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COLLEGE OF VETERINARY MEDICINE

**COLLEGE OF
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RESEARCH DAY**

2023

**BOOK OF
ABSTRACTS**

2023 CVM Research Day Keynote Lecture

Sex Steroid Hormones and Renal Acid -Base
Balance: What's All the Fuss About?



Dr. Autumn Harris, DVM

*Assistant Professor, Small Animal Internal Medicine
Department of Small Animal Clinical Sciences
University of Florida
College of Veterinary Medicine*



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Cellular Senescence in Renal Aging and Disease



Jessica Quimby, DVM, PhD

Associate Professor, Small Animal Internal Medicine
Department of Veterinary Clinical Sciences.

Research focus: Renal pathophysiology, novel strategies, and feline clinical pharmacology focusing on improving supportive care and quality of life in cats with CKD.

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Neutralizing antibody response to SARS-CoV2 infection and mRNA vaccination



Shan-Lu Liu, MD, PhD

Professor, Virology

Department of Veterinary Biosciences

Co-Director of the Viruses and Emerging Pathogens' Program of Ohio State's Infectious Disease Institute

Research focus: Virus-host interaction, particularly host factors that modulate virus entry and release.

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POSTER JUDGES

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

Turi Aarnes

Teresa Burns

Sushmitha Durgam

Jaylene Flint

Autumn Harris

Brian Husbands

Ryan Jennings

Vladi Karniychuk

Haichang Li

Angela Marolf

Stacey Meeker

Sarah Moore

Stefan Niewiesk

Mike Oglesbee

Amanda Panfil

Yasuko Rikihisa

Eric Schroeder

Ramiro Toribio

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

2023 Faculty Chair:
Dr. Jessica Quimby
Associate Professor, Veterinary Clinical Sciences

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

CLINICAL RESEARCH

CR - 1

Title of abstract:	PHARMACOKINETICS AND TOLERABILITY OF MULTIPLE-DAY ORAL-DOSING OF MYCOPHENOLATE MOFETIL IN HEALTHY HORSES
Authors:	<p>K. Bello[*], G. Lorch[*], K. Kim[†], R. Toribio[*], L. Yan[†], Z. Xie[†], K. Hill[†], M. Phelps[†]</p> <p>[*]Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH, USA; [†]Division of Pharmaceutics & Pharmacology, College of Pharmacy, The Ohio State University, Columbus, OH, USA.</p>
Abstract:	<p>Background: Additional efficacious immunomodulatory therapy is needed for the treatment of equine immune-mediated disease. Mycophenolate mofetil (MMF) is an immunosuppressive drug that warrants assessment as a viable therapeutic for horses.</p> <p>Hypothesis/Objectives: To evaluate the pharmacokinetics (PK) of multiple-day oral-dosing MMF in healthy horses and to determine the tolerability of a dosing regimen.</p> <p>Animals: Six healthy Standardbred mares.</p> <p>Methods: Horses received MMF 10 mg/kg PO q 12 h for seven days in the fed state. PK serial sampling was performed over 24 h on days 1 and 7 with trough samples collected every 24 h, immediately before a.m. drug administration. Noncompartmental PK analyses were performed to determine primary PK parameters, followed by calculation of geometric means and coefficients of variation. CBC, biochemical profiles, physical examinations, and fecal scoring were used to assess dose tolerability.</p> <p>Results: Seven days of therapy resulted in a mycophenolic acid (MPA) area under the curve ($AUC_{inf-obs}$) of 22,862 h*ng/ml and terminal half-life ($T_{1/2}$) of 11.3 h, yielding successful hematologic immunosuppression and minor metabolite accumulation in all horses treated. Salmonellosis was detected in the feces of two horses by day 7, while all horses developed hyporexia, decreased gastrointestinal motility, and decreased fecal output by the seventh day of therapy.</p> <p>Conclusion and clinical importance: Administration of MMF 10 mg/kg PO q 12 h achieved hematologic evidence of immunosuppression within one week of treatment. A decreased MMF dose and/or frequency is needed to avoid colic. Therapeutic drug monitoring should include frequent hemograms, biochemical profiles and strict biosecurity protocols.</p>
Keywords for abstract:	Immune-mediated Equine Dermatology Neutropenia Lymphopenia Thrombocytopenia

CR - 2

Title of abstract:	CHARACTERISTICS, SURGICAL TREATMENT AND OUTCOME OF INJURIES INVOLVING THE TARSUS IN GREYHOUNDS
Authors:	<u>M. Biggo</u> ¹ , N. R. Kieves ¹ , S. C. Jones ² , S. Tinga ³ , A. Wanstrath ¹ , B. Carson ¹ , K. Schaul ⁴ , C. Folette ⁵ , and J. Dyce ¹ 1. Department of Veterinary Clinical Sciences, The Ohio State University 2. Bark City Veterinary Orthopedic Surgery Center 3. Department of Clinical Sciences, Cornell University College of Veterinary Medicine 4. BluePearl Pet Hospital Tampa, FL 5. VCA Animal Specialty Group, Los Angeles, Ca
Abstract:	Tarsal injury description, surgical intervention elected, and postoperative complications were retrospectively evaluated in 116 greyhounds. The most common tarsal injuries reported were CTB fractures (67/116; 57.75%), calcaneus fractures (66/116; 56.89%), and joint subluxation/luxation (53/116; 45.69%). The most commonly performed initial surgical intervention was a partial tarsal arthrodesis without additional procedures (44 cases; 37.93%). Of the 115 greyhounds that survived to discharge, 40.00% (46/115) were diagnosed with a surgical site infection (SSI) via positive bacterial culture and 52.17% (60/115) underwent implant removal. When excluding cases that had an open fracture at the time of presentation, the SSI rate was 34.78% (40/115). These numbers are markedly higher than reported in previous literature. Patients diagnosed with a mid-body calcaneal fractures with fissures extending to the distal articular surface had a significantly higher probability of requiring an explantation compared to those cases without a calcaneal fracture. A positive relationship was also demonstrated between increasing anesthesia time and odds of requiring an explantation. Practitioners performing surgical intervention for tarsal injuries in greyhounds should be prepared for the high likelihood that an explantation will be required following healing, particularly with injuries involving mid-body calcaneal fractures with fissures extending to the distal articular surface. Additionally, anesthesia and surgery time should be minimized in these cases to help decrease the chances of explantation.
Keywords for abstract:	Greyhound Tarsus Racing injury Surgical site infection rate Explantation rate

CR - 3

Title of abstract:	MEASURING 25-HYDROXYVITAMIN D IN CATS; COMPARISON OF A WHOLE-BLOOD LATERAL FLOW ASSAY, 2 DRIED-BLOOD-SPOT TESTS, AND SERUM LC-MS/MS
Authors:	<u>Hannah Brodlie</u> , Jessica Quimby, Adam J. Rudinsky, Rene E. Paschall, Katelyn Brusach, Hannah Klein, Jenessa A. Winston, Valerie J. Parker. Department of Veterinary Clinical Sciences, (Brodlie, Quimby, Rudinsky, Paschall, Brusach, Klein, Winston, Parker);Comparative Hepatobiliary and Intestinal Research Program (CHIRP; Brodlie, Rudinsky, Klein, Winston, Parker), College of Veterinary Medicine, The Ohio State University, Columbus, OH, USA.
Abstract:	Measuring 25-hydroxyvitamin D (25D) can be a diagnostic challenge in veterinary medicine because of laboratory accessibility and required sample volume. We compared 2 dried-blood-spot [DBS] tests and a lateral flow assay [LFA] to the gold-standard liquid chromatography-tandem mass spectrometry (LC-MS/MS). We hypothesized that there would be good agreement among the tests, within a clinically significant limit of agreement of ± 25 nmol/L (10 ng/mL). We collected blood from 6 healthy purpose-bred 2-y-old cats at 6 times over 6 wk, and measured 25D concentrations with all tests. Agreement of the 3 candidate tests and LC-MS/MS was evaluated via Bland-Altman analysis, Passing-Bablok regression, and Lin correlation coefficients. Bland-Altman analysis demonstrated that the mean bias was $> \pm 25$ nmol/L (10 ng/mL) for all 3 candidate tests in comparison to serum LC-MS/MS concentrations. The 95% CIs for the mean bias did not include zero, further supporting the presence of significant bias among methods. Additionally, all 3 tests had poor agreement with serum LC-MS/MS concentrations when analyzed by Lin correlation coefficient analysis, and bias between methods was further characterized by Passing-Bablok analysis. Based on these results, none of these 3 tests is recommended as an alternative to LC-MS/MS testing for 25D measurement in cats.
Keywords for abstract:	cats dried-blood-spot test lateral-flow assay vitamin D

