THE OHIO STATE UNIVERSITY
COLLEGE OF VETERINARY MEDICINE

COLLEGE OF VETERINARY MEDICINE RESEARCH DAY

2024

BOOK OF ABSTRACTS

THE OHIO STATE UNIVERSITY

COLLEGE OF VETERINARY MEDICINE

Research Day Keynote Address

Thursday
April 4, 2024

Dunlap Auditorium
Veterinary Medicine Administration Building

"*Scary viruses, killer tapeworms, brain maggots, and nostril ticks: predicting zoonoses in an unpredictable world*"

Presented by:

Dr. Tony Goldberg

*John D. MacArthur Chair
Director, Kibale EcoHealth Project,
Global Virus Network
Professor, Department of
Pathobiological Sciences, School of
Veterinary Medicine, University
Wisconsin-Madison*

Dr. Goldberg is Professor of Epidemiology and John D. MacArthur Research Chair at the University of Wisconsin-Madison, in the USA. He received his B.A. from Amherst College in 1990 in Biology and English, his Ph.D. from Harvard University in 1996 in Biological Anthropology, and his Doctor of Veterinary Medicine and MS in Epidemiology in 2000 from University of Illinois at Urbana-Champaign. Dr. Goldberg's research combines epidemiological study designs with laboratory-based methods in metagenomics to "hunt" for the causes of disease of unknown etiology. He uses methods in the social sciences to link the resulting findings to root drivers of pathogen emergence, many of which hinge on human activities. Dr. Goldberg focuses on diseases that threaten wildlife and imperil ecosystem services, whether or not those diseases are zoonotic. His overarching goal is to improve the health and wellbeing of animals and people while helping to conserve the rapidly changing ecosystems we share.

FACULTY SEMINARS

Metronidazole: Friend or Foe? Shifting theParadigm of Antibiotic Use for Acute Colitis

Adam Rudinsky, DVM, MS, DACVIM

Associate Professor, Small Animal InternalMedicine

Department of Veterinary Clinical Sciences.

Research focus: The interface between microbiota and mucosal surfaces; Microbiology, immunology, urology, and gastroenterology, as it relates to the microbiome and probiotics

DISCOVERY • OUTREACH • EDUCATION • SERVICE

One Health Issues in Dairy and Calf Production

Greg Habing, DVM, MS, PhD, DACVPM

Professor and Interim Chair

Department of Preventive Medicine

Research focus: Antimicrobial use and resistance on livestock farms; Cattle health and welfare; Epidemiology of foodborne pathogens on livestock farms.

DISCOVERY • OUTREACH • EDUCATION • SERVICE

POSTER JUDGES

Thank you to the following faculty for taking time
out of their busy schedules to judge
81 Poster Presentations.

Turi Aarnes	Amanda Berrian
Andrew Bowman	Kara Corps
Sushmitha Durgam	Jaylene Flint
Rebecca Garabed	Tony Goldberg
Greg Habing	Bill Kisseberth
Haichang Li	Jianrong Li
Angela Marolf	Stacey Meeker
Caitlin Moreno	Margaret Mudge
Stefan Niewiesk	Mike Oglesbee
Amanda Panfil	Eric Schroeder
Cody Warren	Gaofeng Xiong

Thank you to Jean Schelhorn for reviewing the
abstracts for potential IP disclosures.

2024 Faculty Chair:
Dr. Stefan Niewiesk
Professor, Veterinary Biosciences

Organized by:
Michele L. Morscher
CVM Office of Research and Graduate Studies

CLINICAL RESEARCH

Title of abstract:	**A COMPARISON OF PRESCRIBED ANALGESIC PLANS FOR AT-HOME CARE BETWEEN DOGS AND CATS POST OVARIOHYSTERECTOMY OR ORCHIECTOMY**
Authors	L. Adams[1], K. Muñoz[1] [1]Department of Veterinary Clinical Sciences, The Ohio State University
Abstract	**Objective:** To investigate variations in pain management after surgical sterilization between dogs and cats, and owner compliance as it relates to administration of prescribed analgesics to their pet at home. **Sample:** 189 owners met the inclusion criteria for the study. **Methods:** An online survey was distributed via email to clients of a high-quality, high-volume low-cost veterinary clinic in August 2022. Owners were asked demographic information of themselves and their pets. Additionally, if their pet was discharged with analgesics they were asked if they were administered as prescribed, and if they thought that their pet showed signs of pain at home. Inclusion criteria included dogs and cats that were sterilized within 6 months of the owner completing the survey, in the current owner's care at the time of the procedure, and being a resident in Michigan, USA. **Results:** Analgesics were prescribed for 13% of pets; a total of 13.8% for dogs and 6.7% for cats. Dogs were more likely to be prescribed analgesics after an ovariohysterectomy as compared to cats ($p = 0.02$), but there was no difference after an orchiectomy ($p = 0.08$). Owner compliance in administering analgesics was reported to be 78.9%. A total of 25.4% of dogs and 13.6% of cats were reported to appear painful at home. **Clinical relevance:** Cats were prescribed analgesics less often than dogs, suggesting that cats' pain may not be appreciated and therefore not managed as well as in dogs. Subjectively, most owners thought their pet's pain was well managed at home.
Keywords for abstract:	cat dog orchiectomy ovariohysterectomy pain scoring

Title of abstract:	**MODIC CHANGES IN DOGS WITH INTERVERTEBRAL DISC DISEASE**
Authors:	<u>D. Agustini,</u> M. K. Heimann, M. Co, B. A. Walter, D. Purmessur, S. A. Moore.
Abstract:	Modic changes (MC) are signs of vertebral pathology visible on magnetic resonance (MR) images that have been associated with low back pain (LBP) and disc degeneration in people. Multiple breeds of dogs also develop MCs and coincident back pain. However, the association between breed, MC, and spinal pathologies has yet to be fully elucidated. This study aimed to identify the prevalence of MC that occur spontaneously in the lumbar vertebral column of dogs diagnosed with intervertebral disc disease (IVDD) and examine their association with demographic criteria and the disc width index (DWI). Medical records and lumbar vertebral column MR images were examined from 104 dogs (831 intervertebral disc spaces and adjacent vertebrae), which were divided into three groups: chondrodystrophic dogs (CD; n= 54) and non-chondrodystrophic dogs (NCD; n= 30) with IVDD as the primary diagnosis, and control dogs (n= 20) with other spinal diseases as their primary diagnosis. Results demonstrate increasing age and a diagnosis of IVDD were significantly associated with MC in dogs ($p < 0.001$ and $p = 0.0062$, respectively). In CD dogs with IVDD, Type 2 MC were most prevalent, whereas, in NCD dogs, Type 3 MC were the most prevalent type. Type 2 MC were distributed nearly equally across the lumbar vertebral column, while Type 3 MC were primarily detected at the level of L7-S1. This study demonstrated that MC developed spontaneously in dogs, are common in dogs diagnosed with IVDD, and the type observed varies by breed. Further research is needed to understand the pathogenesis of MC; however, the increased presence of Type 2 MC in CD dogs, similar to what is found in people with disc degeneration, suggests that CD dogs could serve as models for MC in people.
Keywords for abstract:	Modic changes Intervertebral disc disease Lumbar Disc height index MRI

Title of abstract:	**VITAMIN D BINDING PROTEIN AND VITAMIN D AND THEIR ASSOCIATION WITH DISEASE SEVERITY IN HOSPITALIZED NEWBORN FOALS**
Authors:	Bartish C, Kamr A, Samuels A, Jacobs B, Kelly P, Toribio RE of The College of Veterinary Medicine, The Ohio State University, Columbus, OH Gilsenan W of Rood and Riddle Equine Hospital, Lexington, KY
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). Previous studies in our lab showed that critically ill foals frequently have low vitamin D concentrations. Due to its small size (52-59 kDa), 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 35 hospitalized foals (14 septic and 21 sick non-septic). Preliminary findings showed 13/21 (61.9%) and 8/14 (57.14%) had low 25[OH]D (<7.65 ng/mL) in sick non-septic foals and septic foals on admission, respectively, and 14/21 (66.67%) and 8/14 (57.14%) had low DBP (<14.4 ug/mL) in sick non-septic foals and septic foals on admit respectively. This finding was statistically significant. Descriptive statistics of the healthy foal population determined low measurements. Our findings indicate that low DBP could contribute to hypovitaminosis D in sick foals. This study provided additional insight into the pathogenesis of hypovitaminosis D in critically ill foals.
Keywords for abstract:	Vitamin D 25-hydroxyvitamin D 25[OH]D Vitamin D Binding Protein Foals Neonates

CR-4

Title of abstract:	**COMPARING DEFECATION FREQUENCY BETWEEN CATS WITH AND WITHOUT CHRONIC KIDNEY DISEASE**
Authors:	Z. George, J. Quimby, K. Brusach, L. Lim, S. Jones, A. Rudinksy
Abstrac:t	Cats with chronic kidney disease (CKD) are at higher risk for presenting with constipation. 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. Cats with stable IRIS stages 2-4 CKD (n=9) and healthy control cats (n=9) with no known history of overt constipation were included in this prospective observational study. Serum biochemistry, CBC, T4, urinalysis and blood pressure was performed in all cats to confirm health status. The Petivity™ Smart Litter Box Monitor System was utilized to collect real-time defecation data. Data was collected via the Petivity™ app for 30 days during which medical management and husbandry remained consistent. A Mann-Whitney U test was performed to compare the total number of days without defecation between CKD cats and healthy cats over 14, 21 and 30 days. CKD cats had significantly more total days without defecation than healthy cats at 14 ($p = 0.001$), 21 ($p = 0.0004$), and 30 days ($p = 0.0003$). Median total days without defecation across 14, 21 and 30 days was 5 (1-8), 7 (3-9) and 10 (5-13), respectively, for CKD cats compared to 0 (0-4), 2 (0-4) and 2 (0-7), for healthy cats. Cats with CKD defecate less than healthy cats which may be an indicator of subclinical constipation. This information could allow for earlier interventions and therapies, possibly preventing episodes of overt constipation.
Keywords for abstract:	Constipation Defecation frequency Artificial intelligence Litter box monitor

Title of abstract:	**OCULAR EXAMINATION FINDINGS BEFORE AND AFTER TOTAL EAR CANAL ABLATION AND BULLA OSTEOTOMY IN CATS AND DOGS**
Authors:	B. Hartrum[1,2], T. Webb[1], G. Newbold[2], A. Gemensky-Metzler[2], S. Kennedy[1], B. Carson[2].[1]MedVet Columbus, [2]College of Veterinary Medicine, Ohio State University
Abstract:	***Objective*** To report ocular examination findings before and after total ear canal ablation and bulla osteotomy TECABO) and ventral bulla osteotomy (VBO) in cats and dogs. ***Animals*** Client-owned dogs and cats diagnosed with aural disease in which total ear canal ablation (TECABO) or ventral bulla osteotomy (VBO) was performed. ***Methods*** Ophthalmic examinations were performed in dogs and cats at the Ohio State University and MedVet Columbus for conditions in which a TECABO or VBO was indicated. Exam findings and post-operative complications relating to ophthalmic and/or neuro-ophthalmic diseases were recorded prior to surgery (T0), 1 day (T1), 2-3 weeks (T14), and +/-2 months (T60) post-operatively. ***Results*** Twenty-eight dogs and twenty-two cats underwent 43 TECABO and 20 VBO surgeries, for a total of 63 ears. Reasons for surgery included otitis (52.4%, 33/63), polyps (30.1%,19/63), and aural masses (17.5%,11/63). Facial nerve paralysis was observed preoperatively in 5.7% of surgeries and postoperatively in 47.2% at T1 and 31.3% at T14. Horner's Syndrome was present preoperatively in 11.3% and postoperatively in 45.3% at T1 and 37.5% at T14. Keratoconjunctivitis sicca and corneal ulcers were noted in 5.7% and 17% of cases respectively at T1. Facial nerve paralysis and Horner's syndrome remained present in 29% (5/17) and 36% (5/14) respectively at T60. One dog developed facial nerve paralysis, Horner's syndrome, and a descemetocele that required a conjunctival flap at T14. Overall, 64.2% of surgeries lead to at least one ocular or neuro-ophthalmic complication post-operatively. ***Clinical Relevance*** Cats and dogs undergoing TECABO and VBO procedures should have thorough ophthalmic examinations pre- and postoperatively, as ocular and neuro-ophthalmic complications are common in these patients.
Keywords for abstract:	TECABO VBO aural disease facial nerve paralysis Horner's syndrome

Title of abstract:	**COMPARISON OF TWO ACTIVITY MONITORS IN DOGS**
Authors:	Hilborn EC, Rudinsky A, Kieves N
Abstract:	INTRODUCTION: The FitBark® a is a smartphone linked 3-D accelerometer that collects spatial and movement data. To date its accuracy has not been assessed. Therefore, the objective of this study was to compare the FitBark® device with a previously validated accelerometer (Actical)b to determine its accuracy as an activity tracker. MATERIALS & METHODS: Dogs were fitted with a neck collar with an Actical and FitBark® on it. Dogs wore the devices continuously for one week. Dogs were walked on the same one-mile paved trail once during that week. Step data was evaluated for the entire week, the day of the mile walk, the hour the walk occurred, and the time of the walk itself. Correlations between study variables were measured. RESULTS: Twenty dogs were enrolled. For the set one-mile walk, r=0.75, for the hour the walk occurred in r=0.71, for the day of walk r=0.61, and for the week the walk occurred in r=0.90. R2 values were 0.55 for the walk itself, 0.50 for the hour of the walk, 0.37 for the day of the walk, and 0.81 for the week. DISCUSSION/CONCLUSION: The Actical and FitBark® had a very strong positive correlation for the week and a strong positive correlation for other time periods. This suggests that the FitBark® can be used to evaluate the activity of dogs with some accuracy. Additional studies are needed to further evaluate the ability of the FitBark® to correlate with changes in pet. ACKNOWLEDGEMENTS: There was no proprietary interest or funding provided for this project.
Keywords for abstract:	a FitBark® 2, FitBark, Kansas City, MO (www.fitbark.com) b Animal Actical, Starr Life Sciences Corp., Oakmont, PA.

Title of abstract:	**EFFECTIVENESS OF ACETAMINOPHEN AND MELOXICAM IN REDUCING PYREXIA AND INFLAMMATION IN HORSES INDUCED WITH LPS**
Authors:	B. Jacobs, A. Samuels, P. Kelly, C. Bartish, A. Kamr, R. Toribio. Dept. Of Veterinary Clinical Sciences
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.
Keywords for abstract:	Pyrexia, NSAID, acetaminophen, meloxicam, inflammation, endotoxemia, horses

Title of abstract:	**UNILATERAL NEPHRECTOMY IN DOGS IS ASSOCIATED WITH A HIGH RATE OF INTRAOPERATIVE AND POSTOPERATIVE COMPLICATIONS**
Authors:	<u>C. Johnson</u>, H. Piegols, J. Lapsley, L. Selmic. Of Veterinary Clinical Sciences
Abstract:	Unilateral nephrectomy can be indicated for renal disease in dogs. Intraoperative and postoperative complications have been poorly described. The objective of this study was to report the incidence of complications in dogs undergoing nephrectomy for renal disease and assess factors associated with the development of chronic kidney disease (CKD). Medical records of dogs undergoing nephrectomies for renal disease were reviewed for intra- and postoperative complications. Long-term follow-up was obtained via client telephone interview or referring veterinarian medical records. A Fisher exact test was used to assess the relationship between preoperative measurement of glomerular filtration rate (GFR), postoperative acute kidney injury (AKI), and non-steroidal anti-inflammatory drug (NSAID) administration with long-term development of CKD. 69 dogs were included. Intraoperative complications occurred in 31/69 dogs and postoperative complications occurred in 29/69 dogs, with 7/69 dogs euthanized due to severe postoperative complications. AKI was diagnosed in 12/69 dogs. Long-term follow-up was available for 53 dogs with 24/53 dogs developing CKD. An abnormal GFR was not associated with the development of CKD. Postoperative AKI and NSAID administration were not statistically associated with the development of CKD. Nephrectomy is associated with high rates of intraoperative and postoperative complications CKD was diagnosed in almost 50% of all dogs with long-term follow-up. Limitations of this study were related to the retrospective design and small case number.
Keywords for abstract:	Nephrectomy Complications Kidney Surgery

Title of abstract:	**EFFECTS OF MINING RECLAMATION ON HEPATIC AND SERUM MINERAL VALUES OF WHITE-TAILED DEER IN OHIO**
Authors:	L. Kellow, P. Joyner, P. Dennis, M. Flint. Dept. of Veterinary Preventative Medicine, The Wilds, and Cleveland Metro Parks
Abstract:	Surface mining or strip mining involves excavating soil up to 200m in depth after stripping vegetation, which changes the landscape and alters the soil quality and properties. While the process of reclamation mitigates some of these processes, there is the potential for long-term effects on soil composition and quality, water quality, and diversity of vegetation. White-tailed deer eat a combination of browse, forbs, grasses, corn, and other plants in Ohio, which makes the species a good indicator of vegetation quality and diversity on mining reclaimed land. Previous studies have evaluated baseline hepatic minerals of white-tailed deer, finding that zinc, copper, and barium differed between grazing sites and that mineral concentrations differed depending on reproductive status. There have been no studies to date evaluating hepatic and serum mineral concentrations of white-tailed deer on mining reclamation land and the potential differences between deer from the broader population. In addition, mineral requirements for free-ranging wildlife are underrepresented in the literature, with unknown health implications for these species. This is of particular One Health importance, given the utilization of White-tailed deer as a key hunting species in Ohio. The objective of this study is to continue previous research into the effects of strip mining and mining reclamation by evaluating the effects on the health and nutrition of free-ranging wildlife by assessing and comparing hepatic mineral values, serum mineral values, and baseline health status in White-tailed deer grazing on and off mining reclaimed land.
Keywords for abstract:	white-tailed deer mining reclamation mineral values surface mining One Health

Title of abstract:	**SURVEY OF VETERINARIANS TO EVALUATE TRENDS IN THE TREATMENT APPROACH FOR NONOBSTRUCTIVE FELINE IDIOPATHIC CYSTITIS**
Authors:	<u>LR Krause</u>, E Li, ML Lilly, J Byron, E Cooper, J Quimby. Department of Veterinary Clinical Sciences, The Ohio State University, Columbus, OH, USA
Abstract:	**Objectives** The goal of this study was to gather information on treatment approach and trends for treatment of nonobstructive feline idiopathic cystitis (FIC). **Methods** An internet-based survey of veterinarians was conducted focused on outpatient treatment approaches for cats that are stable, not obstructed, and that exhibit lower urinary signs suspected to be due to FIC, where other causes (e.g. urolithiasis, urinary tract infection, other) have been ruled out. **Results** A total of 606 veterinarians submitted complete surveys for inclusion. Respondents reported that they gathered historical information ≥75% of the time about feline stressors (542/606, 89%), resource set-up (466/606, 77%), and diet (552/606, 91%) when evaluating cats with FIC. Only 31% of respondents (187/606) asked about daily human/cat interaction ≥75% of the time, with 69% (419/606) of veterinarians inquiring about this information 50% of the time or less. Top treatments selected for acute presentations of FIC were analgesics (537/606, 89%), modified litter box management (435/606, 72%), and synthetic feline pheromones (422/606, 70%). Top treatments selected for chronic FIC management were prescription diets (519/606, 86%), modified litter box management (508/606, 84%), and environmental enhancements (493/606, 81%). Owner compliance and expectations were selected as treatment barriers by 81% (486/599) and 62% (372/599) of respondents, respectively. Most veterinarians had never recommended rehoming a cat (382/606, 63%) or euthanasia (547/606, 90%) due to difficulties managing FIC. **Conclusions and relevance** Treatment approach for nonobstructive FIC appears to be multimodal and recommendations vary between acute and chronic presentations. An area of opportunity is client communication and education, which may improve owner compliance and help set appropriate expectations. The importance of human/cat interaction as a management strategy appears under-emphasized.
Keywords for abstract:	idiopathic cystitis FIC survey nonobstructive lower urinary tract FLUTD

CR-11

Title of abstract:	**EXTRAMURAL COMPRESSION AND DORSOVENTRAL NARROWING OF THE LEFT PRINCIPAL BRONCHUS IN LATERAL RECUMBENCY RELATED TO CANINE BODY CONFORMATION**
Authors:	A. Leffler, E. Hostnik. Department of Veterinary Clinical Sciences: Diagnostic Imaging & Radiology.
Abstract:	Tracheal and bronchial narrowing are identified in routine radiography and may implicate airway degeneration. Focal principal bronchial narrowing due to extramural compression has been described while in sternal recumbency (Cote *et. al*.). Authors hypothesize: 1) radiographs overestimate airway size compared CT, 2) bronchi are smaller when in dependent positioning, 3) the LPB height to width (H:W) will be smaller than the right principal bronchus (RPB) H:W while in lateral recumbency, and 4) there is a positive correlation of LPB H:W and thoracic H:W. Dogs received three view thoracic radiographs and two CTs (right lateral and left lateral positioning). All measurements were completed in right lateral recumbency and left lateral recumbency for radiographs and CT. The principal bronchi, descending aorta, and thorax were measured on laterally positioned CTs as outlined by Cote et al. Non-parametric paired analyses compared modalities and positioning. Pearson correlations assessed continuous measurements of thoracic conformation H:W and the principal bronchi H:W. 20 dogs were included. DV diameter measurements of the principal bronchi did not differ between radiographs and CT. Lobar bronchi are significantly smaller when in the dependent position for multiple lobes. There is no significant difference in HU for the accessory lung lobe between right and left lateral positions. The LPB H:W ratio was significantly smaller than the RPB H:W ratio data. Dogs with lower thoracic H:W ratio positively correlates to DV flattening of the LPB while in lateral recumbency. DV narrowing of LPB can be an extramural compression rather than presumed to be solely bronchomalacia.
Keywords for abstract:	Canine Bronchomalacia Extramural Compression Bronchus Radiography CT Thoracic Conformation Narrowing

