have a reduction/elimination of the support cells of the ovaries compared to non-treated cats. 12 young intact female cats were used in this study, with half being injected with the nanocomplex and the other half injected with saline. The cats were observed for several months for signs or lack of sexual behavior. Blood samples from each cat were collected and analyzed for various hormones and other health issues. After being spayed, the ovaries of each cat were collected, fixed in 10% formaldehyde, photographed, and analyzed. Histologic sections of each gonad were analyzed to evaluate gonadal architecture. Data analysis is in progress.
Research Grant	Morris Animal Foundation Grant
Field of Research	Theriogenology

Abstract Title	Identification of the gastric mesenchymal cell types derived from Six2 expressing embryonic progenitors by lin
Authors	Rachel Elder, Gabriella Turnipseed, Esraa Alnahrawy, Fentahun Abate, Pawan Puri
Affiliations	Department of Biomedical Sciences, Tuskegee University CVM, Tuskegee, AL
Abstract	Mesenchymal epithelial crosstalk (MEC) is indispensable for gastric homeostasis. Mis-regulation of the MEC can cause gastric pathologies such as polyposis and cancer. Although mesenchyme is known to be a key player in gastric pathologies, the origin and identity of different mesenchymal cell types remain unknown. We recently characterized a novel conditional mutant mouse Six2Cre+/--PKAcαRfl/wt (CA-PKA) model in which single allele-mediated expression of constitutively active (CA) PKA (PKAcαR) was induced in the gastric mesenchyme using Six2-Cre transgenic mice. CA-PKA mice showed multiple gastric preneoplastic lesions such as marked inflammation, oxyntic atrophy, metaplasia, and invasive glands. The goal of the current study was to identify gastric mesenchymal cells derived from Six2+ve progenitors that may contribute towards the preneoplastic lesions in CA-PKA mice. We hypothesized that Six2 progenitors generate a subset of mesenchymal cells that are altered in CA-PKA mice. Lineage tracing in Six2-Cre;CAG-tdTomato mice along with co-immunofluorescence (Co-IF) were used to identify Six2-progentior-dervied cells. We found that Six2 progenitor-derived cells include ACTA2+ve cells of lamina propria, muscularis mucosae, muscularis externa as well as vascular smooth muscle cells. Gastric endothelial cells (CD31+ve) are not Six2-progenitor-dervied. Six2 progenitor-derived cells include a small subset of FSP1+ve stromal fibroblasts. Further Co-IF analysis showed that all these cell types are markedly altered in Six2Cre+/-;CAG-tdtomato;PKAcαRfl/wt mice. Our results identify Six2 progenitor-derived cells in the gastric mesenchyme that may be directly or indirectly involved in causing preneoplasia in CA-PKA mice.
Research Grant	This research was supported by grants from NIH T35OD010432, NIGMS# 1SC2GM130475 DHHS/HRSA D34HP00001-35-00, and NIH/NIMHD RCMI grant # U54MD007585
Field of Research	Oncology

Abstract Title	Defining the mechanisms of calcium signaling in CAR T cells
Authors	Anna Eringis, Roddy S. O'Connor, and Bruce D. Freedman
Affiliations	School of Veterinary Medicine (Eringis, Freedman) and Center for Cellular Immunotherapies, Perelman School of Medicine (O'Connor), University of Pennsylvania, Philadelphia, PA
Abstract	Over the past decade, chimeric antigen receptor (CAR) T cells have transformed therapeutic approaches to otherwise refractory B cell cancers. CAR T cells are produced by engineering patient T cells to express a single chain variable fragment with specificity for a tumor cell antigen. To be effective, CAR T cells must recognize and rapidly eliminate target cells yet maintain sufficient persistence to provide long term immunity. In their FDA-approved form, CARs are designed with either a CD28ζ or a 4-1BBζ costimulatory domain. CD28ζ CAR T cells undergo glycolytic reprogramming and exhibit enhanced short term cytolytic activity but diminished long term persistence. In contrast, 4-1BBζ CAR T cells undergo oxidative metabolic programming and exhibit poorer short-term killing activity but significantly longer persistence. Importantly, the mechanistic basis for these clinically established differences remains unclear. It is also established that Ca2+ signals regulate T lymphocyte metabolic programming, persistence, and killing. Thus, we hypothesize that intrinsic differences in CAR design give rise to quantitatively different Ca2+ signals, culminating in unique metabolic responses and biological functions. Indeed, preliminary single cell measurements of TCR-induced Ca2+ signals in primary human CD28ζ and 4-1BBζ CAR T cells reveal quantitative differences in cytoplasmic Ca2+ dynamics. Ongoing efforts are geared toward understanding the mechanistic basis for these differences in Ca2+ signaling and how they impact CAR T cell function. Importantly, this understanding will inform improved CAR T design not only for enhancing T cell effector function generally, but also in hostile tumor environments.
Research Grant	NIH R21 AI151334, NIH RO1 CA278837, and Ludwig Research Foundation (Princeton Branch)
Field of Research	Oncology

Abstract Title	A dose-finding study of cannabidiol in dogs with idiopathic epilepsy
Authors	Alyssa Estes, Daniel Gustafson, Breonna Kusick, Krista Banks, Stephanie McGrath
Affiliations	Department of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, Colorado
Abstract	Idiopathic epilepsy is the most common neurologic condition among dogs, affecting approximately 5% of the total population. The exact cause of idiopathic epileptic seizures are unknown, and approximately one third of epileptic dogs are resistant to anticonvulsant treatment. Cannabidiol (CBD) has been shown to reduce seizures in animals and humans, opening the possibility of it being used as an added treatment for idiopathic epilepsy. Currently, no study has identified a therapeutic dose for a large population of dogs. Pilot studies have shown that 5 mg/kg/day oral CBD does not produce a significant change in the number of responders to treatment, but does significantly reduce seizure frequency, suggesting a higher dosage of CBD may be more effective. Human studies have shown doses up to 50 mg/kg/day significantly reduce seizures. The study consists of two phases - Phase 1: to compare various doses of CBD to determine which is most effective in reducing seizure activity in a small number of client-owned dogs with refractory idiopathic epilepsy; Phase 2: to use the target dose from Phase 1 to determine effectiveness in a larger population of dogs. We hypothesized that doses of 20 mg/kg/day will be the effective dose in reducing seizure activity in at least 50% of client-owned canines with refractory idiopathic epilepsy. Results indicate that the 20 mg/kg/day dose of CBD is not statistically significant but is the lowest effective dose - reducing average seizure activity by 50.6%. This study will not only supply further insight into the anticonvulsive effect of CBD on dogs with idiopathic epilepsy, but also potentially relieve a pharmaceutical deficit in epileptic treatment for a large population of patients.
Research Grant	American Kennel Club Canine Health Foundation
Field of Research	Pharmacology and Toxicology

Abstract Title	Evaluation of biomarkers for prediction of equine palmar/plantar osteochondral disease
Authors	Kayla Even, Lauren Pittman, Joanne Haughan, Darko Stefanovski, Kyla Ortved, and Mary Robinson
Affiliations	Department of Clinical Studies, New Bolton Center, School of Veterinary Medicine, University of Pennsylvania, Kennett Square, PA, USA
Abstract	Palmar/plantar osteochondral disease (POD) is a common injury of the distal condyles of the third metacarpal/tarsal bone in racehorses caused by fatigue of the subchondral bone due to repeated overload. POD is thought to precede metacarpal/tarsal condylar fractures. A biomarker test using equine whole blood could be offered as a clinical diagnostic screening tool to identify horses at-risk of injury. The objective of this study was to evaluate changes in candidate biomarkers over one racing/training season in Thoroughbred horses. We hypothesized that racehorses that developed POD would have characteristic changes in pro-inflammatory cytokines and markers of bone metabolism prior to clinical manifestation of the disease compared to healthy horses. Monthly whole blood samples were collected prospectively. Plasma and mRNA were harvested and stored until further analysis. Samples were selected from 4 racehorses that developed POD diagnosed using standing robotic CT (RPOD), 4 racehorses exercised on a high-speed treadmill to simulate race training with no pathology diagnosed by standing robotic CT after 6 months (TMH), and 4 racehorses that continued to race successfully in the ensuing season (RH).Trends in the plasma proteins, C-terminal telopeptide of type I collagen (CTX-I) and osteocalcin, and white blood cell mRNA biomarkers (IL-1β, IL-RA, IL-2, IL-4, IL-6, IL-10, IL-15, IFNγ, TGF-β2, and TNFα) were evaluated using ELISA and PCR, respectively. CTX-I plasma levels did not change significantly over time in the RPOD ($p>0.424$), TMH ($p>0.948$) or RH ($p>0.595$) group. Changes in CTX-I plasma levels over time were not statistically significantly different between groups. Additional results are pending.
Research Grant	None
Field of Research	Pharmacology and Toxicology

Abstract Title	Evaluation of quantitative MRI as a tool to assess intervertebral disc degeneration in canines
Authors	Alaina Falck, Erick Buko, Kayla Chase, Diana Pendleton, Katie McDermott, Olivia Kim, Alexandra Armstrong, Suhail Parvaze, Susan Arnold, Elizabeth Bradley, Arin Ellingson, Christopher Ober, and Casey Johnson
Affiliations	Department of Veterinary Clinical Sciences (Falck, Buko, Chase, Pendleton, McDermott, Kim, Armstrong, Parvaze, Arnold, Ober, Johnson), University of Minnesota, Saint Paul, MN; Department of Orthopedic Surgery (Bradley) and Department of Rehabilitation Medicine (Ellingson), University of Minnesota, Minneapolis, MN
Abstract	Intervertebral disc disease (IVDD) is a canine and human spine disorder characterized by progressive degenerative changes in the composition of intervertebral discs that can lead to chronic pain and disability. To improve clinical management of this condition, new imaging techniques that can better evaluate early and/or progressive degenerative changes are needed. Quantitative magnetic resonance imaging (qMRI) has emerged as a promising imaging modality in human medicine for IVDD; however, no studies have explored this tool to assess spontaneous disease in canines. Dogs seen in veterinary medical centers can provide a comparative, spontaneous animal model to investigate the pathogenesis of IVDD and develop new treatments, with dual species benefit. The purpose of this study was to investigate the sensitivity of qMRI techniques in detecting degenerative changes in the general canine population. We hypothesized that qMRI values would provide noninvasive, correlative measures of physical properties indicative of disc health. In this study, vertebral column specimens were collected from 17 client-owned dogs of varying signalments whose bodies were donated for research following clinical euthanasia. Each specimen was imaged ex vivo using a 3T MRI scanner, and quantitative values of the nucleus pulposus and annulus fibrosus were obtained from 10 discs (T11/T12-L7/S1) using T2, T2*, and T1ρ relaxation time mapping and diffusion mapping. The values from these quantitative maps were compared to the radiological Pfirrmann grade, histologic grade, glycosaminoglycan content, and water content. This study will inform future work in both human and veterinary medicine regarding diagnosis and therapeutic assessment of IVDD.
Research Grant	College of Veterinary Medicine, University of Minnesota
Field of Research	Orthopedics

Abstract Title	Quantifying Tissue Enzymes and Chemical Analytes in Captive Cownose Rays (Rhinoptera bonasus)
Authors	Patrick Farias, Sean Perry, Alexa Delaune, Justin Stilwell
Affiliations	Department of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS (Farias, Perry, Delaune, Stilwell); Mississippi Aquarium, Gulfport, MS (Perry, Delaune)
Abstract	Blood chemistry and enzymes analysis is used clinically to indirectly assess organ health and function. Baseline data regarding tissue origins of enzymes, is limited in fish, particularly in elasmobranch species. The objective of this study was to identify tissue(s) of origin for specific enzymes which is important for interpreting clinical changes in cownose rays (Rhinoptera bonasus) (CNRs) biochemistry profiles. Our hypothesis anticipated that enzymes would exhibit tissue specific tropisms with higher activities in certain tissues when compared to others. Twelve, clinically healthy CNRs were obtained following a mortality event involving a life support system failure at an unaffiliated facility. Fifteen tissues from each animal were sampled and collected via necropsy. Activities were examined for six enzymes and two chemical analytes in each tissue sampled. GGT levels were significantly higher in the kidney, compared to all other tissues. CK and ALT demonstrated tissue-specific tropisms for the esophagus and skeletal muscle, and kidney and liver, respectively. AST was detected predominantly in the rectal gland, esophagus, and liver. Similarly, LDH was predominantly detected in the rectal gland. ALP concentrations were prominent in kidney, spiral valve, and small intestine. BUN and UA demonstrated no tissue specificity. This work establishes baseline tissue enzyme origins for CNRs, which will aid clinicians in diagnostic interpretation of blood chemistries and improve veterinary care for CNRs under human care.
Research Grant	None
Field of Research	Biochemistry

Abstract Title	Preliminary analysis of canine cancer cases and environmental contaminants in Kansas (2021-2022)
Authors	Douglas Farleigh, Avantika Ramekar, Mary Lynn Higginbotham, Timothy Walsh, and Chieko Azuma
Affiliations	Department of Clinical Sciences (Farleigh, Ramekar, Higginbotham, Azuma) and Veterinary Diagnostic Lab (Walsh), College of Veterinary Medicine, Kansas State University, Manhattan, KS
Abstract	The carcinogenicity of various environmental contaminants in humans has been studied extensively in recent years. However, evaluations of carcinogenicity of environmental contaminants in canines in the literature are scant. The present study was to investigate this knowledge gap and evaluate the relationship between canine cancer occurrence and environmental contaminants. Data on diagnoses of carcinomas, sarcomas, and mast cell tumors in dogs from years 2021-2022 were collected from the Kansas State Veterinary Diagnostic Lab (n = 2,803, 39% carcinomas, 21% sarcomas, 40% mast cell tumors). The 3 most reported breeds were the Labrador Retriever, Boxer, and Pit Bull Terrier. The median age was 9 years old (range 0-24 years). The cases were sorted and normalized to human population per ZIP code to reduce reporting bias and identify the top 5 hot spots of reported canine cancer cases. Data on environmentally contaminated sites and spills of hazardous materials were compiled from publicly available databases for the 5 hot spot ZIP codes and adjacent ZIP codes. Spatial autocorrelation revealed a clustered pattern for canine cancer cases. Local Moran's I cluster analysis revealed different types of local distribution patterns. Of the 5 hot spots, 2 did not have significant clustering patterns, 2 clusters followed high or low patterns, and 1 cluster displayed an anomalous clustering pattern. Exploratory regression analysis performed with the environmental data for the 5 hot spots could not adequately explain the occurrence of reported cases of canine cancer. However, these preliminary findings provide a robust foundation for expanding the study to include canine cancer data over two decades in Kansas.
Research Grant	Department of Clinical Sciences, College of Veterinary Medicine, Kansas State University
Field of Research	Oncology

Abstract Title	Evaluation of Hepatocellular Death Associated with Equine Parvovirus-Hepatitis Infection
Authors	Joshua Farris, Samantha Shallop, Joy Tomlinson, Mason Jager
Affiliations	Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY.
Abstract	Equine parvovirus-hepatitis (EqPV-H) is a recently discovered virus that causes disease in horses ranging from mild hepatitis to fulminant hepatic necrosis. In severe cases, massive hepatocellular loss leads to acute liver failure and death, known as Theiler's disease. Previous studies in our laboratory have shown that horses with mild or subclinical disease develop lobular hepatitis with increased individual hepatocyte death. Individual dead hepatocytes in equine parvovirus hepatitis have features of apoptosis, including cell shrinkage, hypereosinophilia, and lymphocyte satellitosis. Apoptosis is the major form of cell death caused by most pathogenic parvoviruses, but necroptosis and necrosis have also been described. This study aimed to examine whether equine parvovirus infection results in regulated cell death of the host cell. To accomplish this, liver tissue biopsies were collected from nine horses before and after experimental EqPV-H infection. Formalin-fixed, paraffin-embedded samples were evaluated for regulated cell death using a fluorescent deoxynucleotidyl transferase-dUTP nick end labeling (TUNEL) assay. Fluorescent microscopy revealed increased levels of fragmented DNA in horses with lobular hepatitis compared to the same horse pre-infection. These findings suggest regulated cell death is important in developing hepatitis during EqPV-H infection. Future studies will examine which regulated cell death pathways are activated in infected hepatocytes. This data is crucial to understanding the complex pathogenesis of this novel virus.
Research Grant	National Institute of Health
Field of Research	Virology

Abstract Title	Clinical signs of HPAI in wild birds presented to US rehabilitation facilities
Authors	Giulia Ferrari and Dr. Barb Wolfe
Affiliations	Colorado State University CVM, Fort Collins, Colorado
Abstract	Highly Pathogenic Avian Influenza (HPAI) H5N1 poses a significant threat to both domestic poultry and wild birds. As wild birds are particularly susceptible to H5N1, understanding the presentation of the disease is crucial for management. Birds presented to wildlife rehabilitation centers provide a unique opportunity to document clinical signs of H5N1. A total of 200 birds presenting to US rehabilitation centers were included in this study, representing 20 species. HPAI diagnosis involved PCR testing of tracheal or oropharyngeal swabs. Clinical signs observed in affected birds were obtained from veterinary records and field observations. The presence and severity of clinical signs were categorized and compared across the four US flyways and across species to identify potential variations. Preliminary results indicate that the clinical signs of H5N1 in presented birds are consistent across the US and include lethargy, anorexia, depression, corneal edema, nasal discharge, and neurological abnormalities. Further analysis and comparisons are underway to identify significant differences in prevalence and severity of clinical signs among the flyways and species. This study was designed to assist wildlife rehabilitators, veterinarians, and researchers in understanding the clinical signs associated with HPAI in wild birds. Early detection and reporting can lead to prompt intervention, preventing the spread of the disease and minimizing its impact on bird populations. A better understanding of the clinical signs of H5N1 will aid in the development of targeted surveillance and management strategies to mitigate the disease's impact on avian populations in rehabilitation settings and in conservation organizations.
Research Grant	None
Field of Research	Wildlife Conservation

Abstract Title	Effects of wildfire on deer mice and hantavirus population dynamics in Sierra Nevada mountains of California.
Authors	Julien Ferrero, Ariel Loredo, Bruno Ghersi, Tracy Drazenovich, Alexandre Tremeau-Bravard, Sarah Smith, and Brian Bird.
Affiliations	One Health Institute, School of Veterinary Medicine, University of California, Davis, CA (Ferrero, Loredo, Drazenovich, Tremeau-Bravard, Smith, Bird); VetAgro Sup campus vétérinaire de Lyon, Marcy-l'Etoile, FRA, Ecole Normale Supérieure de Lyon, FRA (Ferrero); Cummings school of Veterinary Medicine, Tufts University, MA (Ghersi)
Abstract	Sin Nombre virus (SNV) is a zoonotic hantavirus, causing cardiopulmonary syndrome in humans. The deer mouse, Peromyscus maniculatus, is the natural reservoir and is widespread in western North America. Transmission among rodents is mainly due to biting and other aggressive behaviors. Spillover to humans is primarily due to inhalation of virus contaminated aerosols from rodent droppings. Ecological disturbances are associated with changes in SNV prevalence, however the effect of wildfire on this relationship has not been fully explored. Here, we investigate Peromyscus maniculatus and SNV population dynamics in a mixed wet meadow ecosystem impacted by wildfire in 2021. A total of 489 rodents were non-lethally sampled between 2020 and 2023 at burned and unburned sites. Active SNV shedding was detected in 7.49% of sampled P. maniculatus by RT-qPCR, and SNV genome sequence was obtained from 14 individuals using next-generation sequencing approaches. Individual animal dispersal and capture-mark-recapture analyses showed increased movements of rodents in post-fire recovering areas compared to unburned sites. Based on these observed behavior changes, we hypothesize that higher genetic diversity and SNV prevalence will be detected in P. maniculatus populations in burned sites compared to control sites. To assess these differences, 10 to 15 microsatellite genomic markers for population genetics analyses will be applied on 60 randomized sampled individuals stratified over time, location, and SNV status. Population structure will be estimated with STRUCTURE/CLUMPP and Bayesian clustering algorithms. Clusters will be compared to fire exposure as an independent variable, using statistical regression models.
Research Grant	State of California, Wildlife Conservation Board #WC-1856KM; California Department of Fish and Wildlife Green House Gas (GHG) #Q1996007.
Field of Research	One Health

Abstract Title	High prevalence of haemosporidian parasites in Kansas birds: risk of spillover between native & captive birds
Authors	Amanda Fideldy, Bethany McGregor, and Phillip Shults
Affiliations	College of Veterinary Medicine, Kansas State University, Manhattan, KS (Fideldy, Amanda). United States Department of Agriculture, Agriculture Research Service, Manhattan, KS (Mcgregor, Bethany and Shults, Phillip).
Abstract	Avian haemosporidian parasites are vector-borne protozoans that infect a broad range of avian hosts. While native bird populations appear mostly clinically unaffected by these parasites, they pose a significant risk to captive bird species. To assess the transmission risk between these two systems, we conducted a study to characterize the local avian blood parasite diversity and identify their associated vector species. Using a nested PCR assay, we tested 78 avian blood samples (collected in a previous study) for the presence of Haemoproteus and Leucocytozoon spp. Of these, 30% were positive for haemosporidian parasites, with most of these cases occurring in owls and turkeys. Additionally, we conducted 7 weeks of trapping to collect Culicoides biting midges, the suspected vectors, from four different habitat types: a natural area, farm, zoo, and backyard farm. The midges were identified to species and pooled for PCR analysis, however, none of the Culicoides species tested positive for parasites during the initial 4 weeks of collecting. This is potentially due to the limited number of midges tested. Nonetheless, two species, C. haematopotus and C. crepuscularis were identified as potential vector species based on overall abundance and exposure to blood meals infected with Haemoproteus sp. While habitat type affected the Culicoides species diversity, the most likely vector species, mentioned above, were commonly found across all study sites. Our findings suggest that excluding certain avian fauna and implementing control measures for Culicoides populations could help mitigate the risk of transmitting native haemosporidian parasites to captive bird populations.
Research Grant	USDA-ARS NP104 project 3020-32000-018
Field of Research	Parasitology

Abstract Title	Agreement and accuracy of intraoperative sentinel lymph node mapping for skin and subcutaneous tumours
Authors	Diana M. Fitzgerald, Charly McKenna, and Michelle L. Oblak
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Abstract	Sentinel lymph nodes (SLN) are the first nodes receiving lymphatic drainage from a primary solid tumour. If a tumour is metastatic through the lymphatic route, the SLNs will be the first location to harbour metastasis. A current SLN mapping technique uses guidance from indocyanine green (ICG), a fluorescent tracer, which tracks tumour draining lymphatics under near infrared light (NIRF). When surgically staging patients, the anatomically closest regional lymph node (RLN) is often used as a surrogate for the SLN, however the RLN does not always correspond to the SLN. The aim of this study was to establish the agreement between a tumour's RLN and SLN for skin and subcutaneous tumours in the veterinary fluorescence literature, and to report additional cases from the Ontario Veterinary College (OVC). A secondary objective was to evaluate long term outcome in these patients. A systematic search identified studies examining SLNB using ICG-NIRF for skin and subcutaneous tumours in dogs and cats. Extracted results included signalment, tumour location, correspondence of RLN:SLN, ICG dosage, and timing. Four studies (n = 59 tumours upon 55 patients) and 14 OVC patients (2018-2023; n = 14 tumours) were included. RLNs did not correspond to SLNs in 15.1% of tumours (n=11), had partial RLN:SLN correspondence in 38.3% (n=28), and the RLN and SLN corresponded in 46.6% (n = 34). Accuracy of ICG NIRF for detecting metastatic nodes was 90.4% (66/73). No OVC patients developed additional LN metastasis on long term follow up. Based on the findings of this analysis, the RLN is not an accurate method for metastasis staging and SLNB with ICG NIRF can be considered when LN status impacts treatment.
Research Grant	None
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Callitrichine herpesvirus 3 (CalHV-3) in the common marmoset as a model of gammaherpesvirus infection
Authors	Caitlin E. Fitzpatrick, Stacey L. Piotrowski, Allison Tucker, Amanda Lee, Heather Narver, and Steven Jacobson
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Abstract	Callitrichine herpesvirus 3 (CalHV-3) is a gammaherpesvirus in the common marmoset (Callithrix jacchus) that was first discovered in the early 2000s. Although CalHV-3 was found to be phylogenetically related to human Epstein-Barr virus (EBV), the biological similarities between CalHV-3 and EBV have been poorly described. To better characterize the potential utility of CalHV-3 as a model of gammaherpesvirus-related disease, a droplet digital PCR (ddPCR) assay was developed to screen for virus in peripheral blood mononuclear cells (PBMCs), saliva, and formalin-fixed paraffin-embedded (FFPE) tissues. Hematoxylin and eosin (H&E) and immunohistochemistry (IHC) for CD3, CD20, and Iba1 were used in FFPE tissue to confirm neoplastic cell of origin in cases of suspected lymphoma. Naturally occurring prevalence of CalHV-3 in our colony is 19%. In animals infected with CalHV-3, virus was consistently detected in both PBMCs and saliva, with no correlation in viral loads between samples. Lymphoid organs had higher viral loads than non-lymphoid tissues. All cases of B-cell lymphoma in the common marmoset were positive for CalHV-3, with millions of copies of virus in PBMCs and neoplastic tissue. Similar to EBV, CalHV-3 is characterized by persistent infection, viral load fluctuations over time, viral shedding in saliva, and oncogenesis in a small subset of animals. These results suggest that CalHV-3 may serve as a translationally relevant model of EBV infection and associated diseases, such as neoplasia and neurodegenerative disorders like multiple sclerosis (MS) and Alzheimer's disease (AD).
Research Grant	NINDS, Intramural Research Program
Field of Research	Virology

Abstract Title	Investigation of factors related to seroprevalence of Anaplasma marginale in Mississippi cow-calf herds
Authors	Eryn M. Fleming, W. Isaac Jumper, David R. Smith
Affiliations	College of Veterinary Medicine, Mississippi State University, Starkville, MS, USA
Abstract	Anaplasma marginale, the causative agent of bovine anaplasmosis (BA), is a disease of economic importance to the U.S. beef cow-calf industry. Seroprevalence of A. marginale within and between herds in Mississippi is not well described. The objective of this study was to estimate within and between herd seroprevalence of A. marginale in cow-calf herds and investigate herd-level risk factors associated with seroprevalence. Blood samples were collected from all mature cows (i.e., ≥2 years of age) in 20 beef cattle herds across MS. A total of 765 serum samples were tested using a commercially available competitive enzyme linked immunosorbent assay (cELISA). Producers were surveyed on herd demographics, herd management, biosecurity, herd health, and bovine anaplasmosis at the time of sample collection. Most herds were commercial (17/20) and the average herd size sampled was 44 head. Of those herds fed free choice mineral, 47% (9/19) fed free choice mineral containing CTC within the last 12 months. Fifty-five percent (5/9) of herds had access to free-choice mineral containing CTC year-round. Overall, 85% (17/20) of herds tested positive by cELISA, and the average within-herd seroprevalence was 39%. Operations that fed chlortetracycline (CTC)-containing mineral free choice within the previous 12 months had greater odds of increased herd seroprevalence compared to those who did not feed CTC-containing mineral free choice (OR=3.349, 95%C.I.=1.288-7.168). Within herd-seroprevalence varied greatly and is influenced by various management factors. This study is the first to report within and between herd seroprevalence of A. marginale infection in MS cow-calf herds.
Research Grant	Mississippi State College of Veterinary Medicine.
Field of Research	Epidemiology

Abstract Title	Assessing the clinical utility of bendable osteochondral allografts for patellar resurfacing in dogs
Authors	Cassandra Fletcher, Chantelle C. Bozynski, Katherine A. Spack, Gerard A. Ateshian, and James L. Cook
Affiliations	College of Veterinary Medicine (Fletcher), Thompson Laboratory for Regenerative Orthopaedics (Bozynski, Cook), University of Missouri, Columbia, MO, Musculoskeletal Biomechanics Laboratory (Spack, Ateshian), Columbia University, New York, NY
Abstract	While osteochondral allografts (OCA) are already used in treatment of focal arthropathies, there are limitations associated with current techniques, including the size of the defect, the joint affected, and the ability to find a donor match considering the large variability in both size and geometry of the canine joint surface. In this study, a novel bendable OCA (BOCA) was assessed for clinical feasibility, safety, and efficacy of recovery, processing, storage, and transplantation in comparison to standard shell OCAs in a patellar resurfacing model in dogs. We hypothesize that patellar BOCAs will integrate and allow for superior functional outcomes compared to standard shell OCAs. Five skeletally mature purpose-bred hounds, not size-matched to the donor dogs, were evaluated preoperatively with forcemat kinetics, range of motion, lameness scoring and VAS pain metrics. Patellar allografts obtained from 5 canine cadavers were implanted into both knees by hemisecting the native patella to remove the entire articular layer and a portion of the underlying bone then replacing it with either, the grooved BOCA to allow for minor compression and expansion, or standard shell patellar allograft. Remnant patellar allograft and media samples were submitted for microbial culture at time of transplantation and all samples were negative. At 3- and 6-month post-transplant timepoints, all metrics will be re-assessed and radiographs of each knee will be evaluated by one radiologist blinded to each treatment type. At the 6-month timepoint chondrocyte viability and whole joint and patellar graft histology will also be evaluated. If our hypothesis is supported, adaptively conforming OCAs may be a treatment option for canine patients.
Research Grant	Department of Defense US Army Medical Research (CDMRP GRANT) - PRMRP W81XWH1810361
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Assessing efficacy and utility of a point-of-care coagulation analysis tool in the common marmoset
Authors	Alexandra Fong, Ellen Buckley, Martina Jackson, Kelly Metcalf Pate, and Galit Frydman
Affiliations	Cummings School of Veterinary Medicine, Tufts University, Grafton, MA (Fong); Department of Comparative Medicine, Massachusetts Institute of Technology, Cambridge, MA (Fong, Buckley, Jackson, Metcalf Pate, Frydman); Coagulo Medical Technologies, Newton, MA (Frydman)
Abstract	Coagulo Medical Technologies developed a new low volume (50-100uL), rapid (10 minutes), point-of-care (POC) coagulation analysis tool which has previously only been used in human samples. This POC testing system can perform up to 9 coagulation tests simultaneously and evaluate multiple parts of the coagulation pathway. Due to the low volume of blood required, it could provide great use in veterinary medicine, especially for small exotic animal species. Marmoset monkeys (Callithrix jacchus) are a species of new world primates that are known for their small size (< 500 g) and large family groups. In this study, we sought to validate Coagulo Medical Technologies' new coagulation tool using blood samples from individual animals from an active breeding colony. Blood was collected opportunistically under sedation during routine procedures, in which phlebotomy would already be performed. Whole blood samples were placed in 3.2% sodium citrate tubes from 20 individuals (12 male; 8 female) ranging in age from 8 months to 8 years. Manual activated clot times (ACT) were calculated using microliter amounts of platelet poor plasma on printed circuit boards sensors which were compared to the POC device. The median manual ACT was 164 seconds and ranged from 110 seconds to 405 seconds. These values will be compared to the automated ACT derived from the POC device. This study is the first introduction to validating Coagulo Medical Technologies' device in a small exotic animal species and will define a reference range of coagulation parameters for common marmosets. Once validated, this technology may be used to determine the effect and underlying mechanism of clinical conditions, such as pregnancy, on coagulation in this and other species.
Research Grant	None
Field of Research	Clinical Pathology

Abstract Title	Combined MSC-antiviral treatment for systemic inflammation and lymphoid tissue regeneration in cats with FIP
Authors	Rachel Formaker, Patrawin Wanakumjorn, Diego Castillo, Amir Kol
Affiliations	Department of Pathology, Microbiology, and Immunology, School of Veterinary Medicine, University of California, Davis, CA
Abstract	Feline infectious peritonitis (FIP) is a highly fatal disease of young domestic cats that causes severe systemic inflammation and lymphoid tissue destruction. Existing antiviral treatment for FIP (nucleoside analog GS-441524) is not FDA approved and its effects on immune system recovery have not been evaluated. Multipotent stromal cells (MSCs) are somatic cells that can be readily expanded ex-vivo and have been shown to have potent anti-inflammatory properties and facilitate tissue regeneration when administered as a therapeutic. This study investigated the effects of combined MSC and antiviral therapy on inflammation and lymphoid recovery by assessing plasma levels of pro-inflammatory cytokines and blood lymphocyte counts throughout the course of treatment. A randomized, double-blind, placebo-controlled trial with 10 client-owned cats with effusive FIP was performed. Over the course of 11 weeks, all cats received daily antiviral medication GS-441524. Half the cats received two infusions of MSCs on weeks 1 and 3, while the other half received placebo infusions of saline. Blood samples were collected at weeks 0, 1, 3, 7, and 11. Manual 400-cell differential leukocyte counts were performed and used to calculate total lymphocyte counts. Plasma levels of pro-inflammatory cytokines from weeks 0, 7, and 11 were analyzed using a Luminex® assay. Cats in both treatment groups survived to the end of the study and recovered from clinical signs of FIP. Results of this study will elucidate the immunomodulatory effects of MSCs on FIP recovery and provide insight into how the immune system recovers from this disease. It will also provide evidence of the safety and efficacy of MSCs for further exploration as a treatment option for FIP.
Research Grant	National Institutes of Health; National Institute of Child Health and Human Development (1R21HD106027-01)
Field of Research	Immunology

Abstract Title	Validation of Mycobacterium avium spp. paratuberculosis DNA detection in goats with confirmed Johne's disease
Authors	Samantha Frontz, Brittanie Peake, Roger Merkel, Lionel Dawson, Tim Snider, and Jennifer Rudd
Affiliations	Department of Veterinary Pathobiology (Frontz, Peake, Snider, Rudd) and Department of Veterinary Clinical Sciences (Merkel), College of Veterinary Medicine, Oklahoma State University, Stillwater, OK; School of Agriculture and Applied Science (Dawson), Langston University, Langston, OK
Abstract	Johne's Disease (JD) is an economically important ruminant infection characterized by granulomatous enteritis. It is estimated $198 million is lost per year to JD in the US dairy industry alone. The causative agent of JD is the intracellular bacterium, Mycobacterium avium spp. paratuberculosis (MAP). While this disease is well studied in cattle, there is an incomplete understanding of the pathogenesis in small ruminants, particularly goats. Goat kids are exposed early in utero or through ingestion from contaminated feed, water, or the environment. JD has a long "silent" period and clinical signs do not appear until 2-5 years after initial exposure. Current diagnostic assays for MAP detect shedding as bacterial DNA in feces or humoral response to infection; both assays require late stages of infection for reliable detection. Therefore, MAP+ animals contaminate the environment prior to detection, resulting in herd transmission. We hypothesize that utilizing a novel polyclonal enhancement of MAP bacterial DNA detection paired with next-generation sequencing (NGS) can detect an earlier infection stage of JD+ goats when compared with fecal PCR and ELISA for antibody detection. In Phase 1, we optimize PCR on serum from late-stage infected goats and assess the extent of disease and antigen detection in various tissue and fluid samples. Phase 2 (ongoing) will determine the sensitivity of these assays prior to clinical disease and compare non-enhanced MAP DNA with polyclonal antibody-enhanced detection and NGS. The ability to categorize infection stage has future implications in characterizing early-stage immune dysregulation and detection as well as clear advantages to producers struggling with the impact of JD in their herd.
Research Grant	OSU College of Veterinary Medicine RAC Seed Grant, Langston University
Field of Research	Production Animal Medicine

Abstract Title	Prevalence of ESBL and carbapenemase producing Enterobacterales in shelter dog and cat populations
Authors	Taylor Frownfelter, Stephen D. Cole, Brittany Watson, and Chelsea Reinhard.
Affiliations	Department of Pathobiology (Frownfelter, Cole), Department of Clinical Studies and Advanced Medicine (Watson, Reinhard), School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA.
Abstract	The increasing prevalence of infections with extended-spectrum beta lactamase (ESBL) and carbapenemase producing Enterobacterales (CPE) is threatening the future use of commonly used drugs in veterinary practice. In human medicine, the presence of ESBL producing Enterobacterales (EPE) is known to increase mortality risk compared to other causes of bacteremia. Since companion animals are reservoirs for these organisms, it is crucial that we gain a better understanding of the potential sources of infection. These infections were thought to be nosocomially acquired, but increasing reports of EPE and CPE in companion animals demonstrated a need for a more inclusive prevalence study. This study aimed to determine the prevalence of EPE and CPE colonization in sheltered dogs and cats using 4 different shelter populations in the Philadelphia region. We hypothesized that sheltered animals would have a lower prevalence of colonization due to their lower incidences of antimicrobial exposure compared to housed dogs and cats. Fecal samples were collected from sheltered animals within 1 week of intake to the facility. Each specimen was selectively cultured to identify EPE and CPE. Positive samples underwent whole genome sequencing to characterize the molecular mechanism of resistance and genetic lineage. We found that the prevalence of fecal colonization with EPE and CPE are 3.8% (21/550) and 0% (0/550) respectively in sheltered cats and dogs, which is consistent with our initial hypothesis. The importance of β-lactams in veterinary practice highlights the need for continued surveillance among companion animals. This data not only informs future surveillance studies, but also refines preventative and biosecurity measures in shelters.
Research Grant	None
Field of Research	Antimicrobial Resistance

Abstract Title	Role of FAP protease activity on composition, structure and biology of fibroblast derived matrices
Authors	Nathalie Fuhrman, Leslie Todd, Katherine Pelland, Zebin Xiao, Pranidhi Baddam, Ellen Puré
Affiliations	Department of Biomedical Sciences, University of Pennsylvania School of Veterinary Medicine, Philadelphia, PA. Capstan Therapeutics (Baddam, Puré), Philadelphia, PA.
Abstract	Fibroblast activation protein (FAP) is a serine protease and member of the dipeptidyl aminopeptidase family with collagenase activity in vitro. FAP, and specifically its proteolytic activity, is upregulated on fibroblasts in the presence of Transforming Growth Factor Beta (TGF-β). FAP has been demonstrated to play important roles in ECM remodeling, by increasing the accumulation of collagen and fibronectin, and in tumor development, making it a potential therapeutic target. But, a comprehensive look at how FAP itself, either through or independent of its enzymatic activity, impacts the composition and structure of stroma has yet to be conducted. We address this gap by comparing the biophysical and biochemical properties of fibroblast derived ECM (FDMs) generated in the presence and absence of FAP and FAP proteolytic activity to better understand the impact of FAP in matrix production and remodeling. Fibroblasts were isolated from congenic C57BL/6 wild-type, FAP-null (FAP-KO) and FAPS624A (enzymatic dead mutant of FAP) mice and were cultured in either control media or media supplemented with 2ng/ml of exogenous TGF-β for eight days. Flow cytometry was used to characterize their phenotype and the matrix produced was visualized using second harmonic generation imaging microscopy. The cells cultured in a TGF- β enriched environment are expected to have a higher expression of FAP and more fibrillar collagen matrix, as has been seen in human fibroblasts. Regarding the different genotypes, we hypothesize that the wild-type cells will produce a more fibrillar matrix. Comparing the wild type to both a global FAP knock out and the FAP enzymatic dead mutant will allow us to tease out FAP's role in driving the fibrogenic phenotype.
Research Grant	Capstan Therapeutics
Field of Research	Physiology

Abstract Title	An evaluation of pair housing and relationship strength on nonhuman primate sleep quality
Authors	Shaina Furman, Emily Knight, Rachel Choo, Jessica Izzi, Melissa C Painter, and Lydia M. Hopper
Affiliations	Michigan State University, East Lansing MI (Furman), Johns Hopkins University, Baltimore MD (Choo, Knight, Izzi, Painter, Hopper)
Abstract	Understanding the behavior of laboratory animals during the night is essential to ensure enhanced animal welfare, improved clinical decisions, and experimental validity. A recent study suggested that cohousing nonhuman primates (NHPs) extends the time taken for animals to fall asleep and limits time spent asleep, as measured by inactivity. Cohousing is beneficial to wellbeing of NHPs, and is recommended by the Guide, so we further evaluated the sleep quality of paired NHPs via detailed behavioral data. Using direct observation and video recording, we studied 12 pair-housed female rhesus macaques. Daytime evaluations (average: 18/subject) were done cage side once per week, with data recorded every 15 s for 5 min. Nighttime evaluation (3 nights/pair) was taken every minute across 4 30-min segments. Sleep latency, the time from lights off until the first appearance of sleep, and the percentage of time asleep, was calculated. We found video monitoring allowed us to differentiate sleep from inactivity. The average time between social partners to fall asleep was short (average: 6 min ± 8) and monkeys' sleep latency was correlated with their partner's ($t=4.85$, $P=0.008$). The NHPs average sleep latency was 29 mins ± 9, and during the dark light cycle they spent the majority of the time asleep (86% ± 7%), reflecting better sleep quality than that reported in other studies for singly housed NHP. However, monkey's social relationship with their partner, measured by % time in contact during the day, was negatively correlated with time spent sleeping at night ($t=-3.30$, $P=0.008$). These results support the benefits of cohousing as well as promote our need to understand the behavior of laboratory research animals 24/7.
Research Grant	None
Field of Research	Behavior

Abstract Title	Enhancing Medication Delivery: 3D Modeling of the Canine Ear for Treating Otitis Externa Using BIO-PLY
Authors	Jessica Gaine, Linda A. Dahlgren, Jessica Gilbertie, Tessa LeCuyer
Affiliations	Virginia-Maryland College of Veterinary Medicine, Blacksburg, VA (Dahlgren, Gaine, LeCuyer) Edward Via College of Osteopathic Medicine, Blacksburg, VA (Gilbertie)
Abstract	Otitis is one of the most common infections in dogs and is becoming a treatment challenge due to the increasing prevalence of recurrent infections. Discovery of novel approaches to treat otitis is an urgent need. Some otitis pathogens, such as Staphylococcus pseudintermedius and Pseudomonas aeruginosa, create a protective polymeric matrix called a biofilm, which protect bacterial communities from the host immune system and significantly reduce the efficacy of antibiotics. BIO-PLY is a developing adjunct therapy that synergizes with antimicrobials through its anti-biofilm activity. The objective of this project was to develop a BIO-PLY delivery system by creating a 3D model of a canine head and to test different carrier compounds for retention in the model and for their antibiofilm properties. A small hard plastic prototype was used as an outline for feasibility. Then, a larger hard plastic was used to scale the model, which was evaluated by an experienced veterinary anatomist . It was determined that the model's ear canals are slightly larger than average and that the model is anatomically correct. The final model was printed on a Lulzbot Taz 6 with a rigid inner ear structure and more flexible outer ear shape to allow for manipulation of the pinna for inserting medication. The final model was printed with thermoplastic polyurethane filament (TPU) for its elastic properties and ability to be layered to create a rigid surface, allowing TPU to be used for both the inner and outer ear of the replica. Three delivery vehicles were tested: mineral oil, triz EDTA and PEG 400. The vehicles were assessed for anti-biofilm properties and retention in the 3D model after motion.
Research Grant	NIH 2T350D011887-16
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Immunocontraception: zona pellucida antigens with AS03-like adjuvant decreased fertility in mice
Authors	Lea Gamez Jimenez, Ahmed AbdelKhalek, Harm HogenEsch
Affiliations	Department of Comparative Pathobiology, College of Veterinary Medicine, Purdue University, West Lafayette, IN (Gamez Jimenez, AbdelKhalek, HogenEsch) Purdue Institute of Inflammation, Immunology, and Infectious Diseases, Purdue University, West Lafayette, IN (HogenEsch)
Abstract	Wildlife overpopulation has detrimental consequences for the sustainability of ecosystems. Contraceptive vaccination using native porcine zona pellucida (nPZP) proteins isolated from ovaries is among the most humane, safe, and least disruptive options to mitigate this. However, improvements in the longevity, safety, and preparation efficiency of current vaccines are needed. This study compared the humoral response and fertility outcomes in female mice immunized with different vaccine formulations. Antigens included nPZP, recombinant PZP2 and PZP3 and recombinant equine IZUMO1 derived from Chinese hamster ovary (CHO) cells, and PZP3 derived from GnTI deleted HEK293 cells. Antigens were formulated with an AS03-like emulsion adjuvant, AddaS03, or with a combination adjuvant comprised of a plant-derived nanoparticle, Nano-11, and a stimulator of interferon genes (STING) agonist, ADU-S100. Serum antibody responses to nPZP and IZUMO1 were determined by ELISA. The IgG, IgG1 and IgG2b levels were significantly increased after the third dose with the highest titer seen in mice immunized with nPZP with AddaS03. Although least abundant, IgG2a levels were highest in Nano-11/ADU-S100 groups, indicating a more balanced Th1/Th2 response. Fertility was assessed by fetal count, and only the nPZP with AddaS03 group had a significant decrease in fertility. To conclude, the nPZP with AddaS03 formulation appears to be a promising alternative contraceptive vaccine, although trials with wildlife species are necessary for further formulation refinement.
Research Grant	The Humane Society of the United States
Field of Research	Immunology

Abstract Title	Generating exogenic oligodendrocyte progenitor cells for spinal cord injury
Authors	Jessica Garcia, Phoebe Strell, Walter Low
Affiliations	University of Minnesota CVM, Falcon Heights, MN
Abstract	Spinal cord injury (SCI) results in two physiological events marked first by axonal injury, death of neurons and glial cells followed by uncontrolled inflammation and chronic demyelination. Recent studies have found that introducing oligodendrocyte progenitor cells (OPCs) recovers the loss of myelin and improves behavior in mice. Still, there is a short window between the time of injury and the transplant. Furthermore, astrocyte production at the site of injury can limit the successful transplantation of OPCs as they are marked as non-self. To decrease the rejection of these cells, the novel blastocyst complementation (BC) method can be used to generate exogenic cells. BC operates by targeting and ablating a specific gene to the organ or cell of interest in an early-stage embryo to create a developmental niche. Donor stem cells are injected into the genetically modified embryo, then will grow, and fill this developmental niche to generate an exogenic organ or cell. BC has successfully generated the pancreas, kidneys, eyes, and liver. Previous studies in our lab demonstrated that HHEX mouse embryos complemented with mouse iPSCs generate cells found in the forebrain and spinal cord. We hypothesize that by ablating HHEX that we can create a niche for the generation of exogenic OPCs. To test our hypothesis immunohistochemistry (IHC) and spatial genomics will be used to analyze exogenic OPCs in chimeric and wild-type brains. The exogenic OPCs will be identified through a triple positive expression of GFP, PDGFRα, and OLIG2. Spatial genomics will be utilized to determine the transcriptional profile of OLIG2/PDGFRα positive cells to determine if their expression profile is like endogenous OPCs.
Research Grant	Research Grant: NIH R01 AI173804, NIH RF1 AG077772
Field of Research	One Health

Abstract Title	Controlling Neural Activity in a Primate Brain Using Optogenetic Techniques
Authors	Sabrina Garcia, Sebastien Tremblay, Michael Platt
Affiliations	Department of Neuroscience, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania
Abstract	Recent advancements in neuro-technologies have propelled our current understanding of the complex circuitry of the brain and the etiologies and possible treatments of numerous neuropathies. One such tool, optogenetics, presents a powerful method for targeting and manipulating individual neurons using light. In this study, the viral vector AAV1-CaMKIIa-SwiChR++-eYFP was injected into the primate brain, and its genetic cargo incorporated into target neurons. The SwiChR motif is an inhibitory opsin activated by blue light (437 nm) and deactivated with red light (635nm). As such, neurons expressing this opsin can be deactivated by blue light, and reactivated by red light. Through electrophysiology techniques, we are completing preliminary testing to ensure that the infected neurons respond as hypothesized to blue and red light stimulation. The applications of this research are most obvious when looking at neuropathies such as epilepsy where the electrical functioning of the brain is compromised. Through targeted light pulsation, individual neurons could be activated or inhibited in order to regulate misfiring events in neurological patients.
Research Grant	NIH R01 10084477
Field of Research	One Health

Abstract Title	Utilizing 3D Organoid Technology to Model Bovine Mastitis In vitro
Authors	Paulina Garcia, Christopher Zdyrski, Ryan Feauto, Abigail Ralston, Pablo Pineyro, Jonathan P. Mochel, Karin Allenspach-Jorn, and Vengai Mavangira
Affiliations	Iowa State University, Ames, IA(Garcia) Department of Biomedical Sciences(Mochel) Veterinary Diagnostics & Production Animal Medicine(Mavangira) Veterinary Diagnostic Laboratory(Pineyro) Veterinary Clinical Sciences(Jorn) 3D Health Solutions Inc., Ames, IA(Zdyrski, Feauto, Ralston) SMART Pharmacology(Jorn, Mochel)
Abstract	Bovine coliform mastitis contributes to economic losses to the dairy industry due to decreased milk production and compromised animal health. Previous research has been unable to improve the effectiveness of current therapies due to a lack of reliable in vitro approaches for investigating disease mechanisms. The advent of 3D adult stem cell-derived organoids offers opportunities to model the mammary gland and liver in vitro in a way that mimics natural bovine coliform mastitis and allow for the development of effective treatments. We aimed to develop this model from mammary gland and liver tissue samples collected from healthy dairy cattle. Mammary and liver tissues collected postmortem were minced, washed, and plated in Matrigel before incubating at 37˚C in medium with intestinal stem cells growth factors, Rho-associated kinase inhibitor, and glycogen synthase kinase 3β inhibitor. Throughout their culture, mammary organoids were cleaned, passaged, and attempted to be expanded. While initial growth was observed, long-term expansion was not possible with current culture conditions, and we hypothesize additional adjustments to growth factors or culture conditions are needed. For organoids that achieved adequate density, samples were fixed for histopathological analyses and immunofluorescence for various markers, including Cytokeratin 5, Cytokeratin 18, and Vimentin. Our study showed that short-term growth was achieved for mammary gland and liver organoids, and preliminary characterization of the samples was completed on relevant immunofluorescent markers. Our success in isolation and short-term growth of bovine organoids provides an opportunity to improve our model for future studies regarding systemic bovine mastitis.
Research Grant	Iowa Livestock Health Advisory Council (ILHAC) Project, 2023-2024
Field of Research	Production Animal Medicine

Abstract Title	Production and validation of Nipah virus-like particles containing fusion and attachment glycoprotein mutants
Authors	Jacob Gaydos, Viraj Upadhye, Jean Lee, and Hector Aguilar-Carreño
Affiliations	Department of Microbiology and Immunology, College of Veterinary Medicine, Cornell University, Ithaca, NY
Abstract	Nipah virus (NiV) is an emerging, zoonotic paramyxovirus characterized by high mortality, ranging from 40% to 90%, in several outbreaks across Southeast Asia. With no vaccines or antivirals, treatment is limited solely to supportive care, leading to its BSL- 4 and select agent status. Like other paramyxoviruses, virus fusion and entry are mediated by the transient interaction of two surface glycoproteins: the fusion (F) and attachment (G) proteins. Despite the necessity of this interaction for infection, its mechanism is poorly understood, due in part to the instability of the F and G complex. In our lab, it is hypothesized that two mutants of these proteins, NiV F (R3A) and NiV G (N152Q), may increase the stability of the F and G complex, allowing for further investigation of this interaction. To test this hypothesis, we generated virus-like particles (VLPs) containing the mutant F and G proteins for downstream analysis. The VLP system allows for the large-scale production of the mutant proteins for vaccination and analysis of the mutant F and G complex versus wild-type. However, with limited information on the effect of the mutant proteins on VLPs, high-resolution validation is necessary to characterize their morphology and abundance before downstream applications. Here, we utilize electron microscopy and flow virometry to analyze viral protein distribution on the surface of VLPs. The successful production of these mutant VLPs provides a possible medium to resolve the elusive high-resolution structure of the F and G complex. Additionally, our work will inform future vaccine studies, with the goal of targeting and inhibiting the F and G proteins and subsequently, the ability of the virus to infect cells.
Research Grant	NIH/NIAID R01 AI109022
Field of Research	Virology

Abstract Title	Investigating the Pathogenesis and Transmission Pathways of Feline Infectious Peritonitis
Authors	Damilola Gbore, Carolina Menchaca, Ximena A. Olarte-Castillo, Beth N. Licitra and Gary R. Whittaker
Affiliations	Cornell University College of Veterinary Medicine, Ithaca, NY; Faculty of Veterinary Medicine, University of Ibadan, Ibadan, Oyo State, Nigeria (Gbore)
Abstract	Feline Infectious Peritonitis (FIP) is a severe disease of cats that mostly causes death in affected animals. It can be caused by both type 1 and type 2 of the Feline Coronavirus (FCoV), a member of the alphacoronavirus family. While FIP is less common compared to the milder form of the disease caused by the FCoV, it carries a grim prognosis as affected cats have minimal chances of survival if left untreated. However, aspects of this virus remain enigmatic, including its mode of transmission and disease-causing mechanisms, hindering accurate diagnosis and effective treatment. While it is known that the virus can be shed in feces, previous research done in the Whittaker lab has hinted at the possibility of FCoV transmitting via the respiratory route, but this finding requires further investigation. Therefore, the objective of this study is to further unravel the transmission pathways and pathogenesis of FCoV in order to enhance clinical decision-making, diagnosis, and treatment strategies. The research entails the analysis of tissues and fluids from deceased cats suspected of FIP, as well as swabs collected from live cats. Laboratory analysis of these samples will involve viral RNA extraction followed by Real-Time Reverse Transcription-Polymerase Chain Reaction (RT-PCR) and DNA sequencing, for the detection and identification of FCoV using its genetic material. By attempting to shed more light on the behavior of FCoV, especially its transmission patterns and tissue tropism, it is hoped that the findings of this study will pave the way for further research, leading to the development of improved diagnostics for FIP.
Research Grant	Cornell Feline Health Center and Micheal Zemsky Fund for Feline Diseases
Field of Research	Virology

Abstract Title	Evaluating estimated carbon emissions and feedlot production data to address beef sustainability
Authors	Deanna Gennett, Taylor McAtee, David Renter
Affiliations	Center for Outcomes Research and Epidemiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS
Abstract	The beef industry contributes to greenhouse gas emissions via land use as well as cattle production. It is becoming increasingly important to assess the carbon footprint associated with beef production as global demand for beef rises. Our objective is to determine how feedlot factors are associated with emissions to better assess sustainability in beef production systems. It is hypothesized that healthy and efficient cattle contribute less emissions and thus are more sustainable. Operational data were obtained from commercial feedlots and linked by unique lot (cohort) identifiers with outputs from a proprietary life cycle assessment system that estimates carbon equivalents from predicted greenhouse gas production. Descriptive graphs and figures were created for data analysis, visualization, and pattern identification. The primary dataset included 10,665 lots (cohorts) of cattle containing a range of 10-358 animals per lot. Estimated emissions in this data set showed that the cow-calf phase of production contributed roughly 80% of lifetime emissions while the feedlot sector contributed roughly 20%. On a per animal basis, steers had higher lifetime emissions than heifers, while heifers had more lifetime emissions per kilogram of live weight. Lifetime emissions per kilogram of cattle weight (as a measure of beef production) are reduced when days on feed in the feedlot and mortality were minimal and weight gain relative to feed intake was high. The results confirmed that healthy and efficient cattle contribute less emissions and revealed sex and life stage differences. Recognizing how cattle production impacts carbon emissions is a first step towards improving beef sustainability and reducing the associated carbon footprint.
Research Grant	This study was funded by the College of Veterinary Medicine's Center for Outcomes Research and Epidemiology, and the Global Food Systems program, Kansas State University
Field of Research	Epidemiology

Abstract Title	Quantifying defecation frequency between cats with and without chronic kidney disease
Authors	Zachary George, Jessica Quimby, Sarah Jones, Katelyn Brusach, Adam Rudinsky
Affiliations	Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH
Abstract	Cats with CKD are at higher risk for presenting with constipation, and, in a recent survey study, caregivers reported that CKD cats had less frequent bowel movements compared to healthy cats. The purpose of this study was to objectively measure defecation frequency in cats with and without CKD. It was hypothesized that cats with CKD would defecate less frequently than healthy cats. This prospective observational study utilized the Purina® Petivity™ Smart Litter Box Monitor System to collect real-time defecation data. Cats with stable CKD (IRIS stages 2-4) and healthy-control cats underwent health screening to verify their status at enrollment. Data was collected via the Petivity™ app for 21 days in which medical management and husbandry remained consistent. A Mann Whitney test was performed to compare the total number of days without defecation in the 21-day period between CKD cats and healthy cats. 6 CKD cats and 6 healthy-control cats were enrolled. Two co-housed cats with identical weights failed to complete the study as the monitors were unable to distinguish between them. CKD cats had a median of 6.5 days (range 3-7) without defecation during the 21-day period versus 3 days for healthy cats (range 1-6) ($p = 0.04$). Based on these results, cats with CKD defecate less than healthy cats which may be an indicator of subclinical constipation. A limitation was the litter box monitors were unable to differentiate between co-housed cats with similar weights.
Research Grant	Buttons Feline Kidney Research Fund, Petivity™ monitors donated by Nestle Purina®
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Age-related change in routine clinicopathological parameters among apparently healthy dogs
Authors	Elizabeth F. Gibbs, Daniel E.L. Promislow, Jessica M. Hoffman, DAP Consortium, Kate E. Creevy
Affiliations	Texas A&M University School of Veterinary Medicine, College Station, TX (Gibbs, Creevy), Department of Laboratory Medicine and Pathology, University of Washington School of Medicine, Seattle, WA (Promislow), Department of Biological Sciences, Augusta University, Augusta, GA (Hoffman)
Abstract	In the clinical setting, hematological and biochemical laboratory results are routinely utilized in diagnosing and treating canine patients. It is vital that all lab results are interpreted in the appropriate and accurate context. Misclassification can lead to misdiagnosis and/or incorrect therapeutics. Limited prior work suggests that senior and geriatric dogs are likely to have some results outside the reference intervals on routine clinicopathologic tests, even when their owners consider them healthy. By completing this project, our aim was to confirm and build upon these previous findings and provide evidence that these deviations are normal and age-related rather and do not necessarily indicate disease. In the Dog Aging Project (DAP), dog owners enroll their pets by completing a web-based Health and Life Experience Survey (HLES) that collects information including owner-reported overall observations of health, as well as prior and ongoing medical conditions. Hematological, biochemical, and urinalysis data from 966 dogs in the Dog Aging Project's (DAP) Precision Cohort were analyzed. Analysis demonstrated that in dogs with owner-reported "very good" or "excellent" health, and without any owner-reported ongoing chronic conditions, lymphocytes, USG, WBC, and BUN all decreased with age while globulin, ALP, platelets, and total protein all increased with age. These results suggest that although some clinicopathological parameters change as dogs grow older, these changes may not interfere with the quality of life or the healthspan of the dog and seem to indicate the presence of normal age-related change rather than onset of disease.
Research Grant	The Dog Aging Project, and authors KEC and DELP, are supported by U19 grant AG057377 from the National Institute on Aging, a part of the National Institutes of Health, and by private donations.
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Magnetic nanoparticle stimulation of the nucleus accumbens affects opioid reinstatement in rats
Authors	Ian M. Gilbert, Lenah C. Midani, Lorenzo P. Gatti, and Fair M. Vassoler
Affiliations	Department of Comparative Pathobiology, Cummings School of Veterinary Medicine, Tufts University, North Grafton, MA (Gilbert, Midani, Vassoler) Department of Neuroscience, College of Arts and Sciences, Boston University, Boston, MA (Gatti)
Abstract	Opioid use disorder (OUD) is a chronic relapsing disease characterized by cycles of drug seeking followed by periods of abstinence and relapse. Deep brain stimulation of the nucleus accumbens (NAc) can attenuate drug cravings in humans and reduce drug-seeking behavior in laboratory animals but is invasive and comes with a high risk for side effects. We aim to develop a less invasive neural stimulation strategy through external vibration of implanted magnetic nanoparticles (MNP). This study expands on preliminary data suggesting MNP stimulation of the NAc can attenuate opioid reinstatement in rats, a model of relapse. Rats received bilateral stereotaxic injections of either MNP (n=8) or saline (n=8) and were allowed to self-administer intravenous oxycodone (0.1 mg/kg/infusion) by pressing a lever on a fixed ratio schedule of reinforcement. After 21 days, oxycodone was replaced with saline until pressing behavior extinguished (15% of last day of self-administration), at which point rats were injected with a non-contingent priming dose of oxycodone (1 mg/kg, i.p.) to reinstate pressing. Rats underwent two reinstatement sessions, receiving external magnetic stimulation during one of them, and lever pressing was quantified. All rats received magnetic stimulation one hour before euthanasia. Extracted brains will be sectioned and stained via fluorescent immunohistochemistry for c-Fos. C-Fos expression in the NAc and medial prefrontal cortex will be analyzed in order to investigate the effects of MNP stimulation on the activity of neural circuitry involved in OUD. These results will lead to a better understanding of the effects and potential applications of MNP stimulation as a treatment for OUD in humans.
Research Grant	NIH R41 DA045398
Field of Research	Behavior

Abstract Title	Validation of iSperm analyzer for assessing ram semen quality
Authors	Kelli Gillespie, Jamie Stewart
Affiliations	Department of Large Animal Clinical Sciences, Virginia-Maryland College of Veterinary Medicine, Virginia Tech, Blacksburg, VA
Abstract	The objective of this study was to evaluate a portable iSperm semen analyzer for determination of sperm motility and concentration in rams. Ejaculates were collected from 17 rams over 2 replicates and diluted in Optixcell extender. Samples were analyzed on site from 2-3 rams per day using the iSperm (ISPERM1) and preserved in formalin for concentration measurement by hemocytometer. Samples were transported to the lab to be assessed on the iSperm (ISPERM2) and a benchtop analyzer with Spermvision software (CASA). Sperm concentration, total motility (TM), progressive motility (PM), curvilinear velocity (VCL), average path velocity (VAP), straight line velocity (VSL), straightness (STR), and linearity (LIN) were assessed. Data was analyzed in R using ANOVA and Pearson correlation coefficient. Motility and velocity parameters were significantly and positively correlated between the ISPERM1, ISPERM2, and CASA with greater correlations between ISPERM2 and CASA ($r \geq 0.6$, $P<0.01$). TM did not differ between programs ($P=0.24$), but PM was less for ISPERM2 (23±2.5%; $P<0.01$) than ISPERM1 (50±2.9%) or CASA (60±4.1%). VCL was less for ISPERM2 ($P<0.01$) than for ISPERM1 or CASA. VAP, VSL, and STR were greatest in ISPERM1 ($P \leq 0.03$) and did not differ between ISPERM2 and CASA ($P \geq 0.42$). LIN differed between all three ($P<0.01$). Sperm concentration did not differ between the hemocytometer and ISPERM2 ($P=0.65$) but was greater with ISPERM1 ($P=0.03$) and less with CASA ($P=0.01$). In summary, the results of this study show that the iSperm analyzer could be useful for field sperm analyses in rams. Further validation studies are needed to determine if lower dilutions could improve its analysis of sperm motility, velocity parameters, and concentration.
Research Grant	NIH 2T350D011887-16
Field of Research	Theriogenology

Abstract Title	Fecal Microbial Transplant for Parvovirus in the Outpatient Setting: a randomized controlled trial
Authors	Amanda Gimenez, Meghan Hoel, Elizabeth Alvarez, Kelly Schultz, Erin Lashnits
Affiliations	University of Wisconsin - Madison School of Veterinary Medicine, Madison, WI (Gimenez, Hoel) Dept. of Medical Sciences, UW-Madison SVM, Madison, WI (Alvarez, Schultz, Lashnits)
Abstract	Canine parvovirus (CPV) can have high morbidity and mortality in underserved dog populations. This study aims to evaluate commercially available oral-fecal microbial transplant (FMT) capsules as a practical and low-cost option for the treatment of parvoviral enteritis to improve recovery and survival in the outpatient setting. This prospective randomized control trial enrolled dogs diagnosed with parvoviral enteritis at Austin Pets Alive (an animal shelter located in Austin, TX); dogs in both treatment and control groups were treated with standardized outpatient protocols by shelter staff. Dogs were enrolled from 9/17/22 to 5/7/2023: overall there have been 45 dogs enrolled (24 control and 21 FMT-treated). The overall survival of enrolled dogs is 86.7% (39 survived/45 enrolled), with 95.83% survival in the control group (23 survived/24 enrolled) compared to 76.19% survival for FMT-treated dogs (16 survived/21 enrolled) ($p = 0.053$). Excluding dogs that died or were transferred to in-hospital level care, 18 control group dogs and 13 FMT-treated dogs were included in the analysis of symptom duration. When comparing duration to recovery both groups had a median of 5 days from first treatment to recovery (range 3.5 - 8.5 days for control, 4.5 - 10 days for FMT-treated, $p = 0.409$). Though FMT treatment in this small population did not appear to improve the duration of symptom recovery and treated dogs had overall lower survival, future work and enrollment into the study are needed to determine if oral FMT is possibly detrimental or if confounding effects of size or age can explain the findings of this small study.
Research Grant	ASPCA AVC grant 202108-28672 “Fecal Microbial Transplant for Parvovirus in the Outpatient Setting (FMT-POOP): A randomized controlled trial to evaluate a practical and low-cost intervention”
Field of Research	Epidemiology

Abstract Title	The impact of tBHQ on dendritic cell function in the context of influenza A virus (IAV)
Authors	Dr. Cheryl Rockwell, Saamera Awali, Taylor Godfrey
Affiliations	Department of Pharmacology, Toxicology, Human Medicine (Rockwell),Department of Pharmacology (Awali), Michigan State University, Prairie View A&M University (Godfrey)
Abstract	Influenza is a recurring viral infection that continues to evolve, emphasizing the need for further investigation and methods to combat it. According to the Center for Disease Control and Prevention, there was an estimated loss of 5,000 lives in the 2021-2022 flu season. Influenza is still prevalent and its effects can be long lasting on overall immune health and function. Dendritic cells, a key component of the immune system, work overtime when an individual is stricken with IAV by presenting viral antigens to other immune cells for viral clearance. However, research shows that the consumption of certain food additives may hinder immune cell function and capabilities. The purpose of this study is to determine the effect of tBHQ on dendritic cell function after exposure to IAV, specifically on cytokine secretion. Cytokine secretion will be measured by enzyme-linked immunosorbent assays (ELISAs). Food additives are a part of most peoples' diets and the link between consumption of one specific food additive, tert-butylhydroquinone (tBHQ), has been evaluated in the context of immune cells, such as T cells, NK cells, and B cells but dendritic cells have yet to be investigated. This additive is widely used to delay rancidification, or oxidation of fats. tBHQ essentially hinders the relationship between Nrf2, a transcription factor associated with cellular homeostasis, and its regulator KEAP1. The overall concept of this study focuses on tBHQ and the role of Nrf2 on dendritic cell function. This study will aim to shed light on the tBHQ-mediated immunomodulatory role of Nrf2 and how it impairs clearance of the persistent and infectious virus, influenza.
Research Grant	NIH Grant 5R25HL103156-13.
Field of Research	Immunology

Abstract Title	An Investigation of High Pulse Repetition Frequency Histotripsy for Osteosarcoma Ablation
Authors	Noah Goldfarb, Elliana R. Vickers, Lauren Rugger, Eli Vlaisavljevich, Joanne Tuohy
Affiliations	VA-MD College of Veterinary Medicine (NG), Graduate Program in Translational, Biology, Medicine, and Health (ERV), Department of Biomedical Engineering and Mechanics (EV, LR, & ERV), & Department of Small Animal Clinical Sciences, VA-MD College of Veterinary Medicine (JT), Virginia Tech, Blacksburg, VA
Abstract	Osteosarcoma (OS) is the most common primary bone tumor in humans and canines. The treatment options for OS currently include limb amputation, limb salvage surgery, or stereotactic radiation therapy followed by adjuvant chemotherapy. Histotripsy is a traditionally non-thermal, non-invasive and non-ionizing focused ultrasound ablation technique that mechanically disintegrates tissue. Studies have confirmed the safety and feasibility of histotripsy for canine OS ablation, allowing us to advance studies towards in vivo complete tumor ablation . One challenge with ablating large tumor volumes is long treatment times. Ultra-high pulse repetition frequencies (PRFs) can increase the speed of histotripsy ablation but potentially induce thermal rise. This project aims to characterize the temperature rise induced by histotripsy at varying PRFs (500-2500 Hz) delivered ex vivo to canine limbs. We hypothesized that histotripsy treatment at higher PRFs would induce greater temperature rise. PRFs of 500, 1500, and 2500 Hz were tested, and temperature data were recorded pre- and post-focally. Ablation volume, treatment voltage, and dosage were kept constant. We found that higher PRFs led to greater temperature changes. A PRF of 500 Hz resulted in a pre-focal temperature rise of 15.53ºC and a post-focal temperature rise of 15.50ºC, while 2500 Hz resulted in a temperature rise of 21.33ºC pre-focally and 23.00ºC post-focally. The addition of a cooling gel mechanism resulted in a 63% decrease and a 73% decrease in temperature rises pre- and post-focally, respectively. Future work will investigate the use of cooling gel pads to mitigate thermal rise at higher PRFs in order to maximize ablation efficiency while minimizing off-target damage.
Research Grant	NIH National Institute of Biomedical Imaging and Bioengineering
Field of Research	Oncology

Abstract Title	Hypothalamic neurons as hypoxia sensors that facilitate the peripheral chemoreflex
Authors	Jessica Goldner, Jennifer Cornelius-Green and Kevin J. Cummings
Affiliations	Department of Biomedical Sciences, College of Veterinary Medicine, Dalton Cardiovascular Research Center, University of Missouri, Columbia, MO.
Abstract	An inappropriately elevated peripheral chemoreflex (PCR) contributes to obstructive sleep apnea (OSA) and associated cardiovascular diseases such as hypertension and heart failure. Hypothalamic orexin and corticotropin-releasing hormone (CRH) neurons participate in the control of breathing, including the PCR-mediated hypoxic ventilatory response (HVR). However, it is unclear whether these neurons can be intrinsically activated by hypoxia or if their activation is downstream of carotid body excitation. We hypothesize that orexin and CRH neurons are activated by hypoxia and contribute to the HVR in the absence of carotid body input. Using adult rats, we will perform a carotid sinus nerve (CSN) section or sham surgery. Rats will then be exposed to hypoxia (10% inspired O2) for 2 hrs to allow expression of Fos (indicating activation) while recording respiration. Tissues will then be fixed and sectioned, followed by immunohistochemistry to quantify Fos immunoreactivity (IR). We expect that, compared to rats exposed to room air, hypoxia will increase the number of orexin and CRH neurons displaying Fos-IR, even in the absence of inputs from the CSN. We further expect that rats with sectioned CSNs will retain a significant HVR. These results would indicate that orexin and CRH neurons can be intrinsically activated by hypoxia and contribute to the PCR independently of carotid body input. This research will provide new mechanistic insight into the role of the hypothalamus in the PCR, information that could be harnessed to develop therapies treating OSA and associated cardiovascular disease.
Research Grant	NIH grant R01HL098602
Field of Research	Physiology

Abstract Title	Influence of somatic cell counts on oxidant status during bovine sub-clinical mastitis
Authors	Alek Goll, Joe Wilson, and Vengai Mavangira
Affiliations	College of Veterinary Medicine, Iowa State University, Ames, IA (Goll) and Vet Diagnostic & Production Animal Medicine (Wilson, Mavangira)
Abstract	Mastitis significantly impacts the dairy industry with annual economic losses of up to US$2bn. In clinical mastitis (CM), mammary tissue damage is heightened by concurrent alteration in oxidant status (OS) in the mammary gland, whereas subclinical mastitis (SCM) is more prevalent, accounting for a majority of costs to the dairy industry, but the role of OS in SCM pathogenesis and persistence is unknown. Our objectives for this project were to determine OS changes and mammary inflammatory status in cows with SCM based on somatic cell counts (SCC). We hypothesized that cows with SCM experience significant OS changes that correlate positively with mammary inflammatory status. Four groups of cows (n=10/group) were randomly selected into experimental groups based on recent SCC data as follows: normal (N) if SCC <200,000; low SCC mastitis (L-SCC) if 200,000<SCC<1,000,000; high SCC (H-SCC) if SCC>1 million; and, CM based on signs of local and systemic inflammation. OS parameters (reactive metabolites and antioxidant capacity) were assayed and used to determine the OS index. Milk amyloid A was assayed as a marker of mammary inflammation. Correlations between oxidant and inflammatory status and SCC were determined. Our findings indicated cows with SCM have altered OS (P=0.07); however, our study was deficient and precluded the determination of biological relevance correlations among oxidant and inflammatory status in SCM. Follow-up studies will be conducted with more cows and assessment of macromolecular damage related to OS. Our results will provide preliminary information on the potential role of reactive metabolite production during SCM and provide potential intervention to ease inflammation and recover milk production.
Research Grant	Dr. Stephen G. Juelsgaard, Dean's Fellowship in Veterinary Medicine
Field of Research	Production Animal Medicine

Abstract Title	Exploration of Auricular Chondrocytes as a Cell Source of Tissue Engineering of TMJ Disc Cartilage
Authors	Nicole Gonzales, Iris Rivas, and Natalia Vapniarsky-Arzi
Affiliations	Department of Pathology, Microbiology and Immunology, UC Davis School of Veterinary Medicine
Abstract	Temporomandibular joint (TMJ) disorder is characterized by the degeneration and perforation of the cartilaginous disc within the joint. This disorder leads to chronic pain and progressive degeneration of all joint components. Due to to the poor regenerative capacity of cartilage the process is irreversible. Current tissue engineering (TE) therapies are capable of generating biomimetic cartilage constructs derived from costal chondrocytes for implantation; however, there are several limitations to utilizing costal chondrocytes as the primary cell source such as invasiveness of tissue collection and progressive ossification of costal cartilage with age. These limitations have prompted the exploration of novel cell sources that would eliminate both issues. The objective of this study is to determine if auricular cartilage can be used to generate TE cartilage constructs with chondrogenic properties akin to the native TMJ disc. We tested the efficacy of using auricular chondrocytes using scaffold-free cartilage tissue engineering technology. Preliminary findings determined that auricular chondrocytes can be expanded to millions using a small initial stock of cells and that TE constructs have equivocal cartilage morphology histologically. Additionally, we plan to compare biochemical and mechanical properties of these constructs to native TMJ disc tissue. This data is encouraging and shows that auricular chondrocytes are a promising novel cell source for TE cartilage implants for TMJ disorders.
Research Grant	National Institute of Dental and Craniofacial Research (PAR-21-084)
Field of Research	Orthopedics

Abstract Title	A multifaceted approach to improving fish farming in Kenya's Lake Victoria region
Authors	Grace E. Gonzalez, Kathryn J. Fiorella, Eric Teplitz, and Rodman Getchell
Affiliations	Department of Public and Ecosystem Health (Fiorella, Teplitz) and Department of Microbiology and Immunology (Getchell), College of Veterinary Medicine, Cornell University, Ithaca, NY
Abstract	The fishing industry of Lake Victoria is an important source of food security, employment, and income for over 30 million people in the region. In recent decades, declining wild Nile tilapia populations have severely impacted the fishing industry. It is hypothesized that algal blooms, nutrient runoff, overfishing, disease, and poor water quality have contributed to the decline. To meet rising demand for fish as a food source, cage farming of Nile tilapia is rapidly growing. As this method of fish rearing is still new to the area, there are significant gaps in knowledge on how to best manage a cage farm operation amidst the lake's other issues. This project adopts a multifaceted approach to improving aquaculture management practices in Kenya's Lake Victoria region by identifying fish pathogens, measuring algal toxin levels in commonly consumed fish, surveying fish farming practices, and educating the public. Limited existing data influenced our decision to begin this project phase with a literature review of Nile tilapia pathogens and diagnostic services feasible for Kenyan fish farmers. Alongside this, we have begun interviewing cage farmers to assess their current management practices. Using this data, we will create a "Best Management Practices" guide that aims to supplement the farmers' knowledge in cage design, water quality, biosecurity, and fish health. Preliminary survey data suggests some good management practices are implemented, but the areas of biosecurity and fish health are still lacking. The findings of this project provide insight into the areas public health officials, researchers, and farmers should consider when taking action to improve the welfare of the people, fish, and environment of Lake Victoria.
Research Grant	NSF CNH2 (NSF BCS# 2009658), Cornell Atkinson Center Atkinson Venture Fund award and Cornell Center for Social Sciences (to KJF)
Field of Research	One Health

Abstract Title	Understanding the virulence effects of Yersinia pestis through the deletion of T3SS proteins
Authors	Keisha Gray, Deborah Anderson1,2, Rachel Olson1,2 (sponsor)
Affiliations	1Department of Veterinary Pathobiology, University of Missouri, Columbia, MO 2Laboratory for Infectious Disease Research, University of Missouri, Columbia, MO
Abstract	Bubonic plague is a highly virulent disease that has caused the death of millions of humans over several centuries. It is caused by a pathogenic gram-negative bacterium called Yersinia pestis. Y. pestis contains several different virulence factors that aid in its ability to avoid the immune system and effectively kill host cells through the type three secretion system (T3SS) of Yersinia outer proteins (yop). YopK and YopJ are known to contribute to host cell apoptosis, while LcrQ regulates the T3SS. YopK helps fine-tune the T3 secretion process, while YopJ interferes with multiple signaling pathways involved with cell survival. However, whether the deletion of these various proteins affects the ability of Y. pestis to kill the cell is yet to be determined. The overall objective is to understand the inter-related roles of YopJ, YopK, and LcrQ on host cell death and virulence. The objective of this work is to generate mutants that will allow us to study those interactions. We will use KIMD27-derived strains electroporated with YopJ, YopK, and/or LcrQ deletion plasmids (suicide vectors). PCR will then be performed to detect for the gene deletion or reversion to wild-type. In the end, we expect there to be Y. pestis mutants with single, double, and triple deletion of YopJ, YopK, and LcrQ that can be utilized in further research. The deletion of these T3SS virulence factors should cause reduced virulence of Y. pestis in vivo. This, in turn, will provide further insight into the pathogenesis of the Bubonic plague and help guide future research for targeted treatment of the disease as well as the development of effective detection methods.
Research Grant	Provided by the MU Division of Research Innovation and Impact and NIH R01 A129996 (to DMA)
Field of Research	Bacteriology

Abstract Title	Beyond big cats: Public health policy proposals for small non-domestic felids & their hybrids
Authors	Brianna R. Greco and Leslie A. Lyons
Affiliations	Department of Public Health, College of Health Sciences (Greco) and Department of Veterinary Medicine & Surgery, College of Veterinary Medicine (Greco, Lyons), University of Missouri, Columbia, Missouri, USA
Abstract	The trade of wildlife and wildlife products concerns not only animal welfare and wildlife conservation efforts, but also complicates public health and safety. An example is the public safety risk of escaping big cats, especially when first responders are rarely equipped to respond to such events. The Big Cat Public Safety Act (Pub. L. 117-243, 136 Stat. 2336, 16 USC §§ 3371-3378) was enacted in 2022 partly to address these concerns. However, the law does not include small wild felids, such as ocelots (*Leopardus pardalis*), servals (*Leptailurus serval*), and caracals (*Caracal caracal*). These small wild cats are more fractious than domestic cats and face serious concerns regarding their proper housing and nutrition. These cats also frequently escape from their enclosures, posing a potential danger for humans and small pets. To convey the need for legislation covering small non-domestic felids and their hybrids, the Law Enforcement Management Information System of the United States Fish and Wildlife Service will be analyzed to identify the current U.S. trade and ownership of small non-domestic felids and their hybrids. The public health and safety consequences of these cats pose will be evaluated to propose how a policy similar to the Big Cat Public Safety Act legislation could effectively be structured. Additionally, a survey of current veterinary students will evaluate the U.S. veterinary medical education to determine if students are sufficiently prepared to clinically evaluate and treat, properly handle, sedate or recognize the signs of zoonotic disease in these cats. The overall goal is to protect the welfare of citizens and small wild felids and prevent the illicit trade of these cats.
Research Grant	Gilbreath-McLorn Endowed Professor of Comparative Medicine
Field of Research	Exotic Pets and Zoo Animal Medicine

Abstract Title	Determination of the genetic etiology of bilateral anterior hemimelia in Chihuahuas
Authors	Marin Green, Julia Vo, Karen Vernau, Denis Marcellin-Little, Danika Bannasch
Affiliations	Department of Population Health and Reproduction (Green, Bannasch) and Department of Surgical and Radiological Sciences (Vernau, Marcellin-Little), School of Veterinary Medicine University of California-Davis, Davis, CA
Abstract	Bilateral anterior hemimelia (BAH) which has been reported in the Chihuahua breed is the congenital absence of the majority of the bones of the thoracic limbs. Affected dogs have shortened humeri and an absence of the bones and limb distal to the humerus. There are no known syndromes in humans or mice that affect the arms and spare the legs so the variant responsible may aid our understanding of limb specification. To determine the genetic cause of BAH, genome wide association (GWAS) and whole genome sequencing approaches were used. A GWAS was performed using the Illumina HD canine SNP array with 7 cases and 14 controls and a significant association was identified on chromosome 13. The critical interval was further defined based on homozygosity in cases to a 2 Mb pair region. Within this critical interval, there was a compelling candidate gene, RSPO2. Limb deformities affecting all four limbs in humans and Holstein cattle have been linked to mutations of RSPO2. Six affected BAH chihuahuas were whole genome sequenced and variants associated with the disease are being evaluated by comparing to control genomes of dogs with four limbs. No protein coding variants were identified in RSPO2, therefore, we believe the causative variant is in a regulatory domain. WGS data is being analyzed for structural variants and SNPs and small indels across 167 dogs including 6 cases. Candidate variants will be genotyped in silico in public datasets to identify the most likely candidates. Variants will be genotyped in 8 additional cases and 200 control Chihuahuas without BAH. The identification of the variant responsible will enhance our understanding of RSPO2 gene regulation and the developmental difference between thoracic and pelvic limbs.
Research Grant	Maxine Adler Endowed Chair funds
Field of Research	One Health

Abstract Title	Identification of candidate sudden cardiac death causing variants in Thoroughbred racehorses
Authors	Olivia Groth, Joy Stock, Freya Stein, Molly McCue, Sian Durward-Akhurst
Affiliations	Department of Veterinary Clinical Sciences (Groth, Stock, Stein, Durward-Akhurst), Department of Veterinary Population Medicine (McCue), University of Minnesota College of Veterinary Medicine, St. Paul, MN
Abstract	Each year, about 500 apparently healthy U.S. racehorses die while racing. However, only 53% of sudden death cases receive a diagnosis at postmortem. Most fatal arrhythmias don't result in gross or histologic cardiac changes, so it is likely that arrhythmias account for a large proportion of the sudden death cases without a diagnosis. Arrhythmias that cause sudden cardiac death (SCD) in humans without structural heart disease are often caused by genetic variants in ion channel genes. Given the similarities between human and equine arrhythmias, it's likely that variants in genes known to cause arrhythmias and SCD in humans also cause these diseases in horses. Our goal is to identify candidate SCD-causing variants using whole genome sequence (WGS) of 60 SCD cases and 53 controls. Variants were identified using a modified version of the Genome Analysis Toolkit best practices. Using BCFTools and python, we extracted variants present in the SCD cases from the top 100 candidate genes for SCD identified using Phenolyzer. Of these variants; 31, 484, and 949 variants were predicted to have high, moderate, and low impact respectively, using Ensembl-VEP. We will use SnpEff, SNPS&GO and SIFT to establish which variants are most likely contributing to SCD and will genotype these variants in additional SCD cases and controls. We are collecting hair roots from SCD cases and cardiac phenotypes, including ECGs (before, during, and after exercise) and echocardiography from SCD controls. Our long-term goal is to identify the causative variants for SCD in horses to allow for the development of genetic tests to provide non-invasive and affordable methods of detecting horses at increased risk of developing fatal arrhythmias.
Research Grant	Minnesota Racing Commission, University of Minnesota Clinical and Translational Science Institute Pre-K award (ULTR002494)
Field of Research	Equine Medicine and Surgery

Abstract Title	Detection of Theileria orientalis in ticks from Southeastern Oklahoma
Authors	Alanna L Gudmunson, Ruth C Scimeca
Affiliations	College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO (Gudmunson) Veterinary pathobiology, Oklahoma State University, Stillwater, OK (Scimeca)
Abstract	Theileria orientalis is a hemoprotozoan parasite transmitted by Haemaphysalis longicornis ticks, (asian longhorned tick, ALHT). In the USA, T. orientalis genotype Ikeda was first detected in Virginia cattle herds in 2017. Infected cattle display clinical signs similar to anaplasmosis, including anemia, jaundice, and weakness. In Oklahoma neither ALHT or T. orientalis Ikeda have been reported, nonetheless in 2022 two cattle herds from Southeastern OK reported clinical signs consistent with anaplasmosis but with no response to treatment or detection by serology or PCR. Further analysis identified T. orientalis genotype bufeli in these cows. The purpose of this study was to test for the presence of T. orientalis in ticks collected from the area. To collect the ticks, we utilized CO2 traps, flagging and dragging methods. Fed ticks were also removed from cows in the area. A total of 118 Amblyomma americanum (20 nymphs, 98 adults) and 10 Amblyomma maculatum adults were collected. The ticks were dissected to remove internal organs for DNA extraction and PCR amplification of the SSUrRNA and MPSP genes. PCR of the SSU rRNA gene detected a total of 17 (21.7%) positive for T. cervi and 2 (2.5%) positive for T. orientalis. Only ticks removed from cattle tested positive. We did not collect any ALHT from the field and primary results indicate that T. orientalis DNA is only detected from fed ticks in the studied area. However, limitations on the number of ticks and areas tested must be considered. Further analysis includes sequence analysis of the MPSP genes and amplification of the Anaplasma marginale MSP4 gene. Surveillance of the tick vector and protozoan parasite should continue.
Research Grant	Study was funded by Oklahoma State University, College of Veterinary Sciences
Field of Research	Parasitology

Abstract Title	Prenatal oxycodone exposure and adult regulation of the epigenetic regulator MeCP2
Authors	Megan Gulsby, Kelsea Gildawie, Kerri Budge, Sara Isgate, Jillian Celatka, Fair Vassoler, Elizabeth Byrnes
Affiliations	Cummings School of Veterinary Medicine at Tufts University, Grafton, MA
Abstract	Methyl CpG binding protein 2 (MeCP2) is a nuclear protein found in the brain that functions as a transcription regulator and is important in neurodevelopment and maintenance of adult brain parenchyma. It has been established that MeCP2 functions within dopaminergic pathways. Previous findings have reported alterations in brain reward pathways following fetal exposure to opioids. Thus, our hypothesis is that prenatal exposure to the opioid oxycodone leads to dysregulation of MeCP2 in brain regions that regulate reward-related behavior. Female Sprague Dawley rats were surgically implanted with jugular catheters and trained to self-administer oxycodone in operant conditioning sessions (2h/day, 5 days/week for 2 weeks, 6h/day 5 days/week for 1 week; fixed ratio (FR1) schedule; 0.1 mg/kg/infusion). Females were then mated with drug naïve males and once pregnant, were allowed to self-administer oxycodone daily (6hr/day, 7 days/week) until parturition. On postnatal day 1, all oxycodone exposed pups were transferred to drug naïve donor mothers to eliminate the effects of aberrant maternal behavior on adult outcomes. As adults, oxycodone-exposed offspring were sacrificed one hour after receiving an acute injection of either saline or oxycodone, withbrains harvested and stored at -80°C. Tissue micropunches from the striatum were then collected and gene expression using qRT-PCR was conducted to quantify MeCP2 as well as brain derived neurotropic factor (BDNF) and c-Fos. All data will be compared to the offspring of non-oxycodone exposed pups and correlated with dam intake. The results from this study will inform more investigations on the effect of oxycodone exposure on the regulation of MeCP2 in reward-related brain regions.
Research Grant	NIH DA049531
Field of Research	Physiology

Abstract Title	Delta-protocadherin function in axon regeneration in mice
Authors	Jason Gutmann, David M. Lin
Affiliations	Cornell University College of Veterinary Medicine (Gutmann, Lin)
Abstract	Each year in the veterinary field, nerve damage constitutes roughly 2% of all veterinary cases, costing owners thousands of dollars in tests and treatments per case (NCSU). A leading problem in veterinary neurobiology is the lack of understanding of the basic components responsible for nerve regeneration. One group of proteins is of great interest in this field. Delta-protocadherins (δ-Pcdhs) are a group of cell adhesion molecules which allow cells to bind through the high affinity they have for one another (Lin, 2011). Axons are believed to present δ-Pcdhs on their cell membranes, as do the cells they bind to, allowing for guided axon growth and attachment (Zhen, 2023). It is hypothesized that if δ-Pcdhs are essential for axonal growth, then deletion of genetic coding for δ-Pcdhs should diminish regeneration in adulthood. To test this hypothesis, mice were selected as models. Half of the selected mice were wild-type, while the other half were of a mutant genotype and lacked production of a δ-Pcdhs. To allow regeneration to occur in vivo, sciatic nerves were transected and sutured from both wild-type and mutant mice, being allowed to heal for one month before dissection. To determine how growth occurs in vitro, dorsal root ganglia were removed from euthanized wild-type and mutant mice, cleaned of axons, and cultured for 5 days. All samples were stained with fluorescent antibodies, then scanned within a fluorescent microscope. The total growth of axons will then be measured and compared between genotypes. It is our prediction that axon growth will be much greater in wild-type mice than in mutant mice. The goal is to apply these findings for clinical regeneration.
Research Grant	NIH T35 OD010941, Cornell University College of Veterinary Medicine
Field of Research	Physiology

Abstract Title	Verbal description of Tibial Plateau Leveling Osteotomy (TPLO) leads to greater perception of value
Authors	Molly Guyette and Stacy Eckman
Affiliations	Department of Veterinary Integrative Biology, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, Texas
Abstract	There is a lack of formal research assessing the impact of visual aids on client compliance and perception of the value of clinical procedures in veterinary medicine which is important due to the growth of telemedicine. This prospective cohort study determined if the use of purely verbal explanation, verbal and 2D photos, or verbal and 3D model representation of a cranial cruciate ligament rupture and the TPLO procedure leads to improved compliance and perceived value of the cost of the procedure. A link was sent via email to clients that owned medium to large breed dogs with no history of cruciate ligament injury and therefore did not have previous knowledge that would bias their opinion of the procedure. This link landing page contained an embedded audio or video player with either a verbal explanation of the procedure or the verbal explanation accompanied by photos or 3D models. A structured questionnaire about the client's quantitative perception of the procedure was completed by 69 clients. The percentages of clients that agreed or disagreed with the statements provided on the questionnaire were compared. Clients shown the 3D model representation were more likely to disagree that the TPLO is a good value for its average price ($p = 0.01$) compared to those with only verbal explanations. No significant differences were observed between the three methods of explanation when asked if they would pursue the procedure if needed in the future, measuring expected compliance. The client's perception was surprisingly not positively influenced by a 3D model, illustrating how clinicians can help clients can make an informed decision on their pet's health care simply through clear explanation without additional 3D models.
Research Grant	None
Field of Research	Orthopedics

Abstract Title	Tick presence, environmental factors, and risk for tick-borne diseases across a land-use gradient in Oregon
Authors	Lukas Haffner, Simonne Sequeira, Rhea Hanselmann, Michelle Steinauer, Justin Sanders, Brianna Beechler
Affiliations	University of Veterinary Medicine, Hannover, Germany (Haffner), Western University of Health Sciences, CVM, Pomona, CA (Sequeira, Hanselmann), Western University of Health Sciences, COMP, Lebanon, OR (Steinauer) Oregon State University, Carlson College of Veterinary Medicine, Corvallis, OR (Beechler, Sanders)
Abstract	Ticks are responsible for many vector-borne infections such as Lyme disease, Rocky Mountain Spotted Fever, and Anaplasmosis. Our research project is divided into 3 different stages. First, we determined tick presence across 3 different land-use gradients along the Mary's River in the Willamette Valley, Oregon. We collected ticks using carbon dioxide traps and drag-cloth sampling along transects. Based on reports of tick abundance on local human and companion animal populations, we expect differences in tick abundance between land-use types. The second step was to identify and quantify the collected ticks by species, sex, and life stage. In particular, the species Ixodes pacificus, Dermacentor variabilis, Dermacentor occidentalis and Rhipicephalus sanguineus are known ticks in the area. We will determine hosts typical for each land-use gradient which may play a role in the spread of tick-borne diseases. The final step will be to extract and amplify DNA from ticks captured. We will use PCR to screen for the presence of zoonotic pathogens to obtain information on the prevalence of pathogens and thus the risk of tick-borne diseases. Preliminary results show an increased occurrence of ticks in high disturbance areas, with an especially increased occurrence of the genus Dermacentor in the adult stage. We hypothesize that livestock is attractive to ticks, as increased rodent populations are beneficial for the development from larva to nymph, while domestic animals aid the development of the nymph to adult and serve as a final host for the adult. Methods of tick sampling, presence of ticks at study sites, environmental factors affecting tick abundance, and pathogen transmission risks for tick-borne diseases will be discussed.
Research Grant	Oregon State University Department of Biomedical Sciences Intramural support to Beechler, Western University of Health Sciences Intramural Team Grant to Hanselmann and Steinauer
Field of Research	Parasitology

Abstract Title	Immune profiling of horses with and without equine odontoclastic tooth resorption and hypercementosis
Authors	Skyellar Hall-Delarber, Jennifer Hu, Jung Keun Lee, Margaret Brosnahan, Deborah Molehin
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ
Abstract	Equine odontoclastic tooth resorption and hypercementosis (EOTRH) is a debilitating, incurable dental disease in horses. Its cause is unknown, there is no treatment, and the disease process eventually necessitates removal of the affected teeth. One hypothesis of disease is that EOTRH begins with the biomechanical changes that happen naturally as equids age. This causes an increased stress on the periodontal ligaments, most commonly affecting the incisors. Secondary infection takes hold in some horses, leading to severe periodontal disease, alveolar bone resorption, and the condition EOTRH. Why this occurs in some horses as they age, but not all, is unknown; one possibility is a difference in immune function. The immune status of horses with EOTRH has not been investigated. The objective of our pilot study is to examine the saliva, serum and blood leukocytes in horses with EOTRH as compared to young, healthy horses. It is currently unknown exactly where normal aging changes end and pathology begins, however, the use of molecules such as cytokines in saliva and serum, and the immune cells in blood and tissues, may clarify this. This study employed cytokine arrays, ELISAs and flow cytometry on saliva, serum, and peripheral blood mononuclear cells from live horses, and immunohistochemistry on oral tissues of deceased horses, to characterize the immune systems of affected and unaffected horses. If differences in immune cells are detected in our study, a larger study will map the spectrum of immune cells against radiographic and clinical changes in dentition for earlier identification of EOTRH. This will lead to improved diagnostics, and possibly new treatments and preventive strategies to improve equine dental care.
Research Grant	Academic Research Enhancement Award
Field of Research	Immunology