CR - 4

Title of abstract:	ETHICAL CONSIDERATIONS AND OUTCOME MEASUREMENT IN ACCESSIBLE VETERINARY CARE
Authors:	<u>Ellen Bryant</u> , Rebecca Garabed Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio
Abstract:	<p>Access to Veterinary Care (AVC) and the question of how to increase access for those who may otherwise not be able to utilize veterinary services is currently at the forefront of veterinary medicine. Veterinary care, like human healthcare, can be considered a limited or scarce resource for which the demand cannot be satisfied. As such, with the goal of improving access in mind, decisions must be made as to who will and will not be eligible for services, and regarding the desired impact. The ethical frameworks used to allocate these resources are well studied in human bioethics, but the same cannot be said for veterinary medicine. With this study, we will examine the prevalent ethical frameworks that guide decision making in human medicine and correlate these to veterinary medicine. Frameworks can be categorized by whom they aim to support, and their desired result. Broadly speaking, these are broken down into utilitarian principles which maximize overall health benefit or years of life, egalitarianism which offers equal chance of receiving support or equal resources across a population, welfare-based principles which prioritize the most vulnerable or susceptible groups, and desert-based principles which distribute resources relative to individuals' contributions to society or what is "deserved." Focus groups and interviews will be conducted among veterinarians, professionals in low-cost or accessible veterinary services, and clients to assess and compare how these groups employ ethical frameworks to make decisions and achieve desirable outcomes of treatment.</p>
Keywords for abstract:	Bioethics Veterinary ethics Distributive justice Access to veterinary care Subsidized care

CR - 5

Title of abstract:	INCIDENCE OF BRAIN ABNORMALITIES IN DOGS WITH GERIATRIC-ONSET SEIZURES USING 3T MRI AND COMPREHENSIVE SCANNING PROTOCOL
Authors:	<u>M. Cantu</u> , A. Habing, S. Moore, G. Habing, R. Urion. Depts. of Veterinary Preventive Medicine and Veterinary Clinical Sciences
Abstract:	<p>Seizures are one of the most common neurological presentations in dogs and the incidence of structural brain disease as the cause of seizure activity increases with patient age. However, there are still patients for which an imaging diagnosis cannot be achieved, challenging therapeutic decision-making. Magnetic resonance imaging (MRI) is the current gold standard for brain imaging but diagnostic utility is affected by both magnet strength and sequence protocol. The addition of T2*-weighted (T2*w) and fluid-attenuated inversion recovery (FLAIR) sequences may increase sensitivity of detection for blood product and edema-like lesions, respectively, but as magnet strength and sequence selection are not standardized across institutions, this variability may affect the identification of structural brain disease on MRI. We hypothesized that the incidence of structural brain disease in dogs with geriatric-onset seizures would be higher than previously reported when using a high-field (3T) MRI and additional pulse sequences. This retrospective study examined the medical records of dogs with geriatric-onset (≥ 7 years of age) seizure activity which underwent 3T MRI imaging of the brain, including standard pulse sequences as well as FLAIR, T2*w, and pre- and post-contrast T1 sequences. Images were reviewed by two board-certified radiologists and one board-certified neurologist, following which a consensus was sought regarding the presence or absence of structural brain disease and the perceived utility of FLAIR and T2*w sequences. Age, sex, and breed were collected. Data collection and interpretation are still in progress but preliminarily, the use of T2*w images commonly resulted in increased identification of cerebral microbleeds over standard pulse sequences but uncommonly affected identification of other structural brain disease. The use of FLAIR infrequently affected the final diagnosis but provided increased sensitivity for detection of perilesional edema. These results may help guide future imaging recommendations and allow for refined management of these cases.</p>
Keywords for abstract:	MRI Seizures Geriatric Neurology

CR - 6

Title of abstract:	EVALUATION OF A NOVEL TECHNIQUE FOR URETHRAL CATHETERIZATION IN FEMALE CATS AND DOGS WEIGHING LESS THAN 10 KILOGRAMS: A PROSPECTIVE RANDOMIZED CROSSOVER STUDY
Authors:	JA Dornbusch, PE Yaxley, AC Hechler, JK Byron, LE Selmic of the Department of Veterinary Clinical Sciences
Abstract:	<p><i>Objectives:</i> To compare the success rates for urethral catheterization in clinical patients using the traditional and two-catheter techniques when placed by personnel of all experience levels.</p> <p><i>Animals:</i> 38 female cats and dogs weighing less than 10 kilograms that required urethral catheterization at the Ohio State University were prospectively enrolled from August 2020 to November 2022.</p> <p><i>Procedures:</i> Enrolled animals were randomized to have a urethral catheter placed either via the traditional technique or via the two-catheter method under sedation or general anesthesia. Any qualified hospital personnel of any experience level were allowed to place the catheter (veterinary students, technicians, interns, residents, and faculty). If after five minutes the animal was not successfully catheterized, the alternate method was performed. The previous experience of the catheter placer, animal signalment, animal condition that necessitated catheter placement, time to successful placement, and which technique was successful was recorded.</p> <p><i>Results:</i> The two-catheter technique was more successful than the traditional method (60.5% and 34.2%, respectively) for urethral catheterization when used by a variety of hospital personnel. Eight of nine (88.9%) of novice catheter placers that placed their first urinary catheter in this study succeeded with the two-catheter technique and only one was successful with the traditional method.</p> <p><i>Clinical Relevance:</i> Placement of female urinary catheters in small patients that are unable to have concurrent digital palpation can be improved with use of the two-catheter technique. This technique may also be helpful in the inexperienced catheter placer population to aid in guidance into the urethral papilla.</p>
Keywords for abstract:	<p>Bioethics</p> <p>Veterinary ethics</p> <p>Distributive justice</p> <p>Access to veterinary care</p> <p>Subsidized care</p>