CR-12

Title of abstract:	Utility of FitBark to Monitor Activity in Obese Dogs Undergoing a Structured Weight Loss Program
Authors:	H. Lenis, N.J. Nealon, A.J. Rudinsky, H. Klein, V. Parker, J.A. Winston
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.
Keywords for abstract:	Canine Obesity Weight Loss Activity monitors Quality of Life Mobility

CR-13

Title of abstract:	The Cat Chronic Kidney Disease Caregiver Assessment, Reflection on Experience (Cat CKD CARE) Study
Authors:	L. Lim, J. Quimby. Dept. of Veterinary Clinical Sciences, College of Veterinary Meidicne, The Ohio State University, Columbus, OH S. Caney. Vet Professionals, Midlothian Innovation Centre, Roslin, UK
Abstract:	**Background:** Caregiver burden has been documented in management of chronic diseases in companion animals, but it has not yet been explored in its impact on feline chronic kidney disease (CKD). **Hypothesis/Objectives:** To investigate caregiver burden in feline CKD using the abbreviated Zarit Burden Interview (ZBI) adapted and validated for use in pets. We hypothesized that ZBI scores would be significantly higher in the later stages of feline CKD indicating higher caregiver burden. **Animals:** Survey completed by caregivers of CKD cats IRIS stages 1-4 (n=180). **Methods:** Descriptive survey study. Caregivers managing a CKD cat or having previous recent experience were recruited through social media to anonymously participate in the online survey available through u.osu.edu/felinekidneyresearch/care-study/. The abbreviated ZBI was incorporated into the survey to validate assessment of caregiver burden. **Results:** Caregiver burden was significantly higher in IRIS Stages 1&2 (median = 14.00, range = 40.00) versus IRIS Stages 3&4 (median = 18.00, range = 43.00) in CKD cats (P = 0.0098). Caregiver burden was significantly higher in veterinary clients who rarely or never shared (median = 19.00, range = 43.00) versus those who regularly shared (median = 14.00, range = 36.00) care burden (P = 0.0137). Those who spent 30 minutes or longer (median = 19.00, range = 42.00) had significantly higher caregiver burden versus those who spent less than 30 minutes (median = 11.50, range = 40.00) to care for their CKD cat (P = <0.0001). Caregiver burden significantly increased when 4 or more medications were regularly given versus 3 or fewer (P = <0.0001). **Conclusions and Clinical Importance:** Significant caregiver burden exists in feline CKD.
Keywords for abstract:	Cat CKD CARE Study Caregiver burden CKD cats Chronic kidney disease cats Feline CKD Feline chronic kidney disease CKD IRIS stage Abbreviated ZBI Abbreviated Zarit Burden Interview

CR-14

Title of abstract:	**COMPARISON OF ANESTHETIC PROTOCOLS FOR ENHANCING HEALTH ASSESSMENT WELFARE AND HEMOLYMPH COLLECTION SUCCESS IN A FRESHWATER MUSSEL SPECIES *Elliptio insulsa.***
Authors:	R. Long and M. Flint. Dept of Veterinary Preventive Medicine.
Abstract:	Freshwater mussels provide significant ecosystem services that support the health of freshwater systems. However, wild populations continue to be plagued by pressures including invasive bivalve species and environmental degradation. Mass mortality events have also been documented in relatively pristine systems, highlighting the need to identify other relevant health variables in declining populations and expand the currently limited diagnostic and health assessment capabilities in freshwater mussel taxa. Hemolymph collection techniques have been described in freshwater mussels, but these methods involve prying apart the shells of awake mussels, which can be challenging and involves risk of significant injury and stress to these animals. Anesthetic techniques have been described in marine bivalves, but minimal literature exists regarding protocols in freshwater taxa. This work addresses that literature gap and elevates freshwater bivalve health assessment welfare by evaluating two anesthetic protocols frequently used in marine bivalves (magnesium chloride and MS-222) in freshwater mussel species *Elliptio insulsa*. We report that a magnesium chloride bath protocol (50g/L) generally well-tolerated in marine bivalves was poorly tolerated by this freshwater mussel species. MS-222 bath protocols have been reported to induce minimal to variable effects in marine bivalves, but did produce subjectively working anesthesia in *E. insulsa* at 500mg/L. Both protocols decreased the force required to pry open shells and increased hemolymph collection success compared to awake controls. These findings highlight that freshwater and marine bivalves may respond differently to similar anesthetic protocols and demonstrate the value of anesthesia for freshwater bivalve welfare and diagnostic sampling success during health assessments.
Keywords for abstract:	Anesthesia Freshwater mussels Hemolymph collection Invertebrate medicine Invertebrate welfare

Title of abstract:	**LOW-FIELD MRI OF BONE MARROW-TYPE LESIONS IN THE MIDDLE PHALANX OF SPORT HORSES**
Authors:	S. March, R. Urion, R. Mitchell, R. Edwards, C. Cullen, E. Hostnik. Department of Veterinary Clinical Sciences (OSU), Fairfield Equine Associates, and C3 Equine Veterinary Services. 3 C3 Equine Veterinary Services, Westborough, MA
Abstract:	INTRODUCTION: Hyperintense signal within P2 on a T2-weighted (T2w) fat-suppressed sequence is a common finding on equine distal limb MRI. "Bone edema-like lesions" have been reported in few case reports/series and the significance of these lesions remains unclear (Olive et al., 2009; Helweg et al., 2014). This retrospective, cross-sectional study aims to describe low-field MRI P2 bone edema-like lesions in a large population of sports horses. MATERIALS & METHODS: Standing low field (Hallmarq© 0.27 T) MRIs between 2006 and 2017 with P2 edema-like lesions were reviewed by two boarded radiologists and a resident for presence of P2 T2w STIR hyperintense signal. The point of maximum intensity, lesion extension, presence of sclerosis, and presence of phase cancellation artifact were then assessed. RESULTS: A total of 53 horses and 74 MRI studies were included in the study. The majority (52/56) of lesions were distributed in the dorsodistal aspect of P2 with 25/56 central, 17/56 medial, and 14/56 lateral distributions. 52/56 of lesions demonstrated phase cancellation artifact and only 13/56 demonstrated imaging characteristics consistent with sclerosis. The P2 lesions 12/14 fully and 2/14 partially resolved on follow-up examination. DISCUSSION/CONCLUSION: The most common distribution of P2 bone marrow edema-like lesions was the dorsodistal aspect of P2. These lesions commonly demonstrate phase-cancellation artifact and are uncommonly accompanied by sclerosis.
Keywords for abstract:	MRI, horse, bone edema-like lesions, middle phalanx, diagnostic imaging

Title of abstract:	**FECAL AND URINE MICROBIOTA OF COMPNAION DOGS VARY BY BREED AND SEX**
Authors:	Jordan M. Mason,[1] Zachary J. Lewis,[1] Andreas Eleftheriou,[1] Christopher Madden,[1] Sheryl S. Justice,[2] Adam Rudinsky,[3] Jessica Hokamp,[4] Deepika Dhawan,[4] Brian Husbands, [4] Deborah Knapp,[4] Vanessa L. Hale[1]
Abstract:	Recent studies, across host species, have demonstrated a role for host-associated microbiota in cancers, metabolic disorders, urinary tract diseases, and response to therapy. In companion dogs, notable differences in disease incidence occur across breed; for example, Scottish Terriers have a twenty-fold higher risk of developing urothelial carcinoma compared to mixed-breed dogs. A few early studies in dogs have suggested that the gut microbiota may vary according to breed and age, but additional research is necessary to establish stronger links between breed, microbiota, and disease. The healthy urine microbiota remain generally understudied. Here, we analyzed the fecal and urine microbiota of healthy dogs to characterize the impacts of age, sex, and breed on the host-associated microbiota. We collected mid-stream free catch urine and fecal samples from 59 dogs: 32 Scottish terriers and 27 dogs comprising 32 other breeds. 27 dogs were male (8 intact) and 32 were female (25 Intact). DNA was extracted from samples and analyzed via 16s rRNA amplicon sequencing. Sequence processing, diversity analyses, and statistical testing were performed using QIIME2 and Prism. Fecal microbiota differed according to sex: males had significantly lower diversity than females (p=0.0017). The fecal microbiota of Scottish Terriers were significantly more diverse than those of other breeds (p=0.0068). The urine microbiota differed significantly in composition by sex (p=0.015). Additionally, the urine microbiota composition of Scottish Terriers were significantly different from those of other breeds (p=0.019). No differences were found in diversity or composition of the fecal or urine microbiota by age. Our results demonstrate that, as in human studies, there are interactions between sex and the microbiota in companion dogs. We also report that Scottish Terriers differ from other breeds in urine and fecal microbiota diversity and composition, warranting further investigation of the links between breed-related disease and functional differences and the host-associated microbiota.
Keywords for abstract:	Microbiota, Breed, Age, Sex, Urine, Fecal

CR-17

Title of abstract:	**EFFECT OF COMPETITION SURFACE ON COURSE SPEED IN AMERICAN KENNEL CLUB AGILITY TRIALS**
Authors:	Mazzeo G.,1 Shoben A.B.,2 Kieves N.R.,3 Kulchytsky K.S.,1 Szilvas A.M.,1 Pechette Markley A.3
Abstract:	INTRODUCTION: Canine agility competitions are run on a variety of surfaces. Surface composition has been correlated with speed and injury risk in humans and equids, but has not been evaluated in the context of dog agility. The objective of this study was to evaluate types of surfaces found in agility competition facilities and estimate correlations between surface type and speed. We hypothesized that artificial turf would be the fastest and sand slowest. We also hypothesized that surface effects on speed would vary by dog height. MATERIALS & METHODS: Data on all qualifying AKC agility runs from 2012-2022 were obtained from the AKC Event Search & Results webpage. Facilities were contacted by phone, email, or both to obtain information about surface. Linear mixed models were used to estimate differences in speed by surface category, accounting for correlation among runs from the same dog. RESULTS: Surface information was available for 136 of 858 facilities. Differences in speed by surface varied by jump height ($p<0.0001$), with artificial turf the fastest surface across all heights. Shorter dogs experienced a greater decrease in speed on dirt than taller dogs, while the opposite was true on grass. DISCUSSION/CONCLUSION: These effects of surface on speed are likely due to the mechanical differences in the surfaces and are consistent with findings in the human literature. Future studies should consider dog height when planning biomechanical studies on the impact of surface on agility dog performance and injury.
Keywords for abstract:	Agility Canine Sports Medicine and Physical Rehabilitation American Kennel Club Canine Agility

CR-18

Title of abstract:	**AGE-ASSOCIATED CHANGES IN THE GLOBAL, UNTARGETED SERUM METABOLOME OF HEALTHY CLIENT-OWNED DOMESTIC CATS**
Authors:	N.J. Nealon, S. Summers, J. Quimby, and J.A. Winston.
Abstract:	With medical advances, the cat population is aging. To distinguish healthy aging from disease, an improved understanding of age-related metabolism is indicated. Metabolomics, which profiles biomolecules, is routinely used for biomarker discovery. However, with compositional datasets, there is no ideal statistical approach to use when discriminating between study populations. To understand the impact of aging, we compared the global, untargeted serum metabolome of clinically healthy young adult versus mature/senior cats using three multivariate approaches. Healthy, sterilized (male and female) client-owned cats (n = 7 young adult, aged < 7y; n = 13 mature/senior, aged 7y+) were recruited from Colorado and Oregon State Universities. Hematologic, chemistry, and urinalysis profiles were within normal limits for all cats. The serum metabolome was established by Metabolon© using ultra-high performance liquid chromatography tandem mass-spectrometry. Metabolite abundances were compared between young and mature/senior cats using three statistical approaches: A Wilcoxon test, partial least squares regression discriminant analysis variable importance projections (VIP), and random forest mean decrease accuracies (MDA). Metabolites were called meaningful contributors to age differences based on the following criteria: p <0.05, and/or VIP >1, and/or MDA > 0.001094. In total, 914 metabolites were detected, including 209 metabolites differentially abundant between young versus senior cats. These included 37 amino acids, 2 carbohydrates, 13 cofactors/vitamins, 75 lipids, 7 nucleotides, 8 peptides, 37 xenobiotics, and 30 unknown metabolites. A total of 183 metabolites were meaningful contributors to age differences in one model, 20 in two models, and 6 in all three models. These changes support our hypothesis that aging influences the healthy feline serum metabolome. Given that meaningful contributors to age difference varied with the statistical method used, the analysis method should also be considered when discriminating between life stages. These approaches merit further evaluation for their applicability in discriminating between health and disease in aging cats.
Keywords for abstract:	Untargeted Metabolomics Aging and Gerontology Feline Medicine Biomarker Discovery

CR-19

Title of abstract:	**THE EFFECT OF FEEDING ON URINE AMMONIA LEVELS IN CATS WITH AND WITHOUT CKD**
Authors:	Anna Panyutin[1], Lina Lim[1], Ashlie Saffire[2], Autumn Harris[3], Jessica Quimby[1] [1] Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH [2] Faithful Friends Veterinary Clinic, Dublin, OH [3] Department of Small Animal Clinical Sciences, College of Veterinary Medicine, University of Florida, Gainesville, FL
Abstract:	**Background:** Impaired ammonia excretion plays a role in the pathogenesis of metabolic acidosis in CKD, and may have prognostic value. Gold standard evaluation involves measurement of ammonia excretion as urine ammonia-to-creatinine ratio (UACR). The influence of eating on UACR is unknown. **Hypothesis/Objectives:** To investigate the effect of fasting vs feeding on urine ammonia levels in cats with and without CKD. We hypothesized that UACR would increase after feeding and this effect would be blunted in cats with CKD. **Animals:** Cats with stable IRIS stages 1-4 CKD (n=13) and healthy cats (n=10). **Methods:** Randomized, prospective cross-over study. CBC, serum biochemistry, T4, and urinalysis were performed in all cats to confirm health status. Urine was collected at two visits approximately one week apart; once 2-3 hours post meal, and once fasted. Urinary ammonia and creatinine concentrations were measured using commercially available assays and used to calculate UACR. **Results:** UACR was significantly lower in fed (median = 0.77, range 0.11-6.59) versus fasted state (median = 2.55, range 0.49-9.58) in CKD cats ($P = 0.01$). There was no difference in control cats (fed median = 4.305, range 0.19-11.54; fasted median 4.98, range 0.65-10.81) ($P = 0.49$). There was a significant negative correlation between serum creatinine and UACR in both the fed ($r = -0.84$; $P = 0.0006$) and fasted state ($r = -0.92$; $P <0.0001$). **Conclusions and Clinical Importance:** Prandial state affects UACR in cats with CKD, and should be kept consistent in longitudinal sampling.
Keywords for abstract:	Chronic kidney disease Metabolic acidosis Urine ammonia

CR-20

Title of abstract:	**THE EFFECT OF PORUS® ONE ON UREMIC TOXIN CONCENTRATIONS IN CATS WITH CHRONIC KIDNEY DISEASE**
Authors:	<u>R. Paschall</u>, J. Quimby, B. Lourenço, S. Summers, and C. Schmiedt
Abstract:	Background: Serum uremic toxins markedly increase in cats with chronic kidney disease (CKD) and can have deleterious consequences. Porus® One is an oral adsorbent that binds uremic toxin precursors in the gut. Objectives/Hypothesis: Assess the effect of Porus® One on serum uremic toxin concentrations in cats with CKD. Animals: 14 purpose-bred cats (13 IRIS Stage 2, 1 IRIS Stage 3). Methods: Prospective cross-sectional study utilizing cats with remnant kidney model-induced CKD. Cats were treated with standard of care (Days –56 to 0) and then 500 mg Porus® One PO q24h (Days 0 to 56) in food. Serum concentrations of indoxyl sulfate (IDS) and p-cresyl sulfate (pCS) were measured (Days -56, -28, 0, 28, and 56) by LC/MS/MS. Doppler blood pressure (DBP), complete blood cell count, biochemistry, urinalysis, and urine protein: creatinine ratio were measured (Days -56, 0, and 56). Uremic toxin concentrations and clinicopathologic variables were compared before and after administration of Porus® One. Results: Averaged serum IDS and pCS concentrations were significantly decreased after administering Porus® One (Day 28 and 56) relative to averaged baseline (day –56, -28, and 0) concentrations. Indoxyl sulfate decreased from 1,922 ng/ml to 1,592 ng/ml ($p = 0.03$). p-Cresol sulfate decreased from 11,487 ng/ml to 6,956 ng/ml ($p = 0.005$). Doppler BP significantly decreased ($p = 0.03$), and serum bicarbonate concentrations significantly increased ($p = 0.03$) after administering Porus® One. Serum creatinine concentrations were significantly increased at Day 56 relative to Day -56 ($p = 0.002$) but not relative to Day 0. Conclusions and clinical importance: Porus® One decreased uremic toxin concentrations despite mild progression of disease.
Keywords for abstract:	Chronic Kidney Disease Porus One Uremic Toxins

CR-21

Title of abstract:	**POLARIZATION-SENSITIVE OPTICAL COHERENCE TOMOGRAPHY FOR POSITIVE TUMOR IDENTIFICATION FOLLOWING SURGICAL EXCISION OF CANINE SOFT TISSUE SARCOMAS**
Authors:	N. Patel, R. Jennings, G. Fontes, M. Biggo, A. Erickson, J. Dornbusch, N. Jurcak, J. Santana Mignucci, L. Selmic LE. Depts. of Veterinary Clinical Sciences and Veterinary Biosciences
Abstract:	Polarization sensitive optical coherence tomography (PS-OCT) uses birefringence of biologic tissues to illustrate organization of subcellular collagen. The preceding mode of spectral domain OCT (SD-OCT) has been used successfully to identify canine soft tissue sarcomas (STS) from normal tissues. This study's aims were to (1) compare histologic and PS-OCT features of STS and other normal surgical margin tissues, and (2) compare the diagnostic accuracy of paired SD-OCT/PS-OCT imaging to SD-OCT imaging alone in positive tumor identification of canine STS. We hypothesize that histologic features will be agreeable with PS-OCT features and that paired SD-OCT/PS-OCT imaging will be superior compared to SD-OCT alone in discriminating STS from non-cancerous tissue. Forty dogs were enrolled in this prospective study. All STS specimens were imaged post-operatively using the Thorlabs Telesto PS-OCT system prior to sectioning for histopathologic evaluation. Six blinded observers were trained in SD-OCT and PS-OCT tissue type identification, and were subsequently provided with a data set of SD-OCT and SD-OCT/PS-OCT images and videos. Each image was assigned a grade of 1 (no cancer present) to 4 (cancer present). The median sensitivity and specificity of SD-OCT imaging alone were 96.7% and 100%, respectively. The median sensitivity and specificity of paired SD-OCT/PS-OCT imaging were 93.3% and 100%, respectively. Although SD-OCT/PS-OCT may not have proved to be superior to traditional SD-OCT imaging, our results still suggest high diagnostic accuracy with paired imaging.
Keywords for abstract:	Optical coherence tomography Soft tissue sarcoma

Title of abstract:	**ACCURACY AND FEASIBILITY OF POLARIZATION SENSITIVE OPTICAL COHERENCE TOMOGRAPHY IN ASSESSING SURGICAL MARGINS FOR CANINE SKIN CANCER INTRAOPERATIVELY**
Authors:	S. Ramirez, C. Johnson, G. Fontes, R. Jennings, J. Lapsley, H. Piegols, L. Selmic Depts. Of Veterinary Biosciences and Veterinary Clinical Sciences, 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. Fifty-seven dogs with 76 different skin tumors were prospectively enrolled: 27 soft tissue sarcomas (STS), 44 mast cell tumors (MCTs), and 4 benign tumors. All dogs underwent surgical removal of skin tumor which was imaged by one of two trained clinicians, intraoperatively. Areas suspicious of cancer extending to surgical margins were inked and samples were placed in formalin for fixation. PS-OCT surgical margin assessment was compared to PS-OCT interpretation. Clinicians identified MCT, STS, and benign tumors at the surgical margins using PS-OCT in 12/44 (27.3%), 14/27 (52%), and 2/4 (50%) of specimens, respectively. Accuracy in PS-OCT assessment of surgical margins differed between the two clinicians. Clinician A identified incompletely excised MCT, STS, and benign tumor near the surgical margin with a sensitivity of 85.7%, 100%, 100% and specificity of 92.3, 100%, 50%, respectively. Clinician B identified incompletely excised MCT, STS, and benign tumor near the surgical margin with a sensitivity of 28.6%, 66.7%, 100% and specificity of 88.2%, 71.4%, 100%, 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.
Keywords for abstract:	PS-OCT Skin tumors Surgical margins