Abstract Title	Maternal Staphylococcus aureus mastitis immunomodulatory treatment effect on nursing mouse pups
Authors	Stephanie Hall, Jatna Rivas, Sunila Mahavadi, and Benjamin Adu-Addai
Affiliations	Department of Biomedical Science (Hall, Rivas, Adu-Addai), Department of Biology (Mahavadi)
Abstract	Mastitis is a disease that affects the mammary gland of lactating mothers. Mothers with infectious mastitis are recommended to breastfeed while on antibiotic treatment. However, exposure to antibiotics can affect both the mother and the child, therefore the need for an alternate treatment is necessary. IgY, an antibody naturally derived from egg yolk is reported as a safer alternative to antibiotics because of its efficacy, specificity, and safety for oral consumption. One of the indicators of infant health is normal gastrointestinal (G.I.) motility. GI motility can be compromised with poor treatment outcomes. The objectives of this study are to: (1) Compare the health outcome (growth and weight) of pups nursed from Staphylococcus aureus infected dams and treated with anti-SpA IgY, anti-SpA IgY+Vitamin D3, or anti-SpA IgY+Vitamin D3+RP. (2) Evaluate the degree of gastrointestinal motility of pups nursed from Staphylococcus aureus infected dams and treated with each therapy. Fifty pups (five males and five females per treatment) were collected. The litter size and growth rate of these were determined during treatment until they were weaned. Colon samples were collected from each for Angiotensin II receptor (AT1AR and AT1BR) analysis via qPCR. The average weight and growth for all pups were similar, except positive control which was less. Angiotensin receptor (AT1AR) expression in the colon smooth muscle was higher in the positive control, however, angiotensin receptor (AT1BR) expression was the opposite. The same phenomenon that occurred in colon smooth muscle was repeated in the colon mucosa.
Research Grant	TUCVM Veterinary Scholars Program
Field of Research	Immunology

Abstract Title	Determining the functional and temporal role of SOX9 in avian species during craniofacial morphogenesis
Authors	Juliann Hallum, Heddy R. Menendez, Hannah Herron, and Crystal D. Rogers
Affiliations	School of Veterinary Medicine, UC Davis, Davis, CA (Hallum, Menendez, Rogers) and Department of Anatomy, Physiology, and Cell Biology, UC Davis, Davis, CA (Menendez, Rogers), and Department of Biology, Austin College, Sherman, TX (Herron).
Abstract	The neural crest (NC) stem cell population is a vertebrate-specific lineage that forms in the developing central nervous system. NC cells undergo epithelial to mesenchymal transition (EMT) to migrate and differentiate into multiple cell types. This process is conserved as avian craniofacial development retains similar properties to mammalian development. There are gaps in knowledge about the molecular mechanisms that guide the formation of neural crest derivatives. One derivative of neural crest cells is craniofacial bone and cartilage, including the jaw in mammals and the beak structures in birds. This lineage is driven by the SRY-Box Transcription Factor-9 (SOX9), but the timing of SOX9 necessity to drive bone and cartilage formation is unknown. The objective of this project is to: 1) define the role of SOX9 in beak formation in Gallus gallus (chicken) to determine the specific mechanisms regulating beak morphogenesis and 2) identify molecular changes in neural crest- derived tissues after loss of SOX9. SOX9 knockdown at early stages reduces neural crest cell migration, but cells are capable of recovering. Timing is an important factor because genes and proteins must be expressed at the right time and place for normal development. Changes in SOX9 expression leads to congenital abnormalities such as cleft palate. Our objective is to define the timeline for SOX9 necessity, and the downstream morphological changes that occur in its absence. We predict that loss of SOX9 prior to neural crest EMT will inhibit neural crest cell migration and differentiation, leading to abnormal beak morphogenesis. We hope this information about the role of SOX9 in craniofacial development may be translational across animal species.
Research Grant	NSF CAREER grant #21437 to CDR.
Field of Research	Physiology

Abstract Title	Non-apoptotic cell death in naturally occurring Supporting Limb Laminitis
Authors	Abigail Hamilton, Julie Engiles, Jeaneen Kulp, and Andrew van Eps
Affiliations	Departments of Clinical Studies (Hamilton, Kulp, van Eps) and Pathobiology (Engiles), New Bolton Center, University of Pennsylvania, School of Veterinary Medicine, Kennett Square, PA, USA
Abstract	Supporting limb laminitis (SLL), a disease of the equine hoof lamellae, is a significant barrier to successful treatment of orthopedic injuries. Although not fully understood, there is evidence that it is an ischemic process. Experimental models of prolonged preferential weight bearing relevant to SLL showed increased TUNEL positive, caspase negative (non-apoptotic) epithelial cell death adjacent to the keratinized axis of the lamellar epithelium. This unique pattern differs from models of endocrinopathic and septic laminitis and is undocumented in natural laminitis. There is no published evaluation of lamellar epithelial cell death in clinical cases of SLL, our study aims to characterize this. Archived mid lamellar tissue sections of multiple limbs (injured, contralateral, and one additional) from clinical SLL cases (n=8) and matched controls (n=8) were utilized. Formalin-fixed, paraffin embedded sections were stained for DNA fragmentation using TUNEL method (a non-specific cell death marker) and using immunohistochemistry for cleaved Caspase-3 (apoptosis specific). Digital image analysis was used to quantify number of positive cells per primary epidermal lamellae (PEL) and counts will be statistically compared between cases and controls. Results are pending. Based on preliminary observations there is a similar pattern of cell death adjacent to keratinized axes, with predominantly TUNEL positive, caspase-3 negative parabasal cell staining present in multiple limbs from SLL cases. Preliminary results support the likelihood of a non-apoptotic cell death pathway affecting lamellae in SLL. Possible caspase-3 independent cell death mechanisms include necroptosis, aberrant cornification, autophagy or ischemic necrosis.
Research Grant	University of Pennsylvania Laminitis Lab internal funds
Field of Research	Equine Medicine and Surgery

Abstract Title	Guarding the gates: developing a surveillance plan for Japanese encephalitis virus in the United States
Authors	Abdulafees Hamzat, Lee Cohnstaedt, Natalia Cernicchiaro
Affiliations	Department of Diagnostic Medicine and Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS, United States (Hamzat, Cernicchiaro) United States Department of Agriculture, Manhattan, KS, United States (Cohnstaedt) Faculty of Veterinary Medicine, University of Ibadan, Ibadan, Nigeria (Hamzat)
Abstract	Japanese encephalitis virus (JEV) poses a significant threat to both animal and public health, due to its recent global expansion and the suitable conditions in the United States (US) for a potential viral incursion. This study aims to design a comprehensive surveillance system for JEV in the US, to aid early detection, rapid response, and initiation of control measures. The proposed surveillance plan targets the identification of JEV in vectors and hosts populations at high-risk, specifically humans, horses, and swine. Through the use of active and passive data collection methods, diverse data sources will be incorporated, including human health records and clinical data, veterinary laboratory submissions, collection of biological samples at farms or abattoirs and entomological and serological surveys, in areas deemed at high-risk of JEV introduction and transmission. Being free of JE, the US may face several challenges if there is a JEV incursion. Although high morbidity and mortality in animals would be expected upon viral introduction and transmission, few to no farmers or veterinarians would be familiar with the clinical signs. Probably, human cases would be detected and reported first. Limited expertise and diagnostic laboratory capacity, cross-reactivity with other flaviviruses and the non-specific clinical and subclinical presentation in human and animal hosts may contribute to delayed detection. The US is in desperate need of a surveillance and preparedness plan. The proposed surveillance plan integrates multiple data sources and innovative technologies, enabling timely detection, strengthening public health preparedness, improving outbreak response, and reducing JEV's impact on public and animal health.
Research Grant	None
Field of Research	Epidemiology

Abstract Title	Increasing Next Generation Sequencing detectability of Newcastle or Avian Influenza through Host Depletion
Authors	Mark Harden, David Suarez
Affiliations	College of Veterinary Medicine (Harden), Tuskegee University (Harden), Tuskegee (Harden), AL (Harden), Agriculture Research Service (Suarez), U.S. Department of Agriculture (Suarez), Athens (Suarez), GA (Suarez).
Abstract	Avian Influenza (AI) is an Orthomyxovirus that utilize wild aquatic birds as its reservoir host and is capable of transmission to domestic poultry through direct contact, infected equipment, contaminated water, or respiratory droplets. Newcastle disease shares many characteristics to systemic AI in both transmissibility and pathological signs to a point where they're indistinguishable. To combat the spread of AI and Newcastle within the United States' poultry industry understanding gene sequences of current outbreaks is paramount to management and elimination. Next Generation Sequencing (NGS) has the capability to produce rapid, specific results with the goal of identify whole viral genome sequences, however, test sensitivity can decline based on host and bacterial RNA concentrations and viral degradation while samples are in transport. Host depletion is a viable solution to these obstacles by removing host and bacterial RNA that mask sequencing of target viral RNA. In this paper, we develop and investigate various RNA extraction and host depletion methods that significantly reduce chicken host RNA post treatment compared to their pretreated counterpart. Multiple RNA extraction methods were conducted on samples obtained from euthanized specific pathogen free (SPF) birds after addition of Newcastle disease virus to evaluate virus retention. Alteration in host depletion protocols looking at combinations of primer sets, incubation times, and types of DNase/RNase enzymes for degradation are evaluated for greatest depletion of bacterial and host RNA. Post extraction and host depletion treatments are validated using reverse transcriptase real time PCR (RTRT-PRC), producing significantly increased cycle threshold (CT) values.
Research Grant	ARS Funded Research
Field of Research	Virology

Abstract Title	Effect of mRNA-induced antibody on adherence of Tritrichomonas foetus to bovine preputial keratinocytes
Authors	Cassidy Hardy, Merrilee Thoresen, Hannah E. Peck , Daryll Vanover, Philip J. Santangelo, Amelia R. Woolums
Affiliations	Department of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS (Hardy, Thoresen, Woolums) and Wallace H Coulter Department of Biomedical Engineering, Emory University, Atlanta, GA (Peck, Vanover, Santangelo)
Abstract	Tritrichomonas foetus (Tf) infection causes bovine pregnancy loss. There are no approved therapies for infected bulls; currently, control is limited to culling infected animals. TF 1.17 is a surface antigen mediating Tf attachment to host epithelium. Synthetic mRNA encoding antibodies against TF 1.17 at the site of infection could be an effective therapy. Experiments were conducted to determine whether Tf attachment was decreased in bovine preputial keratinocytes (PPK) expressing mRNA for antibody to two TF1.17 epitopes (TF1.15 and 1.17). PPK were transfected with mRNA encoding either secreted or anchored antibodies labelled with NanoLuc® and incubated overnight; transfection efficiency was determined by luminescent assay. Optimal incubation time for the Tf attachment assay was determined by adding 1 x 106 fluorescently labelled Tf/well to PPK in 24 well plates and incubating for 0.5, 1, 1.5, 2 and 3 h. Unattached Tf were washed off, cells were fixed, and actin and nuclei were stained for imaging. Attached Tf were counted in 3 fields at 20X magnification per slide. Using the same methods, labelled Tf were co-cultured with mRNA transfected and control PPK for 3 h, Tf were quantified in 6 fields per slide and experiments were repeated 3 times. Transfection was successful, with antibody to TF 1.15 and anchored constructs most efficiently expressed. Cells producing anchored antibody to TF 1.17 had fewest attached Tf, but due to high variability the decrease was not different from other treatments or controls. In vitro conditions lack host immune mediators that may be necessary for antibody to decrease Tf attachment. Future experiments will focus effects of expressed antibodies on Tf adherence in vivo.
Research Grant	This project was supported by Agriculture and Food Research Initiative Competitive Grant Number 2021-67016-34571 from the USDA National Institute of Food and Agriculture
Field of Research	Immunology

Abstract Title	Morphological and molecular characterization of Versteria tapeworms of North American mustelids
Authors	Rachel Harrell, Keara Monaghan, Kevin Niedringhaus, Caroline Sobotyk
Affiliations	Department of Pathobiology, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, Pennsylvania
Abstract	Mustelids are considered the largest, most diverse group of carnivorous mammals and are known to harbor several species of tapeworm. The family Taeniidae includes clinically important tapeworms in both human and veterinary medicine, which have become increasingly intertwined due to urbanization and landscape fragmentation. Among the genera within the Taeniidae family, Versteria has been recently described and implicated in zoonotic infections in North America; however most species in the genus Versteria lack detailed descriptions and epidemiological data. As mink, fishers, and weasels are known definitive hosts of Versteria sp., we hypothesized that morphological and molecular approaches on tapeworms harvested from these mustelids would provide a complete characterization and taxonomic classification of the zoonotic Versteria sp.. Mustelid carcasses were legally harvested and donated, and gastrointestinal contents were collected. One mink and two fishers were positive for tapeworms. Morphological and molecular analyses are ongoing. Specimens will be cleared in lactophenol and examined under an optic microscope at different magnifications for morphology. Molecular data will be acquired by PCR amplification and sequencing of highly conserved genes. These data will improve the identification and diagnosis of Taeniid infections in domestic and wild animals. Moreover, our findings will contribute to a better understanding of the genetic and geographic variation of this newly described genus as well as provide key information on its evolutionary background, ecology, and potential zoonotic implications.
Research Grant	Institute of Infectious and Zoonotic Disease (IIZD)
Field of Research	Parasitology

Abstract Title	Diet-Induced Pain Signatures in the Brain are Altered by REV-ERB Agonists In Vivo
Authors	Eden Harris1, Sangeet Makhija2, Andrew Aitken2, Vinicia Biancardi2, and Kristine Griffett2
Affiliations	1Tuskegee University College of Veterinary Medicine, Tuskegee, AL 2Auburn University College of Veterinary Medicine, Department of Anatomy, Physiology & Pharmacology, Auburn, AL
Abstract	REV-ERB (NR1D1) is a nuclear receptor that regulates liver glucose metabolism, circadian rhythm, and inflammation. It functions inversely with the retinoic acid receptor-related orphan receptor (ROR) by repressing transcription of et genes while ROR activates them, including genes for inflammation suggesting that REV-ERB has an anti-inflammatory role. Overnutrition, obesity, and metabolic diseases often coincide with chronic inflammation and pain (e.g., diabetic neuropathies), however, most mouse studies in these areas have not evaluated pain signatures in the brain We utilized a nutritional approach to evaluate whether there are CNS changes in pain signatures of obese-diabetic mice on a modified western diet (containing high fat, high fructose, and high cholesterol) as compared to littermates on a control, calorie-matched diet. Based on our previous studies, we hypothesized that mice treated with the REV-ERB agonist would have different inflammatory profiles in the brain as compared to non-treated mice. These differences may include, decreased astrocytes, decreased density of dendritic spines, and fewer glial cells compared to the control mice that were not treated with the compound. To test this hypothesis, we collected brains from mice on a selected diet (2 months of diet) and either treated with vehicle or REV-ERB compound (30 days) and performed immunofluorescence microscopy to analyze the brain for any significant changes between the groups. The data generated will provide support for more comprehensive and multidisciplinary studies evaluating chronic pain with obesity, diabetes, and metabolic disease in the future.
Research Grant	Research Grant: NIH NINDS 1R01NS126204 (KG)
Field of Research	Pharmacology and Toxicology

Abstract Title	Liver abscesses in cattle: Prevalence and assessment of potential involvement of Escherichia coli
Authors	Annie Harris, Alyssa Deters, Harith Salih, Xiaorong Shi, R.G. Amachawadi, and T.G. Nagaraja
Affiliations	Departments of Diagnostic Medicine and Pathobiology and Clinical Sciences, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas.
Abstract	Liver abscesses in feedlot cattle are a purulent bacterial infection enclosed in a fibrous capsule. Fusobacterium necrophorum, a ruminal bacterium, is the primary etiological agent. High-grain diets cause ruminal acidosis and rumenitis, weakening the ruminal epithelium, allowing bacteria into the portal vein then liver to cause abscesses. Microbiome analysis shows phylum Proteobacterium, which includes E. coli, to be the second most dominant phylum in liver abscesses. The goal of the study was to determine prevalence of E. coli in liver abscesses and assess their virulence and involvement in liver abscesses. A total of 96 liver abscesses with matched ruminal and colonic epithelial tissue samples were collected at slaughter. Selective and enrichment media helped isolate and identify E. coli, with liver abscesses yielding higher (64/96) after enrichment than prior (4/96). The prevalence of E. coli in liver abscesses, ruminal and colonic epithelial tissues were 70.8%, 92.7%, and 91.6%, respectively. A total of 245 E. coli strains were obtained and subjected to an 11-plex PCR assay that targeted four enterotoxin genes (elt, estA, estB, and astA), two Shiga toxin genes (stx1 and stx2), three adhesion genes (bfpA, aggA, and eae), and two hemolysin genes (hylA, and ehxA). No strains were positive for stx1, stx2, bfpA, and aggA. Only one strain from liver abscesses was positive for hylA. Ruminal E. coli isolates were positive for eae (2.3%), exhA (1.2%), and astA (1.2%) genes. Colonic isolates were positive for exhA (15.1%), hylA (15.1%), estA (7%), and astA (4.7%). A higher yield of E. coli isolation from enrichment suggests a low concentration in purulent liver abscess material, E. coli is not a likely etiologic agent.
Research Grant	International Consortium for Antimicrobial Stewardship in Agriculture (ICASA)
Field of Research	Bacteriology

Abstract Title	Haemonchus contortus vaccine implant for sheep
Authors	Darby Harris, Jennifer Wilson-Welder
Affiliations	Mississippi State University College of Veterinary Medicine, Mississippi State, MS (Harris), USDA ARS National Animal Disease Center, Ames, IA (Wilson-Welder)
Abstract	Haemonchus contortus, commonly known as the barber pole worm, is a parasitic nematode that resides in the abomasum of small ruminants. These blood-feeding strongyles can be found globally and cause animal suffering and significant economic losses for producers. Given the widespread increase of anthelmintic resistance in H. contortus and other gastrointestinal nematodes, new solutions must be generated. Vaccination against these nematodes has been shown to be effective, but the current commercial vaccine requires serial injections to provide sufficient immunity. The goal of the study is to determine if delivering antigenic targets for Haemonchus contortus in a novel Vaccine Platform for Extended Antigen Release (VPEAR) implant device will induce a strong humoral immune response which could be used as a means of reducing worm burden and disease caused by the parasitic nematodes in sheep. Four different groups of proteins or peptides are compared against a negative control antigen. Forty sheep had a VPEAR implant device surgically placed subcutaneously on the right fore flank a few centimeters caudal to the elbow joint. The immune response is being measured using antibodies detected by indirect ELISA. After measuring the immune response for 8 weeks, all groups will be challenged with oral gavage of live H. contortus larvae. Although this research is still ongoing, the preliminary data shows that a humoral immune response is being generated against Haemonchus contortus antigens.
Research Grant	None
Field of Research	Immunology

Abstract Title	Plasma metabolomic profiling of Canine Cognitive Dysfunction: The canine counterpart of Alzheimer's Disease
Authors	Scarlett Harrison, John Tegzes, Annika Linde, Tonatiuh Melgarejo
Affiliations	Western University of Health Sciences College of Veterinary Medicine, Pomona, California
Abstract	Canine cognitive dysfunction (CCD) is described as a neurodegenerative disease affecting more than 41% of older dogs with most being 11 years of age or older. Clinical signs include slowly progressive alterations in mentation, changes in sleep cycles, other behavioral changes, cerebral vasculature alterations, and brain deposition of β-amyloid proteins. The dog naturally develops this age-related cognitive dysfunction syndrome with brain lesions similar to human Alzheimer's Disease (AD), which makes the dog a highly attractive natural animal model for studying the mechanisms of neurodegeneration in AD. This case-control study aimed at characterizing the plasma metabolomic profiling of client-owned dogs with CCD compared to age-matched controls. Five dogs with a clinical diagnosis of severe CCD and five clinically healthy dogs were included. Fasting plasma samples were collected, frozen (dry ice), and shipped overnight to a third-party metabolomics laboratory (Creative Proteomics, Shirley, NY). Untargeted metabolomics results revealed significant increases (≥ 20 times higher) in plasma vitamin D3 and D4, cholesterol, cholesterol precursors, and progesterone in CCD dogs compared to healthy controls. Additionally, there was a significant decrease (fivefold reduction) in sulfonic acid precursors, phosphatidylcholine, sphingomyelin, and norcotinine plasma concentrations in dogs with cognitive impairment, suggesting that these metabolites may be useful predictors of the clinical progression of CCD. These results align well with the metabolomic signatures of patients with AD. Our data further support that the dog may prove to be a useful naturally occurring animal model to assess the neurobiological mechanisms of AD.
Research Grant	VP Research Office at WU, The True One Medicine Initiative at CVM WU, and the Research Office CVM WU.
Field of Research	Clinical Pathology

Abstract Title	Avian Bornavirus Subunit Vaccine Candidate Produces Robust Humoral Response
Authors	Alyssa Hartmann, Hope Merriam, Sarah Hamer, and Caitlin Mencio
Affiliations	Department of Veterinary Pathobiology, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA
Abstract	Avian bornavirus (ABV) is an enveloped, single-strand RNA virus that is a known etiological agent for proventricular dilatation disease (PDD), or avian ganglioneuritis (AG), in psittacines. PDD is a fatal disease that affects the neurological and gastrointestinal systems and devastates owners of parrots. There is no current antiviral treatment or vaccine against ABV infection. Our first step in testing two novel ABV vaccine candidates was to detect and measure the humoral response following vaccination. Two groups of five cockatiels (Nymphicus hollandicus) were vaccinated via intramuscular injection with either a mix of three purified viral proteins (nucleoprotein (N), phosphoprotein (P), and glycoprotein (G)) or inactivated PaBV-4. Both groups received booster vaccines at week 4. We hypothesized that the viral proteins will produce a stronger antibody response than the inactivated virus. Blood and cloacal samples were collected from all birds one week before and after vaccination then every two weeks to measure antibody levels (ELISA) and confirm ABV absence (PCR). Post vaccination, birds were identified as positive by ELISA when antibody levels were three standard deviations away from the mean of seronegative birds. One week post vaccination 2 of 5 subunit vaccine birds tested positive, and one week post booster 4 of 5 tested positive. 4 birds also showed increasing antibody levels over time. Conversely, only 1 of 5 inactivated virus birds were positive post initial and booster vaccines with inconsistent antibody levels. The protein subunit vaccine's robust response shows the immune system is responding and may be a promising method for ABV protection, making it our top candidate for the next stage of vaccine testing.
Research Grant	NIH T35 OD010991
Field of Research	Exotic Pets and Zoo Animal Medicine

Abstract Title	Dogs as sentinels of American cutaneous leishmaniasis transmission across land use gradients in Panama
Authors	Jeffrey Haydu, Kimberly Archbold, Nicole Gottdenker, Jose Calzada, Azael Saldaña, Vanessa Pineda
Affiliations	Department of Pathology (Haydu, Archbold, Gottdenker), College of Veterinary Medicine, University of Georgia, Athens, GA. Department of Parasitology (Calzada, Pineda), Gorgas Institute, Panama City, Panama. Center for Research and Diagnosis of Parasitic Diseases (Saldaña), University of Panama, Panama City, Panama.
Abstract	Leishmania panamensis is a zoonotic vector-borne protozoan parasite and a cause of the chronic ulcerative skin disease, American cutaneous leishmaniasis (ACL), which is endemic in tropical regions of Latin America. Transmission to humans and domestic animals occurs from wild mammal reservoirs through many species of sandfly vector. Treatments for ACL have variable efficacy and can be toxic, and no vaccines are available. Transmission of Leishmania panamensis is influenced by the prevalence of reservoir species and ecological factors. Aspects of the surrounding environment, such as the scope of farmland, forests, and deforested or reforested areas can have a significant impact on the habitats and prevalence of the vectors, as well as the reservoir hosts, changing the likelihood of exposure to the disease. Therefore, it is critical to understand how the various environments surrounding communities are contributing to rates of infection, so targeted control strategies can best be put to use to prevent disease. The overarching goal of this study is to use dogs, who are often exposed to sandfly vectors and Leishmania spp., as peridomiciliary sentinels to evaluate environmental factors related to Leishmania panamensis infection risk at the household level. Specifically, we aim to develop and standardize an Enzyme-linked immunosorbent assay (ELISA) to detect Leishmania panamensis antibodies in dog serum samples collected from dogs across land-use gradients in rural communities of central Panama. By using dogs as sentinels for peridomestic leishmaniasis transmission across land-use gradients in Panama, we can evaluate which areas are at highest risk of transmission and appropriately target control and prevention strategies.
Research Grant	1924200 CNH2-L: Social and ecological determinants of multi-host vector-borne infections in dynamic tropical landscapes
Field of Research	One Health

Abstract Title	Rational design of common epitope vaccine neutralizing Staphylococcal superantigens and cytotoxins
Authors	Alyssa Heath, Keun Seok Seo, Nogi Park, Youngkyung Park, Justin A Thornton
Affiliations	Department of Comparative Biomedical Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS (Heath, Seo, Park, Park) and Department of Biological Sciences, College of Arts & Sciences, Mississippi State University, Mississippi State, MS (Thornton)
Abstract	One of the most prevalent diseases in dairy cattle today is bovine mastitis. A common cause is Staphylococcus aureus, an opportunistic pathogen known for its resistance to antimicrobials. Vaccines are an alternative method of treatment; however, studies have failed due to S. aureus' evasion of the immune system through various virulence factors. Two important factors are superantigens (SAgs) and cytotoxins, which cause aberrant T-cell activation and lysis of RBCs and WBCs. We hypothesized that immunization with consensus sequences of the receptor binding domain of SAg and cytotoxins will provide cross protection against these toxoids. Sequence alignments showed that the TCR binding domain of SEG, MHC II binding domain of SEI, and stem receptor binding domain of HlgB showed the highest similarity. Recombinant proteins of these binding domains were generated and used for immunizing C57BL/6 mice. Results showed that serum immunized with TCR binding domain was able to neutralize SEC but not SEI. Similarly, serum immunized with MHC II domain was able to neutralize SEI but not SEC. Importantly, SEC and SEI have a higher affinity to TCR and MHC II, respectively, for superantigenicity, indicating that neutralization of a higher affinity interaction between SAgs and TCR or MHC II is important for neutralization. Serum immunized with stem domain of HlgB was able to neutralize HlgB/LukE and LukD/LukE, suggesting cross protection against other cytotoxins. Combined, results suggest that vaccination with consensus sequences can elicit a neutralizing antibody response, providing cross protection against 24 SAgs and 12 cytotoxins. This will be useful to develop an efficacious and affordable bovine mastitis vaccine.
Research Grant	National Institutes of Health Grant T35OD010432
Field of Research	Immunology

Abstract Title	Assessing chemosensory host-seeking behaviour and in vitro impact of emodepside on Ancylostoma caninum
Authors	Shridula S Hegde and Antoinette E Marsh
Affiliations	Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio
Abstract	Ancylostoma caninum, canine hookworm, is a zoonotic intestinal nematode where the infective third-stage larvae (L3) enter the dog via ingestion or skin penetration. This parasite can cause cutaneous larval migrans or patent infections in dogs and humans. There are now drug-resistant isolates in dog populations. It is hypothesized that A. caninum exhibits host-seeking activities using chemosensory behaviour. This study aimed to develop a chemotaxis assay, measure the chemosensory abilities of A. canium, and evaluate emodepside impact on parasite development. Chemosensory stimuli evaluated the attraction to collagen, a protein found in the skin, and urocanic acid (UA), a skin histidine metabolite, mimicking the host odorant. Hookworm eggs were isolated from naturally infected dogs (IACUC: 2019A00000134-R1). Various protocols and reagents (agar, optimal cutting temperature compound (OCT), glycerol, and chloroform) were analysed to develop the chemotaxis assay. In vitro, larval movement on agar towards UA was measured with most L3s in the UA region after 48 hours. The OCT at room temperature did not impact larval viability, whereas at -20°C, most died. To euthanize the L3 for quantification, chloroform treatment at 20% proved ineffective, and at 80%, the larvae died. For emodepside, 40 µg/ml treatment resulted in fewer eggs reaching the L3 stage than the lower concentrations tested. No published studies have evaluated the chemosensory behaviour of A. caninum to UA. The results show that Caenorhabditis elegans chemosensory assays failed to translate to A. caninum directly. Developing and optimizing in vitro laboratory tools is critical to understand A. caninum and prevent its further spread.
Research Grant	The Ohio State University, Canine Research Funds and Duncan Alexander (donor)
Field of Research	Parasitology

Abstract Title	Removing contrast: combining iodine-based contrast-enhanced computed tomography with serial immunostaining
Authors	Paul Heller, Nikita McKnight, Aliza Siebenaller, Kathy Jacyniak, Matthew Vickaryous
Affiliations	FB10, Justus-Liebig-University, Giessen, Hessen (Heller), Biomedical Sciences, Ontario Veterinary College, University of Guelph, Guelph, ON (Heller, McKnight, Jacyniak, Vickaryous), Human Health and Nutritional Sciences, College of Biological Sciences, University of Guelph, Guelph, ON (Siebenaller)
Abstract	Diffusible iodine-based contrast-enhanced computed tomography (diceCT) is an increasingly common tool used to study soft tissues non-invasively. This technique involves incubated specimens in iodine-based solutions. Whether specimens subjected to diceCT can then be re-used for subsequent histological and immunostaining investigations has not been well-explored. Here, we investigate a method for de-staining diceCT-treated tissues and then performing serial histology and immunostaining to explore the brain and associated structures in a representative reptile, the leopard gecko (Eublepharis macularius). Two gecko heads were formalin-fixed for 24 hours, then stored in 70% ethanol. Each head was longitudinally bisected and right sides were stained with 1.25% w/v solution Lugols iodine for either 10 or 21 days. Samples were then micro-CT scanned and de-stained with 1% w/v sodium thiosulfate. Next, both treated (right side) and control (left side) tissues were processed for routine paraffin histology, sectioned at 5 µm and mounted on microscopy slides. We immunostained for markers of cell proliferation (PCNA), neural stem cells (SOX2) and glial cells (GFAP). Our results show robust immunoreactivity for each of the antibodies tested, with no obvious differences between control and both, the 10 and 21 iodine treated tissue samples. Our findings demonstrate that the immunoreactivity of reptile brain tissues can be restored following diceCT-treatment. Further, we outline a methodological workflow to generate digital 3D models and details of protein localization within tissues from a single specimen. Future studies will use morphometric analyses to determine if iodine staining/de-staining results in tissue shrinkage or swelling.
Research Grant	Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery Grant 400358 to MV.
Field of Research	Anatomy

Abstract Title	Effects of sedatives on the plasma corticosterone response of Hispaniolan Amazon parrots (Amazona ventralis)
Authors	Meridith Helms-Pack, Thomas N. Tully, Jr., Breonna Freeman, Keegan R. Stansberry, Chin-Chi Liu, John Tuminello, and Christine R. Lattin
Affiliations	Department of Veterinary Clinical Sciences, School of Veterinary Medicine (Helms-Pack, Tully, Freeman, Liu, Tuminello) and Department of Biological Sciences (Stansberry, Lattin), Louisiana State University, Baton Rouge, LA.
Abstract	Glucocorticoids are steroid hormones that are produced by the adrenal glands and released to regulate an animal's physiology, as well as mediate the stress response. Corticosterone is the major glucocorticoid found in avian species. While corticosterone helps regulate multiple body processes that make life possible, it can also have negative effects such as immune suppression when levels are highly elevated. A previous study showed that plasma corticosterone levels significantly increased when Hispaniolan Amazon parrots (Amazona ventralis) were restrained to mimic routine veterinary handling. The sedatives midazolam and butorphanol are being used more often in veterinary medicine to improve the experience of patient handling for both the patient and caregiver. It was hypothesized that a clinically relevant dose of midazolam and butorphanol would significantly decrease the plasma corticosterone response in restrained Hispaniolan Amazon parrots (n=11) when compared to the control birds (n=11). Overall, the sedative group did not have significantly decreased plasma corticosterone compared to the control groups. However, when we analyzed results by sex, males that received sedatives had a significantly decreased plasma corticosterone response to restraint than male controls, female controls, and females that received sedatives. These results suggest a sex-specific effect in the metabolism of midazolam and butorphanol similar to results that have been seen in other animals (e.g., rodents); pharmacokinetic studies on these sedatives with respect to sex is recommended.
Research Grant	Louisiana State University School of Veterinary Medicine Avian Research Fund
Field of Research	Exotic Pets and Zoo Animal Medicine

Abstract Title	Impact of fed mycotoxins on the vaccine efficacy of non-vaccinated beef cattle
Authors	Karling Hemstreet Graves, Clinton Roof
Affiliations	School of Veterinary Medicine, Texas Tech University, Amarillo, Texas
Abstract	Feed molds and mycotoxin production are naturally occurring processes that are influenced by cool and wet conditions during the growth, harvest, or storage of feed intended for livestock. Mycotoxins in feed result in a reduction of milk production, displaced abomasum, diarrhea, abortion, decreased feed efficiency, and mitigated immune responses in cattle. The most toxic mycotoxin that affects cattle is Aflatoxin B1 (AFB1), with concentrations in feed limited to 300 ppb for growing cattle by the FDA. Unvaccinated cattle moved to a backgrounding or feed yard can be exposed to mycotoxin-contaminated hay, followed by a vaccination protocol days later. However, the effect of mycotoxins on vaccine efficacy in cattle has not been established. We hypothesize that vaccine efficacy in beef cattle is diminished due to decreased immunologic response caused by the presence of AFB1. This pilot study aims to assess vaccine efficacy following administration of mycotoxin-contaminated feed. Beef cattle approximately 8 months of age, considered to be free of maternal antibodies, were acquired. Baseline viral serology for Bovine Rhinotracheitis-Virus (IBR), Bovine Viral Diarrhea Virus (BVDV), Parainfluenza (PI3), and Bovine Respiratory Syncytial Virus (BRSV) was determined. Cattle were randomly fed either mycotoxin-tainted ad lib hay (AFB1 ~300 ppb) or clean visually mold-free ad lib hay for 4 days. Cattle were then given a modified-live vaccine (MLV) against IBR, BVDV, PI3, and BRSV. Feeding continued for an additional 14 days, upon which a repeated viral serology panel was performed. Results from this pilot study will provide key preliminary data for future studies regarding vaccine efficacy in cattle.
Research Grant	None
Field of Research	Production Animal Medicine

Abstract Title	Ocular toxicity, distribution, and shedding of intravitreal gene therapy for uveitis
Authors	Nichol M. Henderson, Kimberly A. S. Young, Jacklyn H. Salmon, Matthew L. Hirsch, Lauren V. Schnabel, and Brian C. Gilger
Affiliations	Department of Clinical Sciences, College of Veterinary Medicine, North Carolina State University, Raleigh, NC (Henderson, Young, Salmon, Schnabel, Gilger) Department of Ophthalmology and Gene Therapy Center, School of Medicine, University of North Carolina, Chapel Hill, NC (Hirsch)
Abstract	Non-infectious uveitis is a painful, recurrent disease that affects ~25% of horses. Current treatments are non-specific and long-term use is accompanied by serious adverse effects. Long-term treatment is needed to prevent vision loss, so novel therapeutics with prolonged action and fewer adverse effects are desired. Adeno-associated virus (AAV) gene therapy was previously explored in rats to elicit the immune tolerance mechanisms of equine Interleukin 10 (eqIL10). This study aimed to evaluate ocular toxicity, distribution of viral transduction, and viral shedding following a single intravitreal (IVT) injection of AAV8-eqIL10 in normal horses. Each horse received an IVT injection in both eyes with either a balanced salt solution (n=1), a low dose of AAV8-eqIL10 ($3.75x10^{11}$ vg, n=2), or a high dose of AAV8-eqIL10 ($3.75x10^{12}$ vg, n=2). Ophthalmic examinations (OEs) were performed on days 0, 1, 3, 7, and weekly thereafter until euthanasia at approximately day 90 post IVT injection. Viral shedding patterns will be determined using blood, tear, urine, and fecal samples. Ocular histology will be performed for signs of toxicity and vector biodistribution on selected ocular tissues and organs will be examined. Serum antibody titers will be run on blood from days 0, 28, and 84. Results of OEs did not indicate a chronic inflammatory response in any treatment group. High dose horses had a statistically significant decrease in intraocular pressure and had keratic precipitates. Shedding, distribution, and toxicity data are still undergoing analysis. While this data is required for a thorough safety assessment of AAV8-eqIL10 IVT injections, the low (expected clinical) dose appears to be well tolerated and promising as a therapy.
Research Grant	North Carolina Biotechnology Center Translational Research Grant
Field of Research	Ophthalmology

Abstract Title	Efficacy of CART Cell Targeting on Central Nervous System B Cells in an Animal Model of Progressive MS
Authors	Sara Hernández Suárez, Hania Kébir, and Jorge Iván Alvarez
Affiliations	Department of Pathobiology, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA
Abstract	Multiple Sclerosis (MS) is an autoimmune inflammatory disease in which the myelin sheath of the Central Nervous System (CNS) is attacked, leading to neurodegeneration with subsequent neurologic signs. Despite devastating clinical outcomes and decades of research, progressive forms of the disease remain difficult to treat. In progressive MS (PMS), the aggregation of B cells in the leptomeninges is predictive of poor clinical outcomes and rapid progression of disability. The gold standard animal model for MS, experimental autoimmune encephalomyelitis (EAE), is unable to mimic the pathophysiology seen in PMS. The Alvarez' lab has developed a progressive EAE (pEAE) model that presents leptomeningeal B cell accumulation associated with underlying pathology as described in PMS. Thus, we aim to interrogate the causal relationship between meningeal B cell responses and progressive disease using a novel therapeutic intervention: the Chimeric Antigen Receptor T cell (CART) therapy. CART cells are re-engineered T cells designed to recognize and kill specific aberrant cells. In order to target B cells, pEAE mice were injected with CART cells directed against CD19, a marker expressed on the surface of B cells. Mice were euthanized 2 and 10 days post-CART administration. The CNS and spleen were then processed for flow cytometry and immunofluorescence analyses. Similar numbers of B cells in the CNS of control and CART-injected mice at day 2 were found by flow cytometry. Interestingly there was a decrease in B cell numbers at day 10 in the CART-injected mice compared to the control group. We now confirming histopathologically, if this correlates with a decrease in B cell leptomeningeal clusters and corresponding subpial injury.
Research Grant	NIH Grant T35 OD 010919-25
Field of Research	Immunology

Abstract Title	Analysis of pathogens from urine cultures of cats and dogs from 2010 to 2021 in Northeast United States
Authors	Maxi Laura Martha Hertel1, Claudia Gisela Cobo Ángel2, Abdolreza Mosaddegh2, Casey L. Cazer2,3
Affiliations	1Faculty of veterinary medicine, Leipzig University, Germany (Hertel) 2Department of Public and Ecosystem Health, College of Veterinary Medicine, Cornell University, Ithaca, NY (Cobo Ángel, Mosaddegh, Cazer) 3Department of Clinical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY (Cazer)
Abstract	Urinary tract infections (UTIs) in dogs and cats are a significant health concern in these species, and the empirical use of antibiotics is common. Understanding the prevalence and types of pathogens is crucial for effective diagnosis and empirical treatment. The objective of this study is to provide an update on the distribution of pathogens among the canine and feline populations with urine cultures. We analyzed data from 31,359 feline and canine urine samples that were cultured at the Cornell University Animal Health Diagnostic Lab between 2010 and 2021. Data were analyzed in STATA v. 18 and MICROSOFT SQL SERVER. For each host species a logistic regression model to predict mixed cultures was created. Overall, the most common pathogens isolated from urine cultures in both dogs and cats was Escherichia coli (11.41% in cats, 15.61% in dogs). For feline samples, Enterococcus faecalis (4.54%) and Staphylococcus spp. (4.08%) were also common. Proteus mirabilis (4.80%) and Staphylococcus pseudintermedius (4.72%) are high prevalent in dogs. In both species, we find a high percentage of mixed infections (more than one pathogen, cats 8.76% and 15.75% in dogs). It should be pointed out that, among all analyzed samples, 37.68% had positive cultures (41.98%) of the canine samples, 27.47% of the feline samples), the rest had no growth. Sampling by voided catch is most likely to result in a mixed culture (dogs: OR=1.58, P< 0.001; cats: OR= 3.7, P<0.001). Appropriate sampling is crucial for accurate diagnosis and targeted treatment. Our results show that sampling by voided catch, for example, is clearly not advisable. No growth results should not be treated with antimicrobials.
Research Grant	Research Grant: None
Field of Research	Epidemiology

Abstract Title	Fitness of Usutu Virus in mosquito and mouse cells
Authors	Annika Heyder, Nisha Duggal
Affiliations	Department of Biomedical Sciences and Pathobiology, Virginia-Maryland College of Veterinary Medicine, Virginia Polytechnic Institute and State University, Blacksburg, Virginia
Abstract	Usutu virus (USUV) is an arthropod-borne flavivirus with an enzootic cycle between Culex (Cx.) spp. mosquitoes and birds. To date, a few human cases have been reported. Some of these are associated with neuroinvasive disease. First isolated in Africa in 1959, USUV has spread widely in Europe in recent years, causing significant bird mortality. During emergence in Europe, USUV may have adapted to cause increased transmission rates in its vector/host over time. We found that USUV Netherlands 2016 had higher titers in birds than Uganda 2012. In contrast, we showed that mice inoculated with USUV Netherlands 2016 had very low viremia, whereas African strains had significant viremia. The aim of this study is to determine the fitness differences between the USUV strains Uganda 2012 and Netherlands 2016 in mouse and mosquito cells. We hypothesized that USUV Netherlands 2016 has adapted better to mosquitoes and thus shows higher replication and fitness than USUV Uganda 2012 in Cx. cells. We also hypothesized that USUV Uganda 2016 has a higher replication and fitness in mouse cells than USUV Netherlands 2016. Growth curves and competition assays were performed to examine the replication and fitness of USUV Netherlands 2016 and USUV Uganda 2012 in Cx. tarsalis and mouse cells. Our results from the Cx. tarsalis growth curve showed no statistically relevant differences between the two USUV strains in replication. Ongoing work will directly measure viral fitness in Cx. tarsalis and mouse cells. Further research on the susceptibility of potential vectors/hosts to USUV and the mechanisms of viral adaptation is urgently needed.
Research Grant	none
Field of Research	Virology

Abstract Title	Feasibility of percutaneous osteotomies in dogs
Authors	Samantha Higgins, Stanley Kim
Affiliations	University of Florida CVM, Gainesville, FL
Abstract	Limb deformity correcting osteotomies are fairly common orthopedic procedures in the antebrachial region of canine patients, with the currently practiced method requiring an open approach. The practice of minimally invasive surgery has rapidly expanded in human orthopedic surgery, especially in the field of foot and ankle surgery. Currently, there has been no veterinary research in the possibility of performing these percutaneous osteotomies on canine limbs, but studies have been done to show the benefits of the percutaneous burr on foot and ankle surgery, which include reduced tissue damage, reduced post-operative pain, and improved healing time. The goal of this study was to examine the feasibility of an minimally invasive approach to the osteotomy using a percutaneous burr inserted in a stab incision. We performed osteotomies on canine cadavers, using the sagittal saw and the percutaneous burr on randomly selected limbs to compare the procedures. We hypothesized that due to the size of the bones commonly affected with canine limb deformity and their comparable size in respect to human foot and ankle bones, percutaneous osteotomies will have lower regional tissue damage with comparable accuracy when performing osteotomies with a saw. We found that there was no significant difference between the tendon damage between the groups and the incision length for the burr group was significantly smaller, but the cutting time and the total procedure time for the burr group was significantly longer. These findings indicate that the use of a percutaneous burr in performing an osteotomy in the antebrachial region is feasible with minimal damage to the small tissue, but it may be challenging given the increased procedure time.
Research Grant	Arthrex Vet Systems for equipment and supplies
Field of Research	Orthopedics

Abstract Title	Bluetongue virus surveillance across domestic ruminants in Northern Colorado in 2022
Authors	Samantha Hilty, Mollie Burton, Christie Mayo
Affiliations	Department of Microbiology, Immunology, and Pathology (Hilty, Burton, Mayo) and College of Veterinary Medicine, Colorado State University, Fort Collins, Colorado
Abstract	Bluetongue virus (BTV) poses a significant threat to both wild and domestic ruminants worldwide. Transmitted by the Culicoides biting midge, outbreaks of BTV in domestic ruminant populations can cause substantial agricultural and economic losses on a global scale, with estimated annual impacts reaching up to 3 billion US dollars. Surveillance of bluetongue virus is essential for monitoring the spread of bluetongue disease and implementing management strategies to help mitigate its impact. This study aims to assess the seroprevalence of bluetongue virus in domestic ruminants in Northern Colorado. Serum samples were collected monthly from May 2022 to December 2022 from domestic sheep, dairy cattle, and beef cattle representing 8 sites and 169 unique animals. The serum samples were screened for the presence of bluetongue virus-specific antibodies using competitive enzyme-linked immunosorbent assay (cELISA). Overall seroprevalence in June was estimated to be 54.6%, with the final seroprevalence in December estimated to be 56.3%. The estimated BTV seroprevalence for the duration of the collection period was 56.9% for sheep sites, 82% for beef sites, 38.5% for dairy sites, and 69.1% for all sites combined. These results underscore the ongoing presence of bluetongue virus in Northern Colorado and the importance of supporting surveillance efforts to inform targeted control strategies to effectively manage bluetongue in Northern Colorado.
Research Grant	United States Department of Agriculture Fellowship, USDA-NIFA AFRI grant number 2019-67015-28982 as part of the joint USDA-NSF-NIH-BBSRC-BSF Ecology and Evolution of Infectious Diseases program.
Field of Research	Virology

Abstract Title	Sedation of great horned owls (Bubo virginianus) for non-invasive clinical techniques
Authors	Rachel M. Hirota, Venus Casagrande, Stephanie Chen, Hugues Beaufrere, Michelle G. Hawkins
Affiliations	School of Veterinary Medicine (Hirota); Department of Animal Biology, College of Agricultural and Environmental Science (Casagrande, Chen); and Department of Medicine and Epidemiology, School of Veterinary Medicine (Beaufrere, Hawkins), University of California-Davis, Davis, CA
Abstract	Wild birds become stressed during the manual restraint required for examination and treatment. Handling stress can lead to acute and chronic physiologic consequences due to catecholamine and glucocorticoid secretions. Reversible, injectable sedation may allow for less stressful completion of clinical procedures by reducing the potential for adverse effects commonly encountered with inhalant anesthesia. While midazolam, dexmedetomidine, and hydromorphone have been explored as sole agents for injectable sedation in several bird species, studies evaluating the sedative effects of these drugs in combination in owls are lacking. The objective of this study was to evaluate the following protocols: (1) midazolam 2 mg/kg IM and dexmedetomidine 0.05 mg/kg IM; (2) midazolam 2 mg/kg IM and hydromorphone 0.6 mg/kg IM; and (3) midazolam 2 mg/kg IM, dexmedetomidine 0.02 mg/kg IM, and hydromorphone 0.3 mg/kg IM in Great Horned Owls (Bubo virginianus) followed by use of specific reversal agents for each drug. Treatments were evaluated for the onset of sedation and recovery; sedation depth via muscle tone and response to stimuli; tolerance of physical examination, venipuncture, and sham radiographic positioning; and venous blood gases before and at the end of sedation. We hypothesized that all 3 treatments will produce sedation sufficient for the completion of clinical techniques and minimize physiological response to manual restraint. Continuous variables will be analyzed via linear mixed models with age, sex, and treatment order as fixed effects and subjects as random effects. Ordinal variables such as sedation scores will be analyzed via ordinal mixed logistic models.
Research Grant	Oiled Wildlife Care Network
Field of Research	Exotic Pets and Zoo Animal Medicine

Abstract Title	Expansion of equine mesenchymal stromal cells using xenogeneic, autologous and allogeneic serum over 7-days
Authors	Cherise Hoagland, Maureen Larson, and Lacy Kamm
Affiliations	Oregon State University, Carlson College of Veterinary Medicine, Corvallis, OR
Abstract	Mesenchymal stroma cells (MSC's) are a therapeutic intervention given to horses with soft tissue injuries or osteoarthritis. MSCs are grown in culture media containing xenogenic serum (fetal bovine serum) as this allows for rapid expansion of the cells and appropriate maintenance of the cell's pluripotent properties. Recent evidence has shown that MSCs cultured in xenogeneic serum exhibit greater immunogenicity when administered as a repeat treatment as compared to MSCs grown in autologous and allogeneic media (Joswig et al. 2017). The aim of this study is to compare the proliferation rates and differentiation ability of equine MSCs when grown in media containing xenogenic, autologous or allogeneic serum. Two females and one castrated male between the ages of 2-17 years were used for bone marrow harvest and serum collection. MSCs were cultured in media for 7 days containing xenogenic serum, autologous serum, pooled commercial allogeneic serum, or combined xenogenic and autologous serum followed by autologous serum prior to harvesting the cells. It is hypothesized that xenogenic media will allow for the greatest MSC proliferation, but autologous and allogeneic serum-containing media will also allow for adequate proliferation. The goal of this study is to determine which autologous or allogeneic media allows for MSC proliferation most like that of xenogenic media. Trilineage capability testing will be performed using xenogeneic and autologous serum to determine if the differing culture conditions affect the pluripotency of the MSCs.
Research Grant	Carlson College of Veterinary Medicine Summer Scholars Program
Field of Research	Equine Medicine and Surgery

Abstract Title	Optical coherence tomography of optic nerve head in dogs with open angle glaucoma: correlation with axon count
Authors	Lisa Hoard1, Shin Ae Park1, Christine D. Harman2, Kelly A. Leary2, Vanessa A Raphtis2, Kate Jongnarangsin2, András M. Komáromy2
Affiliations	1Department of Veterinary Clinical Sciences, College of Veterinary Medicine, Purdue University, West Lafayette, Indiana, USA 2Department of Small Animal Clinical Sciences, College of Veterinary Medicine, Michigan State University, East Lansing, Michigan, USA
Abstract	The gold standard for determining disease progression of glaucoma in research settings involves optic nerve axon counting, which is performed ex vivo. With the advancement of noninvasive imaging techniques, it is possible to image details of the retina and optic nerve head (ONH) in vivo. This study sought to determine the relationship between the number of axons at the ONH and various parameters using optical coherence tomography (OCT) and confocal scanning laser ophthalmoscopy (cSLO) in dogs with various stages of primary open angle glaucoma. Beagles (n=6 eyes) with open angle glaucoma and age matched non-glaucoma dogs (n=2 eyes) were included in the study. OCT and cSLO images were taken of each eye, capturing the ONH, and a built-in software was used to measure neuroretinal rim area, ONH area and diameter, and optic cup diameter. Total retinal thickness, ganglion cell complex (GCC), and outer retinal thickness were also measured. Slides with the ONH samples were scanned and axons were manually counted using Image J software. A strong positive correlation existed when comparing the following parameters to the number of axons: neuroretinal rim area ($r=0.91$, $p<0.01$), ONH area ($r=0.73$, $p<0.04$), total retinal thickness ($r=0.75$, $p=0.02$), and GCC ($r=0.82$, $p<0.01$).There was a strong negative correlation ($r=-0.75$, $p=0.03$) between the number of axons and optic cup area and a moderate negative correlation ($r=-0.70$, $p=0.12$) between number of axons and age. The strong positive and negative correlations between the number of optic nerve axons and the various parameters measured support the utility of OCT and cSLO as useful noninvasive imaging techniques to assess the progression of glaucoma in vivo in dogs with open angle glaucoma.
Research Grant	Research Grant: ACVO Vision for Animals Foundation Resident Research Fund, NIH R01-EY025752, and NIH K08EY030950
Field of Research	Ophthalmology

Abstract Title	Soy isoflavones regulate steroid hormone secretion in the male gonad
Authors	Kristen G. Hoehler, Bamidele Jeminiwa, Samantha Bradley, Kate Wilkinson, Donte Grimes, Benson T. Akingbemi
Affiliations	Department of Anatomy, Physiology, and Pharmacology, Auburn University CVM, Auburn, AL
Abstract	Soy isoflavones are phytoestrogens present in common food items such as soybeans and other legumes, tofu products, and soy-based infant formulas. To identify the mechanisms of soy isoflavone action in the testis, 21-day old Long-Evans rats were fed a control casein diet, control casein diet plus 300 ppm genistein and 200 ppm daidzein (G+D), or control casein diet plus 600 ppm genistein and 400 ppm daidzein (2G+2D). At the end of eight weeks of exposure, animals were sacrificed to collect blood, testes and Leydig cells. Serum and testicular concentrations and Leydig cell secretion of testosterone (T) and estradiol (E2) were measured by RIA. The results showed that T concentrations were decreased in the G+D group but increased in the 2G+2D group compared to control ($p < 0.05$). Additionally, testicular E2 concentrations were increased in the 2G + 2D group while Leydig cell E2 secretion was decreased in the 2G + 2D group ($p < 0.05$). Subsequently, western blots were performed to assess gene expression in testes from all three groups. The results showed that estrogen receptor-α expression was increased in the 2G + 2D group ($p < 0.05$), but Cathepsin D protein was decreased in both treatment groups compared to control ($p < 0.001$). To validate results of RNASeq analysis, Sirtuin 1 was measured, and data showed that this protein was increased in both the G + D ($p < 0.0001$) and 2G + 2D groups ($p < 0.00001$). Taken together, these observations imply that soy isoflavones target the steroidogenic pathway in Leydig cells, inducing estrogenic activity and possibly acting through the sirtuin1 signaling pathway. Therefore, consumption of soy-based foods has implications for male gonadal function.
Research Grant	This study was funded by a research grant from the Animal Disease and Health Research Program at Auburn University College of Veterinary Medicine.
Field of Research	Pharmacology and Toxicology

Abstract Title	Furosemide-induced dilation of pulmonary veins as a prophylactic for exercise-induced pulmonary hemorrhage
Authors	Emily E. Hoffman, Pamela K. Thorne, Kile S. Townsend, Lynn M. Martin, Philip J. Johnson, Warwick M. Bayly, and Darla L. Tharp.
Affiliations	Biomedical Sciences (Hoffman, Thorne, Tharp), Veterinary Medicine and Surgery (Townsend, Martin, Johnson), College of Veterinary Medicine, University of Missouri, Columbia, MO; Veterinary Clinical Sciences, College of Veterinary Medicine, Washington State University, Pullman, WA (Bayly).
Abstract	Horses undergoing intense exercise are routinely diagnosed with exercised-induced pulmonary hemorrhage (EIPH), and furosemide (Lasix™) is the only pharmacotherapy to demonstrate efficacy in reducing the severity of this condition. The use of Lasix™ is controversial since its mechanism of action in the pulmonary system is incompletely understood. Our research aims at elucidating pulmonary vascular mechanisms by which furosemide reduces the severity of EIPH. We hypothesized that furosemide induces dilation of pulmonary veins by inhibition of the Na+, K+, Cl- cotransporter-1 (NKCC1). Pulmonary veins (2 & 3mm diameter) were isolated from the dorsocaudal (DC) and cranioventral (CV) lobes of the right lung obtained from 6 Thoroughbreds. Wire myography was used to assess dilation to furosemide, and as hypothesized, furosemide induced dilation in veins isolated from both DC and CV. Furosemide- induced relaxation was increased in 3 mm veins isolated from DC (94±4%) versus CV (81±5%; ANOVA $p<0.05$), whereas 2 mm veins from both DC and CV responded similarly (88±6%, 85±3%). qPCR was used to determine mRNA expression of NKCC1, and veins isolated from both DC and CV had mRNA expression similar to positive control tissues (kidney, lung, spleen). In future, immunohistochemistry will be used to determine the protein location of the NKCC1 cotransporter in equine pulmonary veins. These data represent the first evidence that furosemide has a direct effect on equine pulmonary vasculature, and that NKCC1 mRNA exists in the lung. These data suggest NKCC1 inhibition is a plausible pulmonary vein-mediated mechanism underlying the efficacy of furosemide for prophylaxis of EIPH.
Research Grant	CVM COR Grant
Field of Research	Equine Medicine and Surgery

Abstract Title	Characterizing occurrence patterns for Infectious Coryza in Ohio
Authors	Brad Hogshead, Dominika Jurkovic, Andreia Arruda
Affiliations	Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio (Hogshead, Arruda) and Ohio Department of Agriculture, Animal Disease Diagnostic Laboratory, Reynoldsburg, Ohio (Jurkovic)
Abstract	Infectious Coryza is a common respiratory disease of chickens caused by the bacteria Avibacterium paragallinarum (APG). The disease causes high morbidity and low mortality and results in decreased production due to lack of feed consumption, stunted growth, and reduced egg production. In layer hens, egg production can be reduced as much as 40%. Outbreaks of Infectious Coryza in the United States have been described; however, the prevalence in Ohio unknown. Prevalence data is important for veterinarians to understand the likelihood of a specific pathogen when investigating disease outbreaks. Thus, the aim of this study was to estimate the prevalence of Infectious Coryza in Ohio. Information on samples submitted to the state diagnostic laboratory, between November 2019 and June 2023, for APG testing via polymerase chain reaction (PCR) were analyzed. Five hundred and twenty samples from 74 different farms were included in the analysis. Overall, the prevalence in Ohio was 29.29%. Licking, Mercer, and Marion counties had the greatest number of sample submissions with 150, 84, and 81 submissions, respectively. Mercer, Darke, and Wyandot counties had the highest percent of positive samples with 29.61%, 19.74%, and 11.18%, respectively. When comparing seasons, the majority of positive samples were seen during the Spring, followed by Winter (56.58% and 28.95%, respectively). This study provides valuable information on the spatial-temporal aspects of Infectious Coryza in Ohio layer flocks that can aid in further prevention of disease outbreaks.
Research Grant	None
Field of Research	Epidemiology

Abstract Title	Cellular targeting and functions for the methionine sulfoxide reductases
Authors	Alexandra Hommer, Carolyn Sevier
Affiliations	Department of Molecular Medicine, College of Veterinary Medicine, Cornell University, Ithaca, New York
Abstract	Reactive oxygen species (ROS) are highly reactive molecules formed by O2 reduction. ROS producing enzymes are distributed throughout the cell in every organelle however, how they cell can sense and respond to these localized sources of ROS is unclear. Protein oxidation by ROS can lead to loss of function or gain of function modifications. Methionine side chains are particularly susceptible to oxidation by ROS resulting in methionine sulfoxide (MetO). This is a stereospecific event resulting in either S-MetO or R-MetO. Enzymes known as methionine sulfoxide reductases, MSRs, are capable of reversing these modifications. While Msr function is well studied, many targets remain unidentified. Humans have multiple MSR enzymes, called MsrA and MsrB, distributed throughout the cell. These enzymes can selectively reduce S-MetO or R-MetO respectively and can be found multiply localized from their respective genes. Interestingly, MsrA and MsrB are found in pairs in every organelle except the ER. The eukaryote, S. cerevisiae has two MSR enzymes: Mxr1 and Mxr2. Mxr1 and Mxr2 are dual localized to the cytoplasm and the mitochondria but are not known to localize elsewhere. We are interested in determining why some cellular locations have one or no copy of these Msr enzymes and how this related to ROS damage and signaling. We aim to better characterize the distribution of Msrs within yeast through cellular fractionation and microscopy utilizing a split-GFP system. Once we have a better understanding of Msr localization, we aim to identify Msr targets within each organelle.
Research Grant	Research Grant: NIH R01 GM105958
Field of Research	Biochemistry

Abstract Title	Super-resolution analysis of chromatin-nuclear lamina interactions in bovine oocytes
Authors	Jaylan Horton, Regan Smith, Claudia Baumann, Xiangyu Zhang, Rabindranath De La Fuente
Affiliations	Department of Physiology and Pharmacology, University of Georgia, College of Veterinary Medicine, Athens, GA
Abstract	Chromosome instability (CIN) poses major challenges to mammalian reproduction, leading to early embryonic demise, implantation failure and high rates of pregnancy loss. For the US cattle industry, embryonic mortality amounts to approximately $2.8 billion/year in lost revenue. Little is known regarding the mechanisms safeguarding chromosome stability in bovine oocytes. Gradual chromatin condensation in the germinal vesicle (GV) of oocytes correlates with increased developmental potential to reach the blastocyst stage. Current oocyte quality parameters for bovine ART rely on coarse morphological assessments. Our goal is to understand the mechanisms regulating major chromatin remodeling in the GV. Bovine oocytes (n=38) were collected from post-mortem ovaries by follicular aspiration. Immunochemistry was conducted using an anti-Lamin A/C antibody and chromatin was differentially counterstained using YO-PRO-1 (for GC-rich domains) and DAPI (for AT-rich sequences). Chromatin nanostructure within the GV was analyzed in relationship to the nuclear lamina using 3D laser-scanning confocal microscopy on oocytes in suspension to allow for 3D spatial reconstruction. We performed high-resolution epifluorescence as well as the first imaging beyond the diffraction limit using super-resolution structural illumination (SR-SIM) to gain insight into changes in mesoscale chromatin organization. Computational image analyses were carried out using IMARIS and ImageJ software. Our results provide insight into the spatial organization of chromatin domains critical for chromosome stability in bovine oocytes and establishes evidence for the relevance of bovine oocytes as a model to study chromosome instability-induced pregnancy loss in humans.
Research Grant	U.S. Department of Agriculture-National Institute of Food and Agriculture-National Institutes of Health (2020-67015-30882) National Institutes of Health-NICHD (HD093383) NSF CMaT (164805)
Field of Research	Theriogenology

Abstract Title	Evaluation of naturally occurring chronic wasting disease (CWD) isolates for evidence of different strains
Authors	Elizabeth Howell, Zoe Lambert, Rylie Frese, Eric Cassmann, and Justin Greenlee
Affiliations	College of Veterinary Medicine, University of Georgia, Athens, GA (Howell) College of Veterinary Medicine, Iowa State University, Ames, IA (Lambert, Frese) Virology and Prion Unit, National Animal Disease Center, Ames, IA (Howell, Lambert, Cassmann, and Greenlee)
Abstract	Chronic wasting disease (CWD) is a fatal neurologic disease of cervids associated with the accumulation of misfolded prion protein in the central nervous system and lymphoid tissues. CWD was first reported in 1967 and has since been identified across the U.S. and internationally in both captive and wild populations, emerging as a disease of economic and ecological importance. CWD isolates can be categorized into different strains based on unique characteristics such as host range, biochemical properties, and neuropathologic features. Previously, western blots of field samples of white-tailed deer CWD from different regions of the U.S. suggested potential strain differences. Cervidized mice (Tg-12) were inoculated with these samples to allow for further evaluation of potential strain differences using enzyme-linked immunosorbent assay (ELISA), western blot, immunohistochemistry, and fibril stability assays. Initial results from mouse bioassays suggest that attack rates are comparable between inocula. The western blot profiles of the mice from different studies did not differ from each other or their respective inoculum. Immunohistochemistry and fibril stability assays are currently ongoing. The preliminary results indicate that CWD strain differentiation is challenging as it is affected by multiple confounding factors and may require the use of multiple assays. Additional passages of these CWD isolates through cervidized mice may help to stabilize the prion agent and allow for better comparison between isolates. Identifying CWD strains may play a role in future management and regulation of CWD in farmed and wild cervids.
Research Grant	USDA ARS NADC CRIS PROJECT: 320-228
Field of Research	Anatomic Pathology

Abstract Title	The effects of a neonicotinoid pesticide on genes that regulate steroidogenesis in canine ovaries
Authors	Justin Huff, Vasiliki Mourikes, and Jodi A. Flaws
Affiliations	University of Illinois College of Veterinary Medicine, Department of Comparative Biosciences
Abstract	Neonicotinoid insecticides are widely used in agriculture, horticulture, forestry and domestic settings to control pests such as fleas and ticks on pets. In insects, neonicotinoids work by binding to the same receptors in the nervous system as nicotine, causing overstimulation of the nervous system which leads to paralysis and death. Imidacloprid (IMI) is a neonicotinoid insecticide commonly used for its high affinity for insect nicotinic cholinergic receptors (nAChRs) and low affinity for mammalian nAChRs. Despite the common use of IMI, limited information exists on how IMI affects the ovary and its functions. Previous studies using mouse ovarian follicles have shown that IMI increased progesterone levels in vitro. Canines are exposed to IMI through flea and tick preventatives, but to our knowledge, the impact of IMI on the canine reproductive system is unknown. To bridge this knowledge gap, we investigated the effects of IMI on the canine ovary. Our hypothesis was that IMI exposure interferes with steroidogenic enzymes and genes that control follicle health in the canine ovarian follicle. To test this hypothesis, antral follicles were dissected from canine ovaries and cultured in media containing vehicle control (DMSO) or IMI (0.2µg/ml - 200µg/ml). After 96 hours, follicles were collected for gene expression analysis of genes that regulate steroidogenesis (Star, Cyp11a1, Cyp17a1, Cyp19a1, Hsd17b1, Hsd3b1) and follicle health (Bcl2 and Bax). We found that IMI did not significantly alter the selected genes. Future studies will investigate hormone production by antral follicles.
Research Grant	NIH F30 ES 033914
Field of Research	Pharmacology and Toxicology

Abstract Title	Treatment of cats with adeno-associated gonadotropin releasing hormone to achieve nonsurgical sterilization
Authors	Chloe S Hume, Aime K Johnson, Kristyn D Burton, Douglas R Martin
Affiliations	College of Veterinary Medicine Oklahoma State University, Stillwater, OK (Hume, Burton) , Scott Ritchey Research Center, College of Veterinary Medicine, Auburn University, Auburn, AL (Johnson, Martin)
Abstract	Stray animals are a problem in the United States and other countries. As of now, surgical sterilization is the most effective solution. However, these methods are expensive, stressful to the animal, and require a veterinarian. A non-surgical technique would eliminate these barriers, remove the physical and psychological stressors associated with surgery, and reduce the number of animals euthanized in shelters. Adeno-associated virus (AAV) is a nonenveloped virus that can be modified to target cells and deliver DNA. Gonadotropin releasing hormone (GnRH) is a hormone produced by the hypothalamus that acts on the pituitary to produce follicle stimulating hormone (FSH) and luteinizing hormone (LH) that act on the gonads and stimulate the release of testosterone in the male and estrogen in the female. Overproduction of GnRH leads to downregulation of GnRH through the receptor. It is hypothesized that administration of AAV containing GnRH (AAV-GnRH) intravenously to male kittens at 6 weeks of age will cause a decrease in testosterone and impaired sperm characteristics leading to infertility. Four treated and three control (untreated) kittens were enrolled. Testicles were ultrasounded once monthly starting at 4 months of age and measurements taken to calculate total testicular volume (TTV), testicular mass, and percent body weight. When the cats reached 6 months of age, they underwent electroejaculation (EEJ) once monthly to analyze sperm characteristics. Blood was obtained every two weeks to compare testosterone production, LH concentrations, and immunologic response to the AAV vector. Results so far indicate there may be a decrease in sperm production and an increase in testosterone concentrations but more data are needed.
Research Grant	“None”
Field of Research	Theriogenology

Abstract Title	Equine and porcine platelet lysates exhibit antimicrobial effects on bacteria isolated from either species
Authors	Edward Hunda, Hannah Kemelmakher, Julie Gordon, and John Peroni
Affiliations	Department of Large Animal Medicine, College of Veterinary Medicine, University of Georgia, Athens, GA
Abstract	Cytotoxic peptides released from platelets are a major contributor to host responses to bacterial infections. These cytotoxic peptides include platelet factor 4 (PF-4), beta-defensin, connective tissue activating peptide 3 (CTAP-3), and thrombocidins. Our lab has focused on collecting and analyzing these platelet-derived bioactive factors in a blood-derived therapeutic known as platelet lysate (PL) and establishing its potential as an antimicrobial alternative for use in veterinary species. Previous work has focused on equine platelet lysate, and now there is interest in developing the porcine equivalent as well as investigating any possible cross-species interactions. Platelet concentrates were collected from healthy horses and pigs via plateletpheresis. Platelet lysate was then manufactured from each donor after a specific process requiring freeze-thaw cycles to activate the platelets to release bioactive factors and filtration to remove cellular debris. The final PL product was pooled from 3 different donors of the same species. In this study, we hypothesized that PL manufactured from horses and pigs would exhibit antimicrobial effects on pathogenic bacteria isolated from either equine or porcine clinical cases. To test this hypothesis we used a well-established growth curve assay to determine the growth dynamics of E. coli and S. aureus when exposed to equine PL (ePL) and porcine PL (pPL). Most PL samples exhibited an antimicrobial effect against the tested bacteria, but we also demonstrated that PL from a cross-species donor proved even more effective. These results will drive further research aimed to broaden the therapeutic use of PL as an antimicrobial alternative in multiple veterinary species.
Research Grant	Morris Animal Foundation
Field of Research	Equine Medicine and Surgery

Abstract Title	Development of cross-reactive hemagglutinin vaccine antigens for swine influenza A (H1N1) viruses
Authors	Brooklin E. Hunt, Salman Latif Butt, Gabriela Mansano do Nascimento, Diego G. Diel
Affiliations	Cornell University College of Veterinary Medicine, Ithaca, New York, USA
Abstract	Influenza A viruses from swine (IAV-S) threaten public health and food security globally. The 2009 H1N1 influenza pandemic cost over 150,000 human lives and culling of hundreds of thousands of pigs. Developing broadly protective vaccines against rapidly evolving IAV-S remains a challenge. Induction of cross-reactive immunity against divergent IAV-S has been accomplished in swine with computationally optimized broadly reactive antigen (COBRA) consensus sequence analysis of the hemagglutinin (HA) protein. We used 961 HA sequences from H1N1 IAV-S in the USA during 2020-2023 to create a phylogenetic tree and subjectively design a consensus HA (conHA) antigen using the COBRA method with 17 primary conHA, three secondary conHA, and one tertiary conHA sequence. These conHA sequences were compared to representative HA sequences objectively selected using the Parnas algorithm. In Parnas, we obtained 17, three, and one representative sequence to compare with COBRA. We generated separate consensus sequences from 17 COBRA primary consensus sequences and 17 Parnas-selected representatives. These COBRA and Parnas consensus sequences were 99.125% similar at the amino acid level. The difference between the mean genetic distances of these two groups was 0.0728 (99.93% similarity). After data curation, the generation of COBRA antigens took over 1 month, whereas Parnas representatives were selected in less than 20 minutes. The high degree of similarity between COBRA and Parnas outputs suggests that Parnas can generate optimal, cross-reactive IAV-S antigens in a fraction of the time. Our work provides an important step in the establishment of methods for rapid development of broadly reactive IAV-S vaccines for use in swine.
Research Grant	USDA-NIFA award no. 2022-67015-36349
Field of Research	Virology

Abstract Title	Assessing the immunoregulatory effect of mesenchymal stem cell extracellular vesicles on stimulated mixed glia
Authors	Startus Hutcherson, Nikolia Darzenta, and Maria Naskou
Affiliations	Scott-Ritchey Research Center (Hutcherson, Darzenta) and Department of Pathobiology (Naskou), College of Veterinary Medicine, Auburn University, Auburn, AL.
Abstract	Neurodegenerative conditions (NCs) such as Alzheimer's, Parkinsons, and Lysosomal storage disorders (LSDs) cause disease by different mechanisms. However, many NCs exhibit some level of neuroinflammation, which is an area of interest regarding therapy of these conditions. With the rapidly evolving and emerging use of stem cell technology in medicine, it has been shown that this technology can be used to decrease inflammation. Specifically, the extracellular vesicles (EVs) from stem cells have shown to modulate the phenotypes of immune cells and downregulate the production of inflammatory cytokines. The focus of this study is to determine the immunomodulatory effect of human mesenchymal stem cell (hMSC) EVs on a cell population of both astrocytes and microglia, the primary immune cells of the CNS, from LSD cat brains. This was done by isolating glial cells from cat brain tissue, treating the cell population with lipopolysaccharide (LPS) to stimulate the production of inflammatory cytokines, and then subsequently treating the cells with hMSC-EVs. Subsequently, ELISA's and qPCR were performed to assess the change in inflammatory cytokine expression and production. Preliminary results showed a decrease in both gene expression and production of inflammatory cytokines. Thus, indicating that hMSC-EVs can downregulate inflammatory cytokine production and should be investigated further in vivo to assess its effectiveness in treating neuroinflammation in live LSD cats.
Research Grant	College of Veterinary Medicine animal health and disease research fund
Field of Research	Immunology

Abstract Title	A novel vaccine strategy to elicit broadly neutralizing antibodies against the CD4 binding site of HIV-1 gp120
Authors	Hyunmook Im, Kavi Raj Acharya, Vikram Srivastava, Michael W. Cho
Affiliations	College of Veterinary Medicine, Iowa State University, Ames, IA (Im, Acharya, Srivastava, Cho) NeoVaxSyn, Inc., Ames, IA (Cho)
Abstract	The development of an effective HIV-1 vaccine has remained a challenge for decades due to high genetic variability and the virus's ability to evade the immune system. The primary objective in developing a vaccine against HIV-1 is to elicit an immune response capable of generating broadly neutralizing antibodies (bnAbs). Numerous studies have indicated that one promising approach is designing a vaccine that targets the CD4 binding site (CD4BS) on the viral envelope glycoprotein, gp120. CD4BS is a conserved region among different HIV-1 strains and plays a crucial role in viral entry into host cells. By targeting the CD4BS, the goal is to induce an immune response that can generate VRC01-like antibodies, which are bnAbs isolated from naturally infected individuals. The objective of this study was to evaluate a novel vaccine strategy we refer to as Incremental, Phased Antigenic Stimulation for Rapid Antibody Maturation (IPAS-RAM) for eliciting bnAbs against the CD4BD. Two different adjuvants (Zn-chitosan and MPLA/ALUM) were compared using the same subunit protein regimen. Transgenic mice encoding the VRC01 germline antibody were used. Mice were immunized five times intraperitoneally or intramuscularly with various combinations of four different proteins (HR1/2-eOD-GT6, eOD-GT6-LS, 426cWT and BG505 DS gp140). Serum samples were collected 13 days after each immunization. Antibody responses were analyzed by an enzyme-linked immunosorbent assay (ELISA). Strong antibody responses were elicited against immunogens in both vaccine groups. We are currently in the process of characterizing antibody responses in greater detail (e.g., mapping target epitopes, determining avidity, and assessing neutralizing activity)
Research Grant	NIH R21 AI-134838
Field of Research	Immunology

Abstract Title	Puppy fecal microbiota allow for Clostridioides difficile spore germination and outgrowth ex vivo
Authors	K.A. Ingram, J.C. Rowe, J.A. Winston
Affiliations	The Ohio State University College of Veterinary Medicine, Department of Clinical Sciences, Comparative Hepatobiliary and Intestinal Research Program, Columbus, OH
Abstract	Clostridioides difficile is an anaerobic, spore-forming, toxin-producing enteropathogen which annually results in 500,000 human infections and 30,000 deaths. Dysbiosis, induced by antibiotics or intestinal inflammation, creates an environment conducive to C. difficile germination and outgrowth leading to toxin production which mediates disease. Despite an 11-30% prevalence in dogs and well-documented and widespread dysbiotic states, including with antibiotics and intestinal inflammation, evidence of C. difficile toxin production resulting in disease in dogs is rare. Coincidentally, in puppies and infants when low microbial diversity exists, a higher prevalence of C. difficile carriage without disease occurs and is attributed to reduced C. difficile pathogenesis in these intestinal environments. The purpose of this study is to evaluate the life cycle of C. difficile ex vivo to characterize disease susceptible states in dogs. Prior to ex vivo inoculation, selective media enrichment isolated C. difficile only from puppies. For the ex vivo model, C. difficile R20291 vegetative cells and spores were then added anaerobically to fresh feces from healthy dogs (n=5) and puppies (n=6). Ex vivo puppy fecal microbiota permitted C. difficile germination and outgrowth while healthy adult dog feces did not. Future directions will include comparison of the canine fecal microbiome and metabolome associated with ex vivo susceptible states and toxin production, and ribotyping/toxin profiling of recovered C. difficile. By identifying and defining C. difficile susceptible states in dogs, a greater understanding of differential pathogenesis is gained which may inform novel microbial directed therapeutics against C. difficile for humans.
Research Grant	J. Winston discretionary start-up funds
Field of Research	Microbiomes

Abstract Title	Tick, tick, boom: investigating ticks and invasive plant species in 2021 and 2022!
Authors	Erica Jackson, Yvette Johnson-Walker, Teresa Steckler, Christopher Evans, Holly Tuten, Christopher Stone, Maung San Myint
Affiliations	Department of Veterinary Clinical Medicine (Jackson, Johnson-Walker, San Myint), College of Veterinary Medicine, University of Illinois Urbana-Champaign, Urbana, IL; Cooperative Extension Services Dixon Springs Agricultural Center (Steckler, Evans), Simpson, IL; Illinois Natural History Survey (Tuten, Stone), Urbana, IL
Abstract	Recent literature has identified the presence of some invasive plant species as risk factors for tick abundance. This study was conducted to assess the association between tick abundance and three species of invasive plants in southern Illinois while controlling for microclimate. Ten plots were identified for data collection at Dixon Springs Agricultural Center. One plot was invaded by Alliaria petiolata (Garlic Mustard), and three plots each were invaded by Microstegium vimineum (Japanese Stilt Grass), and Lonicera maackii (Amur Honeysuckle). Three uninvaded plots were selected to serve as controls. Standard tick drags were performed every three weeks from April to December of 2021 and 2022. At each transect, dataloggers (HOBO) were placed to collect microclimate data every 15 minutes. Ticks were collected, classified by species and tested for pathogens. A total of 941 ticks were collected over the two years of sample collection. There was a statistically significant difference in the mean number of ticks per plot by invasive plant species (ANOVA p=0.001). Plots invaded by Lonicera maackii were 50% more likely to have ticks present compared to the uninvaded plots (Pearson's Chi2 = 9.430, p=0.002 OR = 1.50). Plots invaded by Microstegium vimineum were 30.7% less likely to have ticks present compared to the uninvaded plots (Pearson's Chi2 = 6.397 p=0.011 OR = 0.693). There was a statistically significant difference in the number of ticks present on Lonicera maackii plots compared to Microstegium vimineum plots (95% Tukey Interval 0.1487, 0.5215). Multivariable regression analysis results will be presented to determine the association between plant species and microclimate.
Research Grant	ACES Dudley-Smith Initiative DSynergy Program
Field of Research	One Health

Abstract Title	Effectiveness of acetaminophen and meloxicam in reducing pyrexia and inflammation in horses induced with LPS
Authors	Bryson Jacobs, Amanda Samuels, Payton Kelly, Celine Bartish, Ahmed Kamr, Ramiro Toribio
Affiliations	College of Veterinary Medicine, The Ohio State University, Columbus, OH
Abstract	Pyrexia in horses causes discomfort, lethargy, dehydration, and anorexia. Non-selective cyclooxygenase inhibitors (NSAID), such as flunixin meglumine, are the current medication of choice, but these drugs have serious side effects including renal and gastrointestinal toxicity. Acetaminophen and meloxicam are potential alternative medications to NSAIDs because they have fewer side effects. However, minimal research has been conducted to determine their efficacy in horses to reduce pyrexia and inflammation. The purpose of this study is to investigate whether acetaminophen and meloxicam are effective in reducing pyrexia and inflammation in systemically ill horses. We hypothesize that acetaminophen and meloxicam will effectively control pyrexia and reduce inflammation in an experimental model of endotoxemia. This study enrolled twelve healthy horses and induced endotoxemia using lipopolysaccharide (LPS) infusion. Horses were administered either water (control), flunixin meglumine, acetaminophen, or meloxicam after LPS infusion. To determine the efficacy of each drug, we performed consecutive physical exams and white blood cell counts and kinetically evaluated inflammatory cytokine expression (TNF-α, IL-1β, IL-6, IL-10) using ELISA and RT-PCR. Preliminary results show that both acetaminophen and meloxicam did not have a significant impact on physical exam parameters including rectal temperature, heart rate, and respiratory rate. There was also no difference in total white blood cell, neutrophil, or lymphocyte counts between the treatment groups. Future research could be aimed at utilizing these medications in a clinical trial to better replicate pyrexia and inflammation in clinically ill horses.
Research Grant	Equine Grant No. 2022-16 from The Ohio State College of Veterinary Medicine
Field of Research	Equine Medicine and Surgery

Abstract Title	Assessment of characteristic 'hot-spot' gene mutations of soft tissue sarcomas across veterinary species
Authors	Rebekah James, Isabella Livingston, Leigh Duke, Hannah Pierce, Gregory Lewbart, Tara Harrison, Matthew Breen
Affiliations	College of Veterinary Medicine, North Carolina State University, Raleigh, NC (James, Duke, Pierce, Lewbart, Breen), Department of Molecular Biomedical Sciences, North Carolina State University, Raleigh, NC (Breen, Livingston)
Abstract	Soft tissue sarcomas (STS) are a collection of cancers affecting many veterinary species. The study of recurrent gene mutations in cancers is vital in understanding the drivers of disease, as well as the identification of therapeutic targets and prognostic indicators. In human STS, recurrent mutations have been identified in several genes, including TP53, CDKN2A, PIK3CA, and PTEN. The incidence of these mutations has led to them being termed 'hot-spot' events. While the mutational status of these genes has been investigated in some companion animals (primarily the domestic dog and cat) there is a lack of data for exotic pets and zoologic species. The Exotic Animal Medicine Service (EAMS) at NC State University hosts a collection of tumor biopsies from a range of species. In this study, histopathology confirmed cases of STS in multiple exotic species, including Alces alces (moose), Daubentonia madagascariensis (aye-aye), Crotalus horridus (timber rattlesnake), and Oryctolagus cuniculus (rabbit), were investigated for the presence of signature hot-spot mutations. Tumor and matched tissues for each case were used as the source of genomic DNA. Known genome sequence data for each species (or the closest phylogenetic relative), accessible in the UCSC Genome Browser, were used to design custom PCR primers to amplify target regions of interest. PCR amplicons of both tumor and matched normal genomic DNA for each species were then sequenced and the paired data compared to identify the presence of somatic variants. Results (still pending) indicated that 'hot-spot' mutations associated with human STS (were/were not) detected in the exotic species investigated.
Research Grant	The Cancer Genomics Fund
Field of Research	Oncology

Abstract Title	The effect of psychosocial stress on urinary sphincter regenerative therapy in female cynomolgus macaques
Authors	Jared Jensen, Brett Frye, Autumn Whitt, Hossam Shaltout, Shannon Lankford, James Koudy Williams, Carol Shively
Affiliations	College of Veterinary Medicine, Colorado State University, Fort Collins, CO (Jensen) ; Department of Comparative Pathology (Jensen, Frye, Whitt, Shively), Neurology (Shaltout), and Institute for Regenerative Medicine (Lankford, Williams), Wake Forest School of Medicine, Winston-Salem, NC.
Abstract	Intrinsic urinary sphincter deficiency (ISD) associated urinary incontinence is a result of injury or aging to the urinary sphincter musculature and innervation, resulting in involuntary urine loss. Regenerative therapy with skeletal muscle precursor cells (skMPCs) can repair urinary sphincter integrity, however, variability in patient outcomes have raised concerns regarding its efficacy. Prior nonhuman primate (NHP) studies showed that urinary sphincter regeneration was markedly lower in subordinate female monkeys, which experience greater sympathetic nervous system (SNS) and hypothalamic-pituitary-adrenal (HPA) activation than their dominant counterparts. Local administration of CXCL12 enhances urinary sphincter regeneration by regulating myelopoiesis and the homing of the progenitor cells to the injury site for healing. Due to the decreased CXCL12 production under SNS activation, we hypothesize that psychosocial stress reduces the efficacy of skMPC treatment for ISD. Throughout this study, 29 adult (15 years of age) female cynomolgus macaques (Macaca fascicularis) were group housed and monitored for social hierarchical determination using a Behavioral Ethogram. In addition, interbeat interval from a jacketed external telemetered ECG was analyzed for heart rate variability and spectral frequencies as an index for autonomic nervous system activity. Urinary sphincter injury was surgically induced and 2 months later, a subset of animals (n=13) were treated with either skMPCs or a placebo. Maximum cystometric capacity, maximum urethral pressure, and abdominal leakpoint pressure was assessed at baseline, 6 weeks after ISD initiation, and 6 months after skMPCs as measures of urethral sphincter function. Data is pending.
Research Grant	R01-DK124639-04
Field of Research	One Health

Abstract Title	Novel treatment of white nose syndrome in Myotis lucifugus populations
Authors	Yoomin Jo, Sybill Amelon
Affiliations	College of Veterinary Medicine, University of Missouri, Columbia (Jo); Department of Veterinary Pathobiology, University of Missouri, Columbia, MO; USDA Forest Service, Northern Research Station (Amelon).
Abstract	White-nose syndrome (WNS) has been a major cause of decline of North American bat populations in the past 15 years. White-nose disease is caused by the fungus Pseudogymnoascus destructans, an opportunistic pathogen, which affects bats in torpor. The fungus grows while the bat is immunosuppressed and invades the epithelium, causing the bat to awake in the winter and eventually die of starvation. Fungal lesions emit a characteristic fluorescent orange-yellow color when the wing membrane is transilluminated with 385 nm ultraviolet (UV) light. The objective of this study is to determine the efficacy of treatment using Rhodococcus rhodochrous DAP 96253 (RRDAP) in WNS-infected bats. We hypothesize that treatment with RRDAP increases survival and decreases wing lesions. Little brown bats (Myotis lucifugus) with known diagnoses of WNS were randomly separated into control and RRDAP treatment groups, UV assisted wing photos were taken throughout the treatment period. Wing lesions were quantified using R package “Countcolors” (R Core Team, 2017, Hooper et al. 2020). The RRDAP treatment group showed increased percent survival. We expect bats treated with RRDAP to have decreased wing lesion severity. Results indicate that RRDAP is an effective treatment for WNS in little brown bats. RRDAP is a potential therapeutic approach in increasing survival of bat populations infected with WNS.
Research Grant	0056825 to University of Missouri from Missouri Department of Conservation.
Field of Research	Wildlife Conservation

Abstract Title	INPP4B facilitates resistance to doxorubicin in canine hemangiosarcoma cells
Authors	Ryan Johnson1, Ali Khammanivong1, Yoonkyu Lee2, Ethan Wong1, Zohar Sachs2, and Erin B. Dickerson1
Affiliations	1Department of Veterinary Clinical Sciences, College of Veterinary Medicine, University of Minnesota, St. Paul, MN; 2Department of Medicine, School of Medicine, University of Minnesota, Minneapolis, MN
Abstract	Inositol polyphosphate-4-phosphatase, type II (INPP4B) is a key enzyme that reduces the activity of PI3 kinase/Akt signaling by decreasing the levels PI(3,4)P2. High expression of INPP4B has also been shown to increase resistance to doxorubicin in leukemia and ovarian cancer cells. In canine hemangiosarcoma (HSA), we found that dogs with tumors expressing high levels of INPP4B have poorer overall survival compared to those with low expression. HSA cell lines with low levels of INPP4B were also more sensitive to doxorubicin. These findings led us to hypothesize that increased expression of INPP4B promotes resistance to doxorubicin in HSA cell lines. Overexpression of INPP4B in the Dal-4 cell line (Dal-4-4B) increased the IC50 for doxorubicin by ~ 30-fold and enhanced DNA-damage repair compared to Dal-4 cells transduced with a vector expressing GFP (Dal-4-GFP). Treatment of Dal-4-4B cells with PARP inhibitors restored doxorubicin sensitivity. To explore the mechanisms underlying the observed resistance, we looked for genes that were differentially expressed between Dal-4-4B and Dal-4- GFP cells. Indoleamine 2, 3-dioxygenase 1 (IDO1), which plays a key role in tryptophan metabolism, was significantly down-regulated in Dal-4-4B cells compared to Dal-4-GFP cells. Tryptophan metabolism is also important for generating NAD+, which is essential for PARP activity. Doxorubicin increased the expression of IDO1 in Dal-4-4B and Dal-4-GFP cells, suggesting that doxorubicin activates PARPs through tryptophan metabolism and IDO1. These studies provide a better understanding of the development of doxorubicin resistance in canine HSA and support our long-term goal of improving outcomes for dogs diagnosed with this disease.
Research Grant	Boehringer Ingelheim and the College of Veterinary Medicine
Field of Research	Oncology

Abstract Title	AAV-hTau Seeded Mice as a Screening Model for nSMase2 Inhibitors
Authors	Haley N. Johnson1, Meixiang Huang1,2, Ajit G. Thomas1,2, and Barbara S. Slusher1, 2, 3, 4, 5
Affiliations	Johns Hopkins Drug Discovery1, Neurology2, Oncology3, Pharmacology and Molecular Sciences4, Psychiatry and Behavioral Science5, Johns Hopkins University School of Medicine, Baltimore, MD, 21205, USA
Abstract	Alzheimer's disease (AD) is a neurodegenerative disorder that is increasing in prevalence globally while therapeutic options remain limited. The characteristic pathophysiology of AD that is associated with progressive cognitive decline involves abnormally phosphorylated tau (pTau) proteins spreading along synaptically connected networks in the brain. Recent research has shown that pTau spreads, in part, via extracellular vesicles (EVs) and that attenuating EV biogenesis through small-molecule inhibitors of nSMase2 may be a potential therapeutic approach. However, there are currently no suitable compounds available for clinical development. We have shown that nSMase2 inhibitors can diminish tau propagation in a previously developed AAV Tau seeded mouse model where P301L/S320F mutant human tau was unilaterally seeded into the hippocampus and the spread of pTau to the contralateral hippocampus was monitored. Herein, we monitored the time course of nSMase2 activity elevation after AAV-hTau injection. We stereotaxically injected C57BL/6J mice with AAV-hTau in the CA3 region of the hippocampus and collected the ipsilateral hippocampus at 6, 24, 48, 72 hours, or 1-week post-injection for nSMase2 enzymatic activity assessment. We report that nSMase2 activity (RFU/mg/h) significantly increased at 48 hours post injection, peaked at 72 hours, and then returned to control levels by 1 week post injection compared to the no injection group. These findings suggest that AAV-hTau mice can be used at 48 hours post-injection as an in vivo screening model for new nSMase2 inhibitors to confirm target engagement.
Research Grant	National Institute of Health grants R01 AG063831, R01 AG059799, P30 MH075673, and a grant from the Tau Consortium and Alzheimer's Association (T-PEP-18-579974C) to BSS
Field of Research	Pharmacology and Toxicology

Abstract Title	TLR-MyD88 signaling promotes SARS-CoV-2 membrane (M) protein-induced inflammation
Authors	Paige Johnson, Debarati Chanda, Rudragouda Channappanavar
Affiliations	Department of Veterinary Pathobiology at Oklahoma State University College of Veterinary Medicine
Abstract	Innate immunity is the first line of defense against SARS-CoV-2 infection. However, the exaggerated innate response, characterized by the overproduction of proinflammatory cytokines, is detrimental. SARS-CoV-2 encodes four structural proteins (spike, nucleocapsid, envelop, and membrane), and of these proteins, S, N, and E proteins induce robust inflammation via toll-like receptor (TLR)- 2 and 4 activation. In contrast, the role and immune sensor eliciting M-protein-mediated inflammation are not well characterized. We hypothesized that the M protein utilizes a TLR as its innate receptor to promote inflammation. In this study, using wild-type (WT) macrophages (MQ), we first determined whether M protein stimulates an inflammatory response when compared to cell control, LPS, and Pam3CSK4 (each at 5µg/ml) stimulated MQs. Our results show that M protein does induce significantly increased inflammatory cytokine (TNF) response compared to unstimulated control MQs. Further examination showed reduced TNF levels in TLR2 and TLR4 inhibitor treated- as well as double MyD88/TRIF knock out (but not TRIF-only KO) cells compared to WT control MQs. These findings support our hypothesis that the M protein is sensed by multiple TLRs, and uses the MyD88 pathway to induce a proinflammatory cytokine response. We are currently characterizing the key dominant downstream molecules promoting M-protein induced inflammatory cytokine response.
Research Grant	Oklahoma State University, College of Veterinary Medicine INTERACT
Field of Research	Virology

Abstract Title	Intratumoral injection with stimulator of interferon genes (STING) increases B-cells in canine osteosarcoma
Authors	Sydney Johnson, Brian H. Ladle, Michele Doucet, Emily Kulp, Kathy Gabrielson, and Dara Kraitchman
Affiliations	Department of Oncology (Johnson, Ladle, Doucet, Kulp), Department of Molecular and Comparative Pathobiology (Gabrielson, Kraitchman), Department of Radiology and Radiological Sciences (Kraitchman), School of Medicine, Johns Hopkins University, Baltimore, MD
Abstract	Being the most common bone cancer in dogs, osteosarcoma is a highly malignant bone tumor with high metastasis capability. Due to its aggressive nature, we very much need treatment methods outside of cytotoxic chemotherapy and surgery. Carboplatin is the drug of choice to treat canine osteosarcoma. Stimulator of interferon genes (STING) agonist is a molecule with potential immune-activating and antineoplastic properties. Previous analysis of the STING agonist-treated tumors showed increased T-cell and myeloid cell immune infiltration. However, recent evidence indicates the importance of B-cells for the generation of an effective anti-tumor immune response. We hypothesized that carboplatin along with neoadjuvant intra-tumoral delivery of STING agonist will have an overall greater effect of treating canine osteosarcoma and decrease its recurrence rate by recruiting an increased number of B-cell infiltrates. Using a murine model as the host, we performed a Colorimetric Method (MTS) for determining cell proliferation after dosing with carboplatin and STING agonist, polymerase chain reaction (PCR) for evaluating the presence of STING agonist expression, immunohistochemistry (IHC) to identify the CD3 (T-cells) and CD20 (B-cells) markers, and tumor challenges in vivo to assess tumor-infiltrating lymphocytes (TILs). We found that intra-tumoral injection of STING agonist increased the number of T- and more importantly B-cell infiltrates, suggesting activation of the immune system against the tumor.
Research Grant	National Institutes of Health (NIH), The Children's Cancer Foundation, Swim Across America, and Giant Food Pediatric Cancer Fund
Field of Research	Oncology

Abstract Title	Simultaneous Ndr1 and Ndr2 deletion impairs retinal vasculature development and retinal maintenance in mice
Authors	Annie M. Jones, Catharina Grubaugh, N. Adrian Leu, Gordon Ruthel, Kathleen Boesze-Battaglia, and Francis C. Luca
Affiliations	Department of Biomedical Sciences, School of Veterinary Medicine (Jones, Leu, Luca, Ruthel), and Department of Basic & Translational Sciences, School of Dental Medicine (Boesze-Battaglia, Grubaugh), University of Pennsylvania, Philadelphia, PA
Abstract	Nuclear Dbf2-related (Ndr) 1 and 2 are paralogous protein kinases known to function in a noncanonical Hippo tumor suppressor pathway. Recent data suggest Ndr kinases are important for maintaining retinal health. Notably, an Ndr2 loss of function mutation causes retinal degeneration in young dogs, and in mice, deletion of Ndr1 or Ndr2 causes multiple retinal phenotypes including decreased amacrine cell abundance and aberrant cell cycle activation in a subset of retinal neurons. However, these studies are limited in that they do not reveal the full scope of Ndr1/2 function in the retina, as expression of one Ndr kinase increases in the absence of the other. Moreover, is unknown if the aberrant mitotic retinal neurons in Ndr mutants are caused by developmental defects or due to cell cycle activation in terminally differentiated neurons. Therefore, we generated conditional double Ndr1/2 KO mice (Ndr1/2 cKO), in which floxed Ndr1 and Ndr2 alleles are simultaneously deleted via a tamoxifen-inducible Cre recombinase. We induced Cre expression in neonate mice and conducted IFM on retinal flat mounts to determine how Ndr1/2 deletion influences retinal vasculature development and observed a marked decrease in vascular outgrowth in Ndr1/2 cKO mice when compared to similarly treated control mice. To surveil retinal degeneration and determine whether Ndr deletion reactivates the cell cycle in fully differentiated retinal neurons, we induced Cre expression in adult Ndr1/2 cKO mice and will conduct H&E and IFM analyses with retinal sections. Our initial data reveal a critical role for Ndr kinases in retinal vasculature development and will help elucidate mechanisms that control retinal neuron proliferation and maintenance.
Research Grant	None
Field of Research	Ophthalmology