CR - 7

Title of abstract:	UTILITY OF THE RESPIRATORY RATE-OXYGENATION (ROX) INDEX AS A PREDICTOR OF TREATMENT RESPONSE IN DOGS RECEIVING HIGH-FLOW NASAL CANNULA OXYGEN THERAPY
Authors:	<u>E. Duble</u> ¹ , A. Young ¹ , C. Pouzot-Nevoret ² , K. Kuo ³ , and J. Her ¹ ¹ Department of Veterinary Clinical Sciences, The Ohio State University College of Veterinary Medicine, Columbus, Ohio, USA. ² Intensive Care Unit (SIAMU), Université de Lyon, VetAgro Sup, France ³ Department of Veterinary Sciences, Auburn University College of Veterinary Medicine, Auburn, AL, USA.
Abstract:	<p>High-flow nasal cannula oxygen therapy (HFNC) is a method of escalating oxygen therapy between conventional oxygen supplementation and mechanical ventilation (MV). The respiratory rate-oxygenation (ROX) index (SpO₂:FiO₂ (SF) divided by respiratory rate) have been validated in humans as a predictor of HFNC outcome. The objectives in this study were to determine predictors of HFNC success in dogs and to identify specific cut-off values to guide timely escalation to MV in individuals failing HFNC.</p> <p>88 dogs treated with HFNC were prospectively enrolled. HFNC responders were defined as dogs weaned from HFNC. HFNC non-responders were defined as dogs that were escalated to MV or euthanized due to declining respiratory status. ROX and SF were calculated at baseline and for each hour of HFNC. Variables predicting HFNC success were determined using logistic regression. The overall power of the predictive variables was determined using area under the receiver operating curve (AUC). In a ventilated subgroup analysis, dogs who failed to respond HFNC and were escalated to MV (n = 16) were compared to HFNC responders.</p> <p>Overall success rate of HFNC was 38% (n = 33/88). ROX and SF predicted HFNC success in this population, with acceptable AUC (0.72 and 0.77, <i>P</i> < 0.05). In the ventilated subgroup analysis, ROX and SF were more strongly predictive of HFNC failure (AUC 0.81 and 0.83 respectively, <i>P</i> < 0.05). This relationship was upheld with individual timepoint analysis. At hour 3, ROX < 4.6 (AUC 0.86, 100% specificity, 61% sensitivity) was predictive of HFNC failure. At hour 7, SF < 122 (AUC 0.93, 89% specificity, 100% sensitivity) was predictive of HFNC failure.</p> <p>ROX and SF were found to be excellent predictors of HFNC outcome, particularly in a ventilated subgroup analysis. Future studies are warranted to confirm these findings in a larger population of HFNC non-responders escalated to MV.</p>
Keywords for abstract:	Canine High flow nasal cannula oxygen therapy ROX index SpO ₂ FiO ₂ ratio

CR - 8

Title of abstract:	INFLUENCE OF CLINICAL EXPERIENCE, SIMULATION MODELS, AND CADAVERIC LABORATORY ON THE STRESS RESPONSE OF 3RD YEAR VETERINARY STUDENTS PERFORMING 1ST ELECTIVE SURGERY
Authors:	<u>AK. Erickson</u> , BA. Carson, LE. Selmic, LS. Bednarski, MA. McLoughlin. Department of Veterinary Clinical Sciences.
Abstract:	<p>Objective: To evaluate the role of simulation models and previous surgical experience on subjective and objective stress levels of students performing their 1st elective surgery.</p> <p>Samples: One hundred and forty-one third year veterinary students</p> <p>Procedure: Using a pre-post experimental design, salivary alpha amylase and cortisol were evaluated as markers of physiologic stress response during students' first elective surgery. Student self-reported State-Trait Anxiety Inventory (STAI) scores and quantitative measures of experience were correlated to biomarker results.</p> <p>Results: No association was found for change in salivary biomarkers of stress, alpha amylase and cortisol, between baseline and presurgical samples accounting for gender, age, type of elective surgery performed, previous surgical experience, or simulation model use. Salivary cortisol levels were markedly elevated falling between the 66th and 99th percentile compared to an age and gender matched population. Salivary alpha amylase levels were also two to three times higher than those recorded for other health professionals. Veterinary student STAI scores were high falling between the 65th and 73rd percentile compared to working adults in the general population.</p> <p>Clinical relevance: Veterinary student's salivary cortisol, alpha amylase, and STAI scores fell into the upper 2/3rds of the general population, demonstrating a high level of perceived stress. Simulation models and previous surgical experience were not associated with decreased stress. Further evaluation of the implementation of high-fidelity simulation models, maximizing learner outcomes through challenge point framework, and the role of stress on performance is indicated.</p>
Keywords for abstract:	Simulation models Spay and neuter Salivary biomarkers Stress and learning

CR - 9

Title of abstract:	INFRARED THERMOGRAPHY AS A NOVEL TOOL TO ASSESS SMALL INTESTINAL SURFACE TEMPERATURE IN DOGS UNDERGOING LAPAROTOMY FOR FOREIGN BODY OBSTRUCTION
Authors:	<u>J. Finstad</u> , E. Cooper, S. Ten Cate, P. Yaxley, J. Her, J. Guillaumin
Abstract:	Foreign body obstructions (FBO) are a common cause for laparotomy in small animal veterinary medicine and decision making regarding small intestinal (SI) viability can be challenging. The objective of this study was to evaluate infrared thermography (IRT) as a useful diagnostic tool for evaluating SI perfusion. In this prospective observational study, IRT was utilized to compare mean small intestinal surface temperature differences between intestinal locations at the site of FBO as well as segments oral and aboral before and after surgical resolution of obstruction. Patients in which an enterotomy was not performed acted as controls. These differences were then evaluated for correlation with APPLEfast scoring, lactate, foreign body material (hard vs soft), and blood pressure. A total of 43 client owned dogs with FBO underwent laparotomy and were enrolled in the study. The results demonstrated a statistically significant decrease in average temperature at the segment of intestine directly over the foreign body after resolution of FBO ($P = 0.0043$). With hard FB material the SI segment oral was cooler than the segment aboral to the FB, whereas soft FB material was associated with a warmer temperature oral to the foreign body compared to aboral. However, these differences did not achieve significance ($P = 0.08$). There was not a significant difference in temperature between SI segments at the site of FBO, oral or aboral. There was no correlation appreciated with APPLEfast scoring, lactate, or blood pressure and differences in SI segment temperature. This study demonstrated that infrared thermography may be useful diagnostic modality to identify changes in small intestinal surface temperature relating to FBO. Further investigation is warranted to determine if IRT may be a useful and non-invasive technique to evaluate intestinal perfusion.
Keywords for abstract:	Infrared thermography thermal imaging foreign body obstruction laparotomy

<p>Title of abstract:</p>	<p>THROMBOELASTOGRAPHIC RESULTS AND HYPERCOAGULABILITY IN DOGS WITH SURGICALLY TREATED HEPATOCELLULAR ADENOMA AND CARCINOMA: A VETERINARY SOCIETY OF SURGICAL ONCOLOGY STUDY</p>
<p>Authors:</p>	<p><u>G. Fontes</u>, V. Wavreille, J. Lapsley, E. Cooper, J. Guillaumin, L. Selmic, Depts. Of Veterinary Clinical Sciences</p>
<p>Abstract:</p>	<p>Introduction: Liver lobectomy is performed to treat massive hepatocellular carcinoma. Hemorrhage accounts for 83-93% of intraoperative complications. Due to this risk, preoperative hematological and hemostatic tests are performed. The objectives of this study were to compare the hemostatic status between dogs with a liver tumor and healthy control dogs, and to assess the effect of surgery and anesthesia on their hemostatic status by comparing coagulation and thromboelastographic (TEG) measurements at three time points.</p> <p>Materials and Methods: Liver tumor and healthy control dogs receiving surgery for liver lobectomy or spay, were enrolled between January 2021 and June 2022 at The Ohio State University Medical Center. All dogs had blood work collected at three time points: pre-operatively, 24 hours post-operatively, and 2 weeks post-operatively. Hematological and hemostatic values obtained for statistical analysis included the following: hematocrit, platelet count, prothrombin time, activated partial thromboplastin time, fibrinogen levels and TEG parameters. Comparisons of data across time points in each group was performed using repeated measures ANOVA tests.</p> <p>Results: Eight and ten dogs were enrolled for the control and liver groups, respectively. Platelet count was significantly higher in the liver group than the control group at all time points. The strength of the clot (G-value) was significantly increased for the liver group at all time points.</p> <p>Conclusion: The liver group was hypercoagulable based on elevated G-values at all time points compared to the control group. This hypercoagulability was attributed to the effect of hepatic neoplasia alone, and not secondary to surgery and anesthesia.</p>
<p>Keywords for abstract:</p>	<p>Coagulation Dog Hepatocellular adenoma Hepatocellular carcinoma Thromboelastography</p>