Title of abstract:	**THE LONG-TERM *IN VITRO* BACTERIAL VIABILITY OF LYOPHILIZED AND FROZEN CANINE AND FELINE FECAL MICROBIAL TRANSPLANTATION PRODUCTS**
Authors:	NK Randolph[1,2], D Diaz-Campos[1], J van Balen[1], NJ Nealon[1,2], J Rowe[1,2], L Wetzel[1,2], JA Winston[1,2]
Abstract:	Fecal microbial transplantation (FMT) is the transfer of feces from a healthy donor into the gastrointestinal tract of a diseased recipient to confer a health benefit. The mechanism in which FMT confers a health benefit is linked to the viability and engraftment of microbes and the correction of dysbiosis. Our study aims to quantitate the colony forming units (CFUs) of microbes within canine and feline FMT products using aerobic and anaerobic culture-based techniques. Three screened canine and feline fecal donors each provided three separate fresh fecal samples for processing. Fecal processing techniques include unprocessed and three double centrifuged fecal slurries with the following additives: 0.9% saline, 0.9% saline with 10% glycerol, and 0.9% saline with 25% maltodextrin and trehalose (M:D). FMT products were aliquoted for long-term storage at -20C, -80C, and lyophilized for storage at room temperature. Timepoints for CFU/gram quantitation include baseline, 1, 3, 6, and 12 months. Canine lyophilized products preserved with M:D yielded significantly greater total CFUs compared with other lyophilized FMT products ($p<0.01$). For canine products frozen at -20C, FMT preserved with glycerol and M:D yielded significantly more CFUs than other products ($p<0.01$). All canine FMT products, except 10% glycerol frozen at -80C, exhibited a significant decrease in total CFUs over the 12-month period ($p<0.01$). Under all storage conditions, feline FMT products preserved with M:D exhibited the lowest mean $\log_{10}$ drop over 12-months. All feline FMT products, except 10% glycerol and 25% M:D frozen at -80C, exhibited significant decreases in total CFUs over 12-months ($p<0.01$). For all products, storage at -80C yielded significantly more total CFUs than storage at -20C ($p<0.01$). This study will provide clinicians with evidence for producing and storing FMT in their own practice. Further research is needed to determine whether increased CFUs translates to improved microbe engraftment and ultimately improved clinical outcomes.
Keywords for abstract:	Fecal microbiota transplant canine microbiome feline microbiome gut bacterial viability

Title of abstract:	**BILE ACID DYSMETABOLISM IN FELINE CHRONIC KIDNEY DISEASE IS ASSOCIATED WITH 26 *PEPTACETOBACTER HIRANONIS* VARIANTS**
Authors:	J.C. Rowe[1], S. C. Summers[2], J. M. Quimby[1], J. A. Winston[1] [1]Department of Veterinary Clinical Sciences, The Ohio State University [2]Department of Clinical Sciences, Oregon State University
Abstract:	Background – The microbial-derived secondary bile acid (SBA) ursodeoxycholic acid (UDCA) is decreased in chronic kidney disease (CKD) cats. *Peptacetobacter hiranonis* is the only described SBA producing microbe in cats. Hypothesis/Objectives – Fecal bile acid dysmetabolism occurs in CKD cats, corresponding with reduced abundance of *P. hiranonis*. Animals – Healthy (n = 6) and CKD (n = 28) client-owned cats. Methods – Prospective, cross-sectional study. Targeted liquid chromatography and tandem mass spectrometry metabolomics and 16S rRNA gene amplicon sequencing of fecal samples. Silva taxonomy and NCBI nucleotide BLAST were utilized. Results – Bile acid dysmetabolism characterized by <50% SBAs was present in 8/28 CKD and 0/6 healthy cats. Beta-diversity significantly differed between cats with <50% SBAs and >50% SBAs (Bray-Curtis PERMANOVA $p < 0.0001$). 26 amplicon sequence variants (ASVs) with >97% nucleotide identity to *P. hiranonis* 16S rRNA gene sequence were identified. The combined relative abundance of these 26 ASVs was significantly reduced (median 2.1%) in CKD cats with <50% SBAs compared to CKD cats with >50% SBAs (median 13.9%, Kruskal-Wallis FDR adjusted $p = 0.0002$) and healthy cats with >50% SBAs (median 15.5%, Kruskal-Wallis FDR adjusted $p = 0.0112$). Conventional qPCR primers for *P. hiranonis* would have identified 23/26 (88.4%) of the ASVs. Conclusions and clinical importance – Fecal bile acid dysmetabolism characterized by <50% SBAs occurs in CKD cats. The dysmetabolism is partially explained by reduced abundance of *P. hiranonis*. Currently, methodologies to detect *P. hiranonis* capture similar microbial genetic signatures, but do not provide information regarding functional genetic potential to produce SBAs.
Keywords for abstract:	Feline gut microbiome CKD Microbial-derived bile acids *P. hiranonis* Multi-omics

CR-25

Title of abstract:	**COMPUTED TOMOGRAPHIC FEATURES OF PRESUMED NORMAL HEPATIC LYMPH NODES IN 87 DOGS**
Authors:	J. Santana Mignucci, G. Habing, and E. Green. Depts. of Veterinary Clinical Sciences and Veterinary Preventive Medicine
Abstract:	The hepatic lymphocentrum is a group of lymph nodes located near the porta hepatis. This lymphocentrum usually consists of two nodes, circular to ovoid in shape, located on either side of the portal vein. Previous retrospective studies have described abdominal lymph nodes, including hepatic lymph nodes, on computed tomographic (CT) examinations in a small number of dogs. The purpose of this retrospective study was to describe the number, location, height, width, length, x-ray attenuation (Hounsfield units, HU) of presumed normal hepatic lymph nodes in dogs on abdominal CT scans, to determine if the size of the lymph nodes is correlated to body weight, and to determine a cutoff value for a ratio of lymph node height to aortic diameter that may indicate lymphadenomegaly. Abdominal CT scans of 87 dogs with presumed normal hepatic lymph nodes were included. No cytologic or histopathologic evaluation was performed in any patient. In our presumed normal population, 95% of the patients had a lymph node height to aortic diameter ratio of less than 0.9.
Keywords for abstract:	hepatic lymph nodes computed tomography dog

Title of abstract:	**Evaluation of Optical Coherence Tomography for Identification of Lymph Node Metastases in Canine Oral Malignant Melanomas**
Authors:	Y.-F. Shen[1], G. Fontes[1], C. Johnson, H. Weaver[1], R. Jennings[2], J.M. Lapsley[1], and L.E. Selmic[1] [1]Department of Veterinary Clinical Sciences [2]Department of Veterinary Biosciences
Abstract:	Canine oral malignant melanoma (OMM) has a high potential for lymph node (LN) metastasis. The standard of care involves removal of the primary tumor and regional LNs regardless of metastatic status, but results in a high complication rate. Optical coherence tomography (OCT) is a rapid, noninvasive imaging modality used for intraoperative identification of LN metastasis in humans but not yet translated to canines. The purpose of this study was to (1) correlate normal and metastatic LN OCT imaging features with corresponding histopathology and (2) evaluate the diagnostic accuracy of OCT imaging in identifying metastatic LNs for intraoperative utilization. Dogs with OMM were enrolled and an indirect CT lymphangiogram was performed to identify the sentinel LN. Then surgery was performed to remove the primary tumor and regional LNs. The excised LNs were imaged with OCT and submitted for histopathology. OCT images from the first 5 dogs were compared to digitized histopathology slides to develop descriptive characteristics and a training set for metastatic or normal LNs. The next 15 dog's images were used to generate a test set for observers to evaluate diagnostic accuracy. On OCT images, normal LNs have high intensity grainy lymphoid tissue with striations, clear rounded capsules, and organized adipose tissue. Intensity decreases from superficial to deeper layers with a "comet-like" tail. Lymphoid tissue of metastatic LNs have a diffuse smooth appearance with a loss of striations and intensity, indistinct capsule borders, and blurry disorganized adipose tissue. Reactive lymph nodes have more distinct semi-circular capsules with associated lymphoid hyperplasia with organized or disorganized adipose tissue. Our results indicate a difference in image characteristics between normal and metastatic LNs on OCT imaging. These characteristics, along with further evaluation of observer diagnostic accuracy, may validate intraoperative use of OCT imaging for detection of LN metastasis to reduce patient morbidity.
Keywords for abstract:	Oral Malignant Melanoma Metastasis Lymph Node OCT Imaging

Title of abstract:	**ANTIBIOTIC EXPOSURE AS A RISK FACTOR FOR CHRONIC ENTEROPATHY IN DOGS**
Authors:	<u>A. C. Kavanagh</u>, V. J. Parker, J. A. Winston, A. J. Rudinsky
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 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 IBD 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.
Keywords for abstract:	Chronic Enteropathy Dysbiosis Antibiotic Exposure

Title of abstract:	**INCREASED DIETARY FIBER INTAKE IMPROVES FECAL AND CLINICAL ACTIVITY SCORES IN DOGS WITH CHRONIC ENTEROPATHIES**
Authors:	Isabel A. Muirragui, Rachel Woodfint, Adam J. Rudinsky, Jenessa A. Winston, Valerie J. Parker
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. All data was tested for normality with the D'Agostino & Pearson normality test. Canine inflammatory bowel disease activity index (CIBDAI) and Purina fecal scores were compared at baseline and after dietary modification using a paired t-test. 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 1.4 (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.
Keywords for abstract:	Chronic Enteropathy High-Fiber Diet Fiber Canine Fiber-Responsive Diarrhea

EPIDEMILOGY
AND
APPLIED RESEARCH

EAR-1

Title of abstract:	**ASSESSING *Salmonella* Enterica PREVALENCE AND SEROGROUP DISTRIBUTION IN DAIRY BEEF: IMPLICATIONS FOR FOOD SAFETY AND PUBLIC HEALTH.**
Authors:	A.Arevalo-Mayorga, and G. Habing. Dept. Of Veterinary Preventive Medicine
Abstract:	*Salmonella* enterica, a common foodborne pathogen in livestock, poses significant risks to human health and food safety. However, there is a lack of information regarding its prevalence within dairy beef (cattle originally raised for dairy but later transitioned into beef production), a segment playing a growing role in the U.S. beef industry. **Objective:** This study aims to investigate *Salmonella* from dairy steers at harvest to assess the prevalence of infection and provide insights into serogroup circulation. **Methods:** During the summers of 2023 and 2024, a total of 626 samples were collected from a single commercial processing plant in the Midwest U.S. Each sample consisted of 3-5 mesenteric lymph nodes (MLNs) gathered from animals/viscera per cohort along the production line. Upon collection, *Salmonella* was isolated following the One Herd Lab standard protocol. Suspected colonies were confirmed and serogrouped using latex and slide agglutination tests. **Results:** The samples were collected from 28 cohorts of cattle, representing seven states in the Midwest U.S. *Salmonella* spp. was recovered from 41.5% (n=262) of the samples, corresponding to 82.1% (n=23) of the cohorts. Among 262 MLNs samples, serogroups C and E were predominant (34.7% n=91, and 31.3% n=82, respectively), followed by B (12.2% n=32) and D (1.5% n=4). Additionally, co-infections were detected in 7.3% (n=19) of the MLNs, and 13% (n=34) of the isolates exhibited the rdar-non-typable-phenotype. **Discussion:** Despite MLNs not being part of the food chain supply, the isolation of *Salmonella* is considered evidence of asymptomatic infection and raises concerns about potential transmission to humans. Furthermore, *Salmonella* enterica serogroups B, C, D, and E are of public health importance due to their association with foodborne outbreak serovars. **Conclusion:** These findings contribute to the understanding of Salmonella prevalence in dairy beef, underscoring the significance of monitoring and control strategies in under-researched segments of the beef industry.
Keywords for abstract:	*Salmonella* Prevalence Serogroups Dairy beef Mesenteric Lymph Nodes

Title of abstract:	**THE EXPERIENCES OF ACCESS TO VETERINARY CARE PROVIDERS: A QUALITATIVE ANALYSIS**
Authors:	V. Behmer Porter 1., M. Sumridge 2., J. O'Quin 1., R. Garabed 1. 1. Department of Veterinary Preventative Medicine OSU CVM 2. American Society for the Prevention of Cruelty to Animals
Abstract:	Equitable access to veterinary care (AVC) has been recognized as a shortcoming within the veterinary profession, impacting millions of pets and their families. Surveys conducted by the University of Tennessee's Access to Veterinary Care Coalition found that 23% of respondents were unable to acquire routine preventive care for their pet at some point in the past two years; 80% of those indicated that financial constraints prevented them from obtaining the desired care. Additional barriers also affect AVC, including lack of transportation, inability to confine the animal, inadequate knowledge of where to find care, language barriers, cultural barriers, distrust of health professionals, and fear of judgment. Pet ownership increases every year and expenditure on veterinary services similarly increases every year. Still, not all pets receive the same level of care. To our knowledge, no describtive study has been done on the experiences of providers increasing access to veterinary care. This qualitative study conducted a phenomenological analysis on the interview responses of 27 AVC providers regarding their experiences with various AVC initiatives. Themes were observed regarding interspecies equity, pragmatism, discourse strains, honoring multispecies families (the human-animal bond), lack of resources, the concept of "good medicine," and the veterinarian-owner relationship. This analysis may provide guidance to those interested and currently providing services to underserved owners and pets. Additionally, these findings may further advise additional research and interventions aimed to improve access to veterinary care.
Keywords for abstract:	Access to Veterinary Care Human-Animal Bond Equity One Health One Welfare

Title of abstract:	**UTILIZATION OF ARTIFICIAL INTELLIGENCE TO BETTER UNDERSTAND BEHAVIOR IN AFRICAN WILD DOGS (*LYCAON PICTUS*)**
Authors:	B. Braasch1, M. Flint1, K.A. George2 1 1Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio 2Zoological Association of America
Abstract:	Advancements in technology have proven to benefit animal industries across multiple dimensions, including animal welfare and behavior, which impacts animal management decisions. This study utilizes behavioral data collection and individual identification using advanced technology. This study aims to determine how technological advancements can enhance our understanding of animal behavior, specifically in African wild dogs, to influence management decisions at The Wilds in Cumberland, OH. Video feed will be collected from around the perimeter of the wild dog enclosure, then analyzed using artificial intelligence (AI) software. The three objectives of this study are to (i) determine individuals and basic behaviors within a managed pack of African wild dogs using AI, (ii) compare if the behaviors and spatial use of individuals differ within the pack during three marked time periods: when visitors are present, when visitors are absent, and when interacting with staff; and (iii) test if AI can be used to assess identification of individual personalities when presented with novel enrichment items that may change pack order. The significance of this study to the field of zoological science is further exploration of technological advancements, allowing for greater understanding of the individuality of animals in human care, as well as a better understanding of the sociality of a large carnivore. These advances will aid in determining optimal methods for care regarding enrichment and space.
Keywords for abstract:	African wild dog artificial intelligence machine learning animal behavior animal welfare animal management sociality

Title of abstract:	**DECISION-MAKING IN THE PROVISION OF ACCESSIBLE VETERINARY CARE**
Authors:	E. Bryant, R. Garabed, J. O'Quin, V. Behmer, Dept of Preventive Medicine College of Veterinary Medicine, D. Howard, Dept of Philosophy College of Medicine
Abstract:	As it stands, veterinary care in the United States is not accessible to everyone, and veterinarians regularly face cases of clients who are unable to provide necessary care to their animals regardless of the client's desire to do so. There is currently limited research into how ethics inform the decision-making process regarding when to provide assistance with human medical interventions, and even less is known about how these issues are addressed in veterinary medicine. The concept of who is deserving of or should be prioritized for care fall under the ethical concept of distributive justice. Through this study we have developed and distributed a survey to veterinarians practicing in the United States to identify current trends in how these professionals apply principles of distributive justice in the scope of veterinary medicine. With need currently exceeding the amount of funds and services available, veterinarians are consistently tasked with deciding which cases are most deserving of assistance. We know veterinarians regularly utilize funding or offer discounted services to treat cases that otherwise would go without care, but do not know what aspects of individual cases most influence providers to select one type of case over another for assistance. Ethical frameworks identified in human bioethics research into distributive justice were presented, along with demographic questions, to identify relationships between veterinarian priorities and the scope of their practice and professional experience.
Keywords for abstract:	Access to care, distributive justice, veterinary ethics, bioethics

Title of abstract:	**CUTANEOUS MYIASIS BY CALLIPHORIDAE DIPTERANS IN DOGS FROM CHAD, AFRICA**
Authors:	J. Cox1, R. Ramos2,3, H. Hakimi3, S. Metinou4, W. Danzabe4, M. Overcast1, R. Garabed1, P. T. Ouakou5, B. N. R. Ngandolo6, F. Torres-Velez7, L. Tritten8, M. N. Saleh3, G. G. Verocai3 1Ohio State University, 2Universidade Federal do Agreste de Pernambuco, 3Texas A&M University, 4The Carter Center, 5PNEVG T'Chad, 6Laboratoire de Recherches Vétérinaires et Zootechniques de Farcha, 7High-Consequence Pathogens and Pathology, CDC, 8University of Zurich
Abstract:	In Autumn of 2022, a total of 1,561 dogs from 56 villages along the Chari River in Chad, Africa were inspected for cutaneous myiasis. Dogs are also enrolled in a tethering intervention under the supervision of the Chadian Guinea Worm Eradication Program, with some villages participating in a study of flubendazole and others used as the control arm. Maggots that we found were removed and stored in ethanol for laboratory analysis and morphological identification. DNA of representative maggots was extracted for molecular confirmation of identification and phylogenetic analysis. We created a prevalence map using proportional symbols to display infested dogs in each village, and a data frame for analysis using the information gathered in the field. We then used a multivariable mixed-effects binomial regression model to determine which variables and interactions played a significant role in the risk of cutaneous myiasis. 65 dogs from 21 villages were infested by maggots causing myiasis. A total of 151 maggots were morphologically and molecularly identified as Cordylobia anthropophaga or Chrysomya bezziana. Most of infested dogs were from the southern region and were found to be exclusively infested with one maggot species, but some villages were found to have both maggot species present. The mixed-effects model showed that enrollment in the flubendazole arm, a more northern latitude, and an interaction of study arm and latitude were significantly associated with infestation and indicated no case clustering at any level. Overall prevalence was less than five percent, with 21 of 56 villages having at least one case. While some dogs had multiple maggots present, none were found to be co-infested, even though some villages had cases of both species. The statistical analysis suggested some protective effect of flubendazole against myiasis, which was further amplified in more northern villages.
Keywords for abstract:	Myiasis Africa Anthelmenthic Dog Infestation Mixed-modeling

Title of abstract:	**FIELD VALIDATION AND THE EFFECT OF SAMPLE TESTING CONDITIONS USING A POINT-OF-CARE PCR PLATFORM FOR THE DETECTION OF SWINE INFLUENZA A VIRUS**
Authors:	E. Dalesio, T.Y. Cheng, A. G. Arruda, Department of Veterinary Preventive Medicine, The Ohio State University College of Veterinary Medicine.
Abstract:	Foreign animal diseases such as African Swine Fever present significant risks to the swine industry and, in many cases, the only applicable methods of controlling potential outbreaks are through timely recognition and depopulation. Technological advances have allowed the miniaturization and portability of PCR devices, allowing diagnostic testing to be implemented directly at the point of care (POC). However, the validation of such devices under field conditions is lacking in the literature. Our objective was to validate a POC PCR system under field conditions using swine influenza A virus as a surrogate pathogen. Oral fluids were collected from seven swine farms and aliquoted into four treatments, where PCR was performed on site ("site"), while driving ("ride"), after 24 hours incubation at room temperature ("24rt") and on ice ("24ice"). As a gold standard, samples were also tested at the Ohio Department of Agriculture, Animal Disease Diagnostic Laboratory (ADDL). To compare treatment groups to ADDL results, spearman correlation coefficients were calculated. Ct values were then converted to binary results and the association between treatment and positivity was investigated using logistic mixed regression models. Finally, sensitivity and specificities were computed. Statistical significance was declared at $P < 0.05$. Results showed that POC system's Ct values were highly correlated with the ADDL results (site: $r^2 = 0.93$, ride: $r^2 = 0.94$, 24rt: $r^2 = 0.93$, 24ice: $r^2 = 0.82$). Furthermore, the ride treatment was 83% less likely to return a positive compared to ADDL results ($P = 0.017$). All treatments showed 100% specificity, and site, ride, 24rt, and 24ice groups had sensitivities of 94.44%, 85.71%, 100%, and 83.33%, respectively. Our study showed that the POC PCR system was a promising method for on-site diagnostic testing, providing results consistent with accredited laboratory methods.
Keywords for abstract:	Point of care Swine Influenza A Virus Sample Testing Condition