Abstract Title	Probing host resistance, virulence factors and drug resistance in clinical isolates of Naegleria fowleri
Authors	Håkon Jones, Joseph Dainis, and Dennis E. Kyle
Affiliations	University of Georgia CVM, Athens, GA (Jones, Dainis); University of Georgia CTEGD, Athens, GA (Kyle, Dainis)
Abstract	Primary amoebic meningoencephalitis (PAM) is a deadly disease (>97% fatality rate) that is caused by a pathogenic free-living amoeba, Naegleria fowleri (Nf) The infection ensues when amoebae enter the nasal cavity and migrate along the olfactory nerves into the frontal lobes of the brain, where the amoebae cause significant pathology leading to death within 5-10 days. Recent data from the lab demonstrate Nf isolates show variation with regards to their virulence in host and this has opened some novel avenues of research with amoebic virulence factors, host resistance factors and the quest for a cure. The first of three experiments compared two clinical isolates there were passaged and not passaged over mammalian cells. The rationale are that passaging reestablishes the upregulation of virulence factors not needed by the amoeba when grown axenically. We found that V596 is more virulent, even when not passaged over Vero cells than NF69 in either condition. In regards to search for a cure, we inoculatied CD1-ICR mice with mammalian cell-passaged NF69 to assess efficacy of Quisinostat, an HDAC inhibitor shown to be potent against Nf in vitro. This study is currently underway. Finally, we aimed to determine if copy number variants (CNVs) are associated with resistance induced to a diamidine canidate drug (DB258). We were able to develop qPCR probes and confirm that Nf enolase is a single copy gene and can be used as control for qPCR confirmation of several candidate CNVs identified in whole genome sequencing. In summary, thus far the GVSP scholar has engaged in several experiments that aim to better understand virulence of Nf and to identify a new drug and resistance mechanisms.
Research Grant	Georgia Research Alliance
Field of Research	Parasitology

Abstract Title	Effect of vaccination and marketing strategy on pro-inflammatory cytokines in pre- and post-weaned beef calves
Authors	Alex Jones, Merrilee Thoresen, Kelsey M. Harvey, Brandi Karisch, Matthew A. Scott, Sarah F Capik, Amelia R. Woolums
Affiliations	Dept. of Pathobiology and Population Medicine (Jones, Thoresen, Woolums), and Dept. Animal and Dairy Science (Harvey, Karisch), Mississippi State University, Mississippi State, MS; Dept. of Large Animal Clinical Sciences, Texas A&M University, Canyon, TX (Scott); Tumbleweed Veterinary Services, PLLC, Amarillo, TX (Capik)
Abstract	In some management systems, stocker calves are vaccinated, or co-mingled at auction markets, which may induce inflammation due to immunological stimulation. However, there are few studies explaining how these practices induce inflammation. Our aims were to measure pro-inflammatory cytokines tumor necrosis factor alpha (TNF-α) and interleukin-1 beta (IL-1β) and compare concentrations in calves treated with different vaccination (VAX) and marketing strategies. Angus cross bull calves (n=84) born on the Mississippi Agricultural and Forestry Experiment Station–Prairie Research Unit (MAFES PRU) were randomized into four groups (n=21); VAX + auction market (AM), VAX + direct market (DM), non-vaccination (NVAX) + AM, and NVAX + DM. VAX calves received a modified live 5-way respiratory vaccine (mean age=92 days); baseline blood samples were collected from all groups prior to VAX calves' vaccination. Post-VAX blood samples were collected seven days later. Calves were weaned (mean age=210 days), DM groups remained at MAFES PRU and AM calves were transported to an auction market and then to an order buyer facility, where they were held for 3 days. Pre-marketing samples were collected from all calves prior to AM calves' transport to the auction market. Post-marketing samples (mean age=214 days) were collected from all calves on arrival at Texas A&M Agrilife Research Unit in Bushland TX. Plasma TNF-α and IL-1β were assessed via commercial bovine ELISAs. There was no apparent difference in TNF-α and IL-1β concentrations between VAX or marketing groups, although TNF-α concentrations increased over time in all groups. Further research is needed to understand relationships between common management practices and inflammation.
Research Grant	USDA NIFA Agriculture and Food Research Initiative Competitive Grant #2019-67015-29845
Field of Research	Immunology

Abstract Title	DNA Sequence Variation Assessment of Toll-Like Receptor, Immune Response Gene mgTLRRJ, in Meleagris gallopavo
Authors	Ryan Jordan, Jun Xu, Ed Smith
Affiliations	Virginia-Maryland College of Veterinary Medicine (Jordan), School of Animal and Poultry Sciences (Xu, Smith), Virginia Tech, Blacksburg, VA
Abstract	As demand for food worldwide grows, associated pressure is put on poultry production to increase in tandem. In order to keep pace with demand, poultry are being exposed to increased disease risk factors. It is paramount to find remedies to bolster the innate immune response in production poultry or develop tools that can be used to identify birds with low or high immune response capacity. Toll-Like Receptors (TLR's) are one such molecule which have been identified in other species as vital in the innate immune response. They are responsible for general pathogen recognition. The specific turkey TLR, mgTLRRJ, is a homolog for the chicken TLR21, and human TLR9. The homologs in chickens and humans recognize microbial DNA in their respective species. The chicken gene sequence was used to identify turkey toll-like receptor homologs; additionally, the homologs can be used to identify DNA variants that may be functional. Turkey mgTLRRJ was identified using NCBI blast and comparing GenBank sequences between the chicken and turkey genomes to identify the homolog in turkeys for chicken TLR21. Primers were designed for use in the comparative analyses of the turkey based on Polymerase Chain Reaction (PCR) then screened for DNA variants in the putative turkey TLR-like sequence, DNA from six different strains were used. The amplicons were purified, sequenced, and then analyzed using SeqMan Ultra to identify variants. Putative SNP's (single nucleotide polymorphisms) have been identified in several sequences including a G-T SNP at consensus position 1300, a C-T SNP at 1601, and an A-T SNP at 1449. These results including others will lead to testing of functional variants to enhance the innate immune response in poultry.
Research Grant	NIH 2T350D011887-16
Field of Research	Production Animal Medicine

Abstract Title	Platelet-rich plasma mitigates endometrial inflammation of jennies inseminated with cryopreserved semen
Authors	Carla Joseph, Theodore Blake, Claire Kaplan, Holly Schwarzman, and Lorenzo Segabinazzi
Affiliations	Ross University School of Veterinary Medicine, Basseterre, St. Kitts, West Indies
Abstract	The dramatic decline in the donkey population worldwide has spiked the need to improve the success of reproductive technologies in this species. Although donkey cryopreserved semen presents fair to excellent in vitro post-thaw parameters and fertility in mares; the fertility is extremely poor in jennies. The poor fertility in jennies have been attributed to the higher susceptibility of jennies to post-breeding inflammation. Intrauterine therapy with platelet-rich plasma (PRP) has mitigated endometrial inflammation and improved fertility parameters in mares inseminated with frozen semen. Therefore, the goal of this study is to access the effect of intrauterine infusion of PRP in jennies inseminated with frozen-thawed semen. Jennies (n = 14) had three cycles randomly assigned to receive intrauterine infusions of lactate ringer solution (control), or autologous PRP 4 h post-breeding (PRP and "PRP only"). In control and PRP assigned cycles, jennies were bred with frozen-thawed semen, whereas jennies were not bred in the "PRP only" cycle. Endometrial neutrophils were assessed up to 48 h post-breeding. Pregnancy diagnoses were performed 14 days after ovulation. Data were analyzed with mixed model and multivariate regression. The PRP treatment reduced endometrial neutrophils ($P<0.05$) after breeding compared to the Control assigned cycles, however, did not change the fertility rates of jennies inseminated with cryopreserved semen. Neutrophil counts were reduced in non bred jennies treated with PRP (PRP only) compared to the other groups ($P<0.05$). In conclusion, intrauterine PRP treatment mitigates endometrial inflammation in jennies bred with cryopreserved semen but did not improve fertility rates.
Research Grant	RUSVM Intramural Grant (42011-2022)
Field of Research	Theriogenology

Abstract Title	Understanding how Acrylamide Impacts DNA Damage and Breast Tumor Aggressiveness in Obesity
Authors	Brynna Jovanovich, Brenna Walton, and Lisa Arendt
Affiliations	School of Veterinary Medicine, UW-Madison, Madison, WI (Jovanovich), Molecular and Environmental Toxicology program, UW-Madison, Madison, WI (Walton) and Comparative Biosciences program, UW-Madison, Madison, WI (Arendt)
Abstract	Obesity levels continue rising, yet little is known about how obesity acts with environmental contaminants to promote cancer. Acrylamide is a naturally occurring food contaminant, primarily found in heated starchy foods. When consumed, it is metabolized into glycidamide. Glycidamide is reactive towards DNA and proteins, including the TP53 gene. When TP53 is mutated, DNA damage pathways are affected, allowing tumor formation. We hypothesize chronic exposure to acrylamide will enhance DNA damage, leading to more rapid and aggressive tumor growth. To test this hypothesis, trp53-/- epithelial cells were transplanted into the mammary glands of three-week old mice, then mice were randomly divided into four groups, high-fat diet (HFD) + acrylamide supplemented (AA) water, HFD + vehicle water, low-fat diet (LFD) + AA water, LFD + vehicle water. The mice were monitored until they developed tumors that were 1.5 cm in diameter, or until 1 year of age. They were humanely euthanized, and the tissue was collected. Tumor-bearing mice treated with AA water demonstrated increased metastases to the lungs. To assess tumor cell changes, I used immunofluorescence to stain for BrdU, a marker of cell proliferation, and yH2AX, a marker of DNA damage. Images were taken to quantify cells that expressed either single or both markers, and no significant differences were observed among the four groups. I measured foci of invasive tumor cells at the tumor borders as a marker of aggressive tumor cells, and no differences were observed. Lastly, we quantified hyperplastic mammary ducts on H&E-stained slides to identify early preneoplastic lesions. Further studies are necessary to identify how exposure to acrylamide alters the behavior of tumor cells.
Research Grant	NIH/NCI R01 CA227542
Field of Research	Oncology

Abstract Title	Methods to improve slow freeze cryopreservation of in vitro produced cattle embryos
Authors	Akari Jubashi[1], Jennifer P Barfield[2]
Affiliations	Department of Veterinary Science, University of Miyazaki, Japan[1] Animal Reproduction and Biotechnology Laboratory, Colorado State University, Fort Collins, CO[2]
Abstract	Although the number of in vitro produced (IVP) cattle embryos has been increasing globally recently, cryopreservation of IVP embryos has some challenges. IVP embryos are very sensitive to slow freezing and vitrification, and the survival rate of IVP embryos after thawing/warming is lower than in vivo derived embryos. Selecting the embryos that are most likely to survive the freezing process will reduce the waste of embryos and concerns associated with commercializing IVP embryos. In this research, we focused on slow freeze cryopreservation. Abattoir-sourced oocytes were divided into grades according to their quality based on IETS guidelines immediately after removal from the ovary. Oocytes were matured, fertilized and resulting embryos cultured using a standard IVP protocol. Early blastocysts, blastocysts and expanded blastocysts were slow frozen 7 days after fertilization in 1.5 M ethylene glycol and 0.5 M sucrose using a standard freeze curve for cattle embryos. Survivability of embryos generated from each oocyte grade and stage on day 7 was evaluated 24 hours after thawing. Preliminary results indicate that embryos from grade 3 oocytes do not freeze well, and blastocysts and expanded blastocysts from grade 1 and 2 oocytes have generally higher survivability than others. Knowing which oocytes produce embryos most suitable for slow freeze and which stage of embryos survive cryopreservation best will reduce the waste of embryos and cost. Furthermore, readily available cryopreserved IVP embryos will facilitate efficient production of cattle. This is of particular importance to direct transfer breeding programs where recipient availability is uncertain and commercializing genetics is difficult when germplasm is not frozen.
Research Grant	Boehringer Ingelheim
Field of Research	Theriogenology

Abstract Title	First insight into the expression of melanoma antigen genes (MAGEs) in equine melanomas
Authors	Kayla Justiss, Brooke Foster, Juan Solano, Stephanie Myers, Michael Cruz Penn, and Klementina Fon Tacer
Affiliations	School of Veterinary Medicine, Texas Tech University, Amarillo, Texas and Texas Center for Comparative Cancer Research (TC3R)
Abstract	Most aging grey horses develop melanomas, although at a slow rate of spread. In contrast, colored horses and human melanomas are extremely malignant with a potentially fatal prognosis. Upon resection, melanomas reappear very aggressively, even in grey horses, and the molecular mechanism is still unknown. Over 35 years ago, the first tumor antigen genes, now referred to as melanoma antigen genes (MAGEs), were discovered and targeted for immunotherapy in human melanoma patients; however, their role in animal tumors is virtually unknown. MAGEs normally protect male germ cells in suboptimal environmental conditions, but this same molecular mechanism may also be used by cancer cells for self-preservation and therapy resistance. In this study, we investigated equine MAGE expression in both normal and melanoma tissues. As melanin inhibits reverse transcription (RT) and quantitative polymerase chain reaction (qPCR), we first optimized RNA purification protocols to ultimately perform RT-qPCR analysis. After identifying >40 genes with MAGE homology in the equine genome, we designed equine-specific MAGE gene primers through NCBI's Primer-BLAST software. Levels of gene expression were measured across a panel of >35 normal equine tissues, 15 melanoma samples, and accompanying benign tissue with the intention of revealing their potential role in equine melanoma malignancy. Our preliminary data suggest that equine MAGEs also show tissue-specific expression profiles and are up-regulated in melanoma. Overall, our data will lay the groundwork for comparative research of the MAGE function, which may offer yet unexplored insights into the mechanisms responsible for cancer aggressiveness and novel therapy opportunities for humans and horses.
Research Grant	Texas Tech University Start-Up, Cancer Prevention and Research Institute of Texas Scholar Award RR200059, the Foundation for Prader–Willi Syndrome Research Grant 22-0321 and 23-0447 (all to K.F.T.)
Field of Research	Oncology

Abstract Title	Evidence for chemogenetic control of manual dexterity in a macaque model
Authors	Antonina Kalkus, Sebastien Tremblay, Kristin Gardiner, Michael Platt
Affiliations	University of Pennsylvania School of Veterinary Medicine, Philadelphia, PA (Kalkus, Gardiner), University of Pennsylvania Perelman School of Medicine, Philadelphia, PA (Tremblay, Platt)
Abstract	Numerous neuropathologies involve impairment of motor control. By modulating neuronal activity in a reversible manner, Designer Receptors Exclusively Activated by Designer Drugs (DREADDs) offer potential therapeutic interventions for fine motor impairments in conditions like Parkinson's disease and epilepsy. In this study, we investigated the use of DREADDs in a macaque model to inhibit fine motor control. DREADDs are engineered receptors that can modulate neuronal activity upon administration of specific ligands. We aimed to understand the neural mechanisms underlying precise motor movements in macaques, which closely resemble human motor skills. We used an adeno-associated viral vector to express inhibitory DREADDs in the primary motor cortex. These inhibitory DREADDs reduce neuronal excitability upon administration of a synthetic ligand Deschloroclozapine (DCZ). The effects of DCZ administration on fine motor performance were assessed using the Brinkman Board, a behavioral task that required precise finger movements. The macaque showed decreased ability to perform the task and increased movement variability in tasks when DCZ was administered, demonstrating that DCZ administration led to a reversible impairment in fine motor control. The findings highlight the feasibility of using DREADDs to selectively inhibit fine motor control in macaque models. This approach provides valuable insights into the neural circuits underlying precise motor movements and has implications for understanding motor disorders. We demonstrated the utility of DREADDs as a tool for investigating the neural basis of motor control and opens up possibilities for future research and therapeutic applications in the field of fine motor control.
Research Grant	NIH R01 – 10084477
Field of Research	Behavior

Abstract Title	Optimizing flow cytometry antibody panel for the Shine On Suspicion project protocol
Authors	Isabella Kappenman, Riley Spielman, Jaime Modiano, and Ashley Schulte
Affiliations	Veterinary Clinical Sciences, University of Minnesota CVM, Saint Paul, Minnesota
Abstract	The Shine On project's objective is to develop a reliable test to predict a dog's risk of developing cancer, using that information to then implement an intervention that can prevent or delay the onset of these cancers. Previous studies in our laboratory indicate that the use of an antibody panel and AI can reliably stratify dogs into risk categories, deeming them either high risk or low risk to develop cancer within 2 years. The project now focuses on coupling the screening test with eBAT to assess the drug's efficacy in cancer prevention. To enhance the existing antibody panel, we hypothesized that antibodies could be added, modified, or removed to create a panel that is both functional and efficient. Previous iterations of the panel made use of the conjugated antibodies CD45, CD11b, CD22, and CD5 conjointly in one step of the protocol. When reevaluating this portion of the protocol, titration was used to confirm the lowest antibody amounts that would still sufficiently saturate receptors. Furthermore, flow cytometry was employed to characterize the targets of these antibodies and compare their stained cell populations. Because CD45 is expressed on the surface of most nucleated hematopoietic cells, it is likely that CD45 staining encompasses the cell populations that bind to CD22, CD5, and CD11b. This redundancy could make it feasible to obtain sufficient data using only CD45. However, CD45 also stains a small minority of cells that don't express the antigen of the other trio of antibodies. Thus, replacing the collective panel of antibodies with CD45 could only be done if risk is still appropriately assigned by the Shine On algorithms in the absence of CD22, CD5, and CD11b.
Research Grant	Grant 02806-MOU from the AKC Canine Health Foundation; Funds from the University of Minnesota Animal Cancer Care and Research Program
Field of Research	Oncology

Abstract Title	Pharmacokinetic comparison and bioequivalence of emodepside formulations in dogs
Authors	Greta N. Karwath, Erin J. Mayhue, Theresa A. Quintana, Jeba R.J. Jesudoss Chelladurai, Stephanie E. Martinez
Affiliations	Department of Anatomy and Physiology (Karwath, Martinez) and Department of Diagnostic Medicine and Pathobiology (Mayhue, Quintana, Jesudoss Chelladurai), College of Veterinary Medicine, Kansas State University, Manhattan, KS.
Abstract	Emodepside, administered as the European Medicines Agency-approved canine oral formulation, has been found to be the lone effective treatment for multi-drug resistant (MDR) Ancylostoma caninum (dog hookworm) infections in dogs. In the United States, emodepside is only FDA-approved as a topical product for cats. Veterinarians in the United State have begun administrating the feline topical product orally in an extra-label manner to dogs with MDR hookworm infections despite the unknown pharmacokinetics. Additionally, no studies have been undertaken to determine if the feline topical formulation administered orally results in the same blood concentrations as the effective canine oral formulation (bioequivalence) to determine if both formulations would be expected to yield equivalent effects. Using a crossover design, the topical feline and canine oral emodepside formulations were administered to 7 client-owned dogs. Following drug administration, serial blood samples were taken over a 21-day period. Using liquid chromatography coupled with mass spectrometry, emodepside was quantified in plasma. Non-compartmental pharmacokinetic analysis and bioequivalence testing were carried out using commercially available software. The results of this study are pending but will be utilized to inform the treatment of MDR hookworm infections in dogs.
Research Grant	Kansas State University College of Veterinary Medicine intramural funds
Field of Research	Pharmacology and Toxicology

Abstract Title	Antibiotic Exposure as a Risk Factor for Chronic Enteropathy in Dogs
Authors	A. C. Kavanagh, V. J. Parker, J. A. Winston, A. J. Rudinsky
Affiliations	The Ohio State University College of Veterinary Medicine, Department of Veterinary Clinical Sciences, Comparative Hepatobiliary and Intestinal Research Program, Columbus, OH
Abstract	The incidence of chronic enteropathies (CE) in both people and dogs is increasing. Recent studies have demonstrated that antibiotics are associated with an increased risk of development of inflammatory bowel disease (IBD) in humans. It is unknown whether a similar association exists between antibiotic use and development of CE in dogs. This study aims to assess the impact of antibiotic exposure, including dose–response, timing and antibiotic class, on the risk of CE in dogs. Specific aims include: 1) establishing the prevalence of CE; 2) Investigating antibiotic administration as a risk factor for development of CE, considering class of antibiotics, length of exposure, incidence of multiple exposures, and period between exposure and first office visit for the disease. We hypothesize that antibiotic exposure in dogs is associated with an increased risk of future development of chronic enteropathy. Available medical records will be eligible for study inclusion if they have at minimum of 5 years consecutive follow-up. A sorting pipeline has been developed to screen the electronic database and classify dogs as CE, chronic illness/apparently unhealthy, or apparently healthy. The data search process will then screen up to 5 years of continuous medical records in order to assess antibiotic exposure (e.g., specific antimicrobials, number/duration of prescription, and dose) and medical history. This project is currently preparing for data collection. Incidence rate ratios (IRRs) for CE following antibiotic exposure will be calculated using Poisson regression. If there is an association noted between antibiotic exposure and CE in dogs, this will help further the understanding of the pathophysiology of CE.
Research Grant	None
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Surveillance of Hepatozoon spp. in Nerodia fasciata from southeastern USA and associated hematological factors
Authors	Courtney Kaye, Corinna Hazelrig, Ellen Haynes, Terence Farrell, Christopher Cleveland, Nicole Nemeth
Affiliations	College of Veterinary Medicine (Kaye, Hazelrig), Department of Population Health (Cleveland, Nemeth), Southeastern Wildlife Cooperative Disease Study (Hazelrig, Haynes, Cleveland, Nemeth) University of Georgia, Athens, GA Department of Biology (Farrell), Stetson University, DeLand, FL
Abstract	Hepatozoon spp. are intraerythrocytic protists that infect a variety of vertebrate and invertebrate hosts. More than 300 Hepatozoon spp. have been described with greater than 120 of these species found in snakes. Previous detections of Hepatozoon spp. mainly have been via microscopy or PCR; however, comparisons of the relative effectiveness of these methods have not been performed. Our objectives were to 1) determine the relative sensitivity of microscopy and PCR for detection of Hepatozoon spp. infection in snakes and 2) determine effects of Hepatozoon spp. infection on snake leukocyte counts via leukocyte estimates and differentials. To do so, 46 free-ranging banded watersnakes (Nerodia fasciata) were collected from South Carolina and Florida between May 2022 and May 2023 with four recaptured snakes. Snakes were sampled for Hepatozoon spp. by collecting blood from the ventral coccygeal vein. Fresh blood smears were first made, then remaining blood was deposited in heparinized tubes for subsequent PCR and heparinized blood smears. Of the sampled snakes, 52% (24/46) had either had visible Hepatozoon spp. with microscopy and/or detection via PCR. Of these Hepatozoon spp. infected snakes, 75% (18/24) had both visible gamonts and tested positive by PCR, while three lacked microscopic evidence of infection. There were no distinct trends in leukocyte counts between Hepatozoon spp. infected and non-infected snakes. These results provide a basis for improving screening protocols for Hepatozoon spp. infections in snakes and warrant further research into the effects of Hepatozoon spp. on snake leukocyte responses.
Research Grant	Morris Animal Foundation Established Investigator Grant Proposal Animal Health in Coastal Wetland Ecosystems (D22ZO-046)
Field of Research	Wildlife Conservation

Abstract Title	Comparison of two distal paravertebral block approaches in steers undergoing standing laparotomy
Authors	Maya K. Keefer, Margaret A. Mooring, Jennifer Halleran, Derek Foster, Kelley M. Varner
Affiliations	North Carolina State University College of Veterinary Medicine, Raleigh, NC
Abstract	Standing laparotomies are routine veterinary interventions in bovine practice in the USA. They are commonly performed for abdominal exploratory surgeries, correction of displaced abomasums, and cesarean-sections. It is estimated that over 500,000 cattle will undergo standing laparotomy for one of these conditions in the US this year. Distal paravertebral blocks are one of the described techniques for generating paralumbar fossa anesthesia in cattle. This block aims to desensitize T13, L1, and L2 spinal nerves as the nerve roots cross L1, L2, and L4 transverse processes. Some practitioners report improved perceived efficacy when distal paravertebral (DPV) blocks are also performed at the L3 process. Our study aimed to discover if four injection sites resulted in improved block success, surgical condition scores, and improved postoperative pain scores in steers undergoing standing laparotomy when compared to the traditional three-site injection technique. We hypothesized that four-site distal paravertebral would result in improved surgical conditions and lower pain scores following laparotomy. Two groups of 6 steers (n=12) were randomly assigned to one of two treatment groups (3DPV and 4DPV) and a blinded researcher was provided with the test solution in labeled syringes that corresponded with injection sites. The 4DPV group had 2 mg/kg 2% lidocaine injected at each site. In the 3DPV group, an equivolume of 0.9% NaCl was administered at the L3 process. Physiologic data, reaction scores, and surgical scores were collected at predefined surgical events. Post-operative pain scores and physiologic data were collected at predetermined time points for 24 hours following surgery.
Research Grant	Food Animal Residue Avoidance Database
Field of Research	Production Animal Medicine

Abstract Title	Does host stress influence virulence of Clostridioides difficile?
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Abstract	Clostridioides difficile, a Gram-positive, spore-forming, anaerobic bacterium, is an opportunistic pathogen that causes severe colitis and death in humans and animals. Antibiotic treatment-induced disturbances in the gut microbiota frequently exacerbate infections caused by this bacterium. There is substantial evidence in the literature demonstrating that host stress can lead to changes in the gut microbiota. The gut is the epicenter of hormonal exuberance during stress. Stress modifies the gut physiology while modulating the gut microbiome. Previous studies have shown that norepinephrine, an abundant hormone in the gut experiencing stress, significantly affects the growth and virulence of many Gram positive and Gram negative bacteria. This research project aims to investigate the extent to which norepinephrine influences the virulence of C. difficile. The RNA seq and RT-PCR were performed to study the changes in expression and abundance on virulence genes of C. difficile. The effect of increasing concentrations of norepinephrine on the growth and virulence of C. difficile was evaluated. Our findings provide valuable insights that can inform treatment modalities and guide patient management decision-making processes. Results from this study could help us develop a treatment strategy that could include adrenergic blockers in treating C. difficile colitis.
Research Grant	PVM funds
Field of Research	Bacteriology

Abstract Title	GP5 epitope A specific antibody production after PRRSV exposure
Authors	Alexander Kennedy, Jing Huang, Igor A. D. Paploski, Dennis N. Makau, Declan C. Schroeder, Kimberly VanderWaal and Maxim C-J. Cheeran.
Affiliations	Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, Saint Paul, Minnesota
Abstract	Glycoprotein 5 (GP5) is a major envelope protein of porcine reproductive and respiratory syndrome virus (PRRSV) and its ectodomain contains 3 linear epitopes: epitope A, an immunodominant, non-neutralizing epitope, epitope B, a primary neutralizing epitope, and epitope C, a target for homologous neutralizing antibodies. Studies suggest that antibody binding to epitope A may impede the development and binding of neutralizing antibodies to epitope B. We hypothesize that antibody response to epitope A will vary with PRRSV strains based on N terminal peptide cleavage sites on GP5. Serum obtained from piglets exposed to PRRSV field isolates 3-6 weeks post-infection were tested in an indirect ELISA for antibodies to GP5 peptides containing combinations of the three epitopes. Serum from pigs exposed to a PRRSV lineage 1C field isolate exhibited a significant increase in antibody binding to the GP5 ectodomain including epitopes A, B, and C- compared to uninfected pig serum. No significant difference between infected and uninfected pig serum was observed in antibody binding to the peptide containing only epitope A, indicative of a lack of response to this epitope. In comparison, vaccinated pigs showed a robust antibody response to epitope A. Subsequent analysis of vaccine strains and the L1C field isolate for signal peptide cleavage sites using SignalP 4.1 predicts that epitope A is excised from the final GP5 molecule in the field isolate, compared to the vaccine strain where an alternate cleavage site retains epitope A on GP5. These findings suggest that epitope A may be cleaved from certain PRRSV variants and the antibody response to epitope A in vaccinated pigs may result from retention of the peptide on the vaccine virus.
Research Grant	Funded in part by the joint NIFA-NSF-NIH-BBSRC Ecology and Evolution of Infectious Disease, award 2019-67015-29918, the USDA CARE award 2022-68008-37146 and the USDA AES Multi-state award MN-62-140
Field of Research	Virology

Abstract Title	The unlicensed treatment for feline infectious peritonitis generally contains more GS-441524 than advertised
Authors	Alycia Kent, Nicole Jacque, Su Guan, Wendy Novicoff, and Samantha Evans
Affiliations	Department of Veterinary Biosciences (Evans), College of Veterinary Medicine (Kent), The Ohio State University, Columbus, OH Department of Biochemistry, University of California Davis School of Medicine, Sacramento, CA (Guan) Department of Orthopaedic Surgery, University of Virginia, Charlottesville, VA (Novicoff)
Abstract	Feline coronavirus (FCoV) is endemic within the domestic cat population and can mutate into a much deadlier disease known as feline infectious peritonitis (FIP). There are no FDA-approved therapies available and the disease is 100% fatal when left untreated. The aim of this study was to analyze the content of unlicensed GS-441524-like products being used as a largely successful at-home treatment for cats suspected to have FIP. This study analyzed the actual content of GS-441524 by LC-MS/MS of 127 injectable and oral samples from 30 of the most popular brands of unlicensed manufacturers. The remdesivir content and pH were also measured. In total, 109 (86%) of the 127 samples analyzed in this study contained more GS-441524 than expected. Ninety-five percent of the injectable formulations contained more (on average 39% more) GS-441524 than expected based on the manufacturer's marketing. The average pH (1.30 pH) was well below the physiologic pH conditions recommended for subcutaneous injections. The oral formulations were somewhat more variable with 65% containing more GS-441524 (on average 12% more) than expected and 35% containing less (on average 35% less) than the expected content. There was minimal variability in GS-441524 content between replicate samples in the injectables (CV< 10%) in comparison to the oral formulations (CV ranging between 1% and 32.5%.) Some samples also contained remdesivir. All unlicensed products used for the at-home treatment of FIP contain GS-441524 and generally contain more drug than advertised. Injectable products have very low pH and oral products have more variable drug contents. These findings may inform future clinical use and research into at-home antiviral therapy for FIP.
Research Grant	Donation by Zen By Cat
Field of Research	Pharmacology and Toxicology

Abstract Title	Bold and blue: how lighting environments influence risk-taking behavior in bluefin killifish
Authors	Haley Kenyon, Ratna Karatgi, Jolene Blodgett, Becky Fuller
Affiliations	College of Veterinary Medicine, University of Illinois, Urbana, IL (Kenyon) Department of Evolution, Ecology, and Behavior, School of Integrative Biology, University of Illinois, Urbana, IL (Karatgi, Fuller) College of Agricultural, Consumer, and Environmental Sciences, University of Illinois, Urbana, IL (Blodgett)
Abstract	Phenotypic plasticity is the phenomenon where a single genotype elicits multiple phenotypes in a population because of external factors such as environment, diet, and behavior. In bluefin killifish, (Lucania goodei), sire plasticity is responsible for male color polymorphism. Red and yellow phenotypes are largely genetic and controlled by a locus of large effect. Blue coloration, however, depends on the lighting conditions sires are exposed to. These color morphs exhibit various behavior patterns in different lighting environments: blue males are more dominant and less likely to be targeted by predators in dark waters than red and yellow males. However, it's unknown the extent to which extrinsic and intrinsic factors influence specific behaviors. Boldness is an important behavior to study as it affects how an animal interacts with its environment, which in turn shapes its life history. We evaluated how the extrinsic factor of lighting environment and the intrinsic factor of morph type alter risk-taking behavior in bluefin killifish. Two populations of bluefin killifish from differing light environments were studied. Individual fish from the same population were arranged into a triad that was placed into either a tea-stained or clear water tank. One blue male, one female, and one red or yellow male composed a triad. Each triad member's risk-taking behavior was recorded following the introduction of a predator. Afterwards, the lighting environments were switched to the opposite spectrum, and the triads were observed again. If the risk-taking behaviors of both killifish populations are comparable, this could indicate that the grade of boldness a morph exerts in varied lighting arose because of an evolutionary drive.
Research Grant	University of Illinois research funds
Field of Research	Behavior

Abstract Title	A clinical approach to determining anthelmintic resistance in small ruminants in southern New England
Authors	Eleanor Kharasch, Rachael Gately, Meera Gatlin
Affiliations	Cummings School of Veterinary Medicine, North Grafton, MA (Kharasch), Department of Ambulatory Medicine and Theriogenology (Gately) and Department of Infectious Disease and Global Health, Cummings School of Veterinary Medicine, North Grafton, MA
Abstract	Anthelmintic resistance of gastrointestinal nematodes remains a serious threat to small ruminant producers worldwide. Haemonchus contortus, or the barber pole worm, has been a prevalent strongyle that often leads to significant blood loss of the host and sometimes death. Other strongyles found in small ruminants include Ostertagia and Trichostrongylus species. Previously, anthelmintic resistance has not been studied in southern New England despite an increase in the small ruminant population and an existing market for dairy and meat, both on a commercial and local scale. Parasitism is a major challenge in this region and has resulted in the loss of animals despite anthelmintic treatment and parasite management. We utilized fecal egg count reduction tests (FECRTs) with fenbendazole (brand name Panacur), to determine efficacy against strongyles in sheep and goats from 26 farms in southern New England. Anthelmintic resistance was documented if a FECRT resulted in less than a 90% reduction of eggs. Farm sizes ranged from 2-75 animals, and 100% of farms eligible for the study exhibited resistance. A producer survey was conducted to gather insight on commonly used parasite management strategies including types and frequency of dewormers used on farms. Qualitative data from this survey will be analyzed with quantitative findings to assess potential relationships between management strategies and parasite burden.
Research Grant	Foundation for Food & Agriculture Research Veterinary Student Research Fellowship
Field of Research	Antimicrobial Resistance

Abstract Title	A comparative study of retinal bleaching methods
Authors	Moonhong Kim, Maddison Trawick, Christopher Heesy, Carrie Veilleux, Margaret Hall
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ (Kim, Trawick); College of Graduate Studies, Midwestern University, Glendale, Arizona (Heesy, Veilleux, Hall)
Abstract	The vertebrate retina contains two layers, a neural retina and the non-neural pigment epithelium. In histological studies of the neural retina, during the retinal whole-mount technique, all or part of the pigment epithelium may adhere to the neural retina such that complete removal of pigmented regions may threaten to tear the delicate structure of the neural retina. However, the presence of the pigment obscures the cells of the neural retina and precludes their visualization. In this study we tested several bleaching methods that would allow us to leave the pigment epithelium in place and thereby conserve the neural structure. We obtained two cow retinas from teaching specimens at the Department of Veterinary Anatomy at Midwestern University, Glendale, AZ and performed a retinal wholemount with adherent pigment epithelium. We divided each retina into four approximately equal quarters and placed one quarter from each eye in different solutions, including (1) A control containing only phosphate-buffered saline (PBS), (2) a bleaching solution containing PBS, 30% H_2O_2, and KOH, (3) refractive index matching solution (RIMS), (4) the bleaching solution plus RIMS, and (5) 30% H_2O_2. We left the retinas in solution for 3 hours to depigment the retinas and then stored them refrigerated overnight in a Falcon tube with PBS. Of these methods, only the bleaching solution completely removed the pigment, and it altered the neural retina white. The bleaching solution plus the RIMS caused the entire retina to become completely transparent, making it optimal for accepting stain for further histological work.
Research Grant	Midwestern University intramural funds
Field of Research	Anatomy

Abstract Title	Understanding the regulation of Tinagl1 expression by Sirtuin1 in Triple-Negative Breast Cancer
Authors	Dan Bi Kim, Marc Antonyak, and Richard Cerione
Affiliations	Royal Veterinary College, University of London, London, United Kingdom (Kim), Department of Molecular Medicine, Department of Chemistry and Chemical Biology (Cerione), and Department of Molecular Medicine (Antonyak), Cornell University College of Veterinary Medicine, Ithaca, NY, USA.
Abstract	Triple-negative breast cancer (TNBC) is a highly aggressive subtype accounting for 15% of breast cancer cases. The absence of estrogen, progesterone, and human epidermal growth factor receptor 2 (HER2) receptors limits targeted therapies, and traditional chemotherapies have demonstrated limited efficacy. Therefore, there is an overriding need to develop new strategies for treating this disease. The expression of the NAD-dependent deacetylase Sirtuin1 (SIRT1) has been shown to be reduced in TNBC, resulting in more aggressive phenotypes. We have additionally indicated the loss of SIRT1 leads to increased acetylation of Insulin-like growth factor 2 messenger RNA binding protein 2 (IGF2BP2), subsequently leading to the downregulation of the tumor suppressor Tubulointerstitial nephritis antigen-like 1 (Tinagl1). The primary objective of this study is to investigate the importance of downregulating Tinagl1 in promoting the aggressive features of SIRT1-deficient cells. Preliminary findings suggest that Tinagl1 is secreted as a component of a specific class of extracellular vesicles (EVs) referred to as exosomes, and its expression is lost in exosomes isolated from SIRT1 knockdown cells. I am currently conducting experiments to investigate whether exosome-deficient Tinagl1 promotes cell migration and invasion, and drug resistance. Understanding the interplay between SIRT1 and Tinagl1 secretion via EVs could identify new therapeutic targets for the treatment of TNBC. Ultimately, this work has the potential to advance personalized medicine and pave the way for novel interventions to mitigate the aggressive nature of this breast cancer subtype.
Research Grant	NIH F99 CA274706 NIH R01 CA259195
Field of Research	Oncology

Abstract Title	Utilization of Virtual Reality technology on appropriate personal protective clothing use among dairy workers
Authors	Elizabeth Kim, Pedro Boscan, Isaac Fraire, Morgan Jones, Cyane Tornatzky, Aracely Diaz, Marie Vans, Wenjing Jiang, Sangeeta Rao
Affiliations	Department of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences (Kim, Boscan, Fraire, Jones, Diaz, Rao); College of Liberal Arts (Tornatzky); Department of Systems Engineering (Vans); College of Veterinary Medicine Information Technology (Jiang), Colorado State University, Fort Collins, CO
Abstract	Dairy workers are integral to global food security. However, their working conditions may put them in certain hazards such as physical injuries, exposure to chemicals, and infectious diseases. Training to prevent exposure to these risks includes the use of appropriate personal protective clothing while working on the farm. Although there are various methods of training, the method where individuals best process and utilize what they learned into practice is through an engaging and interactive learning experience. Therefore, this study aims to utilize virtual reality (VR) technology as a training tool that could help educate livestock personnel on the use of appropriate personal protective clothing. This tool surrounds the One Health concept incorporating two important focuses - reducing risk of occupational illness and supporting safe food supply. To perform this study, a VR game was developed where the participant is placed in a locker room within a dairy farm with the option to choose from various protective clothing items. They would need to choose the appropriate items in their correct sequence to progress further. After completing the game, participants were asked to complete a questionnaire on likeability and applicability of the VR tool. Of these participants, 100% responded positively about enjoying the game. The average was 9.8 on 1-10 scale when asked whether VR would be helpful for new workers to know what protective clothing they should be wearing at the farm. The results show a favorable outcome on the effectiveness of VR technology as a training tool, and by gathering more data, this VR tool can advance further to implement more effective biosecurity and biosafety practices within the farm environment.
Research Grant	High Plains Intermountain Center for Agricultural Health and Safety (HICAHS) Emerging Issues Program
Field of Research	One Health

Abstract Title	Anticoagulant Rodenticide Prevalence in Southern California Turkey Vultures and Swainson's Hawks-Pilot Study
Authors	Grace Kinyon, Peter H. Bloom, Emmalee Blumhagen, Jesse Maestas, Alexandra Gresham, Alexandria Koedel, Andrea Bonisoli-Alquati, Robert Poppenga, and Miguel D. Saggese
Affiliations	Western University of Health Sciences, CVM, Pomona, CA (Kinyon, Blumhagen, Maestas & Saggese) Bloom Research Inc., Santa Ana, CA (Bloom) Department of Biological Sciences, Cal Poly Pomona, CA (Gresham, Koedel, Bonisoli-Alquati) CAHFSL, CVM, UC Davis, Davis, CA (Poppenga)
Abstract	Worldwide, anticoagulant rodenticide (AR) use has led to extensive secondary poisoning of non-target wildlife, particularly raptors. They ingest non-target prey and carrion in which ARs accumulate. Even after the 2020 ban on AR use, AR exposure remains highly prevalent in Turkey Vultures (Cathartes aura, TVs), California Condors (Gymnogyps californianus), and other raptors of North-central California. In Southern California (SoCal), where ARs are used extensively, this exposure in TVs and Swainson's Hawks (Buteo swainsoni, SHs) has not yet been assessed. Thus, we investigated the prevalence of exposure to first- and second-generation ARs in the blood of free-ranging TVs (before and after the ban), and in nestlings of SH from SoCal (before the ban) by using liquid chromatography-tandem mass spectrometry. We hypothesized that both species would have detectable AR levels, comparable to findings in North-central California, and that the prevalence of exposure for TVs to ARs should be lower after the 2020 ban. Preliminary results show that only one of the 24 TVs tested so far had detectable levels of one AR (Diaphacinone, 8 ppb). This suggests that TVs in SoCal have an apparent low exposure to ARs. Additional results for eight TVs and nine SHs will be available by the time of the symposium. Overall, the findings of this pilot study will contribute to 1) a better understanding of the risks of AR exposure in these species, 2) assess the effectiveness of the 2020 California AR ban, and 3) refine and validate methodologies for future studies. Current study limitations include relatively small sample size and detection sensitivity issues with blood, which may be remediated by using other tissues for AR investigation in wildlife.
Research Grant	AAV-Avian Health Fund, CVM Matching Funds, Bloom Research, Western U's Office of the Vice-President for Research
Field of Research	Wildlife Conservation

Abstract Title	Unravelling the blood microbiome in healthy and febrile domestic cats via 16s rRNA metagenomics
Authors	Liam Kitson, Ananda Muller, Anne AMJ Becker, Katrin Hartmann, Michele Bergman, Paulina Sepulve-Garcia, and Nivia Canales
Affiliations	Graduate program(Kitson) and Center for Zoonoses and Veterinary Medicine (Muller, Becker), RUSVM, Saint Kitts and Nevis Clinic of Small Animal Medicine(Hartmann, Bergman), Centre for Clinical Veterinary Medicine, LMU Munich, Germany (Canales, Sepulve-Garcia) Facultad de Ciencias Veterinarias, Universidad Austral de Chile
Abstract	This study assessed the blood bacterial microbiome in 300 domestic client-owned cats using 16S rRNA gene sequencing. Genomic DNA samples from the blood of 145 healthy cats (2 months to 15 years, 71 females, 74 males) and 140 febrile cats (3 months to 19 years, 43 females, 77 males, 20 unknown) were analyzed. High-throughput sequencing targeting the 16S rRNA V3-V4 region determined the blood bacterial DNA coverage, composition, and richness. Comparing healthy and febrile groups revealed distinct compositions and diversities. Actinobacteria, Firmicutes, and Proteobacteria were the dominant phyla in both groups, with a lower abundance of Bacteroidetes. Significant differences were observed at the family level. Febrile samples showed an increased abundance of Faecalibacterium, Kineothrix (Firmicutes), and Phyllobacterium (Proteobacteria), while Thioprofundumm (Proteobacteria) decreased significantly. Febrile cats exhibited significant differences in family and genus composition based on affected body systems, except for systemic and oral/gastrointestinal groups. Proteobacteria levels were elevated in systemic and gastrointestinal diseases. Sex did not significantly influence the blood bacterial microbiome, but age had some impact at the family level, particularly between young adult and mature adult groups. Findings indicate age, health status, and disease nature as significant drivers of blood microbiome diversity and composition in cats. Establishing a baseline for the bacterial blood microbiome in healthy cats suggests the presence of "eubiosis" in feline blood. This research expands our understanding of microbial communities in healthy and febrile cats, with implications for future clinical applications.
Research Grant	EveryCat Foundation Grant No EC22-028
Field of Research	Microbiomes

Abstract Title	Evaluating antimicrobial properties of canine platelet lysate in vitro
Authors	Alonza Klopfer, Melika Mollabashi, Matt Murray, Ann Cochran, Thaina Lunardon, Scarlett Sumner, Maria C. Naskou
Affiliations	Scott-Ritchey Research Center (Mollabashi, Murray, Cochran, Lunardon, Naskou), Department of Pathobiology (Mollabashi, Murray, Lunardon, Naskou), Department of Clinical Sciences (Klopfer, Sumner), College of Veterinary Medicine, Auburn University, Auburn, AL.
Abstract	Platelet lysate (PL) is a platelet derived acellular product, that is rich in growth factors and attachment factors. Topical application of PL has shown promising benefits for promoting wound healing. Moreover, PL has also shown antimicrobial properties in vitro and in vivo, which is an attractive attribute for wound therapies since bacterial contamination is one of the most serious complications impairing the wound healing process. The objective of this in vitro study was to compare the antimicrobial activity of PL generated by different methods, against bacteria that are commonly present in canine wounds. Two different centrifugation methods were used to isolate the platelets from canine whole blood. Additional treatment groups were created by performing plasma depletion and/or heat inactivation on the canine PL as plasma and complement activation pathways have unique impacts on bacterial growth. Each treatment group was tested via a spiking assay against bacteria including Escherichia coli, Staphylococcus aureus and Enterococcus faecalis. Colony counts were determined after 3 and 24 hours of incubation. PL treatment resulted in a >1 log reduction in colony counts and higher reduction than other treatment groups for Escherichia coli and Staphylococcus aureus at 3 and 24 hours and for Enterococcus faecalis at 24 hours. Plasma and the complement system likely play a key role in reducing bacterial growth given reduced antimicrobial efficacy in plasma depleted and heat inactivated treatments. PL shows promise as a topical antimicrobial and additional research is warranted in evaluating best manufacturing methods and clinical use.
Research Grant	Scott Fund, Scott-Ritchey Research Center, Auburn University College of Veterinary Medicine
Field of Research	Bacteriology

Abstract Title	Sex-specific assessment of delayed treatment with the LNFPIII therapeutic in a Gulf War Illness mouse model.
Authors	Anthony Kochensparger, Jessica Carpenter, Donald Harn, Brice Hudson, Trevor Kalinowski, Helaina Ludwig, Thomas Norberg, Fabian Tejedor-Rojas, John Wagner, and Nikolay Filipov
Affiliations	Departments of Physiology and Pharmacology (Kochensparger, Carpenter, Hudson, Kalinowski, Ludwig, Wagner, Filipov) and Infectious Diseases (Harn, Norberg), College of Veterinary Medicine, University of Georgia, Athens, GA. Department of Chemistry-BMC (Tejedor-Rojas), University of Uppsala, Uppsala, Sweden.
Abstract	Gulf War Illness (GWI) is a chronic illness affecting 30% of the 700,000 GW veterans, with 7% of the deployed forces being women. Chemical overexposures to pesticides, such as permethrin (PM), and the nerve agent prophylactic pyridostigmine bromide (PB) are linked to GWI's etiology. Symptomology associated with GWI includes neurological abnormalities with neuroinflammatory underpinnings suggestive of neurotransmitter disbalance. However, to date, no studies have evaluated brain neurochemistry in both males and females in a preclinical GWI model that also incorporates a delayed treatment approach. Here, we evaluated the neurochemical effects and benefits of delayed treatment with the immunoprophylactic lacto-N-fucopentaose III (LNFPIII) in both sexes using the PB/PM GWI model. C57BL6/J male and female mice (8-9 weeks old) were co-administered PB and PM (0.7 and 200 mg/kg IP) or a dimethyl sulfoxide vehicle for 10 days. Beginning at 9 months, mice were treated with LNFPIII or Dextran (50 µg/mouse SQ) 2x per week until the time of sacrifice (13 months) to make GW exposures and treatment relevant to veterans with GWI. Brains were collected and processed for HPLC-ECD analyses of dopamine (DA), norepinephrine (NE), serotonin (5-HT), and their metabolites in the pre-frontal cortex, striatum, cerebellum, and brainstem. From the analyses so far, striatal (DA) and cerebellar (5-HT) metabolites were affected the most by the GWI treatment, more in males than females. Male striatal DOPAC was affected significantly, and the LNFPIII treatment restored its GWI-caused decrease. We also observed sex differences at baseline in both striatal DA and cerebellar 5-HT, and they could contribute to the differential effects of GWI/LNFPIII.
Research Grant	Department of Defense Grant W81XWH-21-1-0661 to Nikolay Filipov.
Field of Research	Pharmacology and Toxicology

Abstract Title	MicroRNAs - small molecules with big potential in shaping gut endocrine biology
Authors	Kieran Koch-Laskowski, Heather McCauley, James Wells, and Praveen Sethupathy
Affiliations	Department of Biomedical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY (Koch-Laskowski, Sethupathy); Division of Developmental Biology, Cincinnati Children's Hospital Medical Center, Cincinnati, OH (McCauley, Wells)
Abstract	Gut enteroendocrine cells (EECs) are key regulators of metabolic health. Positioned throughout the gastrointestinal epithelium, EECs sense and respond to luminal contents by secreting a variety of hormones that control appetite, digestion, and whole-body energy balance. Despite the expansion of gut hormone-based therapies as a promising treatment modality for type 2 diabetes and obesity, the mechanisms underlying EEC differentiation and function are not fully understood. Particularly understudied in this context are microRNAs (miRNAs) – small, non-coding RNAs that post-transcriptionally modulate gene expression. While miRNAs have been shown to regulate cell allocation and hormone output in other endocrine tissues, they remain ill-defined in EECs. To address this knowledge gap, we sought to comprehensively profile miRNA expression patterns specific to the EEC lineage. We leveraged murine and human models to isolate intestinal epithelial samples depleted or enriched for EECs, which we analyzed by small RNA-sequencing. Our profiling analyses revealed several conserved miRNAs significantly enriched among different EEC populations, including miR-7, miR-375, and miR-1224. Through ex vivo functional assays, we have found that inhibition of miRNA expression alters EEC abundance in mouse enteroids, and we are currently pursuing additional studies using patient-derived samples. Overall, our findings establish specific miRNAs as conserved regulators of the enteroendocrine lineage and point to molecular targets that may guide future strategies to direct EEC differentiation, function, and ultimately, whole-body metabolism.
Research Grant	American Diabetes Association (1-16-ACE-47 awarded to PS)
Field of Research	Physiology

Abstract Title	Genetic contribution to early onset osteosarcoma in the Irish Wolfhound
Authors	Nyah Kohler, Mehdi Momen, Peter Muir, Gabi Conidi, Brian Davis, and Susannah Sample
Affiliations	Department of Surgical Sciences, School of Veterinary Medicine, University of Wisconsin, Madison, WI (Kohler, Momen, Muir, Conidi, Sample) and Texas A&M University, College Station, TX (Davis)
Abstract	Osteosarcoma (OSA), a highly aggressive cancer with early metastasis and high mortality rates, is common in the Irish Wolfhound (IWH). The IWH has the highest prevalence of OSA among pure-bred dogs and has the youngest age of disease onset. Understanding the genetic contribution and inheritance pattern of OSA in the IWH is important for selective breeding of IWHs. We hypothesize that the majority of OSA in IWHs is highly influenced by a single influential genetic variant in a cancer predisposition gene that, although potentially part of a complex trait, appears to be inherited in an autosomal dominant manner. We propose to identify genetic variants associated with OSA in young IWHs. We undertook 30x depth 150 bp pair-end sequencing of 16 pure-bred IWHs, including 8 pure-bred OSA affected IWHs under 5 years of age and 8 phenotype-negative IWHs. Using a IWH-specific reference genome, we called and identified candidate variants that strongly segregate OSA cases from controls. Genetic variants of interest will be further evaluated using standard bioinformatics protocols, with specific focus on regions of interest that have been identified in prior published work. We expect to identify a subset of strong candidate OSA candidate genetic variants in the IWH. After review of the short read whole genome sequencing results, if a strong candidate variant is identified, we will design a PCR experiment to determine whether candidate loci hold up in a larger population of case and control IWHs. We expect that our results will lead to a genetic test for risk of early onset OSA in the IWH through genotyping of a mutation in a cancer predisposition gene.
Research Grant	American Kennel Club Canine Health Foundation
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Retrospective analysis of risk factors influencing Tragelaphus reproductive health
Authors	Kellie Kokenakes, Chelsey Hamel, Anneke Moresco, Dalen Agnew
Affiliations	Michigan State University CVM, East Lansing, MI Reproductive Health Surveillance Program East Lansing, MI (Hamel and Agnew) Reproductive Health Surveillance Program Morrison, CO (Moresco)
Abstract	Bongos (Tragelaphus eurycerus) are critically endangered with an estimated population of less than 400 individuals remaining in the wild. A thorough understanding of bongo reproductive biology and disease will allow for effective future conservation efforts. Unfortunately, research on this species and related species, including kudu (Tragelaphus strepsiceros and Tragelaphus imberbis), sitatunga (Tragelaphus spekii), and nyala (Tragelaphus angasii) is sparse. This study examines the effect husbandry practices and life history may have on the development of reproductive diseases in this species. We hypothesize that increasing age and parity, and the use of contraceptives increase the likelihood of reproductive disease and infertility. Archived reproductive tracts obtained from 17 bongos, 32 kudu, 6 sitatunga, and 4 nyala collected at necropsy from AZA zoos will be examined grossly and microscopically and reproductive lesions will be identified including inflammation, degenerative changes, and neoplasia. Associations between potential risk factors and disease will be determined using odds ratios and regression analysis. Preliminary examinations have shown leiomyomas, cystic endometrial hyperplasia, and vascular remodeling to be commonly observed lesions. Amyloidosis, associated with chronic inflammation is a common disease in bongo was also observed within some tracts. This information will help guide husbandry and breeding strategies in the future, allowing for healthier bongo, kudu, sitatunga, and nyala populations in captivity and the wild.
Research Grant	MSU Graduate School Fellowship Funds
Field of Research	Anatomic Pathology

Abstract Title	Attitudes, Perceptions, and Expectations for Student Advising in Veterinary Medicine
Authors	Tanner Komlodi*, Susan Fielder, Hui-Fen Chang, Brandy Close, Dan Thompson, Marie Hopfensberger, and Jennifer Rudd
Affiliations	Dept of Veterinary Pathobiology (Komlodi,Fielder,Rudd), OSU Library Services (Chang), Office of Curricular and Education Support (Close,Thompson), College of Vet Med, Oklahoma State University, Stillwater, OK Dept of Large Animal Clinical Sciences (Hopfensberger), College of Vet Med, Michigan State University, East Lansing, MI
Abstract	Academic advising is a core component of most professional programs but little is known about the effectiveness of these mentor-mentee relationships in veterinary medicine programs. Expectations of the institution, advisees, and advisors may vary, limiting usefulness and ability to provide the intended support. These varied perceptions additionally challenge how institutions assess these programs and make improvements. We hypothesize that disconnects in student versus advisor goals for that student's success challenge the effectiveness of the advising program, and more intentional preparation and training should be implemented in advising programs each year. In order to delineate differences in expectations and perceived confidence in advising programs, we developed a Qualtrics® survey that was sent out to advisors and veterinary students throughout accredited veterinary schools in the United States. 237 veterinary students and 74 faculty advisors completed the survey and these data analyzed. While more detailed analyses are ongoing, early findings highlight low frequency of meetings and dissatisfaction among students in this low frequency. Overall, advisors are less likely to consider personal attributes as important to feeling connected in an advisee-advisor relationship than students. Variations in defining advising and student success are also highlighted between groups, and students have less confidence in their advisor's ability to answer their questions than advisors have in their own ability. These findings will be utilized to develop improved, effective advising programs that better meet the needs of both students and the advisors.
Research Grant	None
Field of Research	One Health

Abstract Title	Retrospective study of giraffe (Giraffa camelopardalis) and okapi (Okapia johnstoni) reproductive pathology
Authors	Carrie Kosiba, Anneke Moresco, Dalen Agnew, Ronan Eustace, and Kimberly Thompson
Affiliations	CVM, Michigan State University (Kosiba, Moresco, Agnew, Eustace, and Thompson), East Lansing, MI; Reproductive Health Surveillance Program (Moresco and Agnew), Morrison, CO; Potter Park Zoo (Eustace), Lansing, MI; and Binder Park Zoo (Thompson), Battle Creek, MI
Abstract	With expanding pressures on wild giraffids, giraffe (Giraffa camelopardalis) and okapi (Okapia johnstoni), the importance of sustainable zoo populations and management of the captive breeding population is increasing. Contraceptive methods routinely used in giraffids include castration, separation of sexes, or medications (MGA, MPA, deslorelin, PZP, and improvest), but their effects on the reproductive tract and fertility of giraffids have not been examined. We characterized reproductive lesions in the family Giraffidae and evaluated potential associations between reproductive pathology and age, parity, and contraceptive type. Our study utilized review of tracts in the Reproductive Health Surveillance Program archive and included: 61 female and 16 male giraffes and 14 female and 3 male okapis. Tracts were examined grossly and microscopically, pathologic lesions were characterized, and prevalence of the lesions determined for each species and sex. Neutrophilic inflammation (22/61) was the most prevalent lesion in female giraffes. Ovarian mineralization (6/61) and hydrometra (13/61) were only present in contracepted female giraffes. The most common lesion in female okapis was endometrial hyperplasia (3/14). Common lesions in male giraffes were degeneration (6/16) and hypoplasia (6/16). Epididymal hyperplasia was present in one of three male okapis. These results indicate that reproductive pathology can spontaneously arise in giraffids, and there may be an increased prevalence of some lesions in older, nulliparous and contracepted giraffes.
Research Grant	Reproductive Heath Surveillance Program
Field of Research	Exotic Pets and Zoo Animal Medicine

Abstract Title	Field surveillance of host-seeking ticks on beef cattle pastures in Missouri
Authors	Amanda Kujiraoka, Rosalie Ierardi, Shuping Zhang, and Ram Raghavan
Affiliations	University of Missouri CVM (Kujiraoka); Department of Veterinary Pathobiology, University of Missouri CVM (Ierardi, Zhang, Raghavan); Veterinary Medical Diagnostic Laboratory (Ierardi, Zhang, Raghavan) and Department of Public Health, College of Health Sciences (Raghavan), University of Missouri, Columbia, MO.
Abstract	Ticks and tick-borne diseases pose a major health risk to humans and animals. Two important tick-borne diseases currently transmitted to cattle are bovine anaplasmosis (caused by Anaplasma marginale) and bovine theileriosis (caused by Theileria orientalis). This study utilizes field surveillance to characterize tick populations and A. marginale prevalence on Missouri cattle pastures. Ticks are collected from pastures on four different beef grazing operations in Missouri using flannel drags over 750-meter transects. In 2022, 238 ticks were collected from 79 transects and in 2023, 1905 ticks have been collected from 103 transects between May-July with more collections planned till August. The species composition of this collection includes the lone star tick, Amblyomma americanum (n = 1909), the American dog tick, Dermacentor variabilis (n = 189), the invasive longhorned tick, Haemaphysalis longicornis (n = 29) and occasional minor tick species (n = 16). Our work has revealed for the first time the presence of H. longicornis in Linn and Boone counties of Missouri, with potential implications for human and animal health. Molecular detection of A. marginale among D. variabilis ticks is currently in progress, which will help determine the period-prevalence of this pathogen in beef grazing pastures and the relative significance of the tick vector.
Research Grant	This work is supported by the USDA National Institute of Food and Agriculture, Animal Health project 7003929.
Field of Research	One Health

Abstract Title	Refining cellular reprogramming from engineered endosymbionts using a model transcriptional regulator
Authors	Satyajit Hari Kulkarni, Daisuke Matsumoto, Christopher H. Contag
Affiliations	Comparative Medicine & Integrative Biology (Kulkarni) and Institute for Quantitative Health Science and Engineering (Contag, Kulkarni), Michigan State University, East Lansing, MI Laboratory of Genome and Biomolecular Engineering for Drug Discovery, Hiroshima University, Hiroshima, Japan (Matsumoto)
Abstract	Engineered endosymbionts (EES) are bacteria designed to live in eukaryotic cells and deliver modulators capable of controlling host cell biology. EES engineered to express the endosomal escape protein listerolysin O (LLO) have previously been used to reprogram macrophages towards a pro-inflammatory or anti-inflammatory state and were built on a B. subtilis chassis. However, controlling host cell gene regulation using mammalian transcription factors expressed from EES has yet to be optimized. In this study, we developed a model to refine EES mediated transcriptional control using the reverse tetracycline transactivator (rtTA), a synthetic mammalian transcription factor, to control an optical genetic switch comprised of a tetracycline responsive element (TRE) driving a Luc2-tdTomato fusion protein. In this design, the rtTA is made in the EES under IPTG control, secreted into the cytoplasm using a bacterial secretion system, and transported to the nucleus with a nuclear localization signal (nls). Here, it can activate expression of the reporter gene, under doxycycline control, as a functional readout of EES-mediated transcriptional regulation. J2-immortalized bone marrow-derived macrophages (iBMDM) were nucleofected with the reporter construct and SB100X to generate a stable reporter line and sorted by FACS. rtTA secretion was optimized by screening multiple signal peptide sequences by Western blot and Alphafold. To assess reporter activation, the iBMDM-L2T line was co-incubated with B. subtilis LLO rtTA. Experiments are ongoing.
Research Grant	NSF EAGER 2200991
Field of Research	Immunology

Abstract Title	Polarizing feline CD4 T cells in vitro for feline infectious peritonitis (FIP) therapeutic development
Authors	Emily Kulp, James Cockey, Christian Urbana, Cynthia Leifer
Affiliations	College of Veterinary Medicine (CVM), Cornell University, Ithaca NY
Abstract	Feline infectious peritonitis (FIP) is a near universally fatal disease of cats with no approved treatments. FIP is caused by the feline coronavirus FIPV which infects target cells through spike binding to specific surface receptors. As spike is expressed on infected cells during packaging and egress, it is a promising target for therapy. Our lab is developing a novel chimeric antigen receptor (CAR) system targeting the surface spike protein on FIPV-infected cells. Preliminary data demonstrate that T cells genetically modified to express a spike-reactive CAR specifically detect FIPV spike expressed on target cells. We have developed protocols to enrich and expand feline T cells in vitro to clinically useful numbers; however, feline T cell expansion results in both CD8 and CD4 T cell subsets. While generation of CD4 T cell subsets including Th1, Th2, Th17, and Treg may be clinically useful for adoptive therapies such as CAR, little is known about feline CD4 T cells and whether subsets can be polarized in vitro. Here we aim to generate CD4 T cell subsets using our primary feline cultures with combinations of T cell activators (phorbol myristic acid with ionomycin + IL-2, or concavalin A + IL-2) and polarizing cytokines for Th1 (IL-12), Th2 (IL-4), Th17 (IL-6 + TGFb) and Treg (TGFb). We measured polarization via the upregulation of driver transcription factors Tbet (Th1), GATA3 (Th2), RORgt (Th17) and FOXP3 (Treg) using novel real time quantitative PCR primer sets for these genes identified in the GenBank database. By establishing an optimized protocol to polarize and characterize CD4 T cell subsets in primary feline monocyte culture, this study provides crucial tools to advance studies of engineered cell therapies for FIP.
Research Grant	Cornell Feline Health Center (CAL), Liz Hanson Fellowship (JRC)
Field of Research	Immunology

Abstract Title	Ultrasonographic characterization of lamb lungs during inoculation with Mycoplasma ovipneumoniae
Authors	Ayush Kumar, Sally Madsen-Bouterse, John Mattoon, Paige Grossman, Lilian Moore, Breckan Waite, and Lindsay Piel
Affiliations	Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada (Kumar); College of Veterinary Medicine, Washington State University, Pullman, WA (Madsen-Bouterse, Mattoon, Moore, Waite, Piel); USDA ARS, Animal Disease Research Unit, Pullman, WA (Grossman, Piel).
Abstract	Mycoplasma ovipneumoniae is a bacterial pathogen that can cause mild to moderate respiratory disease in domestic sheep, predominantly affecting lambs. The presence of M. ovipneumoniae can decrease productivity in a flock and can increase susceptibility to other respiratory pathogens, presumably by disrupting mucociliary clearance of commensal bacteria. Previous studies have shown that the lung characteristics of 90% of domestic sheep sent to slaughter exhibit subclinical disease, such as atelectasis and consolidation in the cranioventral lung lobes. Preliminary observations from 2022 revealed cranioventral lung pathology in lambs after infection with M. ovipneumoniae. Predominating clinical signs included abnormal lung sounds upon auscultation and increased respiratory rates. The goal of the present project was to identify lung lobe consolidation by ultrasound imaging following inoculation with M. ovipneumoniae and to correlate these findings to clinical signs, pathogen detection, and gross pathologic lesions during necropsy. Lambs underwent bi-weekly physical exams and weekly ultrasound imaging for approximately 12 weeks' time. Nasal swabs were collected prior to inoculation and at regular post-inoculation intervals to monitor infection status and for other opportunistic respiratory pathogens. Assessment of lung pathology by ultrasound is a novel evaluation method of respiratory disease following M. ovipneumoniae exposure. Use of this imaging technique may help characterize and distinguish lambs which maintain impaired lung function.
Research Grant	USDA (2090-32000-046-000D)
Field of Research	Bacteriology

Abstract Title	Substance P innervation into the central nucleus of the amygdala in mice models
Authors	M. Vitória Kuzolitz, Lauren Beugelsdyk, Miranda Arnold, Ellie Decker Ramirez, and Jesse Schank
Affiliations	Department of Physiology and Pharmacology, University of Georgia, College of Veterinary Medicine, Athens, GA, USA
Abstract	Substance P (SP) is a neuropeptide implicated in stress, anxiety-like behaviors, and drug addiction. Previous studies have shown high expression of SP and its preferred receptor, Neurokinin-1 (NK1R), in the central nucleus of the amygdala (CeA). The CeA is the integrative center of the limbic system that mediates behavioral and physiological responses to fear- and stress-like stimuli. Our objective was to identify the origin of SP projections into the CeA for future studies on drinking and addiction. To investigate this, we infused a retroAAV-hSyn-DIO-mCherry virus into the central amygdala of twelve Tac1-Cre mice using the coordinate AP: -1.1, ML: +/- 2.4, DV: -4.7. When delivered to the CeA of Tac1-cre mice, the cre-dependent retrovirus will drive expression of the mCherry reporter construct in cell bodies of SP positive cells that innervate the CeA, allowing for the identification of SP-specific projection sources. Following a 3-week viral expression period the brains were perfused with paraformaldehyde, sectioned in 30-micron slices, and stained using immunofluorescence to enhance the mCherry signal. Images were then taken on a Zeiss fluorescence microscope for regions where mCherry expression was detected. Results and conclusion are pending. We hypothesize that SP projections originate in the basolateral amygdala, lateral amygdala, paraventricular thalamus, and from the CeA itself.
Research Grant	Unknown.
Field of Research	Physiology

Abstract Title	Investigation of exosome concentration as a potential biomarker for canine cancer
Authors	Courtney H. Labé, Meagan M. Wojtysiak, Mitzi Lewellen, Amber L. Winter, Kelly Reid, Emily L. Myers, Jaime F. Modiano, Kelly M. Makielski
Affiliations	Department of Veterinary Clinical Sciences, College of Veterinary Medicine, University of Minnesota, St. Paul, MN
Abstract	Exosomes are nano-sized extracellular vesicles that are secreted by cells, mediate cell-to-cell communication, and carry cargo including DNA, RNA, proteins, lipids, and metabolites. Exosomal cargo has been significantly associated with various disease states including cancer, highlighting the potential applications of exosomes as biomarkers in liquid biopsy through exosome enrichment and molecular analysis. Previous work in the Modiano Lab has identified an exosome-based blood test that reliably identified the presence of minimal residual osteosarcoma in dogs, providing the rationale for Canine Osteosarcoma Early Detection (COED), a study to develop an exosome-based early detection blood test for canine osteosarcoma. By comparing the exosomal concentrations of dogs enrolled in the COED study from two groups, (1) healthy dogs between 2 and 4 years old, and (2) dogs of any breed, age, and gender with a confirmed diagnosis of cancer, these studies aim to provide a better understanding of exosome shedding and concentration in health and in cancer, and to assess whether exosome concentrations could be one parameter of an early detection exosome-based blood test for canine osteosarcoma and other cancers.
Research Grant	Grant 03032-MOU AKC Canine Health Foundation
Field of Research	Oncology

Abstract Title	Lactobacillus Supplementation Effects on Maternal/Fetal Outcomes of the BPH/5 Preeclamptic Mouse Model
Authors	Jon LaCour, Juliet Flanagan, Kalie Beckers, Kassie Crissman, Jenny L. Sones
Affiliations	Veterinary Clinical Sciences, School of Veterinary Medicine Louisiana State University Baton Rouge, LA 70803 Pennington Biomedical Research Center (Sones) Louisiana State University Baton Rouge, LA 70808
Abstract	Maternal obesity significantly increases the risk of adverse pregnancy outcomes, including preeclampsia (PE). The etiology of this is unknown. Key features of PE, late-gestational hypertension, decidual inflammation, and fetal growth restriction (FGR), are observed spontaneously in BPH/5 mice. Similar to obese preeclamptic women, BPH/5 have increased body weight and gut dysbiosis in pregnancy. We hypothesized that supplementation with anti-inflammatory Lactobacillus sp. in pregnant BPH/5 mice would attenuate obesity, decidual inflammation, and FGR. To test this hypothesis, BPH/5 mice were fed ad libitum (lib) and given 5g/kg L. plantarum and L. pentosus daily or sham treated beginning at embryonic day (e) 0.5 for 6 days. Implantation sites were collected at e7.5 for real-time PCR analyses (n=4/group). BPH/5 treated females had reduced body weight ($p<0.05$) without a change in food intake nor visceral white adipose tissue mass ($p>0.05$). Pro-inflammatory cytokines tumor necrosis factor (TNF)α and interleukin (IL)-6 mRNA were reduced in e7.5 implantation sites from treated mice 10 and 30-fold, respectively ($p<0.05$). BPH/5 treated mice do not have attenuation of late gestational FGR with treatment only in the first third of gestation. In conclusion, maternal weight loss in BPH/5 beginning at conception may improve placental development in this model. Future studies of giving Lactobacillus sp. throughout pregnancy should be performed to see the effects of long-term use on maternal/fetal outcomes. Future investigations are needed to determine the effects on pregnancy outcomes in obese women.
Research Grant	NIH
Field of Research	One Health

Abstract Title	Microbiota-Derived Metabolites Provide Protection from Severe Clostridiodes difficile Infection
Authors	Nicholas N. Laganelli, Joshua E. Denny, Michael C. Abt
Affiliations	School of Veterinary Medicine (Laganelli) and Department of Microbiology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA (Laganelli, Denny, Abt)
Abstract	Clostridiodes difficile infection (CDI) is a major public health threat resulting in over 220,000 hospitalizations and 13,000 deaths annually in the United States. C. difficile is a gram positive, anaerobic, spore-forming bacterium. Following disruption of the intestinal microbiota, C. difficile produces toxins that damage the intestinal epithelial lining. In preliminary studies, our group has found that mice fed two different standard mouse lab diets: Purina LabDiet 5010 & Purina LabDiet 5053 (Diet 1 & Diet 2, respectively) exhibited differences in susceptibility to CDI. Mice fed Diet 1 succumb to severe CDI while mice fed Diet 2 are protected. This protection was independent of C. difficile burden and toxin production. Furthermore, germ free mice are susceptible to severe CDI regardless of diet, suggesting that the protective nature of Diet 2 is acting through the host microbiota. To investigate the role of microbial metabolites produced from these diets in the susceptibility of infection, we compared the growth of C. difficile co-cultured with cell-free cecal supernatants from mice fed Diet 1 and Diet 2. This study was done to confirm the findings from our in-vivo study showing that diet-mediated protection is independent of the pathogen replication. In addition, we explored the role of cecal supernatants derived from mice fed Diet 1 or Diet 2 in modulating intestinal epithelial integrity by measuring the transepithelial electrical resistance across a monolayer of cultured colonic epithelial cells. These findings highlight the importance of microbial metabolites in the protection of mice fed Diet 2 and may inform future studies of diet-based therapeutics.
Research Grant	Crohn's and Colitis Foundation Award Number #1005576
Field of Research	Microbiomes

Abstract Title	MTORC-1 inhibition by Meclizine in Canine Osteosarcoma Cells
Authors	Brandon Lao, Alexey Tomilov, Michael Kent, Gino A. Cortopassi
Affiliations	University of California Davis SVM, Davis, CA
Abstract	Mechanistic Target of Rapamycin (mTOR) is a downstream kinase of the phosphatidylinositol 3-kinase (PI3K) pathway. mTOR has two complexes, mTORC1 and mTORC2. mTORC1 activates p70S6K1 and eIF4E which promotes cell growth and proliferation. Therefore, inhibition of the pathway has been seen as a cancer therapeutic strategy. It has been shown that canine osteosarcomas which have this pathway upregulated are either due to a mutation in PI3K or a deletion of phosphate and tensin homolog (PTEN). Although rapamycin has been shown to be useful in inhibiting cancer cells in vitro, clinical trials have failed to show efficacy. Particularly its use in dogs is limited by its potential toxicity. Previous studies in the lab screened 1600 small molecule human drugs for mTOR binding and discovered several piperazine class drugs that dose-dependently inhibit mTORC1 but not mTORC2. Another study from the lab showed that meclizine dose-dependently killed human glioblastoma stem cells better than rapamycin. We hypothesized that mTORC1 specific inhibition by meclizine would be more effective than rapamycin at inhibiting canine osteosarcoma cells. Drug assays were performed on 3 canine osteosarcoma cell lines exposed to varying concentrations of rapamycin, meclizine, and other compounds that bind to mTORC1. Assays showed that meclizine and other mTORC1 specific inhibitors generally provided less inhibition than rapamycin in all 3 cell lines. While meclizine's effect on cell viability was disappointing, these findings provide a basis for further investigation on the molecular basis for canine osteosarcoma's resistance to mTORC1 specific inhibition.
Research Grant	None
Field of Research	Oncology

Abstract Title	Using Canine Single Chain Trimers to Prevent NK Cell-Mediated Lysis of MHCI-Edited Allogeneic T Cells
Authors	Katie Larsen and Nicola Mason
Affiliations	Department of Clinical Sciences and Advanced Medicine (Larsen, Mason), School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA.
Abstract	Although chimeric antigen receptor T cells (CARTs) show promise in treating humans with hematological malignancies, generating autologous T cells is time-consuming, expensive, and may not be feasible in some patients. To mitigate these issues, CARTs can be derived from healthy donors and cryopreserved so that these allogeneic CARTs would be immediately available for use. However, transfer of allogeneic T cells may elicit an adverse immune reaction. In response, universal CARTs (UCARTs) are generated by removing the donor T cell receptor, as well as beta-2 microglobulin (B2M), a key component of MHC class I (MHCI). However, MHCI null cells such as UCARTs are susceptible to NK cell-mediated lysis. To enable UCARTs to evade NK cell recognition, a non-classical MHCIb molecule can be expressed on their surface in the form of a single chain trimer (SCT). In humans, SCT consist of the HLA-E heavy chain, B2M, and a HLA-E binding peptide linked together and expressed on the MHCI null cell's surface. Relatively little is known about canine MHC (DLA complex); the functional class I gene DLA-88 associates with B2M. We hypothesized that a DLA-88 SCT using canine self-peptide K11 could inhibit NK cell-mediated lysis of MHCI null target cells. K11-DLA88-SCT will be synthesized and used to transduce MHCI null target T cells. Luciferase-based cytotoxicity assays will be performed using canine NK cells co-cultured with T cells for the following conditions: MHCI positive, MHCI null, or expressing K11-DLA88-SCT. If we find that an MHCI-based SCT prevents NK cell-mediated lysis, UCART therapy could provide a safe, effective method to treat patients that may not have the money, time, or functional T cells to generate an autologous product.
Research Grant	None
Field of Research	Immunology

Abstract Title	Salmonella Dublin prevalence in surplus calf environmental samples by multiplex PCR and culture
Authors	Paige Lauder, Samantha R. Locke, Alejandra Arevalo-Mayorga, Greg Habing
Affiliations	Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio
Abstract	Salmonella Dublin (S. Dublin) is a cattle-adapted bacteria known to cause invasive, antimicrobial resistant disease in cattle and humans. Surplus calves are particularly susceptible to infection due to stressors during transportation and marketing. S. Dublin is difficult to recover from environments by culture-dependent methods, limiting our understanding of prevalence and transmission in the surplus calf industry. The objective of this study was to assess prevalence of S. Dublin from environmental samples taken at a surplus calf collection facility by end-point PCR and culture-dependent methods. We hypothesized that the use of PCR as a screening method would increase detection of S. Dublin from surplus calf production environments. Environmental samples were collected from a surplus calf collection facility by walking occupied pen areas in boot swabs. After incubation, pre-enrichment broth aliquots were taken for column-based DNA extraction and PCR using two sets of S. Dublin specific markers. In tandem, samples were cultured using multiple enrichment broths and selective media. Recovered isolates were serogrouped. The prevalence of Salmonella was 100% (38/38) by PCR and 78.95% (30/38) by culture. Fourteen were PCR positive for S. Dublin, but no isolates were recovered via culture. End-point PCR was more sensitive than culture for S. Dublin detection in a surplus calf collection facility, thus this method may be used as a faster and more sensitive test for S. Dublin screening and confirmation. End-point PCR may be used to more efficiently study S. Dublin prevalence and environmental transmission in surplus calf production systems, allowing development of targeted intervention to reduce S. Dublin exposure and infection.
Research Grant	USDA Agriculture and Food Research Initiative
Field of Research	Epidemiology

Abstract Title	Detection of Tetracycline Resistance Genes in Escherichia coli isolates from canines in Grenada, West Indies
Authors	Kaitlin Law, Bhumika Sharma, Andy Alhassan, and Kamashi Kumar
Affiliations	Department of Pathobiology (Sharma, Alhassan), Department of Anatomy, Physiology and Pharmacology (Kumar), St. George's University, School of Veterinary Medicine, Grenada, West Indies
Abstract	Antimicrobial resistance (AMR) in microorganisms poses a great threat to the public health ofhumans and animals worldwide, causing major economic consequences for the global economy. Escherichia coli is a Gram-negative bacterial organism infecting both humans and animals. This bacterium can cause gastrointestinal, urinary tract, and systemic infections. The major impact of AMR development in bacterial organisms is the potential for zoonotic transfer of AMR genes between animals and humans. Recent retrospective studies conducted in Grenada have confirmed the presence of AMR in E. coli isolated from canine samples. Considering the significance of AMR, the present study was designed to evaluate the prevalence of tetracycline resistance and to determine the contributing factor for tetracycline resistance in canine isolates of E. coli in Grenada. Clinical isolates from canine patients collected during April to June 2023 at the Small Animal Clinic, St. George's University, Grenada, were subjected to an antibiotic susceptibility test (ABST) procedure. ABST results confirmed eighteen resistant E. coli isolates. These isolates were further analyzed by Duplex Polymerase Chain Reaction (dPCR), for the presence of tetA and tetB genes. dPCR results confirmed the presence of the tetA gene in 3 out of 18 clinical isolates. Hence, our preliminary studies have confirmed that so far, the contributing factor for tetracycline resistance in E. coli isolates of the canine population in Grenada is associated with the tetA gene. However, further Polymerase Chain Reaction (PCR) studies using more canine E. coli isolates are required to summarize the plasmid-associated AMR pattern in Grenada.
Research Grant	Research Grant: Boehringer Ingelheim Island Veterinary Scholars Program
Field of Research	Antimicrobial Resistance

Abstract Title	Evaluation of optic nerve head and retina using optical coherence tomography in normal canines
Authors	Trang T. Le, Soohyun Kim, Michelle Ferneding, Vanessa Ureno, Maria Do, and Chung-Chih Luo
Affiliations	Comparative Ophthalmology and Vision Science Laboratory and Center for Companion Animal Health, School of Veterinary Medicine, University of California Davis, Davis, CA
Abstract	Glaucoma is defined by a group of neurodegenerative ophthalmic disorders associated with increased intraocular pressure (IOP) that results in irreversible damage to the optic nerve head (ONH) and retina. In canine patients, glaucoma is one of the most common vision-threatening and painful ophthalmic diseases. Effective control of glaucoma can be achieved through therapeutic interventions and prompt management of elevated IOP. Vital features of controlling glaucoma, including timely diagnosis, frequent monitoring, and consistent therapeutics, are necessary to prolonging vision and comfort. In human medicine, repetitive, non-invasive advanced imaging technologies, such as optical coherence tomography (OCT), are utilized in monitoring changes of the ONH and peripapillary retinal nerve fiber layer (RNFL). Due to the anatomical differences of ONH and variations of peripapillary myelination between humans and dogs, the use of OCT with the automatic assessment function is limited for canine patients. Therefore, our study develops an analysis method suitable for measuring the ONH and peripapillary RNFL thickness in canines. Near-infrared reflection and cross-sectional B-scan images of ONH and peripapillary RNFL were obtained with OCT (Spectralis®, Heidelberg Engineering) from 12 dogs with normal ophthalmic findings. The ONH parameters, including cup volume, maximum cup depth, lamina cribrosa displacement and Bruch's membrane opening, were measured using ImageJ. Our goal is to ultimately provide the reference ranges of canine ONH parameters and peripapillary RNFL thickness by OCT to monitor canine patients predisposed to or suffering from glaucoma and prolong vision.
Research Grant	Center for Companion Animal Health # 2022-58-F
Field of Research	Ophthalmology

Abstract Title	The effects of early life seizures on auditory communication in rats
Authors	Catherine LeBlond, Paul Bernard, and Jessica Rock
Affiliations	Department of Biomedical Sciences, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE
Abstract	Early life seizures (ELS) affect approximately 3/1000 infants and are associated with detrimental neurological outcomes, including deficits in socialization. Social behaviors, communicative deficits, and ELS have not been thoroughly studied and mechanistically linked. Our goal is to determine the nature of differences in auditory communication triggered by ELS. We hypothesize that deficits in socially relevant auditory communication underlie the social deficits seen following ELS. This study assesses the differences in vocalizations of Sprague-Dawley rats between treatment groups (ELS/control) and naïve groups and also between male and female gonadal sex. These differences are explored to determine the impact of ELS on receptive and/or expressive auditory communication. Ultrasonic vocalizations (UVs) obtained during social testing underwent complex call analysis in order to determine if call characterization between ELS and control rats are different during a novel social encounter. During complex UV analysis, the experimenters identify call type, duration (ms), and frequency (kHz) while blind to treatment condition. Results are pending statistical analysis, and we anticipate that there will be differences between the treatment groups. Understanding the long term impact of ELS on auditory communication is clinically relevant, yet remains underexplored in the literature. Insights derived from our model may impact our understanding of neurodevelopmental disorders. This model displays broad translational ability in modeling diverse chronic deficits that occur following ELS, as it demonstrates altered synaptic plasticity and mimics behavioral and neurochemical changes associated with neurodevelopmental changes ensuing ELS.
Research Grant	National Institute of Health (NIH)
Field of Research	Behavior

Abstract Title	Bacterial contamination does not influence the diagnostic accuracy of UPC and urine SDS-PAGE
Authors	Alyssa LeComte, Catherine Yeoman, Caroline Gainey, Sara Lawhon, Jing Wu, Kelci Ryan, Jessica Hokamp, Mary Nabity
Affiliations	Department of Veterinary Pathobiology and VMTH Clinical Microbiology Laboratory (Lawhon, Wu), School of Veterinary Medicine, Texas A&M University, College Station, TX, USA
Abstract	Urine samples received for testing commonly contain bacteria, and a recent study found that in dogs with urinary tract infections (UTIs), protein banding patterns on urine sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) were sometimes altered in urine with bacteriuria, even in the absence of hematuria and pyuria. Additionally, a previous study has demonstrated an elevated urine protein:creatinine ratio (UPC) in dogs with experimentally induced UTIs characterized by bacteriuria, pyuria, and hematuria. It is unclear to what extent bacteria and their proteins could contribute to the elevated UPC or SDS-PAGE banding patterns in these studies. This study aimed to determine if the presence of bacteria or bacterial-produced proteins alter the UPC and contribute to the urine protein banding patterns observed with SDS-PAGE. Aliquots of urine from ten clinically healthy, spayed/neutered dogs were inoculated with approximately 105 colony-forming units per milliliter (CFUs/mL) of either Escherichia coli, Staphylococcus pseudintermedius, or Proteus mirabilis and incubated at room temperature (25°C) or 4°C for 2 and 5 days. After incubation, a quantitative urine culture was performed on each aliquot to determine the bacterial CFUs/mL, and the urine supernatant from each condition was collected for UPC and urine SDS-PAGE. No significant increases in UPC and no alterations of banding pattern were observed for any bacteria or condition. Therefore, the diagnostic accuracy of urine SDS-PAGE or UPC are not expected to be altered by bacterial contamination.
Research Grant	International Veterinary Renal Pathology Service; AKC Canine Health Foundation
Field of Research	Clinical Pathology

Abstract Title	Functions of a circular RNA generated from human Survival Motor Neuron genes
Authors	Ji Heon Lee, Diou Luo, Eric W. Ottesen, Ravindra N. Singh
Affiliations	Department of Biomedical Science, College of Veterinary Medicine, Iowa State University, Ames, IA
Abstract	Human Survival Motor Neuron 1 (SMN1) gene produces an essential protein called SMN, a crucial player in various aspects of cellular metabolism. Mutation or deletion of the gene lead to Spinal Muscular Atrophy (SMA), a genetic disorder with high infant mortality due to weakness or wasting of skeletal muscle from losing motor neurons in the spinal cord. Humans also have another SMN gene called SMN2 that is almost identical to SMN1, but it cannot compensate for the loss of SMN1 due to the skipping of exon 7. However, correction of SMN2 exon 7 splicing is a proven approach to treating SMA. Recent reports reveal the generation of circular RNAs (circRNAs) from human SMN genes. However, the function of circRNAs from SMN genes remains unknown. Here we analyze RNA-Seq data from cells overexpressing C2A-2B-3-4, a circRNA multiple genes significantly regulated upon overexpression of C2A-2B-3-4. Employing quantitative real-time PCR (qPCR), we validate the findings of RNA-Seq. We show significant upregulation of NAA15, CELSR3, ELF2, and EN2 by overexpression of C2A-2B-3-4. These findings uncover the critical role of an SMN circRNA in cellular metabolism, including cell signaling, transcription, translation, and macromolecular trafficking. Findings also underscore SMN protein-independent functions of SMN genes in gene regulation and brain development.
Research Grant	NIH R01 NS055925
Field of Research	Biochemistry

Abstract Title	Using filters in the sump for monitoring health of laboratory zebrafish
Authors	Frank Leitgeb, Aidan Horvath, Mollie Madigan, Iris Bolton, Amanda Darbyshire
Affiliations	Laboratory Animal Program, College of Veterinary Medicine, Purdue University, West Lafayette, IN
Abstract	Early detection of pathogens is imperative for the health of laboratory zebrafish and to ensure reproducible scientific results. While most pathogens are present as subclinical or chronic infections, their presence can be a confounding factor in data collection, and some infections can affect zebrafish health and reproduction. Current methods to test for pathogens sample a myriad of sources, including cage swabs, detritus, water collection or filtration, and whole sentinel fish PCR or histopathology. Sentinel mice have been used in the past for mouse health monitoring, but there has been a recent shift to replace sentinel animals with filters in rack exhausts. We wished to see if such methods could be translated from mouse racks to zebrafish systems. We placed filters in the sumps of zebrafish racks to be collected and tested for pathogens at monthly intervals using PCR, and results will be compared to those detected on filters in which water was actively vacuum pumped through, swabs of sump biofilm, and whole fish PCR. We hypothesize that the filters present in the sumps will detect more pathogens than the other methods and may detect more pathogens over time. Should the evidence support the hypothesis, the use of filters could eventually replace the need for sentinel fish for health monitoring purposes of laboratory zebrafish.
Research Grant	VRL Kalter/Heberling Diagnostic Research Grant
Field of Research	Animal Welfare

Abstract Title	Utility of FitBark to monitor activity change in obese dogs undergoing a structured weight loss program
Authors	Hailey Lenis, Nora Jean Nealon, Adam Rudinsky, Hannah Klein, Valerie Parker, and Jenessa Winston
Affiliations	Department of Clinical Sciences, Comparative Hepatobiliary and Intestinal Research Program, College of Veterinary Medicine, The Ohio State University, Columbus, OH
Abstract	Obesity is a prevalent health concern for dogs that is associated with increased mobility issues. Wearable activity monitors (such as the FitBark device) are increasingly used to evaluate canine mobility. While weight loss is widely believed to be associated with improved mobility, there are limited studies using activity monitors to examine mobility changes during structured weight loss programs in dogs. This project aimed to examine relationships between weight loss, activity monitor parameters, and scores on the validated multidimensional canine quality of life survey (QoL) and Liverpool Osteoarthritis in Dogs (LOAD) questionnaire. We hypothesized that weight loss would improve QoL and LOAD scores while increasing activity levels assessed via FitBark. This data is part of the Canine SLIM study, a 24-week clinical trial where 25 client-owned obese dogs underwent a structured weight loss program. Owners completed a LOAD survey every 3 weeks and QoL every 12 weeks. Daily activity was tracked with FitBark devices. QoL scores and fold changes of FitBark activity and LOAD scores were examined for changes over time with repeated measures analysis of variance with significance defined as $p < 0.05$. Initial analyses demonstrated improved physical dimension of QoL scores when comparing baseline to week 24 (Friedman test, $p=0.0075$). Significant changes in LOAD scores were noted between week 12 to 24 (Holm-Sidak's post hoc test, $p < 0.02$). No significant differences in weekly FitBark activity were observed. These results demonstrate that weight loss improves owner perceived physical QoL while maintaining mobility. The FitBark device provides a user-friendly platform to monitor activity levels in obese dogs undergoing weight loss.
Research Grant	American Kennel Club Canine Health Foundation: Canine SLIM Study
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Targeted amplicon next-generation sequencing of phage display libraries reactive with IgG against tick tissues
Authors	Corynn Lewis, Stephan Keller, RW (Bill) Stich
Affiliations	University of Missouri-Columbia
Abstract	Massive parallel sequencing of libraries encoding phage surface proteins is an approach to high throughput screening for peptides that bind to ligands. Intermediate PCR amplification of target sequences allows barcoding for downstream pooling of amplicon libraries. The objective of this project is to generate amplicons encoding random peptides fused to the N-terminus of the pIII surface protein of a commercially available filamentous phage (M13KE) library, preparatory to targeted amplicon next-generation sequencing (NGS). Briefly, M13KE bound to bovine IgG were eluted from protein G-coated magnetic beads, then used as a template for PCR with primers designed to anneal to sequences flanking those encoding the pIII-random peptide fusion protein. Notably, these M13-specific sequences were also flanked with NGS-compatible adapters, to facilitate downstream secondary PCR with barcoding for NGS of pooled amplicon libraries. Two bands, one approximating target amplicon size and the other smaller, were observed after PCR of M13KE. For optimal NGS, two approaches are underway to ensure the target amplicon is predominant. First, work is underway to clone and sequence each band observed, to confirm and utilize these sequences for primer refinement. Second, optimizations of annealing temperature, primer concentration, and cycle number are underway to minimize the smaller band that is observed after standard agarose gel electrophoresis. Future work will involve secondary PCR with NGS-compatible primers and adapters flanking amplicon library-specific barcode sequences, for sequencing of pooled libraries followed by bioinformatic identification, sorting, and characterization of individual M13KE-derived amplicon libraries.
Research Grant	USDA NIFA 17-67015-26630, Foundation for Food and Agricultural Research (FFAR)
Field of Research	Parasitology

Abstract Title	FasR genetic regulation of lipid production in live attenuated vaccine strain of Mycobacterium tuberculosis
Authors	Xiaoxu Lin, Raymond Nietupski, Neharika Jain, Allison Carey, Xin Wang, Eric J. Rubin, Amanda J. Martinot
Affiliations	Dept of Infectious Diseases and Global Health, Tufts University Cummings School of Vet Med, North Grafton, MA (Lin, Nietupski, Jain, Martinot) and Dept of Pathology, University of Utah, Salt Lake City, UT (Carey) and Dept of Immunology and Infectious Diseases, Harvard School of Public Health, Boston, MA (Wang, Rubin)
Abstract	Tuberculosis (TB) remains a major health issue around the globe. BCG is the only licensed vaccine against TB but has variable efficacy in adults. We previously identified a genetic operon, LprG-Rv1410, encoding a lipid transporter, as conditionally essential for Mycobacterium tuberculosis (Mtb) survival in vivo. An Mtb strain lacking the LprG-Rv1410 (delta-LprG; dLprG) operon is severely attenuated and protects mice against TB infection when used as live whole cell vaccine, with superior efficacy and similar safety to BCG. However, the WHO Geneva Consensus recommends that attenuated whole cell vaccines have at least two independent non-inverting gene mutations to be safe. To further improve the safety profile of the dLprG strain, a transposon mutagenesis screen (TnSeq) was performed on the dLprG vaccine to identify additional virulence genes that could be knocked-out. This screen identified the gene, Rv3208 (FasR), encoding for a putative transcriptional activator of the lipid enzyme system, FasI. We hypothesize that lipid efflux via the LprG-Rv1410 operon is functionally linked to cell wall lipid biogenesis through a negative feedback loop tuned by FasR. We used multiplex RT-qPCR on LprG and FasR mutant strains to interrogate FasR function. We first established the relative expression of FasI and FasR across various mycobacterial growth states of BCG. We then used RNA from wild-type, mutant, and complemented LprG and FasR Mtb strains to characterize the functional significance of FasR during Mtb growth. These studies will further elucidate the mechanism of dLprG mediated vaccine protection and help characterize its safety profile.
Research Grant	K08 135098-01A1
Field of Research	Bacteriology