CR - 11

Title of abstract:	EFFECTS OF PIMOBENDAN ON LEFT ATRIAL FUNCTION IN CATS WITH LEFT ATRIAL ENLARGEMENT AND DYSFUNCTION
Authors:	<p><u>E. Herrold</u>¹, K. Schober¹, D. Boothe², J. Rhinehart¹, J. Her¹</p> <p>¹ Dept. of Veterinary Clinical Sciences, The Ohio State University</p> <p>² Dept. of Anatomy, Physiology, and Pharmacology, Auburn University College of Veterinary Medicine</p>
Abstract:	<p>Background – Arterial thromboembolism is a devastating consequence of hypertrophic cardiomyopathy (HCM) in cats due to left atrial (LA) enlargement and dysfunction. Prevention of ATE relies on anticoagulant medication, rather than improving atrial transport function.</p> <p>Hypothesis – Pimobendan improves LA systolic function in cats with HCM and LA enlargement.</p> <p>Animals – 14 client-owned cats with stage B2 HCM.</p> <p>Methods – In a prospective, double-blind, placebo-controlled clinical study, echocardiographic assessment of left atrial and left auricular systolic function was performed before and one hour after administration of a single oral dose of pimobendan (0.2-0.3 mg/kg). Plasma concentrations of pimobendan and o-desmethypimobendan (ODMP) were also analyzed.</p> <p>Results – Nine cats received pimobendan and 5 placebo. Preliminary data analysis demonstrated that LA size based on LA area (cm²) (3.70 +/-1.27 vs. 3.10 +/-0.81; P=.08, power=.24) and LA volume (cm³) decreases (5.11 +/-2.54 vs. 4.55 +/-2.36; P=.19, power=.17), left auricular flow velocity (m/s) increases (.34 +/--.15 vs. .50 +/--.29, P=.14, power=.20), and pulmonary venous atrial reversal flow velocity (m/s) increases (.31 +/--.11 vs. .36 +/--.14, P=.08, power=.32) after pimobendan. Compared to the 6/8 cats with expected plasma concentrations (ng/mL) of pimobendan one hour after administration (7.57-33.98) and ODMP (2.75-11.23), plasma concentrations in 2 cats were notably lower (pimobendan 1.71 and 0.43 ng/mL and ODMP not detectable).</p> <p>Conclusions – Pimobendan may reduce LA size and improve LA transport function in cats with HCM and LA enlargement, but larger a number of cats need to be studied.</p>
Keywords for abstract:	<p>Feline</p> <p>Hypertrophic cardiomyopathy</p> <p>Atrial systolic function</p> <p>o-desmethypimobendan</p> <p>Echocardiography</p>

Title of abstract:	AN EPIDEMIOLOGICAL REVIEW OF “GOOD SAMARITAN” ANIMALS IN THE OHIO STATE UNIVERSITY VETERINARY MEDICAL CENTER FROM 2014 TO 2022
Authors:	YJ Jeong ¹ , J Her ² , C Premanandan ¹ 1 Department of Veterinary Biosciences 2Department of Veterinary Clinical sciences
Abstract:	<p>Introduction Good Samaritan cases are unique to veterinary medicine and are situations in which the clinician provides immediate medical care to animals without an owner of record. The anatomic pathology service at the Ohio State University College of Veterinary Medicine provides postmortem examination of Good Samaritan animals that die under hospitalization in the Veterinary Medical Center (OSU VMC). Although these animals provide an indirect epidemiological survey of unattended animals, there has been a gap in knowledge on major mortality and morbidity of Good Samaritan animals.</p> <p>Objectives The goal of this study is to perform epidemiological review of the major mortality and morbidity in all Good Samaritan animals admitted to OSU VMC and subsequently submitted for autopsy.</p> <p>Methods By cross-referencing the OSU VMC medical records and OSU Anatomic pathology archive from 2014 to 2022, 100 Good Samaritan cases and their medical records were retrieved. The gross autopsy results, histology slides and medical records were reviewed.</p> <p>Results The cohort of 100 Good Samaritan animals consists of 59 felines, 36 canines, 2 raccoons, 1 bat, 1 squirrel and 1 opossum. In all species combined, trauma accounted for 32% of main mortality/morbidity, followed by euthanasia for rabies test (23%), infectious disease (17%), unknown (11%), and other etiologies (17%). Interestingly, infectious disease was the second most frequent morbidity (33%) in dogs, but lower in cats (8%). Rabies tests were requested on 51 animals and all test results were negative.</p> <p>Conclusions This is the first retrospective review of autopsy results of Good Sam animals in the Columbus metropolitan area. Further studies will help raise awareness on the cause of mortality and morbidity in stray and neglected animals.</p>
Keywords for abstract:	Good Samaritan animal Pathology Epidemiology Retrospective study

CR - 13

Title of abstract:	EFFECT OF EQUINE INSULIN DYSREGULATION ON HEPATIC METABOLIC GENE EXPRESSION IN TWO EXPERIMENTAL MODELS RELEVANT TO EQUINE METABOLIC SYNDROME
Authors:	<u>K. Keefer</u> , M. Watts, L. Hostnik, K. Timko, T. Burns. Depts. of Equine Internal Medicine and Veterinary Clinical Sciences
Abstract:	Little is known about function of the equine liver compared to other species, including its role in the pathophysiology of Equine Metabolic Syndrome (EMS) and insulin dysregulation (ID). Insight into the hepatic regulation of specific genes related to metabolism in response to diet and medical treatment will lead to better understanding how these variables affect the liver and its central role in insulin and glucose dynamics. qPCR for genes related to ID was performed on liver collected from equids subjected to two experimental models relevant to EMS. Liver tissue was collected from lean and obese ponies after 7 days of either low or high dietary carbohydrate feeding, and liver biopsies were collected from healthy adult light-breed horses before and after experimentally inducing ID with dexamethasone (DEX) and after treatment with AMPK agonists. GLUT1, ACACb and PEPCK expression increased in response to DEX administration. Further treatment with DEX and one AMPK agonist (aspirin or metformin) increased expression of GLUT1, PEPCK and AMPK while PPARg expression decreased. Combination therapy with metformin and aspirin significantly increased expression of PEPCK. After metformin treatment, PEPCK expression was increased while PPARg was decreased. High-carbohydrate feeding resulted in decreased expression of COX2 in the liver and no significant changes in the other genes. GLUT1, PEPCK, COX2, AMPK and PPARg should be further evaluated for their effect on the equine liver in naturally-occurring ID. Current treatment for ID involves preventative measures and management. Additional information about the pathophysiology of this condition will lead to novel therapeutic approaches and biomarkers to refine diagnosis and prognosis.
Keywords for abstract:	Equine Metabolic Syndrome Insulin Dysregulation AMPK Agonists Dexamethasone Genes