Title of abstract:	**CONCURRENT THERAPEUTIC AND BEHAVIOR INTERVENTIONS REDUCE EMERGING DRACUNCULUS MEDINENSIS WORMS IN DOGS IN CHAD**
Authors:	A.C. Dupper, R. Garabed. College of Public Health, Division of Epidemiology and Dept. of Veterinary Preventive Medicine C.A. Cleveland, M.J. Yabsley. University of Georgia, Athens, Georgia F. Torres-Velez, K. Unterwegner, M. Romero, and A.J. Weiss. The Carter Center, Atlanta, Georgia H. Zirimwabagabo and M. Sidouin. The Carter Center, N'D'jamena, Chad P.T. Oaukou and M.M. Ada. Programme National d'Eradication du Ver de Guinee, Ministry of Health, N'Djamena, Chad
Abstract:	The current study sought to examine the effect of flubendazole (FBZ) at the village level in the presence of existing eradication interventions using secondary data from the Carter Center and a previously published study. Our data set included monthly counts of emerging worms in dogs from January 2019 through September 2021 from 56 villages, of which 11 (19.6%) were involved in the 2019 clinical trial. Models from the individual interventions were fit using a generalized linear mixed models (GLMMs) with a random effect for village. Each model's AIC and BIC values were compared to the AIC and BIC values from a base model where no intervention was present. Models with a difference in AIC and BIC greater than 10 from the base model were selected for inclusion in a final model. Models combining FBZ and proactive tethering were averaged together, and the predicted number of D. medinensis infections per month and 95% confidence intervals were estimated from model averaged fixed effects over the study period. All analyses were performed using R version 4.3.1. The predicted counterfactual number of D. medinensis infections for the average village over the study period with no interventions present was 20.6 (95% CI, 15.3, 27.9). The average estimated number of infections per village remained unchanged in the presence of FBZ alone (20.3, 95% CI, 13.5, 30.6) over the study period. The predicted number of infections decreased in the presence of proactive tethering alone and in the presence of both interventions to 16.8 (95% CI, 12.5, 22.6) and 17.5 (95% CI, 11.8, 26.1), respectively. Though not directly addressing causality, our secondary data analysis supports the hypothesis that flubendazole treatment has a prolonged effect on emerging Guinea worms at the village level. Flubendazole may be an important tool when used concurrently with existing eradication interventions.
Keywords for abstract:	Dracunculus medinensis Parasitology Interventions Flubendazole

Title of abstract:	**ASSESSING THE IMPACT OF A NEGATIVE AIR IONIZATION SYSTEM ON PARTICULATE MATTER AND GASEOUS POLLUTANTS IN SWINE FARM ENVIRONMENT**
Authors:	B.A. Fonseca, Y.-F. Shen, M.R. Campler, and A.G. Arruda Department of Veterinary Preventive Medicine
Abstract:	Poor indoor air quality could be a source of respiratory challenges for swine in commercial farms. Negative air ionization systems (NAIS) have been shown to be effective in reducing airborne particles in human indoor environments, but research is limited for swine-specific farm conditions. The objective of this study is to evaluate NAIS as a technology to reduce airborne particulate matter and gaseous pollutants and its impact on swine production under field conditions. A negative air ionization system (Freshlight LLC) was installed in six farrowing rooms in a 5,000-sow herd. Two treatment groups and one control group were assigned: 1) NAIS installed with lamps ON (L-ON), 2) NAIS installed with lamps OFF (L-OFF), (3) No NAIS installed (NL). Treatment was assigned at room/batch level for three weeks. Particulate matter (PM 2.5 and 10), gaseous pollutant (NH_3, H_2S, CO), temperature, and humidity measurements were taken in each room at pig (2ft) and human (5ft) respiration levels twice a day, two fixed times per week. Daily change in particle counts (morning to evening) and gas concentrations were analyzed using linear regression models built in STATA 17. There were no significant changes in particulate matter concentration between treatment groups. Particulate matter and gaseous pollutant values were similar at 2ft and 5ft and decreased from morning to evening regardless of treatment group. There were higher NH_3 concentrations in NL and L-OFF groups than L-ON group. While treatment had no specific effect on number of pigs weaned and pre-weaning mortality, increases in temperature were associated with increased pre-weaning mortality, while decreases in NH_3 were associated with higher number piglets weaned. Our results show that the NAIS system may be suitable for decreasing ammonia levels but had no effect on particulate matter. The NH_3-lowering capability of NAIS may help improve swine health and farm staff working conditions.
Keywords for abstract:	Negative Air Ionization Swine Ammonia

Title of abstract:	**DETERMINING THE ENVIRONMENTAL FOOTPRINT OF THE VETERINARY OVARIOHYSTERECTOMY**
Authors:	<u>B. Graham</u>, A. Berrian. Dept. of Veterinary Preventive Medicine
Abstract:	The human healthcare industry contributes significant volumes of solid waste, greenhouse gas (GHG) emissions, and environmental pollution globally. However, there is a substantial gap in the literature surrounding waste production and handling in the veterinary sector. The American Veterinary Medical Association supports a One Health (OH) approach to veterinary healthcare, explicitly acknowledging reduction of waste and GHG emissions as an integral part of the veterinarian's role in protecting animals, people, and the environment. Yet, there is little evidence corroborating practice implementation. Additionally, baseline metrics for prioritizing improvements are lacking. We conducted a procedural waste audit to determine the carbon footprint of an ovariohysterectomy procedure, one of the most frequently performed veterinary surgeries, to expand current knowledge surrounding veterinary waste. We created a profile of GHG sources and generation rates using validated waste audit practices established in the human healthcare sector, categorized, and quantified waste, and ascribed monetary costs and GHG estimates by procedure. The study was performed at The Ohio State University's (OSU) College of Veterinary Medicine Spectrum of Care Clinic (SOCC). We monitored and audited 22 surgeries, documented patient (e.g., species, weight), clinician (e.g., number, years of experience), and procedure factors (e.g., length, complications). Mean generation rates by waste type (e.g., fabrics, plastics) were extrapolated to estimate a total by facility/year. Principal Component Analyses (PCA) and regression models were built to determine highest emission and waste contributors. Data will be used to inform sustainable procurement and disposal practices in veterinary healthcare and achieve multisector sustainability improvements.
Keywords for abstract:	Environmental sustainability Greenhouse gas emissions Surgical waste Waste audit

Title of abstract:	**TRANSPOSONS, INTEGRONS AND PLASMIDS; BLA-IMP HORIZONTAL GENE TRANSFER MECHANISMS VARY BY TAXONOMIC FAMILY**
Authors:	S. Grooters, D. Mollenkopf, T. Wittum. Department of Veterinary Preventive Medicine
Abstract:	Antibiotic-resistant infections cause an estimated 3 million illnesses and 35,900 deaths annually in the US, with approximately 9,000 infections from carbapenem resistant bacteria. Carbapenem antibiotics are reserved to treat life-threatening bacterial infections. The bla_{IMP} resistance gene encodes a metallo-beta-lactamase, which confers resistance to all the beta-lactams, including carbapenems. The dissemination of bla_{IMP} among various taxonomic families, shows the diversity and range of horizontal gene transfer. Using whole genome sequencing and bioinformatic tools, we determined the genetic motifs surrounding bla_{IMP} present in 26 bacterial isolates recovered from environmental and agriculture facilities. bla_{IMP} can be found extra-chromosomally on plasmids or found with incomplete and complete Tn7 genetic structures chromosomally. The complete Tn7 containing bla_{IMP} gene cassette within class 2 integrons have been only observed chromosomally in *Shewanella*. Incomplete Tn7 structures, but functional class2 integrons harboring bla_{IMP} gene cassettes were found in species other than *Shewanella*. *Acinetobacter* isolates had truncated and incomplete Tn7s, while conserving the class 2 integron and resistance gene cassettes. Additionally, plasmids carried by *Shewanella*, *Escherichia coli*, and *Proteus* harbored class2 integrons and resistance gene cassettes, but were associated with incomplete Tn3s. Isolates containing bla_{IMP} gene cassettes were found both within class2 integrons, and associated with insertion sequences. Integrons harbor gene cassettes and provide the promoter sequence allowing gene transcription. Class 2 Integrons are associated with and mobilized by Tn7 transposons. Transposons have the ability to carry resistance genes within bacteria from chromosome to plasmid, or vice versa. Tn3 and certain Tn7 transposons, like plasmids, are associated with horizontal gene transfer, sharing resistance genes among different bacterial species. The conserved genetic structure of the complete Tn7 present in *Shewanella* is consistent with *Shewanella* as a potential reservoir from which other bacterial species have acquired certain bla_{IMP} gene cassettes.
Keywords for abstract:	Carbapenemase Antibiotic Resistance Horizontal Gene Transfer

EAR-11

Title of abstract:	**CHARACTIZING OCCURRENCE PATTERNS OF INFECTIOUS CORYZA IN OHIO**
Authors:	B. Hogshead[1], D. Jurkovic[2], A. Arruda[1]. Dept. of Veterinary Preventive Medicine[1] and Ohio Department of Agriculture[2]
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.
Keywords for abstract:	Chickens Infectious Coryza Ohio

EAR-12

Title of abstract:	**EXPANSION OF WILD BIRD AVIAN INFLUENZA RISK ASSESSMENTS IN NORTH AMERICA**
Authors:	MJ Jahid, AS Bowman, and JM Nolting. Department of Veterinary Preventive Medicine
Abstract:	Since the first influenza virus detection in ducks in 1956, subtype diversity and host tropism of influenza A viruses have been increased. Wild migratory birds have been known as the reservoirs and natural hosts for Influenza A viruses (IAVs), perpetuating many subtypes of influenza viruses across Migratory Wild Birds' Flyways. Outbreaks of IAVs have caused devastating consequences in animal health and have impacted farmers' livelihoods, food security, and international food trade. A notable outbreak in the U.S. involved the A(H5) viruses belonging to clade 2.3.4.4b, detected in wild waterfowl in December 2021. As of February 26, 2024, these viruses have been detected in all 50 states, leading to the eradication of 82.02 million poultry and infection of numerous species of wild birds and wild mammals. Detection has occurred in all four U.S. waterfowl flyways, furthering persistence of viral circulation, highlighting the need for increased surveillance.

To define subtype diversity, mammalian adaptation mutations, and antiviral resistance markers, determining the evolving risks to animal and public health, we sampled a diverse species of hunter-harvested wild waterfowl in Wisconsin and Ohio. Cloacal swab samples were collected and screened via RT-qPCR for the IAVs' matrix gene. All positive samples will be further screened for A(H5) 2.3.4.4b using RT-qPCR, following by genomic sequencing of the positive samples for phylogenetic characterization.

To date, we have collected a total of 1,043 cloacal swab samples. Of the 1,042 samples tested, n=187 (17.95%) are IAV positive, accounting for 14 wild birds' species. IAVs continue to be reported in both wild waterfowl and poultry, furthering subtype diversity, host tropism, and widespread distribution. Therefore, a deeper understanding of the evolution within the natural reservoir is crucial to reduce impact on animal and public health. |
| Keywords for abstract: | Influenza A Virus
Wild birds
Poultry
Public Health |

EAR-13

Title of abstract:	**THE EFFECTS OF PAIRED MENTORSHIP ON THE MENTAL HEALTH OF VETERINARIANS**
Authors:	G. Kelly and A. Reinhard
Abstract:	The aim of this study is to evaluate the impact on mental health and wellbeing of a paired mentorship program for both early career veterinarians as well as mentors. In this mixed methods study, a minimum of 100 mentors and mentees will complete pre and post surveys to assess mental health and wellbeing before mentoring and 6 months after the mentoring relationship begins. In addition, 15-20 interviews will be performed to gain a deeper insight of the impact of this program on both mentors and mentees. We hypothesize that this mentorship program will decrease levels of stress, anxiety, and depression in early-career veterinarians as well as their mentors. If this hypothesis is disproved, the qualitative data will be utilized to improve the program for the future. Potential variables that could need improvement include level of training for the mentors, structure for the mentor relationships, and resources available to the relationship.
Keywords for abstract:	Veterinary Wellbeing Stress Anxiety Burnout Resilience

Title of abstract:	**THE POWER OF PROACTIVE SURVEILLANCE: PREVENTING HEALTHCARE-ASSOCIATED INFECTIONS IN VETERINARY MEDICINE**
Authors:	Christy King[1], Dixie Mollenkopf[1], Joany Van Balen Rubio[2], Thomas Wittum[1], Karin Zuckerman[2], Roger Fingland[3], Liv Stepp[2], Chelsea Johnstone[2], Kelley Norris[2], Angela Marolf[3], Edward Cooper[3], Dimitria Mathys[1], Dubraska Diaz-Campos[2] Department of Veterinary Preventive Medicine, The Ohio State University[1]; Veterinary Medical Center, The Ohio State University[2]; Department of Veterinary Clinical Sciences, The Ohio State University[3]
Abstract:	In 2018, the Ohio State University Veterinary Medical Center (OSU VMC) implemented an Antimicrobial Stewardship Program, incorporating an Environmental Surveillance (ES) program as a key element of this initiative. The ES focuses on pathogens recognized as urgent threats to public health by the Centers for Disease Control and Prevention and pathogens that are considered clinically significant in veterinary medicine, including carbapenem-resistant Enterobacterales (CRE). Identification of these pathogens allows the hospital to be aware of contaminated environmental areas, facilitating targeted environmental cleaning strategies to prevent healthcare-associated infections. The ES program involves collecting samples from 86 locations throughout the hospital. Samples are collected using Swiffers® and processed through selective culture media. While the recovery of targeted pathogens is generally low (<10%), an increase in the detection of carbapenem-resistant *Escherichia coli* was observed in and around the intensive care unit in late 2023, persisting even after thorough cleaning and disinfection. In response to this finding, a dedicated CRE response team was established, comprising leaders in hospital administration, epidemiology, microbiology, and clinical care. The team's action plan involved consulting with the University of Pennsylvania, enhancing environmental surveillance and patient CRE screenings, updating infection control and prevention training, managing CRE cases, and developing educational resources. This strategy aimed to identify potential CRE carriers as well as reservoirs for disease transmission. The team also coordinated communication efforts for CRE positive environmental and patient results, which guided both cleaning and disinfection and isolation efforts. This response was critical when one feline patient developed a CRE infection, which was managed without transmission to other patients. Targeted interventions and ES by the team successfully eliminated CRE from the hospital environment, improving patient safety and demonstrating the value of proactive ES in veterinary infection control and prevention. This ongoing effort has enhanced the understanding of CRE risks in veterinary medicine.
Keywords for abstract:	infection control, infection prevention, antimicrobial resistance, environmental surveillance, CRE, healthcare-associated infections

Title of abstract:	**ASSESSMENT OF CLIMATE CHANGE PERCEPTIONS ON ANIMAL HEALTH & WELFARE THROUGH THE LENS OF ANIMAL PRODUCTION**
Authors:	<u>C. Kramer</u>, A. Arruda, J. Flint, M. Flint
Abstract:	To better understand animal industry stakeholders opinions on climate change as an animal health and welfare issue in the United States, we investigated perceptions of animal welfare for a range of environmental issues. Using the Qualtrics XM platform, a thirty-four question survey was used to collect data from seventy production animal stakeholders representing various positions within the industry across the United States. The survey sections included questions on demographics, animal welfare based on the Five Freedoms framework, animal welfare as it relates to environmental issues (i.e. increasing global ambient temperatures, drought, exposure to extreme weather events), and questions for the veterinarian's role in this field. The data analysis for this study was generated using Qualtrics© software, Version November 2023. Results of individuals from twenty-four states representing eleven different production animal industries were recorded. Ninety-two percent of respondents believe that the health of the environment impacted the health and welfare of the animals they worked with. Eighty-nine percent of respondents stated it is either 'Very' or 'Moderately' important to understand the association between the health of the environment and the welfare of the animals they work with. Roughly sixty-eight percent of respondents believe veterinarians are knowledgeable in both animal health and welfare. These results indicate production animal stakeholders not only believe climate change is an animal welfare issue, but that veterinarians may be suited to help find solutions to the pressures this industry is facing. This data can help find relatable ways to engage with production animal stakeholders about climate change as an animal welfare issue, take meaningful action to mitigate climate change causes and effects, and promote sustainable animal welfare practices where applicable.
Keywords for abstract:	Climate Change Animal Production Animal Welfare One Welfare

Title of abstract:	**PREVALENCE OF *SALMONELLA* DUBLIN IN MESENTERIC LYMPH NODES OF SPECIAL-FED VEAL CALVES FROM THE US AND CANADA**
Authors:	S.R.Locke, P. Vinayamohan, A. Arevalo-Mayorga, T. Schaffner, A. Dunmyre, J. Ridolfo, G. Habing
Abstract:	*Salmonella* serovar Dublin is known to cause severe, invasive disease in both cattle and humans. Cattle are the primary reservoir of *S.* Dublin, with calves particularly susceptible to infection and transmission. Previous sampling of special-fed veal calves has documented lymph node carriage of S. Dublin at harvest and may represent a public health concern, but the epidemiology of S. Dublin in special-fed veal is not well understood. The objective of this study was to assess the prevalence of S. Dublin at harvest from special-fed veal calves raised in three different production systems. We hypothesized that *S.* Dublin carriage would be associated with production system. Twenty-two cohorts of special-fed veal calves from two American (n=15) and once Canada (n=9) system were sampled. Mesenteric lymph nodes were collected from 30 calves per cohort for a total of 660 calves sampled. Samples were cultured following a standardized protocol for *Salmonella* isolation and recovered *Salmonella* isolates were then serogrouped. Fisher's exact tests were used to assess the association between Dublin carriage and production system. The overall prevalence of *Salmonella* in mesenteric lymph nodes was 45.9% (303/660). All cohorts had at least one sample positive for *Salmonella*, with cohort-level prevalences ranging from 3-100%. *Salmonella* Dublin carriage was significantly associated with production system (p-value < 0.02). Dublin was recovered from over half of sampled cohorts, with three Canadian and ten US cohorts positive. Dublin was the most frequently recovered serotype from samples (29%) followed by serotypes belonging to serogroup B (23.8%). Special-fed veal calves are a reservoir for *Salmonella* Dublin and Dublin carriage is associated with production system of origin. In order to design and implement effective preharvest interventions, future research should evaluate the extent of S. Dublin endemicity in veal calf production, as well as the timing of Dublin infection.
Keywords for abstract:	*Salmonella* Special-fed veal Lymph node

EAR-17

Title of abstract:	**ANTIGEN DETECTION OF SARS-COV-2 IN A REMOTE POPULATION OF BLACK AND WHITE RUFFED LEMURS**
Authors:	J. Nye, R. Junge, A. Baden, J. Delaney, A. Bowman
Abstract:	SARS-CoV-2, the virus causing the COVID-19 pandemic, has rapidly cycled between human and animal hosts, in wild and captive settings, by exploiting homologous ACE-II receptors expressed across species. Species of high conservation concern, including Malayan tigers and nonhuman primates, have demonstrated susceptibility and ability to spread SARS-CoV-2. Critically endangered Black and White Ruffed Lemurs (*Varecia variegata)* have sufficient ACE-II homology to raise concern for infection of SARS-CoV-2 in wild populations; however, no cases of disease have been documented in wild lemurs thus far and only one case of SARS-CoV-2 serum antibody has been detected in a captive lemur. To look for active SARS-CoV-2 infection in wild lemurs, we collected nasopharyngeal swabs from 14 free-ranging Black and White Ruffed lemurs from a single population in Mangevo, Ranomafana National Park, Madagascar, an area with minimal human activity. SARS-CoV-2 antigens were not present in swabs from any free-ranging lemurs in the sample. Negative results indicate that lemurs in this population are not currently infected with SARS-CoV-2, likely due to their remote geography and limited interaction with other potential carriers, including humans. Future research will include serum antibody testing for anti-SARS-CoV-2 antibodies to screen for past infection in the population and a greater sampling effort to capture a larger and more widespread proportion of the population of lemurs.
Keywords for abstract:	SARS-CoV-2 COVID-19 Lemurs Varecia variegata

Title of abstract:	**CHARACTERIZATION OF A SWINE INTERSTATE MOVEMENT NETWORK FOR DISEASE SPREAD MODELING**
Authors:	L. Ouyang, K. Shaw, A. Arruda, and T. Cheng. Depts. of Preventive Veterinary Medicine and Depts. of Geography at the Ohio State University, and the Ohio Department of Agriculture
Abstract:	Certificate of Veterinary Inspection (CVI) records list animals inspected by veterinarians and are required for interstate animal transportation. Commuter Herd Agreements (CHA) allowing interstate movements only between facilities under same ownership are often neglected in animal tracing. The goal of this study is to visualize the directionality and frequency of Ohio swine movements incorporating two data sources and identify regions with intense movement events using network analysis. We collected CVI and CHA records submitted to the Ohio Department of Agriculture between May and September 2023. Geocoding of addresses was achieved using the cloud-based Google Geocoding service in R program. A zipcode-to-county matching process was performed so that swine movements included the date of transportation, number of transported animals and origin and destination counties. Five interactive dashboards, including total aggregate movements, the import/export from CVI, and the import/export under CHA, were created in R using Leaflet and Shiny packages. Each dashboard consist of a choropleth flow map by origin and destination county, and a histogram of total animal movement by state. From May to September 2023, 2,290 movements (nimport = 674, nexport = 1,616) were identified, moving 1,110,594 heads (485±732.3, range = [1, 8,000]). CHA, constituting 6.3% of total records, accounted for 15.5% of transported animals. The median animal count for CHA records was 1,250, compared to 91 for CVI records. Considering all movements, the highest in-degree (n = 49) was observed for Kentucky, US, indicating the greatest frequency of inbound animal movements to Ohio. Swine was frequently moved to/from Ohio by neighboring states, and a share of swine movements with substantial animal counts was not recorded by CVIs and may be neglected for traditional animal movement tracing approaches. This information should be incorporated to fill gaps in tracking animal movements.
Keywords for abstract:	Swine movement network Disease transmission