Abstract Title	Using natural remedies to reduce fungal (Batrachochytrium salamandrivorans) infection in salamanders
Authors	Kaitlyn N. Linney, E. Davis Carter, Carmen Merolle, Merrie Urban, Matthew J. Gray, and Debra L. Miller
Affiliations	Department of Biomedical and Diagnostic Sciences, University of Tennessee College of Veterinary Medicine, Knoxville, TN (Linney, Miller) Center for Wildlife Health, School of Natural Resources, University of Tennessee Institute of Agriculture, Knoxville, TN (Carter, Merolle, Urban, Gray, Miller)
Abstract	Batrachochytrium salamandrivorans (Bsal), a fungal pathogen identified in 2013, is a causative agent of lethal chytridiomycosis in amphibians. The introduction of Bsal to Europe through the pet trade has devastated salamander populations, and it has the potential to spread worldwide. Previous experiments in our laboratory indicate that curcumin, a compound found in turmeric, demonstrates inhibitory and fungicidal effects on Bsal growth. Other experiments have shown that survival of salamanders exposed to Bsal is temperature dependent, with greater mortality and zoospore load seen when temperatures are closest to the optimum for Bsal growth (15℃). In order to determine the safety and efficacy of curcumin as a potential treatment for Bsal chytridiomycosis, Notophthalmus viridescens adults were collected and individually housed at two different temperatures (13℃ and 20℃). Selected animals were exposed to a Bsal dose of 5x10^3 zoospores/mL for 24 hours. Exposed animals at each temperature were then assigned to one of three treatment groups: simultaneous treatment with 7 µg/mL curcumin, post-exposure (PE) treatment (3 days PE) with 7 µg/mL curcumin, or no fungicide treatment. Each animal was swabbed every 6 days to determine the presence of Bsal DNA via qPCR. Prevalence of Bsal detection in animals treated simultaneously with curcumin was lower than in both post-exposure treated and non-treated animals. Additionally, simultaneous treatment with curcumin reduced average infection load for animals at both temperatures (13℃ and 20℃). Our results suggest that curcumin may be effective at preventing infection and reducing loads of Bsal in N. viridescens but may be less effective at treating animals with established infections.
Research Grant	U.S. Fish and Wildlife Service
Field of Research	Wildlife Conservation

Abstract Title	Exploring correlations between horse behavior and serologic antibody presence for Borrelia burgdorferi
Authors	Tara Long, Rebecca Thompson, Erica Feuerbacher, Virginia Buechner-Maxwell
Affiliations	Summer Veterinary Research Program (Long), School of Animal Sciences (Thompson, Feuerbacher), Center for Animal Human Relationships (Maxwell), Virginia-Maryland College of Veterinary Medicine, Virginia Tech, Blacksburg, VA.
Abstract	Borrelia burgdorferi, the bacteria that causes Lyme disease, is an endemic pathogen to North America that is capable of infecting mammalian hosts via Ixodid tick vectors. Presently, there are only three confirmed clinical disease entities affiliated with borreliosis in horses: pseudolymphoma, neurologic disease, and uveitis. Anecdotal evidence suggests that physical signs like lameness, general stiffness, and behavioral abnormalities may also be implicated with equine Lyme, and this is loosely supported by evidence that B. burgdorferi bacteria remain in muscle tissues and synovial spaces post-infection. Because these and other clinical signs are perceived as being associated with Lyme, borreliosis treatment of horses based solely on clinical discomfort has become common practice. However, more evaluations are necessary to determine whether true correlations exist. This study employed a correlational design to evaluate potential relationships between horse behaviors and Lyme serostatus with the goal of expanding knowledge regarding physical effects of borreliosis. This was accomplished by enrolling a convenient sample of 108 horses in the greater Roanoke and Blacksburg areas. Serum from horses was sent to Cornell University for testing via the Equine Lyme Multiplex Assay and results were compared to Qualtrics behavioral survey responses. Epidemiologic evaluations using R-studio suggest that there are no statistically significant correlations between horse behaviors or lameness and Lyme serostatus. These results contradict suppositions that horse behaviors and general lameness are associated with B. burgdorferi infection, thereby discrediting the presumptive treatment of horses that are only experiencing behavioral signs.
Research Grant	None
Field of Research	Behavior

Abstract Title	Fecal Profiles of Fatty Acids, Sterols, and Bile Acids in Healthy Horses and those with Colitis
Authors	Claire Long, Carolyn Arnold, Chin-Chun Chen, Jan Suchodolski, and Rachel Pilla
Affiliations	Gastrointestinal Laboratory, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA (Long, Chen, Suchodolski, Pilla), Texas Tech University, School of Veterinary Medicine, Amarillo, TX (Arnold)
Abstract	As gastrointestinal disease continues to be a leading cause of death in horses, there is a need for non-invasive biomarkers that differentiate health and disease. Host and microbiome-derived fecal metabolites may provide insight about metabolic pathways perturbed during disease and uncover novel diagnostic and/or therapeutic targets. The aim of this study was to evaluate fecal fatty acid, sterol, and bile acid concentrations in healthy horses (HC=31) and in those with various subtypes of colitis: antibiotic-associated (AAD=13), infectious (INFEC=22) (Salmonella, clostridial), inflammatory (INFLAM=11) (IBD, sand, cantharidin), and undiagnosed (UD=8). We hypothesized that horses with gastrointestinal disease will have alterations in fatty acid, sterol, and bile acid concentrations. Lyophilized feces were assessed for metabolites using a targeted approach with gas chromatography-mass spectrometry (GC/MS). Metabolite concentrations were analyzed using MetaboAnalyst 5.0. When compared with HC horses, there was a significant decrease in myristate (AAD), and significant increases in stearate (INFEC, INFLAM), nervonate, arachidonate, and total fatty acids (INFEC). Among sterols, phytosterol, campesterol:cholesterol, lathosterol:cholesterol and sitosterol:cholesterol ratios were decreased (AAD, INFEC, INFLAM, UD) while concentrations of cholestanol, zoosterol, and total sterol (INFEC, INFLAM, UD), cholesterol (INFEC, UD), coprostanol and lathosterol (INFEC, INFLAM) were increased. No significant differences were detected in bile acids between HC and colitis groups. These results indicate that fatty acid and sterol metabolism is altered in horses with gastrointestinal disease.
Research Grant	None
Field of Research	Microbiomes

Abstract Title	Can Anxiety Fog Your Memory? An Alzheimer's Disease Animal Model
Authors	Danielle Lopez, Stephanie Hall
Affiliations	Department of Anatomy and Physiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS
Abstract	Alzheimer's disease (AD) is a neurodegenerative disease that leads to impaired learning and memory, but largely understudied is AD's influence on stress and anxiety. This relationship becomes compounded by the need for animal models in AD research, as too often high levels of anxiety can lead to misinterpretation of behavioral testing. This study will be the first to statistically correlate anxiety in different ages, genders, and exercise status in AD compared to wildtype (WT). We hypothesize that anxiety will increase with age and AD genotype and decrease in female and those in the exercise group. In addition, it is hypothesized that memory performance will be negatively associated with increased anxiety. Data was analyzed in both the percent time spent in the open arm as well as the percent time spent in the closed arm. Increased time in open arm is indicative of reduced anxiety. Increased time spent in a closed arm is indicative of increased anxiety. Animals with the AD genotype spent significantly ($p<0.05$) more time in the closed arm indicating significantly higher levels of anxiety compared to WT controls. While not statistically significant, strong trends were present that indicated females have more anxiety compared to males, older animals have less anxiety compared to younger animals, and exercise training reduces anxiety compared to sedentary controls. Interestingly, we found no correlation between anxiety level and memory test performance. This indicates that the memory tests were robust enough to overcome any present anxiety. Understanding the effects of anxiety on laboratory animal performance will allow for better interpretation of results.
Research Grant	P20GM113109
Field of Research	Behavior

Abstract Title	Development of a new lipid nanoparticle for microwave triggered delivery of gemcitabine to pancreatic cancer
Authors	Gabriella Lorino, Cesar Aparicio, and Matthew Basel
Affiliations	Kansas State University CVM, Manhattan, KS
Abstract	Pancreatic cancer is the fourth leading cause of cancer deaths, characterized by a surplus of dense connective tissue that surrounds the malignant cells, often making up much of the tumor. This desmoplasia can contain cells and growth factors that aid tumor growth as well as provide a physical barrier to drug delivery. Gemcitabine is a keystone element of pancreatic cancer treatment, but like other chemotherapy drugs, can cause undesirable side effects. By developing a thermosensitive liposome (TSL) nanoparticle to contain gemcitabine, it can be successfully delivered to the pancreatic tumor where it is activated by microwave induced hyperthermia. This hyperthermia causes the nanoparticles to release gemcitabine, increases vascular activity within the tumor improving drug uptake, and targets drug activity to where it is needed most. The targeted delivery reduces gemcitabine's capacity to cause undesirable side effects throughout the body. To determine the kinetics of TSL release, different preparations of TSL containing carboxyfluorescein were exposed to 37 ℃, 42 ℃, and 45 ℃ for 30 minutes with the fluorescence read at 0, 2, 5, 10, 15, 20, 25, and 30 minutes. The carboxyfluorescein is used in place of gemcitabine because its fluorescence is easily detected and measured by the SpectraMax i3x spectrometer. This data indicates which preparation efficiently releases their payload under conditions of hyperthermia while staying intact at lower temperatures. Finally, toxicity of TSL containing gemcitabine is tested on BXPC3 cells exposed to 37 ℃, 42 ℃, and 45 ℃ for 0, 1, 2, 5, 10, and 15 minutes. Results demonstrated that the developed liposomes were thermosensitive and that kinetics for the liposomes could be determined.
Research Grant	Johnson Cancer Research Center Innovative Research Award
Field of Research	Biochemistry

Abstract Title	Type I Interferon Facilitates Klebsiella pneumoniae Survival in Macrophages
Authors	Zachary Lott, Crystal Villalva, and Sunil More
Affiliations	College of Veterinary Medicine, Oklahoma State University, Stillwater, Oklahoma
Abstract	Type I interferons are antiviral proteins induced by viruses and, depending on bacterial species, can be beneficial or detrimental to bacteria. In our mouse model of Klebsiella pneumoniae (Kp) and SARS-CoV-2 coinfection, increased bacterial propagation led to lethality despite a significant increase in macrophages in the lungs. The purpose of this study is to determine the effect of type I interferons on antibacterial functions of macrophages challenged with Kp. Mouse macrophages were treated with Type I interferons (100 ng/mL) for 24 hrs. Post-interferon treatment macrophages were challenged with Kp (MOI of 10). Three hrs post-infection (hpi) the bacterial inoculum was removed and replenished with media. The cells were lysed at 3 and 24 hpi and then plated on nutrient agar. Colony forming units per ml were recorded the next day. We observed that at 3 hpi, the bacterial counts were comparable in both groups. However, interferon-treated macrophages contain significantly higher amounts of bacteria than the control macrophages at 24 hpi. Based on the results, interferon treated macrophages were able to phagocytose Kp at the same rate, but Kp clearance is negatively affected. Therefore, it is likely that type I interferons affect antibacterial degradation mechanisms of macrophages. To conclude, type I interferons confer a survival advantage to Kp within macrophages, despite their recognition of the bacteria. This study highlights the potential detrimental effects of increased interferon induction by SARS-CoV-2 that enhances pathogenicity of secondary bacterial infection with Kp. Further studies on how Kp exploits interferon are required to understand the pathogenesis of coinfection.
Research Grant	College of Veterinary Medicine, Oklahoma State University
Field of Research	Immunology

Abstract Title	Herpes Simplex Virus-1 ICP0 enhancer activity is stimulated by Glucocorticoid Receptor and Sp1 or Sp3
Authors	Sydney Lubbers, Vanessa Santos, Clinton Jones
Affiliations	Department of Veterinary Pathobiology, College of Veterinary Medicine, Oklahoma State University, Stillwater, OK
Abstract	Herpes Simplex Virus-1 (HSV-1) is an important human pathogen that can cause serious ocular disease or encephalitis. HSV-1 initially infects mucosal surfaces and then spreads to neurons during acute infection. A subset of neurons survive infection and establish lifelong latency. Previous studies demonstrated stress triggers HSV-1 reactivation from latency. Additional studies revealed the glucocorticoid receptor (GR) cooperates with specific stress-induced transcription factors to transactivate viral promotors. Genes encoding infected cell protein 0 (ICP0), ICP4, and viral protein 16 (VP16) are believed to mediate HSV-1 reactivation from latency. ICP4 and ICP0 are immediate early genes, which encode proteins that stimulate expression of HSV-1 early and late genes. Sp3 and Sp1, stress-induced transcription factors, are capable of stimulating or repressing transcription by binding specific sites in the promotor. Thus, we hypothesized GR and Sp1 or Sp3 transactivate ICP4 and ICP0 transcriptional promoters. To test this, mouse neuroblastoma cells (Neuro-2A) were transfected with plasmids containing ICP0 or ICP4 (denoted as pα4R) enhancer sequences and then promoter activity was measured using the dual luciferase assay. ICP0 enhancer activity was stimulated more than 6-fold by GR and Sp3 and more than 3-fold by GR and Sp1. Conversely, the pα4R construct was not significantly increased by just the Sp3 transcription factor or GR and Sp3. In summary, GR and Sp1 or Sp3 significantly transactivated the ICP0, but not ICP4, enhancer activity in Neuro-2A cells. Further studies will investigate if GR and Sp1 or Sp3 influence viral replication, reactivation from latency, and other HSV-1 enhancers.
Research Grant	USDA-National Institute of Food and Agriculture (NIFA), National Institutes of Health (NIH)
Field of Research	Virology

Abstract Title	Validation of an Indirect Fluorescent Antibody Test for Sarcocystis neurona infection in California sea lions
Authors	Amalie Luneng Solli, Cara Field, Pádraig Duignan, Andrea Packham, Magdalena Plancarte, Woutrina A. Smith
Affiliations	One Health Institute, School of Veterinary Medicine, University of California, Davis, Davis, CA (Luneng Solli, Packham, Plancarte, Smith). The Marine Mammal Center (Field, Duignan).
Abstract	Sarcocystis neurona is a protozoan parasite that infects California sea lions (Zalophus californianus) and disease may manifest as polyphasic rhabdomyositis, often resulting in death. Seroprevalence of S. neurona has been increasing in marine mammals recently, including in stranded California sea lions where infection prevalence was 5-6% between 1994-2009 and has increased to 14% seroprevalence more recently. To provide a low-cost diagnostic method that can be used to inform treatment plans for stranded animals and in future epidemiologic studies, the SarcoFlour indirect fluorescent antibody test (IFAT) was developed and validated at UC Davis originally for horses, and we aim to validate it for use in California sea lions to benefit wildlife. Our hypothesis is that the IFAT test performance in serum correlates with the gold-standard testing approach of using histopathology and molecular sequencing for detection of Sarcocystis neurona infections in California sea lions. Current aims involve the identification of at least 120 case and control sea lions from The Marine Mammal Center biobank in Sausalito, CA so that gold standard results can be compared to IFAT serology results run at UC Davis for test validation purposes. If Kappa statistical comparison of both testing methods is good, then the SarcoFluor IFAT can be used as an important diagnostic tool for ante- and post-mortem disease investigations.
Research Grant	One Health Institute and The Marine Mammal Center support
Field of Research	Epidemiology

Abstract Title	CORNEAL LESIONS: COMPARING FEATURES SEEN ON ULTRASOUND BIOMICROSCOPY AND HISTOPATHOLOGY
Authors	Vienna Lunking*, Danielle Meritet, Brian Gilger, Annie Oh
Affiliations	Department of Clinical Sciences, NC State CVM, Raleigh, NC.
Abstract	Ultrasound biomicroscopy (UBM) uses high frequency ultrasound to conduct detailed, non-invasive imaging of the cornea and anterior segment. Ophthalmic pathologies affect the echogenicity and appearance of the scan, though the precise changes are unknown. Therefore, the purpose of this study was to compare the characteristics of corneal and anterior segment lesions on UBM to histopathology. We hypothesized that pathological processes which add to cellularity or structural disorder–such as increases in white blood cells, fibrin, or edema–result in hyperechogenicity; fluids relatively low in cells, like aqueous humor, appear dark. Enucleated eyes from 18 canine and equine patients with various corneal pathologies were included in the study, along with two controls. Longitudinal UBM scans in line with the observed lesion were taken dorsally, axially, and ventrally; a histopathology slide of the same cross-section was prepared. Images were compared. Our results support our hypothesis, with inflammatory processes causing increased hyperechogenicity seen in all affected layers of the cornea. Neovascularization could often be identified as hyperechoic areas within the stroma dotted with hypoechoic vessel lumens. Corneal hemorrhage and hyphema presented with increased brightness, likely due to the presence of inflammatory cells. While areas of pathology were identifiable on UBM, different types of cellular infiltrates were not distinguishable. Borders between separate disease features apparent on histopathology were not necessarily seen on UBM if abutted tissues shared similar reflectivity. When used in conjunction with a thorough ophthalmic exam, UBM is a clinically relevant tool for localizing and identifying corneal diseases.
Research Grant	NONE
Field of Research	Ophthalmology

Abstract Title	Energy Dispersive Spectroscopy (EDS) to Evaluate the Forage Quality: An Elk Case Study
Authors	Savannah Lynch, LaRoy S.E. Brandt, Stan C. Kunigelis, Tanner Denton
Affiliations	Lincoln Memorial University College of Veterinary Medicine (Lynch), Lincoln Memorial University School of Mathematics and Science, Department of Biology (Brandt), Lincoln Memorial University, Debusk College of Osteopathic Medicine (Kunigelis), Lincoln Memorial University School of Mathematics and Science (Denton)
Abstract	Often, it may be necessary to supplement the diets of managed wildlife to ensure proper nutritional diets. However, if a population show signs of malnutrition, it may not always be apparent as to what steps may need to be taken. With this in mind, we were asked to conduct a low-cost evaluation of the nutritional quality of the elk forage on a reclaimed, mountaintop removal, coal mining site in SE Kentucky where a population of elk had been re-established. As some elk on site were reported to show symptoms of mineral deficiency and some others had died, we utilized Energy Dispersive Spectroscopy (EDS) to determine the micronutrient and heavy metal composition of elk forage from 3 sources: 1) root tissue samples from grasses and forbs that had been recently foraged by elk in four locations and one offsite location not foraged by elk, 2) gut contents and fecal material from a recently deceased elk, and 3) hair and hoof from the recently deceased elk. From our analysis, we were able to determine some variation in nutritional quality within foraged plants for various trace elements and heavy metals including As, Ca, Cu, Hg, Mg, Mn, Mo, Na, and Zn. Of these elements Cu was nearly non-existent and As levels were much higher than expected. Additionally, some samples contained unexpectedly high levels of Se. As an initial study, our results suggest that wildlife managers might choose EDS as a lower cost alternative to other nutritional analyses prior to making decisions about diet supplementation for wildlife.
Research Grant	None
Field of Research	Wildlife Conservation

Abstract Title	Mapping the male and female rhesus monkey by CT: sexual dimorphism and aging-related pathology
Authors	Jessica Lynch, John Olson, George Schaaf, Brendan Johnson, J. Mark Cline
Affiliations	College of Veterinary Medicine, University of Tennessee, Knoxville TN (Lynch); Department of Pathology, Section on Comparative Medicine, Wake Forest University School of Medicine, Winston-Salem NC (Lynch, Olson, Schaaf, Johnson, Cline)
Abstract	The NIH expects that researchers will include sex as a biological variable when designing and reporting vertebrate animal studies. Implications of sexual dimorphic characteristics in research are not fully known, but are important in developing translational studies and increasing the rigor and reproducibility of experimental design. To date, there are few studies describing the secondary sex characteristics of male and female rhesus monkeys (Macaca mulatta). A few useful anatomical references for this species exist, but no computed tomography (CT) atlas is currently available. The creation of an atlas will allow for visualization of anatomic structures with important clinical and research implications. Documenting common aging pathologies will provide examples of age-associated lesions that might appear frequently on clinical CT scans. This study analyzed CT scans from 58 rhesus macaques, including 11 females and 47 males. Age at most recent evaluated scan ranged from 8.2 to 24.6 years. Axial, coronal and sagittal planes were assessed for each monkey. Any common pathologies associated with aging were documented. Relevant clinical history and pathology reports were compared to CT findings for each animal. So far, CT scans from 49 animals have been evaluated. Preliminary data shows the most common aging pathologies to be spondylosis deformans, osteoarthritis, and colonic diverticulosis, documented in 59%, 49%, and 45% of the cohort respectively. Sexual dimorphisms currently documented are laryngeal air sac size and craniofacial structure, with others pending. The full body CT atlas for both the male and female rhesus is in progress; select images have been labeled with relevant vasculature and anatomical structures.
Research Grant	U19AI067789, U01AI150578
Field of Research	Anatomy

Abstract Title	Linked resistance between arachidonic acid and vancomycin in Staphylococcus aureus
Authors	M.Y. MacIntyre, A.R. Stackhouse, W.N. Beavers
Affiliations	Department of Pathobiological Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	Staphylococcus aureus is a Gram-positive pathogen that causes over 900,000 infections every year. It can infect every niche of the host and colonizes about two-thirds of the human population. The increasing number of antibiotic resistant strains of S. aureus, such as methicillin resistant S. aureus (MRSA), demonstrates the need for new therapeutic targets. Polyunsaturated fatty acids are antimicrobial fatty acids susceptible to oxidation. Arachidonic acid (AA) is a type of polyunsaturated fatty acid that is used in the host immune response for inflammatory signaling. However, our studies showed it can also undergo autoxidation to produce electrophiles toxic to S. aureus. An important observation related to AA is that modifications to cell wall biosynthesis induce AA resistance. These strains are also resistant to vancomycin, a drug of last resort that targets cell wall biosynthesis and is used to treat severe MRSA cases. S. aureus resistance to vancomycin is mediated by the VraRS two-component system. We tested the hypothesis that S. aureus resistance to AA and vancomycin are both mediated through VraRS signaling. Our data revealed that mutant strains with inactive vraR and vraS genes are completely susceptible to vancomycin treatment, while strains with inactive tarO, sgtB, or lcpB (vraS) genes are resistant to vancomycin. The lcpB (vraS) resistance phenotype is likely caused by a single nucleotide polymorphism that constitutively activates VraS. The link between AA and vancomycin resistance will be further investigated to determine if inhibiting VraRS signaling can be used to counter S. aureus's resistance to AA and vancomycin.
Research Grant	K22 AI53677
Field of Research	Bacteriology

Abstract Title	Balancing the equine hindlimb digit using external landmarks: a new standard for equine podiatry
Authors	Peyton Mackey, Ben Nabors
Affiliations	Department of Pathobiology and Population Medicine, Mississippi State University College of Veterinary Medicine, Starkville, MS
Abstract	Lameness accounts for up to $1 billion in economic loss for the horse industry annually [1]. Podiatry is an important method for achieving a functional foot and preventing lameness [2], with most of the healthy foot function revolving around the hoof and the distal interphalangeal joint [3]. Podiatry helps to restore balance, embracing "both shape and function of the foot in relation to the ground, as well as to skeletal structures of the digit, both at rest and at exercise" [4]. Recognizing issues with digital balance would be instructive in dictating the required treatment, or podiatry work, needed [5]. However, to this day, the main principle for podiatry revolves around hoof capsule symmetry and dorsal hoof-pastern axis [6], which would be less important because the dorsal hoof angle does not correlate with digital alignment [2]. If external landmarks can be used to determine alignment of the phalanges, then there will be less reliance on radiographs and less disease associated with lameness, leading to less economic loss. This study aims to establish grossly visible landmarks to determine the digital alignment to the ground compared to the hoof wall angle to the ground. While the idea of using the width of the proximal phalanx to draw an imaginary line has been talked about [2], to our knowledge it has not been executed. We completed three phases within our study, comparing photographs to radiographs of pre trimmed, trimmed, and shod digits. We found with a MANOVA Pillai's trace test that there is a significant difference (p=0.00000165) between the hoof wall angle and the digital angle with an alpha value of 0.001. Our partial Eta2 value was 0.81, which tells us that our angle does influence different measurements.
Research Grant	Mississippi State University College of Veterinary Medicine
Field of Research	Equine Medicine and Surgery

Abstract Title	Analyzing mouse preferences in environmental enrichment using behavioral and physiological parameters
Authors	Mollie Madigan, Frank Leitgeb, Aidan Horvath, Debra Hickman
Affiliations	Department of Laboratory Animal Science, College of Veterinary Medicine, Purdue University, West Lafayette, IN
Abstract	It is well-known that animals in laboratory facilities require environmental enrichment to allow them to display their natural behaviors. Examples of environmental enrichment include, but are not limited to, toys, nesting materials, gnawing materials, food and treats, and additional shelters. However, when given enrichment, it is unknown whether mice actually benefit from a specific enrichment, or if they have a preference as to the specific type of enrichment they receive. To see whether mice do indeed have a preference in their enrichment, several types of commercially available enrichment were placed in cages with singly housed C57BL/6 mice. After a few days of acclimation, acute behavioral trials and physiological analyses were conducted to see how the mice reacted to their enrichment. Later, chronic behavioral trials and physiological analyses were conducted to measure long-term effects of whether the provided environmental enrichment benefited the mice. Using the results from the behavioral trials and blood samples, we will observe the behavioral markers of evident stress along with analyzing the white blood cell counts for evidence of stress. This will allow visualization of any benefits from certain types of enrichment, allowing researchers to purchase that enrichment over others in the future.
Research Grant	None
Field of Research	Animal Welfare

Abstract Title	Engineering retroviruses for targeted cancer therapies
Authors	Maryann Makosiej, Ellen Xu, Michael Birnbaum
Affiliations	Cummings School of Veterinary Medicine, Tufts University, North Grafton, MA, (Makosiej) Department of Biological Engineering, Massachusetts Institute of Technology, Cambridge, MA (Xu, Birnbaum), Koch Institute for Integrative Cancer Research, Cambridge, MA (Xu, Birnbaum)
Abstract	Advancements in veterinary and human immunotherapy have revolutionized the way that cancers are detected by the mammalian body and fought off. As mammals, humans and animals are frequently diagnosed with cancer and may utilize many of the same oncologic and immunotherapy treatments. In some cases, genetically engineering T cells by introducing synthetic receptors may markedly improve how the immune system recognizes and can respond to cancer. In contrast, our lab introduces a variety of function-enhancing genes to boost an anti-tumor response through the use of retroviral vectors. Retroviruses are a class of virus that work by permanently integrating a gene of interest into the host cells' genome. Historically, the viral vectors used to produce engineered T cells exhibit broad tropism. Our lab, however, engineers retroviruses to specifically target antigen-specific T cell subsets, which allow therapeutic genes to be delivered to unique subsets within polyclonal populations. In this project, we explore the delivery and efficacy of different therapeutic cargoes in a murine model of melanoma via targeted murine gamma retrovirus vectors. We hypothesize that a range of therapuetic cargoes could be delivered with our targeted retroviruses to elicit specific T cell phenotypes that are beneficial in the setting of melanoma. These results could be translated to provide a more specific way to treat mammalian cancer.
Research Grant	Damon Runyon-Rachleff Innovation Award
Field of Research	Immunology

Abstract Title	Development of a liposomal amphotericin B induced lameness model in goats (Capra aegagrus hircus)
Authors	Grace Malla, Jessica Garcia, Denae LoBato, Pierre-Yves Mulon, and Joseph Smith
Affiliations	Department of Large Animal Clinical Sciences (Malla, Garcia, Mulon, Smith) and Department of Biomedical and Diagnostic Sciences (LoBato), University of Tennessee College of Veterinary Medicine, Knoxville, TN
Abstract	The goat industry has experienced a steady rise in popularity in recent years, and as such, knowledge of caprine lameness behaviors is essential for animal welfare. Induced lameness models exist using the antifungal Amphotericin B, however, these are typically shorter duration. The goal of this study was to assess lameness behaviors in goats free of lameness and then again after inducing lameness through an intraarticular injection of liposomal Amphotericin B. Ten healthy 6-month-old Kiko-cross goats were used. The goats' pre-induction gait and baseline physiological characteristics were evaluated using tri-axial accelerometry, pedometers, and visual lameness scoring, as well as cortisol and fibrinogen blood analysis. A brief synovitis was induced through an intraarticular injection of liposomal Amphotericin B to the right rear lateral distal interphalangeal joint. The goats' lameness responses were assessed with the same implements at intervals of 6, 12, 24, 48, 72, and 96-hours post-injection. At the time of abstract submission, 5 goats had lameness induced. A statistically significant difference (P = 0.0129) was found for pre-induction and post induction pedometer results (8628 ± 2779 steps pre vs 2315 ± 1809 steps day 1 post induction). No changes in lameness scores were observed between pre-induction and day 1-post. No statistically significant changes were noted in 24hr mean or sum results of the tri-axial accelerometer findings. Blood analysis is pending. While step counts were significantly reduced, more analysis will be necessary for interpretation of tri-axial accelerometry data. Due to the sustained release nature of liposomal Amphotericin B, it may not be as effective as the regular formulation in this model.
Research Grant	University of Tennessee College of Veterinary Medicine USDA Seed Grant
Field of Research	Production Animal Medicine

Abstract Title	Detection and molecular characterization of adenoviruses in captive and free-roaming African green monkeys (Ch
Authors	Diana M. Mancuso, Kerry Gainor, Kerry M. Dore, Christa A. Gallagher, Katalina Cruz, Amy Beierschmitt, Souvik Ghosh
Affiliations	Ross University School of Veterinary Medicine, St. Kitts and Nevis (Mancuso, Gainor, Dore, Gallagher, Cruz, Beierschmitt, Ghosh) CABI/GEF/UNEP project, Ministry of Environment, St. Kitts and Nevis (Dore) Behavioral Science Foundation, St. Kitts and Nevis (Beierschmitt)
Abstract	Although simian adenoviruses (SAdVs, genus Mastadenovirus) have been reported in a variety of monkey species, there is a lack of information regarding adenoviruses (AdVs) in African Green Monkeys (AGMs). In the present study, 31 samples (12 fecals, 9 nasal and 10 rectal swabs) from 28/92 (30.43%, 10 captive and 18 free-roaming AGMs) apparently healthy AGMs in the Caribbean Island of St. Kitts tested positive for AdVs by DNA-dependent DNA polymerase (pol)-, or hexon- based screening PCR assays. Based on partial Pol and hexon sequences, at least two genetic variants of AdVs were identified, and a representative viral strain from each genetic variant/group, group I (strain KNA-08975) and group II (strain KNA-S6), were chosen for molecular characterization of the nearly complete putative Pol, complete hexon, and partial penton base sequences. The group I AdV strains were closely related to SAdV-F/SAdV-18 in both the Pol and hexon, while the group II viruses possessed a SAdV-F/SAdV-18-like Pol, and a human AdV-F(HAdV-F)/HAdV-40-like hexon. The molecular characterization of group II AGM AdVs indicated possible recombination and cross-species transmission events between AGMs and humans. The small Island of St. Kitts is home to a large population of AGMs which frequently stray into human habitats, further supporting the possibility of cross-species transmission. Based on these observations, it is hypothesized that the evolutionary pathways of SAdVs and HAdVs are intermingled, complicated by interspecies transmission and recombination events between AdVs from related host species. This One-Health-based study emphasizes the zoonotic and anthroponotic potential of AdVs, with implications on public health and animal health.
Research Grant	CABI/GEF/UNEP project – 'Preventing the COSTS of Invasive Alien Species in Barbados and OECS Countries' and One Health Center for Zoonoses and Tropical Veterinary Medicine, RUSVM, St. Kitts and Nevis.
Field of Research	Virology

Abstract Title	Prospective observational assessment of water use in a large animal teaching hospital
Authors	Gabrielle Maroulis, Nathaniel Kapaldo
Affiliations	Department of Clinical Sciences (Maroulis, Kapaldo), College of Veterinary Medicine, and the Pollution Prevention Institute (Maroulis), Kansas State University, Manhattan, Kansas
Abstract	Water use in healthcare facilities comprise approximately 7% of total water use in the U.S. commercial sector, accounting for up to 350 gallons per hospital bed per day. There is a paucity of data surrounding this topic in veterinary medicine. Large animal hospitals require frequent use of water for proper sanitation of patient-occupied areas (e.g., stalls, trafficked walkways, cattle-chutes). We hypothesized large animal teaching hospital (LATH) water use, for sanitation purposes only (i.e., hoses and sinks), would comprise more than 10% of the total water entering the building complex encompassing the LATH. Additionally, water use would trend positively with the number of patients seen. A commercially available flow meter was installed on seventy-three hoses and twenty-one faucets in the LATH. The volume of water (gallons/day) consumed each day was monitored a single time and is currently ongoing. Total water volume measured over the course of this investigation (17 days) totaled 39,037 gallons, costing $467. Patient areas were responsible for 79.5% of water measured, accounting for 221 gal/patient/day, costing $2.65 patient/day. Perioperative and operating rooms accounted for 3.0% of water use with an average of 105 gallons/patient/operation, costing $1.25/operation. The LATH water use comprised 15.1% of the building complex's water. These numbers are expected to change as data collection continues. These observations provide objective data on water use for a single LATH. Further investigation on how this data may be harnessed for water conservation strategies, benefiting environmental and financial goals is warranted.
Research Grant	SMM EPA-R7-LCRD-2021 and P2 EPA-HQ-OPPT-2022-001
Field of Research	One Health

Abstract Title	Assessing systemic glucose transport in skeletal muscle of chickens
Authors	Margaret Marsh, Hannah Cavanaugh, Hayley Rejcek, Trinity McMahon, Carson L. Wright, João Brandão, Joshua T. Butcher
Affiliations	Department of Physiological Sciences (Marsh, Cavanaugh, McMahon, Wright, Butcher) and Department of Veterinary Clinical Sciences (Rejcek, Brandão) College of Veterinary Medicine, Oklahoma State University, Stillwater OK
Abstract	Skeletal muscle is the largest glucose sink in most animals, including chickens, with glucose transporters (GLUTs) playing key roles in facilitating diffusion of glucose across cell membranes. Chickens possess notable differences in glucose homeostasis compared to classic mammalian physiology, namely they lack GLUT4 (the primarily insulin-dependent GLUT), are resistant to the action of insulin, and have unusually high plasma glucose. Key questions remain regarding how glucose uptake occurs within skeletal muscle and if the overall distribution of GLUTs are altered within various skeletal muscles. The goal of our project is to identify which GLUT transporters are present (e.g. GLUT1, 2, 3, 5, 8, 9, 12) and assess their distribution in 3 different muscle beds: the cardiac muscle, the pectoralis muscle, and the iliotibialis muscle using qRT-PCR. Initial results in broilers show significant elevations ($p < 0.05$) in insulin-independent GLUT1, 3, and insulin-dependent GLUT8 compared to the heart, particularly in the iliotibialis muscle. Analysis is ongoing and will include expression of other relevant factors involved in glucose transport, including the insulin receptor, insulin-like growth factor-binding protein 1, PGC1□, glucagon, and glucose 6-phosphatase. Further, we intend to determine the comparative expression of the aforementioned indices in layers, typically used for egg laying. Taken together, this study has the potential to inform on glucose homeostasis in the avian species and has implications for overall dietary and nutrition schema in chickens.
Research Grant	NIA K01 AG064121, OCAST HR21-045-1, and the Debbie and Wayne Bell Professorship
Field of Research	Physiology

Abstract Title	Analysis of Piroplasmids in Ectoparasites of snakes in the Peruvian Amazon
Authors	Alexander Marsh, Taylor Mortensen, and Roger Ramirez-Barrios
Affiliations	Virginia-Maryland College of Veterinary Medicine
Abstract	The Amazon Basin has the richest biodiversity on the planet. However, deforestation and habitat degradation jeopardize much of the biodiversity in the area. With rises in native and domestic fauna interactions, there is an increased risk for transmission of diseases through wildlife reservoirs. Snakes are an important, yet understudied, group of pathogenic reservoirs due to their many different life history traits, their presence in anthropogenic environments, and their ability to harbor a range of parasites. However, little is known about snakes' potential as Piroplasmid reservoirs to domestic animals and humans in lowland Amazonia through tick vectors. A total of 26 snake species were found in the Peruvian Amazon. Ectoparasites were collected from 7 species in the Peruvian Amazon and speciated through PCR and Sanger Sequencing. DNA samples were analyzed for Piroplasmids using the same methods with different PCR primers. We hypothesized that we would find different species of ticks and mites on varying species of snakes and the ticks will be positive for Piroplasmid DNA. The discoveries from this study will provide novel insight on snakes as important parasite reservoirs and gives information about ticks as disease vectors in the increasingly anthropogenic Peruvian Amazon.
Research Grant	Summer Veterinary Student Research Program at VMRCVM
Field of Research	Parasitology

Abstract Title	Naproxen exposure during early development inhibits cranial chondrogenesis in axolotl embryos
Authors	Emma J. Marshall and Crystal D. Rogers
Affiliations	Department of Anatomy, Physiology, and Cell Biology, School of Veterinary Medicine, University of California, Davis, Davis, CA
Abstract	Naproxen (NPX) is a non-steroidal anti-inflammatory drug (NSAID) commonly used to alleviate pain and inflammation via inhibition of the cyclooxygenase (COX1/2) enzymes. Embryonic exposures to NSAIDs are linked to preterm birth, neural tube closure defects, abnormal enteric innervation, and craniofacial malformations. Each of these anomalies may be caused by abnormal neural crest cell (NCC) development. NCCs are embryonic stem cells that differentiate into diverse adult tissues including craniofacial cartilage and bone and neurons of the peripheral and enteric nervous systems. Our lab has identified that COX1 and COX2 transcripts are expressed during the early stages of vertebrate embryonic development, and that targeted knockdown of COX2 and its receptor, EP3, leads to aberrant NCC maturation in vertebrate embryos. To investigate the phenotypic and molecular effects of NSAID exposure on craniofacial development, we exposed axolotl embryos to various concentrations of NPX during NCC migration and differentiation stages and then performed immunohistochemistry (IHC) for markers of NC-derived cells. We identified that NPX-exposed embryos exhibit molecular and gross anatomic changes by tadpole stages. Specifically, NPX-exposed embryos have reduced migration of SOX9-positive NCCs resulting in abnormal spatial localization of cells secreting type II collagen (Col2a) and anomalous craniofacial cartilage structures. NPX exposure also disrupts normal expression and patterning in putative lateral line sensory system precursor cells. Future work will define the specific COX signaling pathway effectors involved in normal NCC development and formation of craniofacial bone and cartilage.
Research Grant	NSF 2143217
Field of Research	Pharmacology and Toxicology

Abstract Title	Development of a screening test for ESBL-producing Enterobacterales in canine feces for fecal transplants
Authors	Kira Martin, Bruna C. Lopes, Shannara Welch, Jing Wu, Rachel Pilla, Jan S. Suchodolski, and Sara D. Lawhon
Affiliations	Department of Veterinary Pathobiology (Martin, Lawhon), Department of Small Animal Clinical Sciences (Lopes, Pilla, Suchodolski), and Veterinary Medical Teaching Hospital (Welch, Wu), School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX
Abstract	Fecal transplantation is a therapeutic treatment used to restore healthy microbiota in the diseased gastrointestinal system of canine patients. Transplanting normal gut microbiota carries the risk of transferring antimicrobial-resistant bacteria to the recipient animal, which, albeit rare, can cause serious, life-threatening disease. We determined the limits of detection for a method for screening canine feces for extended spectrum beta lactamase (ESBL)-producing Enterobacterales (ESBLs) using a commercially available chromogenic agar. Growth of ESBL-positive (ESBL+) Escherichia coli or Klebsiella pneumoniae on nonselective and selective media was compared. Both bacteria grew better on chromogenic agar without antibiotics than on blood agar. Canine fecal samples that tested negative for ESBLs were inoculated with a 10-fold dilution series of either ESBL+ E. coli or K. pneumoniae, and individually inoculated onto plates with and without antibiotics selective for ESBLs. The limit of detection for E. coli was 74 colony forming units per gram of feces (CFU/g). The limit of detection for K. pneumoniae was 26 CFU/g. Blinded experiments were performed to evaluate the accuracy of the method at high, medium, and low concentrations of each organism, approximately 50,000, 5,000, and 500 CFU/g respectively with a negative control of 0 CFU/g. ESBL+ E. coli was detected with a 60% accuracy at low concentrations, while its high and medium concentrations and all concentrations of K. pneumoniae tested positive with 100% accuracy. The ability of the chromogenic agar to accurately detect ESBLs confirms the need to link the prevalence of ESBLs within healthy donor feces, as it could be a potential screening tool for fecal transplants.
Research Grant	Additional support for this project was provided by the Texas A&M University Gastrointestinal Laboratory, the Purina Petcare Research Excellence Fund, and departmental funds.
Field of Research	Antimicrobial Resistance

Abstract Title	Evaluating the bleeding effects of specific clopidogrel metabolites
Authors	Vanessa L. Martinez 1,2 , Afolashade Onunkun 2 , Barbara D. Christian 2 , and D. Adam Lauver 2
Affiliations	1Biomedical Research for University Students in Health Sciences (BRUSH),College of Veterinary Medicine, Michigan State University, East Lansing, MI USA 2Department of Pharmacology and Toxicology, Michigan State University, East Lansing, MI USA
Abstract	Clopidogrel is an antiplatelet medication prescribed for prevention of heart attack or stroke in patients with acute coronary syndrome (ACS). A common heart disease, ACS affects millions of people in the United States each year. Acute coronary syndrome involves pathological formation of blood clots, also known as thrombosis, in the coronary or cerebral arteries. Occlusive clot formation results in compromised blood flow and inadequate oxygen delivery to body cells. Clopidogrel, a purinergic P2Y12 receptor antagonist, inhibits induction of adenosine diphosphate (ADP) platelet aggregation and has been demonstrated to be effective in inhibiting thrombosis. However, clinical studies have demonstrated that long-term use of clopidogrel generates a high risk of bleeding. Recent research from our laboratory suggested that non-platelet mechanisms are responsible for unfavorable bleeding events. We hypothesized that specific clopidogrel metabolites directly disrupt the normal hemostatic balance through platelet-independent mechanisms. To test this hypothesis and to assess platelet-independent effects, we evaluated the effects of clopidogrel metabolites on platelet function and bleeding in P2Y12 -deficient mice. Both P2Y12 knockout mice and their wild type littermates were treated orally with either clopidogrel or one of its metabolites (M1,M2, or M15) for five days. Blood samples were collected, and platelet function was evaluated by flow cytometry. Bleeding effects were evaluated via tail bleeding assay. Results suggest that clopidogrel metabolite M 15 possesses non-platelet effects. Together with our previous work, findings demonstrate that specific clopidogrel metabolites may impair vasoconstriction and potentiate bleeding.
Research Grant	National Heart, Lung and Blood Institute (NHLBI) grant R25HL103156
Field of Research	Pharmacology and Toxicology

Abstract Title	Vitrification of Different Volumes of Canine Epididymal Spermatozoa in Semen Straws: Effects on Cryosurvival
Authors	Jamia Mason, Onesimus Nderi, and Gemechu Wirtu
Affiliations	Department of Biomedical Science, College of Veterinary Medicine, Tuskegee University, Tuskegee, Alabama (Mason, Wirtu) and Animal Science Department, Chuka University, Kenya (Nderi)
Abstract	Vitrification, a method of cryopreservation, has advantages over conventional slow freezing including the reduction of intracellular ice crystallization. In our previous study (Mason et al, NVSS 2022), the cryosurvival of canine spermatozoa was better when vitrification pellet size was larger (~10µl vs ~20µl). The present study examined the effects of packaging different volumes in semen straws on the post-thaw cryosurvival. Sperm samples were extracted from cauda epididymis of dogs using PBS, centrifuged, and transferred to an extender containing 20% egg yolk. In Experiment 1, we tested 4 treatments: 20µl, 60µl, 100µl, and 140µl. In Experiment 2, because of improved sperm parameters in the 60µl of experiment 1, more refined volumes of 30µl, 40µl, 50µl, 60µl, and 70µl were evaluated. Resuspend samples were cooled to 4 degrees for 2 hrs, specific volumes were loaded into 0.25 ml straws which were then sealed and placed in 0.5 ml straws. The samples were vitrified by directly plunging the straws in liquid nitrogen. We tested eight testes per experiment. Post-thaw total motility (TM) and total progressive motility (TPM) were evaluated by computer-assisted sperm analysis and data analyzed using one-way ANOVA. In experiment 1, the highest post-thaw motilities were observed in the 60µl with a moderate treatment effect (P=0.07). In experiment 2, volume had little effect on the post-thaw parameters (P>0.7). Our observations indicate that vitrification of spermatozoa in 0.25 ml straws in volumes greater than 30µl supports better post-thaw motility than vitrification in smaller pellets. This counteracts the dogma that vitrification of cells in the smallest volumes supports better cryosurvival.
Research Grant	NIH T35OD010432
Field of Research	Physiology

Abstract Title	Interaction of emodepside with canine MDR1: in silico and cellular assays
Authors	Erin J. Mayhue, Theresa A. Quintana, Greta N. Karwath, Stephanie E. Martinez, Matthew T. Brewer, Jeba R.J. Jesudoss Chelladurai
Affiliations	Department of Diagnostic Medicine/Pathobiology, CVM, Kansas State University, Manhattan, KS (Mayhue, Quintana, and Jesudoss Chelladurai) Department of Anatomy and Physiology, CVM, Kansas State University, Manhattan, KS (Karwath and Martinez) Department of Veterinary Pathology, CVM, Iowa State University, Ames, IA (Brewer)
Abstract	Emodepside is an FDA approved anthelmintic indicated for the treatment of gastrointestinal nematodes in cats. The feline product (Profender) has been used extralabel in dogs with resistant hookworm infection. There have been two reports of neurotoxicity in multidrug resistant 1 (MDR1) mutant dogs after receiving emodepside. We hypothesized that emodepside is transported by MDR1. We evaluated this hypothesis by using three types of assays: in silico, toxicological, and functional. For in silico evaluation, we used ModWeb, PathDock, and PLIP to determine the theoretical binding sites of emodepside on modeled canine MDR1 protein. Results showed that emodepside had multiple binding sites on the MDR1 protein. For both cytotoxicity and functional assays, two Madin-Darby canine kidney (MDCK) cell lines, one with MDR1 (wildtype, WT), one without MDR1 (knockout, KO), were grown to 95-100% confluency in 96 well plates. For the cytotoxicity assay, serial dilutions of emodepside were added to the cells and incubated at 37C with 5% CO2 for 1 week. Crystal violet was then added and absorbance was recorded using a plate reader (A570nm). Emodepside (10uM) did not cause cell death in WT and KO cells and no differences were observed in toxic effects between the two cell lines. For the functional assay, emodepside dilutions and a fluorescent dye (H33342) were added and incubated for 2 hours. Fluorescence was then recorded using a plate reader (Ex/Em 361nm/486nm). The IC50 of emodepside in the H33342 assay was ~2.8nM. These results indicate that emodepside is a substrate of canine MDR1. Therefore, MDR1 mutant dogs given extra label emodepside for resistant Ancylostoma caninum may be at risk of developing neurological side effects.
Research Grant	Kansas State University College of Veterinary Medicine- SUCCESS - FYI awarded to JJC and SEM 2022-2023
Field of Research	Pharmacology and Toxicology

Abstract Title	Effect of Competition Surface on Course Speed in American Kennel Club Agility Trials
Authors	Grace Mazzeo, Abigail B. Shoben, Nina R. Kieves, Kalyna S. Kulchytsky, Angela M. Szilvas, Arielle Pechette Markley
Affiliations	College of Veterinary Medicine (Mazzeo, Kulchytsky, Szilvas); Division of Biostatistics, College of Public Health (Shoben); Department of Veterinary Clinical Sciences, College of Veterinary Medicine (Kieves, Pechette Markley) The Ohio State University, Columbus, OH
Abstract	The sport of dog agility has grown in popularity with a 38% increase in entries to American Kennel Club (AKC) agility competitions in the past decade. Despite this rapid rise of popularity of the sport, few studies have assessed the effects of surface on speed, performance, safety, and injuries in agility dogs. The aim of this study was to analyze the effect of different agility competition surfaces on course speeds. An existing database contained information about all qualifying AKC agility runs from the past decade but did not include information about the surface. Therefore, from May 2023 to June 2023, 495 facilities were contacted by phone, email, or both. Interviews using a standardized form (Qualtrics) were completed with 90 locations (18%). Information collected included general category of surface (grass, dirt, mats, turf, other) and specific information about the surface (e.g., manufacturer, composition of mixture surfaces). Linear mixed models were then used to estimate differences in speed by surface category, accounting for correlation among runs from the same dog. Dog speeds were fastest on turf across all classes and dog heights. The differences in speed between turf and slower surfaces (sand, rubber matting, dirt, grass) differed by height. The effect of dirt and sand was larger for shorter dogs while the effect of grass and rubber matting was larger for taller dogs. These effects of surface on speed are likely due to the mechanical differences in the surfaces and are consistent with the findings in the human literature. The findings of this study suggest that future studies should consider dog height when planning biomechanical studies on the impact of surface on agility dog performance and injury.
Research Grant	None
Field of Research	Orthopedics

Abstract Title	Metabolic consequence of pesticide resistance in Rhipicephalus microplus
Authors	Miranda McClellan, Kayla Earls, Donald Thomas, and Kennan J. Oyen
Affiliations	Michigan State University College of Veterinary Medicine, East Lansing, MI (McClellan), United States Department of Agriculture, Agricultural Research Service (USDA-ARS), Animal Disease Research Unit (Earls and Oyen), USDA-ARS, Cattle Fever Tick Research Laboratory, Moore Air Base, Edinburg, TX (Thomas)
Abstract	Rhipicephalus microplus, or the southern cattle tick, has been eradicated in the United States since 1943. This tick species has cost the cattle industry billions of dollars because it is the main vector for the agents causing bovine babesiosis and bovine anaplasmosis. Bovine babesiosis can result in significant mortality in cattle populations with a range of clinical symptoms including: high fever, anemia, anorexia, ataxia, and lethargy. To control the R. microplus population, various acaricides have been used for decades, but excessive and continual use has led to resistance in several populations further complicating the control efforts globally. The mechanism allowing for this resistance is not well understood but has been attributed to a combination of point mutations and metabolic detoxification. To better understand the role metabolic detoxification has in pesticide resistance, we measured the metabolic rate of four strains of R. microplus eggs. Three of the strains are resistant to different combinations of acaricides while one is susceptible. Metabolic rate infers the energy requirement of the ticks which would indicate if there is an energy tradeoff allowing for resistance. We hypothesized that the different resistant strains would have a higher metabolic rate compared to the susceptible strain. To measure metabolic rate, a flow through respirometry system was used to collect carbon dioxide levels every second over the span of 24 hours. While the analysis of this data is ongoing, preliminary findings show that the susceptible strain had a higher metabolic rate compared to all three resistant strains. Further analysis is required to understand the impact of metabolic detoxification in acaricide resistance.
Research Grant	None
Field of Research	Production Animal Medicine

Abstract Title	Feeding Mice on Cage Floor Does Not Affect Feed Contamination
Authors	Michelle McCorkell, Amber Thompson, Wendy O. Williams, and Glenn Jackson
Affiliations	College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA (McCorkell); Center for Animal Resources and Education (CARE) at Cornell University, Ithaca, NY (Thompson, Williams, Jackson)
Abstract	The Guide for the Care and Use of Laboratory Animals states that animals should be fed uncontaminated diets free of urine and feces and feeders should allow unrestricted access to feed. This suggests that feed should not be placed directly on the cage floor. If feed must be provided on the cage floor for experimental or clinical purposes, guidance suggests that feed be placed in a container that acts as a barrier between the bedding and cage floor. In particular, laboratories that use rodents with cranial implants frequently opt to place feed in a bowl on the floor to limit hopper-associated injury and damage to the implant. In following the Guide by placing the feed in a bowl, husbandry staff have observed that pellets usually end up on the cage floor with bedding and feces accumulating in designated food dishes. Thirty-six heterozygous nude mice (Crl:NU-Foxn1nu) were individually housed and randomly assigned into 2 groups: 19 mice received feed in a metal bowl and 19 mice had pellets placed directly on the cage floor. Photos of the cages were obtained twice a day daily for 2 weeks and the photos were evaluated using a fecal contamination scoring method. This study aims to investigate the potential benefits of feeding mice in a designated food receptacle in comparison to feeding pellets directly on the floor. Based on our prior observations, we hypothesize that there will be no significant difference between contamination scores obtained for cages fed with pellets placed in a bowl versus cages with pellets placed directly on the floor. The results of this study will serve as guidance for feeding mice directly on the floor and provide supporting evidence to laboratory animal care accreditation bodies such as the AAALAC.
Research Grant	Center for Animal Resources and Education (CARE)
Field of Research	Laboratory Animal Medicine

Abstract Title	Disruption of Larp6-Collagen interaction in 5'SL mutant mice improves diastolic function in obese mice
Authors	Tara M. McDaid, Jacob J. Russell, Francisco I Ramirez-Perez, Makenzie Woodford, David A. Brenner, Vincent G. DeMarco, Luis Martinez-Lemus, Jaume Padilla, Bysani Chandrasekar, Shawn B. Bender
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Abstract	Obesity and hypertension cause cardiac diastolic dysfunction via mechanisms including metabolic dysfunction, fibrosis, inflammation, and microvascular dysfunction. The multifunctional ribonucleoprotein Larp6 (La Ribonucleoprotein 6, Translational Regulator) binds the 5' stem loop (SL) region of type I collagen mRNA, thereby increasing its half-life, translation, and deposition upon upregulation in disease states. Thus, we hypothesized that preventing Larp6 binding the 5'SL region of collagen mRNA would decrease the deposition of collagen and cardiac dysfunction in obese, hypertensive mice. Male 5'SL mutant and wild-type (WT) littermate mice were fed a high fat/high sucrose (HFHS) or control diet starting at 6 weeks old for 28 weeks. Echocardiography and histologic assessment of fibrosis were complemented with sequencing of RNA from the left ventricle. Staining will be done for capillary density, macrophage quantity, and other immune cell populations. Prevention of Larp6 binding collagen mRNA in 5'SL mutant mice blunted obesity-associated diastolic dysfunction independent of fibrosis in male mice. Ingenuity Pathway Analysis of differentially expressed genes in the hearts of obese vs lean WT mice predicted activation of diastolic pressure, dyslipidemia, and interferon signaling, while inhibiting D-glucose transport, carbohydrate metabolism, and angiogenesis. In obese mice, transcriptomic changes in the 5'SL mutant mice predicted increased development of endothelial tissue, decreased insulin resistance, quantity of CD4+ T lymphocytes, and mononuclear cells. Accordingly, these data suggest that changes in metabolism, inflammation, and vascular development may underlie the protective effect of the 5'SL mutation in obesity.
Research Grant	NHLBI R01 HL088105, R01 HL136386, R01 HL142770, NIDDKDK130243, SRCS (IK6BX004016), AND MERIT BX005845
Field of Research	Cardiology

Abstract Title	Fetlock Angle Variability With Early Exercise Intervention for Fracture Prevention
Authors	Colleen McDonnell, Melany Opolz, Griffin Sipes, Mariana E. Kersh, and Annette M. McCoy
Affiliations	Department of Clinical Medicine, College of Veterinary Medicine and Department of Mechanical Science and Engineering, Grainger College of Engineering, University of Illinois Urbana-Champaign
Abstract	Fractures in the equine distal limb are a common cause of morbidity and mortality in racehorses. There is a critical need to identify factors that can reduce the number of racing injuries and fatalities. Controlled exercise early in life could increase bone strength, potentially making bones more resistant to fracture, but the ideal exercise regimen is unknown. In silico musculoskeletal models can be used to help predict skeletal responses to exercise but require inputs from in vivo experiments. One such input is joint angles, which allow calculation of vectors of force exerted on the bones. The aim of this study was to determine how fetlock joint angles change over time and with exercise. Twelve foals were enrolled in the study at 8 weeks of age. Six were pasture raised under standard management conditions, while six underwent an 8-week exercise intervention consisting of 1600m trotting at 3.5m/s, 5 days a week. Motion capture videos were collected of age-matched exercised and non-exercised foals prior to the exercise protocol, at the mid-point, and at the end of the protocol. Videos were reviewed using DeepLabCut software and 21 anatomical markers were manually placed to train the software to recognize foal anatomy. Joint angles were measured within DeepLabCut after software training. Changes in joint angles over time will be compared between the exercised and non-exercised foals; foal joint angles will also be compared to adults. If joint angles change with age and exercise, then the forces exerted on bones are different between life stages and with exercise. This will allow us to conclude if it is necessary to input age- or activity-specific joint angles into an in silico musculoskeletal model.
Research Grant	Morris Animal Foundation D21EQ-004, Grayson Jockey Club Research Foundation, Inc.
Field of Research	Equine Medicine and Surgery

Abstract Title	Comparison of nasal viral shedding and disease severity in calves challenged with Bovine Respiratory Syncytial
Authors	Dalton McGeeney, Merrilee Thoresen, Cassandra Barber, Julia Mazanek, William B. Crosby, Santiago Cornejo, Carrie Vance, Florencia Meyer, Amelia R. Woolums
Affiliations	Dept. of Pathobiology and Population Medicine, College of Veterinary Medicine (McGeeney, Thoresen, Barber, Crosby, Cornejo, Woolums) and Dept. of Biochemistry, Molecular Biology, Entomology, and Plant Pathology, College of Agriculture and Life Sciences (Mazanek, Vance, Meyer) Mississippi State University, Mississippi State, MS
Abstract	We are investigating the use of Near Infrared Spectroscopy (NIRS) as a Bovine Respiratory Disease Complex (BRD) diagnostic tool. We have found the biofluids of cattle infected with Bovine Respiratory Syncytial Virus (BRSV) and M. haemolytica have consistently different NIRS spectra than biofluids of healthy cattle. Currently, we are exploring whether spectral differences are related to the viral load and severity of disease. A pilot study was conducted in which groups (n=3) of 6-month-old Holstein bull calves were nebulized with no BRSV, 5x10^3, 5x10^4, or 5x10^5 TCID50 units of BRSV to experimentally create a range of viral loads and disease severity among groups. BRSV F gene copy number was quantified in nasal swabs, collected daily, and tracheal wash samples, collected on day 7, using qPCR to delineate viral concentration. Daily clinical scores were calculated using a previously published scoring system. BRSV was detected on nasal swabs (days 6-8) in all three challenged groups and not the control group. Calves in the high dose group had greater total viral shedding, peak viral shedding, and number of positive samples as compared to other treatment groups, and clinical scores increased in the three challenged groups (days 4 – 8); however, viral shedding and clinical scores were not significantly different from day 0 ($P > 0.05$). On the day of peak virus shedding, clinical score was significantly correlated with BRSV F gene copy number ($P = 0.018$, $r2=0.69$). This challenge did not create a range of disease severity, but calves had a range of viral loads which were related to disease severity. This model will be useful to study the relationship between biofluid NIRS spectra, viral load, and disease severity.
Research Grant	United States Department of Agriculture Award #2022-67016-36978
Field of Research	Virology

Abstract Title	Comparing blood total IgE levels between mice carrying different gut microbiota in mouse model of HDM.
Authors	Maliyah McGowan, Ivon Moya-Uribe, Julia Bell, Susan Ewart, Linda Mansfield
Affiliations	Eastern Michigan University, Michigan State University Department of Food Safety and Toxicology and Large Animal Clinical Sciences
Abstract	Asthma is a chronic inflammatory and respiratory disease that is characterized by airway hyperresponsiveness (AHR) and associated with elevated immunoglobulin E (IgE) levels in the blood. Because it is one of the most common diseases worldwide and can have life threatening impacts, it is vital to find ways to lessen or prevent the side effects of asthma. One area that has been explored is the relationship of the gut microbiota and the risk of developing AHR and asthma. Studies show that gut microbiota influences immune development and can communicate with the lungs through the circulatory and lymphatic system. Metabolites produced by bacteria are absorbed into the bloodstream and travel to the lungs, altering the immune response to allergies and impacting AHR. C57BLACK6 strain mice carrying either humanized gut microbiota or a specific pathogen free microbiota (conventional mouse microbiota) were treated with house dust mite to induce airway allergic responses. To analyze the degree of AHR, three different doses of methacholine were utilized and to determine levels of IgE in the blood, and an ELISA was performed. Correlation tests were used to determine whether there is association between total IgE and airway hyperresponsiveness. I hypothesized the mice with humanized microbiota will exhibit higher levels of IgE and that these elevated levels will correlate with higher airway hyperresponsiveness.
Research Grant	NHLBI grant R25HL103156
Field of Research	Immunology

Abstract Title	Effect of seasonal pyric herbivory on muscid fly populations on cattle gazed in the Kansas Flint Hills
Authors	Megan E. McGraw, Andrea Salazar, Herman Griese, and Cassandra Olds
Affiliations	College of Veterinary Medicine (McGraw, Megan) and Department of Entomology (Salazar, Andrea; Griese, Herman; Olds, Cassandra), Kansas State University, Manhattan, KS.
Abstract	Horn flies, Hematobia irritans, and stable flies, Stomoxys calcitrans, are common blood-feeding ectoparasites that impact cattle health and wellbeing. Blood feeding can result in significant blood-loss, pain and irritation, known as fly worry, culminating in reduced production outputs. Historically, pyric herbivory or prescribed burning has been used for weed suppression, improving forage quality and pest arthropod control throughout the Midwest. Prescribed burning is traditionally preformed seasonally in either the spring, summer, or fall. While the season of burning seems to effect plant growth, little is known of the impact on pest arthropods. This study aims to determine if horn and stable fly populations are impacted by the season of which the burning is preformed. The Kansas State University Beef Stocker Unit is a 1,000 acre facility consisting of 16 pastures with each being assigned to one burn season. Pastures have been burned consistently in their designated season for the past four years and are stocked equally at 246 pound per acre. Starting two weeks after the cattle were released onto pasture, a long-range DSL camera was used to take photographs of different steers in each pasture for nine weeks. ImageJ software was used to manually count both H. irritans and S. calcitrans on each of the photographs over the study period. Preliminary data suggests that burn treatment in spring may impact horn fly populations. With this information, Kansan cattle producers can make a more informed decision on when to burn the fields to help with fly population control.
Research Grant	Elanco Animal Health
Field of Research	Parasitology

Abstract Title	Evaluating the Antibacterial Properties of Bovine Colostrum: The Impact of Postharvest Thermal Processing
Authors	Anna McKane, Trent Westhoff, Suzanne Klaessig, Craig Altier, Katherine Bell, Paulina D. Pavinski Bitar, and Sabine Mann
Affiliations	Department of Population Medicine and Diagnostic Services, College of Veterinary Medicine, Cornell University, Ithaca, NY
Abstract	Providing newborn calves enough high-quality colostrum is a critical calf-management strategy to support health and survival. Colostrum has abundant nutrients and bioactive factors that transfer passive immunity to the immunologically naïve calf. Unfortunately, colostrum may also serve as a fomite for disease when contaminated with pathogens. Thermal processing, including heat treatment (HT) and freezing (FR), are common strategies to manage the microbial load; however, these strategies decrease the concentration and activity of bioactive factors. We hypothesized that HT and freezing bovine colostrum will influence its direct antibacterial properties. Our objective was thus to compare growth of Escherichia coli (E. coli) in raw, HT and FR colostrum. Sterile colostrum was collected and divided into three aliquots. Aliquots were either raw (4°C for 20 h), HT (60°C for 60 min), or frozen (-20°C for 20 h). To simulate contamination that may occur on-farm, all samples were inoculated with one of two strains of E. coli (ECC-Z, associated with chronic mastitis or WM1 060913 P0lA, isolated from bovine feces) and incubated at 37°C in a bacterial kinetics assay. Different strains were selected to investigate the effect of bacterial origin on growth characteristics in colostrum. At 0, 2, 4, 6, 8, and 24h, growth of E. coli was quantified on MacConkey agar plates. Growth curves of each E. coli strain were determined and compared between treatment groups. Our study contributes to understanding the impact of thermal processing on antimicrobial properties of colostrum with the goal of helping to inform colostrum management strategies for dairy producers.
Research Grant	Unrestricted funds (Mann)
Field of Research	Bacteriology

Abstract Title	The association between early childhood pet and livestock ownership and the development of asthma & allergies
Authors	Lauren Wisnieski, Kayla C. Medlin
Affiliations	Lincoln Memorial University: Richard A. Gillespie CVM, Harrogate, TN
Abstract	This research is aimed at exploring the association between early childhood exposure to pets and livestock and the later development of allergies and asthma in a large longitudinal study. Using data from the National Children's Study, we assessed the development of allergies and asthma by 42 months of age (early childhood). Pets involved in this analysis include cats, dogs, small mammals, birds, fish, reptiles, and others. Livestock involved in this analysis include chickens, cows, ducks, geese, goats, guineafowl, hens, horses, mules, peafowl, pigs, pigeons, rabbits, roosters, sheep, turkeys, and others. Statistical analysis was performed in SPSS and a mixed logistic regression will be used for all multivariable analyses. We will include moderators such as indoor/outdoor status and pet sleep location. The first objective is to assess the association between pet ownership during early childhood and the development of asthma and allergies. The second objective is to assess the association between livestock ownership during early childhood and the development of asthma and allergies. The third objective is to assess how pet sleep location and indoor/outdoor status moderate the association between early childhood exposure to pets and the development of asthma and allergies. We expect our results to show a reduced risk of developing allergies and asthma when living in a home that owns pets/livestock. Additionally, we expect children that have an indoor pet and those that sleep in the room with a pet to have even greater protection from the development of allergies and asthma (especially those that share a bed with the pet). The data will be presented upon completion of statistical analysis.
Research Grant	None
Field of Research	One Health

Abstract Title	Combination immunotherapy for the treatment of adrenal tumors with organoid-primed T-cells and PD-1 blockade
Authors	Bryan J. Melvin (presenting author), Dipikaa Akshinthala (co-author), Weilin Li (co-author), Senthil K. Muthuswamy (PI/Mentor)
Affiliations	Laboratory of Cancer Biology and Genetics, National Cancer Institute, Bethesda, MD (Melvin, Akshinthala, Li, Muthuswamy), Comparative Biomedical Scientist Training Program, NIH, Bethesda, MD (Melvin), College of Veterinary Medicine, University of Georgia, Athens, GA (Melvin)
Abstract	Organoid-primed (opT) T-cells are patient-derived organoid (PDO) specific T-cells generated through co-culturing peripheral blood mononuclear cells (PBMCs) with tumor organoids. Programmed cell death protein 1 (PD-1) is a known checkpoint protein that prevents T-cell mediated killing of other cells when bound to its ligand, PD-L1. Previous studies in the Muthuswamy laboratory demonstrated that opT-cells alone could induce efficient tumor-specific killing activity, which, combined with checkpoint inhibition strategies, can synergistically improve tumor response in pancreatic ductal adenocarcinoma. Interventions of checkpoint inhibition are proving to be a promising area of research in cancer biology. The aims of this research are two-fold: to optimize tumor organoid/T-cell co-culture conditions in adrenal cancer, and to determine if combined treatment with PD-1 inhibitor could increase T-cell mediated killing.
Research Grant	National Cancer Institute, Intramural Research Program
Field of Research	Oncology

Abstract Title	Antigenic evaluation and proteomic profiling of excretory-secretory proteins of Sarcocystis neurona
Authors	Sharon Meoli, Annapoorani Jegatheesan, Vishnu Manikantan, Uma Aryal, Sriveny Dangoudoubiyam
Affiliations	Department of Comparative Pathobiology, College of Veterinary Medicine, Purdue University, West Lafayette, IN (Meoli, Jegatheesan, Manikantan, Dangoudoubiyam); Purdue Proteomics Facility, Purdue University, West Lafayette, IN (Aryal)
Abstract	Equine protozoal myeloencephalitis (EPM) is a rare, but economically devastating, degenerative neurological disease caused by Sarcocystis neurona, an intracellular protozoan. Despite high seroprevalence of S. neurona, very few horses develop EPM or present with broad neurological signs of weakness, ataxia, and neurogenic muscle atrophy. Akin to sister genera, S. neurona relies on discharge of excretory-secretory proteins (ESPs) from its apical organelles to invade the host cell and survive intracellularly. Investigation into S. neurona ESPs may reveal important virulence factors associated with EPM progression. Therefore, the aim of this study was to evaluate the antigenicity and generate a proteomic profile of S. neurona ESPs for future studies and development of additional diagnostic tests. Cell-culture derived live S. neurona underwent induced secretion and the ESPs were collected for analysis. Sera and cerebrospinal fluid from five horses of known EPM status were tested for antibodies to S. neurona ESPs by Western blot. Reactivity at two distinct molecular weight ranges was observed and amino acid sequencing is needed to establish the identity of these unknown proteins. Bottom-up proteomics of in-gel digested ESPs was performed via Mass Spectrometry and 92 S. neurona proteins were identified. 21 proteins were found to be from secretory organelles, 22 from other cellular locations, and the remaining are unstudied with unknown localization. Further optimization of sample preparation and data analysis is required for deeper characterization. Overall, this study has provided a glimpse into S. neurona ESPs and establishes a foundation for their use in future research aimed at developing new diagnostic tools for EPM.
Research Grant	Departmental Start-up Grant, Purdue University
Field of Research	Parasitology

Abstract Title	The immune response of Nile Tilapia vaccinated with novel diatom-based oral vaccines against francisellosis
Authors	Collin Meyer, Roshan Shrestha, Ruth Milston-Clements, Sarah Gibson, Taylor Heckman, Zeinab Yazdi, Esteban Soto
Affiliations	Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California, Davis, California (Meyer, Heckman, Yazdi, Soto) Phycovaxx LLC., San Diego, CA (Shrestha) Department of Microbiology, College of Science, Oregon State University, Corvallis, Oregon (Milston-Clements, Gibson)
Abstract	Piscine francisellosis is a highly infectious granulomatous disease caused by Francisella orientalis with a mortality rate up to 95% in tilapia (Oreochromis spp.). There are currently no approved antimicrobials for the treatment of this disease in food fish and no commercial vaccines exist. Recent work in our laboratories has explored injectable vaccination using diatoms as expression vectors of bacterial antigens; however, no oral vaccine trials have been performed in tilapia. Oral vaccines are strongly desired by aquaculturists as they eliminate the need to handle thousands of individuals for injection. We hypothesize that recombinant proteins consisting of IglC (F. orientalis antigen) and flagellin (potent bacterial immunostimulant) expressed in Thalassiosira pseudonana diatoms will act as a self-adjuvanting antigen delivery system to confer a protective immune response against F. orientalis infection in Nile Tilapia (O. niloticus) when administered orally. Fingerling tilapia (n=64 per group) were immunized and provided 0, 1, or 2 boosters over the course of 4 weeks. 30 days after the initial vaccination the fish were exposed to F. orientalis via immersion, then, after 24 hours, gill and internal organs were sampled from each group to assess IL-12, IL-10, IFNγ, and TGFβ gene expression using RT-qPCR. Mortality rates were monitored for 21 days after infection and bacterial load was assessed in survivors using qPCR. Findings indicate significant changes in expression of IFNγ and TGFβ in the immunized groups, but no change to the overall mortality rate in any treatment group. Although the novel delivery method shows promise, further research is needed to provide a safe and effective vaccine against this disease.
Research Grant	United States Department of Agriculture- Small Business Innovation Research
Field of Research	Production Animal Medicine

Abstract Title	Chronic cocaine and alcohol effects on blood biomarkers in Macaca mulatta as a model for polysubstance abuse
Authors	Isabella Michal, Paul Czoty, and Kylie Kavanagh
Affiliations	Wake Forest University School of Medicine, Winston-Salem, NC
Abstract	Cocaine use disorder (CUD) affects more than two million Americans and overdose reports have increased by 70% from 2017 to 2020. Increases in cocaine use means that the number of people with significant medical consequences from CUD will rise, making it public interest to understand the underlying toxicological mechanisms so that that therapies may be developed to mitigate and remediate long-term damage. Previous laboratory animal studies have investigated cocaine in isolation, but this is not an accurate reflection of the clinical picture since up to 90% of those with CUD also abuse alcohol. A cohort of eleven male rhesus monkeys (Macaca mulatta) that was developed to characterize the behavioral and neurobiological effects of chronic self-administration (SA) is the only existing non-human primate model of cocaine-alcohol polysubstance use (PSU). This study utilized serum biochemistry obtained from long-term clinical management of this model to gain information about longitudinal toxicological trends associated with cocaine-alcohol PSU. Additionally, blood-based biomarkers C-reactive protein, pro-collagen I c-terminal propeptide, lipopolysaccharide binding protein-1, plasminogen activator inhibitor-1, CD14 protein, and insulin were analyzed to detect damage to peripheral organ systems following ~7 years of drug administration. Serum biochemistry and blood-based biomarkers values were used to create composite health scores for comparison between monkeys which only SA cocaine with those that SA cocaine and alcohol. The results of this study are pending.
Research Grant	Clinical & Translational Science Institute Ignition Fund
Field of Research	Pharmacology and Toxicology

Abstract Title	Validation of methods used to interrogate the feline endometrium after eCG/pLH-induced ovarian stimulation
Authors	Alyssa I. Miguez, Rhasaan T. M. Bovell, Connor E. Owens, Elizabeth L. Buckles, Pierre Comizzoli and Ned J. Place
Affiliations	Department of Population Medicine & Diagnostic Sciences, CVM, Cornell University, Ithaca, NY (Miguez, Bovell, Owens, Buckles, Place) Smithsonian National Zoo & Conservation Biology Institute, Washington, DC (Bovell, Comizzoli)
Abstract	Assisted reproductive technologies that involve ovarian stimulation (ov stim) induced by exogenous gonadotropins are important tools for conserving endangered felids, but these protocols have had limited success in producing cubs. Exogenous gonadotropins induce supraphysiological levels of ovarian hormones and might induce changes in structure and gene expression in the uterine endometrium that hinder implantation. We are investigating the effects of ov stim on the felid endometrium using the domestic cat as a model. Our initial objective is to validate the methods that we will use to elucidate any potential aberrant effects of ov stim on the feline endometrium. We have used feline reproductive tracts donated by the local SPCA after routine spays. We opened one uterine horn lengthwise to expose and collect endometrial tissue via curettage for subsequent RNA extraction for RNA-sequencing and RT-qPCR. Absence of myometrial tissue was confirmed histologically. We confirmed the quantity and quality of the endometrial RNA and cDNA produced by our methods and are using the cDNA to validate PCR primer sets for 14 target genes that are known to affect implantation in other mammals. We formalin-fixed the proximal, mid, and distal regions of the contralateral horn to evaluate morphological structures, vascular remodeling, and immune cell populations. We have successfully validated our methods for collecting endometrial tissue devoid of myometrial contamination, designing primers for target genes, and preparing 3 uterine horn regions for histology. Collectively, this work facilitates the study in which we will compare the endometrial phenotypes of ov stim cats and cats induced to ovulate by cervical stimulation.
Research Grant	Cornell Feline Health Center (NJP); National Science Foundation Graduate Research Fellowship (RTMB)
Field of Research	Theriogenology

Abstract Title	Morphological evaluation of canine humeral symmetry
Authors	Ciara Miller, Alberto Gines, and Nimar Gill
Affiliations	Veterinary Clinical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	The contralateral limb serves a crucial role in surgical procedures, diagnoses of skeletal diseases, and postoperative assessment and rehabilitation. Existing studies on canine symmetry focus on analyzing specific regions or areas of the bone, but there are no studies that evaluate the whole bone morphology. New three-dimensional (3D) technologies allow the possibility of performing a more precise analysis. The purposes of this study were to describe differences in humeral bone morphology when contralateral limbs are used as a control and to evaluate potential differences between the proximal, middle, and distal parts of the humeri using advanced 3D analysis software. Bilateral humeral computed tomography scans of 11 mixed-breed dogs were performed, enabling the generation of 3D humeral bone models using bone segmentation software. Left and right humeri were superimposed for analysis of more than 200,000 points on each bone. This analysis revealed that proximal, middle, and distal thirds of the bone do not exhibit significant morphological differences ($p=0.2352$). Whole bone analysis illustrated a mean difference of roughly 0.3 millimeters at a given point. These findings demonstrate that bilateral humeral symmetry is present in dogs with non-orthopedic conditions.
Research Grant	LSU School of Veterinary Medicine
Field of Research	Orthopedics

Abstract Title	Whole Body Analysis of Joint Degeneration in the Fetlocks: A Case Study
Authors	Gwyneth P. Miller, Jean Luc Cornille, Ronda Hanning, Alexander K.K. Lee, Elizabeth W. Uhl, Michelle L. Osborn
Affiliations	Dept. Comparative Biomedical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge (Miller, Lee, Osborn) Science of Motion®, Eatonton, GA (Cornille) Field of Dreams Equestrian Center, LLC, Fort Wayne, IN (Hanning) Dept. Pathology, College of Veterinary Medicine, University of Georgia, Athens (Uhl)
Abstract	Lameness is the most common clinical sign in equine veterinary practice and is often associated with the degenerative tissue changes that define degenerative joint disease (DJD). While treatments based on whole body analysis and biomechanical therapies are increasingly common in humans with DJD, they are not routinely applied in equine cases. In this case study, a CT data-based, three-dimensional model of a horse was manipulated using Autodesk Maya® to compare the body positions of a competitive Grand Prix dressage horse with degenerative tissue changes of the hindlimb fetlock joints confirmed during a prepurchase exam. The analysis was performed by modeling positions depicted in photographs of the horse being worked before and after a change to the Science of Motion training approach. This allowed for the comparison of the whole-body working postures of the horse before, during, and after a whole-body exercise regime targeted at reducing the forces acting on the hindlimbs through the correction of spinal function. Angles of the limb joints and position of the head and vertebral column in the three positions were measured using Autodesk Maya® and compared. Our qualitative and quantitative results support a causal relationship between cervical compression and fetlock hyperextension. This case study serves as proof of concept for the feasibility and efficacy of modeling whole-body postures for the purpose of analyzing their relationship to aberrant forces and degenerative joint changes. It also confirms the effectiveness of motion-based therapies for the correction of joint compression.
Research Grant	LSU SVM Charles V. Cusimano Equine Health Studies Program
Field of Research	Anatomy

Abstract Title	Phenotypic resistance of enterococci obtained from feces to erythromycin and vancomycin after in-feed tylosin
Authors	Ivonne M. Miranda Martinez, Julio A. Mojica Perez, Madelyn Schwartz, Laura Neumann, Derek Foster, and Jennifer L. Halleran
Affiliations	Department of Population Health and Pathobiology, College of Veterinary Medicine, North Carolina State University, Raleigh, NC
Abstract	Tylosin is an antibiotic administered during the finishing period in steers to prevent liver abscesses. Subtherapeutic drug concentrations of tylosin in the gut may exert selective pressure on cattle microflora, promoting resistance to antibiotics of critical importance in human medicine. Our objective is to characterize phenotypic resistance of enterococci obtained from cattle feces against erythromycin and vancomycin after in-feed tylosin administration. We hypothesize that resistance to the antibiotics being tested will increase after tylosin administration but rebound back to baseline at the end of the study period. For this study, 6 steers were dosed once daily for three days with in-feed tylosin, and fecal samples were taken daily for a period of 7 days. Feces were serially diluted and plated on Nutrient agar (positive control), m-Enterococcus agar, and m-Enterococcus agar infused with erythromycin (8µg/ml) and vancomycin (32µg/ml), with antibiotic concentrations in the agar being the human resistance breakpoint. Plates were incubated at 37°C for 48 hours. Colony growth was quantified. We expect that the prevalence of erythromycin- and vancomycin-resistant enterococci will increase after administration of tylosin and will return to baseline at the end of the study. Oral administration of tylosin may promote cross-selection of resistant bacteria, leading to macrolide and glycopeptide inefficacy against enterococci and other infectious bacterial species. Although antimicrobial resistance (AMR) can be obtained from multiple sources, establishing an appropriate dosing regimen for tylosin therapy may help reduce the number of resistant bacteria shed into the environment and subsequently, reduce the public health risk.
Research Grant	Start up-FARAD
Field of Research	Antimicrobial Resistance

Abstract Title	Barcoded magnetic beads for tick-borne disease molecular diagnosis: a pathway to rapid and accurate detection
Authors	Nazleen Mohseni, Sean Rowan, Sheema Mir
Affiliations	Western University of Health Sciences, College of Veterinary Medicine
Abstract	Ticks transmit diseases such as babesiosis, anaplasmosis, ehrlichiosis and Lyme disease via blood-borne pathogens in both human and animal hosts. With an increase in the tick population and their migration into new geographical locations, we are seeing a greater prevalence of ticks in new regions, making them a health concern worldwide. Diagnosis of these tick-borne diseases is difficult due to the tick's ability to carry and transmit more than one pathogen and the symptoms of the diseases they cause are not specific to ticks, making diagnosis not only difficult but unreliable. There is a need for a modern approach to tick-borne diseases in both human and veterinary medicine. The development of a multiplex diagnostic assay to diagnose tick-borne diseases can aid in the control and detection of tick-borne pathogens by using a single patient sample. This will allow rapid diagnosis to then provide fast treatment options for infected patients. Our lab has developed a duplex molecular assay for two tick-borne pathogens: Anaplasma phagocytophilum and Borrelia burgdorferi. We used the assay to detect the presence of these two pathogens in twenty-five randomly collected canine samples from Pet Health Center who have had no known diagnosed infection. The goal is to determine prevalence of these two pathogens in the randomly selected canine population with our duplex assay.
Research Grant	Boehringer Ingelheim, CVM Office for Research
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Novel sampling techniques for oral pharmacokinetics of tylosin
Authors	Julio A. Mojica Pérez, Ivonne Miranda Martínez, Madelyn Schwartz, Laura Neumann, Danielle Mzyk, Linda Dillenbeck, Derek Foster, and Jennifer Halleran
Affiliations	College of Veterinary Medicine, North Carolina State University, Raleigh, NC
Abstract	Tylosin is an in-feed antimicrobial used to reduce the incidence of liver abscesses in beef cattle. There are no studies investigating oral tylosin pharmacokinetics. This study aims to understand the pharmacokinetics of orally administered tylosin at the FDA approved labelled dose. While there are reports documenting whole liver tissue residues of tylosin, these are terminal studies and may not reflect accurate tissue concentrations. Collecting portal blood after gastrointestinal absorption may be as close to the site of action to assess accurate tylosin concentrations. Our goal was to test a novel technique for a more accurate drug concentration determination, while not sacrificing the animals. We hypothesize that tylosin concentration will be greater in the portal vein when compared to the peripheral circulation. The animals used were 6-7-month-old crossbred steers. To find a significant difference in drug concentrations between sample sites, a statistical power calculation determined the sample size of 6 steers. Under sedation and with the use of a local block, the portal vein was catheterized utilizing ultrasound as guidance. Steers were administered tylosin orally daily for three days in their feed. Portal and jugular vein blood samples were collected at periodic intervals to measure and compare tylosin concentration via high-performance liquid chromatography analysis. The portal vein catheterization method was successful in 100% of the steers and remained functional for at least 7 days after placement. The described technique has significant potential for future scientific investigations for determining medication concentrations in the liver.
Research Grant	Start-up/FARAD
Field of Research	Pharmacology and Toxicology

Abstract Title	Establishment of an implant-based, prophylactic osteomyelitis rat model
Authors	Emily G. Moles, Luke J. Tucker, Alyssia J. Little, Ezzuddin E. M. Abuhussein, J. Amber Jennings, Lauren B. Priddy
Affiliations	College of Veterinary Medicine (Moles) and Department of Agricultural and Biological Engineering (Tucker, Little, Priddy), Mississippi State University, Starkville, MS Department of Biomedical Engineering (Abuhussein, Jennings), University of Memphis, Memphis, TN
Abstract	Osteomyelitis is an inflammatory response resulting from the infection of bone by a pathogen, typically Staphylococcus aureus, which is prone to antibiotic resistance and biofilm formation. This presents a significant challenge for effectively treating the infection, especially as the concentration of antibiotics needed to treat increases with S. aureus biofilm maturation. Few clinically relevant, implant-based models to study preventative measures for osteomyelitis exist. We hypothesized that an in vivo model that will allow for the repeatable establishment of infection and treatment in the same surgery can be developed using prior data from our and others' chronic osteomyelitis models and further ex vivo experiments. Using an ex vivo model, bacterial burden in the rat femur following implantation time (5 or 15 minutes) of a contaminated screw indicated 5 minutes was sufficient to establish relevant and repeatable infection. Four Sprague Dawley rats underwent a surgical procedure involving the same 5-minute implantation time of a contaminated screw, followed by treatment with membranes loaded with natural antimicrobials. At 72 hours, the femur and soft tissue were homogenized for bacterial quantification. The average bacterial counts of the femur and surrounding soft tissue were 6.38 log CFU and 6.22 log CFU, respectively, demonstrating the establishment of a consistent and repeatable model. This research promotes good antimicrobial stewardship by creating a clinically relevant testbed for evaluating treatments aimed at slowing down the development of S. aureus biofilms, which may decrease the amount of antibiotics needed to treat osteomyelitis.
Research Grant	NIH P20GM103646 DoD W81XWH2110193
Field of Research	Orthopedics

Abstract Title	Development of two novel compounds for atopic dermatitis
Authors	Maria Alejandra Molina Velandia, Chen Xie and Jijun Hao
Affiliations	College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA
Abstract	Atopic dermatitis (AD) is an inflammatory skin disorder characterized by pruritus and dermal lesions. Its etiology involves an interplay between environmental factors, genetic predisposition, and immune dysregulation. Once triggered, keratinocytes express inflammatory cytokines which activate dendritic cells. Activated dendritic cells stimulate Th2 cell production of IL-4, IL-13 and IL-31. In AD, the Th2 cell response is amplified, which leads to skin barrier dysfunction and itch symptoms. We tested two compounds N1 and N2, which are related to NAD+, and hypothesized that they would reduce the level of cytokines and chemokines produced by keratinocytes thereby leading to suppression of Th2 cell response. Additionally, we aimed to understand the signaling pathways by which these two compounds function on keratinocyte-secreted cytokines. To test this hypothesis, HaCaT cells were placed on 6-well plates and pre-treatment with N1 or N2 was performed, then inflammation was induced via addition of TNF-α/IFN-γ. Expression levels of IL-8, MDC, TARC, TSLP, and RANTES in HaCaT cells were examined via RT-qPCR. Western Blot was used to investigate the pathways involved. The results showed that N1 or N2 pretreatment significantly reduced the mRNA expression levels of IL-8, MDC, TARC , TSLP, and RANTES that were induced by TNF-α/IFN-γ. Western blot results showed that pre-treatment with N1 or N2 results in suppression of MAPK (p38) phosphorylation in TNF-α/IFN-γ stimulated HaCaT cells. However, the phosphorylation levels of JNK, AKT, ERK, NF-ƙb, Iƙb were not affected by the tested compounds. These results demonstrated that N1 or N2 may exhibit anti-inflammatory activity in activated HaCaT cells through the MAPK (p38) pathway.
Research Grant	Western University of Health Sciences intramural grant
Field of Research	Dermatology

Abstract Title	Diversity of gastrointestinal helminths and lungworms isolated from mustelids in Pennsylvania and New York
Authors	Keara Monaghan, Rachel Harrell, Caroline Sobotyk, Jennifer Bloodgood, Kevin Niedringhaus
Affiliations	Department of Pathobiology, University of Pennsylvania, School of Veterinary Medicine, Philadelphia, PA (Monaghan, Harrell, Sobotyk, Niedringhaus) Cornell Wildlife Health Lab, Cornell University College of Veterinary Medicine, Ithaca, NY (Bloodgood)
Abstract	Wildlife parasitology is an important field of research as many parasites have a significant impact on wild animal, domestic animal, and human health. Mustelidae is a diverse family of carnivorous mammals that includes weasels, mink, fishers, otters, and others. Many of these species commonly inhabit Pennsylvanian forests and waterways, yet research is limited on the helminth species that infect these animals. The goal of this study was to determine the diversity of gastrointestinal (GI) helminths infecting mustelids in Pennsylvania and potential risks to domestic animals and humans. We collected harvested and donated mustelids from across the state. During necropsy, the GI tract from stomach to rectum was visually examined for adult worms, and intestinal contents were preserved in ethanol. Feces were examined for eggs using centrifugal fecal flotation with Sheather's sugar solution. Larvae were identified using zinc sulfate flotation on intestinal contents. All parasitic life stages were identified and described morphologically using an optic microscope. We discovered a wide variety of GI helminths including Metorchis conjunctus, Aonchotheca putorii, Eucoleus boehmi, Eucoleus aerophilus, Ancylostomatidae, Cystoisospora sp., and Physaloptera sp.. The most prevalent lungworm species found were Crenosoma vulpis and Filaroides sp.. Metorchis conjunctus and E. aerophilus are zoonotic helminths that pose a public health concern, and all isolated parasites possess the ability to infect domestic dogs and cats. These results give us insight to the prevalence, host range, and environmental niches of several GI helminths in Pennsylvania and provides novel information on parasitic disease implications for wild mustelids.
Research Grant	Institute of Infectious and Zoonotic Disease
Field of Research	Parasitology

Abstract Title	Understanding Cardiovascular Disease in Bearded Dragons (Pogona vitticeps)
Authors	Briana S. Moreland, Barton Huber, Curtis Eng
Affiliations	Western University of Health Sciences CVM Pomona, CA
Abstract	Bearded dragon (Pogona vitticeps) ownership is steadily increasing based on increasing numbers seen in private clinical practice. With the expansion in the bearded dragon pet population, the number of clinical case reports of cardiovascular diseases in bearded dragons has increased. As these numbers increase, reptilian medicine can be studied to a greater extent resulting in a better understanding of cardiovascular disease. One specific disease process that is affecting bearded dragons is aneurysms. The cause for aneurysms in bearded dragons has not yet been identified but a current hypothesis is that it may be a sign of cardiac disease and not due to just a weakened vascular condition. While there are very few documented reports of aneurysms (or other vascular anomalies), it appears anecdotally that the most common anatomical locations reported are neck and cranial coelom. The purpose of this retrospective study is to evaluate the medical records of a Southern California exotic animal practice to identify possible influences that will contribute to aneurysms in bearded dragons. Using a minimum of 30 medical cases of bearded dragons diagnosed with aneurysms, the sex, age, body condition score, trauma, nutrition, and other factors will be cataloged, assessed and statistically analyzed to see if any of these are contributing factors. Microsoft Excel and Graphpad will be employed to document each factor of the bearded dragon patient, complete the statistical analysis and graph out any significant influences for this medical condition. While this study should be considered a pilot study, it is hoped that it will serve as an inspiration for further and more detailed studies in this growing medical problem.
Research Grant	None
Field of Research	Exotic Pets and Zoo Animal Medicine

Abstract Title	Transcriptional Profiling of Bone Marrow in a Nonhuman Primate Model of Delayed Radiation Injury
Authors	Jasmine Morgan, John D. Olson, George W. Schaaf, J. Mark Cline, David L. Caudell
Affiliations	Virginia Maryland College of Veterinary Medicine, Blacksburg, VA (Morgan). Section on Comparative Medicine, Department of Pathology, Wake Forest School of Medicine, Winsotn-Salem, NC (Olson, Schaaf, Cline, Caudall)
Abstract	Accidental or intentional radiation exposure may result in life-threatening immunodeficiency due to increased radiosensitivity of hematopoietic cells. Few studies detail the delayed effects of acute radiation exposure (DEARE) on hematopoiesis and subsequent immune function. This is partially due to the limited availability of translational animal models. Evolutionarily conserved Homeobox cluster (HOX) genes transcriptionally regulate hemopoietic stem cell differentiation and self-renewal. To study the hypothesis that DEARE results in reprogramming of hematopoietic niches through regulation of HOX genes we used nonhuman primates (NHP) in the Radiation Survivor Cohort (RSC) at Wake Forest School of Medicine. The study cohort consisted of control (n=15; mean age: 5.17±2.3yr) and irradiated (n=16, 6.5Gy ± 0.12; mean age: 5.17±2.3yr) male Rhesus macaques (Macaca mulatta). Hematologic parameters including complete blood counts (CBC), blood smears, and bone marrow cytology were analyzed for differences in cell numbers and morphology. Pathologic analysis of bone marrow (BM) was performed using light microscopy and immunohistochemistry (MPO, granulocytes; CD163, macrophages; CD3 and CD20, T and B cells; and CD61 and AHSP, megakaryocyte and erythrocytes). RNA isolated from BM was analyzed using nCounter® Pro Analysis System (NanoString, Seattle WA) and ROSALIND (San Diego, CA). Analysis of differential CBC results showed significant difference between control and irradiated NHPs with hemoglobin ($p<0.0001$), neutrophils ($p<0.0001$), lymphocytes ($p<0.0005$), monocytes ($p<0.0022$), and white blood cells ($p<0.0022$). Remaining results are pending. Nonparametric data was analyzed in GraphPad Prism v9.4.1 with significance at $p<0.05$.
Research Grant	U19 AI067798, U01 AI150578, P30CA012197, 2015-IDG-1006
Field of Research	Anatomic Pathology

Abstract Title	Synthesis and in vitro evaluation of irinotecan loaded chitosan nanoparticles against colorectal cancer
Authors	Amol Morrow, Dilip R. Gunturu, Temesgen Samuel
Affiliations	Department of Biomedical Sciences (Morrow, Gunturu); Pathobiology (Samuel), College of Veterinary Medicine, Tuskegee University, AL 36088
Abstract	We investigated the effect of irinotecan, a topoisomerase-I inhibitor, on colorectal cancer cells using chitosan nanoparticles. Colorectal cancer is a common and deadly disease that requires effective treatment. Topoisomerase inhibitors are drugs that induce cell death by interfering with DNA replication. However, they have serious side effects and limited efficacy. Nanoparticle drug delivery systems can enhance the performance of anticancer drugs by improving their bioavailability, biodegradability, and safety. We prepared irinotecan-loaded nanoparticles using chitosan-sodium tripolyphosphate and chitosan-polyethylene glycol-sodium tripolyphosphate. Chitosan is a biocompatible muco-adhesive polymer. We characterized the nanoparticles for their size, shape, and loading efficiency. We also evaluated their cytotoxicity and cell cycle arrest on colorectal cancer cells. Our results showed that chitosan encapsulated irinotecan nanoparticles reduced cell viability more effectively than standard irinotecan. Our study suggests that chitosan nanoparticles can be a promising carrier for irinotecan delivery in colorectal cancer treatment.
Research Grant	This research was supported by grants from NIH T35OD010432, DHHS/HRSA D34HP00001-35-00, and NIH/NIMHD RCMI grant # U54MD007585
Field of Research	Oncology

Abstract Title	The bacterial microbiome of ectoparasites found on snakes in the Peruvian Amazon.
Authors	Taylor Mortensen, Alex Marsh, Roger Ramirez-Barrios, Francisco Carvallo-Chaigneau
Affiliations	Virginia-Maryland College of Veterinary Medicine, Blacksburg, VA
Abstract	The Amazon Basin is a species-rich terrestrial ecosystem that plays an important role in zoonotic disease dynamics. Human expansion into Amazonia threatens urban and agricultural areas with the migration of wildlife. Wildlife is known to be parasitized by various species of ectoparasites, but limited information is available regarding the parasitism of snakes. Snakes are known to be parasitized by over 500 species of mites and ticks, and ticks are accepted as main disease vectors for Rickettsiae, Borreliae, Ehrlichia, and other bacterial diseases. Based on these findings, we hypothesized the bacterial microbiome of ectoparasites collected on native snakes of the Peruvian Amazon would contain bacterial 16S ribosomal RNA consistent with known zoonoses. Ectoparasites were collected on Amazonian snakes in Loreto, Peru. They were crushed and cleaned for genomic extraction, PCR, gel electrophoresis, DNA purification, and Sanger sequencing in order to determine the species of the tick samples. Following DNA extraction, data on the tick's bacterial microbiome was detected using MINion nanopore sequencing technology. A16S ribosomal RNA primer was used to detect the presence of zoonotic disease genomics. These findings will provide novel information on the potential of snake ectoparasites to act as zoonotic disease vectors and snakes to act as disease reservoirs to other wildlife, domestic species, and humans in the Amazon regions of Latin America.
Research Grant	Summer Veterinary Student Research Program
Field of Research	Parasitology