CR - 14

Title of abstract:	A PHASE I DOSE ESCALATION STUDY OF VIP-236 IN DOGS WITH SPONTANEOUS CANCERS
Authors:	<p><u>W.C. Kisseberth</u>¹, D. Nielsen¹, R. Burge¹, A.R. Moeller, B. Stelte-Ludwig², M.M. Frigault³, H.G. Lerchen², R. Izumi³, A. Hamdy³</p> <p>¹Department of Veterinary Clinical Sciences, The Ohio State University College of Veterinary Medicine, Columbus, OH, USA.</p> <p>²Vincerx Pharma GmbH, Monheim, Germany</p> <p>³Vincerx Pharma, Inc., Palo Alto, CA, USA</p>
Abstract:	<p>VIP-236 is a first-in-class small molecule drug conjugate (SMDC) comprised of an $\alpha_v\beta_3$ integrin antagonist linked to a cytotoxic camptothecin (CPT) derivative, designed to selectively release its payload via neutrophil elastase in the tumor microenvironment. Eight dogs with spontaneously occurring cancers [pulmonary carcinoma/adenocarcinoma (3), soft tissue sarcoma (3), metastatic osteosarcoma (1), lymphoma (1)] were enrolled in the clinical trial using a modified 3 + 3 dose escalation design. Dogs were treated with VIP-236 at dosages of 0.75 mg/kg IV weekly for 6 weeks (cohort 1), 0.5 mg/kg given twice weekly 24 hours apart for 6 weeks (cohort 2), or 1.0 mg/kg given twice weekly 24 hours apart for 6 weeks (cohort 3). Overall, VIP-236 was well tolerated when dosed once weekly at a dose of 0.75 mg/kg/dose (0.75 mg/kg/week) or at a dosage of 0.50 mg/kg/dose dosed on 2 consecutive days weekly (1.0 mg/kg/week) for two 3-week cycles. Low grade (grade 1 and 2) gastrointestinal toxicity occurred intermittently in some dogs at these dosages. One episode of grade 1 neutropenia was observed at these dosages. Dose limiting thrombocytopenia (2/2), neutropenia (1/2), and diarrhea (1/2) were observed in the two dogs treated at a dosage of 1.0 mg/kg/dose dosed on 2 consecutive days weekly for two 3-week cycles. These events resulted in life-threatening sequelae (spontaneous bleeding, febrile neutropenia, severe diarrhea) and were designated severe adverse events (SAE). Six dogs had stable disease at the Day 42 response assessment. One dog had progressive disease at Day 19. Based on these data, the maximally tolerated dose (MTD) of VIP-236 when administered to pet dogs with spontaneously occurring cancers by slow bolus infusion for two consecutive days weekly for six weeks is 0.5 mg/kg/dose (total dose 1.0 mg/kg/week). To further refine the MTD, enrollment of an intermediate cohort is recommended.</p>
Keywords for abstract:	<p>VIP-236</p> <p>Camptothecin</p> <p>Small molecule drug conjugate</p>

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Title of abstract:	ASSESSMENT OF THE EFFECT OF GABAPENTIN ON BLOOD PRESSURE IN CATS WITH AND WITHOUT CHRONIC KIDNEY DISEASE
Authors:	Quimby, Jones, Saffire, Brusach, <u>Kurdziel</u> , George, Paschall, Aarnes. Dept of Veterinary Clinical Sciences
Abstract:	<p>Background: Anecdotal evidence suggests that gabapentin may decrease blood pressure (BP) in cats.</p> <p>Objective: Assess the effect of gabapentin on BP in cats with and without CKD.</p> <p>Animals: 30 client-owned cats were enrolled: 14 cats with stable CKD (IRIS Stage 2 and 3) and 16 apparently healthy cats (serum creatinine < 1.6 mg/dL and USG > 1.035).</p> <p>Methods: A randomized, blinded, placebo-controlled crossover study was performed. Cats were evaluated twice, approximately one week apart, and BP (Doppler) was obtained three hours after receiving either a single oral dose of 10 mg/kg gabapentin or placebo. For each cat, BP readings were obtained at each visit using the same Doppler and sphygmomanometer unit, same cat holder and Doppler operator, in the same location.</p> <p>Results: Administration of a single 10 mg/kg oral dose of gabapentin resulted in a significant decrease in BP (median 125 mmHg, range 82-170) when compared to placebo (151, 102-191)(P < 0.001). In the CKD subgroup, gabapentin resulted in a significant decrease in BP (137 mmHg, 96-170) when compared to placebo (157, 102-191)(P = 0.003). In the healthy cat subgroup, gabapentin resulted in a significant decrease in BP (121 mmHg, 82-139) when compared to placebo (137, 102-177)(P = 0.002). Median change in BP was 12 mmHg (-10 to 95) for healthy cats and 20 mmHg (-21 to 43) for CKD cats (no significant difference between subgroups).</p> <p>Conclusions and Clinical Importance: The effect of gabapentin on BP should be taking into consideration when cats receive gabapentin for visit-associated stress.</p>
Keywords for abstract:	Gabapentin Blood Pressure Chronic Kidney Disease Cats

CR - 16

Title of abstract:	HOW VARIABLE IS THE URINARY MICROBIOTA OF HEALTHY DOGS OVER TIME?
Authors:	<u>Andrew McGlynn</u> , Ryan Mrofchak, Rushil Madan, Christopher Madden, Sheryl Justice, Adam Rudinsky, Jessica Hokamp, Vanessa L. Hale
Abstract:	<p>Urine was long thought to be sterile; however, advances in sequencing and expanded culturing techniques have challenged this concept. A few recent cross-sectional studies have characterized the urine microbiota in healthy and diseased dogs. However, the stability of canine urine microbiota over time is unknown. Urine is a highly variable matrix that can change in pH, concentration, and composition withing hours based on a dog's health, diet, and hydration status. Understanding if urine microbial profiles fluctuate within this changing environment will help drive more informed clinical decisions. Based on preliminary culture results, we hypothesized that urinary microbiota would be relatively stable over time within individual dogs but would differ between dogs. To test this, mid-stream free catch urine was collected from 14 healthy dogs (7 female, 7 male) over 12 time points that were hours, days, and months apart. We also collected genital (vulvar and preputial) and perineal swabs and fecal samples from the same dogs at the same time points. DNA was extracted using Qiagen DNA Isolation Kits. The V4 region of the 16S rRNA gene was amplified and sequenced, and the sequence data was processed and analyzed using DADA2 and ZIIME 2™. We used Jaccard, Bray Curtis, and UniFrac distances to assess microbial community similarity and stability within and between dogs. Preliminary results reveal distinct fecal and urine microbial communities that overlap with perineal and genital swab samples. We also observed stability in urinary tract microbiota over three months within dogs, and significant variation in microbial communities between dogs (PERMANOVA, $p < 0.05$). These findings help define normal variation in the urinary microbiota, which can ultimately help better define abnormal changes in urinary microbiota during disease states.</p>
Keywords for abstract:	Microbiota Urine Microbial community Microbial diversity

CR - 17

Title of abstract:	INVESTIGATING CANINE INFERTILITY THROUGH THE EVALUATION OF FULL THICKNESS UTERINE BIOPSIES
Authors:	<u>G. McRae</u> , M. Coutinho da Silva, E. Runcan, and C. Premanandan. Depts. Of Veterinary Clinical Sciences and Veterinary Biosciences
Abstract:	<p>Canine infertility is a frequent problem that is difficult to adequately diagnose and manage. For these infertile bitches there is little information on how to relate canine uterine pathology to infertility and pregnancy loss. In contrast, there is an objective grading system available for endometrial biopsies to determine the likelihood of mares carrying a foal to term. The objective of this study is to compare full thickness canine uterine biopsies with known history of infertility or pregnancy loss submitted to The Ohio State University's Reproductive pathology service website and compare them to full thickness uterine samples of the bitches without a history of infertility or that have successfully carried pregnancies to term. All the control samples are taken at the time of Cesarean section at the hysterotomy site. Previous studies have demonstrated an increased prevalence of chronic inflammation, cystic endometrial hyperplasia and periglandular fibrosis in subfertile bitches. No formal conclusions can be made now as the study is ongoing, but initial characterization of a normal full thickness uterine sample at the time of c-section can be made. Microscopic abnormalities of interest in this study include: lymphocytic and eosinophilic infiltration into the endometrium, endometrial cyst formation, periglandular fibrosis as well as endometrial gland atrophy. 78% percent (18/23) of the subfertile bitch cases exhibited these changes. In comparison, 0.05% percent (1/20) of the control population exhibited these changes. However, a full comparison and grading of the normal and abnormal sample are still in progress. What this study hopes to achieve is a grading scale of abnormalities in full thickness canine uterine biopsies and relate these abnormalities to the ability of maintaining a pregnancy to term.</p>
Keywords for abstract:	Canine Endometrial Biopsy