Title of abstract:	**AN ASSESSMENT OF THREE LARGE-SCALE DEPOPULATION METHDOS FOR SWINE**
Authors:	Janice Y. Park, Magnus R. Campler, Ting-Yu Cheng, Brad L. Youngblood, Dawn Torrisi, Michael D. Cressman, Justin D. Kieffer, Andréia G. Arruda, Andrew S. Bowman Depts of Veterinary Preventive Medicine, Animal Sciences, and Office of the Attending Veterinarian
Abstract:	The threat of foreign animal disease outbreaks to U.S. swine herds warrants effective, scalable, and readily available depopulation methods. Carbon dioxide (CO_2) is one AVMA-recommended method of swine depopulation that has demonstrated higher-volume scalability. However, like other recommended methods, it still faces limitations in scalability to efficiently depopulate the volume of U.S. swine herds. Our objective was to assess and compare outcomes of two large-scale depopulation methods in development: 1) water-based foam (WBF) and 2) high-expansion nitrogen foam (N_2F), to CO_2 on finisher pigs in field conditions. Of 793 enrolled pigs, 84 were implanted with bio-loggers recording electrocardiogram and movement data. Pigs were divided into four replicates per method and loaded into method-specific depopulation trailers, after which depopulation agents were applied. We assessed container fill time, number of aversive behaviors observed during depopulation, overall movement intensity, time to cessation of movement (COM), and time to cardiac arrest. When comparing total fill times for foam-based methods, there was no difference between WBF and N_2F ($P=0.386$). Carbon dioxide had a greater total number of aversive behaviors compared to both foam methodologies ($P<0.01$). Total pig activity was higher in WBF compared to N_2F ($P=0.02$) and CO_2 ($P=0.01$), but no difference between N_2F and CO_2 was observed ($P=0.46$). Mean time to COM (mm:ss, [95% CI]) was longer in WBF (02:01, [01:30-2:43]) than N2F (01:25, [01:03-1:55]) ($P<0.001$). Additionally, N_2F time to COM was faster than CO_2 (04:06, [03:03-5:31]) ($P<0.001$). All three evaluated methods demonstrated high efficacy for rapid, large-scale swine depopulation, achieving 100% mortality rates. Our results support that foam-based technologies are comparably effective as CO_2 and are viable candidates for recommended swine depopulation methods.
Keywords for abstract:	

Title of abstract:	**UNDERSTANDING THE BARRIERS AND DRIVERS FOUND AFTER THE IMPLEMENTATION OF AN ANTIMICROBIAL STEWARDSHIP PROGRAM IN LARGE DAIRY FARMS IN OHIO AND CALIFORNIA.**
Authors:	R. Portillo-Gonzalez1, A. Garzon-Audor2, T.-Y. Cheng1, D. J. Wilson3, R. V. V. Pereira2, G. G. Habing1 1Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, 43210 2Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, CA, 95616 3Dr. Devon Wilson, DVM. 5122 Sherlaw Rd, Chilliwack BC, V4Z1H3.
Abstract:	Ensuring judicious antimicrobial use (AMU) is crucial in the fight against antimicrobial resistance. Farmworkers are responsible for initiating antimicrobial therapy; therefore, they have the responsibility to apply sound antimicrobial stewardship (AMS) practices. This study aimed to identify the barriers and drivers influencing on-farm treatment decisions and to understand farmworkers' impressions of the AMS educational material. This study was part of a quasi-experimental field trial but only the farms that received AMS training were used for this component of the study. Using a semi-structured questionnaire, fourteen trained farmworkers (n = 14) were individually interviewed for approximately 35 minutes. The interviews were audio-recorded, translated (Spanish version), transcribed, and evaluated using thematic analysis. Preliminary results indicated that the most common barriers to receiving training were time constraints and lack of instructors. The most common barriers to using antimicrobials responsibly were lack of information, protocol disagreements, and ownership directions. Farmworkers indicated that they were driven by animal welfare, job success, and financial factors (e.g., drug cost, wasted milk, and withhold times) to use antimicrobials responsibly. Additionally, the qualitative analysis showed that after being trained, farmworkers felt confident rendering treatment and identifying early signs of illness. Farmworkers stated that the educational materials were beneficial and valued each component (e.g., educational modules, summary tables, and benchmark reports); however, it can be improved by shorter didactic sections and more hands-on activities. Farmworkers expressed discreet levels of AMU at the farm they work for and mentioned veterinarians and owners as the most common sources for consultation. In conclusion, farmworkers seemed motivated by animal care, work achievement, and cost-saving to behave as antimicrobial stewards but felt challenged by knowledge gaps, and farm management. Finally, the information obtained through this research project could be used to minimize the barriers and enhance the drivers to improve antimicrobial stewardship on dairy farms.
Keywords for abstract:	qualitative analysis antimicrobials antimicrobial stewardship barriers drivers

Title of abstract:	**WHAT IS THE IMPACT OF INCOMPLETE ANIMAL MOVEMENT NETWORKS IN UNDERSTANDING DISEASE TRANSMISSION DYNAMICS?**
Authors:	Sequeira S1, Habing, G1 Arruda, A. G. 1 1 Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio, United States
Abstract:	Recent concerns with food safety in the United States (U.S.) highlight the importance of traceability systems in the food animal production chain. However, adoption of these systems in the U.S. faces challenges. Interstate Certificates of Veterinary Inspection (ICVIs) are required for interstate animal movements but may be exempted under certain exemptions (e.g., Owner Shipper Statements – OSSs), limiting disease mitigation. Dairy-beef calf networks are understudied, yet important for understanding dynamics of disease transmission between animal and human populations. This study aimed to use Ohio-based movement records to describe calf networks in the U.S. and explore how OSSs impact the structure of calf networks built using ICVIs. We hypothesized that networks built exclusively using ICVIs will differ from those combined with OSSs. Calf movement records to and from Ohio, accessible at the Ohio Department of Agriculture, were obtained through ICVIs and OSSs from June 2021 to June 2022, and analyzed using R. To explore and compare movement patterns, network analysis was performed individually for an ICVI-based network and a network combining both document types, using the R packages igraph and visNetwork. Zip codes were considered nodes and calf movements links. Whole-network (e.g., density, component ratio, etc.) and node-level (e.g., degree, eigenvector centrality, etc.) parameters were calculated for each network. Mann-Whitney U tests were performed to evaluate whether parameters differed statistically ($P < 0.01$), suggesting a discrepancy in their potential to influence dynamics of disease transmission. Lower eigenvector scores in the combined networks indicated a more integrated structure, with fewer influence of individual nodes over the full network ($P=0.01$). There were major differences in the movement structure when incorporating OSSs compared to when using ICVIs exclusively. This study emphasizes the importance of incorporating multiple sources of movement data for the development of targeted disease surveillance strategies.
Keywords for abstract:	Dairy calf; animal movement records; social network analysis; infectious disease; epidemiology.

Title of abstract:	**LONGITUDINAL SWINE-LINEAGE INFLUENZA SURVEILLANCE AMONG YOUTH SWINE EXHIBITORS AT THE HUMAN-ANIMAL INTERFACE**
Authors:	N.N. Tarbuck, H. Cochran, H. Nicholson, J.M. Nolting, A.S. Bowman Dept of Veterinary Preventive Medicine
Abstract:	Exhibition swine are mixing vessels for influenza A virus (IAV), posing a substantial risk to public health through IAV spillover at the human-animal interface. To examine the viral, host, and environmental factors that facilitate interspecies transmission, we launched longitudinal surveillance of youth swine exhibitors frequently exposed to IAV circulating in exhibition swine in 2021. Youth swine exhibitors have been recruited and enrolled at swine exhibitions across the nation with swine samples collected simultaneously. Baseline samples and medical histories were collected from participants at enrollment, followed by annual pre and post exhibition season blood draws. Serum and PBMC samples will be used by collaborators to explore immune response to reference swine-lineage IAV strains circulating in exhibition and commercial swine. Participants self-collect nasal swabs within 7 days of each swine exhibition attendance with an objective to estimate the rate of spillover events. To date, the cohort has enrolled 289 participants across 24 states. 692 nasal swab samples have been tested revealing 5 IAV RT-PCR positive samples. The samples were also tested for influenza B virus, influenza D virus, and SARS-CoV-2, with 9 SARS-CoV-2 RT-PCR positives detected to date. Sequencing conducted on the IAV positive samples identified a variant case, supported by cohesive epidemiological evidence as the sample was collected in July and has a nearly identical genome to swine samples collected at the same show. In 2023, overall prevalence of IAV in swine was approximately 14% at exhibitions where participants were enrolled. Thus, a better understanding of zoonotic IAV dynamics in youth swine exhibitors frequently exposed to divergent swine-lineage IAVs is critical to reduce pandemic potential. Interventions should target reduction of IAV prevalence in the swine population to mitigate IAV spillover at the human-animal interface.
Keywords for abstract:	exhibition swine influenza A virus (IAV) human-animal interface zoonotic

EAR-24

Title of abstract:	**EPIDEMIOLOGICAL ASSESSMENT OF INFLUENZA A VIRUSES IN EXHIBITION SWINE AND ASSOCIATED HUMAN HEALTH RISKS: A COMPREHENSIVE STUDY FROM THE SUMMER OF 2023**
Authors:	L. Terry, D.S. McBride, M. Owsiany, H. Cochran, N. Tarbuck, J.M. Nolting, and A.S. Bowman. Department of Veterinary Preventive Medicine.
Abstract:	Background: 　　Transmission of influenza A viruses (IAVs) from swine to humans represents a significant pandemic risk. In the United States, the predominant instances of zoonotic IAV transmission have been linked to human exposure to swine at agricultural fairs. Effective mitigation strategies are imperative, drawing insights from an understanding of interspecies transmission among exhibition swine. To gain a deeper appreciation of these risks, we investigated the epidemiology of IAVs in exhibition swine and their transmission to humans over the summer of 2023. Methods: 　　Over the summer of 2023, nasal wipes of swine from 46 agricultural fairs across the United States were collected. Nasal swabs of humans at these fairs were collected as part of a NASALS project focused on zoonotic transmission of swine-lineage viruses. Samples were tested for the presence of IAV via polymerase chain reaction (PCR) and Next Generation Sequencing (NGS) methods. Sequencing for the remaining samples is underway. Results: 　　One variant case from a human nasal swab at a fair in Kentucky has been confirmed (H1N2). IAV prevalence in swine at this show was 24%. Additionally, of the 2,402 total swine samples collected over the summer of 2023, 427 samples tested positive for IAV (17.8%). Conclusions: 　　Over the summer of 2023, there was evidence of a variant case and a notable viral load among swine at agricultural fairs nationwide. Without this surveillance, this case would have likely gone undetected, indicating that the prevalence of variant cases at agricultural fairs is being substantially underestimated. According to the CDC, there were four variant cases in the 2022-23 influenza season. Ongoing surveillance of IAVs in both swine and humans at fairs is crucial. Forthcoming sequencing results will provide further insights into the gravity of this issue by determining how many more transmission events have occurred at agricultural fairs.
Keywords for abstract:	Viruses. Pandemic. Zoonotic. Exposure. Mitigation. Interspecies. Risks. IAVs. Humans. Nasal. Agricultural. Swabs. Swine-lineage. Samples. PCR. NGS. Variant. Prevalence. Swine. Positive. IAV. 2023. Fairs. Surveillance. Cases. Underestimated. Influenza. Ongoing. Sequencing. Insights. Transmission.

Title of abstract:	**USING AN ECOSYSTEM HEALTH APPROACH TO EVALUATE THE IMPACT OF DREDGING ON WETLAND HABITATS IN SOUTHWESTERN LAKE ERIE**
Authors:	E. Vincent, J. Flint, A. Bowman, B. Fischer, F. Satern, T. Gabriel, M. Flint Department of Veterinary Preventive Medicine School of Environment and Natural Resources
Abstract:	Confined disposal facilities (CDFs) are diked structures used to contain contaminated dredged materials, but they often become habitats for wildlife, especially in areas where coastal wetlands have been lost due to anthropogenic activities. The impacts of dredging and the use of CDFs on wildlife health and welfare is largely unknown. This study tested the hypothesis that overall ecosystem health would be superior at a protected coastal marsh (PCM) compared to a confined disposal facility (CDF) in southwestern Lake Erie through comparison of wildlife health assessments, freshwater fish assemblages, water quality parameters, and infectious disease surveillance at the two sites. In health assessments of 51 painted turtles (*Chrysemys picta*), turtles from the CDF had significantly higher blood glucose levels and heterophil/lymphocyte ratios but lower total protein and calcium/phosphorus ratios than turtles from the PCM. There was no significant difference in turtle pathogen prevalence by site, with 6/51 turtles testing positive for *Chlamydia*, a single herpesvirus-positive turtle, and no detection of ranavirus or *Mycoplasmopsis* species. A total of 2984 freshwater fish representing 13 species and 2 hybrid sunfish species were evaluated at the two sites. Species diversity and evenness were higher at PCM, with only two species identified at CDF: golden shiners (*Notemigonus crysoleucas*) and goldfish (*Carassius auratus*). There was a higher prevalence of fish ectoparasites at PCM compared to CDF, but there were no significant differences in hematology parameters or health assessment findings. Basic water quality and soil chemistry assessments revealed lower dissolved oxygen and higher dissolved solids at the CDF. We concluded that ecosystem health was negatively impacted at the CDF due to evidence of higher stress levels among freshwater turtles, lower freshwater fish diversity, and worsened water quality. The ecosystem health approach used in this study was valuable in exploring the impacts of anthropogenic activities on coastal wetland habitats.
Keywords for abstract:	Ecosystem health Dredging Coastal wetlands Wildlife health

Title of abstract:	**DEVELOPING A ONE WELFARE ASSESSMENT OF AMERICAN ALLIGATORS (ALLIGATOR MISSISSIPPIENSIS) IN THE UNITED STATES**
Authors:	<u>M. Winans</u>, J. Flint, and M. Flint.
Abstract:	Although animal welfare science has continued to grow since its inception in the 1960s, much of the focus has remained on charismatic, mammalian species. Reptiles, including crocodilian species, remain an understudied taxonomic group in this field. This is especially of concern given the prevalence the American alligator (Alligator mississippiensis) housed in human care setting across the United States, both in the commercial farming industry and zoological industry. As these industries continue to evolve, we must prioritize the welfare of animals in their care, as well as understand the impacts of these facilities on the surrounding environment and human communities, which can be done using a One Welfare approach. The objective of this project will be to assess the One Welfare impacts of zoo-housed crocodilian species across the United States. To evaluate animal welfare, an assessment tool will be developed based in the Five Domains model for assessing animal welfare and adapted for the various crocodilian species and types of institutions. Data for this component of the model will include observations of animal behavior, measuring allostatic load (a range of physiological indicators), and resource-based indicators. Environmental welfare will be included in this approach by way of assessing these institutions' contributions to crocodilian conservation, as well as evaluating the impact of global climate change on the future of the zoological industry. Finally, human/societal welfare will be evaluated by assessing each zoological facility's impact on the local community through measuring the value of educational and/or recreational visitor-animal interactions (direct or indirect), as well as other ways these institutions are supporting their local communities. Together, the three components described here could offer a holistic, One Welfare assessment of zoo-housed crocodilians in the United States.
Keywords for abstract:	One Welfare, alligators, conservation, sustainability, animal welfare

Title of abstract:	**INFECTIOUS HEPATITIS E VIRUS IN THE SPERM HEAD**
Authors:	K.K. Yadav, P. Boley, L. Thamonpan, S. Khatiwada, C. Lee, M. Bhandari, L. Moore, J. Hanson, S.P. Kenney[1] Center for Food Animal Health, Department of Veterinary Preventive Medicine
Abstract:	Hepatitis E virus (HEV) is the leading cause of acute viral hepatitis worldwide and is frequently transmitted to humans via pigs. The presence of HEV in semen of infertile men and chronically ill hepatitis E patients raises the question on the potential transmission of HEV through sperm. The purpose of this study was to develop an animal model to mimic human reproductive tract infection and study the presence of infectious HEV in sperm cells. Pigs are a good natural host animal model to study HEV infection. We hypothesize that during HEV infection, virus can invade mature sperm cells and remain infectious. Randomized experimental design was used to divide 8 pigs (1-month-old, white duroc cross-bred conventional, HEV negative male pigs) into two experimental groups (Human US-2 HEV infected, n1 = 4 and negative control, n2=4). Pigs were intravenously administered with HEV. Active HEV infection was detected in inoculated pigs including virus shedding in feces, virus in the blood, liver, and bile. At 84 days post infection (age = 126 days), pigs were euthanized. Both testicles were collected and stored in a cooled box. Semen was collected from epididymis and sperm cells were separated. We detected HEV in the head of mature sperm cells using an immunofluorescence assay. We found that 19.2% (p < 0.0001) of the sperm cells contained HEV in the infected group using flow cytometry. Altered motility and morphology of sperm cells was noted. HEV within sperm cells was infectious to human liver cells in vitro. Reproductive tissues demonstrated the presence of HEV protein suggesting viral replication in these tissues. Our findings suggest the ability of HEV to possibly be a sexually transmittable disease. Future work will target animal studies demonstrating the sexual transmission of HEV from male to female confirming HEV as a sexually transmittable disease.
Keywords for abstract:	hepatitis E, virus, sperm, infectious, sexual, transmission

Title of abstract:	SALMONELLA DUBLIN PREVALENCE IN SURPLUS CALF ENVIRONMENTAL SAMPLES BY MULTIPLEX PCR AND CULTURE
Authors:	P. Lauder, S. R. Locke, A. Arevalo-Mayorga, G. Habing. Department of Veterinary Preventive Medicine
Abstract:	*Salmonella* Dublin (*S.* Dublin) is a cattle-adapted bacteria known to cause invasive, often antimicrobial resistant disease in cattle and humans. Surplus calves, primarily young males not required in the dairy operation, are particularly susceptible to infection due to stressors during transportation and marketing. *S.* Dublin is difficult to recover from environments by culture methods, limiting our understanding of its prevalence and transmission in surplus calves. The objective of this study was to assess the prevalence of *S.* Dublin from environmental samples utilizing a novel end-point PCR and culture methods. We hypothesized that the use of PCR would increase the detection of *S.* Dublin from a surplus calf production environment. 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 DNA extraction and PCR. Detection of *Salmonella* by culture was performed following a standardized laboratory procedure. The prevalence of *Salmonella* at the genus level was 100% (38/38) by PCR and 78.95% (30/38) by culture. Fourteen samples were positive for *S.* Dublin by PCR, but no isolates were recovered via culture. End-point PCR was more sensitive than culture. 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.
Keywords for abstract:	Salmonella PCR Culture Methods Surplus Calf Dairy

Title of abstract:	**AN ANALYSIS OF ANIMAL CRUELTY LEGISLATION ACROSS STATES IN THE UNITED STATES OF AMERICA**
Authors:	V. Behmer Porter, <u>J. O'Quin</u>. Department of Veterinary Preventative Medicine
Abstract:	We may assume as a society a universal standard for the legal treatment of animals. However, states determine the baseline treatment of animals and animals are legally treated differently between states. Each state in the US has laws against animal cruelty, abuse, and neglect. However, the regulations vary across states. Building off of a previous review of animal cruelty regulations across all of the states in the USA (Behmer & O'Quin, 2023), this analysis evaluates relationships between animal cruelty regulations and multiple variables. Previous work evaluated: the presence and role of humane societies, which professionals investigate animal cruelty complaints, the training and employer of said professionals, cross-reporting regulations, liability and immunity clauses for reporters of suspected animal cruelty, and the classification of specific types of animal cruelty. These data are compared to identify trends in regionality, presence of concurrent laws, cultural phenomena, and political nature of the states. Information from this study can shed light on how animals are treated, classified, and protected in each state. These findings potentially reflect legal and cultural impacts to interventions aimed at decreasing animal cruelty and other violent crimes associated with animal cruelty.
Keywords for abstract:	Animal Cruelty Legislation Animal Welfare One Welfare One Health Public Health