Abstract Title	Increased dietary fiber intake improves fecal and clinical activity scores in dogs with chronic enteropathies
Authors	Isabel A. Muirragui, Rachel Woodflint, Adam J. Rudinsky, Jenessa A. Winston, Valerie J. Parker
Affiliations	From the Comparative Hepatobiliary and Intestinal Research Program (CHIRP), Department of Small Animal Clinical Sciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH 43210
Abstract	Dietary modification, including increasing dietary fiber intake, plays a crucial role in the successful management of a variety of chronic enteropathies [e.g., inflammatory bowel disease (IBD)] in dogs, with up to 50-66% of dogs having food-responsive enteropathies. The aim of this retrospective study is to evaluate the effects of increasing dietary fiber intake on fecal and clinical activity scores in dogs with chronic enteropathies. Dogs (n=14) that presented to The Ohio State University College of Veterinary Medicine's Nutrition service between October 2020 and February 2023 for management of chronic enteropathy and who received recommendations to increase dietary fiber intake were included. Canine inflammatory bowel disease activity index (CIBDAI) and Purina fecal scores were compared at baseline and after dietary modification. Median (range) crude fiber (CF) and total dietary fiber (TDF) at baseline were 0.8 (0.1-1.4) and 1.6 (0.1-2.7) grams per 100 kilocalories (kcal), respectively. The medium (range) of CF and TDF of diets recommended were 1.35 (0.9-1.8) and 4.5 (2.0-6.6) g/100 kcal. Dogs demonstrated a decrease in CIBDAI scores from baseline (median 4, range, 1-6) to recheck (median 1, range, 0-5). Fecal scores decreased from baseline (median 4, range, 3-6) to recheck (median 2.5, range, 2-3). These results support the idea that increasing dietary fiber intake can improve fecal and clinical activity index scores in dogs with chronic enteropathies.
Research Grant	None
Field of Research	Microbiomes

Abstract Title	Molecular detection of Babesia in canine, cattle and small ruminants in Grenada, West Indies.
Authors	Mukarati, Andy Alhassan, Bhumika Sharma
Affiliations	Departments of Pathobiology, School of Veterinary Medicine, St. George's University, Grenada, West Indies.
Abstract	Babesia species are intra-erythrocytic protozoan parasites that infect many wild and domestic mammalian animals especially in tropical and subtropical regions. These blood parasites are commonly transmitted by ixodid tick vectors and cause a disease condition known as babesiosis. Babesiosis is characterized by hemolytic anemia, anorexia, jaundice, organ dysfunction, and acute respiratory distress syndrome in the infected animal. Babesiosis is clinically significant and has an economic impact on livestock as it can affect the quality of meat and milk production. In Grenada, Babesia spp. have been reported in canines and small ruminants however, there is a lack of recent studies conducted to assess the prevalence of Babesia spp. in animals. Therefore, we hypothesize that Babesia spp. DNA will be amplified from at least 10% of the samples analyzed. A total of 125 whole-blood samples, (37 canine; 35 bovine; 38 caprine; 15 ovine), were subjected to Babesia genus-specific polymerase chain reaction (PCR) and gel electrophoresis. Overall, 16% (20/125) samples were PCR-positive for Babesia spp. which mainly includes 14 bovine samples (40%), four caprine samples (10.5%) and two canine sample (5%). The PCR results were further confirmed via direct sequence analyses. The preliminary data confirm the presence of Babesia spp. in animals and an island wide sample collection and analysis is required to estimate the prevalence of these species in Grenadian animals.
Research Grant	None
Field of Research	Parasitology

Abstract Title	Validating gene targets for canine peripheral T-cell lymphoma immunotherapy
Authors	Megan Mulder, Jennifer Holmes, and Paul Hess
Affiliations	Department of Clinical Sciences, NC State College of Veterinary Medicine, Raleigh, North Carolina
Abstract	Canine peripheral T-cell lymphoma (PTCL) is a deadly cancer that responds poorly to chemotherapy alone. Vaccine-based immunotherapy may help eliminate residual chemoresistant cells, improving survival. A vaccine's most critical component is an antigen, a protein that T-cells must "see" for target cell recognition. Valuable cancer vaccine antigens must be 1) present in multiple patients' cancers; 2) absent in normal tissues (no autoimmunity); and 3) absent in thymic epithelial cells (TECs) to avoid deletion of responding T-cells, nullifying vaccine efficacy. PTCL turns on genes called cancer-testis antigens (CTA) which are present in germ cells but silenced in somatic tissue. Using RNA-seq and qPCR, we identified five CTAs that fulfill the first two criteria of a valuable cancer vaccine antigen. Our goal was to determine which of those also met the third. Using endpoint RT-PCR, we performed low-resolution screening in bulk prenatal thymus (0.5% TECs, 99.5% thymocytes). For negative CTAs, re-screening at higher resolution (enriched TECs) would be needed, but TECs have never been isolated in dogs. We hypothesized that canine TECs could be enriched by adapting a murine "panning" method, increasing the probative power of endpoint PCR in meeting the last criterion. All five CTAs were absent in bulk prenatal thymus cDNA and need higher resolution TEC-level screening. Because thymus is scarce, surrogates for TECs and thymocytes were used in panning development. Our panning successfully depleted 83% of "thymocytes" from the model single-cell population, suggesting the potential for significant enrichment of TECs in thymic cell suspensions.
Research Grant	The Shadow Whatley Research Fund
Field of Research	Oncology

Abstract Title	Lineage plasticity of YY1-null pro-B cells enables them to develop features of NK cells
Authors	Clare Munroe, Sarah Naiyer, and Michael Atchison
Affiliations	Department of Biomedical Sciences, University of Pennsylvania School of Veterinary Medicine, Philadelphia, PA
Abstract	The ability to direct cell development from one lineage to another has numerous applications in regenerative medicine. Preliminary data from the Atchison laboratory indicate that knock out (KO) of transcription factor YY1 in pro-B cells enables them to develop features of T lineage cells in appropriate culture conditions. To determine if YY1-null pro-B cells can develop into additional hematopoietic lineages, I cultured them in conditions conducive to natural killer (NK) cell differentiation. I optimized the conditions for NK cell development using hematopoietic progenitor cells, which I exposed to various cytokine and stromal environments. To determine the phenotype of the resulting cells, I used flow cytometry to assess the presence of NK cell surface markers. Using conditions selected based on ease of maintenance, overall cell yield, and generation of cells with NK cell surface markers, I cultured yy1f/f (wild-type (WT)) or Mb-1CREyy1f/f (YY1-null) pro-B cells. After 3 weeks, more YY1-null pro-B cells were beginning to acquire NK cell surface marker NK1.1 compared to WT pro-B cells; however, the fraction of cells expressing NK1.1 was still very low. Ongoing experiments will allow the WT and YY-null pro-B cells to differentiate for longer, and I expect the YY1-null cells to continue to gain NK1.1 positivity, while expression remains low in WT cells. Future experiments will investigate whether the cells generated from YY1-null pro-B cells demonstrate NK cell cytotoxic effector function. If YY1 KO allows cells to develop features of NK cells as well as T cells, it may be possible to direct cells from one lineage to another by manipulating YY1.
Research Grant	NIH Grant R01AI162879 to Michael Atchison
Field of Research	Immunology

Abstract Title	Impact of p53 Truncation Mutants and Their Interaction with Cyclophilin D on Three Types of Cancers
Authors	Morgan A. Murray, Christopher P. Baines
Affiliations	Department of Biomedical Sciences, College of Veterinary Medicine, University of Missouri, Columbia, MO
Abstract	Cancer is one of the leading causes of death in the world. TP53 is a tumor suppressor gene that keeps the cell cycle in check and TP53 mutations are extremely common in cancers. Most mutations result in a loss of its function. However, there is a novel class of truncated p53 mutants, such as p53 213 and 196, that have pro-tumor effects. While wildtype (WT) p53 primarily resides in the nucleus, p53 213 and 196 translocate to mitochondria and interact with a protein called Cyclophilin D (CypD). However, the role that CypD plays in the pro-tumor effects of these novel p53 mutants is unclear. The overall objective is to examine whether CypD contributes to the mitochondrial and proliferative effects of truncated p53 proteins in three different kinds of cancers. We hypothesize that the expression of both p53 213 and 196 mutants will result in increased expression of mitochondrial proteins, proliferation, and ATP levels, and reduced cell death. We will culture colon (HCT116), prostate (LNCaP) and Breast (MCF7) cancer cells. We will overexpress p53 WT, 213, and 196 using adenoviruses. CypD will be depleted using siRNA. Mitochondrial OXPHOS protein and markers of proliferation will be measured by Western blotting. ATP and cell death will be measured by luciferase- and sytox dye-based assays, respectively. In contrast to WT p53, we expect an increase in mitochondrial OXPHOS levels, proliferation, ATP levels and cell survival in response to p53 213 and 196 expression and CypD depletion to attenuate these effects. These results would indicate that binding to CypD mediates the effects of these mutants. This would suggest that targeting of this interaction could be a novel therapeutical approach in the treatment of multiple cancers.
Research Grant	Dr. Baines' Research Incentive Funds
Field of Research	Oncology

Abstract Title	Generation of swine gamma delta CAR T cells
Authors	Purva Nagarajan, Lidia Flor Cuenca, Jack Swain, Hannah Thomas, Nimisha Pattada, Raimon Duran-Struuck
Affiliations	Department of Pathobiology, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA
Abstract	Chimeric antigen receptor (CAR) T cell therapies use T cells engineered to target antigens expressed in cancer cells. Research has been developed to optimize this technology using animal models such as rodents. Unfortunately, rodent models have demonstrated poor clinical predictive value, limiting the translatability to man. Swine share many anatomical, physiological, and immune characteristics with humans, making them ideal for clinical translation. Gamma delta T cells (GDCs) are a subset of CD3+ cells that can be found in the peripheral blood and mucosal tissues and have strong anti-tumor properties and no MHC restriction. This makes them an attractive cell type as there is minimal risk for inducing graft-versus-host disease compared to alpha-beta T cells. We sought to take advantage of both CAR technology and GDC characteristics to generate a large animal CAR GDC. Using swine peripheral blood mononuclear cells, we isolated and expanded GDCs for transduction with a characterized CAR molecule. Optimization of expansion techniques are being studied using zoledronic acid, IL-2, and artificial antigen presenting cells (aAPCs) based on a K562 cells line expressing human CD86 and CD64 loaded with anti-swine CD3. To date, using 5uM ZA, 1000 IU/IL2 and a 10:1 aAPC:GDC ration lead to a >7-fold expansion within 8 days. Flow cytometry data suggests that the majority of these GDCs express CD8αα and are CD4-. We are currently lentivirally transducing our cells with an anti-HLA A2, CD20 or pig allelic antigen CAR, which have been characterized previously in human and swine T cell effector cells. Once validated, cytolytic assays will be conducted to demonstrate their potency.
Research Grant	ITMAT
Field of Research	Immunology

Abstract Title	Antibiotic concentration in the peritoneal fluid of cattle
Authors	Laura Neuman, Danielle Myzk, Jennifer Halleran, Timo Prange
Affiliations	Department of Population Health and Pathology, College of Veterinary Medicine, North Carolina Sate University, Raleigh, NC
Abstract	Intraperitoneal administration of antibiotics is commonly used in bovine surgery to prevent postoperative complications. Though ampicillin is labeled for intramuscular injection, administering this antibiotic intraperitoneal is common in bovine surgery. The objective of this study is to compare abdominal drug concentrations when ampicillin is administered through intraperitoneal or intramuscular route. Our hypothesis is that administering ampicillin intramuscularly will better achieve pharmacokinetic/ pharmacodynamic targets than intraperitoneal administration. 12 six-month old crossbred dairy steers had standing surgery performed. Prior to closure of the abdominal wall, they were randomly allocated to receive 11 mg/kg of ampicillin intraperitoneally or intramuscularly. At surgery, ultrafiltration probes were placed in colon, ileum, peritoneal cavity, and incision. Ultrafiltrate and blood samples were collected for 48 hours. Seven days after the surgery, the steers were euthanized, and tissues were collected to assess drug residues. All the probes placed collected samples 75% of the time during the study. The location with the highest amount of success rate was the ileum with 80% of the samples collected. The locations with fewest samples collected were the peritoneum and colon with 70% success rate. Analysis of drug concentrations is pending. During the study, the animal behavior affected the duration of peritoneal probe sampling. Most of the ultrafiltration probes were functional during the entirety of the study making this method successful for assessment of peritoneal drug concentrations.
Research Grant	FARAD / USDA-NIFA
Field of Research	Pharmacology and Toxicology

Abstract Title	Effects of Colostrum Storage on Health and Welfare of Pre-weaning Calves in Conventional and Organic Dairies
Authors	Victoria Ngo, Allison Warnick, Samantha Lund, Brian Oakley, James Reynolds, and Jose M. Peralta
Affiliations	Western University of Health Sciences, College of Veterinary Medicine
Abstract	High quality colostrum is a crucial component to the health of a neonatal calf, providing it with nutrients, passive immunity, and the first microbial colonists to seed the gastrointestinal microbiome. The purpose of this study is to characterize how the microbiome in colostrum is affected by storage conditions commonly used on conventional and organic dairies. Colostrum samples collected post-calving were first analyzed via a BRIX refractometer to assess total solids concentration, an estimate for colostrum quality. Composite samples from each quarter were collected and aliquots of each sample were frozen at -20 deg C. Because protein and fats can confound DNA extraction, we first modified and validated a protocol to extract DNA in equivalent amounts and quality from samples with a range of Brix values. Next, to discriminate between viable and nonviable microbes, we used two methods - qPCR to validate the use of Promidium Monoazide (PMA), a photo-reactive dye that allows PCR amplification of only viable cells, and aerobic plate counts. These methods have been applied to samples collected from dairies in northern and southern California with collection of additional samples and high-throughput sequencing of 16S rRNA genes still ongoing. We plan to identify specific microbial taxa over- and under-represented in each treatment type. Finally, samples will be tested for Mycoplasma bovis in fresh colostrum. M. Bovis can be an important pathogen in neonatal calves and colostrum is a potential source for inoculating newborn calves.
Research Grant	USDA SARE
Field of Research	Microbiomes

Abstract Title	Student experience with patient stress during abdominal ultrasounds
Authors	Richie Nguyenphat, Emily Smith, Charlotte Bolch
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, Arizona
Abstract	Abdominal ultrasounds are a viable and safe imaging modality for diagnosing abdominal diseases. This technique is non-invasive and is commonly used in conjunction with sedation to ensure the safety of the patient under evaluation and the veterinary operators of the modality. However, some private practices and universities not only teach but utilize abdominal ultrasounds without patient sedation. At the Companion Animal Center (CAC) at Midwestern University, veterinary students are tasked to assist in restraining and observing patients undergoing abdominal ultrasounds. Since patients are not under sedation, they can move with limited motion under restraint and show signs of stress, such as vocal production of distress, dilated pupils, and attempts to escape. This perceived patient stress may then be experienced by veterinary students, which could impact their learning abilities. The overall objective of this proposed research aims to quantify veterinary students' stress levels when assisting or observing abdominal ultrasounds of distressed patients. An online survey consisting of 17 questions has been created and is currently being distributed to veterinary students who have consented. The results of this project will provide a framework for optimizing the learning environment of abdominal ultrasounds for veterinary students and recommend the use of sedation in patients to be used in practice to decrease student distress and decrease patient distress.
Research Grant	None
Field of Research	One Health

Abstract Title	Mutational and transcriptomic patterns in canine malignant peripheral nerve sheath tumors differ from human
Authors	Noelle Niemi 1, Brandan Wustefeld-Janssens 2, Brian W. Davis 1,3
Affiliations	1 Veterinary Integrative Biosciences, School of Veterinary Medicine, Texas A&M, College Station, TX. 2 Clinical Sciences, College of Veterinary Medicine, Colorado State, Fort Collins, CO. 3 Small Animal Clinical Sciences, School of Veterinary Medicine, Texas A&M, College Station, TX.
Abstract	Malignant peripheral nerve sheath tumors (MPNST) are aggressive soft tissue sarcomas prevalent in humans and dogs, but canine etiology is unknown. In both, there is a high incidence of metastasis and regrowth after resection, making MPNST life threatening as no effective treatment exists outside surgery. Human studies show functional loss of NF1, TP53, and CDKN2A contribute to tumor progression, as does loss of PRC2 function through inactivation of SUZ12 and EED. This study examines somatic changes in canine MPNST and compares them with human cancers. We sequenced whole genomes of eight tumors, four subcutis and four from the brachial or lumbosacral plexus, and assessed single nucleotide, small insertion-deletion, and large copy number variants, as well as gene expression perturbation. NF1, TP53, and all PRC2 components were expressed normally. However, CDKN2A is significantly upregulated across tumors along with other similarities to human cancer. Mutated genes across tumors are implicated in human adenocarcinoma of the lungs and kidneys. Transcriptional dysregulation of pathways involved in multiple human cancers, cell injury/stress, cellular immune response, nervous system signaling, and cellular growth/proliferation. The FAK pathway is affected, which is not associated with human MPNST but is with multiple other cancers. Many copy number alterations involving tens of megabases exist in seven of eight tumors. This study is the first to utilize whole genome and transcriptome analysis to understand canine MPNST. This first step in determining interspecies congruence can help better link the molecular mechanisms underpinning neoplastic function towards potential implementation of effective treatments in both species.
Research Grant	Internal GINN grant through the Department of Small Animal Clinical Sciences, Texas A&M University.
Field of Research	Oncology

Abstract Title	Effects of sedation on rectal temperature during equine dental procedures performed in different seasons
Authors	Amanda Norman, Colleen M. Turner, Jennie Soule, Jane M. Manfredi
Affiliations	Pathobiology and Diagnostic Investigation (Norman, Soule, Manfredi), Large Animal Clinical Sciences (Turner) Michigan State University College of Veterinary Medicine, East Lansing, MI; Veterinary Dental Referral Services (Turner), Davison, MI.
Abstract	Sedation is a key tool for a safe equine dental procedure, but it is unknown if there is a higher risk of sedation causing hypothermia in procedures performed during cold months. We hypothesize the effects of sedation for a dental procedure will significantly decrease rectal body temperature in cold as compared to warm ambient temperatures. Adult horses (N=246), from a private equine dentistry practice, that needed dental equilibration were used. Sedation was administered intravenously (0.011 mg/kg detomidine and 0.009 mg/kg butorphanol) and intramuscularly (0.55 mg/kg xylazine and 0.028 mg/kg acepromazine). Ambient and serial rectal temperatures (pre-sedation (PRE), 15 minutes after sedation (POST15), and 30 minutes after sedation, or if before, at the end of the procedure (POST30)) were recorded. Statistics included Shapiro-Wilks test, Spearman's correlation coefficient, and a Friedman test with Dunn's post hoc test (all significant at $p<0.05$). Ambient temperatures ranged from -7.8 to 30°C. The median (95% CI) of rectal temperature was PRE: 37.4 (37.2-37.7) °C, POST15: 37.5(37.2-37.8) °C, and POST30: 37.4 (37.1-37.7) °C. POST15 temperatures were significantly increased from PRE ($p=0.001$) and POST30 ($p=.005$) temperatures. PRE to POST30 temperatures were not significantly different ($p>0.9$). There was a weak positive correlation between ambient temperature and POST15 ($rho= 0.26$, $p<0.001$) and POST30 ($rho= 0.25$, $p<0.001$). Three horses became hypothermic (<36°C). Rectal body temperature in horses after sedation at ambient temperatures between -7 to 30°C remains at a safe level in most instances, suggesting sedated dental procedures can be performed during cold months.
Research Grant	MSU CVM & Graduate Office Fellowship funds
Field of Research	Equine Medicine and Surgery

Abstract Title	Using PROTAC Technology to Create Live-Attenuated Porcine Diarrhea Epidemic Viruses as Vaccine Candidates
Authors	Shawn O'Brien, Xiang Chi, Xufang Deng
Affiliations	Department of Physiological Sciences, College of Veterinary Medicine, Oklahoma State University, Stillwater, OK, 74074
Abstract	Porcine epidemic diarrhea virus (PEDV) is a swine enteric coronavirus that causes severe diarrhea, dehydration and death in neonatal piglets with a 90-100% mortality. Without access to a safe, effective vaccine, PEDV has been a significant threat to the pork industry. PROTAC is a proteolysis-targeting chimera technology that links the proteins of interest via a linker to an E3 ubiquitin ligase, leading to ubiquitination and subsequent proteasomal degradation of the targeted proteins. The overarching goal of this project is to develop live-attenuated PEDV vaccine candidates using PROTAC. We designed a linker that is composed of proteasome-targeting peptide (PTP) fused with the TEV protease (TEVp) cleavage motif. We expect that PROTAC will attenuate the virus due to viral protein degradation in conventional cells but not in the TEVp-expressing cells in which the PTP is cleaved off the targeted proteins. The specific aims of my work include generating a stable cell line expressing TEVp and inserting the linker sequence into the genome of PEDV. Using a lentivirus, we engineered the genome of Vero-81 cells to express TEVp. Puromycin resistance corroborated successful lentiviral infection of TEVp into the Vero-81 cells. DNA sequencing confirmed successful PTP insertion into the genomic cDNA of the PEDV infectious clone. Our next studies include rescuing the recombinant PROTAC PEDV and evaluating the attenuation of the virus in cell cultures and in animals. It is our expectation that PROTAC is an effective approach to attenuate PEDV, thus providing vaccine prototypes for comprehensive assessment.
Research Grant	USDA-NIFA AFRI competitive grant (2023-67015-39096) and USDA-AES Hatch project (OKL03251)
Field of Research	Virology

Abstract Title	IL-33-dependent skin barrier alterations mediate acquired immunity to penetration of Strongyloides ratti
Authors	Nicole Oey, E. Evonne Jean, De'Broski Herbert
Affiliations	Department of Biomedical Sciences (Oey) and Department of Pathobiology (Jean, Herbert), School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA
Abstract	Soil-transmitted helminth (STH) infections affect approximately 1.7 billion individuals, and while humans typically experience recurrent infections, data has shown that mice are able to develop acquired resistance. Historically, STH infection research focuses on protective immune responses at mucosal barriers. Thus, the architecture and immune cell repertoire of the skin in the context of re-exposure to STH infection has not been studied. Data shows that penetration of S. ratti is reduced upon secondary exposure to infectious third stage larvae (iL3). Our lab has shown this resistance requires IL-33-expressing, antigen-presenting myeloid cells (APCs) and expansion of gd-T cells. Our data suggests that IL-33 is required to recruit gd-T cells to the skin, which have been shown in literature to increase skin barrier integrity in response to tissue damage. Cytokine production by gd-T cells and myeloid cells that leads to neutrophil infiltration and keratinocyte proliferation. We hypothesize that a major component to secondary resistance is this skin barrier integrity and IL-33-dependent mobilization of gd-T cells and myeloid cells. A qPCR array was performed targeting murine extracellular matrix (ECM) genes and cell adhesion markers on skin homogenates from secondary infected IL-33-deficient mice. Immunofluorescence assays (IFA) were performed on naïve and secondary-infected skin from the footpad to visualize how IL-33 controlled immune cell localization at the site of infection. Future experiments will focus on determining the function of genes of interest (GOI) that were found to be increased due to secondary infection, where they are expressed, and how they are expressed in an IL-33 dependent manner.
Research Grant	NIH U01AI163062 [and] NIH 1R21AI171740
Field of Research	Parasitology

Abstract Title	Assessing zoonosis in Texas snakes: Cryptosporidium and Giardia prevalence in captive and wild-caught snakes
Authors	Kelsey O'Hara, Cora Garcia, Maureen Kelly, Joe Luksovsky, Guilherme G. Verocai, Meriam N. Saleh
Affiliations	Texas A&M University SVM, College Station, TX
Abstract	The number of US households with pet reptiles has been steadily increasing. Parasitic infections in pet reptiles are common, and Cryptosporidium and Giardia are protozoan parasites that pose a zoonotic risk. However, little is known about the prevalence of Cryptosporidium and Giardia in snakes. Cryptosporidium serpentis and C. parvum, which infects people, have been previously documented in snakes. The increase in reptile ownership could lead to an increased risk for zoonosis from these parasites. We surveyed 21 different species of captive (n=101) and wild-caught (n=16) snakes from Texas to determine the prevalence and zoonotic potential of Cryptosporidium and Giardia. A commercial direct immunofluorescence assay (IFA) for the detection of Cryptosporidium and Giardia was used to screen excreta. The prevalence of Cryptosporidium in both captive and wild-caught populations was 12.0% (14/117); the captive population had a prevalence of 7.9% (8/101) while the wild-caught population had a prevalence of 37.5% (6/16). Prevalence rates between the two populations were compared with Fisher's exact test. The prevalence of Cryptosporidium in wild-caught snakes was significantly higher than the captive population ($p = 0.0040$). All samples were negative for Giardia on IFA. Positive samples are currently being analyzed via PCR and sequencing for species determination and genotyping. These initial results support our hypothesis that the incidence of Cryptosporidium is higher in wild-caught snakes. These findings should be considered when acquiring wild-caught snakes, in addition to routine husbandry and hygiene. A wider geographic range and larger sample size is warranted in future studies to support these findings.
Research Grant	None
Field of Research	Parasitology

Abstract Title	Urine specific gravity's effect on urine antigen load in canines with Blastomycosis
Authors	Brianna Ohm, Jessica Pritchard
Affiliations	School of Veterinary Medicine, University of Wisconsin - Madison, Madison, WI
Abstract	Blastomycosis is an infection caused by the fungus Blastomyces dermatitidis which produces spores that are inhaled by dogs. The spores transform into yeast which prevent the pathogen from exiting the lungs and allow for dissemination to other tissues. Diagnosis is often obtained by measuring urine Blastomyces antigen levels - a diagnostic tool performed by MiraVista laboratories with nearly 100% sensitivity. This tool has prognostic value, including measuring success of treatments, but prior research has only shown urine antigen levels of <5ng/ml being associated with increased survivability. Urine antigen levels exceeding this threshold have variable survivabilities. Based on previous observations, my hypothesis is that urine specific gravity impacts urine antigen levels and dilute urine, often seen with hospitalized patients on intravenous fluids, corticosteroids, etc. are providing artificially low results. In order to explore this question, at least 36 dogs diagnosed with Blastomycosis will be recruited and their urine specific gravity will be measured at three different time points throughout a 24 hour period and sent to MiraVista laboratories to determine antigen concentration. Among recruited dogs, it has been consistently observed that urine specific gravity can vary significantly in a 24 hour period and naturally among dogs without any interventions including intravenous fluids or increased water consumption. These observations should allow for increased probability of variation in urine antigen among samples. Identifying significant variation in urine antigen associated with urine specific gravity could change submission protocols for samples sent to MiraVista laboratories to increase prognostic value.
Research Grant	None
Field of Research	One Health

Abstract Title	Characterization of Biomarkers in Canine Cognitive Decline
Authors	Kassandra Oldham, Masa Ukai, Stephanie McGrath, Amanda S. Lathan, Breonna Kusick and Julie A. Moreno
Affiliations	Department of Clinical Sciences (Oldham, Ukai, McGrath, Kusick) and Department of Environmental and Radiological Health Sciences (Lathan, Moreno), College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO.
Abstract	Canine cognitive dysfunction syndrome (CCD) is a naturally occurring progressive neurodegenerative disease that commonly affects geriatric dogs, with age being the number one risk factor. Similar to humans with Alzheimer's disease (AD), it is known that the canine population has similar pathologic changes, yet the overall pathogenesis of CCD is poorly understood. Two characteristic features of AD are the post-mortem presence of neurofibrillary tangles (NFTs), composed of abnormally phosphorylated tau (P-tau), and the deposition and accumulation of the protein beta amyloid (Aβ), forming plaques. These extracellular depositions prevent the proper function of neuronal cells, eventually leading to cell ischemia and cell death. Increases in glial inflammation accompany the Aβ and NFTs, causing tissue damage and contributing to the clinical signs seen with AD. Recent studies of post-mortem aging canine brains have demonstrated an increase in glial inflammation, accumulation of Aβ, and tau phosphorylation (P-tau). Specifically, these studies have displayed increased P-tau in CCD positive dogs, presenting a potential indicator for this disease. The only current antemortem diagnostic for CCD is owner questionnaires combined with veterinary physical and neurological examinations. This study aimed to investigate P-tau, Aβ, and microglial concentrations as possible biomarkers of CCD onset and prognosis, expecting an overall increase in CCD positive dogs. Utilizing a cohort of presumptively diagnosed CCD positive and a cohort of CCD negative geriatric canines, we investigated these neurodegenerative proteins via immunohistochemistry staining and microscopy image analysis.
Research Grant	Dog Aging Project; Institute of Cannabis Research, Colorado State University (Pueblo); Panacea Life Sciences
Field of Research	Anatomic Pathology

Abstract Title	Detailed Histological Study of the Nidamental and Accessory Nidamental Glands in Euprymna scolopes
Authors	Patrick O'Leary, Wael Khamas, Josep Ruttlant, Curtis Eng
Affiliations	Affiliations: Western University CVM, Pomona, Ca
Abstract	Euprymna scolopes, a Hawaiian sepiolid, exhibits an intriguing symbiotic relationship with the bioluminescent bacteria Vibrio fischeri, a trait that enhances its camouflage during moonlit hunts. Central to this partnership is the evolution of a unique organ, the lumen, that E. scolopes uses to modulate the emitted light, thereby eliminating its shadow and rendering it invisible in the water. The ability of the lumen to host V. fischeri exclusively opens avenues for further research. The bacteria living symbiotically in the bobtail squid's organ, the accessory nidamental gland, play a critical role in the squid's development and reproductive processes. However, the challenge of breeding E. scolopes in captivity beyond F1 generation has been a persistent obstacle. Our study seeks to overcome this limitation by examining the histology of wild-caught E. scolopes, with a particular focus on the Nidamental Gland and Accessory Nidamental Gland. Applying standard histological procedures, we performed tissue collection, fixation, embedding, sectioning and staining using routine stain (Hematoxylin and Eosin). Glands and tissue were photographed, digitized, and photographs of these selected organs were montaged together to prepare a high-detail whole organ cross section. These analyses will provide a vital baseline for understanding E. Scolopes's macro- and microscopic anatomy and physiology. The anticipated findings and their implications are expected to pave the way for future immunological studies, facilitate strategies for successful captive breeding of E. scolopes, and offer opportunities for comparative analysis with captive-bred individuals in subsequent research planned for the coming year.
Research Grant	WesternU Research Committee
Field of Research	Anatomy

Abstract Title	Histology of the nidamental and accessory nidamental glands in the bobtail squid, Euprymna scolopes
Authors	Patrick O'Leary, Wael Khamas, Josep Rutllant, Curtis Eng
Affiliations	Western University CVM, Pomona, Ca
Abstract	Euprymna scolopes, a Hawaiian sepiolid, exhibits an intriguing symbiotic relationship with the bioluminescent bacteria, Vibrio fischeri, a trait that enhances its camouflage during moonlit hunts. Central to this relationship is the evolution of a unique organ, the lumen, that E. scolopes uses to modulate the emitted light, thereby eliminating its shadow and rendering it nearly invisible in water. The ability of the lumen to host V. fischeri exclusively opens avenues for further research into the immunological function that permits this monoculture. However, the challenge of breeding E. scolopes in captivity beyond F1 generation has been a persistent obstacle in deepening our understanding of this relationship. To address sustainability and reduce harvesting from the wild, our study seeks to examine and define the histology of the reproductive organs of wild-caught E. scolopes, the nidamental and accessory nidamental glands. All provided specimens either died due to natural causes or were euthanized for reasons outside of this study. Applying standard histological procedures, we performed tissue collection, fixation, embedding, sectioning, and staining using routine stain (Hematoxylin and Eosin). Glands and tissues were photographed and digitized to prepare a high-detail whole organ cross section. These analyses will provide a vital baseline for understanding E. scolopes' macro- and microscopic anatomy and function. The anticipated findings and their implications are expected to pave the way for future immunological studies, facilitate strategies for successful captive breeding of E. scolopes, and offer opportunities for comparative analysis with captive-bred individuals in subsequent research planned for the coming year.
Research Grant	Western University of Health Sciences, Student Research Fellowship Program
Field of Research	Anatomy

Abstract Title	Comparison of the probing duration of Culicoides sonorensis and Aedes aegypti using electropenetrography
Authors	Babatunde Ibrahim Olowu, Anastasia M. W. Cooper, Favour Ajibade, Vivienne Velic, Dana N. Mitzel, Kristopher Silver, and Kathryn E. Reif
Affiliations	University of Ibadan, Ibadan, Nigeria (Olowu, Ajibade) Kansas State University, Manhattan, KS, USA (Cooper, Silver, Reif) University of Veterinary Sciences, Brno, Czech Republic (Velic) National Bio and Agro-defence Facility, USDA, Manhattan, KS, USA (Mitzel)
Abstract	Hematophagous arthropods, such as mosquitoes and biting midges, require a blood meal to complete their gonotrophic cycle. During blood-feeding, hematophagous arthropods can serve as vectors and transmit various pathogens, many of which produce disease in vertebrate hosts, including humans and livestock. Pathogen transmission often occurs during blood-feeding activities, such as probing, salivation, and ingestion. Thus, the time spent engaging in these activities may reflect the likelihood of pathogen transmission. The electropenetrography (EPG) technique has been adapted to study the blood-feeding behaviors of hematophagous arthropods, allowing for events such as probing, salivation, and ingestion time to be precisely quantified. The present study uses EPG to compare the probing duration of Culicoides sonorensis biting midges and Aedes aegypti mosquitoes on human hosts to determine which insect spends the most time probing and, thus, potentially has the greatest opportunity to transmit pathogens. Preliminary data suggest that Ae. aegypti spends significantly less time probing than C. sonorensis (4.42±0.49 min vs 9.38±1.87 min) but tends to probe more frequently (3.07±0.84 vs 1.29±0.18). This investigation provides new insight into the basic biology and behavior of blood-feeding insects. Future work will determine the amount of pathogens these hematophagous arthropods transmit within each probing period and test the hypothesis that C. sonorensis transmits more pathogens within equally specified feeding times than Ae. aegypti. This research will help investigate if there is a timeline for disrupting feeding before pathogen transmission and if probing duration is important for determining vectorial capacity.
Research Grant	USDA Research, Education, and Economics Workforce Development Agreement (#58-3022-0-002) and the Hatch Multistate Project (NE1943).
Field of Research	Parasitology

Abstract Title	Quantifying the Impact of Metaphylaxis on the Abundance of Key Members of the Respiratory Microbiome in Cattle
Authors	Alison Olsen, Molly McClurg, Matthew Scott, John Richeson, Lee Pinnell, Paul S Morley, and Robert Valeris-Chacin
Affiliations	VERO, Veterinary Medicine and Biomedical Sciences, Texas A&M University, Canyon, TX (Olsen, McClurg, Scott, Pinnell, Morley, and Valeris-Chacin); Department of Agricultural Sciences, College of Agriculture and Natural Sciences, West Texas A&M University, Canyon, TX (Richeson)
Abstract	Bovine Respiratory Disease (BRD) leads to substantial economic losses in the beef industry. A common control strategy is the use of antimicrobial drugs (AMD) in cattle upon facility arrival (metaphylaxis). However, limited knowledge exists on the impact of metaphylaxis on the bacterial populations in cattle over time. The aim of this study was to quantify the effect of metaphylaxis on the abundance of BRD-related bacteria in post-weaned beef cattle. In this study, tulathromycin (TU), florfenicol (FL), and oxytetracycline (OX) were evaluated along with a negative control (NC) (15 animals per treatment group). Nasopharyngeal swabs were taken at six time points (Days 0, 3, 7, 14, 21, and 56). DNA was extracted from the swabs using PowerSoil Pro Kit. The absolute abundance of Mannheimia haemolytica, Mycoplasma bovis, Histophilus somni, and Pasteurella multocida was quantified using digital qPCR in a microfluidic platform (QuantStudio Absolute Q digital PCR system, Applied Biosystems). Generalized linear mixed models (binomial distribution, complementary log-log link, animal ID as random intercept, and $P<0.05$) were used to compare the pathogens' absolute abundance between treatment groups and time points. All AMDs significantly reduced the M. haemolytica abundance in comparison to NC on days 21 and 56. A significant reduction of M. bovis abundance on days 21 and 56 was detected only in TU. Despite an initial decrease, P. multocida abundance on day 56 in the OX group was significantly higher than in the other groups. Overall, H. somni abundance was very low in all groups. In conclusion, the abundance of BRD-related bacteria was significantly lowered with TU in the long term when compared to the other AMDs.
Research Grant	Texas A&M AgriLife Research FY23 equipment grant, Texas A&M University startup funds, and FFAR Veterinary Summer Fellowship
Field of Research	Epidemiology

Abstract Title	Assessment of fracture risk in racehorses using digital radiography and helical standing computed tomography
Authors	L. O'Neil, S. Irandoust, P.H.L. Ramzan, S.E. Powell, S.H. Brounts, S.J. Loeber, D.L. Ergun, C.R. Henak, P. Muir
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Abstract	About 25% of catastrophic injuries resulting in euthanasia of Thoroughbred (TB) racehorses are condylar stress fractures. Repetitive high impact causes fatigue injury in the parasagittal groove (PSG) of the distal third metacarpophalangeal/metatarsophalangeal (MC3/MT3) or cannon bone which can lead to stress cracks that can propagate into complete condylar fractures. Digital radiography (DR) is insensitive to these fatigue injury changes, and misdiagnosis can be fatal. Standing computed tomography (sCT) has overcome this barrier as distal limb scans can be performed with low risk and no interruption to training. sCT can better identify structural changes indicative of fatigue injury, but assessment of condylar fracture risk by DR and sCT has not been compared in detail. We aim to evaluate the detection of PSG fatigue injury in racing TBs using DR and sCT ex vivo. DR and sCT image sets from 31 fetlocks with lesions of varying severity were blindly evaluated by 4 veterinarians of varying experience. A gold standard diagnostic estimate used CT and pathology of the articular surface after cartilage removal. Sensitivity was lower for DR regardless of reader but were improved with sCT for all readers. The intraclass correlation agreement against the gold standard was higher for sCT than for DR, as well as the agreement between readers. Though fatal injuries are uncommon overall, detection of risk for injury must be sensitive. Recently, public concern for racehorse and jockey welfare has highlighted this even more. Our results confirm that sCT improves diagnostic capability for risk assessment of condylar fracture risk, relative to DR. Therefore, this work advances understanding of fetlock injury prevention in TB racehorses.
Research Grant	Grayson-Jockey Club Equine Research Foundation
Field of Research	Equine Medicine and Surgery

Abstract Title	Investigating the Impact of Wildfires on Gastrointestinal Helminths in Coyotes and Elk from New Mexico
Authors	Ortiz Soto, G.D (1), Padilla, C. (2), Gomper, M. (2), Pulaski, C (3), Yabsley, M.J (4), Cleveland, C.A (4).
Affiliations	Georgia Veterinary Scholars Program, CVM, UGA, Athens, GA (1) Department of Fish, Wildlife and Conservation Ecology, New Mexico State University, Las Cruces, NM (2) Department of Infectious Diseases, CVM, UGA, Athens, GA (3) Southeastern Cooperative Wildlife Disease Study, CVM, UGA, Athens GA (4)
Abstract	Natural disturbances can have profound impacts on ecological relationships, habitat use, and ecosystem health. Wildfires are examples of significant natural disturbances and are increasing in frequency and intensity as a result of global climate change. The effects of wildfires on parasite-host interactions are an understudied area of research. Of particular importance is increasing our understanding of the effect's wildfires have on gastrointestinal parasites of large mammals. To address this knowledge gap, we examined 100 coyote (Canis latrans) feces and 100 elk (Cervus canadensis) feces from wildfire burned and unburned areas in New Mexico. We found two parasite taxa in coyotes located in burned areas: Taenia and Isospora species, and in unburned areas, two different parasite taxa were found: Capillaria species and Moniezia benedini. We found no parasite taxa in elk located in burned areas. In unburned areas one taxa was found: Isospora species. We detected a greater diversity of GI helminth species recovered from unburned areas than burned areas. Our results indicate that wildfires may have direct impacts on the helminth diversity in ungulate and predator species in a wildfire affected habitat, however, more work is needed to fully appreciate the long-term effects. Understanding the impacts of natural disturbances, such as wildfires, on the ecological relationships between hosts and parasites is critical to increasing our understanding of One Health in natural systems.
Research Grant	None
Field of Research	Parasitology

Abstract Title	Method development to cast the vasculature of the rat larynx
Authors	Tara Paarlberg, Abigail Cox
Affiliations	Department of Comparative Pathobiology (Cox), Purdue University College of Veterinary Medicine
Abstract	Understanding the vascular anatomy of commonly used laboratory animals is necessary to improve research outcomes of studies focusing on image analysis (e.g. magnetic resonance angiography) and surgical approaches of comparative models. The rat is a popular model to use in experimental studies. However, due to the small size of the rat it can be difficult to visualize some of the anatomical details we wish to study. Attempts to perfuse the vascular system of the rat often omit the smallest of vessels. This method development study aims to determine the best procedure to generate casting of the rat laryngeal vascular system. Various combinations of saline, latex, and formalin were used for casting of the vascular system. Perfusion was attempted with both a perfusion pump and the rat heart pumping. Freeze thaw specimens fixed with formalin and latex produced the best cast, with the superior thyroid artery visible. Rats that were formalin fixed and then casted with latex produced the best perfusion results. In the future, a dehydration study is planned that will study how dehydration changes the effect of estrogen on ultrasonic vocalizations, blood vessel geometry, and the vocal fold tissue of the rat larynx. These casting method results will be used as a model for that dehydration study.
Research Grant	NIH/NIDCD R01 DC020179
Field of Research	Anatomy

Abstract Title	Molecular signature profile of cancer biomarkers in feline renal carcinoma
Authors	Andrea Paredes and Annelise Nguyen
Affiliations	Texas Tech University, Amarillo, TX
Abstract	Domestic cats often diagnosed with chronic kidney disease. Recently, a renal tumor was isolated and identified as atypical epithelioid cells suspected to be of renal epithelial or possible mesothelial origin. A cell line of neoplastic cells harvested from the primary tumor, OBKI, was successfully established. Thus, the goal of this research project is to characterize primary tumor cells and determine the molecular signature profile to develop anti-cancer drug treatment. The approach is to perform Western Blot analysis and immunohistochemistry assay for detection of biomarker expression. Various biomarkers have been screened. Results show that vimentin is highly expressed in OBKI cells compared to other human cancer cell lines. Furthermore, vimentin was visually detected using immunofluorescence assay as well. E-cadherin and VEGF showed lower expression when compared to expression of vimentin in both Western blot and IFA analyses. These suggest that OBKI cells derived from feline renal carcinoma may have undergone epithelial-mesenchymal transition (EMT). Overall, we identified a unique molecular signature that helps further focus on treatment of feline kidney carcinoma.
Research Grant	Texas Tech University Start-Up Fund
Field of Research	Oncology

Abstract Title	Establishing an allogeneic mesenchymal stem cell bank for regenerative medicine research in dogs and cats
Authors	Luis Parera and Helena D. Zomer
Affiliations	University of Florida College of Veterinary Medicine, Gainesville, Florida
Abstract	Mesenchymal Stem Cells (MSCs) have been increasingly used for regenerative medicine in both human and veterinary medicine in the past two decades. MSCs are multi-potent cells that can differentiate into cells of mesodermal origin like muscle, bone, and adipose tissue. MSCs have immune modulation capacity that can improve tissue healing in wounded/sick patients. Despite all their known benefits, MSCs clinical potential hasn't been extensively used in veterinary medicine. To aid in research and future clinical use of MSCs in veterinary medicine, we set out to establish a dog and cat allogeneic MSC bank for regenerative research at the University of Florida Small Animal Hospital. Young, healthy female dogs and cats (n=6/species) undergoing ovariohysterectomies were selected to isolate, cultivate, and expand adipose tissue derived MSCs. MSC cultures were expanded to passages 1 and 2 for dogs and cats, respectively, and then cryopreserved for future use. On average, there were 3,474,911 cells/gram of adipose tissue (SD: ± 2,483,604.81 cells/gram) for our dog samples, which resulted in an average of 10 cryotubes/sample (SD: ± 0.8 cryotubes) each containing one million cells. Viability tests were performed to confirm cell survival after being cryopreserved, which resulted in more than 88% of viability after thawing for our dog samples. We were able to successfully differentiate our dog MSCs into adipocytes, chondrocytes, and osteocytes and cat assays are currently ongoing. Our next experiments will confirm cell identity by immunophenotypic analysis to CD34-, CD45-, CD73+, CD93+, and CD105+. Overall, six dog MSC lines were established with ongoing cat colonies, cryopreserving millions of MSCs for future research.
Research Grant	Department of Physiological Sciences, College of Veterinary Medicine
Field of Research	Physiology

Abstract Title	Tracking skeletal health in canine skeletal metastasis of prostate carcinoma
Authors	Leena Park, Kristina V. Wells, and Damian C. Genetos
Affiliations	Department of Anatomy, Physiology & Cell Biology, School of Veterinary Medicine, UC Davis, Davis, CA
Abstract	Prostate cancer (PCa) is the second leading cause of death in human men, with prognosis dramatically decreasing upon metastasis to bone. Dogs may serve as a preclinical model for studying PCa metastasis, for canine PCa shares important clinical features such as spontaneous disease development, age-associated disease and skeletal metastasis. PCa can subjugate osteoblasts and osteoclasts within bone to form osteoblastic or osteolytic lesions, respectively, and to increase the overall rate of remodeling. Because osteocytes regulate osteoblast and osteoclast activity, we sought to understand how PCa crosstalks with osteocytes in a pre-clinical translational canine model. 129 cases of PCa were identified from the UC Davis Veterinary Medical Teaching Hospital from 1988 to 2023, in intact (28/129=21.7%) and castrated (101/129=78.3%) male canine patients. Nine cases (9/129=6.98%) reported confirmed metastasis to bone. Median age was 8 (range: 4-13) years. All metastases were located in the axial skeleton, specifically in the vertebrae (4/9=44.4%), ribs (2/9=22.2%), or multiple sites (vertebrae and rib; 3/9=33.3%). Histological slides of bone metastases were prepared from 4 cases; hematoxylin and eosin with Alcian blue and Ploton silver staining were performed for osteocyte viability and connectivity. Both cortical and trabecular bone elaborated markers of remodeling, including cement lines, new osteoid, and osteoclast presence. This was most evident in regions near the tumor, whereas hallmarks of remodeling decreased in both cortical and trabecular bone distant from the tumor site. Understanding crosstalk between PCa and osteocytes will be clinically significant in preventing and treating skeletal metastasis and its sequelae.
Research Grant	NIH/NIAMS R01AR073772
Field of Research	Orthopedics

Abstract Title	Correlation between serum B12 and small intestinal histopathologic changes in cats with chronic enteropathy
Authors	Mina Park, Paula Giaretta, Chee-Hoon Chang, Stefan Keller, Judit Magnusson Wulcan, Valerie Freiche, Sina Marsilio
Affiliations	Dept. of Medicine & Epidemiology (Park, Marsilio) and Dept. of Pathology, Microbiology & Immunology (Keller, Magnusson Wulcan), University of California SVM, Davis, CA, US Dept. of Small Animal Clinical Sciences (Giaretta, Chang), Texas A&M SVM, College Station, TX, US L'école nationale vétérinaire d'Alfort, Maisons-Alfort, FR
Abstract	Cobalamin (Vitamin B12) is essential for mitochondrial metabolism, DNA synthesis, and cellular regeneration including that of rapidly dividing enterocytes. While commonly used as a surrogate marker for intestinal absorption, the correlation between cobalamin deficiency and histopathologic lesions in the small intestine in cats has not been investigated. We hypothesized that the serum cobalamin concentration will be negatively correlated with the degree of lesions in small intestinal biopsies from cats with chronic enteropathy (CE). In this study, the databases of the Veterinary Teaching Hospitals at UC Davis, Texas A&M University, and Alfort National Veterinary School were searched for cases of feline CE. Cases were categorized into normocobalaminemia (NC, >400ng/L), hypocobalaminemia (HC, ≤400ng/L, ≥150ng/L), or severe hypocobalaminemia (SHC, <150ng/L). Hemotoxylin and eosin (H&E) stained slides of the upper small intestine and ileum were blindly scored by a board-certified pathologist on a World Small Animal Veterinary Association (WSAVA) scale. Outcomes were assessed based on medical records and client questionnaires. A modified Feline Chronic Enteropathy Activity Index (FCEAI) was used to quantify gastrointestinal symptoms at baseline and follow-up. A total of 56 cases (18 NC, 19 HC, 19 SHC) were identified and analyzed. There were no differences in FCEAI between groups at baseline or follow-up. However, cats with SHC had the highest rate of clinical remission at follow-up (37.5%) compared to NC (15.4%) and HC (11.1%) cats. The result of this study may indicate that cats with severe hypocobalaminemia show the most overall improvement, possibly due to a bigger benefit of the correction of their hypocobalaminemia.
Research Grant	Comparative Gastroenterology Society, IDEXX
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Transcriptomic responses in synovial fluid cells and leukocytes in horses with progressive osteoarthritis
Authors	Ashana Patel, Gabriella Piquini, Lyndah Chow, Renata Impastato, Dean Hendrickson, Steve Dow, and Lynn Pezzanite
Affiliations	Department of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Fort Collins CO
Abstract	Given the protracted asymptomatic pre-radiographic phase of OA in many cases, improved understanding of the early changes occurring both within the joint and in circulating leukocytes could improve our ability to diagnose the disease and tailor treatments. The objective of this study was to investigate the transcriptomes of synovial fluid cells and circulating leukocytes in horses with and without progressive OA, using RNA sequencing. This study will address the overall hypothesis that horses with OA will have a unique transcriptome response in both blood and synovial fluid that can be identified using recently available next-generation sequencing techniques. Blood and synovial fluid were collected from 6 horses with OA presenting for arthroscopy and 12 healthy horses without OA. Horses were determined to either have OA or be disease free via musculoskeletal palpation, lameness evaluation and radiographic examination. RNA was extracted from synovial fluid cells and peripheral blood mononuclear cells and subjected to full RNA sequencing using an Illumina-based platform. Our early results indicate that synovial fluid cell transcriptomes are significantly different in horses with OA, and importantly the circulating leukocyte responses are also significantly different. Thus, the use of next gen sequencing tools can provide unique new insights into the pathogenesis of OA in horses, and suggest important new diagnostic tools for non-invasive diagnosis and monitoring of disease activity.
Research Grant	US Department of Agriculture Fellowship
Field of Research	Equine Medicine and Surgery

Abstract Title	The regulation of IL-1β production and NLRP3 inflammasome activity by Tumor Progression Locus 2 (TPL2)
Authors	Niki Patel, Denise Fahey, Wendy Watford
Affiliations	Department of Infectious Disease, College of Veterinary Medicine, University of Georgia, Athens, GA
Abstract	IL-1β is a pro-inflammatory cytokine that facilitates innate immunity to pathogens and contributes to the pathogenesis of numerous autoinflammatory diseases. Due to its inflammatory potency, IL-1β is tightly regulated by the multimeric protein inflammasome complex. Stimulation of host pattern recognition receptors (PRRs) (priming) induces transcription of IL-1β and NLR family pyrin domain containing 3 (NLRP3). Activation of the NLRP3 inflammasome cleaves pro-IL-1β via caspase-1. The serine-threonine protein kinase, tumor progression locus 2 (TPL2), transduces signals by host PRRs to mediate inflammation. TPL2 ablation significantly increases the production of IFN-β after LPS stimulation. IFN-β, a type I interferon, has been shown to downregulate NLRP3 inflammasome activity and decrease IL-1β production. We hypothesized that TPL2 is required for macrophage inflammasome activation either through its kinase/scaffolding functions or suppression of IFN-β. Bone marrow-derived macrophages (BMDMs) from wild type, Tpl2-/-, IFNAR-/-, or Tpl2-/- IFNAR-/- mice (DKO) were treated with TPL2 inhibitor before LPS priming, but prior to inflammasome activation with extracellular ATP. Genetic ablation or pharmacological inhibition of TPL2 significantly decreased IL-1β transcription and secretion. NLRP3 expression was reduced by TPL2 genetic ablation, but not pharmacological inhibition, suggesting a possible scaffolding function for TPL2. Production of IL-1β and select inflammasome components were regulated by TPL2 but not by IFN-β signaling. A better understanding of the role of TPL2 in regulating inflammasome activation will help clarify the use of Tpl2 inhibitors as a potential therapeutic target to treat IL-1β-mediated inflammation.
Research Grant	NIH-NIAID Award Number R21AI147003-01. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.
Field of Research	Immunology

Abstract Title	Development of lymphohematopoietic tumor cell lines for the establishment of a porcine model of cancer
Authors	Nimisha Pattada, Lidia Flor Cuenca, Jack Swain, Hannah Thomas, Purva Nagarajan, and Raimon Duran-Struuck
Affiliations	Department of Pathobiology, University of Pennsylvania College of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA
Abstract	Animal models of human disease have always played a central role in biomedical research, but the predictive value gap between humans and rodent models have hindered the applicability of these discoveries. Swine are ideally positioned as a cancer model as their anatomy, physiology, and immunology closely resemble that of humans. However, the current lack of transplantable hematologic cancers limits the use of swine as a model for cancer studies. The Oncopig model is a transgenic swine model that recapitulates human cancer through development of site and cell specific tumors following Cre recombinase induced expression of heterozygous KRASG12D and TP53R167H , mutations that have been demonstrated to be key drivers of human cancer. We have previously determined lymphoid leukemias can be generated in vivo by injection of Adenovirus Cre-recombinase into secondary lymphoid organs surgically in three Oncopigs. We found that this procedure resulted in lymphadenopathy, suggestive of lymphoma. Flow cytometry data from tissue samples showed a massive predominance of CD8+ T cells. We are now transforming isolated Oncopig PBMCs and CD3+ T cells in vitro with the goal of generating T cell specific leukemias to later be transplanted back into the host swine. To date, we have isolated CD3+ T cells from Oncopigs and transformed them by Cre-mediated oncogene activation. Preliminary flow cytometry data from these samples have also shown a predominance for CD8+ T cells to expand, corresponding with the results seen in vivo. This study aims to generate a series of transplantable swine tumor cell lines, with the goal to establish a reliable and reproducible swine cancer model and increase the predictive value of pre-clinical cancer studies.
Research Grant	ITMAT, Internal funds
Field of Research	Oncology

Abstract Title	Understanding the role of CD4+ T-cells in mammary carcinomas resistant to immune checkpoint blockade therapies
Authors	Samantha Paucar, Anushka Dongre
Affiliations	College of Veterinary Medicine, Long Island University, Greenvale, NY (Paucar) and Department of Biomedical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY (Dongre).
Abstract	Immune checkpoint blockade therapy is a promising therapy for breast cancer patients. However, epithelial to-mesenchymal transition (EMT) endows carcinomas with resistance to immune checkpoint blockade therapy (ICB). This resistance is due to mesenchymal tumors expressing factors such as CD73, an ectoenzyme that generates immunosuppressive adenosine. Strikingly, tumors with CD73-knockout (sgCD73) responded to anti-CTLA4 ICB. However, this effect was not achieved when combined with anti-PD1 ICB. The reason for this could be that anti-PD1 reinvigorates a progenitor stem cell-like subset of exhausted CD8+ T-cells while anti-CTLA4 mobilizes both CD8+ and CD4+ T-cells to the tumor core. Thus, the objective of this study was to determine if a lack of CD4+ T-cells is responsible for the continued resistance to anti-PD1. We performed immunohistochemical staining for CD4+ on tumor sections from control mice or those treated with anti-PD1, anti-CD73, anti-CTLA4 and combinations of the three. Interestingly, we observed more CD4+ T-cells in the tumors treated with both anti-PD1 and anti-CTLA4 in combination with anti-CD73 relative to control tumors or those that had received each antibody on its own. Importantly, CD4+ T-cells from within a sgCD73 tumor that responded to anti-CTLA4 ICB displayed enhanced cancer-killing. Our work identifies that although CD4+ cells are present in anti-PD1 treated tumors, they do not appear to have the same cancer cell killing capacity that they do in anti-CTLA4 responder tumors. These findings prompt us to explore whether different CD4+ T-cell subsets are prevalent in tumors treated with anti-CTLA4 or anti-PD1 ICB. This could reveal avenues for further optimization of ICB for breast cancer.
Research Grant	K22 CA255420, NCI, NIH
Field of Research	Oncology

Abstract Title	Treatment of equine fungal keratitis in vitro using ultraviolet-C light: a pilot study
Authors	Jessica L. Payne, Ronald W. Griffith, Amy Griffith, Melissa A. Kubai
Affiliations	Department of Veterinary Microbiology and Preventative Medicine, Department of Veterinary Clinical Sciences, College of Veterinary Medicine, Iowa State University, Ames, IA.
Abstract	Fungal keratitis is a significant infection of the cornea that increasingly affects equine patients worldwide. Common fungal organisms impacting the equine cornea include Aspergillus spp. and Fusarium spp. Pathogenic fungal infection of the cornea can compromise globe integrity and long-term vision. Fungal keratomycoses are difficult to treat, and cases often require long-term aggressive treatment with topical antifungals. There is a clinical need to develop an alternative treatment strategy for infectious keratitis. Ultraviolet-C light has been previously shown in human medicine to have antimicrobial and antifungal properties. UV-C light has also previously been found safe and non-carcinogenic at low doses. This study uses a cheap, affordable, handheld Ultraviolet-C light device to treat common fungal pathogens in culture. These fungal pathogens include Aspergillus fumigatus, Aspergillus flavus, Fusarium solani, and Fusarium oxysporum. We will then be able to determine the minimum UV-C treatment duration in vitro that is necessary to inhibit fungal growth. With this data, we will investigate UV-C light use in ex-vivo studies of fungal keratitis in harvested equine corneas. Safety studies for the cornea with the UV-C light device will also be determined.
Research Grant	Unknown
Field of Research	Ophthalmology

Abstract Title	Investigation of a Genetic Etiology for Multiple Ocular Coloboma in the Captive Snow Leopard Population
Authors	Jennifer J. E. Pederson, Leslie A. Lyons, Annajane B. Marlar, Timothy A. Georoff, Hong An, Lyndon M. Coghill
Affiliations	Department of Veterinary Medicine and Surgery, University of Missouri, Columbia Mo (Pederson, Lyons); Marlar Veterinary Consulting, Arlington, TX (Marlar); North Caroline Zoo, Asheboro, NC (Georoff); RSCH Core Facilities (Hong An), Department of Veterinary Pathobiology (Coghill), University of Missouri, Columbia, MO
Abstract	Multiple ocular coloboma (MOC) is a congenital disease of the ocular tissue caused by failure of the fetal optic fissure to close properly. Clinical presentations include, but are not limited to, eyelid aplasia, persistent pupillary membranes, congenital cataracts, retinal cysts and/or retinal dysplasia. MOC has been a long-standing health concern for captive snow leopard populations. The lesions affect each cat to a varying degree and often require surgical correction of the deformity. However, despite being first reported in 1960's and 70's, the etiology of the disease remains undetermined. Although suspected as heritable, a causal genetic variant has yet to be discovered. Consequently, the objective of the current study is to identify DNA variance in the snow leopard genome that is associated with embryonic development and correlate with disease presentation. The long-term goal is to genotype the DNA variance in the captive snow leopards to prevent the production of affected animals. Whole genome sequencing of both affected and unaffected snow leopards has been conducted and data from approximately 65 additional wild felids and 404 domestic cats has been used to prioritize candidate variance. Sanger sequencing will be used to validate the genetic variance within the snow leopard population. Studbooks and health records will be used for segregation analysis to define a mode of inheritance. A causal DNA variance is expected to segregate concordantly with disease. This knowledge will improve the health and welfare of both individual snow leopards and the long-term success of the snow leopard Species Survival Plan.
Research Grant	ACVO – Vision for Animal Foundation Grant Gilbreath-McLorn Endowment
Field of Research	Exotic Pets and Zoo Animal Medicine

Abstract Title	Evaluation of a commercially available water supplement to promote hydration in clinically ill cats
Authors	Maria Peralta, Amy Nichelason
Affiliations	Department of Medical Sciences, School of Veterinary Medicine, University of Wisconsin-Madison, Madison, WI
Abstract	Dehydration is common in clinically ill cats, and can result from vomiting, diarrhea, decreased water intake, and increased urinary water losses. Promotion of water consumption in cats is challenging. As such, rehydration often relies on administration of intravenous or subcutaneous fluids, which can add cost and stress for clients and patients. Purina Hydra Care™ is a commercially available liver-flavored oral hydration supplement consisting of osmolytes such as glycerin and amino acids. Hydra Care™ has been shown to be palatable and increase water consumption in healthy cats, but it is not known whether it is effective in improving hydration in clinically ill cats. Our primary aim is to determine whether this hydration supplement improves urea nitrogen concentrations and other measures of dehydration in clinically ill cats within 48 hours. Our secondary aim is to determine whether Hydra Care™ invokes a minimum fluid intake of 30ml/kg/day and improves quality of life assessments in cats within 48 hours. It is hypothesized that Hydra Care™ will improve hydration in clinically ill cats in the outpatient setting as assessed by physical exam and laboratory markers of hydration. Clinically ill cats eligible for outpatient management are being recruited. Laboratory parameters including BUN, albumin, PCV, TP, calculated serum osmolality, and body weight, will be compared between baseline and recheck using Wilcoxon matched pairs signed rank tests, with $P < 0.05$ considered significant. The overall goal of this study is to determine the utility of a water supplement for rehydration in clinically ill cats. If effective, this could provide a stress-free and cost-effective alternative for improving hydration in clinically ill cats.
Research Grant	Purina
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Crimean-Congo hemorrhagic fever virus surveillance in Hyalomma spp. ticks collected from cattle in Tanzania
Authors	Nicole Perry, William Swain, Alex Tremeau-Bravard, Mac Farnham, Woutrina Smith, Zikankuba Sijali, Mwokozi Mwanzalila, Walter Simon, Robinson Mdegela, Rudovik Kazwala*, and Brian Bird
Affiliations	College of Veterinary Medicine, University of Florida, (Perry); One Health Institute, School of Veterinary Medicine, University of California, Davis (Swain, Tremeau-Bravard, Farnham, Smith, Bird) and Sokoine University of Agriculture, Morogoro, Tanzania (Sijali, Mwanzalila, Simon, Mdegela, Kazwala [*deceased])
Abstract	Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne zoonotic disease that is wide-spread across multiple continents including Africa, Asia, and parts of Europe. CCHF virus (CCHFV) can infect a wide variety of livestock, birds, and other wildlife, but does not cause clinically apparent disease. In contrast, humans develop severe and often fatal disease with case fatality ratios exceeding 40%. CCHFV is maintained and transmitted primarily by Hyalomma spp. ticks, with other hard tick species also serving as competent vectors. The geographic range of CCHFV appears to be expanding and climate change is expected to further increase Hyalomma spp. tick ranges globally introducing CCHFV into further previously unaffected areas. To understand the ecological drivers of CCHFV and tick host ecology, ticks and cattle were sampled in two contrasting climactic zones in the Iringa/Ruaha region (higher elevation, low precipitation) and Kilombero river valley region (lower elevation, high precipitation) in Tanzania throughout 2020 and 2021. Hyalomma spp. ticks were tested via RT-qPCR for the presence of CCHF viral RNA as part of this project and results are pending. Serological analyses of sampled cattle in the study regions revealed approximately 30% IgG seropositivity (N=113/383 total) to CCHFV among adult animals. We hypothesize higher prevalence of CCHFV infection will be found among ticks from the Iringa region due to increased contact with Hyalomma spp. tick hosts (ground birds, hares, and other wildlife) and more favorable climatic conditions for tick persistence across the greater Ruaha ecosystem.
Research Grant	In partnership with the United States Department of Agriculture, Agricultural Research Service (NACA 58-3022-2-024 and NACA 58-8064-9-015).
Field of Research	One Health

Abstract Title	Surveillance and Characterization of Avian Pathogenic E. coli using Molecular Serology
Authors	Tristan Perryman, Klao Runcharoon, Catherine Logue
Affiliations	Department of Population Health, University of Georgia College of Veterinary Medicine, Athens, GA
Abstract	Avian Pathogenic E. coli (APEC) is the causative agent of colibacillosis and represents one of the most economically costly pathogens affecting the global poultry industry. APEC classification has traditionally involved identifying serogroups. The literature indicates that the most historically common serogroups linked with disease are O1, O2, and O78; however, recent studies have shown that these serogroups may no longer be the most prevalent. Our hypothesis is that the commercially available vaccines targeting the O1, O2, and O78 serogroups may have caused a shift in the APEC that are commonly causing disease. The first goal of this study is to characterize the serogroups that are currently present in broiler operations by running 1500 isolates from disease positive birds through multiplex PCR to identify the most common serogroups in circulation. These isolates will then be screened through another multiplex PCR that targets 9 genes associated with APEC virulence. These results will be used to determine which serogroups represent the most virulent strains. In addition to 15 isolates will be screened for biofilm formation and serum resistance, as these both represent important mechanisms of environmental persistence for APEC. Finally, the allantoic cavity of 12-day-old chicken embryos will be inoculated with 10 novel hot strains of APEC in order to perform an embryo lethality assay. Strains causing embryo death of >29%, 10%-29% and <10% are considered as, virulent, moderately virulent, and avirulent strains. The result showing that all 10 novel hot strains were virulent as they caused embryos mortality >70% within 4 observation days. Interestingly, both O15 and O152 cause 90% mortality at 2 days post infection.
Research Grant	Funded by USDA
Field of Research	Epidemiology

Abstract Title	Non-invasive measurement of skin sympathetic nerve activity in dogs with naturally acquired arrhythmias
Authors	Luís Dos Santos and Charlotte Peterkin
Affiliations	Department of Veterinary Clinical Sciences, Purdue University College of Veterinary Medicine, West Lafayette, IN
Abstract	It has been shown that changes in sympathetic innervation to the heart are correlated with arrhythmogenesis, as it can lead to heterogeneous changes in cardiac electrophysiology. The cervicothoracic (stellate) ganglia are one of the final common pathways for extrinsic cardiac sympathetic fibers, and thus changes in its activity have been linked with arrhythmia development. Traditionally, stellate ganglia nerve activity (SGNA) has been measured invasively by surgically implanting electrodes directly into the ganglia or the subcutaneous space above them. More recently, studies have shown that sympathetic nerve activity can be measured on the skin's surface, and that this method is accurate in estimating SGNA. Currently, the canine research models have relied on artificially induced arrhythmia. However, this method does not capture the change in nerve activity that occurs during progressive heart disease. The present study examined skin sympathetic nerve activity in dogs with naturally occurring arrhythmias via a non-invasive recording technique. Conventional ECG electrodes were placed over the approximate area of the stellate ganglion, on either side of the body. Simultaneously, traditional ECG activity was recorded using standard clips and procedures. Ganglion activity in dogs with good cardiac health was also obtained to evaluate sympathetic tone in diseased versus healthy patients. Examining sympathetic activity in the skin of dogs with naturally occurring cardiac disease can provide more clinically applicable insight. Understanding how the sympathetic nervous system affects cardiac electrophysiology, can lead to the design of more efficacious treatments for malignant arrhythmias in the future.
Research Grant	None
Field of Research	Cardiology

Abstract Title	Development of an in vitro model of glucose stimulated GIP secretion in equine duodenal organoids
Authors	Breanna Sheahan, Lara Madding, Jillian Petersen
Affiliations	College of Veterinary Medicine, North Carolina State University, Raleigh, NC
Abstract	Glucose-dependent insulinotropic polypeptide (GIP) is an incretin secreted by duodenal epithelium that regulates insulin secretion and inhibits gastrointestinal motility. Thus, GIP dynamics may be relevant to horses with equine metabolic syndrome and/or postoperative colic horses suffering from ileus. Mechanisms of altered GIP secretion can be interrogated by comparing glucose-stimulated in vivo GIP secretion to in vitro secretion in duodenal organoids. The purpose of this study was to develop a platform for assessment of GIP secretion in equine duodenal organoids. An oral sugar test [OST] was performed on healthy horses (n=11) to determine in vivo GIP secretion. Plasma [GIP] and serum [insulin] were measured via ELISA. Plasma [GIP] increased after the oral sugar test. Plasma [GIP] was highest in horses that were insulin resistant (IR). This suggests that GIP may influence insulin concentrations in IR horses. To study in vitro secretion, endoscopically-guided duodenal biopsies were obtained from the same horses after the OST to produce duodenal organoids. After passaging, organoids were incubated in control, glucose, or maximally-stimulated solutions with a DPP4 inhibitor for 2 hours to stimulate GIP secretion. Organoid secretion [GIP] was at or below the detection limit of the assay. It is unknown whether the lack of GIP present in the organoid secretion is due to buffer dilution, low cell concentration in the cultures, or some other factor. Optimization is ongoing to enhance GIP secretion in equine duodenal organoids. Once optimized, future studies will compare GIP secretion in vivo and in vitro between patient populations of interest (post-operative colics or horses with equine metabolic syndrome) and healthy horses.
Research Grant	Dr. Sheahan's start up funds [or] NCSU CVM Intramural grant 2022 [or] Fund for Discovery
Field of Research	Equine Medicine and Surgery

Abstract Title	Customized 3D printed casts for external fixator pin placement in canine antebrachium deformities
Authors	Elaina L. Peterson, Mu Young Kim, Stanley E. Kim
Affiliations	Department of Small Animal Clinical Sciences, University of Florida College of Veterinary Medicine, Gainesville, FL
Abstract	External skeletal fixation (ESF) is a minimally invasive technique used to correct fractures and forelimb deformities in dogs. The current techniques for ESF lack consistency and present patient-specific challenges. This study investigates the application of virtual surgical planning (VSP) with customized 3D printed casts to achieve accurate pin placement in ESF of the canine radius. Building upon successful findings in veterinary and human orthopedics with VSP and 3D printed guides for forelimb/forearm injuries, we hypothesized that pin placement using our methods would deviate no more than 1.5 mm and 2.5° from the planned position at each pin set. We performed computed tomographic scans on canine cadavers (n=5) with normal forelimb anatomy, generating 3D bone and soft tissue models. We designed 3D printed casts using Materialise® software, which were attached to the forelimbs with screws and nuts. The cast featured cylindrical openings serving as drill entry point guides for K-wire placement through the marked locations and radius before removing the cast. Postoperative CT scans compared the actual pin location with the planned, revealing minor average deviations from the preoperative plan of 1.5°, 7.5°, and 2.5° on frontal, sagittal, and transverse planes. Among the 20 pin sets tested, the majority hit the radius (59/60 pins total) and fell within the desired 1.5 mm and 2.5°. To conclude, virtual surgical planning and customized 3D printed casts for ESF demonstrate feasibility, streamline the procedure, reduce reliance on the surgeon's tactile sensation. These findings provide a promising approach for pin placement in ESF, although further work is needed to explore the applicability on forelimbs requiring correction.
Research Grant	Edward Debartolo Gift to the University of Florida College of Veterinary Medicine
Field of Research	Orthopedics

Abstract Title	Phenotyping of HIV-1 ASP in an Inducible CD4+ Cell Specific Transgenic Mouse Model
Authors	Aria Phan, Isabella A. Caico, Cory Brayton, and Fabio Romerio
Affiliations	Department of Molecular and Comparative Pathobiology, Johns Hopkins University School of Medicine, Baltimore, MD (Phan, Caico, Brayton, Romerio) University of California Davis School of Veterinary Medicine, Davis, CA (Phan)
Abstract	The HIV-1 genome contains 9 genes encoding 15 viral proteins. A tenth gene encoding the antisense protein, ASP, is exclusively present in pandemic group-M HIV-1 strains and absent in all other primate lentiviruses. Suppression of ASP expression reduces viral replication through an unknown mechanism. To better understand the effects of ASP, we generated an inducible CD4+ cell specific ASP transgenic mouse model in which the ASP open reading frame (ORF) is expressed under its natural negative sense promoter (NSP) in the HIV-1 3'LTR. Expression of ASP is blocked by a STOP cassette between NSP and the ASP ORF. We screened 37 transgenic mice by PCR on genomic DNA from tail samples to confirm presence of the ASP construct. Ten mice (27%) were positive and 27 (73%) negative. Positive transgenic mice were backcrossed to isolate homozygotes. To induce ASP expression exclusively in CD4+ cells (natural targets of HIV-1), homozygous 3LTR-STOP-ASP transgenic mice will be crossed with a transgenic mouse carrying the Cre recombinase gene under the CD4 promoter (CD4-Cre-ERT2). The Cre recombinase is fused to two copies of the estrogen receptor, which sequesters Cre in the cytoplasm and prevents excision of the STOP cassette. Removal of the STOP cassette and expression of ASP in CD4 cells in double transgenic mice will be induced via Tamoxifen treatment leading to nuclear translocation of the CreERT2 fusion protein. Phenotyping of the double transgenic mice before and after tamoxifen treatment will include morphologic, anatomical, clinical, and immunologic assessments. The ASP transgenic mouse model will support future studies into the role of ASP in viral replication.
Research Grant	NIH/NIAID R03AI172665 (F.R.)
Field of Research	Immunology

Abstract Title	Evaluating the presence of Cryptosporidium and Cyclospora in rabbits and mice
Authors	Elora Pierce, Alison Li, Doaa Naguib, Randi Turner, Matthew Valente, Hannah S. Tiffin, Glen Scoles, and Asis Khan
Affiliations	Mississippi State University CVM (Pierce), Boston University (Li), Mansoura University, Mansoura, Egypt (Naguib), University of Georgia, Athens, GA (Turner), USDA, ARS, Animal Parasitic Disease Laboratory (Turner, Valente, Khan) and Invasive Insect Biocontrol and Behavior Lab, Beltsville, MD (Tiffin, Scoles)
Abstract	Species of Cyclospora and Cryptosporidium cause health challenges for humans across the globe. Cyclospora cayetanensis and Cryptosporidium hominis occur exclusively in humans. Unfortunately, progress in studying host-pathogen interactions and developing new therapeutics has been hampered by the lack of small animal models and in vitro systems for long-term cultivation. This research hoped to identify genetically similar species from fecal samples of C. hominis in rabbits and mice and C. cayetanensis in mice. 100 rabbit stool samples were received from Egypt and were scanned using a sensitive and specific qPCR assay for Cryptosporidium. Of 100 samples, 7 samples were considered positive using qPCR. Separately, PCR and gel electrophoresis on these samples showed a faint band of expected size which confirmed the presence of Cryptosporidium in sample 31. Additionally, 17 wild mice samples collected from Beltsville, MD showed that 12 out of 17 samples were positive for Cryptosporidium on qPCR. The mice samples were also scanned using two C. cayetanensis 18S rRNA-specific qPCRs including BAM19 primers developed by the FDA and Pancyclo 18S rRNA primers. qPCR results indicated 14 out of 17 samples gave a CT value of less than 40. Sanger sequencing was conducted on three of the positive mice samples, which showed a 99% match to Isospora and a 95% match to C. cayetanensis. Further microscopic examination and sequencing of genetic loci will be conducted in the future to characterize these samples in order to identify and develop a rabbit/mice-adopted animal model for Cryptosporidium and Cyclospora.
Research Grant	NIH Grant 1R01AI148667-01A1
Field of Research	Parasitology

Abstract Title	Developing a canine antibody phagocytosis assay to study maternal antibodies specific for canine parvovirus
Authors	Ana Alice Pimenta Pereira, Sarah A. K. Woodyear, Tawny L. Chandler, Agnes Yang, Wendy S. Weichert, and Sarah Caddy.
Affiliations	Baker Institute for Animal Health, Cornell University, Ithaca, NY (Pimenta-Pereira, Woodyear, Chandler, Yang, Weichert, Caddy); Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil (Pimenta-Pereira).
Abstract	Neonatal infections pose a significant threat to puppies, with mortality rates ranging from 10% to 30%. Among these infections, canine parvovirus (CPV) stands out as a highly dangerous viral disease which primarily affects young dogs with underdeveloped immune systems. During this critical phase, puppies rely on the transfer of antibodies from their mother through the placenta and colostrum to fortify their defense mechanisms. Research conducted on human breast milk has demonstrated that the antibodies it contains exhibit superior phagocytic activity compared to antibodies found in maternal serum. However, at present the biology of maternal antibody transfer in dogs is poorly understood and little is known about phagocytic clearance and neonatal protection against CPV. To determine whether antibodies in colostrum and cord blood promote heightened phagocytic activity, we aimed to devise a phagocytosis assay based on a method developed in 2011 for analyzing clinical samples in humans. We first made canine parvovirus (CPV) virus like particles (VLPs) using a baculovirus BacMid and Sf9/Hi5 insect cells to produce CPV VP2 protein on a large scale. We then conjugated VLPs to fluorescent beads using biotinylation. Future work aims to incubate these beads with clinical samples containing maternal antibodies and then introduce them to cultured macrophages (human THP1 and canine DH82 cells). Flow cytometry will be employed to determine the percentage of macrophages that have successfully engulfed the fluorescent immune complexes. This antibody-dependent cellular phagocytosis assay should allow us to better study antibody-mediated phagocytosis and maternal antibody transfer in dogs.
Research Grant	Riney Canine Health Centre grant to Dr Sarah Caddy.
Field of Research	Virology

Abstract Title	Impact of Blood Plasma Transfer on the Survival Rate of Young Kittens in Shelters
Authors	Antoinette Piraino, Kelly Min, Pedro P. Diniz, Jacqueline Noble, Zarah Hedge, Jonathan Chapman
Affiliations	Western University of Health Sciences, College of Veterinary Medicine, Pomona, CA (Piraino, Diniz, Chapman) and San Diego Humane Society, San Diego, CA (Min, Noble, Hedge, Chapman)
Abstract	The San Diego Humane Society annually supports over 20,000 kittens. Despite optimal care, some kittens still perish or are humanely euthanized. One leading cause of this is Failure of Passive Immunity (FPT), which increases the risk of infectious disease and death. Previous research shows that subcutaneous plasma injection produces satisfactory serum IgG levels in FPT kittens. However, the efficacy of improving survival rates remains unknown. This study aimed to evaluate the impact of feline blood plasma transfer (FBPT) on the survival rate of shelter kittens. Since 2009, the San Diego Humane Society has been implementing FBPT. Due to intake constraints, not all kittens receive FBPT. We reviewed medical records of 96 kittens, 34 recipients of FBPT and 62 who were not (control). Information about FPT was not available. Confounding factors and concurrent disease were reviewed and analyzed. Preliminary analysis suggested age, weight, and presence of diarrhea as factors affecting kittens' survival. To delve deeper into the impact of FBPT, we designed a retrospective case-control study, controlling for the effects of age, weight, and presence of diarrhea. Records from 582 kittens were reviewed with a goal to reach a 2:1 case-control of 200 kittens. We successfully identified all records to adequately fulfill the case-control design requirements. Data analysis will be performed to evaluate if FBPT has a protective effect on the survival of kittens. The study's findings may advocate for the usage of feline blood plasma transfer in kittens to improve the survival rate, especially for those who are suspected to have FPT. Future plans include a randomized clinical trial to establish the optimal dosage, given its high cost.
Research Grant	San Diego Humane Society and The Office for Research, College of Veterinary Medicine, Western University of Health Sciences
Field of Research	Shelter Medicine

Abstract Title	A novel approach using side population sorting to identify intestinal stem cells in wild-type pigs
Authors	Lydia Poisson, Caroline McKinney-Aguirre, John M. Freund, and Liara M. Gonzalez
Affiliations	Department of Clinical Sciences and Comparative Biomedical Sciences, North Carolina State University, College of Veterinary Medicine, Raleigh, NC
Abstract	Severe intestinal ischemia is an emergency diagnosis in human and veterinary medicine, with mortality rates reaching 80%. Improved animal models are needed to study the reparative processes driven by intestinal stem cells (ISCs). Pigs closely approximate human anatomy and physiology, but methods to study porcine ISCs (pISCs) are limited: Most require fixation, precluding in vitro work, or use of a single available transgenic model. Thus, we sought to implement an alternative method of identifying pISCs. Side population (SP) analysis via flow cytometry (FCM) has proven effective for analyzing mouse and human ISCs. SP analysis functions by using a cell-permeable dye, DyeCycle Violet (DCV), that is pumped out of cycling cells, such as ISCs, via ABC membrane transporters. In contrast, non-cycling cells (e.g., epithelial cells) retain DCV, thereby fluorescing as a separate population upon FCM analysis. Verapamil, a Ca2+ channel blocker, is used as a control to inhibit the ABC transporters and prevent DCV efflux. Cell surface markers CD45 (leukocytes) and CD166 (goblet, Paneth cells) are used to assess SP heterogeneity. We employed chemical and mechanical dissociation to produce a single-cell suspension containing a SP upon FCM analysis. Consistent with cycling cells, verapamil incubation prevented this SP. Subsequent analyses will include CD45 and CD166. Future directions will implement cell sorting for downstream analyses such as 3D ISC culture and novel surface marker identification. These data represent the first description of using SP in a porcine intestinal model. The ability to isolate pISCs will broaden our understanding of these cells to potentially leverage their regenerative capacity to develop novel therapies.
Research Grant	U.S. Department of Defense PR181265
Field of Research	Physiology

Abstract Title	Impact of ovariectomy on PFOS-induced cardiovascular function in rats
Authors	Karina Porfirio, Pankaj Yadav, Sri Vidya Dangudubiyyam, Jay S. Mishra, Sathish Kumar
Affiliations	Comparative Biosciences, School of Veterinary Medicine, University of Wisconsin-Madison, Madison, WI
Abstract	Per- and polyfluoroalkyl substances (PFAS) are pervasive environmental pollutants frequently detected in drinking water worldwide. Reports linking PFAS exposure to cardiovascular disease have increased significantly in recent years. Furthermore, women appear to be more susceptible to the adverse effects of PFAS. However, the potential role of ovaries in the increased vulnerability of females to PFAS-related health effects remains unknown. In this study, we investigated the influence of ovariectomy (OVX) on the cardiovascular function of female rats exposed to perfluorooctane sulfonate (PFOS), a prominent PFAS. Bilateral OVX or sham surgeries were performed in 8-week-old female SD rats. Following recovery from surgeries, the rats were given drinking water containing 50µg/mL of PFOS for 3 weeks. Control groups received PFOS-free water. PFOS exposure significantly reduced body weight but increased blood pressure similarly in both intact and OVX rats. Echocardiography analysis revealed that PFOS exposure decreased cardiac output, end-systolic volume, and end-diastolic volume in intact rats but not OVX rats. Vascular function studies demonstrated that PFOS equally reduced endothelium-dependent and -independent relaxation responses in intact and OVX rats. The endothelium-independent contractile responses were more pronounced in both intact and OVX rats. eNOS protein levels were similarly decreased in both intact and OVX rats. In conclusion, these findings indicate an intricate interplay among PFOS exposure, hormonal status, and cardiovascular function. PFOS appears to impact cardiac function through hormone-dependent mechanisms, while vascular function is impaired independent of ovarian hormonal status.
Research Grant	National Institutes of Health R01ES033345
Field of Research	Physiology

Abstract Title	The effects of epigenetic manipulation on chemotherapy response in somatic versus germ cell tumors
Authors	Christine Powell, Ratnakar Singh, Michael J Spinella
Affiliations	College of Veterinary Medicine, University of Illinois, Urbana-Champaign, Urbana, IL, 618101 (Powell) Department of Comparative Biosciences, University of Illinois, Urbana-Champaign, Urbana, IL, 618101 (Singh and Spinella)
Abstract	Relative to other tumor types, testicular germ cell tumors (TGCTs) are highly sensitive to the chemotherapy drug cisplatin, but the mechanisms behind this sensitivity are unclear. Cisplatin has been used to treat many types of cancer and acquired resistance remains a major challenge to therapy. Previous work in our lab has shown that cisplatin resistance in TGCTs can be overcome with combination therapy that includes agents manipulating the epigenome. This study tested whether a specific epigenetic mechanism influencing cisplatin resistance (i.e. histone tri-methylation at H3K27) in TGCTs can be applied to somatic cell cancers to alter cisplatin response. A total of five cancer cell lines, colon adenosarcoma, osteosarcoma, breast adenosarcoma, and control cisplatin-resistant and cisplatin-sensitive TGCTs, were utilized. First, dose-sensitivity assays were performed to establish appropriate cisplatin concentrations for each tumor type. Cells were treated with cisplatin concentrations ranging from 0 to 20 uM for 6 hours and cell viability was measured after 72 hours using a luminescent based cell viability assay. Next, each tumor type was pretreated with either GSK-126 (H3K27 methyltransferase inhibitor), GSK-J4 (H3K27 demethylase inhibitor), or vehicle control (DMSO). Cells were then treated with previously established doses of cisplatin and measured for cell viability as described above. RT-PCR and immunoblot analysis confirmed H3K27me3 alterations. The results of this head-to-head comparison of TGCTs and other cancers will help us further understand the mechanisms for the unique hypersensitivity of TGCTs to cisplatin.
Research Grant	National Institutes of Health Grants R01-CA211875 and DOD PRCRP Impact Award W81XWH2110903
Field of Research	Oncology

Abstract Title	Understanding contact between humans and deer in Illinois to identify routes of cross-species COVID-19 spread
Authors	Ambrielle Pratt, Tara Prezioso, Nohra Mateus-Pinilla, Kimberly Pepin, Rebecca Smith
Affiliations	College of Veterinary Medicine (Pratt), Department of Pathobiology (Prezioso, Mateus-Pinilla, Smith), Department of Animal Sciences, Department of Natural Resources and Environmental Sciences (Mateus-Pinilla), University of Illinois Urbana-Champaign, Urbana IL; USDA APHIS (Pepin)
Abstract	First manifesting in 2019, SARS-CoV-2 has been found in multiple species, including dogs, cats, minks, and cervids. Multiple regions in the United States, including Illinois, have identified SARS-CoV-2 infections in the wild white-tailed deer (WTD) population. The seroprevalence in Illinois has been estimated at 6.9%; with an overall seroprevalence of 40% estimated across 4 different states. Although the exact path for spillover into wild cervids is unknown, the virus has been shown to replicate within and spread among WTD. There is concern that the virus may spill back into the human population from a wildlife reservoir, potentially following viral evolution. However, transmission requires contact between WTD and humans. The aim of this cross-sectional survey was to understand the frequency and type of close contact between the general public in the state of Illinois and WTD, and to identify populations at highest risk for such contact. The survey was distributed electronically using convenience sampling, recruiting participants from list serves, social media, and community partners or extension liaisons. Questions addressed frequency and distance of contact with WTD, encompassing live animals and bodily fluids. Summary statistics were stratified by regions of Illinois, property type, and demographics, and logistic regression was used to identify risk factors. The survey is part of a broader study that seeks to establish whether disease spread in wild cervids correlates to disease spread in humans. We hypothesize that Illinois residents surrounded by deer habitat, and in occupations that involve cervid exposure, will have higher risk of close contact with WTD.
Research Grant	None
Field of Research	Epidemiology

Abstract Title	Update on synovial fluid analysis in adult dairy cattle
Authors	Trace Presley, Andrew Muir, Maxey Wellman, Andrew Neihaus, Susan Smith, Mackenzie Long
Affiliations	Veterinary Clinical Sciences (Presley, Muir), School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA Veterinary Clinical Sciences (Wellman, Neihaus, Smith, Long), College of Veterinary Medicine, Ohio State University, Columbus, OH
Abstract	Synovial fluid composition in cattle was first described in "Observations on Normal Synovial Fluid of Cattle: I. The Cellular constituents and Nitrogen Content" authored by A Bauer in 1930. This study set the precedent for reference intervals that have been used to evaluate synovial fluid samples in cattle since its publication. Conformation of today's cattle has changed drastically to meet industry demands to produce a larger, more feed efficient, and heavier muscled animal in beef cattle, and larger animals with increased milk production in dairy cattle. Synovial fluid acts to maintain the integrity of the joint and acts as a medium for shock absorption produced from mechanical stress on the bones and joint capsule in affiliation with movement. This study serves to update the synovial fluid reference intervals used in cattle in terms of color, viscosity, turbidity, total protein, and specific gravity to determine if changing bovine structural composition has affected these values. Samples from twenty Holstein cows were evaluated for these parameters. Cattle included in this study were determined to be free of musculoskeletal and systemic disease by undergoing a brief physical examination, gait analysis, and a complete blood count. Synovial fluid was collected from the stifle joint split evenly between the left and right hindlimbs. It was hypothesized that minor changes are to be expected in total protein, specific gravity, and viscosity due to changes in the structural composition of today's cattle, which results in increased mechanical load on the joints, but overall values and composition of synovial fluid should not be significantly altered. Results of this study are still pending.
Research Grant	None
Field of Research	Clinical Pathology

Abstract Title	Coordinating laryngeal and orofacial movements in a mouse model
Authors	Kuirsten Preston, Tobias Riede
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ (Preston); College of Graduate Studies, Midwestern University, Glendale, AZ (Riede)
Abstract	In human speech, laryngeal sound production and orofacial movements must be precisely coordinated to generate characteristic sounds. Although such complex movement is of great importance in vocal communication, little is known about the coordination of laryngeal and orofacial movements in nonhuman mammals. Here we look at the California mouse (Peromyscus californicus), a species that generates a stereotypic vocal pattern with prominent orofacial movements. Both neonates and adults produce calls that consist of 1 to 6 syllables, about 150 ms in duration with an average fundamental frequency of 18 to 24 kHz. We investigated the coordination between laryngeal sound production and orofacial movements during the first four weeks of life. Nine pups were audio and video recorded on multiple postnatal days for a total of 1657 syllables. Syllables were analyzed for fundamental frequency, sound intensity, onset and offset time. Mandible movement was analyzed for onset and offset time, and mouth gape. On postnatal day 1, mandible depression precedes syllable onset on average by 27 ms (±20 ms) and exceeds syllable offset on average by 127 ms (±38 ms). Mouth gape was significantly associated with both fundamental frequency ($r^2 = 0.17$; $p<0.05$) and sound intensity ($r^2 = 0.54$; $p<0.001$). In 6 additional pups, temporary immobilization of the mandible resulted in a decrease in fundamental frequency and intensity, supporting a functional association between mouth opening and acoustic parameters. Current results support the theory that orofacial movement is coordinated with vocal production in California mice. Continued data analysis will investigate whether movement coordination changes over the first four weeks of life.
Research Grant	None
Field of Research	Physiology

Abstract Title	Determining whether 16S rRNA is an in vivo biomarker for intestinal permeability in swine
Authors	Sydney Puda, Kyan Thelen, Joseph Hoadley, and Adam J. Moeser
Affiliations	Department of Large Animal Clinical Sciences, College of Veterinary Medicine, Michigan State University, East Lansing, MI
Abstract	Gut health is an essential component of overall health and thus is a focus of the animal health industry. However, monitoring gut health remains a significant challenge due to a lack of reliable biomarkers. Among the essential components of gut health is integrity of the intestinal barrier. This barrier, formed by intestinal epithelial cells, serves a crucial function of preventing intestinal microbes from translocating from the intestinal lumen into systemic circulation. When the barrier is compromised, often due to various stressors, microbes can invade the bloodstream, leading to increased inflammation and tissue damage. There is a growing need for more sensitive and non-invasive biomarkers to evaluate intestinal barrier integrity and, by extension, gut health. The purpose of this study is to investigate blood 16S rRNA, a gene specific to bacteria, as a potential biomarker that reflects changes in intestinal permeability in swine. We hypothesize that 16S rRNA expression in blood will increase in response to weaning stress and can serve as a sensitive and non-invasive biomarker for detecting changes in intestinal permeability. We induced weaning stress in castrated male pigs (n=10) at 18d of age and collected blood samples at 0h, 3h, 24h, and 7d postweaning. DNA was extracted, and 16S rRNA was quantified via qPCR. Statistical analysis will be performed using a one-way ANOVA on repeated measures with a Tukey's post hoc test. If successful, this research will provide a more sensitive, non-invasive in vivo measure of intestinal permeability that could provide opportunities for real time analysis and further our understanding of intestinal barrier-related health issues.
Research Grant	USDA NIFA Grant 2019-67015-29483 (AJM)
Field of Research	Physiology

Abstract Title	Development and validation of a self-prepared phenol red thread test
Authors	Bryan E. Puentes, Erin A. Hisey, Michelle H. Ferneding, Vanessa N. Ureno, Maria A.H. Do, Sara M. Thomasy, and Brian C. Leonard
Affiliations	Department of Surgical and Radiological Sciences, School of Veterinary Medicine, University of California- Davis, Davis, CA, USA and Department of Ophthalmology & Vision Science, School of Medicine, University of California Davis, Davis, CA. USA.
Abstract	The phenol red thread test (PRTT) is the preferred diagnostic tool to quantify aqueous tear production in small animals due to ease of placement under the eyelid margin and short testing duration. Despite its benefits, commercial PRTTs have been discontinued, creating a need for an alternative source. Therefore, we proposed to develop and validate a self-prepared PRTT. We dyed cotton thread (dia: 0.25 mm, length: 110 m) in PR (a liquid pH indicator), then dried and cut the PRTT into 75 mm segments and UV sterilized them in sealed pouches for 1 hr. The wicking potential of the PRTT was tested at various time intervals (5s-40s) and in solutions of varying pH (range: 7.2-8.0). A one phase decay regression was performed on these data. We performed PRTTs in vivo on 10 mice (5 females, 5 males) in both eyes 3x/week using the commercial PRTT for one week, then using our PRTT the subsequent week. A mixed effects analysis of variance and Bland-Altman analyses were performed to determine differences between the self-prepared PRTT and the commercial PRTT. Our in vitro results revealed that at a pH of 7.6, the absorptive capacity of the thread plateaus at 33.17 mm and that measurement variability was largest between 15 and 25s. Ongoing studies will test differences in wicking with different pH solutions. In wild type mice, the commercial test had a median PRTT of 3.55 (25th percentile: 2.27, 75th percentile: 4.41). Studies with the self-made PRTT are ongoing. If there are no differences between thread types, our self-prepared PRTT can act as a substitute for researchers and clinicians to continue to utilize the PRTT to determine normative tear production across veterinary species and to assist in the diagnosis of dry eye disease.
Research Grant	Startup funds (Leonard)
Field of Research	Ophthalmology