Title of abstract:	TO SAMPLE OR NOT TO SAMPLE: CAPTURING FELINE FECAL MICROBIOME CHANGES WITH HIGH-FREQUENCY SAMPLE COLLECTION
Authors:	<p><u>N.J. Nealon</u>¹, H. Klein¹, M. Salerno¹, V.J. Parker¹, J. Quimby¹, A. Rudinsky¹, J. Howard¹, and J.A. Winston¹</p> <p>¹. Department of Veterinary Clinical Sciences. The Ohio State University, College of Veterinary Medicine. Columbus, Ohio. 43210.</p>
Abstract:	<p>Microbiota-based fecal evaluations are promising feline diagnostic tools. While once-weekly sampling is standard in research, daily fecal microbiota changes make the ideal sampling frequency unknown. The objective of this study is to evaluate how sampling frequency impacts the resolution of fecal microbiota data. Our hypothesis is that daily high frequency fecal sampling is more effective than less frequent sampling at capturing significant microbiota alterations in cats.</p> <p>Six healthy, sterilized adult laboratory cats (3 male, 3 female) were assessed. To initiate an abrupt microbiota disturbance, a rapid diet change was performed. Feces was collected prior to diet transition and then daily for five weeks. 16s rRNA microbiota analysis (V4 region) was performed using the DADA2 pipeline. To examine impacts of sampling frequency, twelve sampling schemes, representing once-weekly to everyday sampling, were compared for their ability to identify microbial shifts over time. For each scheme, pairwise PERMANOVA and DESeq2 differential abundance testing were used to identify time-dependent microbiota compositional and taxonomic changes respectively. Significance was defined as $p < 0.05$ following posthoc corrections.</p> <p>When comparing sampling schemes, high frequency daily sampling provided the best resolution for identifying microbiota alterations over time ($p < 0.01$) compared to low frequency once-weekly sampling ($p = 0.015$). Sampling frequency schemes differentially estimated fold changes in Fusobacteriota, a phylum important in protein metabolism, where daily sampling identified a 5.31-fold reduction in Fusobacteriota abundance between baseline and study week one ($p = 9.41E-20$) whereas the once-weekly sampling scheme identified a 3.13-fold decrease ($p = 0.0034$).</p> <p>The results from this study support that high frequency sampling may be needed to accurately capture microbial community shifts occurring in response to an inciting agent, including diet and/or medical treatments. Ongoing analysis will integrate this data with daily feline dysbiosis index values, a widely used feline microbiota diagnostic tool, to further assess the impact of sampling frequency on biologically-relevant taxa.</p>
Keywords for abstract:	Gut Microbiome; Sampling Frequency; Feline Medicine; 16s rRNA Sequencing; Microbiome Study Design

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Title of abstract:	MULTISYSTEMIC EOSINOPHILIC EPITHELIOTROPIC DISEASE (MEED) WITH EXTENSIVE HEPATIC INVOLVEMENT IN A HORSE
Authors:	<u>J.Y. Park</u> , A. Thriffiley, J.P. Cronin, C. Premanandan, M.E. Schreeg. Dept of Veterinary Biosciences
Abstract:	<p>Multisystemic eosinophilic epitheliotropic disease (MEED) is a rare equine disease of unidentified cause that most commonly manifests in the skin and gastrointestinal tract. Few reports detail gross and histologic lesions, and extensive hepatic involvement is not documented. An 18-year-old Rocky Mountain Horse mare presented for a week-long history of hyperthermia, anorexia, and intermittent diarrhea. Physical examination revealed tachycardia, tachypnea, multifocal alopecia and crusting, and abdominal distention. Serum biochemistry panel showed moderately to markedly elevated ALP, GGT, and SDH. Antemortem duodenal and rectal biopsies revealed submucosal eosinophilic granulomas with minimal to mild neutrophilic inflammation; MEED or parasitism were considered as differentials. Due to lack of clinical resolution, the mare was euthanized and submitted for postmortem examination. Postmortem samples were routinely collected and processed for histologic evaluation. Gross examination revealed too numerous to count, variably sized, firm, light yellow to tan, green-tinged nodules throughout the liver, mesentery, mesenteric lymph nodes, and to a lesser extent, the lung. Nodules affected approximately 10-20% of the liver parenchyma. The small intestines were transmurally moderately thickened. Histopathology of affected tissues revealed marked eosinophilic and granulomatous inflammation with extensive fibrosis. No etiologic agents were identified with GMS or PAS stains. These findings are consistent with an atypical manifestation of MEED in a horse with extensive hepatic involvement. MEED may be considered as a cause for nodular hepatopathy and/or elevation of liver enzymes in horses.</p>
Keywords for abstract:	Liver Hepatopathy Equine MEED Hypersensitivity

CR - 20

Title of abstract:	EFFECTS OF JUMP HEIGHT ON FORELIMB LANDING FORCES IN BORDER COLLIES
Authors:	<u>Joanna Pogue</u> , DVM; Chris Zink, DVM, PhD, DACVP, DACVSMR; Nina R. Kieves, DVM, DACVS-SA, DACVSMR
Abstract:	<p>Objective: The objective of this study was to evaluate the effects of jump height on the landing forces of dogs.</p> <p>Animals: Client-owned Border Collies experienced in agility competition, n = 9</p> <p>Procedures: The study involved client owned border collies with the same AKC standard jump height of 20 inches and preferred height of 16 inches. An AKC regulation bar jump was placed over a previously validated pressure sensitive walkway (PSW). The peak force (N) and peak contact pressure (kPa) of the landing forelimbs were evaluated for all dogs.</p> <p>Results: There was no significant difference in landing force between the two jump heights for either peak force as a percentage of body weight or peak contact pressure.</p> <p>Conclusions & Clinical Relevance: Our findings demonstrated no significant difference in active landing forces of peak contact pressure and peak force on the forelimbs of dogs when jumping at a standard jump height versus a preferred jump height when controlling for velocity. These results suggest that the recommendation of decreasing jump height for older animals or injured animals may not provide a significant decrease in the impact on the forelimbs. It is likely that other factors contribute to the total forelimb kinematics picture during competition. Veterinarians and trainers should consider additional ways to decrease impact for canine athletes as they recover from injury.</p>
Keywords for abstract:	Agility Jump Landing forces

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Title of abstract:	VALIDATION OF NONINVASIVE METHEMOGLOBIN AND CARBOXYHEMOGLOBIN MEASUREMENTS USING PULSE CO-OXIMETRY IN HEALTHY DOGS
Authors:	<u>J. Roh</u> ¹ , J. Her ¹ . ¹ Department of Veterinary Clinical Sciences, The Ohio State University College of Veterinary Medicine, Columbus, Ohio, USA.
Abstract:	<p>Co-oximetry measures the various species of hemoglobin and the oxygenation status by using multiple wavelength spectrophotometry. Pulse co-oximetry is a non-invasive method that also utilizes multiple wavelength spectrophotometry to provide serial measurements of the concentration of methemoglobin (MetHb) and carboxyhemoglobin (COHb). To date, there are no studies that evaluate the agreement between pulse co-oximetry and blood co-oximetry in healthy dogs. Thus, the aim of this study is to compare the levels of MetHb and COHb measured by pulse co-oximetry with those measured by blood co-oximetry in healthy dogs.</p> <p>The study included 45 client-owned healthy dogs of various breeds, genders, and ages (1-13 years old). The levels of MetHb and COHb were measured simultaneously using both pulse co-oximetry (Masimo Radical 7) and blood co-oximetry (Stat Profile Prime Plus). The data was analyzed using Spearman correlation, intra-class correlation (ICC), and Bland-Altman analysis.</p> <p>The Spearman correlation analysis revealed at most weak positive correlation between pulse co-oximetry and blood co-oximetry MetHb (rho 0.00, 95% Confidence Interval; CI -0.3-0.3) and COHb (rho 0.03, 95% CI -0.27-0.32). The ICC showed poor agreement between pulse co-oximetry and blood co-oximetry, with MetHb ICC coefficient 0.00 (95% CI -0.12-0.15) and COHb ICC coefficient 0.03 (95% CI -0.27-0.32). Additionally, Bland-Altman analysis demonstrated a low bias but wide limits of agreement (LoA) between pulse co-oximetry and blood co-oximetry, with pulse co-oximetry overestimating MetHb by 0.7% (95% LoA -0.5 to 2.0) and COHb by 0.2% (95% LoA -4.6 to 5.0).</p> <p>In conclusion, this study suggests that the Masimo Radical 7 pulse co-oximetry cannot be recommended as a substitute for direct measurement in healthy dogs due to the wide LoA. Further studies are required to validate the reliability of pulse co-oximetry in other clinical conditions.</p>
Keywords for abstract:	Canine Co-oximetry Pulse co-oximetry Methemoglobin Carboxyhemoglobin