IMMUNOLOGY
AND
INFECTIOUS DISEASES

IMID-1

Title of abstract:	**RESISTANCE-INDUCING PROTEIN OF EHRLICHIA — A NOVEL IN VIVO VIRULENCE FACTOR OF EHRLICHIA SPECIES**
Authors:	R.C. Chien, M. Lin, Y. Rikihisa. Department of Veterinary Biosciences
Abstract:	Ehrlichiosis is a potentially life-threatening disease caused by infection with *Ehrlichia* sp., tick-borne bacteria. *Ehrlichia japonica* provides a mouse disease model to study ehrlichiosis as it recapitulates full-spectrum and lethal human ehrlichiosis. We found *E. japonica* transposon mutant Δ*ripE* does not express resistance-inducing protein of *Ehrlichia* (RipE, *EHF0962*). While Δ*ripE* proliferates similarly to wild-type *E. japonica* in macrophage cell culture, it is attenuated in mouse infection and virulence. Although *Ehrlichia* sp. are obligate intracellular bacteria, they need to endure a brief extracellular stage to initiate a new cycle of infection. *ripE* mRNA was upregulated at the start of the exponential replication stage, and the majority of RipE protein was found in the smaller and CtrA-positive *Ehrlichia* populations that are primed to be liberated from the host cells. Extracellular Δ*ripE* contained significantly less ATP and lost infectivity more rapidly in culture compared with wild-type *Ehrlichia*. Reconstitution of Δ*ripE* with *ripE* gene insertion or overexpression of RipE in wild-type *Ehrlichia* significantly increased ATP, and RipE overexpressing *E. japonica* killed mice more rapidly than wild-type *E. japonica*. In addition, RipE is a bacterial surface-exposed protein and recombinant RipE (rRipE)-immunization of mice induced *Ehrlichia in vitro* infection-blocking antibody, and significantly delayed onset of illness and prolonged survival time following a lethal dose of *Ehrlichia* challenge. Our findings strongly suggest that RipE energizes *Ehrlichia* and confers resistance at the extracellular stage to initiate new infection and spread in demand in the *in vivo* environment, and thus a potential vaccine candidate and a therapeutic target against ehrlichiosis.
Keywords for abstract:	Human monocytic ehrlichiosis *Ehrlichia japonica* Virulence factor Bacterial resistance

Title of abstract:	**EVALUATING THE ZOONOTIC POTENTIAL OF SIMIAN ARTERIVIRUSES THROUGH CD163 RECEPTOR CHARACTERIZATION**
Authors:	Jared D. Compaleo[1,2], Devra Huey[1,2], Makky Mousa-Makky[1,2], Tony L. Goldberg[3], Jens H. Kuhn[4], and Cody J. Warren[1,2,5,6]
Abstract:	Simarteriviruses (family *Arteriviridae*) are endemic in African monkeys. On rare occasions, these viruses cross species barriers and infect new hosts. The results of these host-switching events can be severe, including fatal cases of hemorrhagic fever. Previously, we discovered that CD163 (a monocyte/macrophage-specific membrane protein) acts as an intracellular receptor for the simarterivirus simian hemorrhagic fever virus (SHFV). Here, we demonstrate that reconstitution of CD163 expression in nonpermissive monkey and human cell lines renders these cells permissive to SHFV infection. Further, we demonstrate that a distantly related simarterivirus, Kibale red colobus virus 1 (KRCV-1), is also dependent on CD163 expression and can replicate to high titers in human cell lines engineered to express human CD163. Prior studies with porcine reproductive and respiratory syndrome virus 1 (PRRSV-1), a betaarterivirus that also uses CD163 for virion entry, concluded that the scavenger receptor cysteine-rich (SRCR) domain 5 of CD163 is essential for this process. To determine whether these findings also hold true for simarteriviruses, we engineered CD163 receptor-knockout cells to stably express chimeric CD163 receptor molecules. We conclude that SRCR domain 5 is not the sole determining factor for SHFV entry, indicating that the receptor interface may be more complex than once thought. Future studies are focused on pinpointing the precise virion interaction interface of CD163 and developing specific inhibitors that block arterivirus-receptor interactions.
Keywords for abstract:	Coronaviruses and Arteriviruses Receptor Biology

IMID-3

Title of abstract:	**SARS-COV-2 SPIKE MUTATION I692V DRIVES DESTABILIZATION OF SPIKE AND ATTENUATES VIRAL INFECTIVITY**
Authors:	J. Faraone, J. Evans, K. Xu, S.-L. Liu
Abstract:	Throughout the COVID-19 pandemic, SARS-CoV-2 has demonstrated the ability to infect a variety of animal hosts. Some of these infections, particularly in farmed mink, have resulted in new variants of the virus. One such variant, called mink cluster five variant (MC5V), carries five mutations in the spike protein including I692V and M1229I in the S2 subunit. While MC5V has been reported to have reduced pathogenicity in humans compared to the ancestral Wuhan strain, the underlying mechanism is unclear. Here we conducted mutational analyses of ancestral and MC5V spike proteins and characterized the impacts of these key residues. We identified the I692V mutation, located near the furin cleavage site, as the key determinant of the low infectivity of MC5V. Specifically, we observed that introduction of I692V into D614G reduces the spike furin processing, impairs spike-mediated cell-cell fusion, and diminishes pseudotyped lentivirus infectivity. Consistently, introducing the V692I reversion mutation into MC5V greatly restored MC5V spike processing and fusogenicity and increased pseudotyped virus infectivity to levels comparable with D614G. Additionally, we have found that I692V mutation promotes instability of the spike trimer, evidenced by increased spontaneous S1 shedding, as well as contributes to conformational changes, demonstrated by disruption of binding to RBD-targeting monoclonal antibody S309. This destabilization of spike can be explained through homology modeling that shows the loss of critical hydrophobic interactions upon mutation of the residue. The results of this study suggest a critical role for the I692V mutation, which is not in the receptor-binding domain of S1, for impacting furin cleavage site accessibility, therefore underscoring the critical role of non-RBD spike mutations in modulating viral infectivity, transmission capability and pathogenesis of SARS-CoV-2.
Keywords for abstract:	SARS-CoV-2 reverse zoonosis MC5Vspike protein evolution

Title of abstract:	**ASSOCIATION BETWEEN INNATE IMMUNE DYSREGULATION AND RISK OF ATHEROSCLEROSIS IN SEVERE COVID-19 PATIENTS.**
Authors:	Manuja Gunasena1,2, Mario J. Alles1, Yasasvi Wijewantha1, Will Mulhern1, Dhanuja Kasturiratna3, Joseph Bednas1, Thorsten Demberg4, Nicholas Funderburg1 and Namal P.M Liyanage1,2 1 The Ohio State University, College of Medicine, 2 The Ohio State University, College of Veterinary Medicine, 3Northern Kentucky University, 4 Marker Therapeutics Inc., Houston, TX, United States.
Abstract:	There is evidence that patients with COVID-19 have an increased risk of atherosclerotic cardiovascular diseases (CVDs), while the exact pathways are unknown. Although macrophages and monocytes were previously shown to be linked to atherosclerosis, it is unknown how Natural Killer (NK) cells, specifically in COVID-19 associated atherosclerosis, function. In this study, we investigated selected biomarkers of CVD risk in COVID-19 patients at different disease states to explore potential mechanisms associated with cardiovascular complications in severe COVID-19 patients. Using Spectral flow cytometry and plasma biomarker assays, we investigated changes in immune subsets in whole blood and plasma biomarkers of CVDs in Healthy (n=17), severe Covid-19 (n=29), and recovered individuals (n=30). Our findings reveal that severe COVID-19(ICU) patients display elevated levels of neutrophils, intermediate monocytes, and activated NK cells with some inflammatory subsets persisting even after recovery (p<0.05). Activated (CD69+) subsets of NK cells identified by CD56 and CD16 expression showed an increase that suggest homing to vascular tissue and influence the uptake of plasma oxidized LDL (oxLDL) into macrophages within the vessel walls, providing novel insights into the underlying mechanisms observed in ICU patients. In terms of cardiometabolic markers, ICU patients had significantly higher levels of CRP (C-Reactive Protein), MCP-1 (Monocyte Chemotactic Protein-1) and FABP4 (Fatty Acid-Binding Protein 4), indicating a risk for CVDs. It's interesting to note that OxLDL levels decreased (p<0.05) even in recovered people, indicating higher OxLDL uptake from macrophages and increased likelihood of foam cell formation, both of which indicate a long-term risk for atherogenesis. Furthermore, our invitro studies conclusively demonstrated that NK cells derived from ICU patients actively facilitate the uptake of ox-LDL by monocytes derived macrophages in the presence of autologous plasma from ICU patients. Collectively, our study provides valuable new insights into the underlying mechanisms of atherogenesis, coagulopathy, and CVDs in COVID-19 patients, specifically those in intensive care units.
Keywords for abstract:	SARS-CoV-2 Atherosclerosis Natural Killer cells

Title of abstract:	**ASSESSING CHEMOSENSORY MECHANISM FOR HOST SEEKING BEHAVIOUR AND IN VITRO IMPACT OF EMODEPSIDE ON ANCYLOSTOMA CANINUM**
Authors:	<u>S. Hegde</u> and A. Marsh. Department of Veterinary Preventive Medicine
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℃, most died. To euthanize the L3 for quantification, chloroform treatment at 20% proved ineffective, and at 80%, the larvae died. For emodepside, 40* μ*g/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.
Keywords for abstract:	Ancylostoma caninum Chemotaxis Urocanic acid

Title of abstract:	**INTRANASAL MEASLES VIRUS AND MUMPS VIRUS-BASED SARS-COV-2 VACCINES EXPRESSING PREFUSION SPIKE OF OMICRON XBB.1.5 PROVIDE BROAD AND COMPLETE PROTECTION AGAINST CURRENTLY DOMINANT OMICRON SUBVARIANTS**
Authors:	Cheng Chih Hsu[1], Michelle Chamblee[1], Sung J. Yoo[1], Yajie Liu[1], Pei Li[1], Mohamed M. Shamseldin[2], Chengjin Ye[3], Jiayu Xu[1], Yuexiu Zhang[1], Ilada Thongpan[4], Mahesh KC[4], Xueya Liang[1], Luis Martinez-Sobrido[3], Prosper N Boyaka[1,5], Shan-Lu Liu[1,2,5], Purnima Dubey[2,5], Mark E. Peeples[4, 5, 6], Jianrong Li[1,5] [1]Department of Veterinary Biosciences, The Ohio State University, Columbus, OH, USA [2]Department of Microbial Infection and Immunity, The Ohio State University, Columbus, OH, USA [3]Texas Biomedical Research Institute, San Antonio, TX, USA [4]Center for Vaccines and Immunity, Abigail Wexner Research Institute at Nationwide Children's Hospital, Columbus, OH, USA [5]Infectious Disease Institute, The Ohio State University, Columbus, OH, USA [6]Department of Pediatrics, The Ohio State University, Columbus, OH, USA
Abstract:	The currently approved SARS-CoV-2 vaccines are delivered intramuscularly and induce strong serum antibodies but not mucosal immune responses. With the continuous emergence of highly immune-evasive SARS-CoV-2 Omicron variants and subvariants, there is an urgent need to develop an intranasal SARS-CoV-2 vaccine that can protect against severe illnesses but also virus infections. Here, we developed intranasal, monovalent and trivalent SARS-CoV-2 vaccine candidates expressing the six proline-stabilized prefusion spike proteins (preS-6P) of ancestral SARS-CoV-2 WA1 and two Omicron variants, BA1 and XBB.1.5, based on the attenuated measles virus (MeV) and mumps virus (MuV) Jeryl Lynn (JL1) and JL2 vaccine strains. Golden Syrian hamsters intranasally immunized with 3×10^5 PFU of monovalent rMuV-JL2-WA1-preS-6P, monovalent rMuV-JL1-XBB.1.5-preS-6P, or trivalent vaccine containing rMeV-BA.1-preS-6P, rMuV-JL2-WA1-preS-6P, and rMuV-JL1-XBB.1.5-preS-6P (1×10^5 PFU each) induced high levels of serum IgG and IgA antibodies. Antibodies produced against the monovalent rMuV-JL1-XBB.1.5-preS-6P and trivalent vaccine candidates but not monovalent rMuV-JL2-WA1-preS-6P vaccine efficiently neutralized the currently dominant Omicron variants, XBB.1.5, EG.5, XBB.1.16, and JN.1. Importantly, hamsters immunized with monovalent rMuV-JL1-XBB.1.5-preS-6P and trivalent vaccine candidates provided complete protection against challenge with Omicron BA.1, EG.5, XBB.1.5, and JN.1 strains, whereas monovalent rMuV-JL2-WA1-preS-6P only provided partial protection. In addition, high levels of Omicron XBB.1.5-specific neutralizing antibodies (NAbs) were detected in monovalent rMuV-JL1-XBB.1.5-preS-6P and trivalent vaccine groups even when hamsters had been pre-immunized with monovalent rMuV-JL2-WA1-preS-6P vaccine, suggesting that immune imprinting has a limited impact on the efficacy of intranasal vaccine candidates. Both intranasal and subcutaneous immunization routes of the trivalent vaccine induced strong serum NAbs in IFNAR$^{-/-}$ mice. However, intranasal but not subcutaneous immunization generated high levels of S-specific mucosal IgA antibodies as well as resident memory T cells in the lungs. In summary, we have developed intranasal monovalent and trivalent vaccines expressing preS-6P of Omicron XBB.1.5 that induce broad NAbs and protect against currently dominant Omicron variants.
Keywords for abstract:	Vaccines, VOCs, SARS-CoV-2, MMR, Vectored vaccine

Title of abstract:	**QUANTIFICATION OF VIRUS-INFECTED CELLS USING RNA FISH-FLOW**
Authors:	Huey D1, Barbachano-Guerrero A2, Yang Q2, Worden-Sapper ER2, Sawyer SL2, and Warren CJ1 1 Department of Veterinary Biosciences, The Ohio State University 2 BioFrontiers Institute, Department of Molecular, Cellular, and Developmental Biology, University of Colorado Boulder
Abstract:	Researchers frequently use viruses that have been genetically manipulated to encode a fluorescent reporter gene (e.g., enhanced green fluorescent protein [eGFP]) to visually assess viral infection in cells. However, there are numerous caveats with this approach, including, 1) effects of the reporter gene on virus fitness, 2) genetic instability of the reporter gene, and 3) significant effort required to generate and validate reporter virus clones. Given these caveats, we sought to develop an alternative approach for the rapid quantification of virus infected cells. Here, we describe a flow-cytometry-based protocol for intracellular detection of viral RNA in mammalian cells using fluorescence in situ hybridization (FISH). This method, which we call RNA FISH-Flow, can be easily adapted to measure infectivity of diverse RNA viruses. It takes only a few hours to perform this protocol, uses standard buffer recipes, and can even be multiplexed with fluorescently labeled antibodies for simultaneous protein and RNA measurements. Further, using an eGFP reporter virus clone, we show that RNA FISH-Flow is equivalent to eGFP in discriminating infected vs uninfected cells by flow cytometry. Taken together, our data highlights RNA FISH-Flow as a valuable new method for the rapid and high-throughput quantitation of viral infection in cells.
Keywords for abstract:	NA virus infection, fluorescence in situ hybridization, flow cytometry.

Title of abstract:	**THE PUPPY FECAL MICROBIOTA SUPPORTS GERMINATION AND OUTGROWTH OF *CLOSTRIDIOIDES DIFFICILE EX VIVO***
Authors:	K.A. Ingram, J.C. Rowe, J.A. Winston
Abstract:	*Clostridioides difficile* is an anaerobic, spore-forming, toxin-producing enteropathogen which annually results in over 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 pathogenesis in these intestinal environments. Previous studies report a relative dysbiosis in the puppy fecal microbiome before 5-6 weeks of age. The purpose of this study is to evaluate the life cycle of *C. difficile ex vivo* to characterize disease susceptible states in puppies, as well determine the status of naturally acquired *C. difficile* carriage. 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 added anaerobically to fresh feces from healthy dogs (n=5) and three litters of puppies (n=18). *Ex vivo* puppy fecal microbiota permitted *C. difficile* germination and outgrowth while healthy adult dog feces did not. Puppies from three litters were found to naturally carry *C. difficile* without signs of clinical disease from as early as the first week of life. Future directions will include comparison of the canine fecal microbiome and metabolome associated with *ex vivo* susceptible states and toxin production, and ribotyping and toxin profiling of recovered *C. difficile*. By identifying and defining *C. difficile* susceptible states in dogs, a greater understanding of differential *C. difficile* pathogenesis is gained which may inform novel microbial-directed therapeutics against *C. difficile* for humans.
Keywords for abstract:	*Clostridioides difficile* Puppy microbiome Canine microbiome Dysbiosis *Ex vivo* model

IMID-9

Title of abstract:	**CHARACTERIZING THE ROLE OF N-6-METHYLADENOSINE IN THE ONCOGENIC RETROVIRUS HTLV-1**
Authors:	<u>Emily King</u>, Amanda Midkiff, Amanda R. Panfil
Abstract:	Human T-cell leukemia virus type 1 (HTLV-1) is an oncogenic retrovirus that infects 5-10 million people worldwide. Approximately 10% of those infected will develop disease (adult T-cell leukemia/lymphoma, myelopathy/spastic paraparesis, inflammatory disease) after a clinical latency period of several decades. However, HTLV-1 patient prognosis is poor with few effective therapeutic options available. Two viral genes, *Tax* and *Hbz*, have been previously identified as critical to viral persistence and pathogenesis. Methylation of the N6 position of adenine (m^6A) is the most common post-transcriptional modification, which until now has not been documented in HTLV-1. This dynamic modification is identified by cellular reader proteins (YTHDF1-3, YTHDC1-2) that can recognize the m^6A modifications and regulate target gene expression. Given our current understanding of HTLV-1 and m^6A, we hypothesized that dynamic m^6A modification of HTLV-1 RNA will regulate viral gene expression. Using cross-linked immunoprecipitation assays (CLIP) we found that both *tax* and *hbz* mRNAs contain m^6A modifications and that these transcripts bind to reader proteins YTHDC1 and YTHDF1. RT-qPCR analysis revealed that siRNA-mediated knockdown of reader protein YTHDC1 decreases sense-(*tax, gag, env*) and antisense-strand (*hbz*) viral transcripts, decreases Tax protein, and decreases infectious viral particle (p19) release in HTLV-1-transformed T cells. Upon further evaluation, we found YTHDC1 promotes nuclear export of *tax* transcripts, which is dependent on m^6A-modifications of the *tax* mRNA. Similarly, shRNA-mediated knockdown of reader protein YTHDF1 resulted in decreased sense and antisense transcripts, Tax protein production, and p19 release in HTLV-1-transformed T cells. Sites of m^6A modification were mapped in HTLV-1 immortalized cells using methylated RNA immunoprecipitation sequencing (meRIP-seq). Mapping experiments identified enrichment of m^6A in the RNA genomic regions encoding *tax* and *hbz*. Experiments are ongoing to map the location of m^6A modification to the single nucleotide level using RNA nanopore sequencing. This work helps further define the mechanisms of HTLV-1 infection and is critical for understanding viral pathobiology.
Keywords for abstract:	Retrovirus m6A Epigenetics RNA Pathogenesis

Title of abstract:	**SWINE CELL LINE SUSCEPTIBILITY TO PORCINE EPIDEMIC DIARRHEA VIRUS (PEDV) FOR GENOMIC CRISPR KNOCKOUT SCREENS**
Authors:	T. Laocharoensuk[1,2], L.J. Saif[1,2], Q. Wang[1,2], F. Grey[3], S.P. Kenney[1,2] [1] Center for Food Animal Health, Department of Animal Sciences, College of Food, Agriculture and Environmental Sciences, The Ohio State University, Wooster, OH, US [2] Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, OH, US [3] Royal (Dick) School of Veterinary Studies, The University of Edinburgh, UK
Abstract:	Porcine epidemic diarrhea virus (PEDV) is a swine enteric coronavirus, causing significant economic losses in swine industry due to high mortality in newborn and suckling piglets. Entry receptors and other host factors facilitating PEDV infection remain poorly understood. Characterizing the interaction between the virus and these host factors provides a foundation for uncovering potential therapeutic targets and breeding animals that are less susceptible to specific pathogens. Genomic CRISPR knockout (GeCKO), a newly developed high throughput genetic assay, has provided an invaluable tool for a rapid identification of host genetic factors critical for viral infection. In this project, we propose to utilize GeCKO to identify critical host factors contributing to PEDV infection. Ideally, a cell line that is highly permissive to PEDV and matches the primary host species and primary site of infection must be used for both positive and negative GeCKO screening. Therefore, porcine cell lines were screened for permissiveness to PEDV. IPEC-J2 cells from porcine small intestine, LLC-PK1 cells derived from porcine kidney, swine testicular (ST) cells, and neonatal porcine tracheal (NPTr) cells were tested for permissiveness to PEDV using dORF3-EGFP reporter virus. We found that NPTr cells, ST cells, LLC-PK1 cells, and IPEC-J2 cells were only partially susceptible to infection with PEDV and produced infections that were multiple folds less in magnitude than Vero cells, which are the cell line primarily used for PEDV propagation due to its ability to produce high titers of virus. To enable appropriate screening via GeCKO, modification of existing cell lines to increase potential virus receptors, or to reduce the interferon response may be necessary to achieve appropriately high permissiveness to enable host factor screening.
Keywords for abstract:	PEDV Permissiveness Genomic CRISPR knockout High throughput genetic assay