Abstract Title	Effects of OVLT/MnPO lesion on the gut microbiome
Authors	Sejla Pujagic, Nayara Pestana-Oliveira, Timothy Johnson, John Collister
Affiliations	Veterinary Biomedical Sciences, College of Veterinary Medicine, University of Minnesota Twin Cities, Saint Paul, MN
Abstract	Hypertension is a multifaceted condition affecting 700 million people worldwide, and despite decades of study, several aspects of its complex pathophysiology remain unclear. Changes in the gut microbiome have been associated with hypertension, though the cause and effect is not well defined. Previously, circumventricular organs in the brain, such as the OVLT, have been shown to play a role in hypertension. Our lab has previously demonstrated that OVLT lesioned hypertensive rats had attenuated hypertension in addition to a gut microbial population more closely resembling normal controls, compared to sham lesioned rats. Further studies have also pointed to the importance of a downstream site, the MnPO, in modulating multiple models of hypertension. The goal of this study was to further define the relationship between presence of an OVLT or MnPO lesion and changes in the gut microbiome. Male Sprague Dawley rats underwent lesion or sham operation using stereotaxic surgery. After 7 days, brain and gut tissues were harvested for analysis. Gut microbiome data from OVLT lesioned and sham rats was analyzed, and results suggest statistically significant differences in microbiome composition between lesioned and sham rats in most gut regions. Generally, sham rats had a more diverse microbial population than lesioned rats, though both had relatively similar spread of species abundance. There was also a higher relative abundance of Ligilactobacillus spp. in lesioned rats. These findings suggest the OVLT lesion itself has effects on the diversity of the gut microbiome, which may contribute to attenuating hypertension. Further, we are currently collecting gut tissues from verified MnPO lesioned rats for future analysis.
Research Grant	University of Minnesota Grant-In-Aid #546839
Field of Research	Physiology

Abstract Title	Combined antiviral-MSC treatment for T cell injury in cats with spontaneous feline infectious peritonitis
Authors	Rachel W. Qiao, Patrawin Wanakumjorn, Diego Castillo, Amir Kol
Affiliations	Department of Pathology, Microbiology, and Immunology, School of Veterinary Medicine, University of California, Davis, CA
Abstract	Feline infectious peritonitis (FIP) is a lethal disease of young cats that results from an aberrant immune response to coronaviral infection and involves severe multisystem inflammation and lymphoid tissue atrophy. Cats with FIP often present with peripheral lymphopenia due to apoptosis, with previous studies suggesting especially marked decreases in T cells. T cell exhaustion occurs during many chronic infections and is suspected to contribute to the complex pathogenesis of late-stage FIP. GS-441524 is a viral RNA polymerase inhibitor that has been used to successfully treat FIP in previous experiments, though its capacity to support lymphoid tissue regeneration is poorly understood. Multipotent stromal cells (MSCs) are somatic cells that have been studied as a potential therapeutic for inflammatory diseases due to their immunomodulatory and regenerative properties. We hypothesized that a combined antiviral-MSC treatment will support restoration of lymphocyte populations and rejuvenation of exhausted T cells in cats with FIP. Ten cats with effusive FIP were enrolled in a double-blinded, 11-week veterinary clinical trial. The cats were randomized into two treatment groups and received either a combined antiviral and MSC therapy or an antiviral and placebo treatment. Peripheral blood mononuclear cells (PBMCs) were isolated at each visit and interrogated via flow cytometry. Specifically, major lymphocytes subsets (CD21, CD5, CD4, and CD8) were determined along with T cell cytokine secretion capacity (CD5, CD4, CD8, TNFα, and IL-2). Data collection and analysis are currently ongoing. Findings from this research will help elucidate the immunopathogenesis of FIP and inform the development of novel therapeutics using MSCs.
Research Grant	National Institute of Child Health and Human Development 1R21HD106027-01
Field of Research	Virology

Abstract Title	Preparing Pets and their People
Authors	Joedy Quintana, Valeria Sanchez, Lindsey Viola, Danielle Scott, and Colleen Duncan
Affiliations	Colorado Department of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Fort Collins, CO
Abstract	In December 2021 over 1,000 pets died in their homes when the Marshall wildfire spread in Boulder County (6). Climate change has made disasters, and the associated health risk, more frequent and severe. Despite this growing risk, a 2022 study revealed that 55% of adults in the US do not have a disaster plan (11). For those who have disaster plans, it remains unknown how many of these plans include pets. The objective of this project was to explore the potential for veterinary teams to facilitate the development of a pet-inclusive disaster plan by discussing the topic at routine veterinary visits. We hypothesized that the topic of disaster preparedness was not typically covered during veterinary visits, but that pet owners would be receptive to learning about the topic from their veterinary team. We conducted two separate anonymous surveys, one for veterinary teams and one for veterinary clients in the US. Veterinary teams were asked how often disaster plans are discussed with veterinary clients and if their clinic had a disaster plan in place. Pet owners were asked if they have disaster plans that include their pets, if their veterinary team ever discussed the topic and if they would be interested in learning more about disaster plans involving their pet. Data collection is underway; the first survey is currently distributed through veterinary networks (social media, emails, conferences). The second survey is distributed through Amazon Mechanical Turk. Results of this project will serve as a foundation upon which to promote disaster planning at veterinary clinics. Such efforts could potentially increase the number of animal lives saved during a natural disaster.
Research Grant	Boehringer Ingelheim Fellowship
Field of Research	One Health

Abstract Title	Single-cell transcriptomics of the TAZ-deficient murine cornea reveals changes in gene expression associated w
Authors	Raneesh Ramarapu, Sangwan Park, Nayeli Echeverria, Michelle Ferneding, Sophie M. Le, Monica Ardon, Vijay Raghunathan, Crystal Rogers, Brian C. Leonard, Sara M. Thomasy
Affiliations	Dept of Surgical & Radiological Sciences (Ramarapu, Park, Echeverria, Ferneding, Le, Ardon, Leonard, Thomasy) and Dept of Anatomy, Physiology and Cell Biology (Rogers), School of Veterinary Medicine, UC Davis, Davis, CA. The Ocular Surface Institute (Raghunathan), College of Optometry, University of Houston, Houston, TX.
Abstract	Fuchs' endothelial corneal dystrophy is a polygenic disease affecting >300 million globally and is characterized by accelerated and progressive loss of corneal endothelial cells (CEn) with guttae formation in Descemet's membrane (DM) due to accumulation of aberrant extracellular matrix. Our lab has modeled the late-onset form of the disease in mice through a deficiency in Wwtr1 (TAZ; transcriptional co-activator with PDZ-binding motif), a key component of the Hippo pathway, affecting mechanotransduction, the cytoskeleton, cell adhesion and proliferation. We have recently generated single cell RNA-sequencing (scRNA-seq) data from wildtype (WT) and homozygous knockout (KO) mice from 3 age groups - 2, 6 and 11 months old. The purpose of this study was to elucidate the transcriptomic changes seen in the cornea across the genotypes in the context of aging. Our results indicate significant transcriptomic differences between the WT and KO CEn, with KO demonstrating an upregulation of endoplasmic reticulum stress (Hspa5, Lamp1, Xbp1, Hsp90b1) and mitochondrial dysfunction (downregulation of Mt1 and Mt2). Additionally, significant transcriptomic differences were noted in the limbal stem cells. We noted a downregulation of genes of keratinization (Krt6a, Krt16, Krt17) but an upregulation of corneal amplifying cell marker Txnip. This indicates the integral function of TAZ in not only the progression of CEn dysfunction but also in the homeostasis of the epithelium.
Research Grant	NIH R01
Field of Research	Ophthalmology

Abstract Title	Single-cell transcriptomics of the TAZ-deficient murine cornea reveals changes in gene expression associated w
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Affiliations	Dept of Surgical & Radiological Sciences (Ramarapu, Park, Echeverria, Ferneding, Le, Ardon, Leonard, Thomasy) and Dept of Anatomy, Physiology and Cell Biology (Rogers), School of Veterinary Medicine, UC Davis, Davis, CA. The Ocular Surface Institute (Raghunathan), College of Optometry, University of Houston, Houston, TX.
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Research Grant	NIH R01EY016134, P30EY12576, K08EY028199
Field of Research	Ophthalmology

Abstract Title	Accuracy and feasibility of polarization sensitive technology in detecting canine skin cancer intraoperatively
Authors	Stephanie Ramirez, Gabrielle Fontes, Ryan Jennings, Janis Lapsley, Hunter Piegols, Laura E. Selmic
Affiliations	Departments of Veterinary Clinical Sciences and Veterinary Biosciences, The Ohio State University, CVM, Columbus, OH
Abstract	In veterinary medicine, only a small portion of surgical margins are assessed with current pathology methods. Margin assessment informs clinicians of patient prognosis and need for further treatment to decrease the risk of local recurrence. Polarization-sensitive optical coherence tomography (PS-OCT) has a high accuracy for margin imaging for breast cancer in human clinical trials. The use of this technology has not been reported in veterinary medicine. The purpose of this study is to assess the accuracy and feasibility of intraoperative PS-OCT assessment of surgical margins for skin tumors in dogs. Twenty-five dogs with 33 skin tumors were prospectively enrolled: 8 soft tissue sarcomas (STS), 21 mast cell tumors (MCTs), and 4 benign tumors. All dogs underwent surgical removal of skin tumor which was imaged intraoperatively. Areas suspicious of cancer extending to surgical margins were inked and samples were placed in formalin for fixation. Pathology assessment of surgical margins was compared to PS-OCT interpretation. PS-OCT identified MCT, STS, and benign tumors at the surgical margins in 7/21 (33.3%), 5/8 (62.5%), and 2/4 (50%) of specimens, respectively. PS-OCT assessment of surgical margins detected incompletely excised MCT, STS, and benign tumor near the surgical margin with a sensitivity of 85.7%, 100%, 100% and specificity of 92.9%, 100%, 66.7%, respectively. This technology shows promise for intraoperative surgical margin assessment to permit real-time decisions with removal of further tissue or allow opportunity for intraoperative application of adjuvant therapies to decrease the risk of local recurrence.
Research Grant	Philanthropic donation
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Equine placental-derived extract enhances the regenerative capacity of equine intestinal epithelial cells
Authors	Mara P. Ramos Cabrera, Caroline McKinney-Aguirre, and Liara Gonzalez
Affiliations	North Carolina State University, College of Veterinary Medicine, Raleigh, NC
Abstract	Colic is the most common presenting complaint and the leading cause of death in horses aside from old age. Severe manifestations of colic cause intestinal hypoxia resulting in neutrophilic influx, endotoxemia, and epithelial cell injury. Despite the substantial danger of colic-induced hypoxic intestinal injury, therapeutic options are limited. Placental-derived therapeutics have been demonstrated to improve intestinal health by supporting the stem cell niche in mouse epithelial disease. We aimed to determine if equine acellular placental-derived extract (PE) would have similar therapeutic effects on epithelial cell proliferation and barrier repair after intestinal injury. We hypothesized that PE would promote intestinal epithelial cell repair in an equine in vitro injury model. To test this, monolayers were derived from banked jejunal enteroids obtained from full-thickness biopsies. Once confluent, monolayers were subjected to 4 hours of 1% hypoxia followed by a scratch assay. Experimental wells were treated with three doses of PE (0.05mg/mL, 0.075mg/mL, 0.150mg/mL) or bovine serum albumin as control (BSA, 0.075mg/mL). To assess the effect of PE on epithelial healing, time to defect closure, changes in transepithelial electrical resistance (TEER) after closure, and changes in proliferative cell biomarker expression were evaluated. Preliminary results show that PE significantly accelerates epithelial wound closure at 6H after injury (BSA: 33%, 0.075mg/mL: 77%, $p<0.0001$). However, TEER data shows no significant contribution to tight junction recovery. The use of PE to improve epithelial restitution could be a clinically effective treatment in colic cases with intestinal hypoxia and injury.
Research Grant	North Carolina Horse Council
Field of Research	Equine Medicine and Surgery

Abstract Title	Investigating the role of pro-crossover factors in mammalian spermatogenesis
Authors	Ana M. Ramos-Bartolomei, Anna Wood, and Paula Cohen
Affiliations	Cornell University College of Veterinary Medicine, Ithaca, NY (Ramos-Bartolomei), Department of Biomedical Sciences and Cornell Reproductive Sciences Center, Cornell University, Ithaca, NY (Wood and Cohen)
Abstract	Meiosis is a type of cellular division in sexually reproducing organisms in which one round of DNA replication is followed by two divisions to form haploid gametes. During prophase I, homologous chromosomes reciprocally exchange DNA through crossing over to prevent nondisjunction. Crossing over is initiated by the formation of DNA double strand breaks (DSBs) in early prophase I. In mice, 200-300 DSBs form, but only ~24-26 are repaired as crossovers (COs) and the rest are repaired as non-COs with no reciprocal exchange. While the distribution of COs across the genome is critical to ensure that every chromosome pair segregates properly at the first meiotic division, it remains unclear how these CO sites are selected. We studied how the pro-CO factors MLH1, CDK2 and CNTD1 affect CO choice. MLH1 is a final marker of crossing over in mice, while CDK2 localizes to developing CO sites, and CNTD1 regulates CO frequency and/or placement. We performed prophase I chromosome spreads on testes of Mlh1 and Cntd1 wildtype (+/+) and knockout (-/-) mice. We observed the accumulation of MLH1, CDK2, and CNTD1 during prophase I in Mlh1+/+ mice, whereas only CDK2 and CNTD1 accumulated in Mlh1-/- mice. As expected, the MLH1 protein is not formed without a functional Mlh1 gene. In Cntd1+/+ mice, we observed MLH1, CDK2, and CNTD1 foci, while in Cntd1-/- mice, we saw no foci for these pro-CO factors. This implies that CNTD1 plays a role in establishing the final CO number and that it may be acting upstream of MLH1.This study contributes to our knowledge of the temporal accumulation of pro-CO factors. Studying the mechanisms that regulate CO formation helps us understand how defects in COs contribute to aneuploidy, infertility, and birth defects.
Research Grant	Eunice Kennedy Shriver National Institute of Child Health & Human Development (NICHD) of the National Institutes of Health under award no. R01HD041012
Field of Research	Biochemistry

Abstract Title	Association between extracellular vesicles and peripheral blood neutrophils in non-human primates
Authors	Ann Ramsey, Erin Shirk, Tom Driedonks, Blanca Rodriguez, Linglei Jiang, Bianca Pachane, Olesia Gololobova, and Kenneth W. Witwer
Affiliations	Department of Molecular and Comparative Pathobiology, Johns Hopkins University School of Medicine, Baltimore, MD
Abstract	Extracellular vesicles (EVs) are membrane-bound, cargo-carrying vesicles with therapeutic applications in both human and veterinary medicine. Released by most cell types, they facilitate intercellular communication by transporting molecular content to target tissues. Understanding the mechanism by which EVs interact with immune cells is crucial to determining the efficacy of EVs engineered for therapeutic purposes. EVs are known to associate with peripheral blood mononuclear cells; however, few reports discuss EV interaction with granulocytes such as neutrophils. Neutrophils are circulating myeloid leukocytes that respond to acute inflammation in defense against pathogens. In this study, we examined associations between blood cells and EVs harvested from Expi293F (human embryonic kidney) cells and engineered to contain a dual nanoluciferase/GFP label. EVs were 1) intravenously injected into non-human primates, followed by blood collection at different time points, or 2) spiked into whole blood from donor animals. Flow cytometry revealed that EVs associated with peripheral blood neutrophils. Ongoing research aims to elucidate the type of association between neutrophils and EVs (i.e. surface binding versus internalization and fusion) as well as its implication in physiologic and therapeutic contexts.
Research Grant	US NIH (NIAID AI144997)
Field of Research	Immunology

Abstract Title	Ticks on the Trail: Canine tick exposures in Northeast Georgia greenspaces
Authors	Benjamin Randolph, Michael Yabsley, Nikole Castleberry, Nicholas Friedeman, Kaylon Coats, Kevin Richmond, Uriel Rivera
Affiliations	Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA.
Abstract	Dog owners who walk their pets in greenspaces are potentially exposed to ticks and tick-borne pathogens. Enhancing urban greenspace is a priority, but little is known about the risks of ticks in urban/suburban greenspaces. The objectives of this study were to 1) determine the prevalence and diversity of ticks and their pathogens in Northeast Georgia public greenspaces and a natural forest and 2) determine behaviors and practices of dog owners that affect canine tick exposure. From June-July 2023, we sampled ticks from nine public greenspaces in northeast Georgia and one non-public, UGA-owned natural forest. Ticks were collected using both tick drags and CO2 traps. Collected ticks were identified and tested for the presence of Ehrlichia and Rickettsia species. Applicable data from a 2020 study where ticks were collected from the same sites were combined for analyses. We also conducted an online anonymous survey on dog owner lifestyle, behavior, and practices to understand tick exposure risk. Overall, 61 ticks of three species were collected from greenspaces compared with 254 ticks of two species from the natural forest. Pathogen testing of ticks is underway. Survey results showed that dogs allowed off of established trails and/or dogs allowed off-leash were more likely to have reported ticks attached compared to those that stayed on the trail or were maintained on a leash. While we found that the potential for tick exposure is less likely in sampled urban/suburban public greenspaces compared to a natural forest area, ticks were still found and represent a risk. Our findings highlight important factors related to tick exposure risk that can be used to educate the public to improve canine and human health.
Research Grant	Cooperative Agreement with USDA APHIS
Field of Research	Parasitology

Abstract Title	Evaluation of safety of AlHV-1ΔORF73/OVHV2-ORF8 chimeric virus vaccine for Malignant Catarrhal Fever in bison
Authors	Madeline O. Rech[1], Katherine N. Baker[2], Daniela D. More[2], Maria Herndon[3], Brett Webb[4], Cristina W. Cunha[2]
Affiliations	1-Mississippi State University, Mississippi State, MS 39762 2-Animal Disease Research Unit, Agricultural Research Service, USDA, Pullman, WA 99164 3-Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164 4-Department of Veterinary Sciences, University of Wyoming, Laramie, WY 82070
Abstract	Malignant catarrhal fever (MCF) is caused by a group of viruses that belong to the family Herpesviridae, genus Macavirus. Ovine herpesvirus 2 (OvHV-2) is the causative agent of sheep-associated MCF (SA-MCF), which is endemic in most sheep populations and can often cause fatal disease once introduced to susceptible species, such as American bison. Domestic sheep are considered the subclinical reservoir, where the virus usually establishes latency. In North America, SA-MCF is one of the most important infectious diseases for bison producers, causing large financial and herd losses. Effective vaccines are necessary to avoid these losses. A vaccine targeting MCF in bison should be non-replicating in order to reduce transmission risk among individuals. This study aimed to evaluate the transmission risk of a novel SA-MCF vaccine candidate in bison. The vaccine candidate is a chimeric virus containing a recombinant, non-pathogenic strain of alcelaphine herpesvirus-1 (AlHV-1) encoding the OvHV-2 ORF8 to express gB (AlHV-1ΔORF73/OvHV-2-ORF8). This vaccine mixed with adjuvant (Emulsigen®) was given intramuscularly and boosted twice at two-week intervals. No clinical signs or adverse effects were observed in any of the vaccinated animals. To evaluate AlHV-1 shedding, nasal swabs, saliva, and buffy coat samples were collected, total DNA was extracted, and viral genomes detected/quantified using PCR. There was no significant amplification in any of the samples. These results show that the chimeric virus used as a vaccine vector does not cause disease, has a very low transmission/infection risk and therefore is considered safe to give to American bison.
Research Grant	USDA-ARS 2090-32000-045-00D
Field of Research	Virology

Abstract Title	Serum C1q concentrations are associated with rhodococcal pneumonia in foals irrespective of plasma transfusion
Authors	Danyelle Reiskind, Patricia Flores-Ahlschwede, Scott Ahlschwede, Jocelyne M. Bray, Angela I. Bordin, Noah D. Cohen
Affiliations	Equine Infectious Disease Laboratory, Department of Large Animal Clinical Sciences, School of Veterinary Medicine & Biomedical Sciences, Texas A&M University, College Station, TX (Reiskind, Bray, Bordin, Cohen) and Rood & Riddle Equine Hospital in Saratoga Springs, NY (Flores-Ahlschwede, Ahlschwede).
Abstract	Rhodococcus equi causes disease and death from pneumonia in foals worldwide. Transfusing plasma from donor horses hyperimmunized against R. equi (RE HIP) to newborn foals reduces R. equi pneumonia incidence. Antibodies in RE HIP are considered to mediate opsonophagocytic killing of R. equi in concert with complement (C) and neutrophils. However, if RE HIP transfusion increases serum C concentrations and if increased serum C concentration is associated with reduced risk of pneumonia in foals is unknown. The objectives of this study were to determine serum concentrations of C component 1 q antigen (C1q) before and after transfusion of foals with RE HIP, and to examine whether C1q concentrations after transfusion were lower in foals that went on to develop pneumonia. We hypothesized that serum concentrations of C1q would significantly increase in foals following transfusion and that concentrations of C1q following transfusion would be significantly lower in foals that developed pneumonia. Serum samples from 205 foals from 2 R. equi-endemic farms in New York were collected immediately before and after transfusion at age < 48 hours with RE HIP from a single manufacturer. C1q concentrations were determined by enzyme-linked immunosorbent assay. Data were analyzed using generalized linear modeling. Concentrations of C1q were significantly ($P > 0.0001$) decreased following transfusion. Lower serum concentration of C1q pre-transfusion was significantly ($P < 0.05$) associated with development of R. equi pneumonia. These findings indicate that transfusion with RE HIP does not mediate protection by increasing serum C1q concentrations, but C1q concentrations are inversely associated with the risk of rhodococcal pneumonia.
Research Grant	Advancement in Equine Research Award from Boehringer-Ingelheim Animal Health. Additional support from the Link Equine Research Endowment and the Glenn Blodgett Chair in Equine Studies.
Field of Research	Equine Medicine and Surgery

Abstract Title	Dexmedetomidine-midazolam sedation in Sonoran Desert toads: effect on cardiorespiratory function and activity
Authors	Hayley Rejcek, Hannah Cavanaugh, Margaret Marsh, Joshua T. Butcher, Trinity McMahon, Landon Butler, João Brandão
Affiliations	Department of Veterinary Clinical Sciences (Rejcek, Brandão) Department of Physiological Sciences (Cavanaugh, Marsh, Butcher), College of Veterinary Medicine, Oklahoma State University, Stillwater, OK.
Abstract	Compared to other animal groups, such as mammals and birds, there is limited research on amphibian sedation. Overall, it is accepted that amphibians require higher doses of sedative drugs, but dose determination studies, evaluation of cardiovascular side effects, and impact of sedation on activity and behavior are not well studied. Therefore, the goals of this project were to 1) determine the effective dose 50 (ED50) of intramuscular (IM) midazolam- and dexmedetomidine-alone, 2) evaluate the cardiorespiratory effects of IM midazolam-dexmedetomidine at ED50, and 3) evaluate the short-term impact (up to 2 hours) on activity using a Noldus EthoVision XTTM following sedation reversal in Sonoran Desert toads (Incilius alvarius). A total of 21 toads were available for this study. Using a clinically applicable sedation score, ED50 IM dexmedetomidine was 0.5 mg/kg and midazolam was 5 mg/kg when calculated with the Dixon's Up-and-Down method. Although no morbidity or mortality was noted during the study, when midazolam (5 mg/kg IM) was combined with dexmedetomidine (0.5 mg/kg IM), statistically significant cardiopulmonary depression was noted during the 30 min post-treatment administration, when compared to the control group. Animals recovered quickly after reversal administration. Activity is currently undergoing statistical analysis. Based on the current results of this study, high doses of dexmedetomidine and midazolam are needed to achieve a sedative status that allows for clinical procedures. Although no morbidity or mortality were detected at any point, the cardiorespiratory side-effects are substantial and should be taken into consideration when sedating toads, in particular, non-healthy animals.
Research Grant	Debbie and Wayne Bell Professorship in Veterinary Clinical Sciences
Field of Research	Pharmacology and Toxicology

Abstract Title	Safety and pharmacokinetics of bacteriophage therapy in an ovine model of fracture-related infection
Authors	Jennifer Resnick, Daniel Arens, Caroline Constant, and Christian Peez
Affiliations	AO Research Institute - Preclinical Services and Musculoskeletal Infection, Davos, Switzerland
Abstract	Treating fracture-related infections (FRI) with antibiotics has become increasingly challenging due to antibiotic resistance of pathogens. Phage therapy offers a novel approach to eradicating multi-resistant bacteria. Lytic bacteriophages (phages) viruses that can lyse, infect, and kill bacteria by disrupting their metabolism, regardless of their antimicrobial resistance. Immediately after infection, the bacterial cell is redirected to manufacture phage particles, which are released in large numbers when the host cell lyses. Newly formed virus particles then infect additional bacterial cells. Although this new strategy seems appealing, further research is required to optimize treatment protocols and indications. This study aims to provide fundamental safety information on phage therapy in clinically relevant ovine models. Phages were initially injected into three non-infected sheep. In the second phase, phage therapy was initiated after induction of a FRI by an injection of a staphylococcus aureus of human origin into twelve sheep. The mode of administration of the phage was also tested, in saline locally or intravenous for ten days. Drain and serum were collected throughout to detect the distribution of phages and any changes, the development of phage resistance, and the production of anti-phage antibodies. After euthanasia, samples were collected from all sheep to quantify bacterial burden, determine phage titer, and histological comparison of the safety and efficacy of both administered therapies.
Research Grant	AO Trauma
Field of Research	Orthopedics

Abstract Title	The effect of green light phototherapy on equine lameness
Authors	Lynsie T. Rhegness, Sarah Jacob, Jack Kottwitz, Amelia Munsterman
Affiliations	College of Veterinary Medicine, Michigan State University, East Lansing, MI
Abstract	Musculoskeletal diseases resulting in pain and lameness are the most common disorders that affect horse's health. Current recommended treatments include non-steroidal anti-inflammatory drugs, gamma aminobutyric acid analogs, opioids, and/or stall rest. However, pharmaceuticals can have adverse side effects with narrow margins of safety. Green light phototherapy (GLP) has shown promising results for both soft tissue and neuropathic pain in rodents and humans. The analgesic effects appear to be mediated by intrinsically photosensitive retinal ganglion cells via release of endogenous opioids within the central nervous system. The purpose of this study was to evaluate the effects of GLP on equine lameness. Our hypothesis was that GLP would increase endogenous opioids, adrenocorticotrophic hormone (ACTH) and cortisol levels with a concurrent reduction in lameness scores. A total of 10 horses with chronic lameness were treated with either GLP (5 horses) or white lights (5 control horses) for 6 hours a day over 6 days. Lameness exams were conducted daily using an inertial sensor that measures gait asymmetry, along with scoring of lameness videos by two blinded observers. Cervical cerebrospinal (CSF) samples were collected at the beginning and end of the treatment period to monitor endogenous opioids (b endorphin, proenkephalin), ACTH, and cortisol levels. Comparison of lameness progression and CSF hormones will be performed within and between the control and treatment groups. We anticipate that lameness will improve in treated horses, with a concurrent increase in CSF hormone levels. A positive outcome will support GLP as a non-pharmacological treatment method for equine lameness.
Research Grant	MSU Professional Development Funds
Field of Research	Equine Medicine and Surgery

Abstract Title	Got Lyme?: Prevalence of Borrelia burgdorferi in Ixodes scapularis ticks collected from horses across the USA
Authors	Hanna E. Rhoads, Makaela Hedberg, and Brian H. Herrin
Affiliations	Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS
Abstract	Borrelia burgdorferi is a spirochete transmitted by Ixodes spp. ticks and is responsible for Lyme in humans, dogs, and horses. Although I. scapularis ticks are present across most of the Eastern and Midwestern United States, the prevalence of B. burgdorferi in its tick vector is variable throughout the range, and there are few studies on the prevalence of this pathogen in ticks collected from horses. As part of the National Equine Tick Survey (NETS), ticks were collected from horses across the country and morphologically identified as Ixodes scapularis. Submissions were sorted based on state of origin and previously established regions defined in other parasite epidemiologic studies. Ticks identified as I. scapularis were dissected, had their DNA extracted, and were tested via nested PCR for B. burgdorferi. A total of 330 adult male and female I. scapularis ticks were submitted; 92 from the Midwest (M), 198 from the Northeast (NE), 38 from the Southeast (SE), and 0 from the West (W). Prevalence of B. burgdorferi was 20% overall, 23% for NE, and 15% for SE and M. The number of submissions was highly variable across states with 161 submissions from Pennsylvania and many enrolled states submitting zero or only one tick. Higher number of submissions from states may represent higher populations of I. scapularis as well as increased concern about tickborne disease. Further study is warranted to assess tick feeding behavior on horses and its relationship to B. burgdorferi prevalence.
Research Grant	Startup Funding Kansas State University College of Veterinary Medicine
Field of Research	Parasitology

Abstract Title	Influence of Tnf deficiency on inflammation, coagulation, and oxidative stress in malaria during pregnancy
Authors	Marc A. Rivas, Julie M. Moore, Alicer K. Andrew
Affiliations	Department of Infectious Diseases and Immunology, College of Veterinary Medicine, University of Florida, Gainesville, FL
Abstract	Plasmodium falciparum infection in pregnant women manifests as placental malaria (PM), causing severe pregnancy and birth complications. Infected erythrocytes sequester in the intervillous space of the placenta, leading to severe maternal inflammation, oxidative stress, and dysregulated coagulation involving proinflammatory cytokine release in the placenta. We hypothesize that the physiological pathways of inflammation, coagulation, and oxidative stress are intimately linked in malaria pathogenic processes and thus disruption of one of these regulatory pathways, via selective gene manipulation, will improve pregnancy outcome by altering all of the pathways. Prior studies demonstrated that C57BL/6J (B6) mice deficient in the inflammatory cytokine, tumor necrosis factor (Tnf), have improved pregnancy outcomes. Our study, utilizing a murine model that simulates human PM with infected Tnf deficient (Tnf-/-) mice, aimed to support those findings. Transcript analysis of infected Tnf-/- mouse conceptuses compared to intact conceptuses showed a thirteen-fold reduced expression of the pro-inflammatory cytokine, interleukin-1-beta (Il1-β), while expression of Tnf was unchanged. Similarly, procoagulant tissue factor (Tf) expression did not change in Tnf-/- embryos, while endothelial protein C receptor (Epcr) transcripts had a three-fold increase, suggesting suppressed coagulation. Expression of antioxidant genes, Sod1 and Sod2, did not significantly change in Tnf-/- mice. This research will aid in the understanding of the interactions between the major pathways of inflammation, coagulation, and oxidative stress in malaria pathophysiology and may assist in development of potential therapies to improve pregnancy outcomes.
Research Grant	University of Florida College of Veterinary Medicine funds to Julie M. Moore
Field of Research	Immunology

Abstract Title	Immune activated cellular therapy for treatment of osteoarthritis
Authors	Meagan Rockow, Lyndah Chow, Renata Impastato, Dean Hendrickson, Kelly Santangelo, Steven Dow, Lynn Pezzanite
Affiliations	Department of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Fort Collins, CO
Abstract	Despite the high prevalence of osteoarthritis (OA), there remains a lack of effective treatment options. Cellular therapies such as mesenchymal stromal cells (MSCs) are increasingly popular for treatment of OA, but their effectiveness may be improved by pre-activation before injection. We hypothesized that activation of MSCs with a nucleic acid ligand for Toll-like receptor 3 would improve efficacy to treat OA. To address this question, we used a mouse model in which OA was induced via surgical medial meniscal destabilization. Mice received intra-articular injections at 3 and 5 weeks postoperatively with either needle insertion alone, non-activated MSC, or TLR-activated MSC, and their activity level was monitored weekly until week 8. Outcome parameters assessed were mouse mobility evaluated by motion-activated camera (AnyMaze®) and bulk RNA sequencing of injected joint tissues. Additionally, an in vitro model was used to assess the effects of activated vs non-activated MSC on macrophage inflammatory responses as a model for synovial immune responses. Gait analyses indicated that mice treated with TLR-MSCs traveled further total distances, spent greater time mobile, and had greater mean speeds compared to those receiving sham injections. Analysis of joint transcriptomes revealed significant differences in tissues of mice treated with activated MSC, indicating significant differences in tissue responses. Ongoing macrophage modeling studies will include both cytokine and transcriptome analysis. These studies therefore provide support for the hypothesis that activated MSC may be more effective than non-activated MSC in treating OA in animals and humans, and point to new directions for understanding mechanisms of action.
Research Grant	CSU Department of Clinical Sciences, CSU, Young Investigator Grant in Companion Animal Studies, Carolyn Quan and Porter Bennett
Field of Research	Orthopedics

Abstract Title	PCR for antigen receptor rearrangement: Benchmarking performance of a clonality assay in diverse canine sample
Authors	Frank Rodriguez, and Mohamed Abouelkhair
Affiliations	Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, The University of Tennessee, Knoxville, TN.
Abstract	In the field of veterinary medicine, the use of molecular diagnostic tools is on the rise. However, unlike traditional diagnostic tests, such as hematology and chemistry, molecular diagnostic tests in veterinary medicine lack a well-established history of benchmarking and standardization. One area where molecular diagnostics are increasingly employed is in the differential diagnosis of lymphoma in dogs. Distinguishing between malignant lymphoid tumors and benign reactive hyperplasia can be challenging in certain cases, such as early-stage lymphoma with intact nodal structure or nodular lymphoma resembling normal nodal architecture. Polymerase chain reaction (PCR) for antigen receptor rearrangement (PARR) is a molecular test that enables the discrimination of these lymphoid malignancies, providing valuable insights for accurate diagnosis and treatment. PARR assay variations have been described and are commercially available, but performance metrics are not uniformly reported. The objective of our study was to assess the accuracy, sensitivity, and specificity of the PARR assay. To achieve this, we extracted total DNA from a diverse range of samples, including leftover samples submitted for routine diagnostics such as flow cytometry, using a Qiagen DNA/RNA Extraction Kit in the clinical immunology lab at UTCVM. Assay performance was determined for 5 blood samples and 31 fine-needle aspirates (20 lymphoma, 11 non-lymphoma) from a total of 36 dogs (20 B-cell lymphoma, 1 T-cell lymphoma, and 15 non-lymphoma). Performance metrics were lower in most cases for discrimination of B- or T-cell versus non-B- or non-T-cell samples than for lymphoma versus non-lymphoma.
Research Grant	None
Field of Research	Immunology

Abstract Title	Characterization of Postmortem Trauma After Fall from Heights in Dogs and Cats.
Authors	Taína Rodríguez, Nanny Wenzlow
Affiliations	Louisiana State University, PBS-LADDL
Abstract	After perpetrators commit acts of cruelty in the form of blunt-force trauma, they might conceal their acts by dropping the cadaver from heights, which causes additional lesions to the body. Hemorrhages allow the distinction between ante- and postmortem changes in fresh bodies but is much less useful in decomposed cadavers. Freshly euthanized puppies (n=10), adult dogs (n=10) and kittens (n=8) were separated into two groups and dropped from 40 feet and 80 feet respectively. All animals had pre-necropsy radiographs taken. Liver lacerations were present in 100% of animals. Of both species, 65% had skull fractures (puppies (93%) and kittens (50%)). Rib fractures were present in 80% of all dogs and mostly in puppies (76%). Although true pulverization of the solid inner organs was not observed, 27% of animals showed rupture of the kidney capsule, and 13% showed fragmentation of the liver into multiple, smaller, detached pieces. Limb fractures were present in 44% of cases, 42% of which were adult dogs and 2% were puppies. Fractures of the spine were seen in 17% of animals. Pre-necropsy radiographs were essential to the identification of most bone fractures. The histology of all fractures confirmed the absence of vital reaction or repair, with pointy sharp edges of the bone fragments typical of wet fractures. The distribution of these lesions is different from those seen in animals with high-rise syndrome, motor-vehicle trauma, and accidental or non-accidental injuries (NAI).
Research Grant	Research Grant: Dr. Wenzlow's Start-up Fund. Student Support: None
Field of Research	Anatomic Pathology

Abstract Title	Evaluating the effects of AFFFs with and without PFAS on the development and behavior of larval zebrafish
Authors	Patrik Rollefson, Pranup Adhikari, Demetrius McAtee, Mohamed Ateia, Ahmed Abdelmoneim
Affiliations	Department of Comparative Biomedical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA (Rollefson, Adhikari, McAtee, Abdelmoniem) Department of Chemical and Biomolecular Engineering, George R. Brown School of Engineering, Rice University, Houston, TX (Ateia)
Abstract	Per and polyfluoroalkyl substances (PFAS) are a diverse group of chemicals widely used in consumer and commercial products due to their resistance to oil, water and heat. In military settings, PFAS-containing aqueous film forming foams (AFFF) play a critical role in extinguishing fires involving Class B materials. However, with recent studies highlighting the ubiquitous presence and persistence of PFAS in the environment and their potential adverse health effects, federal initiatives to develop PFAS-free AFFF for fire suppressants have emerged. The objective of this study was to evaluate the effects of developmental exposure to a PFAS-containing AFFF (Buckeye) and a PFAS-free alternative (BioEx Ecopol A3+) on the development and behavior using the zebrafish model organism. Enzymatically dechorionated wild-type zebrafish embryos were individually plated in prefilled 96-well plates, with exposure media consisting of a 5-fold dilution series starting from 0.1% of the working concentration of the target AFFFs. The exposures extended between 6 and 120 hpf (hours post fertilization) to encompass embryonic and early larval development. Daily media changes (50%) were performed using a robotic liquid handling system. At the end of the exposure period, multiple endpoints were evaluated, including mortality, overall development, prevalence of morphological defects, and behavioral activity under baseline conditions and in response to acute stressors. This study underscores the importance of evaluating the safety of chemicals and their alternatives as it pertains to environmental and human health.
Research Grant	LSU
Field of Research	Pharmacology and Toxicology

Abstract Title	Diet Manipulation in Macaques with Enteric Disease and the Effects on the Gastrointestinal Microbiota
Authors	Gabrielle Roque, Paul Makidon, Keely McGrew
Affiliations	Mississippi State College of Veterinary Medicine, Inotiv, Charles River Laboratory
Abstract	In captive import/export macaque facilities, idiopathic diarrhea is a common health concern. Enteric disease incidences in captive breeding population have a great impact for the animal, as well as the economic and human disease modeling industry. The etiology of diarrhea can be multifactorial including commonly described pathogens, behavioral stress, dietary issues, and operationally related factors. It is well understood that gut microbiota plays a major role in susceptibility to diarrheal diseases. Yet, the relationship between the disease and microbiota in captive NHP is not well described. Thankfully, there are numerous opportunities for therapeutic intervention. These include antibiotics, dietary manipulation, fiber symbiotics, and behavioral manipulation. Standard of care for numerous veterinary species and humans dictate the use of diets that are bland in nature, non-inflammatory, and non-challenging to the intestinal tract. A suggestion is a bland diet will promote “healthier” gut microbiome. In this study, we compared a group (N=13) of NHPs with diarrhea who were placed on a bland diet vs. a group (N=13) of were fed a standard primate chow. In addition to characterizing the microbiome, animals were clinically assessed by a clinical scoring system. Although there were a few differences identified in the clinical scoring between NHPS treated with bland diet vs. standard primate chow, we did observe less remission in the bland diet group. The remission rates are supportive of the idea that the gut microbiome shifted to a healthier phenotype in the bland diet group compared to the control. This evidence-based medicine provides a framework for informing future herd management of diarrhea in captive macaques.
Research Grant	Inotiv
Field of Research	Laboratory Animal Medicine

Abstract Title	RISC-y business: Impact of siRNA knockdown of nonstructural protein 1 on bluetongue virus replication
Authors	Danny Rosen, Stacey Scroggs, Taylor Steele, Jessica Gutierrez, Barbara S. Drolet
Affiliations	College of Veterinary Medicine (Rosen), Kansas State University, Manhattan, KS. Arthropod-Borne Animal Diseases Research Unit (Rosen, Scroggs, Steele, Gutierrez, Drolet) Agricultural Research Service, USDA, Manhattan, KS
Abstract	Bluetongue virus (BTV) causes hemorrhagic disease in domestic and wild ruminants. BTV is transmitted by Culicoides biting midges. There are at least 26 serotypes of BTV worldwide, with 17 serotypes either established or reported in the US. RNA interference (RNAi) is an immune response in these vector insects that degrades intracellular viral RNA through the RISC protein assemblage. We investigated if inducing an RNAi response with a small interfering RNA (siRNA) targeting the BTV protein synthesis regulator, nonstructural protein 1 (NS1), would suppress the replication of BTV in a Culicoides cell line (W8). W8 cells were transfected with either NS1 or luciferase control siRNAs, then infected at 24 h with BTV at low and high dose. Virus was collected from the cells and media at a range of time points. Infectious virus was quantified via plaque assay on Vero cells and viral RNA was quantitated by reverse transcription real time quantitative PCR (RT-qPCR). Viral RNA showed down regulation by NS1 dsRNA very early (1 hour) by RT-qPCR and had lower infectious titers at 24 and 48 hours by plaque assay. Both assays showed viral recovery by 96 hours. Unexpectedly, infectious virus was detected earlier for both siRNA treatments compared to the untreated control. This may suggest that experimental introduction of small dsRNAs distract the innate immune system, as has been reported for other insect-transmitted viruses. These preliminary data highlight the complexity of developing RNAi-based control measures to decrease viral replication. Further research will be needed to evaluate RNAi as a means of controlling BTV in Culicoides biting midges or determine if another knockdown target would prove successful.
Research Grant	USDA, NP103: 3020-32000-020-00D
Field of Research	Virology

Abstract Title	Beads of Discovery: Use of Barcoded Magnetic Beads for Tick-Borne Disease Molecular Diagnosis and Surveillance
Authors	Sean Rowan, Nazleen Mohseni, Sheema Mir
Affiliations	Western University of Health Sciences, College of Veterinary Medicine
Abstract	Tick-borne diseases pose a significant threat to both humans and animals as a wide range of pathogens, can be transmitted from ticks to vertebrates. Surveillance of tick-borne diseases within the population still requires advancements in diagnostic tools. In the field of human medicine, the current standard is a nucleic acid-based multiplex diagnostic assay tool. This powerful tool enables simultaneous screening of 384 patient samples for various tick-borne pathogens. To address the need for improved diagnostics in veterinary medicine, our lab has developed an assay using barcoded magnetic bead technology on the BioCode 2500 system. This assay allows for the simultaneous detection of canine tick-borne pathogens from a single test sample. Our lab has developed a duplex assay for two two major tick-borne pathogens, namely A. phagocytophilum and B. burgdorferi species. The objective is to determine the prevalence of these two pathogens in a randomly selected canine population consisting of 25 samples collected at the Pet Health Center, Pomona. Future goal is to include R. rickettsii, B. canis, and E. canis to the duplex to enhance the diagnostic capacity of the assay. Given the close association between tick-borne infections in humans and animals, it is essential to integrate data from veterinary and human reporting systems to effectively control these diseases. Multiplex diagnostic assays play a crucial role in this integration process. This canine multiplex diagnostic assay holds the potential to serve as a quick and accurate tool for identifying tick-borne pathogens, facilitating timely treatments, effective public health interventions, and improved surveillance of tick-borne diseases in the population.
Research Grant	United States Department of Agriculture (USDA)
Field of Research	Laboratory Animal Medicine

Abstract Title	Incidence of bilateral temporohyoid osteoarthropathy in horses presented to CSU-VTH between 2013 and 2023
Authors	Kaila Rowe, Yvette S. Nout-Lomas
Affiliations	Colorado State University CVM, Fort Collins, CO
Abstract	Temporohyoid osteoarthropathy (THO) is a condition in horses in which the stylohyoid bone of the hyoid apparatus fuses with the petrous temporal bone of the skull. THO usually presents with unilateral neurological signs when the fusion affects cranial nerve function, compromising the safety of the horse. Most cases of THO are reported to be unilateral as they present with unilateral neurological signs, yet upon further examination many of these horses appear to have bilateral disease. The goal of this project is to test the hypothesis that the majority of THO cases are bilateral. Horses with undiagnosed bilateral THO that undergo a unilateral ceratohyoidectomy may be at risk for complications including neurologic dysfunction occurring from the opposite untreated temporohyoid joint in the future. A retrospective analysis of medical records from 20 cases of THO presented to Colorado State University (CSU) from 2013-2023 was performed. Presence of THO is detected via radiography, endoscopy, and computed tomography (CT), with CT being the gold standard diagnostic tool. Interestingly we show that CT was able to differentiate more accurately between bilateral and unilateral disease than endoscopy and radiography by overriding their findings 57% of the time in regards to changing diagnosis from unilateral to bilateral. Furthermore, 86% of CTs showed bilateral disease. Of the 7 horses diagnosed with unilateral THO only one underwent a CT scan. The clinical implication of this work is to emphasize the importance of CT to diagnose this condition. Future follow-up studies are necessary to determine if this information should change the current way of managing and recommending diagnostic and surgical procedures for these horses.
Research Grant	Yvette S. Nout-Lomas, Equine Neurology Fund
Field of Research	Equine Medicine and Surgery

Abstract Title	Nosema ceranae infection alters honey bee (Apis mellifera) queen behavior and reproductive capacity
Authors	Madison Rowe, Abigail Martinez, Keegan Nichols, Dr. Tonya Shepherd, Dr. Juliana Rangel
Affiliations	School of Veterinary Medicine & Biomedical Sciences, Texas A&M University, College Station, TX (Rowe); University of Texas Rio Grande Valley, Edinburg, TX (Martinez); Department of Entomology, Texas A&M University, College Station, TX (Nichols, Shepherd, Rangel)
Abstract	The Western honey bee, Apis mellifera, plays a vital role in agriculture, especially as the key pollinator of several crops. Thousands of managed honey bee colonies are often transported across state lines to fulfill pollination services. This leads them to intermingle in the fields, making communicable diseases a major concern. The takeover of the microsporidian Nosema ceranae over N. apis as the main honey bee gut pathogen has revealed a knowledge gap regarding how N. ceranae affects colony health. While the general consequences are well-substantiated, the long-term effects on behavior of queens are understudied. The queen is responsible for laying up to 1,500 eggs per day, making her health critical for colony productivity. In this study, we explored the effects of N. ceranae infection on queen egg-laying capacity and mobility, as well as worker retinue behavior. We hypothesized that queens would lay fewer eggs, be less mobile, and elicit a smaller retinue after inoculation with N. ceranae compared to their initial response. We set up observation colonies headed by sister queens and fed each a sucrose solution. We monitored the queens' egg-laying capacity, mobility, and retinue size for six consecutive days. We then inoculated each queen with a sucrose solution containing N. ceranae spores and conducted similar measurements for six days. We found a significant increase in mobility and egg-laying capacity with a significant decrease in retinue after inoculation. N. ceranae impacts colony health via altered queen vitality and reproductive output alongside the known consequences in workers. This makes N. ceranae a multi-focal threat to the agriculture industry through its simultaneous weakening of workers and queens.
Research Grant	Boehringer Ingelheim VSP
Field of Research	Behavior

Abstract Title	Confirmation of chelonid alphaherpesvirus 5 infection in green and Kemp's ridley sea turtles from Mississippi
Authors	Sarah Rubelowsky, Justin Stilwell, Caroline Betbeze, Debra Moore, Lyndsey Howell, and Natalie Stilwell
Affiliations	Mississippi State University CVM, Mississippi State, MS (Rubelowsky, Stilwell, Betbeze, Moore, Stilwell), National Oceanic & Atmospheric Administration, Pascagoula, MS (Howell)
Abstract	Fibropapillomatosis (FP) is a neoplastic disease associated with chelonid alphaherpesvirus 5 (ChHV5) infection in threatened and endangered sea turtles worldwide. Due to its transmissible nature, high disease prevalence in some areas, and potential for severe disease among affected individuals, FP negatively impacts sea turtle health and creates challenges for rehabilitation programs. To our knowledge, FP remains unreported in Mississippi. Over a 6-month period in 2022-2023, one Kemp's ridley sea turtle (Lepidochelys kempii) and three green sea turtles (Chelonia mydas) stranded off the Mississippi coast with FP-suggestive lesions. The objectives of this study were to molecularly confirm and phylogenetically characterize ChHV5 strains from the recent Mississippi cases. Conventional PCR assays targeting three ChHV5 genes were performed on genomic DNA from FP lesion, skin, and blood samples collected at necropsy. Positive detections were confirmed using Nanopore sequencing. Results confirmed ChHV5 infection in all four cases as well as another stranded, asymptomatic Kemp's ridley sea turtle from the Mississippi region. Phylogenetic analysis of the concatenated genes revealed that ChHV5 strains from the Mississippi turtles were most closely related to strains from Florida, the Caribbean, and Atlantic seaboard, but were relatively unrelated to strains from Texas, suggesting a possible east-to-west dissemination pattern. These results offer the first confirmation of FP-associated ChHV5 infection in sea turtles from the Mississippi coast. Importantly, the detection of ChHV5 in an asymptomatic Kemp's ridley turtle underscores the need for additional surveillance to understand the prevalence of this pathogen in Mississippi.
Research Grant	The National Fish and Wildlife Foundation under the Mississippi Department of Environmental Quality Agreement No. 18-00081, Department of Clinical Sciences ECFVG funds
Field of Research	Wildlife Conservation

Abstract Title	Comparison of an opioid versus a non-opioid anesthesia protocol on canine gastroesophageal reflux incidence
Authors	Haley Rubia, Colleen Hickey, Erin Wendt-Hornickle
Affiliations	Department of Veterinary Clinical Sciences (Hickey, Wendt-Hornickle), College of Veterinary Medicine, University of Minnesota, St. Paul, MN
Abstract	Gastroesophageal reflux (GER) occurs when gastric acid or bile backflows into the esophagus and threatens to damage the mucosa. GER incidence varies from 40% to 60% in anesthetized dogs compared to < 1% in awake dogs. Consequences of GER include esophagitis, regurgitation, esophageal strictures, and aspiration pneumonia. Opioid-mediated decreases in gastrointestinal motility and reduction in lower esophageal sphincter tone are likely contributing factors to perianesthetic GER. To date, no study has directly compared opioid and non-opioid protocols and the subsequent development of GER. We hypothesize that an opioid-free anesthetic technique will decrease GER incidence compared to an opioid-containing protocol in anesthetized healthy dogs for elective hindlimb orthopedic procedures. Hydromorphone hydrochloride, the premedication and analgesia option, is the independent opioid factor that will be removed in the randomized experimental group. Since opioids are the gold standard for the treatment of acute peri-operative pain, steps were taken to ensure patients in the experimental group do not experience pain. During surgery, if there is over a 20% increase in baseline heart rate and mean arterial pressure for more than 5 minutes and the patient is receiving an adequate inhalant anesthetic, an additional dose of analgesia is administered. After tracheal intubation, a 6.4-French-calibrated esophageal pH probe is placed in the esophagus via the oral cavity for continuous pH measurements during surgery. Esophageal reflux is defined when the pH is < 4.0 for gastric reflux or > 7.5 for biliary reflux for more than 30 seconds. These findings will bring us one step closer to finding factors associated with GER occurrence.
Research Grant	2023 CVM Resident & Graduate Student Research Grants (RAF #755)
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Differential detection of biofilm-producing and non-producing Salmonella by MALDI-TOF MS and IR Biotyper
Authors	Phoebe Rychener, Smriti Shringi, Samuel Ajulo, Juned Ahmed, and Devendra H. Shah
Affiliations	School of Veterinary Medicine, Texas Tech University, Amarillo, Texas
Abstract	Salmonella, the world's leading foodborne pathogen, is one of the many types of bacteria that have certain strains that can produce biofilms. Biofilms are slimy layers that aid in the long-term persistence of Salmonella in the food animal and food processing environment, often related to their ability to resist chemical disinfection, antibiotic treatment, and host immune responses. The aim of this study was to employ MALDI-TOF and IR biotyping technologies for rapid differential detection of biofilm-producing and non-producing Salmonella. The pure cultures of a total of 156 strains of the twelve most prevalent poultry-associated Salmonella serotypes that were previously determined to be biofilm producers (n=72) and non-producers (n=84) will be evaluated by MALDI-TOF and Bruker IR Biotyper. The MS and IR spectra generated will be evaluated to determine the distinguishing peaks/markers between biofilm producers and biofilm non-producers. These will then be used to generate a super spectrum to which all future test samples can be compared for rapid detection of Salmonella along with discrimination based on biofilm phenotype. If successful, the approach developed in this study will provide an easier and faster way to identify biofilm-producing bacteria compared to current conventional procedures. The rapid detection of biofilm-producing Salmonella will aid in predicting and mitigating the risks associated with the biofilm-driven persistence of Salmonella strains in food animals and food processing environments.
Research Grant	TTU School of Veterinary Medicine
Field of Research	Bacteriology

Abstract Title	An in-vitro study of feline calicivirus (FCV) as a corneal pathogen utilizing feline corneal epithelial cells
Authors	Daniela I. Saade, Erinn P. Mills, Ugochi Emelogu, Andrew C. Lewin
Affiliations	Veterinary Clinical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	Feline calicivirus (FCV) is a common viral pathogen of domestic cats. Information on FCV's role in feline ocular surface disease is scarce. An emerging body of evidence supports the role of FCV as a primary ocular surface pathogen in domestic cats, yet confirmation of replication and cytopathogenic effect (CPE) of FCV in feline corneal epithelial cells (FCEC) remains unassessed. The objective of this study was to determine whether FCV replicates in FCEC, leading to cellular CPE. We hypothesized that FCV is capable of replicating in FCEC with associated CPE. This would suggest that FCV is capable of acting as a primary corneal pathogen in domestic cats. Superficial keratectomies were performed to isolate FCEC of cats euthanized for unrelated reasons, which were cultured in-vitro. Using 7 previously archived FCV samples, viral RNA was extracted for subsequent sequencing using Illumina MiSeq. Following reference-based assembly, whole viral genomes were annotated and assessed. The 3 most genomically diverse FCV isolates were used to infect FCEC at two different multiplicity of infection (MOI) ratios (0.1 and 0.01 (PFU/cell)). Once infected, FCEC were monitored for up to 48 hours for visible CPE. Feline herpesvirus type 1 (FHV-1) was used as a positive control. Following FCEC infection, viral titer (using Crandall Rees Feline Kidney cells) was performed and viral identity was re-confirmed by quantitative PCR. Maximum (100%) CPE was observed 24 hours following infection for FCV (MOI 0.01/0.1) and 48 hours following infection for FHV-1 (MOI 0.01/0.1). Viral titers and qPCR for re-confirmation of identity are pending. These preliminary results support our hypothesis that FCV is capable of replicating in FCEC.
Research Grant	LSU Startup funds (Lewin)
Field of Research	Ophthalmology

Abstract Title	Veterinary collaboration prior to emergent ophthalmic referrals can lower costs and improve patient care
Authors	Allyson Sabatelli, Esteban Fernandez-Juricic, Bret A. Moore
Affiliations	Department of Small Animal Clinical Science, University of Florida College of Veterinary Medicine, Gainesville, Florida. (Sabatelli, Moore) Department of Biological Science, Purdue University, West Lafayette, Indiana. (Fernandez-Juricic)
Abstract	Collaborative care in veterinary medicine offers clients the most efficient and effective options for managing patients and can help establish the need for referral to a specialist. This retrospective pilot study aimed to characterize the diagnostic and treatment complexity, costs, and urgency of emergency referrals to a veterinary ophthalmology service to predict the alternative outcome of virtual collaborative care with an ophthalmologist. Emergency referral cases (86) seen by the University of Florida Ophthalmology service from 1/1-6/30/23 were included. Electronic medical records were reviewed for diagnosis, treatment, and cost. Diagnostic and treatment complexity was categorized based on core competencies of the veterinary curriculum as able to be managed successfully by a general practitioner or requiring an ophthalmologist. Patients and clients remained anonymous throughout the study. Data analysis was conducted on GraphPad Prism version 9.5.1. A greater proportion of cases were at the educational level required for successful management by a general practitioner (68.67%) than that of a specialist (31.33%), and it was estimated that the mean expense incurred by referral of a case not requiring specialty care was $506.80 (95% CI, $410.00 to $603.70). These findings suggested that client costs such as travel, diagnostics, and treatment, for emergent referrals could be reduced by virtual collaboration when not requiring immediate care by an ophthalmologist. Future analysis of a larger data set will include generalized linear mixed modeling to better guide the development of new methods to improve the referral process and collaboration between general and specialty medicine in this hospital and profession wide.
Research Grant	None
Field of Research	Ophthalmology

Abstract Title	SK2 Expression of the Motor Thalamus in Normal Motor Function, and their Dysregulation in Parkinson's Disease
Authors	Phillip Saint-Martin, Tashonda Vaughn, Olalekan M. Ogundele
Affiliations	Department of Comparative Biomedical Sciences, Louisiana State University School of Veterinary Medicine.
Abstract	SK2 channels are small conductance Ca+2 -activated K+ channels found widely in the CNS and are central to many of the vital brain functions such as the transmission of information, memory, learning and synaptic plasticity. Post-synaptic densities that harbor SK2 channels also contain domains with Calcium-calmodulin-dependent kinase II (CaMKII). During an excitatory synaptic neurotransmission, CaMKII auto-phosphorylates at the Thr (T) 286. In this self-activated state, it continues to function even after the absence of Ca+2 flux. Because these two proteins (i.e., SK2 and CaMKII) are pertinent to synaptic excitation, and its suppression, thereafter, the proposed research will examine activity-coupled regulation of these proteins in excitation-induced Parkinson's' Disease (PD). Here, we used a hemi-parkinsonian mouse model to ascertain how SK2/CaMKII expression is altered in excitatory synapses of the motor thalamus following the loss of inhibitory striatal inputs. Induced PD was verified through a motor function test for fine and coarse motor skills. The results of this project will demonstrate a novel mechanism activity coupled regulation of excitation in the motor pathway.
Research Grant	NSF Grant
Field of Research	Physiology

Abstract Title	Measles virus infection induces IP-10 release but not inflammasome activation in respiratory epithelial cells
Authors	Brittany Salciccioli, Jacqueline Brockhurst, Diane E. Griffin
Affiliations	College of Veterinary Medicine, University of Georgia, Athens, GA (Salciccioli) Cellular and Molecular Medicine, Johns Hopkins School of Medicine, Baltimore, MD (Brockhurst) W. Harry Feinstone Department of Molecular Microbiology & Immunology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD (Griffin)
Abstract	Measles virus (MeV) infection is an important cause of childhood mortality and is spread through the respiratory route. MeV suppresses the innate immune response systemically by inhibiting interferon (IFN) release, allowing MeV replication, and spread. Much is unknown about the host immune response in the respiratory tract, including how the virus establishes efficient infection of respiratory epithelial cells. MeV induces inflammasome activation in macrophages, but this has not been well studied in the respiratory tract. Our goal is to explore the innate immune response following MeV infection using differentiated tracheal epithelial cells (TEC) from rhesus macaques. Using TECs, we looked for evidence of inflammasome activation as evidenced by cell death (TUNEL assay, LDH) and the release of inflammasome products (IL-1β and IL-18). We also looked at IP-10/CXCL10 production which is detected systemically during MeV infection. TEC cultures were infected at MOI = 1 with wildtype Bilthoven MeV (WT) or vaccine strain Edmonston-Zagreb (EZ). Samples were collected from mock or MeV-infected TEC cultures over the course of infection. Markers of cell death (TUNEL/LDH) and inflammasome activation (IL-1β and IL-18) were not different between infected and mock-infected TEC cultures. EZ and WT MeV-infected TECs showed higher IP-10 release (two-way ANOVA, $P<0.0001$) that correlated with viral titers in cultures. These data suggest MeV infection does not induce inflammasome activation in respiratory epithelial cells but does induce IP-10 which may play a role in the innate immune response. Further analysis of the innate immune response is warranted.
Research Grant	US National Institutes of Health/National Institute of Allergy and Infectious Diseases: R01 AI153140 (DEG)
Field of Research	Immunology

Abstract Title	Glucose homeostasis achieved via consumption of early glycation products in mice fed a Western diet
Authors	Matheus Sartorato, Fatma A Eldefrawy, Tai L. Guo
Affiliations	Department of Biomedical Sciences (Eldefrawy, Guo), College of Veterinary Medicine, University of Georgia, Athens, GA
Abstract	Cooking foods at high temperatures for long durations form advanced glycation end products (AGEs). AGEs are commonly found in Western diets and are proven to have negative effects on health, specifically being associated with a higher risk of diabetes. In contrast, early glycation products (EGPs) can be formed through a well-controlled glycation reaction. Preliminary data propose EGPs as a strategy to improve the physicochemical properties of food proteins. It is hypothesized that EGPs might attenuate disease manifestation of type 2 diabetes mellitus (T2DM) through modulating immune homeostasis and gut microbiota. This study evaluates how EGPs affect the gut microbiota-associated metabolic pathways in male and female C57BL/6 mice. Sequencing analysis of rRNA genes was conducted using fecal samples from male mice fed with a Western diet ad libitum and exposed to EGPs and non-reacted (NR) samples for 6 months at a dose of 600 mg per kg body weight by gavage. Glucose Tolerance Tests (GTT) and Insulin Tolerance Tests (ITT) were conducted every month in addition to weekly glucose measurement. Significant decreases in the blood glucose levels were observed for the mice following EGP exposure when compared to NR, indicating an increased glucose tolerance and decreased insulin resistance. EGP-treated males had decreased incidence of diabetes and females treated with EGPs showed a significant decrease in body weight. The profiles of gut microbiome were altered in the EGPs treated males. In sum, this study revealed an association among EGPs exposure, gut microbiota alteration, glucose homeostasis and T2DM, suggesting that EGPs might have a sex-specific effect in Western diet-induced T2DM with more protection observed in male mice.
Research Grant	This work was supported by NIH R41DK121553, and in part by NIH R41AT009523, R21ES24487 and USDA National Institute of Food and Agriculture [Grant #2016-67021-24994/project accession no. 1009090].
Field of Research	Pharmacology and Toxicology

Abstract Title	The effect of femur angle during computed tomography scan on three-dimensional model compliance
Authors	Zachary Sayre, Sun Young Kim
Affiliations	Purdue University College of Veterinary Medicine, West Lafayette, IN
Abstract	Three-dimensional (3D) modeling using computed tomography (CT) scans is becoming increasingly popular in veterinary medicine. CT scans create a series of images that can be used to generate 3D models. Error during 3D modeling has been reported. In human medicine, femurs are positioned perpendicular to the CT scan, but anatomical differences in veterinary medicine do not allow for this positioning. Standard procedures for CT scans used in the generation of 3D models have not yet been developed in veterinary medicine. The goal of this research is to examine the effect of femur angle during CT scan on 3D modeling. Soft tissue was dissected from three pairs of femurs from beagles. All six femurs were placed on a custom jig in a CT scanner and one scan was obtained at each 0, 20, 40, 60, and 80 degrees relative to the table. From these scans, 3D models were generated using open-source 3D modeling software. This yielded five models of each femur, one at each listed angle. Surface area and volume of each segmentation were calculated. The five models of each femur were overlayed and an iterative process was used to minimize error. Hausdorff distances were calculated and heat maps generated comparing models from each angle to the model from the 0 degree angle scan. Repeated measures ANOVA will be run to analyze the effect of femur angle during CT on surface area, volume, and maximum and mean Hausdorff distances. We expect a decrease in surface area and volume and an increase in maximum and mean Hausdorff distances as femur angle increases. We expect errors in the model to be localized to the proximal and distal ends of the femur where bone geometry is more complex.
Research Grant	Purdue University, College of Veterinary Medicine
Field of Research	Orthopedics

Abstract Title	Strolling with shelter cats
Authors	Julianna Scardina (1), Allie Andrukonis (2), Yasmeen Gomez (2), Yhakira Gray (2), Yanran Sheng (2), Virginia Buechner-Maxwell (1), and Erica N. Feuerbacher (2)
Affiliations	1. Virginia-Maryland College of Veterinary Medicine, Blacksburg, VA 2. Virginia Polytechnic Institute and State University, College of Agriculture and Life Sciences, School of Animal Sciences, Blacksburg, VA
Abstract	Animal shelters can be extremely stressful environments for cats and offer limited opportunities for environmental enrichment, which can negatively affect cat welfare and behavior. Less social and interactive behavior is correlated with longer lengths of stay in the shelter, which are linked to poorer health and adoption outcomes. While dogs in shelters are routinely taken for walks by volunteers, shelter cats are typically confined to kennels or restricted indoor areas for the duration of their stay. In addition, cats are less often taken for walks by their owners than pet dogs, which limits benefits of pet ownership such as exercise and facilitation of the human-animal bond experienced by pet owners. By utilizing a pet stroller, risks of allowing cats outdoor access may be limited while providing the welfare benefits of environmental enrichment. To examine the impact of taking shelter cats for walks in strollers on their behavior and welfare, we tested whether prior training with a stroller would impact behavior that cats and kittens exhibit during a stroller outing. We worked with cats and kittens at Montgomery County Animal Care and Adoption Center in Christiansburg, VA. The training group underwent desensitization and counter conditioning to the stroller by being positively reinforced for approaching and jumping into the stroller. For both cats and kittens, we also tested a control group that was taken for walks in the stroller without positive reinforcement training experience. We recorded videos of the cats in their kennels to determine if training had any effect on in-kennel behavior; during training sessions to assess highest training level achieved; and in stroller to assess welfare during a stroller ride.
Research Grant	Virginia-Maryland College of Veterinary Medicine
Field of Research	Behavior

Abstract Title	Aquimarina emerges as a potential primary pathogen involved in epizootic shell disease of American lobsters
Authors	Anna Schaubeck, Dianjun Cao, Vincent Cavaleria, Seyoung Mun, and Soo Jin Jeon
Affiliations	College of Veterinary Medicine (Schaubeck, Cao, Jeon), Long Island University, Old Brookville, NY New York State Department of Environmental Conservation (Cavaleria) Dankook University (Mun), Republic of Korea
Abstract	Epizootic Shell Disease (ESD) is a destructive condition affecting the American lobster (Homarus americanus) population of the Long Island Sound (LIS). Symptoms can present as pitting, melanization, and eventual erosion of the carapace. Past studies have only confirmed a link between a dysbiotic shift in the carapace microbiota and ESD. In this study, American lobsters were collected from west LIS, 50 miles south of Montauk, and east LIS to identify the specific bacterial taxa and their potential involvement in the disease pathogenesis. We employed high-throughput 16S rRNA gene sequencing to analyze the carapace microbiota of healthy (HTH) lobsters and those exhibiting varying stages of ESD, which revealed a significant difference in the relative abundance of Aquimarina, representing 13.5% of carapace microbiota in ESD and 4.2% in HTH. Of the carapace core bacterial genera shared by all lobsters in each group, Aquimarina, Halocynthiibacter, Tenacibaculum, and Cohaesibacter were higher in ESD compared to HTH, but no significant differences were found. Further analysis of the core bacterial genera in the green gland, hepatopancreas, and testis organs revealed the presence of Aquimarina and Halocynthiibacter in ESD but absent from the same internal organs in HTH. Our data suggests that Aquimarina may be the primary etiologic agent of ESD due to its increased relative abundance on the carapace, ability to degrade the lobster carapace via the enzyme chitinase, and invade internal organs, particularly the green gland. These findings provide novel insights into the disease dynamics, viable targeted interventions, and the basis for future studies of interactions Aquimarina may have with other carapace or internal microbiota.
Research Grant	None
Field of Research	Bacteriology

Abstract Title	Wolbachia-detection via qPCR as an alternative to molecular and classical heartworm microfilariae detection
Authors	Mary Schech, Maureen Kelly, Emily Orr, Hassan Hakimi, Guilherme G. Verocai
Affiliations	Department of Veterinary Pathobiology, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX
Abstract	Canine Heartworm Disease, caused by Dirofilaria immitis, has the greatest morbidity and mortality of all vector-borne diseases affecting dogs in the United States. Currently, heartworm diagnosis relies on a combination of antigen- and microfilariae- (mf) detection tests, but discrepant results could benefit from additional laboratorial tests. Wolbachia, an intracellular endosymbiont of filarial nematodes, has recognized importance within the inflammatory response of CHD and maturation of D. immitis. Molecular detection of Wolbachia in blood of canine patients may provide an alternative diagnostic target to be used in tandem with routinely used tests, or as a confirmatory test when other test results are discrepant. We analyzed whole blood samples of dogs (n=484) from Central Texas using a probe-based real-time polymerase chain reaction (qPCR) for detection of D. immitis Wolbachia. Results were compared to those obtained through a qPCR targeting D. immitis DNA, modified Knott's (MK), and the commercially available DiroCHEK® antigen test pre- and post-immune complex dissociation (ICD) via heat-treatment. Overall, 158 (32.6%) tested positive in at least one technique. Within those positives, Wolbachia was detected in 99 (62.7%) samples and D. immitis DNA was detected in 92 (58.2%) samples. The MK detected D. immitis mf in 81 (51.3%) samples. Pre-ICD DiroCHEK® detected 107 (67.7%), while post-ICD detected 130 (82.3%). Additionally, our novel qPCR assay detected Wolbachia in 24 samples found negative in all other tests. These data suggest that Wolbachia-detection via qPCR can be a viable confirmatory test for heartworm and may reveal infections that are missed by other diagnostic techniques.
Research Grant	None
Field of Research	Parasitology

Abstract Title	Unraveling Auditory System Dysfunction: Assessing Mitochondrial Role in Fragile X Syndrome via Brain Culture
Authors	Rachel Scherer, Elizabeth McCullagh, and Giulia Bertolin
Affiliations	College of Veterinary Medicine, Oklahoma State University (Scherer), Department of Intergrate Biology Oklahoma State University (McCullagh) Insitute of Genetics and Development of Rennes (Bertolin)
Abstract	Fragile X Syndrome (FXS) is a genetic disorder that is sex linked and is often presented as attention deficit disorder, mild to severe intellectually disability, and extreme sensitivity to sensory stimuli, including hearing. FXS is a condition that impacts humans but can also be generated in other animals such as mice to understand some of the biological mechanisms that underly FXS. The mitochondria of a cell provides adenosine triphosphate (ATP), or energy. Neurons in the brain use large amounts of ATP; FXS mice with hypersensitivity to hearing have a greater response to auditory stimuli and consequently utilize more energy. Mice postnatal days 9 – 12 were sacrificed and the brains are removed. The medial nucleus of the trapezoid body (MNTB), where part of the auditory system is located, and the surrounding area were sliced into 200 micrometer thick samples and grown in an organotypic culture. After 7 days, mitochondria trackers were used to stain the mitochondria and assess biological function. The goal is to be able to compare the function of mitochondria in FXS mice compared to controls. Currently the results are pending; however, preliminarily observations indicate brain culture growth suggesting that we will be able to assess mitochondrial function in culture in this brain region and understand potential dysfunction in FXS.
Research Grant	NIH R15 from NICHD, and FACE Foundation
Field of Research	Laboratory Animal Medicine

Abstract Title	Designing a method to deliver non-invasive pulsed electromagnetic field therapy to raptors.
Authors	Dominic Scheurer, Nicole Torres, Lorrie Hale-Mitchell, Mark Mitchell, Kielyn Scott
Affiliations	Department of Clinical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	Pulsed electromagnetic field (PEMF) therapy can be used as an adjunct to treatment of diseases and injuries by manipulating cellular magnetic fields. When electromagnetic waves interact with tissues, a cascade of biological processes are affected. Use of PEMF therapy in veterinary medicine is expanding, with many devices designed for use in companion animals. PEMF therapy is underdeveloped in the field of avian medicine due to the necessary restraint of the patient, leaving them vulnerable to stress-related complications. Testing the efficacy of PEMF therapy in avian species is difficult, and determining the efficacy of PEMF is necessary for exploring its applications. This study sought to develop a method for administering PEMF therapy to raptors without restraint. An elevated platform was constructed using materials that the PEMF can penetrate. Four captive raptors were trained on the platform once-daily for up to 30 minutes for 25 days without administration of PEMF to acclimate them to the new platform. After this period, they were trained on the platform once-daily for up to 30 minutes for 25 days while being administered PEMF. Body language cues displayed during PEMF therapy were observed and documented using a Body Language Score. The time that the raptors were willing to remain on the platform near the PEMF device was recorded. It was hypothesized that the administration of PEMF therapy at 5Hz would significantly affect the time that raptors are willing to remain on the platform near the PEMF device. Initial findings indicated no significant relationship between the use of PEMF and the time that raptors were willing to remain on the platform, but the research is currently ongoing.
Research Grant	None
Field of Research	Behavior

Abstract Title	The effect of castration on social behavior between familiar cohorts of weaned beef cattle after commingling
Authors	Jordan A. Schroeder, Rebecca L. Parsons, Caleb M. Brezina, Grant A. Dewell, Renee D. Dewell, Anna K. Johnson, Derek B. Haley, Suzanne T. Millman
Affiliations	Veterinary Diagnostic & Production Animal Medicine (Schroeder, Parsons, Brezina, G. Dewell, Millman), Center for Food Security & Public Health (R. Dewell), Biomedical Sciences (Millman), CVM, ISU, Ames, IA, and Animal Science, CALS, ISU, Ames, IA (Johnson), and Population Medicine, CVM, University of Guelph, Guelph, ON (Haley)
Abstract	Commingling is a common practice in beef production where cattle from various sources are mixed together at different points in the production cycle such as at livestock auctions and feedlots. Commingling familiar cattle with unfamiliar conspecifics is shown to be a major source of stress linked to increased susceptibility to respiratory diseases and behavioral changes associated with disruptions of the established social structure. Social buffering, the reduction of stress while in the presence of a closely bonded companion, may reduce the negative effects of commingling; however, little research has been conducted on the social bonds between familiar beef cattle prior to or following commingling. In this study, we analyzed the frequencies of affiliative and agonistic behaviors between bull-calves pre- and post-castration to understand if a major stressful event affects the social bonds between familiar beef calves in a commingled group. We hypothesized that a major stressful event will alter the affiliative and agonistic behavioral frequencies between familiar beef calves housed with unfamiliar pen-mates. Seventeen pens, each housing three familiar and three unfamiliar weaned bull-calves, were enrolled on Day 0 and castration occurred on Day 14. The affiliative and agonistic behavioral frequencies between individuals were quantified over 15-minute intervals between Day 7 and Day 21. The results of this study will determine if social bonds form between familiar groups of beef cattle and how having familiar pen-mates influences the response to a major stressful event such as castration while housed in a commingled group.
Research Grant	USDA NIFA Animal Health and Production and Animal Products: Animal Well-Being Program [grant no. 2019-67015-29572/ project accession no. 1019068] from the USDA NIFA
Field of Research	Animal Welfare

Abstract Title	Radiographic Validation of External Landmarks to Assess Equine Forelimb Digit Alignment
Authors	Anna Grace Scrimager, Ben Nabors
Affiliations	Mississippi State College of Veterinary Medicine
Abstract	Loss of performance use in sport horses costs the horse industry up to $1 billion annually, a quarter of that resulting from forelimb digit lameness. Podiatry is the most effective method to mechanically balance the digit and directly affects the distal limb. Skeletal and soft tissue structures comprising the digit, along with the two principles of locomotion, elastic recoil and concussion absorption, function optimally when balanced. Balance is created when the digital phalanges are aligned, allowing internal structures to absorb concussion evenly and permitting elastic recoil to govern limb locomotion untethered. We hypothesized that external landmarks can be employed to identify a difference in the pastern angle (proximal and middle phalanx) and hoof angle (distal phalanx) indicating an unbalanced phalangeal alignment. This would obviate the need for radiographs in the process of achieving balanced phalangeal alignment in the digit. Seven horses were imaged, taking photographs and radiographs of the forelimb digit. External landmarks were utilized to assess digital alignment on photographs and validated with radiographic digital alignment measurements. Analysis of measurements via MANOVA found a significant difference ($p=0.007646$) between the hoof wall and the digital angle with an alpha value of 0.001. In all seven horses, gross external landmarks directly represented internal digit alignment radiographically.
Research Grant	Mississippi State College of Veterinary Medicine
Field of Research	Equine Medicine and Surgery

Abstract Title	Optimizing Cell Blocks and Storage Media Conditions of Fine Needle Aspirates from Canine Livers
Authors	Francyrette A. Seda Gómez, Jessica Lambert, Alexander Tufano and Erika Gruber
Affiliations	Department of Population Health and Pathobiology, College of Veterinary Medicine, NC State University, Raleigh, NC.
Abstract	Fine needle aspiration (FNA) is crucial in identifying and differentiating types of cancer in dogs. Similar to small biopsies, cell blocks (CBs) prepared from freshly collected aspirates have been found to provide sufficient material for microscopic evaluation of tumors. To make CBs more accessible to veterinarians and patients beyond academic institutions, our aim was to determine if CBs from aspirates stored at 4°C for up to 72 hours would be comparable to those made immediately after collection. We also investigated if protein in the storage medium could improve sample quality. FNAs were collected from the livers of recently euthanized healthy dogs. Aspirated material was expelled into tubes containing Hanks buffered saline solution (HBSS), 100% fetal bovine serum (FBS), 10% FBS in HBSS, or 5% bovine serum albumin (BSA) in HBSS. At 0h, 24h, and 72h, tubes were centrifuged, and the supernatant was replaced with 50µL of 3% agarose gel to create the CB. For microscopic analysis, the CBs were fixed in 10% neutral buffered formalin for paraffin embedding, sectioning, hematoxylin & eosin staining. Preliminary results suggest that storing aspirated liver in HBSS for 24 and 72 hours decreases cellularity and lessens intact morphology. Improved cellularity and morphology were observed in aspirates stored in 100% FBS, 10% HBSS, and 5% BSA. Hepatic aspirates stored in media containing either BSA or FBS retain morphologic features suitable for incorporation into CBs for microscopic evaluation.
Research Grant	NCSU Population Health and Pathobiology Faculty startup funds
Field of Research	Clinical Pathology

Abstract Title	Immunomodulation using a celastrol-loaded cyclodextrin nanoparticle on cardiac tissue in mice after ischemia r
Authors	Dominic, Andrew Belec, Rachel Wilson, Joyce Ho, Preston So, Chaitanya Karimanasseri, Christopher Rodell, and Pavan Atluri
Affiliations	School of Veterinary Medicine (Seiberlich) and Department of Surgery (Patel,Iyengar,Weingarten,Dominic,Belec,So,Ho,Karimanasseri,Atluri) Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA; School of Biomedical Engineering, Science, and Health Systems (Soni,Rodell), Drexel University, Philadelphia, PA
Abstract	Cardiac ischemia reperfusion (IR) injury causes sterile inflammation that can lead to cardiac remodeling and decreased function. Modulation of the immune response following ischemia can have improved long-term outcomes. Celastrol is a compound known to convert pro-inflammatory M1 macrophages to pro-healing M2 macrophages. The aim of this study was to characterize the macrophage immune response after IR injury in mice and to determine the immunomodulatory potential of celastrol in cardiac tissue following IR. In this study, a macrophage-targeting cyclodextrin nanoparticle (CDNP) was utilized to deliver celastrol to inflamed cardiac tissues. Adult C57BL/6 mice underwent a left thoracotomy, and the left anterior descending (LAD) artery was ligated for 45 minutes and then released to allow for reperfusion. To characterize the immune response, animals were separated into Day 1, Day 3, Day 5, and Day 7 post injury cohorts. The left ventricular infarct and border zone tissue was processed for flow cytometry, which demonstrated peak numbers of M1 macrophages on Days 2 and 3 post IR injury. To assess the biodistribution of the CDNP, live near-infrared imaging studies on animals treated with labeled CDNP were performed on the day of peak M1 expression (Day 2). Imaging demonstrated an accumulation of CDNP in the inflamed heart within 24 hours of injection (Day 2) and retention for up to 72 hours (Day 5). Using this information, animals were treated with 10 mg/kg IV of celastrol-loaded CDNP on Day 2 following IR injury to coincide with peak inflammation. Flow cytometry post treatment showed a decrease in M1 numbers compared to control animals, suggesting favorable immunomodulation following IR injury in treated animals.
Research Grant	University of Pennsylvania
Field of Research	Cardiology

Abstract Title	Effect of land use and climate on ticks and tick-borne pathogens in Eastern Oregon
Authors	Simonne Sequeira, Lukas Haffner, Kimberly Gerstner, Brianna Beechler, Michelle Steinauer, Justin Sanders, Rhea Hanselmann
Affiliations	Western University of Health Sciences, CVM, Pomona, CA (Sequeira, Hanselmann), University of Veterinary Medicine, Hanover, Germany (Haffner), Oregon State University, Carlson College of Veterinary Medicine, Corvallis, OR (Beechler, Gerstner, Sanders), Western University of Health Sciences, COMP, Lebanon, OR (Steinauer)
Abstract	Ticks are significant disease carriers, posing a growing global public health concern. Yet, there is a vast knowledge gap regarding the geographic distribution of ticks and tick-borne pathogens. The increasing change of our world's physical environment associated with climate change, is likely to drive changes in tick distributions, and thus continued monitoring is necessary. Our project investigates tick presence and abundance in Oregon's high desert region, specifically the White River Watershed near Tygh Valley. We collected ticks using CO2 bait traps and drag-cloth sampling across different land-use areas spanning pristine mountain habitat, agricultural fields and rural towns and recorded ambient temperature at each site. By comparing tick presence and abundance across sites, we aim to assess the impact of human land use and temperature on tick distribution and associated pathogen exposure risk. We will compare our findings to previous data from the same sites to detect temporal changes. In a next step, ticks will be submitted for DNA extraction and pathogen analysis via PCR and results will again be compared across sampling sites and years. We anticipate higher tick density in moderately to highly disturbed areas, especially sites near livestock. Our study contributes valuable insights into identifying high-risk areas for ticks and tick-borne diseases, which has important implications for human and animal health.
Research Grant	Western University of Health Sciences Intramural Team Grant to Hanselmann and Steinauer; Oregon State University Department of Biomedical Sciences Intramural support to Beechler
Field of Research	One Health

Abstract Title	Characterization of the Distribution of EcoHIV Infected Cells in a Mouse Model of HIV Pathogenesis
Authors	Annushka Sewrathan, Claire E. Lyons, Yeji Cho, Alyssa L Chalmin, Aileen J. Feng, Bess W. Carlson, Zahra Gholizadeh, M. Riley Richardson, Selena M. Guerrero-Martin, Daphne Pariser, Zeli Shen, Kelly A. Metcalf Pate
Affiliations	Division of Comparative Medicine, Massachusetts Institute of Technology, Cambridge, MA
Abstract	Approximately 38.4 million people are infected with HIV worldwide. While antiretrovirals prevent AIDS, HIV-associated neurocognitive impairment still manifests partially due to cellular reservoirs that house latent virus within sanctuary tissues. HIV-induced inflammatory responses in the CNS lead to increased BBB permeability and proinflammatory leukocyte invasion in the brain. One of these inflammatory responses is platelet activation, which may drive platelet-monocyte aggregates (PMAs) via P-selectin/PSGL-1 interactions during HIV infection, as seen in our lab's previous work. Formation of these PMAs may facilitate the migration of infected and infectable monocytes into the brain, perpetuating the latent reservoir. We will utilize the EcoHIV-infected murine model to characterize viral distribution via Q-PCR in the spleen, liver, and brain, and define the effect of P-selectin/PSGL-1 interactions on EcoHIV distribution by comparing organ viral loads in wild-type versus PSGL-1-knockout mice. Our results show that EcoHIV-infected wild-type mice carry a significantly higher viral load in their spleens compared to livers ($P < 0.05$). Within the spleen, viral loads peak at day 3 post-inoculation then plateau as infection progresses on days 9, 11, and 15 ($P < 0.05$). Within wild-type livers, viral loads between day 3 and day 11 were the only groups significantly different ($P < 0.05$). It is important to note that infection was shown to still be present at day 15 in both wild-type spleens and livers. We found no evidence of biological sex playing a role in wild-type mice's viral distributions within the spleen and liver. Overall, our data supports that EcoHIV mouse models can be a valuable tool for understanding HIV latency.
Research Grant	None
Field of Research	Virology

Abstract Title	Is there a Good Microbiome for Survival?
Authors	Taylor Sheridan, Darla DeStephanis, Shannon Scarberry, Masha Long, and Kylie Kavanagh
Affiliations	College of Veterinary Medicine, University of Georgia, Athens, GA (Sheridan), Wake Forest University School of Medicine, Department of Pathology, Winston-Salem, NC
Abstract	The gut microbiome is a complex community made up of billions of bacteria, viruses, archaea, and fungi. The composition of this community is increasingly being studied as an important influencing factor on the development of gastrointestinal, metabolic, neurologic, and immunologic diseases, and any shift in constitution may play a role in health and disease. Amongst the billions of residents in the gut microbiome, three bacterial "indicator species" have come to light as possible proxies for a healthy microbiome in human and nonhuman primates. These species are Faecalibacterium prausnitzii, Lactobacillus reuteri, and Lachnospiraceae bacterium. This study aims test the hypothesis that these indicator bacteria are enriched in two species of nonhuman primates with superior health spans and lifespans. One arm of the project compares these indicator species in fecal microbiomes sourced from radiation survivor rhesus macaques with divergent health outcomes following exposure. The other arm of the project assesses indicator species in long-lived versus short-lived, diabetic versus non-diabetic, vervet monkeys by retroactively assessing indicated species at various life stages. The ultimate goal is to establish biological markers for a healthy microbiome and lay the groundwork for development of probiotics to combat age-related disease onset/progression. To assess this, fecal samples from 9 rhesus macaques and 29 vervet monkeys were collected and stored at -80 °C until the time of the study. DNA was extracted and qRT-PCR performed to quantitate fecal abundances, normalized to microbial 16S ribosome levels. Full data set and results pending.
Research Grant	U01AI150578, UL1TR001420, R01HL142930, P40OD010965
Field of Research	Microbiomes

Abstract Title	Altered serotonergic and GABA signaling in the gut in a mouse model of impaired maternally inherited UBE3A
Authors	Hyun Min Shin, Jelissa Reynoso-Garcia, and Melanie Gareau
Affiliations	Department of Anatomy, Physiology and Cell Biology, School of Veterinary Medicine, University of California Davis, Davis, California
Abstract	Angelman syndrome (AS) is characterized by the deletion or mutation of the maternally inherited ubiquitin ligase E3A (UBE3A) gene expression in neurons. Deficient neuronal UBE3A leads to neurological impairments, including neurodevelopmental delays and seizures. Interestingly, concurrent gastrointestinal (GI) issues including constipation, poor feeding, and reflux, are common in AS patients, suggesting impairments along the microbiota-gut-brain (MGB) axis. We previously identified gut microbiota dysbiosis correlated with neuropsychiatric disorders across different animal models of AS including mice, rats, and pigs. We hypothesized that gut-brain impairments, including reduced GI motility, would be present in AS mice. To assess whether alterations in the gut microbiome contributed to GI pathophysiology, Ussing chamber studies and qPCR was performed. Ussing chambers revealed AS mice had increased gut permeability and decreased ion transport in the ileum and distal colon compared to wild-type (WT) control mice. qPCR was performed to assess serotonergic signaling and GABA signaling in gut and brain (ileum, colon, hippocampus). AS mice demonstrated increased expression of serotonergic signaling in the gut (Tph1, Tph2, Sert) and GABA signaling (GABA1b, GABA2a) in both the gut and brain. Together these findings support altered motility in AS mice which may provide insight to the mechanisms of constipation in AS patients. Since MGB axis impairments are common in many human and animal disorders, better understanding the signaling patterns in neuronal-induced altered motility has the potential to serve a larger patient population.
Research Grant	Foundation for Angelman Syndrome Therapeutics (FT2022-007)
Field of Research	Physiology

Abstract Title	Interactions between 11KT, gonadal composition, brain, and behavior in A. ocellaris undergoing sex change
Authors	Monica Shotwell, Emma Ibanez, Gabriel Graham, Meghan Connolly, Justin S. Rhodes
Affiliations	College of Veterinary Medicine, (Shotwell), Department of Psychology, (Ibanez, Graham, Rhodes), Neuroscience Program (Connolly, Rhodes), University of Illinois, Urbana-Champaign, IL
Abstract	Amphiprion ocellaris clownfish exhibit protandrous sex change from male to female. Clownfish live in small hierarchical groups with only a single reproductive pair and up to several non-breeding subordinate males. The female is the largest and dominant fish. When a female is displaced, the male changes to female, while the largest subordinate completes the pair. Similarly, when males are paired together, the largest changes sex to female, and the smaller stays a male. There is much to learn about the mechanisms behind sex change regarding involvement of the brain, gonads, and circulating sex hormones. The purpose of this study was to examine the composition of the gonads, sex steroid hormone levels, cellular composition of the brain, and behavior in clownfish undergoing protandrous sex change. Sex change was induced in 10 fish by pairing males together or removing the female. At 6 months, blood was taken to measure sex steroids. The fish were then euthanized for analysis of gonadal composition and brain gene expression. The body was sectioned and stained with H&E. Gonadal composition was determined by outlining ovarian, testicular, and connective tissues using Adobe Photoshop. Preliminary results show 3 fish changed sex as indicated by the presence of vitellogenic oocytes in the gonads or complete loss of testicular tissue. This was associated with low plasma levels of 11-ketotestosterone (11KT) and female-typical behavioral displays. The remaining fish displayed male-typical behavior and 11KT levels and had varying levels of testicular tissue. Analysis of the telencephalon is currently underway using single nuclei RNA sequencing. Results will provide new insight into the neuroendocrinology of sex change in clownfish.
Research Grant	None
Field of Research	Physiology

Abstract Title	Diminished angiogenesis impairs fracture healing in a mouse model of Down Syndrome.
Authors	Kayleigh Shumaker, Catrina Silveira, Lindsay A. Dawson, Kirby M. Sherman, Dana Gaddy, and Larry J. Suva
Affiliations	Department of Veterinary Physiology & Pharmacology (Shumaker, Silveira, Dawson, Sherman, Suva), and Department of Veterinary Integrative Biosciences (Gaddy), School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX.
Abstract	Down Syndrome (DS) results from trisomy of human chromosome 21 and occurs in approximately 1 in 800 live births. DS individuals are predisposed to enhanced inflammation, reduced bone mineral density (BMD), and increased fracture risk. We have shown low BMD in DS individuals is secondary to low bone mass accrual, and that DS mouse models have deficient fracture healing leading to non-union. Angiogenesis is long established as an essential component of fracture healing; therefore, its dysregulation may promote development of fracture non-union. We hypothesized the observed fracture healing impairment and subsequent non-union in DS may result from altered angiogenesis. The TS65 DS mouse model was used to investigate fracture repair using the middle phalanx (P2) fracture model. Bilateral P2 fractures were induced on digits II and IV in 16-week-old male and female WT and TS65 DS mice. Longitudinal changes in bone volume, morphology, and fracture bridging were analyzed by weekly in vivo µCT. Digits were harvested 14 days post fracture (DPF) and immunohistochemical analysis performed to quantify angiogenesis by examining endomucin positive cell area and density. Vascular density and vascular area were measured in 6 sections per genotype at 14 DPF. Interestingly, both vascular density and vascular area were significantly lower in male TS65 DS mice compared to WT controls ($p<0.05$). Similarly, vascular area was significantly reduced in DS female mice, but no significant difference in vascular density was observed ($p=0.8029$). These data implicate diminished angiogenesis in impaired fracture healing of murine DS and justify further investigation of the relationship between angiogenesis and fracture non-union in DS patients.
Research Grant	NIH R01 HD102909-01A1 (Suva)
Field of Research	Orthopedics

Abstract Title	Development and validation of a new coma scale and long-term outcome scoring system for dogs with head injury
Authors	Britta Siegenthaler, Claire Tucker, Tracy Webb, Ayla Mollen, Katy Walrond, Kelly Hall
Affiliations	Colorado State University, Department of Clinical Sciences, Fort Collins, CO
Abstract	Head injury and associated traumatic brain injury (TBI) are common causes of emergent presentation, morbidity, and mortality in dogs and humans. The Modified Glasgow Coma Scale score is the only validated neurologic scoring system for use in dogs. However, it is not specific for TBI, and patients with spinal cord injuries or in hypovolemic shock may be incorrectly categorized as having intracranial central nervous system injury. Using literature from pediatric neurology, veterinary retrospective studies, and clinical expertise, we developed the Veterinary Glasgow Coma Scale (VetGCS), de-emphasizing spinal cord reflexes and simplifying the brainstem reflexes to pupillary light responses. We hypothesize that the VetGCS, measured at presentation, will be more specific for early identification of head injury patients with TBI and predict outcome in trauma patient populations. We have also designed a modified version of the Glasgow Outcome Scale – Extended Pediatric version from human medicine, called the Veterinary Glasgow Outcome Scale (VetGOS), that we hypothesize will correlate with the VetGCS and provide a similar long-term outcome scoring system that is not currently available in veterinary medicine. To validate these scoring systems, dogs presenting to the Colorado State University Veterinary Teaching Hospital with evidence of head injury will be enrolled and scored using the VetGCS during hospitalization and with the VetGOS at two weeks, one month, and six months post-head injury. We anticipate using these scoring systems to enhance the ability to leverage canine TBI as a translational model in future clinical trials evaluating novel therapies and to ultimately improve trauma patient outcomes.
Research Grant	None
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Development of a Surgical Model for Rotator Cuff Tendon Degeneration in the Rat
Authors	Travis Montoya, Brennan Silliman, Sierra Batson, Sam Winston, Lynn Pezzanite, Kirk McGilvray, Jeremiah Easley, Katie Sikes
Affiliations	Preclinical Surgical Research Laboratory, Department of Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences Orthopedic Bioengineering Research Laboratory, Department of Mechanical Engineering, Walter Scott Jr. College of Engineering, Colorado State University, Fort Collins, CO
Abstract	Tendons of the rotator cuff play an important role in stabilizing the shoulder. Tendinopathy, or chronic tendon degeneration, resulting from overuse occurs in 5-7% of the general population, with rates as high as 40% in high-risk populations including athletes, military personnel, and occupational workers. Despite these high rates of occurrence, there is no gold standard for treatment. Current small animal pre-clinical models to evaluate therapeutic options focus on acute injuries (transection) or rely on intensive protocols (downhill treadmill running for one hour per day for 8-16 weeks). Therefore, the goal of this study was to develop a surgical model of chronic rotator cuff tendon degeneration. For this, fifteen male, skeletally mature, Sprague Dawley rats were randomly assigned to one of three groups (n=5/group): 1) naïve, 2) bilateral comb fenestration (10x midsubstance striations using a 25G needle) surgery of rotator cuff tendons, or 3) overuse injury through daily treadmill running. Voluntary gait pattern and dynamic weight bearing of each animal was measured weekly using the Tekscan rodent walkway. After 8 weeks, animals were humanely euthanized. One limb/animal was taken for histological processing to evaluate tendon pathology and one limb/animal was taken for biomechanics. We hypothesize that animals receiving the comb fenestration surgery will have a quicker on-set and progression of tendon degeneration as evidenced by decreased fore limb weight bearing and increased histopathological score relative to animals receiving treadmill running. Establishment of a surgical model for chronic tendon degeneration will assist researchers and clinicians in the study of rotator cuff disease.
Research Grant	None
Field of Research	Orthopedics