Title of abstract:	GUT MICROBIOTA PROMOTING PROPIONIC ACID PRODUCTION ACCOMPANIES DIET-INDUCED INTENTIONAL WEIGHT LOSS IN CATS
Authors:	<u>J. C. Rowe</u> , J. A. Winston, V. J. Parker, K. E. McCool, J. S. Suchodolski, C. Gilor, and A. J. Rudinsky. Dept. of Veterinary Clinical Sciences, The Ohio State University (JCR, JAW, VJP, AJR); Dept. of Clinical Sciences, North Carolina State University (KEM); Dept. of Small Animal Clinical Sciences, Texas A&M University (JSS); Dept. of Small Animal Clinical Sciences, University of Florida (CG)
Abstract:	<p>The gut microbiota influence regulation of host metabolic function through microbial-derived metabolite production during states of obesity and weight loss. Specifically, microbiota production of short-chain fatty acids (SCFAs) can become altered in obese people and perpetuate metabolic states associated with obesity, including insulin resistance. These dynamics are minimally explored in feline medicine where it is estimated that 60% of cats in the United States are overweight or obese. In this study, overweight or obese research cats (n = 7) were transitioned from a maintenance diet to a weight-loss diet fed <i>ad libitum</i> for seven days, then calories were restricted to achieve 1-2% weight loss per week for an additional 77 days. Cats then received their original maintenance diet again for 14 days. Significant intentional weight loss was noted after the calorie restriction phase (adjusted p < 0.05). Fecal samples were collected during the four study phases, and both 16S rRNA amplicon sequencing and targeted SCFA metabolomics were performed. Amplicon sequence variants (ASVs) were generated using DADA2, and taxonomy was assigned using SILVA database. Alpha diversity did not significantly change across study phases; however, beta diversity analysis of Bray-Curtis distances demonstrated differences in microbiota composition between the four study phases (PERMANOVA adjusted p = 0.011). Differentially abundant taxa driving the compositional differences were identified using LEfSe, which included four <i>Blautia</i> genus ASVs that were significantly enriched either during or following weight-loss diet administration (adjusted p < 0.05). During weight-loss diet administration, significantly greater concentrations of the SCFA propionic acid were detected in feces, while branched chain SCFAs were significantly reduced (adjusted p < 0.05). These data demonstrate that intentional weight loss in obese or overweight cats in response to dietary intervention is accompanied by shifts in gut microbiota composition promoting production of propionic acid, which is implicated in preventing obesity-associated inflammation.</p>
Keywords for abstract:	<p>Gut Microbiome Weight Loss Short-chain Fatty Acids Obesity Feline</p>

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Title of abstract:	UNLICENSED MOLNUPIRAVIR IS AN EFFECTIVE RESCUE TREATMENT FOLLOWING FAILURE OF UNLICENSED GS-441524-LIKE THERAPY FOR CATS WITH SUSPECTED FELINE INFECTIOUS PERITONITIS
Authors:	<u>M. Roy</u> ¹ , N. Jacque ² , W. Novicoff ³ , E. Li ¹ , R. Negash ¹ , and S.J.M. Evans ¹ . ¹ Department of Veterinary Biosciences, College of Veterinary Medicine, The Ohio State University ² Independent Researcher, San Jose, CA ³ Departments of Orthopedic Surgery and Public Health Services, School of Medicine, University of Virginia
Abstract:	Feline infectious peritonitis (FIP) is a complex and historically fatal disease, though recent advances in antiviral therapy have uncovered potential treatments. A newer therapeutic option, unlicensed molnupiravir, is being used as a first-line therapy for suspect FIP and as a rescue therapy to treat cats who have persistent or relapsed clinical signs of FIP after GS-441524 and/or GC376 therapy. Using owner-reported data, treatment protocols for 30 cats were documented. The 26 cats treated with unlicensed molnupiravir as a rescue therapy were treated with an average starting dosage of 12.8 mg/kg and an average ending dosage of 14.7 mg/kg twice daily for a median of 12 weeks (IQR = 10–15). In total, 24 of 26 cats were still living disease-free at the time of writing. One cat was euthanized after completing treatment due to a prolonged seizure, and the other cat underwent retreatment for relapsed clinical signs. Few adverse effects were reported, with the most notable—folded ears (1), broken whiskers (1), and severe leukopenia (1)—seen at dosages above 23 mg/kg twice daily. This study provides a proof of principle for the use of molnupiravir in cats and supports the need for future studies to further evaluate molnupiravir as a potentially safe and effective therapy for FIP.
Keywords for abstract:	FIP Coronavirus Antiviral EIDD-2801 Black market

CR – 24

Title of abstract:	GASTROINTESTINAL RELEASE SITE FOR DELAYED RELEASE AND GELATIN CAPSULES IN HEALTHY DOGS
Authors:	Charlie Stone ^{1,2} , Simone March ¹ , Rebecca J. Urion ¹ , Adam Rudinsky ^{1,2} , and Jenessa A. Winston ^{1,2} Affiliations: ¹ Department of Veterinary Clinical Sciences. The Ohio State University, College of Veterinary Medicine. Columbus, Ohio. 43210. ² Comparative Hepatobiliary and Intestinal Research Program, The Ohio State University, College of Veterinary Medicine. Columbus, Ohio. 43210.
Abstract:	Fecal microbiota transplantation (FMT), delivery of fecal material from a healthy donor into a diseased recipient, is routinely administered as a slurry via enema or nasogastric tube but can also be encapsulated for convenient oral administration. Traditionally, in veterinary medicine capsular FMT is uncommon and if performed clinicians have utilized gelatin capsules. However, this likely results in delivery of fecal material into the stomach, due to the rapid dissolution of gelatin capsules in the low pH environment in the stomach, instead of the desired location in the small intestines. Delayed release capsules (Lonza DR Caps) are an alternative to gelatin capsules, which are designed to resist pH dependent dissolution allowing small intestinal release of the FMT. This study aimed to determine the gastrointestinal release site for DR and gelatin capsules in healthy dogs. We hypothesized that DR capsules would deliver contents in the small intestine compared to gelatin capsules releasing contents in the stomach. This randomized double-blinded crossover experiment included six client-owned healthy dogs. Fasted dogs were randomly assigned to receive either gelatin or DR capsules filled with barium impregnated polyethylene spheres (BIPS) orally with 20 grams canned Purina EN. Serial radiographic imaging (prior to capsule administration, immediately following, 5 minutes post, 15 minutes post, followed by every 30 minutes) was performed to determine the gastrointestinal release site of BIPS for each capsule type. A minimum 7-day washout was completed between crossovers. In fasted dogs, both capsule types released their contents in the stomach with no capsules reaching the small intestine. Studies evaluating the impact of a meal size on gastric emptying, gut motility, and capsule release location are ongoing. This study is the first to provide evidence-based insights into DR capsules in dogs, and its significance extends beyond FMT as drug delivery to the small intestine is sometimes required.
Keywords for abstract:	Fecal microbiota transplantation Delayed release capsules Gelatin capsules Barium impregnated polyethylene spheres (BIPS) Healthy dogs