Title of abstract:	**DELAYED MATURATION AND MIGRATION OF DENDRITIC CELLS IN GERIATRIC COTTON RATS INFECTED WITH RESPIRATORY SYNCYTIAL VIRUS**
Authors:	J. Miller, C. Leedale, S. Niewiesk
Abstract:	Elderly adults are at increased risk of severe disease resulting from respiratory syncytial virus (RSV) infection, with elevated rates of hospitalization and death in individuals over 65 years of age. RSV clearance is delayed in elderly people, contributing to a more severe disease course. Geriatric cotton rats mimic this prolonged clearance kinetic, serving as a useful animal model for studying age-associated factors that contribute to impaired clearance. RSV-specific CD8+ T cell responses are delayed in lungs and secondary lymphoid tissues of geriatric cotton rats following infection, implicating impaired development of cell-mediated immunity in this age group. To investigate the cause of delayed CD8+ T cell responses in geriatric cotton rats, we measured dendritic cell (DC) activation in lungs and migration to mediastinal lymph nodes following RSV infection. Using CCR7 expression as a marker of maturation, we found that pulmonary DC activation is delayed in geriatric cotton rats compared to adults. DC migration to mediastinal lymph nodes is also delayed in geriatric cotton rats. Treating geriatric cotton rats with anti-inflammatory drugs including a pan-cyclooxygenase (COX) inhibitor, COX-2 specific inhibitor, or prostaglandin D_2 (PGD2) synthase inhibitor improved their clearance of RSV, maturation of pulmonary DCs, and CD8+ T cell responses. These results provide early evidence that age-associated inflammation contributes to delayed DC maturation and CD8+ T cell activation following RSV infection, and highlight PGD2 as a key mediated of impaired cell-mediated immunity.
Keywords for abstract:	Respiratory syncytial virus Aging Cotton rat Prostaglandin D_2

IMID-12

Title of abstract:	**IFN-INDUCIBLE PHOSPHOLIPID SCRAMBLASE 1 (PLSCR1) MODULATES SARS-COV-2 ENTRY IN A TMPRSS2-DEPENDENT MANNER**
Authors:	P. Qu, Y.-M. Zheng, S.-L. Liu. Depts. Of Veterinary Biosciences
Abstract:	Accumulating evidence indicates that viral infection, in particular the step of entry, is affected by host scramblases and flippases which regulate the asymmetrical distribution of phosphatidylserine on the plasma membrane. Here we show that an IFN-inducible phospholipid scramblase 1 (PLSCR1) is a critical host factor that regulates SARS-CoV-2 entry in a TMPRSS2-dependent manner. In low-TMPRSS2 expressing cells, such as in A549-ACE2 and 293T-ACE2, PLSCR1 restricts entry of SARS-CoV-2 at the virion fusion step. However, this inhibitory effect is lost by overexpressing TMPRSS2 in 293T-ACE2 cells, or completely reversed in high-TMPRSS2 Calu-3 cells. We observed that PLSCR1 inhibits the processing of the S2 subunit by cathepsin L/B in endosomes upon entry yet enhances the processing of S2 subunit by TMPRSS2 on the plasma membrane. Together, our study reveals complex functional roles of PLSCR1 in viral entry, the activity of which is modulated by additional critical host factors.
Keywords for abstract:	Interferon Phospholipid scramblase 1 SARS-CoV-2 TMPRSS2 Cathepsin L/B Entry

Title of abstract:	**A STEPWISE APPROACH TO IDENTIFY SWINE INFLUENZA VIRUSES WITH ZOONOTIC POTENTIAL**
Authors:	Christina G. Sanders, Devra Huey, Janice Park, Phylip Chen, Andrew S. Bowman, Mark E. Peeples, and Cody J. Warren. Departments of Veterinary Biosciences and Veterinary Preventive Medicine, The Ohio State University College of Veterinary Medicine, and Center for Vaccines and Immunity, Abigail Wexner Research Institute at Nationwide Children's Hospital
Abstract:	Emerging infectious diseases are a constant threat to global human health, with three out of every four being of zoonotic origin. Swine influenza viruses are priority pathogens --viruses known to cause outbreaks or pandemics in humans -- for pandemic preparedness research. Thus, new studies are warranted to assess the ability of diverse swine influenza viruses to effectively replicate in humans. We have developed a stepwise approach to experimentally assess the zoonotic potential of swine influenza viruses. This approach involves the following: 1) identification of new viral variants through active swine surveillance, 2) isolation, propagation, and evaluation of viral growth in primary human airway epithelial cultures, and 3) assessments of immune evasion mechanisms. We demonstrate that viruses with known zoonotic transmission are more efficient at replicating in primary human airway epithelial cultures when compared to closely related, non-zoonotic isolates. In addition, we find that some isolates appear to have no barriers to propagation in the human airway and are potentially poised to cross the species barrier. Another influenza virus pandemic could occur at any time, and it is imperative that we prepare ourselves by identifying and monitoring for viruses with high zoonotic potential.
Keywords for abstract:	emerging viruses influenza virus zoonosis pandemic preparedness virus surveillance primary human airway cultures

Title of abstract:	**NEUTROPHIL ELASTASE INHIBITOR ENHANCES EARLY IMMUNE RESPONSE TO SARS-COV-2 VACCINE IN CYSTIC FIBROSIS MICE**
Authors:	<u>S. Yoo</u>, L. Mazik, H. Steiner, Y. Ganesh, E. Kim, M. Joldrichsen, E. Cormet-Boyaka, P. Boyaka
Abstract:	Cystic fibrosis (CF), a genetic disorder caused by a malfunctioning CFTR protein, weakens the immune system, making patients more susceptible to infections. This impaired immune function emphasizes the need to understand the impact of CFTR deficiency on vaccine efficacy, particularly since existing data on vaccine effectiveness in CF patients has shown inconsistencies across different vaccines. Our prior research showed that neutrophil elastase inhibitor (NEI) supplementation in vaccines enhances antibody and T cell responses and promotes mucosal immunity. Therefore, we investigated the effects of CFTR deficiency on the immune response to the SARS-CoV-2 spike (S) protein vaccine in wild-type (WT), heterozygous, and knockout (KO) mice. Mice were immunized with an alum-adsorbed hexapro-Spike protein (6ProSpike). We further assessed the effects of NEI supplementation on these responses. We found that CFTR KO mice generated comparable antigen-specific serum IgG antibody levels against the 6ProSpike compared to WT mice. Interestingly, NEI supplementation significantly enhanced the magnitude, affinity, and breadth of the antibody response early (1 and 2 weeks) after vaccination in all three groups. NEI supplementation also conferred cross-reactivity against SARS-CoV-2 variants of concern, and induced serum and mucosal IgA responses. These NEI effects were more prominent in early time points than later time point (4 weeks). These findings suggest that NEI supplementation holds promise for accelerating and broadening the early immune response, potentially benefiting CF patients.
Keywords for abstract:	Cystic Fibrosis (CF) Neutrophil Elastase Inhibitor (NEI) SARS-CoV-2 Vaccine efficacy Antibody responses

IMID-15

Title of abstract:	**EHRLICHIA EFFECTOR TRP120 MANIPULATES BACTEREMIA TO FACILITATE TICK ACQUISITION**
Authors:	T. Zhang, R. C. Chien, K. Budachetri, M. Lin, P. Boyaka, W. Huang, and Y. Rikihisa. Depts. Of Veterinary Biosciences
Abstract:	*Ehrlichia* species, obligatory intracellular bacteria exist in nature via cyclical transmission and infection between ticks and mammals. Accidental infection of humans may lead to potentially fatal illness called human ehrlichiosis. *Ehrlichia japonica* provides a mouse disease model to study ehrlichiosis as it recapitulates full-spectrum and lethal human ehrlichiosis. Here, we developed a tick-transmission model of *E. japonica* and characterized the mouse pathogenicity and tick transmission of *E. japonica* wild-type and a transposon mutant that lacks tandem repeat protein (TRP)120 (ΔTRP120). Wild-type and the isogenic mutant ΔTRP120 could proliferate similarly in cultures of mammalian and tick cells. Upon inoculation into mice, both wild-type and ΔTRP120 multiplied exponentially in various tissues, and caused similar clinical chemistry and hematologic changes, proinflammatory cytokine induction, and fatal disease. Thus, TRP120 is not required for clinical disease. In blood, however, ΔTRP120 became almost undetectable within 24 h, whereas the abundance of wild-type increased exponentially. >90% of TRP120 protein was released from infected cells into the culture medium. Native TRP120 protein in the culture supernatant, significantly reduced mouse blood monocytes expressing transmigration-related surface markers of Ly6C and CD11b. Larval ticks attached to mice infected with either wild-type or ΔTRP120 imbibed similar amounts of blood and molted to nymphs at similar rates. However, unlike wild-type, ΔTRP120 was minimally acquired by larval ticks and subsequently transmitted to molted nymphs, and thus failed to transmit to naïve mice. These findings suggest a novel manipulation of infected blood monocytes by an obligatory intracellular bacterium to sustain its lifecycle of mammal-tick transmission.
Keywords for abstract:	*Ehrlichia japonica*, TRP120, bacteremia, tick acquisition/transmission, blood, mouse, monocytes

Title of abstract:	**SARS-COV-2 LACKING RNA CAP 2'-O-METHYLTRANSFERASE IS**
Authors:	Jiayu Xu, Yuexiu Zhang, Michelle Chamblee, ChengChih Hsu, Xueya Liang, Jianrong Li. Depts. Of Veterinary Biosciences
Abstract:	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) employs various regulatory mechanisms to evade recognition by the innate immune system. The viral genome of SARS-CoV-2 encompasses 16 non-structural proteins (Nsps), four structural proteins, and nine accessory proteins, collectively orchestrating the suppression of interferons (IFNs) production and their signaling pathways. Like all coronaviruses, viral Nsp16 is an RNA ribose 2′-O-methyltransferase (MTase), catalyzing the transfer of a methyl group to the cap structure of mRNA. In addition, Nsp16 plays an important role in innate immune evasion. The Nsp16 contains a conserved lysine-aspartic acid-lysine-glutamate (KDKE) tetrad which is the catalytic site for the 2'-O MTase activity. Methylation of the mRNA 5′ cap by MTase facilitates efficient translation and shields the viral RNA from the detection by the innate immune system. To explore the function of Nsp16 of SARS-CoV-2, we recovered five recombinant SARS-CoV-2 mutants, each harboring one or two mutations in the conserved KDKE motif of Nsp16 which abolish the 2'-O MTase activity. Our results reveal that these recombinant SARS-CoV-2 Nsp16 mutants are attenuated in vitro. Mechanistically, these mutants display a significantly higher sensitivity to type I IFN compared to the wild-type SARS-CoV-2. In summary, our findings underscore the pivotal role of SARS-CoV-2 Nsp16 in evading host innate immunity. Our study also suggests that Nsp16 is a promising target for generating live attenuated SARS-CoV-2 vaccine and a target for developing therapeutic intervention.
Keywords for abstract:	SARS-CoV-2, Nsp16, 2′-O-methyltransferase, IFN

Title of abstract:	**THREE SARS-COV-2 SPIKE PROTEIN VARIANTS DELIVERED INTRANASALLY BY MEASLES AND MUMPS VACCINES ARE BROADLY AND HIGHLY PROTECTIVE**
Authors:	Yuexiu Zhang1‡, Michelle Chamblee1‡, Jiayu Xu1‡, Panke Qu1#, Mohamed M. Shamseldin3,4,5#, Sung J. Yoo1#, Jack Misny2#, Ilada Thongpan2, Mahesh KC2, Jesse M. Hall3, Yash A. Gupta3, John P. Evans1, Mijia Lu1, Chengjin Ye6, Cheng Chih Hsu1, Xueya Liang1, Luis Martinez-Sobrido6, Jacob S. Yount3,8, Prosper N Boyaka1,8, Shan-Lu Liu1,3,8,9, Purnima Dubey3,8, Mark E. Peeples2, 7, 8, Jianrong Li1,8
Abstract:	The outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has led to worldwide disruption and loss of life. As the pandemic continues and new variants of concern (VoCs) such as the Omicron subvariants emerge, there is still an urgency to develop vaccines that are able to overcome the immune escape prevalent within these variants and provide broad protection. Here, we have developed highly efficacious, intranasal trivalent SARS-CoV-2 vaccine candidates based on the three components in MMR vaccine: measles virus (MeV), mumps virus (MuV) major component Jeryl Lynn (JL1) strain and MuV minor component JL2 strain. Specifically, we constructed MeV, MuV-JL1, and JL2 vaccine strains expressing a stabilized prefusion spike protein with six prolines (preS-6P) of SARS-CoV-2 WA1, B.1.1.7, B.1.351, and B.1.617.2 VoCs. All these recombinant viruses are genetically stable and grow to high titers in Vero CCL81 cells. The preS-6P of each VoC was also highly expressed by all three vectors. Subsequently, MeV, MuV-JL1, and MuV-JL2 vaccine strains, each expressing preS-6P of different VoCs were combined to generate trivalent vaccine candidates. Intranasal immunization of IFNAR -/- mice with these trivalent SARS-CoV-2 vaccine candidates generated high levels of S-specific serum IgG and mucosal IgA antibodies as well as resident memory T cells in the lungs. Furthermore, intranasal immunization was more efficacious than subcutaneous immunization or combination of intranasal and subcutaneous routes. Golden Syrian hamsters immunized with these trivalent vaccine candidates also induced high levels of IgG antibodies, serum IgA antibodies, and broad neutralizing antibodies against multiple VoCs and were protected when challenged with SARS-CoV-2 ancestral WA1, B.1.617.2, and Omicron BA.1 strains. In summary, we have developed a panel of MeV and MuV-based trivalent SARS-CoV-2 vaccine candidates that can induce broad neutralizing antibodies and protection against multiple SARS-CoV-2 VoCs through intranasal administration.
Keywords for abstract:	SARS-CoV-2 Coronavirus Vaccine

MOLECULAR
AND
CELLULAR BIOLOGY

Title of abstract:	**CHARACTERIZING THE ROLE OF PRMT5 IN HTLV-1 DISEASE PATHOGENESIS**
Authors:	<u>K. Ernzen</u>, C. Phelps, S. Niewiesk, P. Green, and A. Panfil. Dept. of Veterinary Biosciences
Abstract:	Human T-cell leukemia virus type 1 (HTLV-1) is an oncogenic retrovirus and the causative agent of adult T-cell leukemia/lymphoma (ATL), a fatal malignancy of CD4+ T-cells. Given that ATL is a chemotherapy-resistant disease that lacks an effective long-term therapy regimen, there is an urgent need to characterize novel therapeutic targets for infected patients. Protein arginine methyltransferase 5 (PRMT5) is a type II PRMT enzyme that has been directly implicated in the tumorigenesis of several different lymphomas through the transcriptional regulation of relevant oncogenes. Our group recently has shown that PRMT5 RNA and protein is overexpressed in HTLV-1-transformed T-cell lines, during HTLV-1-mediated T-cell transformation, and in ATL patient samples. The primary objective of this study was to assess how PRMT5 activity impacts HTLV-1 gene expression, transformation, and disease pathogenesis. Chromatin immunoprecipitation (ChIP) experiments in newly-immortalized HTLV-1-infected T-cells (PBL-HTLV-1) revealed a significant enrichment of symmetrically di-methylated histones within the long terminal repeats (promoter regions). Affinity pulldown and proximity ligation assays in transfected HEK293T cells demonstrated that PRMT5 targets p30, a viral accessory protein that plays a role in regulating viral gene expression and T-cell transformation. Using a co-culture model of infection and immortalization, we identified that the small molecule PRMT5 inhibitor EPZ015666 is capable of preventing HTLV-1-mediated T-cell immortalization, indicating that PRMT5 enzymatic activity is necessary for the transformation process of HTLV-1 *in vitro*. To determine the importance of PRMT5 activity *in vivo*, EPZ015666 was administered to NSG xenograft and HTLV-1-infected humanized immune system (HIS) mice, resulting in significantly decreased tumor burden and improved survival outcomes, respectively. Altogether, these findings illustrate that the epigenetic regulator PRMT5 is essential for the transformation and pathogenesis of HTLV-1, demonstrating the potential utility of this cellular enzyme as a therapeutic target for the treatment of ATL.
Keywords for abstract:	HTLV-1 ATL PRMT5 EPZ015666 Transformation

Title of abstract:	**FUNCTION OF SITE-SPECIFIC N6-METHYLADENOSINE (M6A) MODIFICATIONS OF HIV-1 RNA IN VIRUS-HOST INTERACTIONS**
Authors:	S. Golconda, G. Lee, A. Baek, and S. Kim Dept. Of Veterinary Biosciences
Abstract:	Decoding the dynamics between HIV-1 RNA and its host interactions is crucial to unraveling the pathways essential to HIV-1 survival, potentially leading to the discovery of novel drug targets for controlling the late stages of viral replication. However, the structure complexity, chemical modifications, and stability of HIV-1 RNA limit in-depth studies of its multifaceted roles in viral replication. Recently, we have demonstrated nucleotide-resolution mapping of chemical modifications on full-length HIV-1 RNAs using innovative Nanopore direct RNA sequencing and tandem mass-spectrometry. Our data unveiled a surprisingly simple modification landscape on HIV-1 RNAs, revealing only three predominant modification peaks near the 3' end. Each of these modification peaks indicates site-specific, high-stoichiometry N6-methyladenosine (m^6A) modifications that are crucial for maintaining normal levels of HIV-1 RNA splicing and translation. Additionally, we discovered these m^6As possess unique functional properties and deposition patterns on HIV-1 RNAs, distinct from those typically observed in cellular transcripts, suggesting HIV-1-specific and context-dependent roles for these m^6As. Given the crucial role of host machineries in viral RNA expression and post-transcriptional modifications, we explored whether knocking out the site-specific m^6As on HIV-1 RNA affects host gene expression in virus-producing cells. Interestingly, principal component analysis and hierarchical clustering showed a clear separation of the samples into 2 distinct groups: wildtype (WT) vs. mutants. Cells producing any of these m^6A mutant HIV-1, either single or triple knockout of the three m^6As, exhibited similar gene expression profiles distinct from those of WT virus-producing cells, further supporting the redundant functions of these m^6As. Differential profiling and gene set enrichment analysis comparing WT- and triple-mutant-producing cells identified several sets of cellular transcripts differentially expressed between these cells potentially important for viral RNA production and replication, including those known to interact with m^6A readers and those involved in viral RNA transcription, elongation, and RNA splicing and transport. These key findings provide insight into a novel evolutionary strategy of HIV-1, utilizing its site-specific m^6As, as well as the molecular mechanisms underlying m^6A-mediated interactions between viral RNA and host functions.
Keywords for abstract:	HIV-1 RNA m6A Virus-Host Interactions Transcriptome

Title of abstract:	**NANOPORE DIRECT RNA SEQUENCING REVEALS SITE-SPECIFIC M6AS CRUCIAL FOR REGULATING HIV-1 RNA AND PROTEIN EXPRESSION**
Authors:	<u>G. Lee</u>, A. Baek, S. Golconda, A. Rayhan, B. Addepalli, P. Limbach, L. Wu, and S. Kim. Depts. Of Veterinary Biosciences
Abstract:	While the significance of chemical modifications on RNA has been demonstrated, the specific roles of these modifications in HIV-1 replication remain unclear and even controversial. Previous studies provide only low-resolution, type-specific RNA modification site mapping and relied on indirect analyses of phenotypic effects through overexpression or knockdown (knockout) of host effectors. These approaches overlook site-specific and context-dependent functions of viral RNA modifications. In this study, we introduce a novel Nanopore direct RNA sequencing (DRS) library preparation method for full-length HIV-1 RNAs. Our analysis unveiled a surprisingly simple HIV-1 modification landscape, with three dominant site-specific N6-methyladenosine (m6A) modifications located near the 3' end. Confirmation of these m6A sites was achieved through site-directed mutagenesis, oligonucleotide LC–MS/MS, and in vitro treatments with a m6A eraser, ALKBH5. Interestingly, in our m6A-knockout-virus experiments, all the single mutants – lacking one of these three m6As – showed no notable reductions in any of the examined replication steps, including total HIV-1 RNA production, viral protein expression, virion production, and infectivity. However, the removal of all three dominant m6As (triple mutation) showed a significant reduction in full-length HIV-1 RNA and protein translation. To further investigate the defects of triple mutant in producing full-length RNA, we analyzed alternative splicing patterns of HIV-1 RNAs by quantifying the splicing donor and acceptor usage rates. The triple mutants exhibited a significantly lower fraction of unspliced RNAs and a higher utilization of splicing donors and acceptors compared to the WT, suggesting the crucial roles of the three m6As in the regulation of HIV-1 RNA isoforms. Our HIV-1-specific m6As knockout and full-length DRS analyses have shed light on the functional and evolutionary significance of these site-specific m6As in HIV-1 replication. The technological innovations presented here will also serve as a useful reference for future explorations of the complex RNA biology.
Keywords for abstract:	Human immunodeficiency virus Viral epitranscriptome RNA modifications Direct RNA sequencing