Abstract Title	Equine blood microbiome in a cohort of clinically healthy trail riding horses
Authors	Noel Simms, Joseph Bertone, Tonatiuh Melgarejo, Caitlin O'Shea, Theros T. Ng, and Annika Linde
Affiliations	Western University of Health Sciences, College of Veterinary Medicine, Pomona, CA
Abstract	Emerging research suggests the presence of a blood microbiome in clinically healthy individuals. Studies have linked dental procedures in horses with transient bacteremia, yet little is known about the equine blood microbiome. This study aimed to characterize the bacterial composition and abundance in blood from clinically healthy horses using 16S next-generation sequencing. We examined 20 hack horses of varying breeds (8 - 14 yrs. old) living on a dry-lot pasture in Colorado (7,680 feet elevation). The herd shares water troughs and feed, but lives isolated from other horses. Blood was collected from the jugular vein into Serum, Zymo Research DNA/RNA Shield Blood Collection and EDTA tubes. Samples were submitted for microbiome analysis (CosmosID) and blood work (CBC, Chem). Our results show that blood is not sterile in healthy horses. Alpha Diversity showed that microbial taxonomic diversity in individual samples ranged from 48 to 76 with a median of 61 species. Beta Diversity (principal coordinate analysis) investigating microbial structure diversity reflected large variability of the data with no obvious clustering, indicating dissimilarity between bacterial populations in different horses. Considering the relative isolation of the herd, the diversity was surprisingly heterogeneous. A heat map of microbial taxonomy & abundance showed the presence of Corynebacterium, Moraxella, and Neisseria in 95%-100% of the samples. Genera with the highest relative abundance in the samples were Acinetobacter, Gardnerella, and Lactobacillus. Establishing a baseline of the abundance and diversity of the bacteria in clinically healthy horse blood provides new insight into possible microbiome shifts that may result in clinical disease.
Research Grant	WesternU CVM Office for Research and True One Medicine Initiative
Field of Research	Microbiomes

Abstract Title	Effect of Crinkle Paper Nesting Material on the Ability of Animal Care Workers to Perform Cage Checks
Authors	Jacob Simpson, Daniel J. Davis, Elizabeth C. Bryda
Affiliations	Department of Veterinary Pathobiology, College of Veterinary Medicine, University of Missouri, Columbia, MO College of Veterinary Medicine, NC State University, Raleigh, NC
Abstract	The Guide for the Care and Use of Laboratory Animals recommends environmental enrichment for all laboratory animals to promote species specific behavior and deter abnormal stress behaviors. Nesting material for lab mice has been shown to eliminate ambient cold stress, improve reproduction, and decrease stereotypical behavior. The University of Missouri has instituted the use of 8 grams of crinkle paper in addition to a nestlet as enrichment for mice. It has been suggested that this additional paper material may compromise the ability to visualize animals while evaluating their health status. Our objective was to determine the effect crinkle paper has on worker ability to assess animals during routine cage checks. Three separate trials were completed with eight individuals evaluating twenty-one cages of mice per trial. Cages were divided into three enrichment groups: 8 grams of crinkle paper and a nestlet, 4 grams of crinkle paper and a nestlet, and a nestlet with no crinkle paper. Each group contained eight simulations of common issues found during routine cage checks with each appearing once per group over all trials. Time to perform individual cage checks and ability to identify simulation conditions were recorded for each evaluator. An approximate 11% increase in cage check time for cages with 8g of paper, no significant time difference between 4g and nestlets alone, and a trend of better simulation identification with less paper material were found. We recommend the use of 4g of paper for enrichment instead of 8g and for future studies to explore this reduction's measurable physiological impact on mice.
Research Grant	Bryda Lab Research Incentive Funds
Field of Research	Laboratory Animal Medicine

Abstract Title	Ketamine interventions in a mouse model of Alzheimer's Disease
Authors	W Sitterson, C Lee, J Kara, Y Zermeno , P St. Martin
Affiliations	Comparative Biomedical Sciences
Abstract	Alzheimer's disease (AD) affects more than six million Americans, ranking as the seventh leading cause of death in the United States. It is characterized by diminished cognitive abilities, memory loss, an array of decreased visuospatial skills, changes in personality, and depression. Several treatments have been proposed to combat the symptoms associated with Alzheimer's disease, and recent findings suggest that N-methyl-D-aspartate (NMDA) receptor antagonists such as ketamine can provide neuroprotection with a decrease in neuropsychiatric symptoms from AD. Studies show that AD acts in a way that increases the levels of quinolinic acid (QUIN), which is a potent neurotoxin that binds NMDA receptors. AD also increases neuronal and glial cell death. Given ketamine's possible neuroprotective action on neurons, glial cells, and astrocytes, it could demonstrate therapeutic benefit, and even slow the onset of symptoms in patients. In this study, we propose to examine the prospective neuroprotective effects of ketamine treatments in a mouse model of Alzheimer's disease. We will utilize novel object recognition, Y maze, and forced swim test in an AD mice model that harbors a single amyloid precursor protein (APP) mutation associated with AD. These mice will be treated with ketamine, and their performances will be compared to mice given saline as a placebo.
Research Grant	Unknown
Field of Research	One Health

Abstract Title	Regulation of canine Neutrophil Extracellular Trap formation by immune-mediated hemolytic anemia therapeutics
Authors	Madison Smith, Liming Shen, Terri Higgins, Rie Watanabe, Dana LeVine
Affiliations	Departments of Clinical Sciences (Smith, Shen, Higgins, LeVine) and Pathobiology (Watanabe), College of Veterinary Medicine, Auburn University, Auburn, Alabama
Abstract	Immune-mediated hemolytic anemia (IMHA) is an autoimmune disease in dogs resulting in life-threatening anemia. IMHA has a tragic mortality rate of up to 80% due to fatal thromboemboli (TE). One probable cause of TE in IMHA is exuberant neutrophil extracellular trap (NET) formation; NETs are extracellular strings of DNA, histones, and granular proteins released by activated neutrophils. NETs are prothrombotic and increased circulating NET markers are associated with death in IMHA dogs. There is little evidence to support the ideal immunosuppressant or antithrombotic regimens for IMHA. We hypothesized that, based on their mechanisms of action, some IMHA therapies (heparins, aspirin, cyclosporine, mycophenolate), but not others (dexamethasone, azathioprine), would inhibit NETosis, providing a rationale for their preferred use. In an ex vivo model, neutrophils from healthy dogs were isolated and treated with each drug at various concentrations prior to stimulation with a NET inducer, phorbol-12-myristate-13-acetate (PMA). Cells were stained with a mixture of cell permeable dye (SYTO green), staining intracellular DNA, or intact neutrophils, and impermeable dye (SYTOX orange), staining extracellular DNA, or released NETs. Using a fluorescence microscope, the percent NET forming neutrophils was determined for each treatment. Of the antithrombotics tested, low molecular weight heparin (enoxaparin) ($p \leq 0.0001$, 160 U/ml) and unfractionated heparin ($p \leq 0.001$, 0.7 U/ml) inhibited NETosis, while aspirin did not. None of the tested immunosuppressants (dexamethasone, azathioprine, mycophenolate, cyclosporine) impacted NETosis. Heparins may be superior antithrombotics in dogs with IMHA due to their capacity to inhibit NETosis.
Research Grant	None
Field of Research	Small Animal Medicine and Surgery

Abstract Title	The impact of sea-level rise on disease transmission: A dengue fever case study
Authors	Whitney E. Smith and Amy C. Kinsley
Affiliations	Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, St. Paul, Minnesota
Abstract	Sea-level rise threatens the habitat of humans and animals that populate coastal regions worldwide. Consequently, sea-level rise is expected to impact the mass movement of humans and animals, directly affecting zoonotic disease potential. While the implications of climate change on zoonotic diseases have been examined, further understanding of sea-level rise's role in zoonotic disease transmission and emergence is needed. This study examines the connections between sea-level rise, human migration, and disease transmission. We used dengue fever, a mosquito-borne viral disease rapidly expanding worldwide, as a case study focused on Florida, USA. One major factor affecting the spread of dengue fever is increased human mobility. Therefore, we designed an SIR compartmental model to assess the impact of sea level rise on human migration. Within the model, we simulated human and mosquito populations at origin and destination locations to examine dengue fever transmission dynamics. Projections for sea-level rise and known parameters for dengue fever were used to inform the model, highlighting the impact of human migration due to sea-level rise on disease transmission. This One Health approach will be the foundation for additional disease modeling and aid future transdisciplinary approaches to reduce zoonotic disease emergence and transmission.
Research Grant	None
Field of Research	One Health

Abstract Title	Load and shoe effects on third phalanx displacement measured in healthy and laminitic equine hoof radiographs
Authors	Emily Smith, Rita Aoun, Catherine Takawira, Mandi J. Lopez
Affiliations	Laboratory for Equine and Comparative Orthopedic Research, School of Veterinary Medicine, Louisiana State University SVM, Baton Rouge, LA
Abstract	Laminitis is a hoof pathology that can result in separation of the third phalanx (P3) from the hoof wall. Shoes, used as a supportive non-invasive tool can prevent P3 rotation or sinking. The objective of this study was to compare effects of open-heel (OH), heart-bar (HB), egg-bar (EB), and wooden clog (WS) shoes on radiographic P3 localization in unaffected and laminitic hooves during compressive loading. It was hypothesized that rotation and sinking would be greater in laminitic hooves with increasing load, and WS would reduce displacement, followed by HB, EB, OH, then US. Disarticulated fore digits with and without laminitis were fixated at the deep digital flexor tendon and proximal interphalangeal joint. The proximal portion of the specimen was stabilized in polyvinyl chloride pipe and resin to fit a mechanical testing system mimicking a ground reaction force during a 550 Kg-horse step cycle. Radiographs were acquired at 25% increments of maximum load. The position of P3 was determined by measuring the coronary-P3 extensor process distance (CE) and sole depth (S) contributing to the degree of sinking; and proximal and distal horn-lamellar zones (PHL, DHL) and parietal surface angle (A2) contributing to the degree of rotation. Preliminary results show that S was decreased in healthy unshod hooves versus other shoeing conditions. In laminitic hooves, HB and EB resulted in the highest A2, PHL, and DHL, while WS resulted in the opposite trend. Increasing load induced significant changes in radiographic measurements. WS decreased the rotation of P3 with increasing load in laminitic hooves compared to other shoes. Stabilizing P3 in affected hooves with shoes such as WS can reduce the worsening consequences of laminitis.
Research Grant	Tynewald Foundation
Field of Research	Equine Medicine and Surgery

Abstract Title	Effect of Iodochlorhydroxyquin on the large intestinal microbiota of horses
Authors	Mikaila Z. Smith, Kile S. Townsend, Lynn M. Martin, Aaron E. Ericsson, Philip J. Johnson
Affiliations	Departments of Veterinary Medicine and Surgery (Smith, Townsend, Martin, Johnson) and Pathobiology (Ericsson), College of Veterinary Medicine, University of Missouri CVM, Columbia, MO
Abstract	Fecal Water Syndrome (FWS) in horses is a concern because the fecal water running out of the anus pollutes the tail and legs and can even cause lesions, when severe enough. Etiology is identified in only ~20% of horses affected with diarrhea and FWS. Colonic bacterial dysbiosis likely plays a role in these conditions. Whereas treatment with iodochlorhydroxyquin (IQ) is often helpful, its mechanism of action is unknown, especially with regard to its effects on the colonic microflora. Consequently, our objective is to investigate the effect of IQ on fecal microflora in healthy adult horses. We hypothesize that orally administered IQ treatment elicits changes in colonic microflora that benefit fecal consistency in affected horses. Following 7 days of acclimation, 8 horses will be treated with IQ at a standard dose (10 g, PO, daily for 7 days). Feces will be obtained daily (frozen until analyzed as a batch) for DNA extraction and characterization of bacteria composition using next generation sequencing (NGS) before, during, and for 7 days after discontinuation of treatment. Bacteria will be classified from NGS data based on specific amplicon sequence variant (ASV) designation. We do not anticipate adverse health effects or changes in stool consistency during treatment of healthy horses with IQ. We expect IQ treatment will cause beneficial alterations in the bacterial population of the colon and that there will be an effect (on colonic bacteria) of discontinuing treatment. By identifying bacterial populations that are affected (increased or decreased) by IQ treatment, this information will help to inform broader studies (focused on specific taxa) in the future, especially pertaining to horses affected with diarrhea and FWS.
Research Grant	Animal Health Foundation of St Louis
Field of Research	Equine Medicine and Surgery

Abstract Title	DNA repair kinetics in canine osteosarcoma and patient-derived melanoma cells evaluated using γ-H2AX analysis.
Authors	Tiernan M. Smith, Angelynn Simenson, and Charles A. Maitz
Affiliations	Department of Veterinary Medicine and Surgery, College of Veterinary Medicine, University of Missouri, Columbia, MO
Abstract	Ionizing radiation, which induces cell death through the formation of DNA strand breaks, is a treatment commonly used in the management of cancer. Upregulation of DNA repair mechanisms in cancer cell lines can limit the efficacy of radiation therapy. The primary aim of this study is to assess the efficacy of varying radiation doses by measuring the level of dsDNA breaks and repair in canine osteosarcoma cell lines (HMPOS, D-17, Abrams) as well as a patient-derived melanoma cell line (Geddy). HMPOS, D-17, Abrams, and Geddy cell lines were cultured and incubated to reach confluence. They were then irradiated at varying doses (0 Gy, 2 Gy, 4 Gy, and 8 Gy), after which the cells were fixed and permeabilized to a slide for imaging. Using Gen5 software to perform dual-mask individual nuclei foci analysis, γ-H2AX foci were quantified as a measure of dsDNA break formation and then compared to the total nuclei count to determine the % DNA damaged in response to irradiation. This data was used to generate a dose-response curve for the individual cell lines. It is expected that higher doses of radiation will induce a higher amount of dsDNA breaks. Additionally, the repair kinetics of each cell line will be examined and compared at clinically relevant radiation doses of 3 Gy and 8 Gy by performing the γ-H2AX analysis at varying time points after irradiation. Different cell lines are expected to display unique repair kinetics that impact their response to radiation. These findings will allow for further elucidation of the mechanisms underlying these dosing regimens and their effectiveness at initiating DNA damage and cell death, generating useful insight into how to strategically administer radiation therapy in a clinical setting.
Research Grant	UM System Tier 1 Project Grant, faculty startup, and oncology support fund
Field of Research	Oncology

Abstract Title	The effect of common laboratory ultrasounds on rat behaviour and physiology
Authors	Veronica K Sohasky, Logan J Bigelow, Clare P Lee, Jonathan Spears, Paul B Bernard
Affiliations	Department of Biomedical Sciences, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, Canada
Abstract	Our perception is dictated by our sensory capabilities, which capture only a fragment of the available information. Sensory capacities, including hearing, vary across species dictating a unique experience. Unfortunately, differences in hearing capacities can make it difficult to identify aberrant environmental sounds which may be a source of stress. The laboratory space is rife with ultrasounds emitted from a variety of sources including ventilation, electronics, and lighting, which unfortunately cannot be detected by the human ear without specialized equipment. These sounds may not only be causing stress to animals but may affect their communicative capacities, which includes vocalizing in the ultrasonic range. As a means of understanding the significance of ultrasounds in the environment, we assessed the effects of ultrasound exposure on behavioural and physiological markers of stress in the rat. Rats were exposed to ultrasounds at 40 kHz, a frequency commonly present within the laboratory space and tested using classic and novel assessments of anxiety. Behavioural anxiety assessments including the open field test and elevated plus maze were supplemented with physiological measurements including body temperature and adrenal gland integrity. We hypothesized that rats exposed to ultrasounds would show behavioural and physiological indications of increased stress compared to rats exposed to no noise. The results of this study will not only lead to improved validity of rodent research by the identification and assessment of a confounding variable, but it will also be beneficial to pet owners who may be inadvertently exposing their pets to ultrasounds.
Research Grant	Sir James Dunn Animal Welfare Centre
Field of Research	Animal Welfare

Abstract Title	Characterization of contamination events during gloving & gowning amongst veterinary students
Authors	Karly M. Souders, Stanley E. Kim
Affiliations	University of Florida College of Veterinary Medicine, Department of Small Animal Clinical Sciences, Gainesville, FL
Abstract	Maintenance of proper aseptic technique is essential for limiting surgical site infections. While many studies highlight the contamination rates of surgeons intraoperatively, the incidence of breaches in aseptic protocol (BAP) of veterinary students has not been explored. This study aimed to assess the frequency of breaches in protocol amongst veterinary students scrubbing, gowning, and gloving into surgery, and identify factors that may be associated with increased risks of contamination. Students on clinical rotations at the University of Florida CVM in the surgical specialties of Orthopedics, Soft Tissue, Oncology, & Neurology were included (n= 97). Students were observed while scrubbing, gowning, and gloving into surgery and breaches in protocol were recorded. Dates, service type, start and end time of donning the surgical attire, previous surgical experience, and prompts regarding proper technique from the technicians or clinicians were also reported for each event. Of the 97 reportable events observed, 45 (46.3%) made at least one BAP. The most common mistakes noted were improper use of the towel (17.5%), contact of the gown with non-sterile surfaces (15.4%), touching objects with bare hands (13.4%) and improper scrubbing technique (13.4%). There was no statistical significance between factors such as service type ($p = 0.96$), previous scrub experience ($p = 0.29$) and stage of rotation ($p = 0.36$) and breaches in aseptic protocol. On average, those that made a BAP had longer gowning and gloving times (4.6 ± 1.4 min) than those who did not make a BAP (3.71 ± 0.91 min). These findings may help to highlight substandard practices in the operating room and promote the future development of aseptic technique protocols.
Research Grant	Research Support: Edward Debartolo Gift to the University of Florida
Field of Research	Small Animal Medicine and Surgery

Abstract Title	CRISPR gene editing in canine cells for pyruvate dehydrogenase kinase 4 to treat dilated cardiomyopathy
Authors	Sasha Spada-O'Neill, Arielle Admonius, Cole English, Noble II. Noble, Amara Estrada, Christina Pacak, Chris Vulpe, Chris Martyniuk
Affiliations	Physiological Sciences, CVM, University of Florida, Gainesville, FL (Spada-O'Neill, English, Noble, Vulpe, Martyniuk) Small Animal Clinical Sciences, CVM, University of Florida, Gainesville, FL (Admonius, Estrada) Neurology, CoM, University of Minnesota, Minneapolis, MN (Pacak)
Abstract	Cardiovascular disease is a leading cause of mortality in both humans and canines, one of the most common forms being dilated cardiomyopathy (DCM). In the Doberman Pinscher, DCM is linked to two known genetic mutations. One is a 16 base pair deletion located at the donor splice site of an intron in the pyruvate dehydrogenase kinase 4 (PDK4) gene. This mutation results in an altered splice product, which effects metabolic capacity of cardiomyocyte cells. The objectives of this study are to determine the efficacy of homology-independent targeted insertion (HITI), a CRISPR/Cas9 gene editing strategy, to correct the PDK4 mutation. We designed single guide RNA (sgRNA) using two approaches: one approach was to drop out the exon adjacent to the mutation, while the other approach was to target and cut the unique mutant sequence to enable the replacement of the deleted region using a HITI approach. We tested five sgRNAs in vitro using ribonucleoprotein (RNP) based cleavage assay. Four sgRNA candidates showed evidence of cutting in vitro in the homozygous DNA template. To further evaluate the candidates, we carried out transfection using RNPs in vivo. Cleavage efficiency was assessed by Sanger sequencing and computational analysis. For the two sgRNA candidates designed to exon drop, post-nucleofection analysis showed up to 100% total editing efficiency and up to 71% editing efficiency specific to the exon deletion. However, post-nucleofection analyses did not detect editing efficiency for sgRNAs designed to cut the mutant sequence for integration. Our results suggest that the CRISPR/Cas9 HITI approach may be used to edit the PDK4 mutation, advancing potential for genetic therapies in veterinary medicine.
Research Grant	Morris Animal Foundation, Doberman Pincher Health Foundation, ACVIM Pacemaker Fund Diplomate Grant
Field of Research	Cardiology

Abstract Title	Hyperglycemia from diabetes potentiates osteocalcin-induced insulin secretion in pancreatic β-cells.
Authors	Speight V(1), Channuwong P(1,2), Yuan Y(3), Yao S(3), Yoshimura M(3), Bauermann F(4), Ranjan A(1), Adisakwattana S(2), Cheng H(1)
Affiliations	(1) Dept. of Physiological Sciences and (4) Veterinary Pathobiology, Oklahoma State University CVM, Stillwater OK (2) Dept. of Nutrition and Dietetics, Faculty of Allied Health and Sciences, Chulalongkorn University, Bangkok, Thailand (3) Dept. of Comparative Biomedical Sciences, Louisiana State University SVM, Baton Rouge, LA
Abstract	Osteocalcin (OCN) is a hormone secreted by osteoblasts that functions to strengthen bone during mineralization. In addition to being a biomarker for ongoing bone formation, it also regulates glucose homeostasis by stimulating insulin secretion from pancreatic β-cells. However, its effect on β-cells under hyperglycemic diabetic conditions as well as its mechanism of action is unknown. The goal of our project was to investigate how OCN affected β-cell function under high glucose conditions. Using rat pancreatic β-cells (INS-1), we performed static incubation and ELISA to quantify insulin secretion, real-time calcium imaging analysis to measure intracellular calcium signals, and RT-qPCR to determine its effect on glucose-induced insulin secretion genes. The results revealed that OCN significantly increased insulin secretion under hyperglycemic conditions compared to lower glucose levels. This effect was also dose dependent at a fixed glucose concentration. Because insulin secretion relies on intracellular calcium signals, we confirmed that OCN increased intracellular calcium in a concentration dependent manner. RT-qPCR analysis revealed that OCN significantly upregulated the expression of the insulin, glucose transporter 2 (GLUT2) and ATP sensitive K+ channel (KATP) genes under hyperglycemic conditions. In conclusion, OCN increased insulin secretion and upregulated glucose-induced insulin secretion genes via an intracellular calcium mechanism, which was potentiated under high glucose levels. These findings provide a better understanding of the endocrine system control of insulin secretion in diabetes.
Research Grant	Oklahoma State University CVM Research Advisory Committee Thai Royal Golden Jubilee Research Program, Thailand
Field of Research	Physiology

Abstract Title	Optimizing lysis of canine red blood cells for flow cytometry
Authors	Riley Spielman, Isabella Kappenman, Jaime Modiano, Ashley Schulte
Affiliations	Veterinary Clinical Sciences, University of Minnesota CVM, St. Paul, Minnesota
Abstract	Flow cytometry measures and analyzes cell populations for the Shine On Suspicion test to detect dogs at higher risk of cancer. Cells are processed through lasers and their resulting light scatter and fluorescence are recorded to determine cell types. Red blood cells are removed using hypotonic lysis with ammonium chloride-based buffers. In the hypotonic environment, NH4Cl enters erythrocytes by osmosis, causing them to swell and rupture. White blood cells can respond to and survive in the hypotonic environment for a short period of time, but red blood cells cannot, providing a method for the selective depletion of erythrocytes and platelets. The proper proportion of lysis to blood samples is important when trying to conserve the highest amount of non-erythrocytic cells and keep them alive. Red blood cell lysis buffer is a combination of ammonium chloride, potassium carbonate, and EDTA, commercially available as 10x solutions. The standard procedure in our lab involves diluting 10x RBC lysis buffer to 1x with DI water and using 40mL of the diluted solution with 2 mL of the blood sample. Most commercially available RBC lysis buffers are formulated for mouse or human samples; the purpose of my summer project is to determine if changing these parameters will increase the total non-erythrocyte cell count and viability for canine cells. We hope to establish a consistent method for using canine blood by conducting experiments that explore conflicting procedures in the literature. Our hypothesis is that these changes will impact overall cell counts, erythrocyte removal, and cell viability.
Research Grant	Grant 02806-MOU from the AKC Canine Health Foundation; Funds from the University of Minnesota Animal Cancer Care and Research Program
Field of Research	Oncology

Abstract Title	Prevalence of Salmonella enterica across the beef-on-dairy cattle production system
Authors	Faith Stapleton, Raghavendra G. Amachawadi, Harith Salih, Taghreed Mahmood, Logan Druecker, Tera Barnhardt, Phillip A. Lancaster, and T. G. Nagaraja
Affiliations	Departments of Clinical Sciences (Stapleton, Amachawadi, Salih, Mahmood, Druecker, Lancaster), Diagnostic Medicine/Pathobiology (Nagaraja), College of Veterinary Medicine, Kansas State University, Manhattan, KS. Consulting Veterinarian (Barnhardt), Southwest KS.
Abstract	Salmonella enterica is a foodborne pathogen of major public health concern. Cattle harbor Salmonella in the gut and lymph nodes, which are the main sources of food, including ground beef. The use of beef cattle semen to breed dairy cows to produce calves, called, beef-on-dairy crosses, for beef production has greatly increased in the past 5 years. The life cycle of beef-on-dairy calves typically includes three phases: a calf ranch phase with calves housed individually, a grower phase with calves housed in pens and a feedlot phase. There are no studies on the prevalence of Salmonella in beef-on-dairy cattle. Our objectives were to conduct an analysis of feeding and management practices, including data on morbidity and mortality, from birth to harvest to determine their associations with the Salmonella prevalence in feces and lymph nodes. A total of 141 pen floor fecal samples were collected randomly from calf ranches (n=80) and grower yards (n=61) located in Colorado (n=20), Kansas (n=80) and Texas (n=41). Salmonella isolation and identification were by culture method, agglutination and PCR detection of invA and pagC genes. Overall prevalence of Salmonella was 10.6% (15/141). The prevalence was 13.7% (11/80) and 6.5% (4/61) in calf ranch and grower phases, respectively. Fecal prevalence from Colorado, Kansas, and Texas were 5% (1/20), 8.7% (7/80), and 17.1% (7/41), respectively. Among grower yard samples the prevalence was 5% (1/20) and 7.3% (3/41) from Colorado and Kansas, respectively. Efforts are ongoing to collect lymph nodes and more fecal samples, feeding and management data to assess Salmonella prevalence and relate prevalence to feeding and management practices.
Research Grant	National Cattlemen's Beef Association (NCBA)
Field of Research	Bacteriology

Abstract Title	Associations between demographics, clinical signs, and geographic location of SARS-CoV-2 in shelter cats
Authors	Gianna Stark, Rachael Kreisler, Ogi Okwumabua, Louis Badang, and Nancy Bradley-Siemens
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ, USA
Abstract	Cats cohoused with experimentally infected cats shed SARS-CoV-2 for 5-10 days, starting as early as 1-day postexposure and generate antibodies within 7 days. The aim of this study was to associate demographic, exam, and geographic data with incidence and seroprevalence of SARS-CoV-2 in shelter cats. Cats >1 kg undergoing anesthesia were convenience sampled (pharyngeal/conjunctival swabs and serum) from April to December 2020 at a Phoenix metro shelter. Medical records were blindly coded. Normal data were compared with t-test, non-normal by nonparametric equality-of-medians test, and count by Fisher's exact. Intake zip code was mapped for comparison to human case rates (per 100,000). There were 354 cats sampled with 14 (4%) positive by ELISA (95% CI [2-7%]) and 7 (2%) positive by PCR (95% CI [4-18%]). Of the PCR+ cats, 5/7 (71%) were sampled in September. Strays accounted for 150 (42%) cats and surrender for 161 (45%). The median length of stay before sampling (LOSBS) was 5 days (IQR 2-17), with 8 of the ELISA+ cats having a LOSBS of ≤5 days. The mean weight was 3.2 kg (SD 0.9), and the median age was 12 months (IQR 6-24). The mean temperature was 101.0°F (SD 1.1), heart rate 152 bpm (IQR 136-168), and respiratory rate 30 bpm (IQR 25-40). Clinical signs were found in 41/354 (12%) of cats. There was no difference in demographic or exam findings between positive and negative cats for PCR or ELISA. There was no difference in human case rates at the zip code level for ELISA+ (P = 0.141) or PCR+ (P=0.058) cats. Eight of the seropositive cats had a LOSBS of ≤5 days, suggesting community-acquired infection. The median LOSBS for 5 PCR+ cats was greater than the SARS-CoV-2 infectious period, suggesting in-shelter transmission.
Research Grant	None
Field of Research	Epidemiology

Abstract Title	Response of the VCM Vet™ Viscoelastic Testing Monitor to Simulated User Error and Delayed Filling
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Affiliations	Interdisciplinary Veterinary Medicine, School of Veterinary Medicine, Texas A&M University, College Station, TX Department of Small Animal Clinical Sciences, School of Veterinary Medicine, Texas A&M University, College Station, TX
Abstract	VCM Vet is a novel viscoelastic tool that provides an analysis of blood coagulation as a sample clots, strengthens, lyses or retracts. Training veterinary staff to appropriately use the VCM Vet likely impacts the reliability of the results, and user error may increase the chance of misdiagnosis or inaccurate findings. The objective of this study was to assess the susceptibility of the VCM Vet to simulated user error via sample cartridge underfilling, overfilling, and delayed filling, compared to operating as the manufacturer recommends. Four sample cartridge handling groups were used: A) control group filled as directed by the manufacturer, B) underfilling to ½ to ¾ of the cartridge, C) overfilling the cartridge, and D) appropriate cartridge filling delayed by four minutes. Seven healthy volunteer dogs were recruited. Fresh whole blood samples were collected, and each sample underwent all treatment groups, loading the delayed filling cartridge after the time delay. Underfilling, overfilling, and control groups were loaded in a random order determined prior to each collection. Results were compared between conditions using a Friedman test, and if significant (P-value < 0.05), were followed by a Wilcoxon test for paired samples. Clot formation time (P = 0.00043), alpha angle (P = 0.00959), A10 (P = 0.00566), LI45 (P < 0.00001), and baseline (P = 0.00966) were significantly different among groups. All three test groups had significant differences from the control group. Veterinary practices should appropriately train staff to properly run the VCM Vet monitor to ensure valid results. Underfilling, overfilling, or delayed filling of the cartridge impacts VCM Vet test results.
Research Grant	None
Field of Research	Clinical Pathology

Abstract Title	Complex microbial interactions in DSS-induced colitis severity
Authors	Amy Steeneck, Trevor R Rodriguez, Kevin Gustafson, Aaron Ericsson, Craig L Franklin
Affiliations	Biomedical Sciences Department, Carlson College of Veterinary Medicine, Oregon State University, Corvallis, OR (Steeneck); Comparative Medicine Program and Department of Veterinary Pathobiology, College of Veterinary Medicine, University of Missouri, Columbia, MO (Steeneck, Rodriguez, Gustafson, Franklin, Ericsson)
Abstract	Differences in gut microbiota (GM) have been shown to significantly impact rodent disease model phenotypes. Previous studies in our lab demonstrated that GM transfer methods and richness of donor and recipient GM affect the severity of dextran sodium sulfate (DSS)-induced colitis in mice. Notably, mice with a highly diverse GM exposed to a less diverse GM through co-housing showed the most severe disease response. We speculate that high richness GM prevents colonization of novel microbes from a low richness donor leading to limited tolerance. When exposed to DSS, which disrupts epithelial integrity, the mucosal immune system is more readily exposed to these immune naïve microbes, resulting in a worsening of disease severity. To assess if this is microbe driven, weanling C57BL/6 mice with high and low richness GMs were exposed to the opposite GM by co-housing or weekly fecal microbiota transfer (FMT) and bedding transfer for consistent exposure to novel microbes. At 7 weeks of age, mice were administered 2.5% DSS to induce colitis. Fecal samples were collected at 3 and 7 weeks of age, and DNA was sequenced to determine GM makeup. At 9 weeks of age, colon length was measured and samples collected for cytokine analysis. With both co-housed and FMT transfer methods, low to high richness GM transfer groups had increased weight loss, mortality, and decreased colon lengths compared to other groups. We anticipate that these mice will also have increased pro-inflammatory cytokine expression following induced colitis and that putative causative microbes will be identified through microbiome analysis. Such results would indicate that tolerance to novel microbes is limited in mice with a natively high richness microbiome.
Research Grant	U42 OD010918, Mutant Mouse Resource and Research Center at the University of Missouri
Field of Research	Microbiomes

Abstract Title	Assessing population stress in Atlantic salmon (Salmo salar) with fecal corticosteroid metabolites
Authors	Kisa Storey, Laura Groves, Sara Purcell, Shona Whyte, Mark Fast, Sonja Saksida
Affiliations	Department of Pathology and Microbiology, University of Prince Edward Island AVC, Charlottetown, PEI
Abstract	Aquaculture production of Atlantic salmon (Salmo salar) faces the unique challenge of rearing and maintaining fish while incorporating the growing standards on welfare in farmed animals. The ability to quantify negative affective states in non-mammalian animals has proved difficult. Plasma cortisol is the current gold standard method to measure stress in teleosts, however, this is an invasive handling method that often induces hypothalamic-pituitary-interrenal (HPI) axis activation in the fish, and only provides an individual's snapshot of stress out of a tank population. In this study, fecal corticosteroid metabolites (FCM) were measured from feces sampled from Atlantic salmon tanks, using a corticosterone immunoassay. The goal is to determine if this non-invasive method of measuring FCM can provide a good measure of stress at the population level. Twelve tanks of Atlantic salmon with sixteen fish each were enrolled, six tanks were exposed to Chaetoceros spp. culture three times, to replicate common harmful diatom blooms in the marine phase of grow out, and then challenged with Tenacibaculum maritimum, a bacterium known to cause severe skin lesions in Atlantic salmon. The other six tanks acted as controls (unstressed). Feces were collected from the tanks 24 hours after each stress event and samples for FCM over the course of 6 weeks. The study will assess whether FCM levels measured from feces collected from tanks can be used to detect stress in a population. Quantification of population stress allows for early intervention during disease outbreaks or stressful events, and a humane way to assess the welfare of fish as our understanding of this topic develops.
Research Grant	Sir James Dunn Animal Welfare Research Grant
Field of Research	Production Animal Medicine

Abstract Title	A novel co-culture model highlights extrinsic modulation of TNBC therapy responses by primary lung fibroblasts
Authors	Claire Stratton, Marika Klosowski, Daniel Regan
Affiliations	Department of Microbiology, Immunology, and Pathology and Flint Animal Cancer Center, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO.
Abstract	Triple negative breast cancer (TNBC) has a poor prognosis due to high metastatic incidence, lack of molecular drug targets, and chemoresistance. Cancer associated fibroblasts extrinsically drive chemoresistance in primary TNBC tumors, but it is unclear if resident fibroblasts of distant metastatic tissues, such as the lung, influence TNBC drug sensitivity. Thus, we developed a breast cancer cell (BCC) - donor-derived lung fibroblast (LF) co-culture model, and hypothesized that anti-cancer drug screening using the TNBC cell line MDA-MB-231 in this model would uncover mechanisms of LF-mediated chemoresistance and therapeutic vulnerabilities relevant to lung metastasis. A high-throughput screen of 900 kinase inhibitor compounds revealed that while MDA-MB-231 drug resistance broadly increased in co-culture compared with monoculture, co-culture sensitivity increased to only three drugs, of which two were vacuolar protein sorting 34 inhibitors (VPS34i). Validation of prioritized compounds across a dose range confirmed enhanced co-culture resistance to MCB-613, a steroid receptor coactivator stimulator, and sensitivity to VPS34i drugs. As VPS34 is a key inducer of autophagy, we sought to determine if autophagy is a mechanism for MDA-MB-231 LF-mediated chemoresistance. Indeed, combined therapy with a VPS34i reversed LF-mediated resistance to TNBC standard-of-care doxorubicin. Ongoing experiments will compare autophagic flux between mono- and co-culture and determine if VPS34i therapy also reverses resistance to MCB-613, whose metabolic effects are known to be mitigated by autophagy. Together, these data support BCC-LF co-culture as a relevant in vitro model of lung metastatic TNBC that can inform preclinical drug development.
Research Grant	National Institutes of Health K01OD022982
Field of Research	Oncology

Abstract Title	A comparison of methods for preparation of equine platelet-rich plasma used for treatment of PBIE
Authors	Madeleine Stroh, Yazmin Osornio, Tracey Chenier
Affiliations	Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON
Abstract	Persistent breeding-induced endometritis (PBIE) occurs when affected mares fail to clear the normal, transient, post-breeding inflammatory response within 48-72 hours after breeding. Platelet-rich plasma (PRP) has been proposed as a treatment for PBIE as platelets are rich in factors that down-regulate inflammation. No standard PRP dose exists in the literature when treating PBIE-susceptible mares. This study aimed to compare platelet counts produced by double centrifugation to the Arthrex ACP double-syringe system. We hypothesized that PRP prepared by double centrifugation would yield higher platelet concentrations, but with more variation, compared to the Arthrex system. Whole blood (WB) was collected from light-horse breed mares (n=8) via jugular venipuncture. WB samples were collected into a vacutainer containing EDTA. Blood was drawn into a 15mL Arthrex ACP double-syringe pre-loaded with 1.5mL of CPDA-1, and centrifuged at 1100 rpm for 5 minutes. Plasma was drawn into the 6mL inner syringe, and the bottom and top 1mL were each sampled as PRP and PPP respectively. Samples were submitted to the University of Guelph Animal Health Laboratory for automated determination of platelet, RBC and WBC counts. Mean platelet concentration in WB, PRP, and PPP were 131.5x109/L (±19.9), 148.6x109/L (±60.0), and 148.1x109/L (±52.2) respectively. The enrichment factor (%) of platelets in PRP and PPP compared to their respective WB counts averaged 1.13 (±0.42) and 1.14 (±0.41). PRP and PPP concentrations were not significantly different ($p = 0.48$). These findings suggest that preparation by the Arthrex system produced plasma and not PRP and PPP specifically. Ongoing work will evaluate a double centrifugation preparation method.
Research Grant	Equine Guelph, OMAFRA
Field of Research	Theriogenology

Abstract Title	Prednisolone pharmacokinetics in dogs with protein-losing enteropathy
Authors	Jessica L. Strohmeyer, Sara A. Jablonski, John P. Buchweitz, Andreas F. Lehner, and Daniel K. Langlois
Affiliations	Michigan State University College of Veterinary Medicine (Strohmeyer), Small Animal Clinical Sciences (Jablonski, Langlois) Veterinary Diagnostic Laboratory (Buchweitz, Lehner)
Abstract	Intestinal diseases associated with proteins loss across the diseased intestinal tract are referred to as protein-losing enteropathies (PLE). Dogs with PLE are commonly affected with either chronic inflammatory enteropathy (e.g., inflammatory bowel disease), lymphangiectasia, or a combination of both. Orally administered steroids such as prednisolone are mainstays of treatment, yet up to 50% of PLE cases are non-responsive. It is unknown if steroid malabsorption contributes to poor outcomes. The objectives of this study were to determine the pharmacokinetics of orally administered prednisolone in dogs with PLE. Ten dogs with well-characterized PLE and 5 healthy controls were enrolled in this prospective clinical study. All dogs were administered 1 mg/kg prednisolone once daily for approximately 3 weeks. Serum biochemistries were determined at baseline and at study conclusion. Serum prednisolone concentrations were measured immediately before and at 1, 2, 4, 6, and 8 hours after the initial and final prednisolone doses of the study period. Statistical testing was performed to determine if there were differences in variables between PLE and control dogs or if there were differences between treatment responders and non-responders within the PLE population. The clinical study has concluded, but measurements of prednisolone concentrations are ongoing. Four of 10 PLE dogs remained severely hypoalbuminemic despite treatment. We speculate there will be no significant differences in pharmacokinetics variables between PLE and control dogs or between treatment responders and non-responders within the PLE population. These results would have immediate clinical impact as it would influence treatment practices for dogs with PLE.
Research Grant	Michigan State University College of Veterinary Medicine Endowed Research Funds.
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Sex-related differences in autoimmune diseases is linked to changes in T cell development
Authors	Rebecca A. Stuhrmann, Isabel M. Forlastro and Brian D. Rudd
Affiliations	University of Veterinary Medicine Hannover, Germany (Stuhrmann) and Department of Microbiology and Immunology, College of Veterinary Medicine, Cornell University, Ithaca, NY (Forlastro, Rudd)
Abstract	A large number of epidemiological studies have indicated that females are more prone to autoimmune diseases than males. However, the underlying basis for these sex-related differences is unclear. An important question is whether altered susceptibility to autoimmune diseases relates to sex-specific differences in thymic development. To address this question, we harvested thymuses and spleens from male and female B6 mice and compared the amounts of self-reactivity, clonal deletion and proliferation using flow cytometry. Interestingly, we found that female B6 mice express higher levels of CD5 (a marker of self-reactivity) and have higher rates of clonal deletion compared to males. We also evaluated thymic selection in male and female non-obese diabetic (NOD) mice which are more prone to type I diabetes. Notably, the amount of self-reactivity in CD8+ T cells from female B6 mice is comparable to what is found in their counterparts from NOD mice. However, the mature female CD8+ T cells undergo more clonal deletion in NOD mice. Lastly, we examined whether sex-specific differences in T cell development are associated with changes in the thymic environment. For this experiment, we isolated RNA from thymic cells, ran qPCR and are currently gathering results about the cytokine composition. Collectively, these findings suggest that susceptibility to autoimmune diseases corresponds to changes in self-reactivity during thymic development and that female CD8+ T cells in healthy animals are generated with inherently more self-reactive T cell receptors (TCRs) than male CD8+ T cells.
Research Grant	R01AI110613
Field of Research	Immunology

Abstract Title	The wild ones: the effects of genetic re-wilding on depression and anxiety scores of C57BL/6 lab mice.
Authors	Erin Tan, Daniel Chang, Michael J. Sheehan, Matthew N. Zipple
Affiliations	Laboratory for Animal Social Evolution and Recognition, Department of Neurobiology and Behavior, Cornell University, Ithaca, NY, USA
Abstract	Lab mice are the go-to biomedical model organism for understanding human health and disease. However, recent results have shown inconsistencies between the effectiveness of drugs in lab mice and humans, leading to calls by scientists and the media to re-think the lab animal approach to drug development. This issue might be especially pronounced for behavioural disorders like anxiety and depression – the leading psychiatric disorders in humans – which are so dependent on animals' social and physical experiences. One of the problems with lab mice is that they are genetically uniform and have undergone multiple generations of artificial selection and adaptation to captivity. This selection may have led to lab mice developing depression and anxiety phenotypes that render them less valid models of such human disorders. For example, lab mice may have a higher innate level of learned helplessness, a set of behavioural changes which leads to the development of depression and anxiety in mice. Here, we tested whether crossing C57BL/6 lab mice with wild strains affected their escape motivation, a trait linked to the level of depression-like behaviour in mice. We found that some strains of outbred mice showed significantly higher escape motivation than lab mice. We are also currently running depression and anxiety assays on lab mice and outbred mice to compare if outbreeding significantly affects other aspects of anxiety and depression. These findings will be helpful in creating more valid mouse models of depression and anxiety – and other disorders at large – and will further the development of more effective drugs to treat these disorders in humans.
Research Grant	Cornell Klarman Postdoctoral Fellowship Program, Animal Models for the Social Dimensions of Health and Aging Network
Field of Research	Behavior

Abstract Title	Effects of neonatal estrogen and progesterone administration on adulthood fertility in female rats
Authors	Kayla Tando, Behrokh Marzbanabbasabadi, Po-Ching Patrick Lin, CheMyong Jay Ko
Affiliations	Department of Comparative Biosciences University of Illinois Urbana-Champaign, Urbana, IL, USA (Tando, Lin, Ko) and Amol University of Special Modern Technologies, Amol, Iran (Marzbanabbasabadi)
Abstract	Kisspeptin (KISS1), a neuropeptide that controls GnRH secretion, is expressed by KISS1 neurons which are found mainly in the anteroventral periventricular nucleus (AVPV) and arcuate nucleus (ARC) of the hypothalamus, influencing estrous cyclicity, and also in the amygdala, influencing sexual behaviors. Estrogen induces apoptosis of KISS1 neurons and progesterone (P4) is known to antagonize effects of estrogen. Prior studies have shown a neonatal estrogen injection disrupts estrous cycling and causes infertility in adult canines while a neonatal estrogen/P4 injection does not affect cycling but causes infertility. In this study, estrogen and P4 were given to neonatal female rats to evaluate effects on estrous cycling and KISS1 expression in the AVPV, ARC and amygdala. We hypothesize estradiol benzoate (EB) treated rats will have reduced hypothalamic KISS1 expression and abnormal estrous cycling while EB+P4-treated rats will have normal hypothalamic KISS1 expression and estrous cycling but decreased KISS1 expression in the amygdala. On postnatal day (PND) 1.5, groups were injected with EB, EB+P4 co-treatment, or a control vehicle. Estrous cyclicity was monitored during PND 40-50. At PND 70, AVPV, ARC, amygdala, uterus and ovary samples were collected. Anovaginal distance (AVD) and vaginal opening size were also evaluated. The EB group mainly exhibited proestrus while the EB+P4 group fluctuated between proestrus, diestrus and metestrus. AVD was consistent among all groups. EB-treated and EB+P4-treated groups had smaller vaginal openings and smaller ovaries. Histological results are still pending. Results of this study may have implications regarding neonatal sterilization of animals and even human sexuality.
Research Grant	INSIGNA TTA
Field of Research	Physiology

Abstract Title	Quantifying the effect of vial septa passage on peak penetration force: a blinded randomized control trial
Authors	Julia Tawil, John Mitchell, Emma Vitello, and Rachael Kreisler
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ (Tawil, Vitello, Kreisler); College of Dental Medicine, Midwestern University, Glendale, AZ (Mitchell)
Abstract	Veterinarians often change needles before injection after drawing up a vaccine due to concerns for needle dulling. The aim of this study was to determine whether needles commonly used by veterinarians dull after passage through vial septa. The peak force required to penetrate a standard material by the most common brands (3) and sizes (4) of single-use hypodermic needles reported by veterinarians in an anonymous internet survey (IRBAZ-5222) was measured using a Wagner FDIX ForceOne force gauge. Multivariable linear regression was used to determine the association between peak force and number of passages (0, 1, 2) through a vaccine vial septum while controlling for needle brand (a, b, c), gauge (20, 22, 25, 29), and vaccine vial penetration force (VVPF). There were 330 needles analyzed. New 20 G needles of brand a (referent) required 1.05 N to penetrate the standard material. Two passes through a septum required additional 0.20 N of force ($P<0.001$) while one pass only required an additional 0.08 N ($P=0.035$). Compared to brand a, brand b and c required an additional 0.12 and 0.10 N, respectively, both $P<0.0001$. Smaller needles required less force, with 22, 25, and 29 G needles requiring -0.06, -0.23, and -0.47 N, respectively (all $P<0.003$). VVPF increased the peak force by 0.03 N for each additional 0.5 N ($P=0.003$) during the first septum penetration but was not significant for a second penetration ($P=0.337$). The R2 was 77%. These findings suggest that careful needle brand and size selection and slow insertion into the vial are more important than changing needles to minimize peak penetration force. The clinical relevance of these peak force differences is unknown.
Research Grant	None
Field of Research	One Health

Abstract Title	Validation of Trueperella pyogenes identification in clinical bovine samples using MALDI-TOF
Authors	Keegan Taylor, Stephanie Myers, Jason Fritzler, and Michael Cruz Penn
Affiliations	Texas Tech University, School of Veterinary Medicine, Amarillo, TX
Abstract	Bovine respiratory disease complex (BRD) is a significant disease affecting the cattle industry. The disease attributes to 70% of feedlot deaths and results in an annual economic loss of $640 million. Both viruses and bacteria contribute to the development of clinical lesions. Diagnostic tools that are critical for identifying these pathogens include matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF). Resulting spectra are compared to a reference library to allow fast identification of specific organisms. However, reproducibility can be limited due to sample preparation and bacterial strain, thus requiring either robust validation or the development of a super spectrum library containing many strains grown under multiple conditions. In this study, we validated the identification of Trueperella pyogenes, a bacterial pathogen implicated in the BRD complex, using MALDI-TOF against the SARAMIS database. Two isolates of T. pyogenes were acquired: one from the American Type Culture Collection (ATCC; NCTC 5224; source: swine) and one from the Texas Veterinary Medical Diagnostic Laboratory (TVMDL; source: bovine) in Canyon, TX. Bacterial isolates were grown using blood agar or brain heart infusion agar at three temperatures (26, 32, and 37 degrees Celsius) for 24, 48, or 72 hours. The TVMDL isolate was confirmed as T. pyogenes. However, the ATCC isolate was unable to be confirmed due to contamination. These findings highlight two important concepts: 1) sample preparation and validation are crucial for accurate results, and 2) these methods can be applied to other bacterial isolates where a super spectrum may be needed.
Research Grant	None
Field of Research	Bacteriology

Abstract Title	Optimizing an enzyme-linked immunosorbent assay for transgelin-2 to diagnose feline infectious peritonitis
Authors	Lily Tees, Alora LaVoy, and Gregg Dean
Affiliations	Department of Microbiology, Immunology, and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO
Abstract	Feline infectious peritonitis (FIP) is a systemic disease that is devastating in young and immunocompromised cats. FIP is caused by feline infectious peritonitis virus (FIPV), which is thought to arise from a genetic mutation of the common feline coronavirus (FCoV) among other host and environmental factors. Diagnosis of FIP is challenging because it is usually accomplished post-mortem using immunohistochemistry (IHC) on formalin-fixed tissues. There is a need to develop a noninvasive ante-mortem diagnostic test to detect the disease and begin treatment before clinical signs worsen. Three plasma proteins have been identified through proteomic analysis as potential diagnostic biomarkers for FIP: neural cell adhesion molecule-1 (NCAM1), transgelin-2 (TAGLN2), and tropomyosin-4 (TPM4). The expression of these proteins was altered in cats with FIP compared to healthy cats and cats with other viral diseases. We hypothesized that enzyme-linked immunosorbent assays (ELISA) can be developed against the feline proteins and used in combination to identify cats with FIP. To achieve this, a TAGLN2 sandwich ELISA was optimized using recombinant feline TAGLN2 and plasma from healthy cats. Different concentrations and reagents for coating, detection, and secondary antibodies against TAGLN2 were tested in addition to multiple horse radish peroxidase (HRP) substrates until the strongest signal: noise ratio was achieved. An ELISA for feline NCAM1 has already been optimized and a TPM4 ELISA is under development. Future experiments will involve repeated screening of the original samples used in the proteomic study with the optimized assay for each protein, followed by a clinical trial to test plasma samples from cats with and without FIP.
Research Grant	Morris Animal Foundation
Field of Research	Clinical Pathology

Abstract Title	Pilot study of the dimensions of forelimb navicular suspensory apparatus in mature non-lame Quarter horses
Authors	Kyndal Terry, Bo A. Brock, Abbi Brock, Joshua Rowe, Myra Barrett, James A. Brown
Affiliations	Texas Tech University SVM, Amarillo, TX (Terry, Brown, Rowe), Brock Veterinary Clinic, Lamesa, TX (B. Brock, A. Brock), Colorado State University, Fort Collins, CO (Barrett)
Abstract	Forelimb foot lameness is a major limitation in performance horses. Within the foot, the navicular bone and bursa, navicular suspensory ligament (NSL), deep digital flexor tendon (DDFT), and transverse lamina of the DDFT (TLDDFT) are common sites of pathology. The NSL and TLDDFT combined form the T-Ligament. Fibrous adhesions between one or more of these structures leads to impairment of the normal biomechanics and fibrosis of the NSL and TLDDFT is often identified during bursoscopy. Dimensions of the NSL and TLDDFT in mature non-lame horses are not yet described and such information could greatly assist in identifying pathology. In this pilot study, cadaver forelimbs of two mature non-lame horses were subject to magnetic resonance imaging (MRI) prior to proximal to distal (PrD) and dorsal to palmar (DoP) measurements of the NSL, and PrD measurements of TLDDFT, at three sagittal section sites (medial, midline, lateral) on gross dissection. Abaxial (medial and lateral) measurements were made at 15.34 ± 3.46mm and 11.35 ± 2.56mm from midline for the NSL and TLDDFT, respectively. NSL PrD measurements at the midline sagittal ridge were less than abaxial locations (7.22 ± 0.92mm versus 9.74 ± 0.97mm). NSL DoP measurements were similar across the three locations (midline; 4.41 ± 0.37mm, abaxial; 5.17 ± 0.76mm) as were TLDDFT PrD measurements (midline; 8.34 ± 0.29mm, abaxial; 9.13 ± 1.07mm). MRI measurements pending. Length (PrD) of the NSL was the only measurement found to vary upon location along the navicular bone. This study provides preliminary NSL and TLDDFT dimensions. Future studies with a greater sample size to provide reference ranges and normal variation for comparison to horses with foot-related lameness are needed.
Research Grant	Brock Veterinary Clinic, Hallmarq Veterinary Imaging
Field of Research	Equine Medicine and Surgery

Abstract Title	Do female rats demonstrate heightened anxiety, fear, and sensory sensitivity post-TBI compared to males?
Authors	Rachel Tevere, Emma Halter, John A. Wolf
Affiliations	1 Center for Brain Injury and Repair, Department of Neurosurgery, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania 2 Center for Neurotrauma, Neurodegeneration & Restoration, Corporal Michael J. Crescenz Veterans Affairs Medical Center, Philadelphia, Pennsylvania
Abstract	Mild traumatic brain injury (mTBI) affects millions of people per year. mTBI has recently gained more attention as it is highly comorbid with post-traumatic stress disorder (PTSD), however their relationship is still not well understood. Research investigating the effects of TBI in both humans and animals has largely only included male subjects up to this point, therefore there is a need to investigate sex differences when studying the effects of TBI. In this study, female and male Long-Evans rats underwent a 5mm left lateral craniotomy followed by a fluid percussion injury (FPI) to model mTBI, and control rats underwent a sham procedure. Anxiety behaviors were assessed both pre and post-injury in an open field and elevated plus maze. To test for sex differences in sensitivity to sensory stimuli we evaluated the freezing response to seven 30 second presentations of novel white noise 48 hours post-injury. Finally, to understand how TBI alters fear memory, rats underwent a single trial of fear acquisition one day before surgery; rats received a series of 10 0.7 mA foot shocks. On days 15 and 16 post-injury rats underwent four trials of fear extinction. On day 35 post-injury one trial of reinstatement was conducted in which rats received a single 0.7 mA foot shock; this was followed by an additional three trials of fear extinction. We hypothesize that FPI females will demonstrate more anxious behaviors, freeze more in response to a novel sensory stimulus, and take longer to extinguish learned fear when compared to all other study animals. Understanding how TBI alters anxiety levels, fear memory and sensory processing, and how sex influences those responses, may contribute to our understanding of TBI-PTSD comorbidity.
Research Grant	NIH Grant T35 OD 010919-25
Field of Research	Behavior

Abstract Title	Effects of branched-chain amino acid supplementation in calves pre-weaning
Authors	Hannah L. Thom, Carley C. Mills, and Francisco A. Leal-Yepes
Affiliations	College of Veterinary Medicine, Washington State University, Pullman, WA.
Abstract	As dairy calves are weaned from milk and transitioned to a solid diet, they often become nutritionally deficient, resulting in growth and developmental setbacks, decreased productivity, and economic losses for producers. To study the potential to eliminate nutritional deficiencies, calves were supplemented with branched-chain amino acids (BCAA; 17 g/d Val, 27 g/d Leu, 11 g/d Ile) from day 2 until weaning at day 56 of life and compared to a group receiving unaltered milk (n=11). We aimed to better understand how BCAA supplementation can benefit dairy calves during the weaning period and hypothesized that supplementation may result in increased protein synthesis and muscle gain. Statistical analysis was performed using repeated measurements ANOVA (SAS 9.4, SAS Institute Inc.). We observed that the BCAA calves had a greater average daily gain (ADG) when compared with the control calves. The BCAA averaged 0.73 kg/day, with a 95% confidence interval (95% CI) [0.63, 0.82]. The control group ADG was 0.58 kg/day, 95% CI [0.49, 0.66], (P=0.02). No difference in daily intake was observed. On average, the BCAA calves drank 6151.8 ml of milk/d (P=0.33), 95% CI [5868.1, 6449.1], and the control group drank 6338.7 ml of milk/d, 95% CI [6071.6, 6619.1]. The BCAA calves consumed 0.12 kg of grain/d (P=0.62), 95% CI [0.07, 0.19], and the control calves consumed an average of 0.10 kg of grain/d, 95% CI [0.06, 0.16]. Ultrasonography of the longissimus dorsi muscle was used to measure muscle width at day 35 and 58 of life. We did not observe a difference in muscle diameter (P=0.63). As observed, BCAA supplementation pre-weaning results in the continual increase in gain throughout a period typically associated with loss for dairy calves.
Research Grant	WSU CVM Summer Research Fellowship
Field of Research	Production Animal Medicine

Abstract Title	Biomarker discovery in pregnant cattle infected with bovine viral diarrhea virus
Authors	Heather Thomasovich, Andrea Lear, and Jon Beever
Affiliations	Department of Large Animal Clinical Sciences, College of Veterinary Medicine (Thomasovich, Lear) and Department of Animal Science (Beever), University of Tennessee, Knoxville, TN
Abstract	Placenta-derived exosomes are released from the trophoblast along with pregnancy associated glycoproteins (PAGs), and both can be indicators of fetal health. Exosomes are a subset of extracellular vesicles (EVs) that carry proteins, nucleic acids, and lipids and act as intercellular communication. Higher numbers of exosomes can be measured in pregnant females than in non-pregnant females, but it is unknown how pathology affects exosome content in pregnant cattle. Bovine viral diarrhea virus (BVDV) can invade the fetal compartment, causing disease in the fetus without the dam displaying symptoms. The objective of this study is to identify biomarkers in the blood of the dam that are associated with fetal BVDV infection. Nulliparous pregnant beef heifers were divided into 2 treatment groups, a PI group (heifers carrying a PI fetus, n=4), and a CTRL group (heifers carrying a non-infected fetus, n=4). Cattle were intranasally inoculated with BVDV-1b strain (BJ6) or sham media at 75 days of gestation. Whole blood was collected at 45 and 95 days of gestation and plasma isolated. Using density gradient centrifugation, the exosome population was isolated from plasma and placental exosomes were further isolated by immunoprecipitation, using placental alkaline phosphatase (PLAP) conjugated dynabeads. Flow cytometry was used to confirm the presence of CD63+ and PLAP+ placenta-derived exosomes, which were then evaluated by proteomics and RNA extraction. Serum was used to determine PAG concentration using a commercially available ELISA. We expect that PAG concentrations and EV content will differ between heifers with healthy and BVDV infected fetuses.
Research Grant	USDA- Center of Excellence
Field of Research	Virology

Abstract Title	Virulence and genetic diversity of Klebsiella pneumoniae from California sea lions (Zalophus californianus)
Authors	Madeleine Thompson, Zeinab Yazdi, Carlos Rios, Pádraig Duignan, and Esteban Soto
Affiliations	Aquatic Animal Health Laboratory, Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California, Davis, CA (Thompson, Yazdi, Soto) The Marine Mammal Center, Sausalito, CA (Rios, Duignan)
Abstract	Klebsiella pneumoniae is a gram-negative, aerobic, encapsulated, non-motile bacillus with a broad host range, including humans. Within the last decade there has been an unexplained increase in the prevalence of hypermucoviscous (HMV) K. pneumoniae in marine mammals, especially California sea lions (Zalophus californianus) (CSLs), contributing to disease and strandings. Using murine models of infection, the HMV phenotype isolated from human patients has been associated with increased virulence. However, this association has not been established using isolates recovered from animal hosts. To explore this association we initially typed 37 isolates collected from CSLs at The Marine Mammal Center in Sausalito, CA during 2022 for the presence of 12 virulence factors thought to be associated with greater pathogenicity in members of the family Enterobactericeae. Thirty-three out of the 37 isolates had the capsular serotype K2 gene (K2wzy). Within the K2 serotype four distinct genetic profiles were observed, with one over-represented clade containing 28 of the 33 K2 K. pneumoniae. Next-generation sequencing confirmed genetic heterogeneity within the recovered K2 HMV isolates. The in-vitro virulence of representatives from each of these identified clades will be assessed using Vero cells, a kidney epithelial cell line extracted from African green monkeys (Chlorocebus sabaeus), a known susceptible host of HMV K. pneumoniae. Cytotoxicity post-infection will be assessed through quantification of lactate dehydrogenase as an indicator of disrupted cellular plasma membranes. These findings demonstrate genetic diversity within the K2 serotype, and our planned investigation of differences in their virulence will further characterize them.
Research Grant	Donations to the Aquatic Animal Health program
Field of Research	Bacteriology

Abstract Title	Bridging the gap: overcoming DNA degradation challenges in Sea Turtle genetic analysis with mtDNA targeting
Authors	Sarah Thurman, Mark Arick II, Chuan-yu Hsu, Theresa Madrigal, Debra Moore, Beth Peterman, Atilla Karsi
Affiliations	Department of Comparative Biomedical Sciences (Thurman, Karsi) & Department of Pathobiology and Population Medicine (Moore, Peterman), CVM & Institute for Genomics, Biocomputing, & Biotechnology (Arick II, Hsu), & Global Center for Aquatic Health (Moore, Peterman, Karsi), MSU, Starkville, MS IMMS (Madrigal)
Abstract	Kemp's ridley sea turtles (Lepidochelys kempii) are a critically endangered species found in the Gulf of Mexico. The Institute of Marine Mammal Studies in Gulfport, MS, has played a vital role as a rehabilitation facility for cold-stunned sea turtles stranded along New England shores. These turtles receive veterinary care from MSU veterinarians, are tagged with satellite trackers, and released into the Mississippi Sound. Tracking efforts have revealed that these rehabilitated turtles remain within the Gulf, particularly off the coasts of Mississippi and Louisiana. This evidence suggests that the Northern Gulf Coast now supports a significant population of released sea turtles, emphasizing the importance of understanding this population at a genetic level for effective conservation. To this goal, blood samples were collected from turtles undergoing rehabilitation, and tissue samples were obtained from deceased stranded turtles along the Gulf Coast. The genomic DNA extracted from these samples presented challenges as most exhibited poor quality and varying degrees of degradation. Consequently, mitochondrial DNA (mtDNA) amplification and sequencing emerged as the most viable approach for genetic analysis. Multiple universal primer sets were designed to amplify the complete 16 kb mtDNA or two overlapping fragments. While amplification of the entire 16 kb mtDNA proved unsuccessful, one of the two fragments was successfully amplified using three specific primer sets. We will optimize the conditions to obtain the second fragment required to amplify the entire mtDNA. Assessment of genetic diversity is expected to be a foundation for future studies aimed at analyzing several important factors that will contribute to conservation.
Research Grant	Mississippi Department of Marine Resources (Gulf of Mexico Energy Security Act) Mississippi State University College of Veterinary Medicine
Field of Research	Wildlife Conservation

Abstract Title	Histologic Characterization of Brood X Cicadas
Authors	Sara Tonissen, Johanna Rawlings, Elise E. B. LaDouceur, Ellen Klinger, and Megan E. Schreeg
Affiliations	Department of Veterinary Biosciences, College of Veterinary Medicine (Tonissen, Rawlings, Schreeg), and Department of Ecology, College of Food, Agriculture, and Environmental Sciences (Klinger), The Ohio State University, Columbus, OH. Joint Pathology Center, Silver Spring, MD (LaDouceur).
Abstract	Several observational studies have followed the distribution of different periodical cicada broods, but no studies have looked at population histology. The overall aim of this project was to histologically characterize Brood X cicadas and we hypothesized that we would identify underlying histologic lesions that contributed to mortality in the cicadas that were found dead. 50 Brood X cicadas (30 found dead; 20 caught live and euthanized) were collected in Powell, OH and examined. Gross features were used to differentiate between males and females as well as the three species within Brood X (Magicicada septendecim, M. cassini, and M. septendecula). Males were overrepresented in the found dead group while females were overrepresented in the live group. Cicadas were fixed in Davidson's solution for 3-13 days, trimmed using combined serial transverse and sagittal sections, then processed routinely. To date, 39 cicadas (22 found dead; 17 caught live) have been examined. Tissues identified histologically included: cuticle (39/39), epidermis (39/39), skeletal muscle (39/39), foregut (26/39), midgut (30/39), hindgut (12/39), fat body (30/39), Malpighian tubules (27/39), heart (10/39), aorta (6/39), vessels (15/39), tracheae and tracheoles (39/39), brain (34/39), peripheral nerves (31/39), compound eyes (37/39), and reproductive system (37/39). Preliminary lesions identified: fat body atrophy (9/39), cuticular fungal mats near the ovipositor (3/39), and Massospora fungal infection (1/39). Multi-systemic bacterial and fungal overgrowth from postmortem degradation was common in cicadas that were found dead, and overt causes of death in cicadas examined were not apparent.
Research Grant	Megan Schreeg OSU-CVM Start-Up Fund
Field of Research	Anatomic Pathology

Abstract Title	Characterization of organoids cultured from normal and mucocele canine gallbladders.
Authors	Nicole K. Torres Machado, Jennifer Holmes, and Jody L. Gookin
Affiliations	Department of Clinical Sciences, College of Veterinary Medicine, North Carolina State University, Raleigh, North Carolina.
Abstract	Mucocele formation results from the accumulation of thick and dehydrated mucus within the canine gallbladder leading to gallbladder rupture. Surgical removal of the gallbladder can be curative but carries a high mortality. The cause of mucocele formation is unknown and there are currently no models to study disease pathogenesis. The cystic fibrosis transmembrane conductance regulator (CFTR) is an epithelial chloride channel responsible for hydration of gallbladder mucus. Prior studies of CFTR knockout laboratory animals demonstrate a gallbladder pathology similar to dogs with mucocele formation. The objective of our study was to establish an organoid culture model to investigate CFTR in healthy and mucocele gallbladders. We hypothesized that organoids cultured from dogs with mucocele formation would have abnormal CFTR expression or secretory function. Organoids were cultured from healthy and mucocele gallbladders using methods established for intestinal epithelium. Immunofluorescence imaging was performed to visualize CFTR expression. Organoid swelling in response to cAMP agonists was measured to quantify epithelial chloride secretion. Healthy gallbladder organoids express CFTR and swell in response to CFTR stimulation. Mucocele organoids lacked CFTR expression but retained the ability to swell. Results suggest that mucocele gallbladder organoids may be capable of cAMP-mediated secretion that is independent of CFTR expression. Further studies to determine the dependence of mucocele organoid swelling on CFTR activity are needed. Discovery of alternative pathways for secretion by mucocele organoids could provide treatment targets to promote mucus hydration in dogs with gallbladder mucocele formation.
Research Grant	AKC Canine Health Foundation #03145
Field of Research	Physiology

Abstract Title	Perivascular adipocyte progenitors' adipogenesis is modulated by ECM stiffness and anatomical location
Authors	Alanis J. Torres Berríos, Carolina Lopez, C. Javier Rendon, G. Andres Contreras
Affiliations	Department of Large Animal Clinical Sciences, College of Veterinary Medicine, Michigan State University, East Lansing, MI, United States (Torres, Alanis) (Lopez, Carolina) (Rendon, C. Javier) (Contreras, G. Andres) Department of Biology, University of Puerto Rico – Mayagüez, Mayagüez, Puerto Rico. (Torres, Alanis)
Abstract	The pathogenesis of hypertension involves changes in the anatomical structure of the vasculature. Mechanical forces on the vessels promote collagen deposition in the tunicas media and adventitia, changing vascular structural properties and enhancing their deleterious impact. This process remains poorly understood in the outermost layer: the perivascular adipose tissue (PVAT). During hypertension, mechanical forces limit adipogenic potential of PVAT adipocyte progenitors (AP), which may drive AP to a fibroblastic fate, affecting their vasoactive functions and promoting vascular stiffness. Thoracic aortic PVAT (aPVAT) contains 3 long strip fat depots: one anterior to the aorta (A-aPVAT), and two lateral to the posterior wall (L-aPVAT). Previous research indicates L-aPVAT adipocytes arise from progenitors different than those in A-aPVAT, we hypothesized that ECM stiffness and anatomical location influences the adipogenic potential of AP. L-aPVAT and A-aPVAT were collected from 10-week-old male Sprague Dawley rats by outgrowth expansion. To determine the effects of ECM stiffness on adipogenic potential, progenitors were cultured in a collagen matrix at different stiffness degrees. Adipogenesis and lipogenesis were quantified based on lipid droplet accumulation using IncuCyte Live-Cell® imaging and triglyceride quantification. Proliferation was evaluated with EdU staining. RNA from progenitors and adipocytes were sequenced in Illumina NextSeqData, and differentially expressed genes identified. We expect that with higher ECM stiffness, adipogenic capacity of AP will be reduced, and that L-aPVAT will have higher adipogenic potential. These results will help us understand the remodeling process of PVAT during hypertension.
Research Grant	NIH NHLBI P01 HL152951
Field of Research	Pharmacology and Toxicology

Abstract Title	The Effect of Targeted Pulse Electromagnetic Field Therapy on Canine Osteoarthritis of the Coxofemoral Joint
Authors	Nicole Torres, Anais Musso, Catherine Takawira, Mandi Lopez, Mark Mitchell, Dominic Scheurer, Kielyn Scott, Lorrie Hale-Mitchell
Affiliations	Department of Veterinary Clinical Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	Osteoarthritis (OA) affects 25% of the population of dogs and is a common form of arthritis seen. There are currently three approaches to managing OA, medical, surgical, or a mix of both. A surgical approach is costly, time-consuming, and provides a temporary fix. The medical approach relies on pain control using nonsteroidal anti-inflammatory drugs, which have adverse effects on the gastrointestinal and renal systems with long-term use. Other medical approaches, such as rehabilitation, joint supplements, and weight loss, are costly and require time and patience. Pulse electromagnetic field therapy (PEMF) has been shown to be an effective medical treatment for minimizing pain and inflammation. This study assesses if targeted PEMF (tPEMF) therapy on the coxofemoral joints of dogs with OA will have an effect on their activity, gait, and range of motion. Daily activity was measured using activity trackers placed on their collars for 6 weeks, gait kinetics was analyzed using a force platform to calculate the percentage change of ground force reactions (GFR) once weekly for 6 weeks, and range of motion was analyzed using a goniometer once a week. This study used ten research dogs, with eight dogs that have confirmed hip OA from diagnosis, standard 2-D radiographs, and computed tomography; the other two dogs were used as a control to see if tPEMF has any negative effects on healthy joints. We hypothesized that using tPEMF will improve daily activity, gait, and range of motion which is statistically significant after thrice weekly treatments for 4 weeks. The relevance of this data is to provide scientific evidence of another treatment option for OA by improving quality of life with improved activity, range of motion, and gait.
Research Grant	Louisiana State University School of Veterinary Medicine
Field of Research	Orthopedics

Abstract Title	Effect of tertiary lymphoid structures on prognosis and outcome in canines with soft tissue sarcomas
Authors	Sophia Torres, Christine Olver
Affiliations	Department of Microbiology, Immunology, and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO
Abstract	Tertiary lymphoid structures (TLS) are defined as aggregates of lymphocytes found in sites external to lymphoid tissue – including tumors. These structures are associated with improved prognosis in certain human cancers, including sarcomas, which have similar features to canine soft tissue sarcomas (STS). TLS in canine sarcomas have been recently described in our laboratory, but we have not explored the prognostic potential or the immune environment of these structures. The aim of this study is to evaluate the effect that TLS presence has on prognosis in patients with STS. Additionally, we sought to further assess the immune cell distribution and activation state within TLS. Through a retrospective study, prognosis will be calculated through median survival and recurrence times derived from the medical records of patients who had STS submitted through the CSU Veterinary Diagnostic Laboratory. Both TLS and non-TLS containing cases will be evaluated to determine differences between the two populations. We hypothesized that patients diagnosed with TLS-containing STS will have improved survival and recurrence times when compared to those without TLS. Further exploration using flow cytometry and immunohistochemistry will identify the immune cell population and the presence of T cell “exhaustion markers” within TLS containing tumors, with the long-term goal of determining whether the immune environment is susceptible to checkpoint inhibitor therapy. While TLS are novel in canine immunology, we hope the results from this study further develop a translational model for cancer immunotherapies in TLS-containing tumors.
Research Grant	College Research Council, CVMBS. Young Investigator Award, Center for Companion Animal Medicine
Field of Research	Immunology

Abstract Title	Quantifying the presence of the tapetum lucidum in Aotus lemurinus
Authors	Maddison Trawick, Moonhong Kim, Christopher Heesy, Carrie Veilleux, Margaret Hall
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ (Trawick, Kim, Heesy, Hall); College of Graduate Studies, Midwestern University, Glendale, AZ (Heesy, Veilleux, Hall)
Abstract	The tapetum lucidum is a reflective layer found in many nocturnal mammals that can be found either behind a clear pigment epithelium or in front of the pigment epithelium, the non-neural layer of the retina. The function of this structure is to reflect light and give the photoreceptor layer a second chance to capture it. The owl monkey, Aotus lemurinus, is the only nocturnal anthropoid, the group that includes monkeys, apes, and humans, and it is unknown whether they possess a tapetum, since conflicting reports of eyeshine exist in the behavior literature and no histological studies yet exist. For this study, we obtained the eyes of three owl monkeys from MD Anderson, Bastrop, TX. We analyzed three retinae and compared them to cow, dog, and goat, all of which have tapeta, and pig, which does not. All comparative specimens were obtained from teaching specimens in the College of Veterinary Medicine at Midwestern University. We excised the eyes, removed the retinae, and prepared the sclera and non-neural retina. We embedded scleral pieces in paraffin and cut these using a cool-cut HM325 manual rotary machine to 5-micron thick samples. Sample sections were floated onto slides in a 40□C bath and stained with H&E using a Lecia ST520 machine to ensure uniform staining. We captured representative images of different samples from four different species. In the owl monkey sample, we found a thin layer of collagen that contained fibroblasts in the same position as the cow and goat tapetum, sclerad to the pigment epithelium and vitread to the choroid. While this layer was significantly narrower than the tapeta found in cow and goat, it was otherwise consistent with the morphology of a tapetum fibrosum.
Research Grant	Midwestern University Intramural Funds
Field of Research	Anatomy

Abstract Title	High-velocity impact points to canine integument
Authors	Christina Ulsh, Nanny Wenzlow
Affiliations	Department of Pathobiological Sciences - Louisiana Animal Disease Diagnostic Laboratory, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	The characteristics of canine gunshot wounds (GSWs) and correlated distance estimates are missing from much of the medical literature. Therefore, veterinary pathologists must extrapolate what is known about human GSWs to guide their findings, which can have implications in court decisions in cases of animal abuse and cruelty. This study aimed to provide insight on GSWs to canine integument for clinical and diagnostic veterinarians. Four firearms (12-Gauge shotgun, .38 special handgun, .22 handgun, .22 rifle) were fired from three distances [0 inches (contact), 6 inches (close-range), 3 feet (intermediate-range)] to the head, chest, abdomen, and hindlimb on euthanized canine cadavers (n=27) and on four different-colored canine hides. Dense fur coats and darker colors interfered with the gross examination. Contact and close-range entrance GSWs only caused soot deposition but not tattooing or stippling, as described in humans. Intermediate, entrance GSWs may be well hidden by long fur and only cause searing of the wound edges. While entrance wounds show bullet wipe, presence of bullet wipe on exit wounds is unpredictable. Gunshot-entrance wounds do have a somewhat different appearance on dogs' skin than on humans. The distance evaluation is much less specific and less useful to shooting reconstructions. Growth in the veterinary forensics field not only holds weight in upholding animal welfare but also in detecting individuals who pose a threat to society.
Research Grant	Start-up funds from Nanny Wenzlow
Field of Research	Anatomic Pathology

Abstract Title	Metagenomic Amplicon Sequencing Identifies Hosts for Parasites & Bacteria in Raw Cat Foods.
Authors	Marie Umbarger, Aaron Malkowski, Guillaume Reboul, Yunman Gu, Kelly Sams, Laura B. Goodman
Affiliations	Department of Public and Environmental Health, College of Veterinary Medicine, Cornell University, Ithaca, NY
Abstract	Many pet owners are moving away from conventional diets, opting for more “natural” or “homemade” diets for their beloved companions. Despite the lack of studies to assess risk and benefit, increasing demand for biologically appropriate raw food (BARF) diets among dog and cat owners have led to increased availability in local pet stores and online storefronts alike. This raises concern, not only for the health of the animals, but also for potential risks to pet owners. A collection of 112 commercially available frozen, refrigerated, and freeze-dried raw meat food products were found to have varying levels of parasitic and bacterial loads. The same samples were tested using an 815 primer AmpliSeq AMR panel. Evidence of increased antimicrobial resistance genes in these raw foods was found. Meat sources, or hosts, were then determined by mitochondrial 16S PCR amplification followed by metagenomic sequencing. Host sequences were successfully amplified from 112 of the products as visualized by gel electrophoresis, and data from the MiSeq Illumina system is currently being analyzed using Qiime2. Analysis of host barcoding data will not only verify the advertised meat sources, but will also determine if particular meat sources are associated with more virulent parasitic or bacterial communities. The ultimate aim of this study is to assess the pathogen exposure risk to felines and their owners, quantify the prevalence of AMR genes in the microbial communities in raw food diets, and offer health and safety recommendations to the general public.
Research Grant	Cornell Feline Health Center Natural Nutrition Award
Field of Research	Microbiomes

Abstract Title	The role of cognitive behavioral batteries and questionnaires in diagnosing canine cognitive dysfunction
Authors	Mikayla Underwood Aguilar, Evan Maclean, Stephanie Hargrave, Stephanie McGrath
Affiliations	School of Veterinary Medicine, UC Davis, Davis, CA (Mikayla U. Aguilar), Canine Cognition Center, School of Veterinary Medicine, University of Arizona, Tucson, AZ (Evan Maclean, Stephanie Hargrave), Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, CSU, Fort Collins, CO (Stephanie McGrath)
Abstract	Canine cognitive dysfunction (CCD) is a neurodegenerative disease that affects upwards of 22.5% of dogs over the age of 9 years. CCD is characterized by changes in cognition, such as delayed memory and behavioral changes. Studies have been conducted looking at various diagnostic methods for CCD, but few, if any studies have focused on a cohort of dogs presumptively diagnosed with moderate to severe CCD. To improve our diagnostic acuity, we assessed the role of canine cognitive batteries in conjunction with validated questionnaires, as a method for accurately diagnosing CCD in affected animals' antemortem. We hypothesized that animals who scored higher on both Canine Cognitive Dysfunction Rating Scale (CCDR) and Canine Dementia Scale (CADES), would be negatively correlated with their cognitive battery scores. We also expected to see a decline in overall performance when comparing affected with unaffected dogs. To test our hypotheses, we used a cognitive battery to access various components of memory, latency, and accuracy of decision making. Summary scores for each task were analyzed using principal components analysis. We then used these scores as an input variable to generate a total summary score for the cognitive battery. Each analysis was performed using R programming. The results show a negative correlation between age and memory-related tasks and lower total battery summary scores in affected dogs compared to the unaffected dogs. Collectively, these findings show that cognitive dysfunction may be accurately diagnosed by using a cognitive battery exam in agreement with CCDR and CADES scores. With refinement these batteries may be an effective, economical method of diagnosing and monitoring the progression of CCD.
Research Grant	Institute of Cannabis Research, Colorado State University (Pueblo); Panacea Life Sciences; Dog Aging Project
Field of Research	Behavior

Abstract Title	Evaluation of a LSD1 inhibitor as a radiosensitizer for feline oral squamous cell carcinoma
Authors	Ryan Unnerstall, Oscar Maldonado, Ann Chan, and Marilia Takada
Affiliations	Department of Small Animal Clinical Sciences, College of Veterinary Medicine, University of Florida, Gainesville, FL
Abstract	Feline oral squamous cell carcinoma (SCC) is often diagnosed in late stage of disease, when surgical removal is no longer a feasible option. Radiation therapy alone has shown suboptimal results, so the use of pharmacologic agents as radiosensitizers is appealing to enhance the local disease control. Here, we investigated the inhibition of lysine-specific demethylase 1 (LSD1), known to attenuate HR and NHEJ-mediated DNA repair capacity, as a tool to consolidate the radiation-mediated DNA damage to the tumor cells, augmenting tumor killing. Our results demonstrated that SP-2577 (Seclidemstat), a LSD1 inhibitor, effectively inhibited the growth of three SCC cell lines in a dose-dependent manner (IC50s of 240nM, 407nM and 487nM, vs. 53uM from normal feline fibroblasts). The combination of ionizing radiation and SP-2577 decreased the surviving fraction in a clonogenic survival analysis when cells were treated with drug concentrations below IC50 (100nM and 250nM). Ionizing radiation at 4 Gray resulted in increased DNA fragmentation after 24 hours, in a Comet Assay (single-cell gel electrophoresis), however, the combination therapy did not result in a higher degree of DNA damage. We demonstrated that cell apoptosis, quantified by Caspase-Glo 3/7 Assay, was not a major mechanism of cell death by either modality of treatment. Here, we demonstrated that SP-2577 has an additive inhibitory effect to radiation therapy in SCC cell lines. Although no synergistic effect could be proven, SP-2577 could be a potential therapeutic drug for feline SCC. Further in vivo studies and clinical trials are needed to fully evaluate therapeutic potential of this multimodal treatment for SCC.
Research Grant	NA
Field of Research	Oncology

Abstract Title	Effects of supplemental pre-milking stimulation on milking performance, udder health and welfare in dairy cows
Authors	John Armand Valdevieso and Matthias Josef Wieland
Affiliations	Department of Population Medicine and Diagnostic Sciences, Cornell University CVM, Ithaca, NY
Abstract	Adequate udder stimulation of dairy cows is critical before milking to harvest high-quality milk. It facilitates the milk-ejection reflex to obtain the alveolar milk, which represents 80% of udder's milk volume. Currently, conventional machine-milking methods fail to accommodate for this physiological requirement resulting in poor milking performance, compromised udder health, and decreased well-being of dairy cows. This study is aimed to investigate the effects of additional stimulation using automated pre-milking stimulation (APS) techniques to supplement conventional milking practices on commercial dairy farms. In a randomized controlled trial conducted at a commercial dairy farm in New York State, 491 Holstein cows have been assigned to treatment and control groups for a period of 60 d. Treatments consist of high (APS300 = 300 cycles/min) and low (APS100 = 100 cycles/min) frequency pulsation stimulation for a maximum of 20 seconds with a pulsation ratio of 25:75. Cows in the control group (CON) receive traditional stimulation only by means of manual forestripping for 8 s. Milking characteristics (milk yield, milking duration) have been measured with on-farm milk flow meters. Short- and long-term changes in teat tissue condition have been assessed visually on a bi-monthly basis. Composite milk samples have been analyzed once per month for somatic cell count. The occurrence of clinical mastitis has been documented by farm personnel. Generalized linear mixed models will be used to study the treatment effects on the outcome variables of interest. Results on milking performance, udder health indices, and teat tissue condition will be presented.
Research Grant	Research Grants Program in Animal Health
Field of Research	Production Animal Medicine

Abstract Title	Linking and Elucidating Ontogeny of Acanthostomum (Digenea) in Alligator mississippiensis Using DNA Barcoding
Authors	James Valentine, Thomas G. Rosser, Ethan Woodyard, Wes Baumgartner, Divya Rose, Celene Slifka
Affiliations	Department of Comparative Biomedical Sciences (Thomas G. Rosser), College of Veterinary Medicine, Mississippi State University, Starkville, MS
Abstract	The genus Acanthostomum Looss 1899 (Digenea, Cryptogonimidae) consists of over 20 described trematode species that parasitize fish, alligators and other crocodilians, causing damage to the gut tissue of their hosts. Acanthostomum has a complex 2 to 3-host life cycle, including snails, reptiles and fish. Despite a rich history consisting of novel host and geographic records, there are still many questions remaining about their taxonomy and systematics, pathogenesis in each host and their life histories. Morphological characteristics have been used to identify Acanthostomum spp., but two areas that require further investigation include (1) elucidating the various life stages and (2) conducting phylogenetic analyses using molecular data to infer evolutionary relationships among different species. Several Acanthostomum spp. have been reported from crocodilians globally, but molecular data assessing their diversity and intraspecific variation have not been fully explored. In this study, ribosomal and mitochondrial data were sequenced from adult Acanthostomum spp. collected from American alligators Alligator mississippiensis and larval metacercariae from the muscle of spotted gar Lepisosteus oculatus from the southeastern United States. At least 3 hologenophores were prepared by cutting a section from each worm, extracting its DNA, and then permanently staining and mounting them. Additionally, a whole worm was processed for DNA analysis. The DNA was used to assess the utility of DNA barcoding for linking individuals to specific species and to infer phylogenies using both ribosomal and mitochondrial DNA in conjunction with novel morphological characteristics.
Research Grant	Mississippi State University College of Veterinary Medicine
Field of Research	Parasitology

Abstract Title	Investigating the presence of Neorickettsia spp in different potential (in)vertebrate hosts in Ontario
Authors	Florance van Dam1,2, Olivia Anderson2, Jutta Hammermueller2, Cornélie Westermann1, Luis Arroyo Castro3, and Brandon N Lillie2
Affiliations	1 Clinical Sciences, Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands 2 Dept. of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada 3 Dept. of Clinical Studies, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada
Abstract	Potomac horse fever, which is caused by Neorickettsia risticii and N. findlayensis, can primarily induce colitis and other clinical signs in horses. Trematodes that parasitize snails and aquatic insects are proven as intermediate hosts, but the extent of the potential definitive hosts remains poorly understood. In this study, a polymerase chain reaction (PCR) was performed on liver samples obtained from different wildlife species including bats, muskrats, raccoons, opossums, and skunks as well as several invertebrates to investigate the presence of Neorickettsia spp. Neorickettsia spp. DNA was identified in many invertebrates as well as 4/133 (3 %) vertebrates sampled (two bats, one skunk, and one muskrat). The findings of this study suggest that Neorickettsia spp. circulate among different wildlife species, indicating a broader natural reservoir for these bacteria than previously recognized. These results contribute to the understanding of the life cycle, epidemiology, and potential transmission options for these bacteria. Further research is warranted to clarify the role of wildlife species in the maintenance and spread of Neorickettsia spp.
Research Grant	Equine Guelph and the Ontario Animal Health Network (OAHN)
Field of Research	Epidemiology

Abstract Title	Unraveling the Role of X-Chromosome Linked Copy Number Variations in Equine Early Pregnancy Loss
Authors	Willeke van den Boer, Donald Miller, Jessica Lawson, Charlotte Shilton, Amanda de Mestre
Affiliations	Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Ithaca, NY, USA
Abstract	Equine early pregnancy loss (EPL) poses a significant challenge to reproductive health, with 5-10% of pregnancies failing within two months of conception. Recently, evidence has emerged associating genetic structural variants in embryos with pregnancy outcome in mares. In our laboratory, preliminary studies have identified copy number variations (CNVs) specific to EPL conceptus genomes but absent in normal placentas and adults. In continuation, our current study explores the potential association between X-chromosome CNVs and equine EPL. We hypothesize that microdeletions on the X chromosome in the fetus and/or placenta, that impact the gene dosage of key developmental genes, lead to lethality of male conceptuses within the first two months of pregnancy. We received 123 conceptuses (EPLs lost before 65 days of pregnancy) from veterinary practices. These samples were hybridized on the Axiom™ Equine 670k SNP Genotyping Array alongside 175 controls, including manually terminated clinically normal pregnancies, healthy adults, and term placentae. After filtering aneuploid and low-quality samples, we analyzed 52 EPLs and 130 controls using the Axiom™ Analysis Suite, specifically targeting CNVs larger than 50kb base pairs. So far, we identified 0 deletions and 10 duplications that were unique to male EPL conceptuses, along with 3 deletions and 178 duplications unique to female EPLs. To investigate smaller deletions in male samples, we will utilize the DNAcopy package in RStudio. Subsequently, we will investigate the linkage between these CNVs and developmental genes by means of ENSEMBL, aiming to identify potential targets for future treatments and diagnostic tests enhancing the clinical management of affected mares.
Research Grant	None
Field of Research	Equine Medicine and Surgery

Abstract Title	Elucidating sex differences in the response to anterior cruciate ligament injury following mechanical rupture
Authors	Emily M. Van Zeeland, Brandon Kassel, Travis Montoya, Kelly S. Santangelo, Jeremiah T. Easley, and Katie J. Sikes
Affiliations	College of Veterinary Medicine & Biomedical Sciences, Colorado State University, Fort Collins, Colorado
Abstract	Following anterior cruciate ligament (ACL) injury, up to 87% of individuals develop post-traumatic osteoarthritis (PTOA) in their knee joint. Although it is well established that females are more likely to experience an ACL injury compared to males, it is poorly understood if sex differences contribute to the development of PTOA. The aim of this project was to examine the variable injury responses of males and females following ACL rupture using a refined mechanical rupture model. Unilateral ACL rupture was achieved via mechanical compression in male and female mice. Longitudinal mobility analyses were conducted prior to ACL rupture and weekly out to eight weeks post-injury. No significant differences were observed between male and female mice at baseline for all parameters. Relative to uninjured baseline values, male mice exhibited decreased voluntary distance traveled compared to female mice at five weeks following ACL injury ($p=0.0086$). Compared to female mice, males showed increased hindlimb stance width on a flat treadmill relative to baseline values ($p=0.0271$). These changes suggest male mice are minimizing voluntary movement after ACL rupture. Further, increased hindlimb stance width seen in male mice compared to females suggests male mice are modifying their gait due to a pain response and/or compensating for decreased stability. These observations could indicate differences in injury responses, pain perception, and/or PTOA development between males and females. Understanding the early injury differences between males and females may elucidate novel therapeutic mechanisms and surgical reconstruction techniques for an overall goal of improving ligamentous healing following rupture to mitigate PTOA progression.
Research Grant	CSU CVMBS College Research Council Award & CSU Center for Companion Animal Studies Young Investigator Award
Field of Research	Orthopedics

Abstract Title	The visual field of the Argentine Black and White Tegu (Salvator merianae)
Authors	Sharleen Vargas-Godoy1, Jacob Morris1, Esteban Fernandez-Juricic2, Bret A. Moore1
Affiliations	Department of Small Animal Clinical Science, University of Florida College of Veterinary Medicine, Gainesville, Florida. (Vargas-Godoy, Morris, Moore) Department of Biological Science, Purdue University, West Lafayette, Indiana. (Fernandez-Juricic)
Abstract	The Argentine Black and White Tegu (Salvator merianae) is an invasive lizard that predates on threatened and endangered species native to Florida. With successfully established populations in multiple counties of south and central Florida and one rapidly emerging on the southeastern area, this lizard poses a true conservation threat. In order to better understand their ecology and how they hunt, we describe the visual fields of the Argentine Black and White Tegu for the first time and characterize how they manipulate their visual fields by coordinated eye movements. This species has a narrow binocular field with a small to minimal convergent eye movements, but wide lateral fields and a small blind area. Such a visual field configuration, without alignment or indication toward a specific foraging behavior, is not uncommon for animals with a generalist diet that often includes scavenging. Having a wide total visual field may enable scanning large areas for prey and potential predators. Further studies to determine the retinal topography and the visual acuity will offer a better understanding of their visual behaviors that relate to predation and that could serve a purpose on the conservation of imperiled species in Florida.
Research Grant	None
Field of Research	Ophthalmology

Abstract Title	An interactive web application to calculate and analyze 16 indicators of antimicrobial use by dairy farmers
Authors	Ashley Varnadoe, Ece Bulut, and Renata Ivanek
Affiliations	Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY
Abstract	Antibiotic resistance (AMR) is one of the most concerning modern threats to global health and will remain as such unless antimicrobial use (AMU) is reduced to be more judicious. One aspect of AMR can be attributed to AMU in veterinary medicine, including dairy farm therapeutics. An effective strategy to control AMR on farms is to collect and analyze data on AMU in dairy cattle to improve on-farm antimicrobial stewardship, and it has been suggested that improving farmer confidence in treatment decisions via farmer-led initiatives has led to reduced AMU. Many methods for quantifying AMU have been described, but 16 indicators (5 count-based, 2 mass-based, and 9 dose-based) were selected from the literature for the development of a web application. The programming language, R Studio, was used to generate preliminary code that imports farmers' AMU data into R and calculates the 16 selected indicators. A preliminary web application is also designed to provide farmers an interface for the import, analysis, and calculation of their data and the 16 indicators via the R package, Shiny. The developed Shiny app is based on a reactive programming model, which allows for interactive explorations of the various functions within the app, including the visualization and distribution of imported data. The interactive interface for tracking AMU on a farm will provide decision support to the user about the meaning of AMU indicators and which specific indicators are advisable in certain situations and priorities. This will aid farmers and veterinarians in optimizing AMU on their dairy farms and thereby controlling AMR.
Research Grant	USDA NIFA Hatch [7000433]
Field of Research	Epidemiology

Abstract Title	Discovering putative disease-causing alleles for CSNB in Brazilian horses using a candidate gene approach
Authors	I.A. Vasdev, J.L. Marlowe, L. Hughes, A.S. Borges, M.E. McCue* S.A. Durward-Akhurst* *(Co-senior Authors)
Affiliations	Summer Scholars Program (Vasdev), Department of Veterinary Clinical Sciences (Marlowe, Durward-Akhurst) Department of Veterinary Population Medicine (Hughes, McCue), University of Minnesota, St. Paul, MN; Department of Veterinary Clinical Science, São Paulo State University, São Paulo, Brazil (Borges)
Abstract	Congenital stationary night blindness (CSNB) is a condition that causes blindness in low-light environments. Seventeen genes are associated with CSNB in humans. By contrast, only two genes (TRPM1, GRM6) have been associated in horses. Our understanding of the pathophysiology and genetic causes of CSNB in horses remains incomplete. Collaborators in Brazil identified a trio of Mangalarga Marchador horses who present with CSNB-like signs, but do not have any known causative variants. In this study, we aimed to identify novel putative disease-causing alleles for CSNB using a candidate gene approach. Phenolyzer, Online Mendelian Inheritance in Man (OMIM), ClinVar, OpenTargets, and Endeavor databases were searched to generate a list of candidate genes associated with CSNB. 135 candidate genes were present in at least two databases and were prioritized for further use. In the trio of horses, 561 variants with high or moderate likelihood of pathogenicity as predicted by Ensembl-VEP annotation were identified. 32 variants had an allele count of at least 3 with allele frequencies under 10%. 26 variants were found in all three horses which created a short list of putative CSNB-causing variants. Further predictions of pathogenicity of these variants were made using SNPs&GO, SIFT and PhD-SNP. Additional research confirming the causative variant will allow identification of the causative gene for these CSNB-like signs. This can improve understanding of the pathophysiology of this disease. These results can also be used as future targets for genetic testing to increase affordable and accessible tests to veterinarians and owners hoping to diagnose or make informed breeding decisions.
Research Grant	University of Minnesota College of Veterinary Medicine
Field of Research	Equine Medicine and Surgery

Abstract Title	New treatment for feline osteoarthritis: soluble epoxide hydrolase inhibition
Authors	Katherine Vedros, Alonso Guedes, Kristi Flynn, Martin Kennedy
Affiliations	Department of Veterinary Clinical Sciences, College of Veterinary Medicine, University of Minnesota, St Paul, MN
Abstract	Osteoarthritis (OA) is a prominent and prevalent condition in companion animals, especially cats. Our prior studies suggested that inhibition of the lipid-metabolizing enzyme soluble epoxide hydrolase (sEH) can improve mobility and pain associated with OA and protect against apoptosis of articular chondrocytes. Our hypothesis is that sEH inhibition will significantly improve mobility and quality of life (QOL) compared to placebo in cats with impaired mobility associated with naturally occurring OA. Our goal is to determine the effects of sEH inhibition on the mobility and QOL of cats with naturally occurring OA. Our study will assess the mobility of client-owned cats (n = 24) with naturally occurring OA via a collar-mounted activity monitor and client-specific outcome measures questionnaire (CSOM) as well as owner-perceived QOL. Cats will be treated with sEH inhibitor (t-TUCB) or placebo orally, twice daily for 7 days each in a randomized, crossover design with one-week washout between treatments. Preliminary results from 7 enrolled cats suggest there is no difference in mobility (activity level and CSOM) and QOL between placebo and t-TUCB treatments; however, a potential carry over effect is evident in cats treated first with t-TUCB on week 2 followed by placebo on week 4. The carry over effect is evident during the washout and placebo treatment weeks (3 and 4, respectively), suggesting a delayed onset with a possibly long-lasting effect (at least 2 weeks) of t-TUCB. The potential for a carry-over effect has prompted a revision of the experimental protocol. Activity will now be monitored for 2 additional weeks after the last treatment week to determine if there is evidence suggesting a delayed onset of t-TUCB efficacy.
Research Grant	Morris Animal Foundation (Grant #D22FE-031 to A. Guedes)
Field of Research	Pharmacology and Toxicology

Abstract Title	Cleavage as an estimator of the development capacity of bovine in vitro fertilized embryos.
Authors	Angelique Velasquez, John Gibbons, Jessica Looman, Sydney Hickerson, Kassandra Holguin
Affiliations	School of Veterinary Medicine, Texas Tech University, Amarillo, TX
Abstract	In vitro production of bovine embryos enables ranchers to produce more genetically-valuable calves. The number of bovine embryos produced in vitro worldwide has supplanted the number of embryos produced via superovulation/embryo transfer. The objectives of this study were to: 1) manipulate the in vitro embryo culture environment to maximize blastocyst development and 2) evaluate and document daily changes in development. We hypothesized that cleavage would be an effective estimator of developmental capacity and cleaved IVF embryos would develop more efficiently than imaged controls and culture controls (ova not removed from the incubator for evaluation). Follicles (5-10 mm) were aspirated from slaughterhouse ovaries, selected oocytes were matured, fertilized, the cumulus cells removed, and randomly placed into culture groups of 10 (50µL culture drops). Cleaved embryos (≥2 cells) were selected after 24 hours and re-cultured as a single group. Image controls and cleaved controls were photographed each day of culture (Days 1-7 post fertilization). On Day 7 of culture, cleavage and blastocyst development rates were evaluated in all culture groups and analyzed via Chi Square. Cleavage was not affected by treatment (culture controls =64.4+/-3.84,% timage controls =56.9+/-4.4%, treated =67.9+/-4.0%). Blastocyst development in the culture controls (27.5+/-3.5%) tended (p =0.06) to be higher than the treated group (16.4+/-3.1%) while image controls served as an intermediate (20.0+/-3.5%). The process of taking embryos out of the incubator to collect images suppressed blastocyst development but did not affect cleavage. Cleavage, while an important biological process, was not a useful estimator of blastocyst development.
Research Grant	Foundation for Food and Agriculture Research
Field of Research	Theriogenology

Abstract Title	Can Pain-Associated miRNAs be Used as Biomarkers for Colic in Horses?
Authors	Janay Velez-Leon, Britta Leise, Jeannette Cremer
Affiliations	Department of Veterinary Clinical Sciences and Equine Health Studies Program, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA.
Abstract	Pain assessment in horses can be challenging, particularly in colic where clinical signs vary greatly. Subjective pain scoring systems have been evaluated in horses using facial expressions, location in the stall, and response to external stimuli. However, having the ability to utilize an objective measurement of pain through biomarkers would allow for better assessment of response to pain management in clinical cases. Specific microRNAs (miRNAs) have been proposed as biomarkers for pain in horses with laminitis (miR-23b-3p, miR-145-5p and the miR-200b-3p) and for assessment post-castration (miR-126-5p, miR-145, miR-let7e). The following miRNAs have also been proposed as biomarkers for visceral pain in other species: miR-29a, miR-199, miR-181a, and miR-449b. Therefore, the objective of this study was to determine if miRNA expression could be correlated with subjective pain scores in horses with colic. We hypothesized that horses with colic would have increased expression in pain-associated miRNAs compared to healthy horses. Horses were placed into one of 3 groups: healthy (no pain), colic-medical management, colic-surgical management. On presentation, 10mls of blood was collected and stored for later miRNA analysis. Horses were subjectively assessed for pain and videos were recorded for additional pain assessment by veterinarians that were unaware of patient outcome. Additional, blood samples, pain assessment score, and videos were taken at 24, 48 and 72 hours post-arrival. This research is ongoing, however, we expect to see increased expression of miRNAs in horses with colic, particularly those requiring surgery and a substantial decrease in expression after treatment.
Research Grant	LSU School of Veterinary Medicine Equine Health Studies Program.
Field of Research	Equine Medicine and Surgery

Abstract Title	Investigation of a novel mosquito wiring procedure for electropenetrography
Authors	Vivienne Velic, Anastasia M. W. Cooper, Favour Ajibade, Babatunde Ibrahim Olowu, Dana N. Mitzel, Kristopher Silver, and Kathryn Reif
Affiliations	University of Veterinary Sciences, Brno, Czech Republic (Velic) Kansas State University, Manhattan, KS, USA (Cooper, Silver, Reif) University of Ibadan, Nigeria (Ajibade, Olowu) National Bio and Agro-defense Facility, USDA, Manhattan, KS, USA (Mitzel)
Abstract	Electropenetrography (EPG) allows us to better understand the feeding behaviors of hematophagous insects by indirectly visualizing waveforms (i.e., electrical signals) generated during probing. EPG is based on current capacity moving through the electrical circuit and the connection between the host (i.e. CD1 Mus masculus) and the blood-feeding insect (i.e. Aedes aegypti). Properly attaching the conductive gold wire to the surface of the pronotum on a selected insect is one of the key components to successful EPG recording. However, an insect's cuticle is an excellent insulator. Thus, this study aimed to test a method that would reduce resistance due to the cuticle by bringing the wire into contact with the epidermal cells below the cuticle. Inserting the wire without causing major trauma to the mosquitoes (Ae. aegypti) was achieved by using a micro needle to create a hole for wire placement. After inserting the conductive gold wire, conductive silver glue was used to secure it in place. Our results show that over 58% of Ae. aegypti blood-fed on artificial feeders 24 hours after microneedle penetration, and 40% of Ae. aegypti blood-fed 24 hours after wire insertion through the cuticle. Further efforts are needed to overcome mortality and low feeding rates associated with invasive wire placement, handling challenges, and long exposure to CO2 during immobilization. In addition, work is needed to determine if waveform appearance is altered due to subcuticular wire placement. Development of different wiring procedures to connect the insect to the electrical circuit is important to increase the sensitivity and reliability of EPG, to improve waveform interpretation, and to understand feeding behaviors in finer detail.
Research Grant	This research was supported by the USDA Research, Education, and Economics Workforce Development Agreement (#58-3022-0-002) and the Hatch Multistate Project (NE1943).
Field of Research	Parasitology

Abstract Title	Microscopic analysis of single-use hypodermic needles after vaccine vial penetration
Authors	Emma Vitello, Gina Agostini-Walesch, John Mitchell, Julia Tawil, and Rachael Kreisler
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, AZ (Vitello, Tawil, Kreisler); College of Dental Medicine, Midwestern University, Glendale, AZ (Agostini-Walesch, Mitchell)
Abstract	There is no primary literature on veterinary needle changing practices or the effect on needle conformation after vial penetration. This study aimed to investigate needle tip deformation after one or two penetrations of a vaccine vial septum for common brands and gauges of single-use hypodermic needles. A survey to determine the most common brands and gauges of needles, as well as needle changing practices was promoted to veterinarians and staff via social media from 5/5-5/12/23 (IRBAZ-5222). Surface scans of the 3 most common brands and gauges (20, 22, 25 G) of needles were captured via 3D infinite focus microscopy (Alicona MeasureSuite) after passage through the septum of one or two vials. Pairwise comparisons of tip deformation between 0 to 1 and 1 to 2 passages were performed using GOM Inspect Professional 2016 by overlaying one scan onto another and calculating the difference at the tip of the needle. Linear regression was used to determine associations between number of passages and tip deformation controlling for brand, gauge, and vial penetration force. Sample size analysis indicated that 8 needles from each of the 6 brand and size combinations scanned 3 times (after 0, 1, and 2 passages) would be required. Over 75% of survey respondents (365/482) reported changing a needle used to draw up a vaccine to a new needle before injection. The majority of those who changed (356/365) reported concern for dulling as a reason. For each of the 3 brands, 3 needles of each size were scanned 3 times for a total of 27 scans and 54 pairwise comparisons. No variable was significant in either univariable or multivariable regression at current enrollment. Data collection will continue until full enrollment is achieved.
Research Grant	None.
Field of Research	One Health

Abstract Title	Assessing the phenotype of Orthobunyaviruses in Louisiana mosquitoes
Authors	Jordan Vivien, Erik Turner, Samantha Clark, Rebecca Christofferson
Affiliations	Department of Pathobiological Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA.
Abstract	Climate change increases the threats that arboviruses pose. Rising climate temperatures accelerate many biological processes affecting arbovirus transmission. Geographic expansion of mosquito-borne diseases has also resulted from climate change, increasing the transmission of dengue, chikungunya, and Zika in temperate areas like Europe. Recent cases of malaria transmission in Texas and Florida have incited conversations of vector-borne disease threats in the Gulf South. Aedes albopictus and Ae. aegypti are two mosquito species of interest as they are known to transmit various viruses of concern and have become endemic to the Gulf Coast While many areas in this region have robust mosquito control programs, interruptions occur during extreme weather events and with substandard housing lacking the infrastructure necessary to interrupt mosquito-human contact. There is no information regarding vector competence of Louisiana Aedes mosquitoes for Batai virus. BATV shares many transmission similarities with West Nile virus and can infect Ae. albopictus. The initial transmission period for WNV in LA is May-June when the average temperature is 26.6°C. This project tested the vector competence of Ae. albopictus to transmit BATV under conditions aligning with IPCC climate projections for 2030, an increase of 1.5°C. Ae. albopictus juveniles were collected from Baton Rouge, LA and reared to adults. Females were blood-fed BATV and maintained at 28°C. Mosquitos were force salivated and tested for the presence of BATV in the saliva and midgut using qRT-PCR. Vector competence rates were calculated and the potential for Ae. albopictus in South LA to transmit this arbovirus discussed.
Research Grant	None
Field of Research	One Health

Abstract Title	Detection and characterization of Giardia and Cryptosporidium in ranched North American bison from Texas
Authors	Carmen Volz, Kaylee Kipp, Maureen A. Kelly, Joe L. Luksovsky, Meriam N. Saleh, Guilherme G. Verocai
Affiliations	Faculty of Veterinary Medicine, Ludwig-Maximilians-Universität, Munich, Germany (Volz) Department of Veterinary Pathobiology, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, Texas, USA (Kipp, Kelly, Luksovsky, Saleh, Verocai)
Abstract	Protozoan parasites such as Giardia duodenalis and Cryptosporidium cause production loss in many livestock species, directly impacting weight gain and health. North American bison have gained importance as a production animal in the US, where it is managed similarly to cattle. Most data on parasites of ranched bison focus on helminths, but little is known on protozoans. Fecal samples of 194 bison of different age groups were collected from 14 ranches across Texas. An Immunofluorescence Assay (IFA) and a coproantigen-detection test (QC) were used to detect Giardia and Cryptosporidium infections. Giardia and Cryptosporidium were found in 9 (64.3%) and 4 (28.6%) ranches, respectively. Overall, 8.3% and 20.6% animals tested Giardia-positive, and 3.1% and 2.6% tested Cryptosporidium-positive in IFA and QC, respectively. Co-infections were found in 5 (2.6%) animals. Regarding age class, Giardia was more common in calves (16%) compared to mature (3.6%). Out of 7 Cryptosporidium-positive samples, 6 were calves (3.1%) and one was an adult (0.5%). There was a significant difference ($p<0.0001$) between IFA versus QC results for Giardia. However, there was no difference between IFA versus QC for Cryptosporidium. Most protozoan infections occurred in calves, suggesting a greater age susceptibility. Molecular characterization of Giardia assemblages and Cryptosporidium species are presented. This study provides the first comprehensive assessment for Giardia and Cryptosporidium infection in bison and has shown that these protozoans are relatively common within bison ranches in Texas. While their clinical and economic impact remain unclear, management strategies may reduce risk of infection and transmission to other susceptible livestock.
Research Grant	None
Field of Research	Parasitology

Abstract Title	Genetic examination of Feline Chronic Gingivostomatitis using a candidate gene approach
Authors	Teresa Wahl, Shawna R. Cook, Jessica Hayward, Santiago Peralta, and Jacquelyn M. Evans
Affiliations	Baker Institute for Animal Health (Wahl, Cook, Evans), Department of Biomedical Sciences (Hayward), and Department of Clinical Sciences (Peralta), College of Veterinary Medicine, Cornell University, Ithaca, NY School of Veterinary Medicine, Freie Universität Berlin, Berlin, Germany (Wahl)
Abstract	Despite broad investigation, the understanding of the etiopathogenesis of Feline Chronic Gingivostomatitis (FCGS) is incomplete. FCGS is characterized by chronic inflammation and ulceration of the caudal oral mucosa. It is thought to be related to antigenic stimulation followed by an abnormal response of the immune system. Viral and bacterial infections as well as non-infectious conditions like stress, medication, nutrition, and trauma are suspected triggers; however, a causal role has yet to be proven. Clinically similar diseases in humans have been linked to genes involved in inflammation, immunopathology, and autoimmunity. The aim of this study was to analyze genetic variants possibly associated with FCGS using the candidate gene approach. Whole genome sequencing data from 13 cats with FCGS were manually scanned for coding variants in 73 candidate genes. In silico prediction was used to estimate effects on protein function, and allele frequencies were investigated in publicly available cat genomes. Variants at low frequency in the general cat population and predicted to have a damaging effect on protein function were prioritized for further study. Association studies in a larger case-control cohort as well as investigation of intergenic and regulatory variants are required. The etiology of the disease is assumed to be multifactorial, and a polygenic inheritance cannot be excluded. The identification of genetic variants connected to FCGS can support the understanding of the pathogenesis and may lead to new treatment modalities.
Research Grant	Cornell Feline Health Center, Foundation for Veterinary Dentistry, Hill's Pet Nutrition
Field of Research	One Health

Abstract Title	Exploring the role of childhood obesity in cancer: structural changes in adipose tissue stroma
Authors	Jessica Wakeman, Alyssa Miles, Nora Springer
Affiliations	University of Tennessee College of Veterinary Medicine, Knoxville, TN
Abstract	In the United States, childhood obesity has reached epidemic levels. With the increase in incidence of colorectal cancer correlating to childhood obesity, an understanding of the underlying mechanisms between obesity and adipose tissue is needed to develop preventive and interventional treatment modalities for cancer. It is known that in obesity, structural and biochemical changes occur in adipose stroma cells (ASCs) and extracellular matrix (ECM) that mimic the tumor microenvironment. Given this evidence, it is predicted that juvenile obese and aged adipose tissues will share features such as ASC cellular aging and ECM fibrosis; essentially, obesity will result in premature aging of ASCs, and this effect is irreversible with weight loss. ASCs in this study were isolated via a diet-induced obesity (DIO) mouse model consisting of the following cohorts: lean/low fat diet (LFD) juvenile mice, obese/high fat diet (HFD) mice, formerly obese mice, and lean aged mice. For each ASC line, immunofluorescence microscopy was used to assess myofibroblast differentiation, cellular proliferation by BrdU incorporation, and ECM composition by fibronectin, collagen I and VI immunostaining. Myofibroblast differentiation is increased in the HFD cell lines relative to lean, formerly obese, and aged cell lines. HFD cells were less proliferative than other cell lines. Data for ECM composition is pending analysis. The effects of obesity studied in this project appear to be reversible with weight loss. Aged lean ASCs were similar to lean and formerly obese ASCs isolated from younger mice.
Research Grant	Johnson Cancer Research Center Innovative Research Award
Field of Research	Clinical Pathology

Abstract Title	The analysis of CD8 T cell and macrophage infiltration during female reproductive tract infection
Authors	Olivia P. Wallace and Weidang Li
Affiliations	College of Veterinary Medicine, Midwestern University, Glendale, Arizona.
Abstract	Chlamydia trachomatis is a sexually transmitted infection associated with significant reproductive tract pathologies. The goal of our study is to explore the pathogenesis of chlamydia in the female reproductive tract of mice, with a focus on identifying the host immunological factors that may contribute to genital pathology. Using a mouse model infection with Chlamydia muridarum, a close analog of C. trachomatis in humans, we will investigate the role of CD8 T cells and macrophages in the pathogenic mechanisms. Numerous Chlamydia muridarum infection models in mice have been contrasted to C. trachomatis infections in humans as both models have suggested homologous pathogenic mechanisms. The mice will be hormonally manipulated with a progesterone injection to enhance the infection process, and genital tissue cells will be analyzed at five different stages of infection. We hypothesize that CD8 T cells and macrophages will exhibit different key markers between early and later stages of chlamydia infection, potentially related to the progression of chlamydia-induced pathology. To investigate this, we will employ flow cytometry analysis to identify specific markers and core gene regulators associated with pathogenic CD8 T cells and macrophages during the course of infection. The data generated from this research will not only advance our understanding of chlamydia-induced reproductive pathologies but will also provide valuable insights for the development of targeted anti-chlamydia vaccines.
Research Grant	Midwestern University and National Institutes of Health
Field of Research	Immunology

Abstract Title	Honey, I shrunk the patients: an introduction to honey bee medicine and management for veterinary professional
Authors	Courtney Wallner and Meera Gatlin
Affiliations	Cummings School of Veterinary Medicine at Tufts University (Wallner), Department of Infectious Disease and Global Health (Gatlin), Cummings School of Veterinary Medicine, North Grafton, MA.
Abstract	The instability of honey bee (Apis mellifera) health poses a large threat to the global food supply and overall health of most environments. Over 80% of flowering plants are pollinated by honey bees, including more than 130 varieties of fruiting crops worldwide. In 2021, more than 21% of honey bee hives in the United States died over the winter, representing a 9% increase in losses from 2020. The Food & Drug Administration tasked veterinarians with overseeing the usage of antibiotics in honey bees in an effort to combat antimicrobial resistance in food-producing animals in 2017. Honey bees, however, are the only food-producing animals that American veterinarians do not receive mandated education on while in school. To rectify this gap in knowledge, which has yet to be uniformly addressed by US accredited veterinary schools, we are creating educational honey bee medicine modules designed specifically for veterinary professionals. By increasing the exposure that veterinary professionals have to honey bee medicine, we predict that the number of professionals competent, comfortable, and willing to see honey bees as patients will also increase. The success of the modules will be measured by assessing the change in individual knowledge on core honey bee competencies and overall willingness to see bees as patients. This project shall serve as both a resource and a guide for veterinary schools looking to implement honey bee medicine in their curriculum and sustainable teaching hives on their campus. By increasing access to care for the 27 million honey bee hives across the country, veterinarians can further reinforce the systems protecting ecosystem health and food security within the United States.
Research Grant	Foundation for Food and Agriculture Research Veterinary Student Research Fellowship
Field of Research	One Health

Abstract Title	Ex vivo Comparison of Kinamed SuperCable and Standard Metal Cerclage Wire in a Canine Femoral Fracture Model
Authors	Natalie Walls, Seila Day, Steven Elder, Michael Jaffe
Affiliations	Department of Clinical Sciences Mississippi State University of Veterinary Medicine (Day, Selia) Department of Biomechanical Engineering Mississippi State University (Elder, Steven), Department of Clinical Sciences Mississippi State University of Veterinary Medicine (Jaffe, Micheal)
Abstract	Standard metal cerclage wires are commonly used as an implant in veterinary orthopedic surgery in conjunction with other repair and fixation methods to provide interfragmentary compression of bone fragments. While metal cerclage wire has been used historically there are known complications that may be sustained under physiological conditions. The goal of this study is to evaluate the Kinamed SuperCable orthopedic cable and compare it to standard cerclage wire configurations under cyclic loading until failure. Failure was deemed to occur when a permanent bone-implant construct displacement of greater than or equal to 2mm was seen. It was hypothesized that the Kinamed SuperCable would prove to be superior to standard cerclage wire methods when tested under cyclic 4-point bending for use in veterinary small animal surgery. When the Kinamed SuperCable was compared to standard single loop metal cerclage wire it proved to be superior in both the amount of load (N) and number of cycles it was able to withstand until failure. The Kinamed SuperCable's superior load bearing capabilities make it a practical option as a more effective and efficient way to stabilize small animal orthopedic surgical cases, particularly fractures.
Research Grant	Research Grant: Kinamed Inc
Field of Research	Orthopedics

Abstract Title	Investigating glial fibrillary acidic protein to diagnose and predict outcome in canine traumatic brain injury
Authors	Katy Walrond, Claire Tucker, Kelly Hall, Britta Siegenthaler, Ayla Mollen, Tracy Webb
Affiliations	Colorado State University, Department of Clinical Sciences, Fort Collins, CO
Abstract	Biomarkers can be leveraged as point-of-care tests that aid in accurately diagnosing and predicting outcomes after head injury and associated traumatic brain injury (TBI). In humans, the time course and prognostic value of the biomarker glial fibrillary acidic protein (GFAP) has been relatively well-established, with a blood test approved by the U.S. Food and Drug Administration in 2018. GFAP is expressed by astrocytes, and its expression is upregulated after injury to the central nervous system. In dogs, head injury and associated TBI are usually treated with supportive care due to a dearth of evidence-based research and challenges with definitively diagnosing TBI without advanced imaging. Although GFAP has been measured in dogs, it has not been assessed in dogs with head injury. This study is evaluating the utility of measuring serum GFAP levels in dogs after head injury to diagnose TBI and predict patient outcome (survival to discharge) non-invasively. Serum GFAP concentration will be measured from time of presentation to Colorado State University's Veterinary Teaching Hospital through 72-hours post-head injury. The study will also assess trends in GFAP levels with changes in patient neurologic status using validated veterinary scoring systems. Analysis will include ANOVA testing and identification of cut-points for diagnosis of TBI as compared to clinical gold standard and survival to discharge. If found to have satisfactory sensitivity and specificity, use of GFAP in canine trauma patients can support more informed patient care and enhanced translational applications.
Research Grant	Koster Endowment
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Prevalence of endoparasites in native wildlife presented to the Wildlife Hospital of Louisiana
Authors	Corrine Wang, Adriano Vatta, and Mark A. Mitchell
Affiliations	Department of Veterinary Clinical Sciences (Wang, Mitchell) and Department of Pathobiological Sciences (Vatta), School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA
Abstract	Anthropogenic activities have led to detrimental changes in the ecosystems of native wildlife, including habitat loss and fragmentation. These changes have led to wildlife being forced into smaller home ranges, increasing their risk for exposure to parasites. Methods for the transmission of parasites between parasitized and susceptible animals include fecal-oral, bloodborne, physical contact during social behaviors, and resource sharing. Parasites have been found to decrease an organism's fitness by altering host behavior, lowering their immune defense, and decreasing nutrient intake. These changes in the host lead to increased susceptibility to infection, disease transmission, and predation. The Wildlife Hospital of Louisiana (WHL) is a medical facility focused on rehabilitating native wildlife in Louisiana. We hypothesized that parasite prevalence in native wildlife presented to the WHL will exceed 25%, and patients receiving treatment for endoparasites will have a reduced parasite burden at time of release. Fecal samples were processed using a direct smear, double spin flotation using Sheather's Sugar solution, and sedimentation; ova were visualized with light microscopy. To date, 82 wildlife cases have been screened for parasites (3 classes: 4 reptiles, 64 birds, and 14 mammals). The prevalence of endoparasites in this population is 54.8% (45/82, 95% CI: 43.7-65.2), and there was no significant difference in the likelihood of shedding parasites by animal class (p=0.68) or species (p=0.10). Information obtained from this study can be used to evaluate and improve treatment plans not only for the WHL, but also for other wildlife rehabilitators facing the same challenges.
Research Grant	Fluker Farms Zoological Fund
Field of Research	Parasitology

Abstract Title	Safety evaluation of pevonedistat treatment in cats with lymphoma, a phase I dose finding study
Authors	Tammy Xiong Wang, Tricia Hu, Christen Montesanto, Ruthanne Chun, Xuan Pan
Affiliations	Department of Medical Sciences, School of Veterinary Medicine, University of Wisconsin-Madison (Wang, Hu, Montesanto, Chun, Pan) and Wisconsin Blood Cancer Research Institute (Pan), Madison, WI, USA
Abstract	Feline alimentary lymphoma is the most common form of lymphoma in cats. Cytotoxic chemotherapy drugs are available as treatment options, but they indiscriminately attack rapidly dividing cells whether they are cancerous or not. Alternatively, targeted therapy drugs can be utilized to interfere with the cell signaling pathway unique to cancer cell proliferation or apoptosis. Pevonedistat (MLN4924) is a potent and selective NEDD8-activating enzyme (NAE) inhibitor. Phase I clinical trials of pevonedistat investigated in human patients have demonstrated a promising safety profile. Additionally, previous studies conducted in our laboratory have revealed that pevonedistat effectively induces canine lymphoma cell death and inhibits the proliferation of cancer cells. These encouraging findings make pevonedistat a compelling candidate for the treatment of feline lymphoma patients. We hypothesize that a well-tolerated targeted therapy protocol with pevonedistat will be established using a standard 3+3 phase I trial approach. In our preclinical trial, we administered a single injection of pevonedistat at the 40 mg/m^2 dose in three healthy, one-year-old cats. Repeated bloodwork, urinalysis, and physical exams at 7, 21, and 28 days post-administration yielded no significant health effects or adverse events. We have thus identified that pevonedistat is well tolerated at a dose of 40 mg/m^2. Moving forward, we will continue to escalate the dose according to a standard open-label phase I dose-cohort escalation design at 50 mg/m^2, 60 mg/m^2, 70 mg/m^2, and 80 mg/m^2.
Research Grant	SVM Feline Health Fund and Short-term Research Training for Veterinary Students in Wisconsin [or] NIH NIH T35OD011078 (PI Joan Jorgensen)
Field of Research	Oncology

Abstract Title	The effects of Hypoxia Inducible Factor-1α stabilizer deferoxamine on murine traumatic brain injury
Authors	Jingjing Wang, Jacquelyn Dayton, and Lillian Cruz-Orengo
Affiliations	School of Veterinary Medicine, University of California,Davis, Davis, CA
Abstract	Traumatic brain injury (TBI) commonly causes deaths and disabilities in both humans and animals. TBI can lead to increased blood-brain barrier (BBB) permeability and secondary neuroinflammation that further impairs cognition and motor functions. Yet there is no pharmacologic therapy available to ameliorate the damage caused by TBI and its secondary neuroinflammation. It has been suggested that hypoxia-inducible factor-1α(HIF-1α), a transcription factor, promotes gene expression related to cell proliferation, and survival. HIF-1α also inhibits the transcription of genes associated with inflammation and apoptosis. Although the mechanism remains unclear, HIF-1α is vital for the neurorepair and recovery after stroke, retinopathy, among others, and putative cerebrovascular protection to TBI. Deferoxamine (DFO), an FDA-approved iron chelator, stabilizes HIF-1α by inhibiting the activity of HIF-prolyl hydroxylase. We hypothesized that daily administration of DFO facilitates faster recoveries and better outcomes after TBI by prolonging the presence of HIF-1α. Ten-week-old C57BL/6J mice underwent controlled cortical impact to model TBI, or sham surgeries. DFO was administered daily for 14 days post-injury (DPI). Myriad behavioral assays were utilized to determined neurologic function: rotarod and beam walk, to evaluate motors skills and novel object recognition and Barnes' maze to assess cognitive function. Mice were euthanized for molecular assays, sodium fluorescein BBB permeability and Western blot, at 3-, 7-, and 14-DPI to determine HIF-1α expression levels in the brain tissues and BBB permeability. These findings would provide evidence for the beneficial effects of DFO in the treatment after TBI.
Research Grant	Dr. Lillian Cruz-Orengo SVM PI Bridge Funds and Dr. Jorge Contreras SOM Start-up funds
Field of Research	Physiology

Abstract Title	Canine parvovirus infection: what makes a receptor?
Authors	Kari E. Waring, Wendy S. Weichert, Brian R. Wasik, Colin R. Parrish
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Abstract	Canine parvovirus (CPV) is an important canine pathogen; causing high morbidity gastroenteritis and myocarditis. During infection CPV can bind both its receptor and circulating antibodies. CPV's primary receptor is transferrin receptor type-1 (TfR), where apical domain binding is critical for viral entry and infection. This study investigates the significance of TfR in mediating CPV cellular infection by receptor modification to determine the specific necessary engagements to support replication. Two main modifications are being examined: (1) replacing the TfR ectodomain with an antibody as a single-chain variable fragments (scFv); (2) replacing only the apical domain with the scFv. Previous studies have shown that these modifications enable CPV binding, but it remains inconclusive whether cell infection and replication can also occur. To evaluate the effects of TfR modifications, TRVb cells (CHO cells lacking endogenous TfR) were transfected with plasmids encoding modified TfRs and infected with CPV. Fluorescent antibody staining was utilised to quantify transfection and infection levels. The virus was also incubated with TfR apical domains (sAp) prior to infection to investigate potential outcomes. Preliminary results indicate that the modified TfRs facilitate CPV binding and cellular uptake with minimal infection. An additional emerging aspect of this study is the pre-infection incubation of CPV with a sAp and whether this receptor-domain interaction alters the CPV infectious process. Furthering the understanding of CPV could allow future contributions to novel vaccines, anti-virals, and diagnostic tool development.
Research Grant	None
Field of Research	Virology

Abstract Title	Expression of Mu opioid receptor in the equine hoof lamellar interface in health and laminitis.
Authors	Jessica R. Warwick, Angelynn P. Simenson, Dae Y. Kim, Philip J. Johnson, Thomas E. Childs
Affiliations	Departments of Veterinary Medicine and Surgery (Warwick, Simenson, Johnson), Veterinary Pathobiology (Kim) and Biomedical Sciences (Childs), College of Veterinary Medicine, University of Missouri, Columbia, MO
Abstract	Laminitis is a common, painful affliction of the equine hoof and, in refractory cases, failure of analgesic strategies to control pain often necessitates resort to euthanasia. When administered locally, the use of Mu opioid receptor agonists, such as morphine, is emerging as an effective adjunctive anti-inflammatory and analgesic treatment for arthritis. Although Mu opioid receptors have been demonstrated in equine synovial tissue, the presence of these receptors in either healthy or laminitic hoof lamellar tissue has not been investigated. The extent to which Mu opioid receptor expression can be identified will be compared between healthy and laminitic lamellar tissue using immunohistochemical methods. We hypothesize that Mu opioid receptors are constitutively expressed in healthy lamellae and that the level of expression is increased during laminitis. Using a validated antibody, we will undertake chromogenic immunohistochemical examination of archived equine hoof lamellar tissues for the presence and distribution of the Mu opioid receptor in both the healthy and laminitic conditions. We anticipate that Mu opioid receptors will be identified in healthy lamellae and, to a greater extent, in lamellae obtained from laminitic horses. Demonstration of Mu opioid receptors in the equine hoof would support the employment of opioid agonist treatments for anti-inflammatory and analgesic management of laminitis.
Research Grant	Animal Health Foundation of St Louis, MO.
Field of Research	Equine Medicine and Surgery

Abstract Title	Defining minimum deliberate practice time needed to learn direct and indirect fundoscopy on simulation models.
Authors	EH Washburn S Hooper* E Artemiou* EM Scott
Affiliations	Ross University School of Veterinary Medicine, St Kitts Ross University School of Veterinary Medicine, St Kitts Texas Tech University School of Veterinary Medicine Cornell University College of Veterinary Medicine
Abstract	Purpose. Direct and indirect fundoscopy are day one skills for new graduate veterinarians. This study aims to determine the minimum deliberate practice time needed to identify structures on the fundus on a low-cost canine fundoscopy simulation model via direct and indirect fundoscopy. Methods. Forty-eight Ross University School of Veterinary Medicine students were recruited and randomly split into three groups based on time (12 min, 24 min, 36 min). Students rated their confidence in fundoscopy techniques and were subsequently trained using the principles of deliberate practice followed by a second questionnaire. Students took a self-guided Objective Structured Clinical Examination (OCSE) which assessed their ability to identify the shape, color, and location for the optic nerve and lesions. Wilcoxon signed-rank tests were used to assess changes between pre- and post-lab questionnaires. Generalized linear mixed models assessed the impact of cohort time, years worked as a veterinary technician and number of times pre-lab videos were watched with students as a random effect. Results. Students reported a significant increase in confidence with both direct and indirect fundoscopy after practice sessions ($p < 0.001$). Students in the 24- and 36-min cohorts had significantly increased overall OSCE scores ($p < 0.05$) and indirect OSCE scores ($p < 0.05$). Conclusions. Indirect fundoscopy is a harder skill to master and our results suggest students require at least 24 minutes in deliberate practice to identify structures using indirect fundoscopy competently. Conflict of interest: None.
Research Grant	Funding sources: Morris Animal Foundation, RUSVM The Center for Research and Innovation in Veterinary and Medical Education (Intramural grant number: 44025-2024)
Field of Research	Ophthalmology

Abstract Title	The effects of NV-5138 administration on mTOR pathway signaling in the forebrain of mice
Authors	Haley Watters, Michael Cahill
Affiliations	University of Wisconsin-Madison SVM, Madison, WI
Abstract	NV-5138 is a recently composed pharmacological agent that upon oral administration facilitates mTOR pathway activity in the prefrontal cortex of rats. The actions of NV-5138 on mTOR signaling are largely attributed to its inhibition of the sestrin complex, which acts as a partial brake for mTOR activation. However, whether NV-5138 affects mTOR pathway activity in other forebrain regions remains unknown. Furthermore, whether the established biochemical effects of NV-5138 on mTOR signaling in the rat brain also occur in mice is not known. To address these current gaps in knowledge, we examined the activity profile of known mTOR targets in multiple forebrain regions following oral NV-5138 administration in mice. Biochemical profiling was performed using SDS-PAGE and subsequent Western blotting. The outcome of this study could further illuminate the mechanisms by which NV-5138 exerts its behavioral effects, including its antidepressant properties.
Research Grant	1R21HD112147-01
Field of Research	Biochemistry

Abstract Title	Characterization of the Toxoplasma gondii LETM1, a mitochondrial calcium proton transporter.
Authors	Emily Weant, Baihetiya Baierna, and Silvia N J Moreno
Affiliations	University of Georgia CVM, Athens, GA (Weant), Center for Tropical and Emerging Global Diseases, University of Georgia, Athens, GA (Baierna, Moreno), and Department of Cellular Biology, University of Georgia, Athens, GA (Baierna, Moreno).
Abstract	Toxoplasma gondii is a zoonotic intracellular parasite that infects most warm-blooded species, including humans, causing the clinical disease toxoplasmosis. The definitive host for T. gondii are felines, who excrete oocysts into the environment that sporulate and can be infective to other species via ingestion of contaminated material. Infection can also occur by ingestion of undercooked meat from animals chronically infected with T. gondii or transplacentally from an infected mother to fetus. The current treatments for animals include sulfadiazine and pyrimethamine or clindamycin, both of which are only beneficial during the acute phase and do not prevent disease progression. No drugs are effective against the chronic stage of infection. The mitochondrion is essential for the replication of T. gondii and is a promising target for the inhibition of parasitic growth. In this project we focused on the characterization of the T. gondii LETM1 protein, a homologue of the mitochondrial Calcium Proton exchanger present in other eukaryotes. We hypothesized that the LETM1 protein is important for optimal mitochondrial function, contributing to parasitic replication, differentiation, and infectivity. We used CRISPR Cas9 to insert an HA tag at the C-terminus of the TgLETM1 gene. After validating the insertion of the tag, we obtained a clonal population with stable expression. We validated its mitochondrial localization and expression by immunofluorescence assays with anti-HA antibodies. We also used CRISPR to generate a clonal conditional knockdown cell line, in which expression of the TgLETM1 gene is regulated by anhydrotetracycline. We are presently characterizing the phenotypes of these mutants.
Research Grant	NIH R01169846
Field of Research	Parasitology

Abstract Title	Reducing respiratory disease transmission from humans to chimpanzees in Uganda
Authors	Taylor Weary, Tressa Pappas, Patrick Tusiime, Shamilah Tuhaise, Elizabeth Ross, James Gern, and Tony Goldberg
Affiliations	Department of Pathobiological Sciences (Weary, Goldberg), School of Veterinary Medicine and Department of Pediatrics (Pappas, Gern), School of Medicine and Public Health, University of Wisconsin-Madison, Madison, WI The Kasiisi Project (Tusiime, Tuhaise, Ross), Fort Portal, Uganda
Abstract	Respiratory disease is a major cause of morbidity and mortality among people in the developing world and also threatens great apes across Sub-Saharan Africa. Studies of wild chimpanzees in Kibale National Park, Uganda, have identified the causative agents of respiratory disease outbreaks as “common cold” pediatric human pathogens, but reverse zoonotic transmission pathways have remained unclear. Between May 2019 and July 2022, we collected 1,976 paired respiratory symptoms surveys and nasal swabs from 264 local children and forest workers and 445 fecal samples from 55 chimpanzees as part of a prospective cohort study. We characterized respiratory pathogens using a multiplex PCR panel and examined the transmission risk of detected pathogens and potential risk factors such as demography and seasonality. Children exhibited high incidence rates and symptom severities, whereas adults were largely asymptomatic. COVID-19 lockdown in 2020-2021 significantly decreased respiratory disease incidence. Human symptoms peaked in February. In chimpanzees, the most common month for respiratory disease outbreaks was March. Rhinovirus (RV), which caused a lethal 2013 outbreak among Kibale chimpanzees, was the most prevalent human pathogen and most likely to be carried asymptomatically by people. Our data suggest that respiratory pathogens circulate in children living near Kibale, and that adults become asymptomatically infected and may carry the pathogens into the forest and infect chimpanzees. The “Healthy Children, Healthy Chimps” program reflects our hope that reverse zoonotic disease transmission to chimpanzees can be mitigated through a One Health approach that considers the health of chimpanzees and local people to be linked.
Research Grant	NIH R01AG049395 Morris Animal Foundation D20ZO-052 Arcus Foundation Disney Conservation Fund
Field of Research	One Health

Abstract Title	Studies on Chronic Wasting Disease – Effects of Prion Genotypes with RT-QuIC Performance
Authors	Devin-Danielle V. Webb, Joseph Darish, Margaret Krueger, Srinand Sreevatsan
Affiliations	Department of Pathobiology, Department of Diagnostic Investigation, College of Veterinary Medicine, Michigan State University, East Lansing, MI
Abstract	Transmissible Spongiform Encephalopathies (TSEs) are neurodegenerative diseases. TSEs manifest themselves in several species such as Sheep (Scrapie), Cattle (Bovine Spongiform Encephalopathy), Humans (Creutzfeldt-Jacob Disease), and Deer (Chronic Wasting Disease or CWD). The pathogenesis for all manifestations of TSEs is shared across species; amyloid fibrils, created by the proliferation of misfolded prion proteins in the brain. The genetic predisposition of CWD susceptibility has been hypothesized to be a result of polymorphisms of prion protein (PrnP) at codons 95, 96, 116, and 226. Real-Time Quaking-Induced Conversion (RT-QuIC) is an assay that increases sensitivity in the detection of prion proteins in CWD. We hypothesize that prion genotypes susceptible to misfolding amass at a faster rate, thus, reducing time to positivity by RT-QuIC.
Research Grant	NHLBI grant R25HL103156
Field of Research	Virology

Abstract Title	Influence of H. pylori coinfection on enterotoxigenic B. fragilis-induced intestinal tumorigenesis
Authors	Yi Wen, Zhongming Ge, Yan Feng, Nicola Parry, Melody H. Guo, Zeli Shen, James G. Fox
Affiliations	Division of Comparative Medicine, Massachusetts Institute of Technology, Cambridge, MA (Wen, Ge, Feng, Parry, Guo, Shen, Fox); College of Veterinary Medicine, Kansas State University, Manhattan, KS (Wen)
Abstract	Epidemiological data suggests that enterotoxigenic Bacteroides fragilis (ETBF) infection is implicated in colorectal cancer (CRC), and in some studies Helicobacter pylori (Hp) is associated with increased CRC. ETBF infection has been established to promote colonic tumorigenesis in B6 Apcmin/+ (multiple intestinal neoplasia, Min) mice. However, how ETBF's pathogenicity is affected by coinfection with other gastrointestinal (GI) pathogens remains unclear. In this study, we orogastrically dosed ETBF with or without Hp in female B6 Min mice. Stomach, duodenum, jejunum, ileum and colon were collected for histopathology, bacterial culture and DNA/RNA extraction. Quantitative PCR was performed to document Hp or ETBF colonization levels and cytokine mRNA expressions. Our data showed that ETBF infection significantly increased the polyp number in duodenum/jejunum, but this was attenuated by Hp coinfection (P=0.025). Intriguingly, the polyp number was increased in the ileum of coinfection mice compared to mono-ETBF mice (P=0.015). However, Hp coinfection did not affect ETBF-promoted polyps and histological activity index in the colon, whereas mRNA levels of colonic IL-17A and Foxp3 were significantly upregulated in the coinfected group compared to mono-ETBF mice (P<0.05). Furthermore, ETBF efficiently colonized the stomach and colon tissues, which were not significantly influenced by Hp coinfection. In summary, our findings demonstrated that Hp coinfection differentially affected ETBF-induced tumorigenesis quantitated in different GI tissues. Additional investigations such as longitudinal infection studies are warranted to shed light on the mechanisms underlying effects of Hp coinfection on ETBF-induced intestinal tumorigenesis.
Research Grant	Division of Comparative Medicine (DCM)/Fox research funds
Field of Research	Oncology

Abstract Title	Identification and characterization of compounds that remove bacterial biofilms of bovine respiratory disease
Authors	Wei Man Weng1, Yue-Jia Lee1, Bindu Subhadra1, Nancy Vogelaar2, Pablo Sobrado2, and Thomas Inzana1
Affiliations	1Long Island University CVM, Brookville, NY 2Virginia Tech, VT Center for Drug Discovery Screening Laboratory
Abstract	Bacteria that become established in host sites readily form biofilms, following attachment and production of an extracellular matrix. We have previously established that the primary etiological agents of bovine respiratory disease (Histophilus somni, Pasteurella multocida, and Mannheimia haemolytica) can form individual and polymicrobial biofilms in vitro and in the host cardio-respiratory tract. Bacteria within a biofilm are more resistant to antimicrobial therapy and host immune defenses, and therefore tend to cause more chronic infections. The application of compounds that can remove bacterial biofilm should enhance the efficacy of antibiotics and resolve the infection sooner. Over 5000 compounds from the Virginia Tech Center for Drug Discovery Screening Laboratory were tested for the capability to remove an established H. somni biofilm in vitro, as determined by crystal violet staining. Three compounds at 10-100 µm concentration removed greater than 80% of the biofilm, probably through disrupting the ECM. These compounds were also effective at removing the biofilms of P. multocida and M. haemolytica, though the effectiveness of each compound with each bacterium varied. The compounds demonstrated little to no toxicity for bovine epithelial cells, bovine pulmonary endothelial cells, or bovine uterine endometrial cells at concentrations tested up to 100 µm. The effectiveness of these compounds to remove an established biofilm from bovine cell lines is currently being investigated, as well as whether the compounds interact with ECM or interfere with bacterial adherence. These results indicate that the addition of an anti-biofilm compound with antibiotics may enhance bovine recovery from, or prevent, respiratory disease.
Research Grant	Foundation for Food & Agriculture Research
Field of Research	Antimicrobial Resistance

Abstract Title	Determining the volume of lavage to reduce microbial growth below 10^5 CFU/ml in a subcutaneous tissue model
Authors	Cody Westmoreland, Sara Lawhon, Jing Wu, Nicholas Jeffrey, and Vanna Dickerson
Affiliations	Department of Veterinary Pathobiology (Lawhon, Wu) and Department of Small Animal Clinical Sciences (Jeffrey, Dickerson), School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX
Abstract	Surgical site infections (SSIs) are a recurrent surgical complication that increases the incidence of incisional dehiscence, illness, sepsis, and death. Current standards indicate that intra-peritoneal lavage promotes the removal of bacteria that may have been translocated during abdominal surgery, with a recommended volume of 200-300 ml/kg of body weight. Given that subcutaneous tissues may also be contaminated secondary to wounds or during procedures such as gastrointestinal surgery, we sought to quantify the volume of lavage required to decrease the bacterial load present. The silicon skin model was inoculated with a 0.48-0.52 McFarland standard of isolated Staphylococcus pseudointermedius for 20 minutes. Pre-inoculation and post-lavage cultures were taken to verify sterility and quantify the remaining bacteria, respectively. Lavage volumes of 2.5 ml/cm, 5 ml/cm, and 10 ml/cm were applied with subsequent removal of the remaining volume to be plated for bacterial quantification. Microbial growth decreased incrementally compared to increasing lavage volumes, with a reduction of bacterial colonies below a clinically significant standard of 10^5 CFU/ml in 0% of models lavaged with 2.5 ml/cm, 40% with 5 ml/cm, and 85% with 10 ml/cm. The data supports that a 10 ml/cm volume of subcutaneous lavage can be used in cases of contamination with wounds or gastrointestinal surgery to reduce the bacterial burden below 10^5 CFU/g where SSIs remain a greater concern.
Research Grant	Internal Texas A&M University GINN grant
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Virulence of Mycoplasma tullyi modeled by Galleria mellonella
Authors	Brittany Whitcher, Alexandra Burne, Dina Michaels, and Mary Brown
Affiliations	University of Florida CVM, Department of Infectious Diseases and Immunology, Gainesville, FL
Abstract	Mycoplasmas are the smallest self-replicating bacteria with a wide host-range, impacting both human and veterinary medicine. A number of new Mycoplasma spp. have been discovered in wildlife hosts, creating a need for determining their pathogenic potential. Experimental infection of the natural host is not feasible; therefore an alternative model is needed. Galleria mellonella, the greater wax moth, is a well-defined invertebrate model system that has shown successfully mirrored the pathogenic potential of a number of bacterial and fungal species. The aims of this study were to determine the pathogenic potential of Mycoplasma tullyi, a putative pathogen of penguins, using G. mellonella as an alternative host system. G. mellonella larvae (n=24) were injected with a low and high dose of 3 strains of M. tullyi and monitored for 28 days for successful pupation and emergence, as well as mortality events. M. tullyi infection was confirmed by PCR of hemolymph and whole body larvae. Here, we report that M. tullyi isolates are pathogenic in the G. mellonella model, suggesting that they may also have pathogenic potential in penguins. This study supports that the G. mellonella model is a significant tool to determine the pathogenic potential of new Mycoplasma spp. in wildlife, providing new knowledge for wildlife conservation in both wild and captive animals.
Research Grant	None
Field of Research	Exotic Pets and Zoo Animal Medicine

Abstract Title	Developmental toxicity of dichloroacetic acid (DCA) in zebrafish (Danio rerio)
Authors	Charlotte Whitmer, Katharine Horzmann
Affiliations	Department of Pathobiology, College of Veterinary Medicine, Auburn University, Auburn, AL
Abstract	Dichloroacetic acid (DCA) is a by-product of drinking water chlorination and is a major metabolite of Trichloroethylene (TCE) and Tetrachloroethylene (PERC). TCE and PERC are major environmental toxicants commonly used as industrial solvents and metal degreasers during the mid-twentieth century. TCE, PERC, and DCA can be found in numerous groundwater sources, which is concerning since TCE and PERC are linked to short- and long-term health effects. One of the major health effects is developmental toxicity in mammals and aquatic life, with reports of cardiac abnormalities, stunted growth, and fetal death. The zebrafish (Danio rerio) biomedical model organism was used to test the hypothesis that DCA contributes to TCE and PERC-related developmental toxicity. Wild-type zebrafish embryos were statically exposed to 0, 5, 50, or 500 parts per billion (ppb; µg/L) DCA from 1-120 hours post fertilization (hpf). Embryo survival and hatching were monitored every 24 hours for 120 hpf and larval morphology, heart rate, and behavior, via a visual motor response assay, were evaluated at 120 hpf. There were no changes in survival and hatching or heart rate between groups; however, the 5 ppb exposure group had significantly decreased body length and head length compared to controls on morphological assessment. Additionally, the visual motor response assay showed the 50 ppb exposure group had a decrease in distance moved and velocity compared to controls and the 50 and 500 ppb exposure groups had decreased time spent moving. This data indicates that DCA does significantly contribute to TCE and PERC-related developmental toxicity and continued investigation is warranted.
Research Grant	National Institute of Environmental Health Sciences (R15 ES033361)
Field of Research	Clinical Pathology

Abstract Title	Parity number is negatively associated with day of embryonic attachment in dairy cattle
Authors	Lindsey Wichman, Florentino Paz Jose da Silva Junior, Marcelo El Azzi, Martina Mancheno Valarezo, Dan Ponce-Aguilar, Madeline Zutz, Iago Leao, Thiago de Oliveira Cunha, and João Paulo N. Martins
Affiliations	School of Veterinary Medicine University of Wisconsin-Madison, Madison, WI
Abstract	Early pregnancy losses remain an impediment to optimal fertility in lactating dairy cows and occur more frequently in cows than heifers. This study aimed to determine the effect of parity on the dynamics of pregnancy-specific protein B (PSPB), an indicator of embryonic attachment in cattle. Previous studies indicated that later PSPB increase is associated with a higher risk of pregnancy loss. We anticipate that parity would be negatively associated with day of increase in serum PSPB concentrations. Nulliparous (n=34), primiparous (n=11), and multiparous (n=21) females received a similar synchronization of ovulation protocol and timed-artificial insemination on the same day (d0). Blood samples were collected once (d 14–26) or twice (d 18–24) daily to assess serum PSPB concentrations. Pregnancy diagnosis was determined by ultrasound on d28 by the presence of embryo heartbeat. Day of embryonic attachment was defined by a significant increase (> 3 SD) in basal PSPB within individual (mean PSPB d 14–18). A total of 52.9% (18/34) nulliparous, 63.6% (7/11) primiparous, and 38.1% (8/21) multiparous were pregnant at d28. Nulliparous had the earliest day of embryonic attachment (d 19.3). Also, primiparous (d 20.1) had an earlier embryonic attachment than multiparous (d 20.9). These findings indicate that parity number is negatively associated with day of embryonic attachment, which may be related to an impairment in embryonic development.
Research Grant	None
Field of Research	Theriogenology

Abstract Title	Pathway analysis identifies adrenergic receptor signaling as potential mechanism of CMVD-associated FOG2S657G
Authors	Elissa Williams, Mikaela Castillo, Sharavana Gurunathan, Susannah Elwyn, Donna Conlon, Daniel Rader, Marie Guerraty
Affiliations	University of Pennsylvania School of Veterinary Medicine (Williams), Philadelphia, PA Department of Genetics (Rader) and Department of Medicine (Castillo, Gurunathan, Elwyn, Conlon, Rader, Guerraty), University of Pennsylvania Pearlman School of Medicine, Philadelphia, PA
Abstract	Coronary microvascular disease (CMVD), defined as a disease of the coronary pre-arterioles, arterioles, and capillaries, is a significant cause of ischemic heart disease. Increased sympathetic tone, which is mediated by adrenergic (Adr) receptors, has been implicated in the pathogenesis of CMVD. Cardiomyocyte Fog2 is a transcriptional co-regulator crucial for the development and maintenance of the coronary microvasculature. In prior work, we identified a variant of FOG2 (A1969G, S657G) which is associated with an increased risk of CMVD. The mechanism of how FOG2S657G contributes to CMVD is not known. We created a mouse model expressing human FOG2S657G and another expressing wild-type FOG2. We hypothesize that Fog2S657G promotes CMVD via dysregulation of cardiac adrenergic receptor expression. RNAseq gene expression data from 8-week-old mouse hearts showed that FOG2S657G increased adrenergic gene expression. Gene set enrichment analysis of the top differentially regulated genes identified Adr receptor activity as the top gene ontology (GO) molecular function (Enrichment score (ES) 7.92, nom_p=3.64E-4). This was driven by increased expression of Adrb1, Adrab1, Adrab2, and Adrad1. We confirmed that Adrb1 and Adra1b were increased in FOG2S657G mouse hearts and iPSCs through qRT-PCR, Western blot, and immunofluorescence. We analyzed electronic health record data from 11,105 patients with genomic data in the Penn Medicine Biobank: 8,206 AA, 2,665 AG, and 234 GG (FOG2S657G homozygotes) and found no significant differences in heart rate (HR) or blood pressure (BP). Future studies are needed to define the mechanism by which FOG2S657G interacts with transcription factors to regulate expression of Adr and influence risk of CMVD.
Research Grant	Burroughs Welcome Fund
Field of Research	Cardiology

Abstract Title	Alterations in Pulmonary Glucose Metabolism during Diabetes
Authors	Ally Williams, Matthew Rochowski, Ionsei Hastings, Allison Campolo, John Balcerak, Véronique A Lacombe
Affiliations	Oklahoma State University, College of Veterinary Medicine, Stillwater, Oklahoma
Abstract	Diabetes has recently been identified as a significant independent risk factor for the increased rate and severity of respiratory infection. Diabetes is characterized by chronic hyperglycemia, which may lead to excess glucose available in the lung for invading pathogens to replicate. We previously demonstrated that glucose concentration is elevated in the airway of diabetic mice, although the regulation of glucose transport in the lung is not well known. Glucose transport is regulated by a family of specialized proteins called the glucose transporters (GLUTs). GLUT 4 is a major insulin-sensitive GLUT that is responsible for glucose uptake into fat and muscles, although its role in the lung is not elucidated. AS160 is an AKT substrate that is phosphorylated downstream of insulin action that leads to increase GLUT4 trafficking to the cell surface to enhance glucose uptake. Thus, we hypothesized that GLUT protein expression of the lung would be altered during type 1 diabetes through an AS160 dependent pathway, and rescued with insulin treatment. Type 1 diabetes was induced via streptozotocin and rescued via subcutaneous semi-osmotic insulin pump for 8 weeks. Total expression of GLUT, AS160, and AKT (total and phosphorylated) were quantified via Western blotting of homogenized adult whole lung. Diabetic mice demonstrated significant decreases of protein expression of pulmonary GLUT -4 and -8 (a novel isoform), which was rescued with insulin treatment. Results are pending in regards to AS160 and AKT protein expression. These alterations in pulmonary glucose homeostasis could be a potential therapeutic target to help mitigate the severity of pulmonary infection during diabetes.
Research Grant	National Institute of Health
Field of Research	Biochemistry

Abstract Title	Identification of alleles and genes that underlie recurrent exertional rhabdomyolysis in racehorses
Authors	Caro Wilson, Kirsten Dimmler, James Mickelson, Molly McCue
Affiliations	University of Minnesota CVM, St. Paul, MN
Abstract	Recurrent exertional rhabdomyolysis (RER), also known as 'tying up', is a painful muscle condition that affects 10% of Thoroughbred (TB) and 25% of Standardbred (STBD) racehorses. Acute episodes of exertional rhabdomyolysis (ER) can cause life threatening electrolyte imbalances and renal damage. Even in the absence of acute ER, horses may suffer from subclinical signs such as muscle pain. Although no specific causative genetic variants have been identified, previous work demonstrated that approximately 42% and 45% of disease risk is attributable to additive genetic effects in TBs and STDBs. To further understand the pathophysiology of RER we will identify specific alleles, genes, and biological pathways that contribute to the disease. Alleles associated with RER were selected for inclusion in a custom genotyping assay based on 1) Significant allele frequency differences between cases and controls 2) located within 500 kb of a GWAS region of interest (ROI); 3) located within 100 kb of a random forest (RF) ROI; 4) located within a biological candidate gene; 5) located within a positional candidate gene; and 6) predicted functional effect. Using data from 1,579 STDBs and TBs genotyped on the custom assay, I will build a logistic regression to identify alleles with a moderate to high contribution to disease risk both within breeds and across breeds. Gene Ontology (GO) term enrichment analysis will be performed to identify biological pathways that are overrepresented in the set of genes and thus provide insight into the molecular basis of RER. We expect to have identified specific alleles, genes, and biological pathways that underlie RER pathogenesis which may guide personalized treatment and management for affected horses.
Research Grant	Grayson Jockey Club research Foundation
Field of Research	Equine Medicine and Surgery

Abstract Title	Investigating the pathogenesis and infective dose of Campylobacter hepaticus in white leghorn laying hens.
Authors	James Wilson, Roel Becerra, Catherine M. Logue
Affiliations	Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA 30602
Abstract	Spotty Liver Disease (SLD), caused by Campylobacter hepaticus, is characterized by multifocal 1-2mm white spots on the surface of chickens' livers. C. hepaticus SLD infections have not been seen in the US since the 1960s but have recently emerged in free range and cage free rearing layer systems. With increasing potential for SLD to become widespread in egg laying breeds, investigation into the pathogenesis of C. hepaticus is needed. The objective of this study was to determine the amount of C. hepaticus needed to cause clinical disease in white leghorn (WL) laying hens and the pathogenesis of the bacterial infection. For this study, 30 WL layers at 60 weeks of age, were divided into three treatment groups and orally challenged with 108, 109, or 1011 cfu/ml of C. hepaticus. An unchallenged sentinel bird was added to two groups to monitor transmission. Birds were housed in battery cages in colony houses and were euthanized weekly beginning four days post challenge. SLD lesion scores were recorded for each bird. Bile, blood, feces, and eggs were collected from euthanized birds and plated on blood agar to assess C. hepaticus presence. All C. hepaticus colonies were confirmed by PCR. The expected outcome is that challenging 1011 cfu/ml will produce greater lesion scores and greater recovery of C. hepaticus from sampled tissues. It is also expected that C. hepaticus will be detectable in feces but absent in eggs. To the author's knowledge, there is currently no research on the infective dose of C. hepaticus required to cause SLD in layers or the bird-to-bird transmission route. This research allows us to examine the level of C. hepaticus necessary to cause SLD, and what dose is appropriate for development of a live vaccine.
Research Grant	None
Field of Research	Bacteriology

Abstract Title	Inter-investigator Reliability on Measuring the Rotation of the Canine Stifle
Authors	Morgan Winters, Dominique Griffon, and Emma Faulkner
Affiliations	College of Veterinary Medicine, Western University of Health Science
Abstract	Cranial cruciate ligament deficiency (CCLD) is a common orthopedic disorder affecting the dog's stifle joint. While multiple factors contribute to its development, excessive internal rotation of the stifle is a common characteristic, exerting increased pressure on the cranial cruciate ligament. Internal rotational instability (RIS) plays a significant role in the pathogenesis of CCLD and can also result from it. However, the normal range of internal stifle rotation in susceptible breeds remains unknown. This study aimed to establish the normal range of stifle rotation in healthy canine stifles and investigate how breed influences this range. Additionally, it looked to examine the impact of CCLD on rotational range in affected stifles. Reliability of rotational measurements within dogs and among different clinicians was also assessed. Measurement techniques include fluoroscopy, 3D kinematics, and goniometry. Goniometry, a cost-effective and minimally invasive option, offers good reliability and can guide clinical interventions. It was used to measure the neutral position, internal rotation and external rotation of each limb. The study hypothesized that breeds predisposed to CCLD, as well as affected limbs, will exhibit increased internal rotation compared to the control group. Furthermore, the measurements have demonstrated excellent reliability within dogs and good reliability across different clinicians. This research contributes to preventing and managing CCLD in dogs, shedding light on rotational instability as a causative and consequential factor. Determining the normal range of stifle rotation and reliable measurement techniques enhances our understanding of these conditions and aids in intervention strategies.
Research Grant	VCA matching grant, BI
Field of Research	Orthopedics

Abstract Title	Capacity-building for serosurveillance of zoonotic diseases in the Democratic Republic of the Congo
Authors	Danae A Witte, Nicole A Hoff, Megan Halbrook, Anne W Rimoin, and Lisa E Hensley
Affiliations	University of Florida College of Veterinary Medicine, Gainesville, FL (Witte); Fielding School of Public Health, University of California, Los Angeles, CA (Hoff, Halbrook, Rimoin); Zoonotic and Emerging Disease Research Unit, United States Department of Agriculture (USDA) Agricultural Research Service, Manhattan, KS (Hensley)
Abstract	Several zoonotic diseases endemic to the Democratic Republic of the Congo (DRC), including Ebola virus, Crimean-Congo Hemorrhagic Fever virus, and mpox virus, are of significant public health concern. Lack of infrastructure and resources in the DRC creates a challenging environment to cultivate national surveillance and disease reporting systems; as a result, the risk of pathogens to humans and livestock is relatively unknown. An initiative to launch a cross-sectional sentinel serosurveillance study for these among livestock populations in collaboration with the Institut National de Recherche Biomédicale (INRB) and the Laboratoire Vétérinaire Centrale de Kinshasa (LVC) has been developed. Prerequisite to initiating these efforts, research capacity-building strategies were implemented to prepare local teams for conducting animal field studies in low-resource settings. The key areas for development identified for local veterinary professionals included the implementation of electronic data collection and standardization of the nutritional assessment of animal participants. In this study, we transitioned from paper records to electronic data collection using REDCap®, a secure web application that can be used for either online or offline data capture, making it ideal for field research settings. We also introduced local veterinary partners to a standardized assessment for body condition scoring, which allows for quantification of the energy needs of each participant. Further capacity-building efforts will support a robust and functional national surveillance program for zoonotic emerging infections, and improvements by this project have formed a valuable foundation on which to build an interdisciplinary network.
Research Grant	USDA ARS 58-3022-2-020 Ecological and Epidemiological Investigations of High-Consequence of Zoonotic Pathogens at the Livestock, Wildlife and Human Interface
Field of Research	Epidemiology

Abstract Title	Investigation of radiation on canine appendicular osteosarcoma with metasurface-enhanced infrared spectroscopy
Authors	Lea Witzke, Alizeh Khan, Steven Huang, Gennady Shvets, and Parminder Basran
Affiliations	Cornell University College of Veterinary Medicine, Ithaca, NY
Abstract	Canine appendicular osteosarcoma is a common bone tumor in dogs that severely impacts their mobility and overall health. Treatment options are limited, often involving limb amputation combined with chemotherapy and sometimes radiotherapy. Given the mixed results of radiotherapy, further research is required to clarify its role and efficacy as a less invasive treatment option. This study aims to monitor the effect of radiation using metasurface-enhanced infrared spectroscopy (MEIRS). By manipulating light at the nanoscale and enhancing cellular infrared signals, MEIRS can identify changes in cell morphology, adhesion, and lipid composition. It is hypothesized that MEIRS detects significant differences between irradiated and non-irradiated cells. OSCA78 canine osteosarcoma cells were cultured, seeded at confluency in 60mm Petri dishes, and incubated for 24 hours. The cultured cells received 3Gy and 5Gy irradiation doses, while an unirradiated control group was included. Cells were then trypsinized and transferred to the metasurface. MEIRS non-invasively measured various cellular responses of live cells on the metasurface. Additionally, microscopic images were taken before and after radiation to evaluate potential morphological changes. Preliminary results indicate noticeable qualitative distinctions in cellular morphology between irradiated and non-irradiated cells, indicating greater damage in the irradiated group. It is expected that the MEIRS measurements will further validate these cellular disparities. In conclusion, this study has great potential to improve our understanding of the cellular response to irradiation in canine appendicular osteosarcoma and contribute to the development of improved treatment strategies.
Research Grant	Cornell Richard P. Riney Canine Health Center Research Grants Program
Field of Research	Oncology

Abstract Title	Relationship between nutrition support plan and outcome in hospitalized dogs at a veterinary teaching hospital
Authors	Reed E. Wixon, Lauren M.W. Tseng, Jacqueline M. Parr
Affiliations	Department of Small Animal Medicine and Surgery, College of Veterinary Medicine, University of Georgia, Athens, GA
Abstract	Objective: This study aimed to determine the nutrition support plan of hospitalized dogs through analyses of electronic medical records at a veterinary teaching hospital over a 12-month period and to determine the relationship to hospital outcome (euthanasia/death versus discharge). Animals: A total of 95 client-owned dogs and 100 hospitalizations at the University of Georgia College of Veterinary Medicine from February 1, 2022-February 28, 2023. Methods: Data pertaining to signalment, weight, body condition score, muscle condition score, nutrition support plan, appetite, enteral nutrition (EN), parenteral nutrition (PN), and outcome were analyzed. After ranking patients from longest to shortest time of hospitalization, the 100 longest hospitalizations were selected for inclusion. Results: Length of hospitalization ranged from 193.9-880.6 hours (mean 283.5 hours). During 94 hospitalizations, patients lost weight with a mean loss of 7.9%. When comparing patients that died (n=18) to patients that were discharged (n=82) using a cutoff of 50% of appetite treatments, 77.8% versus 41.5% of hospitalizations were hyporexic and 72.2% versus 26.8% were anorexic. Additionally, 61.1% versus 28.0% received EN (31 nasoesophageal/nasogastric, 12 esophageal, and 2 gastric feeding tubes), 11.1% versus 1.2% received PN, and 55.6% versus 29.3% received appetite stimulants to address hyporexia/anorexia. Clinical Relevance: Hospitalized patients that died were more likely to be hyporexic/anorexic versus patients that were discharged. This resulted in a higher percentage of assisted feeding (both EN and PN) and use of appetite stimulants for patients that died versus patients that were discharged.
Research Grant	None
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Comparison of plasma preparations to optimize exosome enrichment for early detection of canine osteosarcoma
Authors	Meagan M. Wojtysiak, Courtney H. Labé, Mitzi Lewellen, Emily L. Myers, Amber Winter, Kelly Reid, Jaime F. Modiano, Kelly M. Makielski
Affiliations	Department of Veterinary Clinical Sciences, College of Veterinary Medicine, University of Minnesota, St. Paul, MN
Abstract	Osteosarcoma is a common, terminal disease of dogs with cancer and has limited treatment options. While lesions commonly occur in the appendicular skeleton, the lesions are heterogeneous in nature; furthermore, the prognosis and metastatic potential for virtually all the tumors are guarded to poor. In this complexity lies the need to develop a test capable of early detection, which might enhance the probability of treatment success. We developed the Canine Osteosarcoma Early Detection (COED) project to fulfill this need. Our goal is to create biomarkers based on exosome transcript patterns, similarly to what we previously showed was effective to predict minimal residual disease in dogs with osteosarcoma. Exosomes are microvesicles secreted by all cells that serve as important biological vehicles for communication and waste disposal, and they are found in circulating blood of all dogs. This study is focused on optimizing protocols for exosome enrichment and processing for downstream analyses with NanoSight and qRT-PCR. Specifically, we will compare exosome enrichments using plasma preparations from blood samples collected in EDTA anticoagulant tubes and separated at the point of care, or after shipment and upon receipt in the lab (defined as “plasma” and “plasma control”, respectively). We will establish if differences exist between the fresh and delayed plasma preparations with an emphasis on exosome yields, uniformity, and quantity of known transcripts found in exosomes secreted by osteosarcoma cells in situ. These results will help to credential the most efficient steps for exosome processing helping to optimize the protocols that will be implemented for the COED project.
Research Grant	Grant 03032-MOU AKC Canine Health Foundation; University of Minnesota Animal Cancer Care and Research Program
Field of Research	Oncology

Abstract Title	The effect of Janus Kinase inhibitors on healthy canine lymphocytes
Authors	Dianne M. Wolfsen, Satoshi Suzuki, Troy A. Myers, Kristina Meichner
Affiliations	Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands (Wolfsen) Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, GA (Suzuki, Myers, Meichner)
Abstract	Lymphoma is one of the most common malignant cancers in dogs. Response to chemotherapy is high initially but dogs usually succumb to their disease and alternative treatment options are clearly needed to improve outcome. Activation of the Janus Kinase (JAK)/Signal Transducer and Activator of Transcription (STAT) pathway is critical in both physiologic lymphopoiesis and lymphoid malignancies and JAK inhibitors (I) are used for the treatment of human lymphoma in clinical trials. Our laboratory tested the effect of JAK-Is in canine lymphoma cell lines but no studies investigated the effect of different JAK-I in non-neoplastic lymphocytes. We hypothesized that JAK-Is alter T and B cell proportions in healthy canine lymphocytes. Peripheral blood mononuclear cells were isolated via density gradient centrifugation from blood collected from four healthy dogs and treated with JAK-Is (oclacitinib, AZD-1480, tofacitinib, itacitinib) at 1 µM following stimulation with canine recombinant (cr) interleukin (IL)-2, cr-IL-6 and Concavalin-A for a total of 120h. Cell viability, lymphocyte subsets (T helper, T cytotoxic, B cells), lymphocyte activation (CD25, MHC-II), and proliferation (Ki-67) were measured via flow cytometry. Compared to untreated control cells, all JAK-Is caused a decrease in all lymphocyte subsets ($p < 0.0001$), likely via inhibition of T cell activation ($p < 0.0001$) and proliferation, and increase in cell death ($p = 0.005$), but response between different dogs was variable. AZD1480, a JAK-2-I, and tofacitinib, a pan-JAK-I, were most potent. These in vitro findings suggest a lymphocytolytic effect of these JAK-Is and form a base for future in vivo studies in dogs with lymphoma but also autoimmune diseases.
Research Grant	None
Field of Research	Oncology

Abstract Title	Histological analysis of distribution & correlation of nanoparticle and tumor-related cells in mammary tumor
Authors	Theresa W. Wong, Preethi Korangath, Robert Ivkov
Affiliations	Johns Hopkins University, Department of Molecular and Comparative Pathobiology, Department of Radiation Oncology and Molecular, Radiation Sciences, and Department of Oncology (Korangath, Ivkov), School of Medicine, Baltimore, MD Western University of Health Science, College of Veterinary Medicine, Pomona, CA (Wong)
Abstract	Iron oxide nanoparticles (NP) are potential drug carriers to target tumor cells when coated with cancer-specific antibodies (Ab). Previous studies show that targeted NPs seldom reach the target (tumor) from complex interactions with host immune and stromal cells when injected systemically. This study aims to investigate correlations between patterns of spatial distribution of Ab conjugated and unconjugated NP with antigen-expressing tumor cells and tumor-associated stromal cells (TASC) within mammary tumors (MT) grown in mice. The intent is to determine if correlations between NP and TASC may provide clues to mechanisms of NP retention in the tumor microenvironment (TME). Female FVB/NJ mice bearing murine-derived human epidermal growth factor receptor (HER2) MT implant were IV injected with either PBS or Bionized nano ferrite NP. NP was conjugated with Herceptin® (BH), polyclonal isotype IgG (BIgG), or plain unconjugated (BP). MTs were harvested 24hrs post-injection for staining by immunohistochemistry with markers for fibroblast, T cell, macrophage, tumor cell, endothelium, and dendritic cell, and Prussian blue for iron, and Mason's Trichrome for collagen. Histology slides were digitized and analyzed in quartile and duo-decile sections from outermost to innermost region, using ImageJ. BH and fibroblast both showed similar spatial distribution with three-fold higher accumulation in the outermost quartile, compared to the innermost quartile, whereas HER2 distribution appeared uniform. Quantitative analysis is ongoing. Our preliminary, conclusion is that BH distribution within the tumor is associated more with stromal cells than with HER2 within the TME.
Research Grant	Jayne Koskinas Ted Giovanis (JKTG) Foundation for Health and Policy and NIH/NCI grant 5P30 CA006973
Field of Research	Oncology

Abstract Title	Serum Glucose and Lactate Concentration Changes Over Time in Room-Temperature and Refrigerated Canine Whole Bl
Authors	Katherine Woolf, M. Ryan Smith, Chin-Chi Liu
Affiliations	Department of Veterinary Clinical Sciences, Lousiana State University, School of Veterinary Medicine, Baton Rogue, LA
Abstract	Serum glucose and lactate concentrations are important clinical values in the assessment of canine veterinary patients. Delays in sample processing and analysis are known to result in increased lactate and decreased glucose concentrations due to ongoing cellular metabolism, which can affect result interpretation significantly. The purpose of this study was to evaluate the efficacy of refrigeration on slowing the rates of concentration change compared to samples held at room-temperature. Whole blood samples were taken from 10 healthy canines. Glucose and lactate values were assessed immediately and at 2, 4, 6, 12, and 24 hours after blood collection. The rate of concentration change of both lactate and glucose was accelerated in room-temperature samples compared to refrigerated samples.Glucose concentration change was found to be clinically significant after 4 hours in room-temperature samples, but not clinically significant through 24 hours in refrigerated samples. Lactate concentration change was found to be clinically significant for both room-temperature and refrigerated samples at 2 hours.
Research Grant	None
Field of Research	Clinical Pathology

Abstract Title	Molecular characterization of Listeria monocytogenes isolated from the cow calf farming system of Central AL
Authors	Sabria Wooten, Woubit Abebe, Rawah Faraj.
Affiliations	Center for Food Animal Health, Food Safety, and Food Defense, Department of Pathobiology, College of Veterinary Medicine, Tuskegee University, Tuskegee, Alabama, USA
Abstract	Listeria monocytogenes is a ubiquitous microorganism and the causative agent of listeriosis. L. monocytogenes can be found in moist environments, soil, water, and animals. This study analyzed 50 fecal samples collected from cow-calf farming systems between May 2023 and July 2023 from different farms in central Alabama, USA. We examined the prevalence, virulence factors, and phylogenetic distribution of the hlyA gene of L. monocytogenes isolated from the cow-calf farming system. The prevalence of contamination with L. monocytogenes was 11 (22%) out of 50 fecal samples. Serotypes and virulence genes of all L. monocytogenes positive samples were characterized using multiplex PCR. All isolates were positive for inlA, inlB, plcB, prfA, iap, actA, hly, hlyA, and Lmo0733 genes. PCR-based serotyping showed the isolates belonged to serotype 4d (4/11, 36%), 1/2b (2/11, 18 %), 4a (3/11, 27%), and 1/2a (2/11, 18%). The presence of variations of the hlyA genes among the isolates was analyzed using geneious prime software. The results of hlyA gene alignment from all isolates revealed high similarity with strains reported from different parts of the world (GenBank Database). This gene will be used to understand the evolutionary distance of the current L. monocytogenes isolates with respect to those available in public domains. The high percentage of L. monocytogenes isolation in this study may reflect an increased risk of infection through direct or indirect contact with cow fecal samples. Regular screening of animals for L. monocytogenes is beneficial for preventing listeriosis in farms and, subsequently, the food system.
Research Grant	Research Support: USDA/NIFA/CBG 2021-38821-34710, MSU/USDA/NIFA RC113747TU.
Field of Research	Bacteriology

Abstract Title	Ampakines and functional bladder recovery from spinal cord injury
Authors	Austen J Yan, Sabhya Rana, Robert C Martinez, Firoj Alom , David D Fuller, Aaron D Mickle
Affiliations	Department of Physiological Sciences, College of Veterinary Medicine (Yan, Alom, Mickle), Department of Physical Therapy, College of Public Health (Rana, Martinez, Fuller) University of Florida, Gainesville, FL McKnight Brain Institute, University of Florida, Gainesville, FL (Yan, Rana, Martinez, Mickle, Fuller)
Abstract	In America, more than 17,000 people suffer from spinal cord injuries yearly, with one of the most common complaints being the loss of urinary control. Ampakines are allosteric modulators of AMPA-type glutamate receptors and enhance glutamatergic synaptic transmission. Glutamate signaling is present in many neural circuits that are involved in bladder sensation and voiding. We hypothesized that ampakines can enhance the function and survival of spinal cord neurons, resulting in a reduction of bladder deficits related to SCI. Adult female Sprague Dawley rats received a T9 spinal contusion (n=12) and six randomly chosen rats received ampakine CX1739 (5mg/kg) daily post contusion, four received the HPCD vehicle injection daily post contusion, and two received CX1739 starting 5 days post injury for thirty days. Spontaneous voiding frequency and volume were recorded weekly in metabolic cages, in addition to fecal weight, BBB, and urine analysis. At the endpoint, we performed cystometry under urethane anesthesia. Data showed that the pressure threshold for inducing bladder contraction and the interval between bladder contractions were reduced in ampakine treated rats compared to HPCD vehicle rats. Due to the severe injury model, many rats died before the four-week endpoint, making it difficult to draw concise conclusions. However, it appears that chronic ampakine may provide reduced voiding deficits following SCI. Current therapies for spinal cord injured persons with bladder dysfunction are aimed at relieving patients of symptoms, rather than curative solutions. Here, we demonstrate that intraperitoneal delivery of an allosteric modulator of AMPA receptors may provide long term improvements to bladder function following SCI.
Research Grant	NIH 1R01HL139708-01A1, SCIRTS Craig H. Neilsen Foundation, Rita Allen Foundation Scholars Program Fund, Community Foundation of New Jersey, NIH NIBIB Trailblazer award (R21 EB031249)
Field of Research	Physiology

Abstract Title	Characterising tumor-associated macrophage behavior in the tumor microenvironment of canine osteosarcoma
Authors	Katherine Yang, Alaina Ryan, Amanda Martinot, Cheryl A. London and Heather L. Gardner
Affiliations	Cummings School of Veterinary Medicine, Tufts University, North Grafton, MA
Abstract	Recent research focusing on the role of immune cells in the tumor microenvironment identified macrophages as having an important role in supporting tumor growth and creating an immunosuppressive environment. Subsequent clinical trials in dogs with canine osteosarcoma (OS) using immunotherapy combinations designed to target the immune microenvironment have shown evidence of activity, but it is unknown how macrophage activity changes in dogs between the primary tumor and development of metastatic disease in the lungs. It is hypothesised that companion dogs with naturally occurring OS will have a higher macrophage infiltration with immunosuppressive signatures in lung metastases compared to the primary tumor. It is also predicted that these immunosuppressive signatures will be associated with disease-free interval and an M2 phenotype, which have pro-tumor properties. To begin to characterise the macrophage behavior in canine OS, RNA was extracted from patient-matched primary and pulmonary metastatic tissues to obtain differential gene expression signatures using the Nanostring nCounter CanineIO panel. Patient-matched formalin-fixed tissue will be evaluated using the GeoMx digital spatial profiler to evaluate macrophage infiltration and associated gene expression changes. Regions of interest will be evaluated for degree of macrophage infiltration, and gene expression signatures will be determined and correlated with progression-free survival. These findings will provide valuable information on macrophage behavior in the canine OS microenvironment and may identify outcome-associated biomarkers for future prospective validation.
Research Grant	NIH U01 CA224182
Field of Research	Oncology

Abstract Title	Pharmacokinetics of Buprenorphine - Extended Release on 2/3 Partial Hepatectomized Mice
Authors	Emily Yang, Patricia Arreola, Ingrid Mejia Santos, Naomi Lee*; *Corresponding author email: naolee@coh.org
Affiliations	Office of Research, College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA (Yang) Center for Comparative Medicine, Beckman Research Institute, City of Hope, Duarte, CA (Arreola, Santos, Lee)
Abstract	Two-thirds partial hepatectomy is a commonly employed surgical technique in studying liver functions and regeneration. The liver plays a crucial role in metabolizing compounds through chemical modifications with phase 1 and phase 2 enzymes. An opioid commonly used in veterinary species, extended-release buprenorphine (Buprenorphine-ER, Zoopharm, Loveland CO) for effective analgesia, is metabolized by the liver. However, mice that undergo hepatectomy and given the same dosage of Buprenorphine-ER (Bup-ER) often exhibit overt depressive like states, poor post-operative recovery, reduced activity, and decreasing body weight. This study investigates the metabolism of Bup-ER with a goal of refining a more appropriate dosage for mice in the hepatectomy model, which is expected to have compromised liver function. Our experimental design consists of one control (n=10), sham surgery (laparotomy) (n=10), and 2/3 partial hepatectomy (n=10) group. Each group has an equal number of females (n=5) and males (n=5), is injected with 1 ml of saline during the pre-operative period, and is treated with 1 mg/ml dosage of Bup-ER post-operatively. Serial blood collections are performed with each mouse at five timepoints (7 days prior to the study to establish the baseline and 6, 24, 48, and 72 hours post administration of Bup-ER). The blood samples are analyzed with liquid chromatography with tandem mass spectrometry (LC MS/MS). We hypothesize that the circulating buprenorphine level would be statistically higher in the hepatectomy group compared to the surgical sham and control group. It is also hypothesized that circulating buprenorphine levels would have no statistical difference in surgical sham and control group.
Research Grant	City of Hope Center for Comparative Medicine - Animal Care Program Western University College of Health Sciences - College of Veterinary Medicine
Field of Research	Laboratory Animal Medicine

Abstract Title	Electrophoretic urine protein banding patterns in healthy cats and cats with kidney or urinary tract diseases
Authors	Catherine Yeoman, Jessica Quimby, Katelyn Brusach, Sarah Shropshire, Alyssa LeComte, Caroline Gainey, Kelci Ryan, Mary Nabity, and Jessica Hokamp
Affiliations	Texas A&M University SVM, Department Veterinary Pathobiology, College Station, TX; Department of Veterinary Clinical Sciences, Ohio State University Veterinary Medical Center (Quimby, Brusach), Columbus, OH; Colorado State University CVM, Clinical Sciences (Shropshire), Fort Collins, Colorado, USA
Abstract	Current methods of urine protein evaluation in cats with chronic kidney disease (CKD) do not accurately predict origin (glomerular or tubulointerstitial (TI)) or severity of renal damage. Electrophoretic urine protein banding patterns can predict location and severity of renal damage in proteinuric dogs, but evaluation of urine protein banding patterns in healthy and diseased cats has been limited. We sought to establish urine protein banding patterns in clinically healthy cats and determine banding pattern differences in cats with renal and urinary tract diseases. Urine from 14 clinically healthy cats, 51 cats with renal disease (37 with CKD but without confirmatory biopsy; 6 with biopsy-confirmed immune complex mediated glomerulonephritis (ICGN); 3 with biopsy confirmed non-ICGN glomerular disease; 5 with biopsy confirmed TI disease), and 14 cats with lower urinary tract infections (UTI) or pyelonephritis was resolved with 1D gel electrophoresis. Healthy cat urine consistently contained 3 protein bands compatible with albumin, cauxin, and Tamm-Horsfall protein. All disease categories had significantly increased low (LMW) and intermediate (IMW) molecular weight proteins while pyelonephritis/UTI, CKD, ICGN, and non-ICGN categories had significantly increased high molecular weight (HMW) proteins compared with healthy cats. While cats with pyelonephritis/UTI, non-ICGN, and ICGN all had significantly increased bands > 200 kDa, numbers of bands > 200 kDa were highest in ICGN cats and could distinguish ICGN from pyelonephritis/UTI and CKD cats. Electrophoretic urine protein banding patterns might be useful to identify ICGN in cats.
Research Grant	International Veterinary Renal Pathology Service
Field of Research	Clinical Pathology

Abstract Title	Extending a flow cytometric assay to assess Rickettsia parkeri infectivity in skin-infiltrating leukocytes
Authors	Xiaochen Yuan, John Stokes, and Andrea Varela-Stokes
Affiliations	Department of Comparative Pathobiology, Cummings School of Veterinary Medicine, Tufts University, North Grafton, MA.
Abstract	Rickettsia parkeri is a tick-borne obligate intracellular pathogen in the spotted fever group Rickettsia spp. (SFGR) that causes spotted fever rickettsiosis (SFR). Our lab studies SFR using the guinea pig model and R. parkeri transmission by its primary vector, the Gulf Coast tick. Here, we expand a previously developed flow cytometric (FCM) assay for immunophenotyping cellular infiltrates in guinea pig skin to identify host cells targeted by R. parkeri. Specifically, we are testing an anti-SFGR antibody designed for immunohistochemistry (IHC) in an in vitro FCM experiment using differentiated THP-1 cells (human leukemia monocytic cell line) prior to moving to an animal study. First, we determined the number of THP-1 cells required to seed a 6-well plate to recover 1 x 106 viable differentiated cells per well. Then, we confirmed the percentage of formaldehyde required to inactivate R. parkeri when fixing cells in the FCM protocol. Next, we are determining the minimum time necessary for R. parkeri (MOI of 10) to invade host cells. We will apply those data to identify the multiplicity of infection (MOI) required to infect approximately 20 percent of the host cells for testing our FCM assay. We labeled the anti-SFGR antibody with the fluorophore CF405L in-house and are performing a titration to tell us if the antibody would be useful for flow cytometry and, if so, at what optimal dilution. We anticipate expanding our FCM assay to detect infected leukocytes in spiked guinea pig blood before moving to in vivo studies. Ultimately, this work will allow us to better understand disease progression and pathogenesis during infection after natural tick transmission in the guinea pig model.
Research Grant	Varela-Stokes Start-Up Funds and Department of Comparative Pathobiology, Cummings School of Veterinary Medicine, Tufts University
Field of Research	Immunology

Abstract Title	Evaluation of AAV9-pGUSB-NPC1 for treating NPC1 disease
Authors	Caroline Zagoren, Rebecca Campbell, and Charles H. Vite
Affiliations	Department of Clinical Sciences and Advanced Medicine, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA
Abstract	Niemann-Pick disease type C1 (NPC1 disease) is an inherited disorder caused by loss-of-function mutations in the NPC1 gene, leading to lysosomal accumulation of cholesterol and sphingolipids. Disease onset is typically in childhood and presents as clumsiness or learning disability. Symptoms include cerebellar ataxia, cognitive impairment, dystonia, supranuclear gaze palsy and dysphagia. Disease in the feline model follows an orthologous mutation to that in humans and recapitulates symptoms observed in patients. In previous works, biweekly administration of 2-hydroxy-propyl-beta-cyclodextrin (HPßCD) in the cisterna magna prevented ataxia and Purkinje cell storage and death, but was ototoxic and did not resolve all symptoms. In prior gene therapy studies, affected cats treated with 1E14 vg of AAV9-pGUSB-NPC1 administered at the cisterna magna showed increased Purkinje cell survivability and diminished ataxia. We hypothesized that optimizing IC administration of AAV9-pGUSB-NPC1 would optimally transduce cells in the cerebellum and result in a more uniform outcome. Using immunological markers for Purkinje cells and NPC1, we identified improved viral transduction of Purkinje cells and concomitant increases in cell survivability and axonal preservation in cats treated optimally. Treated cats also displayed normal gaits and saccadic eye movements, and did not experience ototoxicity. These data suggest that treating NPC1 disease with a viral vector is effective in minimizing Purkinje cell loss and cerebellar disease. This study highlights the potential of AAV9-mediated gene therapy to successfully treat inherited cerebellar neurodegenerative disorders.
Research Grant	R01-NS-115869-01
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Prevalence of campylobacter, giardia, coccidia and other enteric pathogens in dog breeding facilities
Authors	Zoey Zentkovich, Jeanette O'Quin, Thomas Wittum, and Antionette Marsh
Affiliations	Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, Ohio
Abstract	Commercial dog breeding is a major industry in the US with more than 2.1 million dogs purchased from these facilities each year. Within the state of Ohio alone, there are 548 licensed high volume breeders producing dogs for the pet trade. Dogs can be infected with bacteria and parasites of potential risk to people and other animals; however no prevalence studies have been published in commercial dog breeding facilities. In the US, two outbreaks of multidrug resistant Campylobacter jejuni sickening 169 humans across 17 states were recorded from 2016 to 2021 that trace back to pet store puppies, which are primarily sourced from commercial dog breeders. This study aims to identify the prevalence of MDR campylobacter in dogs housed in commercial dog breeding facilities as well as the prevalence of other enteric pathogens including coccidia and giardia, which the breeders report to be a problem in their populations. To determine presence of these infectious agents, several dog breeding facilities will be visited to collect fresh fecal samples and environmental samples using Swiffers. Data on housing, flooring, antiparasitic and antibiotic use as well as facility size and co-housing will be collected. Diagnostically, fecal and Swiffer samples will be cultured to grow Campylobacter spp., Salmonella spp., and carbapenem resistant bacterales. Fecal samples will also be analyzed through double centrifugation and flotation with sugar solution to identity coccidia, giardia, round worms and hook worms. This data will provide pathogen prevalence and can be used to identify potential risk factors useful in evaluating preventive care protocols to reduce prevalence.
Research Grant	Life of Riley
Field of Research	Bacteriology

Abstract Title	Crossed Corticothalamic Projections of the Mouse Prefrontal Cortex Modulus
Authors	Yan Zermeno, Charles Lee
Affiliations	Department of Comparative Biomedical Sciences
Abstract	The prefrontal cortex (PFC) plays a key role in accomplishing goal-oriented tasks. Alterations to the neuroanatomy and chemical imbalances in the PFC have been linked to disorders such as schizophrenia, autism spectrum disorder, and post-traumatic stress disorder. Transgenic mouse models have been subsequently developed to better understand these disorders and the neuroanatomy responsible for them. Ipsilateral corticothalamic projections are regarded as modulatory pathways, but contralateral corticothalamic connections (CCCs) from the PFC have been largely overlooked. The goal of this study is to elucidate transgenic mouse lines and the characteristics of neurons involved in prefrontal CCCs. Evidence suggests neurons from cortical layer 6 typically form corticothalamic connections and neurons from layer 5 tend to project to subcortical structures. This led us to hypothesize that mouse cell lines that emphasize layer 6 neurons are likely to have the strongest CCCs followed by layer 5 neurons. In this study, the Allen Mouse Brain Connectivity Atlas was utilized to analyze the strengths of CCCs originating from the prefrontal modulus of the mouse and to determine the transgenic mouse lines best present CCCs. Injections into wild-type mice prefrontal cortices were performed to confirm the presence, pattern, and strength of these contralateral projections. Transgenic mouse line Syt6-Cre KI148, which outlines layer 6 neurons in the prefrontal cortex demonstrated the strongest CCCs. Ntsr1-Cre GN220, which outlines layer 6 neurons in sensory areas, demonstrated weak CCCs. Rbp4-Cre KL100, which outlines layer 5 neurons, demonstrated stronger CCCs than Ntsr1-Cre GN220 but weaker than Syt6-Cre KI148.
Research Grant	None
Field of Research	One Health

Abstract Title	Duration of adrenocortical suppression after long-term immunosuppressive oral prednisolone therapy in dogs
Authors	Mary Zhou, Mathieu Paulin and Elisabeth Snead
Affiliations	Small Animal Clinical Sciences, Western College of Veterinary Medicine/University of Saskatchewan, Saskatoon, Canada
Abstract	Despite the high prevalence of corticosteroid use in veterinary medicine, long-term effects including hypothalamic adrenocortical axis (HPAA) recovery from immunosuppressive doses remain elusive. The objective of this study was to evaluate changes in the HPAA function after abrupt discontinuation of immunosuppressive doses of oral prednisolone following 35 days of therapy in eight healthy beagle dogs. Dogs were administered a placebo (10 mg lactose) for 14 days, followed by 2.2-2.6mg/kg prednisolone orally daily for 35 days. HPAA suppression was assessed with adrenocorticotropin (ACTH) stimulation testing, endogenous ACTH (eACTH) monitoring and ultrasound measurements of the length and width of each adrenal gland. Assessments were performed at the end of the placebo period (baseline; T0), 17 days (T1), day 35 (T2), and every two weeks post prednisolone until HPAA recovery was evident in all dogs. Notable HPAA suppression occurred by T2. Two weeks post-treatment, 2/8 dogs had clinically normal post ACTH cortisol values indicating that in some dogs, recovery as early as 2 weeks after abrupt discontinuation of steroid therapy may be possible. Significant adrenal atrophy occurred by T2 as measured by L cranial pole ($p = 0.0033$), L caudal pole ($p = 0.0007$), and R caudal pole ($p = 0.0001$) with no significant changes seen in L adrenal lengths ($p = 0.1916$). Adrenal size measurements continued to be significantly depressed 2 weeks post-treatment. In dogs adrenocortical functional recovery with ACTH stimulation appears individually variable and precedes recovery of adrenal size. Other parameters assessing the HPAA including assessment of eACTH are pending before complete clinical recommendations can be made.
Research Grant	Companion Animal Health Fund
Field of Research	Small Animal Medicine and Surgery

Abstract Title	Validating KLF4 as a key control for miR-145 initiated α-SMA expression in canine VICs
Authors	Runzi Zhou, Dawn Meola, and Vicky Yang
Affiliations	Department of Clinical Sciences, Cummings School of Veterinary Medicine, Tufts University, North Grafton, MA.
Abstract	Myxomatous mitral valve disease (MMVD) is the most common acquired heart disease in dogs, characterized by degenerative changes in the mitral valve, leading to regurgitation and congestive heart failure. The etiology of this disease remains unknown. Histologically, valvular interstitial cells (VICs) in MMVD transition from fibroblasts to myofibroblasts, marked by increased alpha-smooth muscle actin (α-SMA) expression. We have demonstrated elevated expression of miR-145 in VICs obtained from diseased canine mitral valves and its direct inhibition of KLF4, an important transcription factor in cellular processes. We hypothesized that KLF4 regulates α-SMA expression and the fibroblast-to-myofibroblast transition in VICs. We performed KLF4 loss/gain of function experiments. VICs from diseased canine mitral valves (n=3) were cultured with recombinant human KLF4 protein at concentrations of 0.1 and 1.0ng/ml for 24 hours in growth factor-depleted media. RNA and protein were extracted with miRVana RNA kit and M-Per, respectively. Western blotting revealed KLF4 stimulation at 0.1ng/ml significantly decreased α-SMA expression ($p = 0.015$; one way ANOVA with Dunnett's multiple comparison test), with a fold change of 0.87 ± 0.09 compared to the control group. Real-time PCR will be used to assess α-SMA gene expression. Further loss-of-function experiments using KLF4-specific siRNA with Lipofectamine RNAiMAX in VICs from normal mitral valves will be conducted. Our data showed that KLF4 indeed controls VIC α-SMA expression. Therefore, inhibition of KLF4 is expected to increase α-SMA expression. These findings will provide insights into MMVD pathogenesis and offer potential therapeutic targets in the miR-145 – KLF4 pathway.
Research Grant	NIH K01OD028205
Field of Research	Cardiology

Abstract Title	Epizootic hemorrhagic disease virus (EHDV) prevalence in white-tailed and mule deer in northeastern Colorado
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Abstract	Epizootic Hemorrhagic Disease Virus (EHDV) is a segmented Orbivirus transmitted by the Culicoides genus of midges. Wild ruminants are particularly susceptible to this disease, with white-tailed deer (Odocoileus virginianus) seeming to be more acutely affected than mule deer (Odocoileus hemionus). Infected white-tailed deer demonstrate hemorrhage and acute mortality, while male mule deer develop peruke (deformed) antlers with evidence of the virus causing sclerosis of testicular tissues. As white-tailed deer populations expand into Colorado from the Northeast, we expect an increase in both white-tailed EHDV-related deaths and male mule deer with peruke antlers in areas where EHDV is circulating. In this study, a total of 40 white-tailed and mule deer were captured and sampled from Weld and Larimer counties in Colorado. Serum samples were taken to test for the prevalence of EHDV from both male and females, and testicular aspirates were taken from males. These results will be important to identify the prevalence and epidemiology of EHDV in Colorado as the deer populations continue to change in our state.
Research Grant	United States Department of Agriculture Fellowship, USDA-NIFA AFRI grant number 2019-67015-28982 as part of the joint USDA-NSF-NIH-BBSRC-BSF Ecology and Evolution of Infectious Diseases program.
Field of Research	Epidemiology