MCB-4

Title of abstract:	**STANDARDIZING METHODS FOR CHARACTERIZING THE CANINE URINARY TRACT MICROBIOTA**
Authors:	Zachary J. Lewis,[1] Angela Scott,[1] Christopher Madden,[1] Sheryl S. Justice,[2] Adam Rudinsky,[3] Jessica Hokamp,[4] Vanessa L. Hale[1] Depts. Veterinary Preventive Medicine, College of Nursing, Veterinary Clinical Sciences, and Veterinary Biosciences
Abstract:	Recent studies highlight the role of microbiota in cancer development and therapeutic response. However, efforts to characterize urinary microbiota and its role in bladder cancer (BC) have been limited due to technical challenges including low microbial biomass and potentially high host cell shedding in urine. While a few studies have identified links between the urobiome and BC, additional mechanistic studies with standardized methods are needed. In this project, I evaluate urine sample volume and host cell removal on urobiome profiles in healthy dogs. We collected urine from five dogs and fractionated samples into 0.1-5.0 mL aliquots before DNA extraction and 16S rRNA or shotgun metagenomic sequencing. To evaluate effects of host cell removal, we collected urine from seven dogs. We extracted each sample using six methods (Bacteremia (B), DNA Microbiome (D), Molysis, NEBNext, HostZero, and Propidium Monoazide). Total and bacterial DNA concentrations were measured via Qubit and qPCR. Bacterial sequences were analyzed using QIIME2, MetaPhlAn4, and R. The microbial community profiles (16S), observed in ≥3.0 mL urine samples had significantly lower abundances of contaminating microbial sequences (p=0.026) and less variable communities than samples with lesser urine volumes (p=0.005). Method B maximized total and bacterial DNA yield. Method D demonstrated effective host cell removal. Urobiome studies have been limited to characterization via culture and 16s rRNA sequencing. Few studies have attempted shotgun metagenomic sequencing and none, to our knowledge, have reported metagenome-assembled microbial genomes (MAGs) and genome-resolved analyses of the urobiota. Method D maximized taxa identification (p=0.01) and MAG recovery (p=0.04) in spiked samples from the shotgun dataset, but overall identifiable diversity was lower than in the 16S dataset. Initial results from shotgun sequencing suggest the construction of MAGs is feasible, but that community and functional analyses of the urobiome may be limited to the gene-resolved, rather than genome-resolved, level.
Keywords for abstract:	Canine urine microbiome Shotgun metagenomics 16S sequencing Urinary tract Host cell removal

Title of abstract:	**THE NEONATAL FC RECEPTOR (FCRN) IS AN ESSENTIAL ARTERIVIRUS ENTRY FACTOR**
Authors:	M. Mousa-Makky, T. Shaw, D. Huey, J. Compaleo, F. Jiang, H. Li, A. Bailey, C. Warren
Abstract:	Simian arteriviruses are endemic in African nonhuman primates yet remain largely unstudied and uncultured *in vitro*. These viruses can cause Ebola-like diseases that are fatal to Asian macaques but are not yet known to infect humans. The reasons for this are unclear. Receptor binding is a primary barrier to the cross-species transmission of viruses from animals to humans. Thus, we undertook a study to identify and characterize the cellular receptors required for simian arterivirus infection. First, using a genome-wide CRISPR-Cas9 genetic screen, we identified CD163 and the neonatal Fc receptor (FcRn) as candidate simian arterivirus receptors. We demonstrate that FcRn knockout abrogates simian arterivirus infection, and that receptor complementation restores virus infection. Next, we showed that FcRn acts at the stage of viral entry using viral genome-transfection experiments and virus particle internalization assays. Further, we show that heightened FcRn expression in normally permissive cells enhances virion uptake. To determine whether both CD163 and FcRn are necessary for arterivirus infection, receptor null Vero cells were engineered to stably express both receptors. Interestingly, we found that expression of both receptors renders Vero cells wholly permissive to arterivirus infection, including high-titer virus production and robust cytopathic effects. We conclude that both CD163 and FcRn join forces to support arterivirus infection. Future studies are focused on unraveling the mechanisms of arterivirus-receptor interactions.
Keywords for abstract:	Arteriviruses

Title of abstract:	**TARGETING TBL1X TO PROMOTE GENOMIC INSTABILITY IN MANTLE CELL LYMPHOMA**
Authors:	B Pray, E Baiocchi, J Williams, J Carvajal-Moreno, KC Wing, J Yalowich, L Alinari Depts of Veterinary Bioscience, Internal Medicine, and Pharmacology
Abstract:	Mantle Cell Lymphoma (MCL) is an incurable B-cell lymphoma characterized by significant genomic instability. MCL patients who progress on targeted therapies, such as ibrutinib, have a short survival; there is thus an urgent need for novel therapeutic strategies. Our group has shown that transducin β-like protein 1 (TBL1X) stabilizes key oncogenic proteins, such as PLK1 and c-MYC, in diffuse large B-cell lymphoma through interaction with a SKP1-CUL1-F-box protein supercomplex. The function of TBL1X in MCL, however, was previously unexplored. Our data show that unlike normal B cells, MCL cells express abundant levels of TBL1 and that genetic knockdown of TBL1 and treatment with tegavivint (Iterion), a first-in-class small molecule targeting of TBL1, promote MCL cell death in vitro and in vivo. Moreover, treatment of MCL cells with tegavivint induces significant DNA damage and depletion of key DNA damage response (DDR) and cell cycle regulatory proteins, including Rad51 and cyclin D1, the latter being a key driver of MCL pathogenesis for which targeted therapeutic interventions do not currently exist. The results of this project (1) elucidate the oncogenic role of TBL1X in maintaining genomic stability in MCL and (2) establish TBL1 as a novel therapeutic target in MCL, thus facilitating the development of a novel therapeutic strategy for patients with this incurable disease.
Keywords for abstract:	cancer, mantle cell lymphoma, TBL1X, DNA damage response

Title of abstract:	**ANAPLASMA PHAGOCYTOPHYLUM T4SS EFFECTOR EGEA HIJACKS ER-GOLGI PROTEINS TO PATHOGEN-OCCUPIED INCLUSIONS FOR MULTIPLICATION**
Authors:	L. Wang, M. Lin, L. Hou, and Y. Rikihisa. Depts. Of Veterinary Biosciences
Abstract:	Human granulocytic anaplasmosis (HGA) is an emerging tick-borne infectious disease that causes a potentially fatal, severe influenza-like illness. The causative agent of HGA, *Anaplasma phagocytophilum (Aph)*, is an obligatory intracellular bacterium that proliferates in the membrane bound compartment "inclusions" in the cytoplasm of neutrophils. Mechanisms by which *Aph* infects, survives, and proliferates in these host defensive cells remain mostly unknown. *Aph* has Type IV secretion system (T4SS) that can secrete effector molecules into human cells. We predicted the APH0874 protein is a new *Aph* T4SS effector using bacterial two-hybrid system. To validate APH0874 as a bona fide T4SS effector, cellular localization of native APH0874 and FLAG-tagged APH0874 with/without its C-terminal secretion signal expressed by *Aph* mutants were examined by immunofluorescence labelling. Results showed that both native APH0874 and FLAG-APH0874 are secreted and localized to *Aph* inclusions, while the fragment without secretion signal localized within *Aph* inclusions. To determine roles of APH0874 in *Aph* infection, APH0874 was knocked down using anti-sense peptide nucleic acid (PNA) of APH0874. Results showed that APH0874 PNA knockdown significantly reduced *Aph* infection. By constructing GFP-tagged full-length or truncated APH0874, we observed that both full-length and C-terminal half of APH0874 localized to the Golgi apparatus in uninfected cells, and on *Aph* inclusion membranes in infected cells. Pulldown assay for proteomics analysis and yeast two-hybrid screening indicates that APH0874 interacts with two ER-Golgi proteins. ER stress markers were analyzed by RT-qPCR and results showed that ER stress is not activated by *Aph* infection or overexpression of APH0874.These results demonstrated APH0874 is a T4SS effector that plays an important role in *Aph* infection of human cells by employing ER-Golgi to facilitate biogenesis of *Aph* inclusions and alleviate ER stress. The findings will help uncovering molecular targets for HGA therapies alternative or adjunctive to doxycycline.
Keywords for abstract:	*Anaplasma phagocytophilum* Human granulocytic anaplasmosis Type IV Secretion System effector *Anaplasma* inclusions ER Golgi

Title of abstract:	**SRPK1 INTERACTS WITH THE HTLV-1 HBZ MRNA AND INFLUENCES CELLULAR PROLIFERATION**
Authors:	R.Zalidvar, J. Seth, T. Wilkie, P. Green, A. Panfil
Abstract:	Human T-cell leukemia virus type 1 (HTLV-1) is an oncogenic retrovirus which causes persistent infection through clonal expansion of infected CD4+ T cells. Among HTLV-1 encoded genes, Hbz is critical for disease development. Hbz is encoded from the antisense strand of the integrated viral genome. Several groups have found that Hbz is multi-functional, playing significant roles in both the RNA and protein form throughout infection and establishment of latency. Hbz is expressed early after viral infection in an animal model, and hbz RNA is expressed in all virally-induced tumor cells. It was recently demonstrated that hbz RNA is predominantly nuclear in infected T cells. We hypothesize cellular protein interactions with hbz RNA secondary structure translates to cell signaling pathways important for viral persistence and cellular proliferation. Mass spectrometry was used to identify cellular proteins that differentially interact with hbz and an hbz RNA sequence containing a silent mutation (SM) that disrupts the RNA secondary structure. Our proteomics data identified an mRNA splicing factor serine/arginine protein kinase 1 (SRPK1) binding to hbz RNA. Cross-linking immunoprecipitation (CLIP) assays in HEK293T and in HTLV-1 tumor derived T-cell lines (ATL-ED) further validated this interaction. Expression vectors encoding hbz RNA only (hbzTTG) and hbz with silent mutations (hbz SM) were generated and proliferation assays in Kit-225 cells demonstrated that cells stably expressing hbzTTG showed a proliferative advantage. shRNA-mediated knockdown of SRPK1 in Kit-225 hbzTTG cells and ATL-ED cell lines was performed and localization of hbz RNA was examined using cellular fractionation and RT-qPCR. SRPK1 knockdown in Kit-225 hbzTTG cells and ATL-ED cells decreased cellular proliferation and caused redistribution of hbz from the nucleus to the cytoplasm. In conclusion, Hbz RNA proliferative abilities depend on nuclear localization and at least one cellular factor which controls this localization is SRPK1.
Keywords for abstract:	HTLV-1, Retrovirus, persistent, Hbz RNA, cellular proliferation, RNA secondary structure, SRPK1, latency

STRUCTURE/FUNCTION

SF-1

Title of abstract:	**UNLICENSED ANTIVIRAL PRODUCTS USED FOR THE AT-HOME TREATMENT OF FELINE INFECTIOUS PERITONITIS CONTAIN GS-441524 AT SIGNIFICANTLY DIFFERENT AMOUNTS THAN ADVERTISED**
Authors:	A. Kent. The Ohio State College of Veterinary Medicine S. Guan. Department of Biochemistry, University of California- Davis W. Novicoff. University of Virginia, School of Medicine N. Jacques. San Jose, CA S. Evans. Dep. Of Biomedical Sciences, Colorado State University
Abstract:	This study analyzed the content of unlicensed GS-441524-like products being used as a largely successful at-home treatment for cats suspected to have FIP. The remdesivir content and pH were also measured. The study included 127 injectable and oral samples from 30 of the most popular brands of black market producers. Unlicensed GS-441524-like products were procured through donations and tested for GS-441524 and remdesivir content by liquid chromatography with tandem mass spectrometry. A pH meter measured the pH of injectable samples. Of the 87 injectable formulations, 95% contained more (on average 39% more) GS-441524 than expected based on the producer's marketed concentrations. The average pH (1.30 pH) was well below the physiologic pH conditions recommended for SC injections. The oral formulations were more variable, with 43% containing more GS-441524 (on average 75% more) than expected and 58% containing less (on average 39% less) than the expected content. There was minimal variability in GS-441524 content between replicate samples in the injectables formulations (measured by coefficient of variation). One injectable and 2 oral samples additionally contained remdesivir. All unlicensed products used for the at-home treatment of FIP that we tested contain GS-441524. The injectables generally contain significantly more drug than advertised at a below-physiologic pH. Unlicensed oral products vary more widely in drug content and suffer from unconventional dosing and labeling. These data should highlight the need for regulation of these products and the development of legal pathways to procure GS-441524.
Keywords for abstract:	FIP GS-441524 liquid chromatography mass spectrometry remdesivir

Title of abstract:	**EMBRYO SIZE CLASSIFICATION AT TIME OF EGG COLLECTION AND ITS RELATIONSHIP TO HATCH SUCCESS AND UMBILICAL SCARRING IN FLORIDA ALLIGATORS (*ALLIGATOR MISSISSIPPIENSIS*)**
Authors:	N. Lordi, J. Flint, and M. Flint. One Welfare and Sustainability Center of Dept. of Preventive Medicine
Abstract:	The alligator industry is a multi-million dollar enterprise with farms across most of the southeastern US. The main source of revenue comes from harvesting hides. The presence of umbilical scars decreases the value of hides and has been identified as a significant issue in the industry. Umbilical scarring or defects are believed to be caused by incomplete absorption of the yolk sac and/or incomplete healing of the navel. The exact mechanism of scarring contributed during incubation is unknown. Objectives included: examining the hatch success and incidence of umbilical scarring in American alligators in comparison to the embryo size classification at early candling, and to develop a non-lethal staging scheme to broadly classify the stage of embryo development during field collection of eggs. 369 eggs from 12 clutches and two locations were incubated. Eggs were candled at least once to assign a developmental size classification and record any key anatomic features or measurements. Post-hatch data included hatch success, umbilical assessment, length, and weight. We hypothesized that a lower hatch success and umbilical scarring would be more common in embryos that are at an earlier stage of development at time of collection. The overall hatch success was 62%. A significant difference in hatch success was appreciated between small and large embryos ($\rho=0.03$). 9 of the 204 hatchlings had an umbilical defect. A significant relationship between embryo size, length, weight, and umbilical scarring was not determined. A non-lethal embryo classification scheme included measurements and anatomical features such as body length, limb morphology, tail flexion, and body pigmentation. Findings highlight the potential for improved hatch success by allowing embryos to develop more prior to collection. The non-lethal staging scheme also provides farms with the ability to classify embryo size by selecting eggs based on embryologic development with relative ease in the field.
Keywords for abstract:	American alligator Incubation Alligator hatchlings Umbilical scarring Hatch success Alligator farms

Title of abstract:	**THE EFFECT OF PROPOFOL ON SIGNS AND ENDOCRINE VARIABLES OF NAUSEA IN DOGS AFTER MORPHINE ADMINISTRATION**
Authors:	C.B. Seger1, K.A. Muñoz1*, L. Adams1, A. Kamr1, A. Wanstrath1, and R.E. Toribio1 1Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State University, Ohio, USA
Abstract:	Postoperative nausea and vomiting is an unpleasant sensation experienced by humans. Adrenocorticotropic hormone (ACTH), cortisol, arginine vasopressin (AVP), and 5-hydroxyindoleacetic acid (5-HIAA) objectively assess nausea in humans. Sub-hypnotic doses of propofol provide anti-nausea effects in humans. No data exists in animals. To evaluate anti-nausea effects of sub-hypnotic intravenous doses of propofol, 6 healthy dogs were randomized into 4 groups: saline at 0.1 ml/kg (S), propofol at 0.5 mg/kg (P1), propofol at 1.0 mg/kg (P2), and propofol at 1.5 mg/kg (P3). At the zero-timepoint, nausea scores were determined and morphine (0.5 mg/kg) administered intramuscularly immediately thereafter. At 20 minutes, nausea scores were recorded and dogs received their assigned treatment (S, P1, P2, or P3) intravenously. Blood was collected at 0, 10, 20, 50, 200 and 380 minutes for measurement of ACTH, AVP, cortisol and 5-HIAA concentrations. Nausea scores increased ($p < 0.05$) at 5 minutes (all groups), 10 minutes (P2), 20 minutes (P3), 50 minutes groups (S, P1, P2), 80 and 140 minutes (all groups), and 200 minutes (S, P2 and P3). ACTH increased ($p < 0.05$) at 10 minutes (P1, P3) and 50 minutes (S, P1). ACTH was lower ($p < 0.05$) in P2 versus P1, P2 versus S, and P3 versus S. Cortisol increased at ($p < 0.05$) at 50 minutes (S, P1, P2) and at 200 minutes (P2). At 50 minutes, cortisol was lower ($p < 0.05$) for P3 versus S, P2 versus S, and P3 versus P1, and at 200 minutes for P1 versus P2. There was no significant difference in AVP and 5-HIAA. Propofol (1.5 mg/kg) appeared to decrease signs of nausea for approximately 60 minutes in dogs. At 50 minutes, increasing doses of propofol reduced biomarker indicators of nausea. This study provides evidence that propofol alters clinical and endocrine variables associated with nausea in dogs.
Keywords for abstract:	Biomarkers Canine Nausea Propofol Vomiting

Title of abstract:	**ECHOCARDIOGRAPHIC EVALUATION OF PULMONARY VASCULAR RESISTANCE IN DOGS WITH PULMONARY HYPERTENSION**
Authors:	<u>A. Stavri</u>, M. Krasnow, K. Schober Dept. of Veterinary Clinical Sciences, The Ohio State University
Abstract:	Background: Pulmonary vascular resistance (PVR) is an important hemodynamic variable in the development and classification of pulmonary hypertension (PH), has prognostic relevance, and may aid in therapeutic decision-making. There is a lack of data on PVR in dogs with PH. Hypothesis/Objectives: Echocardiographic estimation of PVR in dogs is feasible and can be used to differentiate between pre-capillary PH (pre-PH), isolated post-capillary PH (Ipc-PH), and combined post- and pre-capillary PH (Cpc-PH) and provides valuable hemodynamic information beyond that derived from tricuspid regurgitation (TR) based estimation of PH. Animals: 459 dogs with PH and 38 control dogs with TR. Methods: Retrospective observational study. Eighteen clinical and 60 echocardiographic variables predicting PH and PVR were evaluated. PVR (pulmonary artery pressure divided by pulmonary flow) was calculated using 3 equations validated in people. Dogs with pre-PH, Ipc-PH, and Cpc-PH were compared using common statistical tests for large group comparisons. A p-value <0.05 was considered significant. Results: Normal values were derived from the control dogs. There were 213 dogs with pre-PH and 246 dogs with post-PH. Average PVR was 2.5 ± 0.9 WU in control dogs. Median was 8.8 WU (min to max, 1.5 – 28.0), 4.6 WU (1.2 – 6.1), and 9.2 WU (6.1 – 26.8) in dogs with pre-PH, Ipc-PH, and Cpc-PH, respectively. PVR was disproportionally increased (8.8 ± 2.1 WU) in 21 dogs with mild Cpc-PH (TR velocity 3.19 ± 0.16 m/s) and normal (4.4 ± 1.2 WU) in 7 dogs with severe Ipc-PH (TR velocity 4.19 ± 0.40 m/s), identifying subpopulations where estimation of PVR could be particularly beneficial. Conclusions: Echocardiographic estimation of PVR is feasible and clinically useful.
Keywords for abstract:	Pulmonary vascular resistance Echocardiogram Pulmonary hypertension Pre-capillary pulmonary hypertension Post-capillary pulmonary hypertension

Title of abstract:	**HISTOLOGIC CHARACTERIZATION OF BROOD X CICADAS**
Authors:	Sara Tonissen1, Johanna Rawlings1, Elise E.B. LaDouceur2, Ellen Klinger3, and Megan E. Schreeg1 1The Ohio State University College of Veterinary Medicine, Department of Veterinary Biosciences, Columbus, OH, 2Joint Pathology Center, Silver Springs, MD, 3The Ohio State University College of Food, Agriculture, and Environmental Sciences, Department of Ecology, Columbus, OH
Abstract:	Several ecological observational studies have been performed on periodical cicadas, but population histology has not been characterized. The aim of this project was to histologically characterize Brood X cicadas. We hypothesized that we would identify lesions contributing to mortality in cicadas found dead. Fifty-one Brood X cicadas (31 found dead (FD); 20 caught live (CL)) were collected in Powell, OH and examined. Gross features were used to differentiate between sex and the three species within Brood X (Magicicada septendecim, M. cassini, and M. septendecula). Males were overrepresented in the FD cicadas and underrepresented in the CL cicadas. Cicadas were fixed in Davidson's fixative for 5-13 days, trimmed using serial transverse and sagittal sections, then processed routinely for histologic evaluation. After initial evaluation, 16 FD cicadas were excluded due to severe postmortem autolysis. Tissues identified included: cuticle (35/35), epidermis (35/35), skeletal muscle (35/35), mouthparts (30/35), cephalic glands (35/35), tracheae and tracheoles (35/35), brain (34/35), peripheral nerves (33/35), compound eyes (35/35), foregut (33/35), epidermal glands (34/35), midgut (35/35), hindgut (23/35), fat body (34/35), Malpighian tubules (25/35), heart (9/35), aorta (28/35), vessels (33/35), and gonads (34/35). Minor lesions in the cuticle (8/15 FD; 12/20 CL), epidermis (2/15 FD; 12/20 CL), skeletal muscle (7/15 FD; 8/20 CL), and mouth parts (3/15 FD; 7/20 CL) were most common. Evidence of systemic disease (Massospora cicadina infection, n=2; bacterial sepsis, n=1; protozoal infection, n=1) was rare and only identified in CL cicadas. Bacterial/fungal overgrowth was common in FD cicadas, and causes of death were not apparent.
Keywords for abstract:	Brood X cicadas Massospora cicadina Found Dead Caught Live Lesions Systemic Disease