Title of abstract:	HIGH-PROTEIN MEAL FEEDING IS ASSOCIATED WITH POST-PRANDIAL HYPERINSULINEMIA IN HORSES WITH EXPERIMENTALLY-INDUCED INSULIN DYSREGULATION
Authors:	<u>A. Thriffiley</u> , M. Watts, K. Timko, E. Pinnell, K. Keefer, O. Gorman, L. Hostnik, T. Burns. Department of Veterinary Clinical Sciences
Abstract:	<p>Background: Dietary management is the most important treatment for equine insulin dysregulation (ID) and often involves feeding low non-structural carbohydrate (NSC), high-protein ration balancers and grass hay. Data suggest that post-prandial hyperinsulinemia can be exacerbated by a high-protein meal in patients with ID, creating concern about the safety of this nutritional intervention.</p> <p>Hypothesis: Consumption of a low-NSC, high-protein meal will induce post-prandial hyperinsulinemia, which will be amplified after induction of ID in horses.</p> <p>Animals: Seven adult, light-breed horses with normal endogenous [ACTH].</p> <p>Methods: Each horse underwent a frequently-sampled insulin-modified IV glucose tolerance test to characterize systemic insulin and glucose dynamics, followed by a feed challenge test (1 kg ration balancer [min 32% crude protein, max 13% NSC] consumed within 15 minutes, with [insulin] and [glucose] measured at baseline and every 30 minutes for 240 minutes after the meal). Both tests were repeated after induction of ID (dexamethasone 0.08 mg/kg PO once daily for 7 days). Outcomes were compared between baseline and ID conditions.</p> <p>Results: ID was associated with exacerbation of post-prandial hyperinsulinemia and hyperglycemia after high-protein meal feeding. ID AUC_{INS} ($548.9 \pm 150 \mu\text{U}/\text{mL} \times \text{min}$) was significantly higher than baseline AUC_{INS} ($216.2 \pm 104.4 \mu\text{U}/\text{mL} \times \text{min}$; $P = 0.003$). ID AUC_{GLU} ($89.5 [60-115] \text{mg}/\text{dL} \times \text{min}$) was significantly higher than baseline AUC_{GLU} ($75 [34.9-94] \text{mg}/\text{dL} \times \text{min}$; $P = 0.03$).</p> <p>Conclusions and Clinical Importance: Horses with experimentally-induced ID displayed significantly higher glycemic and insulinemic responses to a high-protein meal than at baseline, suggesting that high-protein ration balancers may complicate nutritional management of equine ID.</p>
Keywords for abstract:	Insulin Dysregulation Equine Metabolic Syndrome

Title of abstract:	POLARIZATION SENSITIVE OPTICAL COHERENCE TOMOGRAPHY IMAGE CHARACTERISTICS FOR GASTROINTESTINAL TUMORS AND TISSUE AT SURGICAL MARGINS IN DOGS
Authors:	<u>H. L. Weaver</u> ¹ , G. S. Fontes ¹ , Y.-F. Shen ¹ , R. N. Jennings ² , J. M. Lapsley ¹ , and L. E. Selmic ^{1,2} . ¹ Dept. of Veterinary Clinical Sciences, ² Dept. of Veterinary Biosciences
Abstract:	Gastrointestinal tumors in dogs are uncommon, usually asymptomatic until the later stages of disease. Definitive treatment for these tumors is surgical excision with wide margins. Normally, histopathology is used to assess the tumor margins. Real-time surgical margin assessment with optical imaging technologies is currently being investigated for different tumor types. Optical coherence tomography (OCT) is a noninvasive imaging modality that uses light scattering and polarization to identify tissue types on cross section. Spectral domain OCT (SD-OCT) allows differentiation based on light scattering properties and polarization sensitive OCT (PS-OCT) differentiates based on tissue polarization birefringence. In this study, our objective was to characterize different tissue types present in GI tumor excision sites using OCT. We hypothesized that OCT imaging could accurately identify incomplete margins and neoplastic tissue. Samples were imaged following surgical resection of oral, hepatic, and other GI tumors (pancreatic, gastric, and intestinal). Samples were fixed in formalin, mounted, and stained with hematoxylin and eosin as well as picosirius red. OCT images and histology slides were compared, and the tissues were characterized based on structure, SD-OCT light scattering, and PS-OCT birefringence. Our results showed that SD-OCT is a good modality for identifying fat, which has a net pattern of increased light scattering. PS-OCT can differentiate muscle from other tissues that appear as increased light scattering with SD-OCT with alternating high and low birefringence bands. Neoplasms have a uniform, dense structure of increased total intensity on SD-OCT and have increased birefringence throughout the tissue on PS-OCT. These results indicate that it is possible to differentiate normal tissue from tumor tissue based on OCT images, which could eventually be utilized intra-operatively to confirm surgical margins and complete excision.
Keywords for abstract:	Optical coherence Tomography Margins of excision Gastrointestinal neoplasia Canine

<p>Title of abstract:</p>	<p>IN VITRO BACTERIAL VIABILITY OF COMMERCIALY AVAILABLE VETERINARY FECAL MICROBIOTA TRANSPLANTATION PRODUCTS</p>
<p>Authors:</p>	<p><u>Lisa Wetzel</u>^{1,2}, Nina Randolph^{1,2}, Dubraska Diaz-Campos¹, Joany van Balen¹, Jenessa A. Winston^{1,2}</p> <p>¹. Department of Veterinary Clinical Sciences. The Ohio State University, College of Veterinary Medicine. Columbus, Ohio. 43210.</p> <p>². Comparative Hepatobiliary and Intestinal Research Program, The Ohio State University, College of Veterinary Medicine. Columbus, Ohio. 43210.</p>
<p>Abstract:</p>	<p>Fecal microbiota transplantation (FMT) is the transfer of feces from a healthy donor into the gut of a diseased recipient to modulate the recipient's gut microbiome and confer a health benefit. Although the exact mechanism of action of FMT is unknown, engraftment of viable microbes is critical. In veterinary medicine, screening fecal donors and processing feces for FMT is expensive, making FMT preparation impractical and cost-prohibitive for most veterinary practices. AnimalBiome[®] offers encapsulated lyophilized canine and feline FMT products for direct sale to pet owners and veterinarians. This study aimed to assess and compare the bacterial viability of The Ohio State University Companion Animal Fecal Bank (OSU CAFB) FMT products to AnimalBiome[®] FMT products using culture-based techniques in aerobic and anaerobic environments. Three AnimalBiome[®] products (DoggyBiome, DoggyBiome from raw fed donors, KittyBiome) and two OSU CAFB products (freshly processed with 10% glycerol and lyophilized with 10% glycerol) were tested in duplicate. Total CFUs/gram were not significantly different between AnimalBiome[®] and OSU CAFB lyophilized products (p>0.999). Freshly processed canine and feline samples yielded significantly higher CFUs/gram compared with lyophilized products (dogs, p=0.0001; cats, p=0.0002). All FMT products exhibited <i>in vitro</i> viability, with the greatest viability observed under anaerobic conditions. No Gram-negative growth was observed in any AnimalBiome[®] or OSU CAFB lyophilized product under aerobic and anaerobic conditions. These results indicate that freshly processed FMT provides the highest "dose" of CFUs/gram and more robust diversity compared with lyophilized FMT products. An important limitation of this study is that the majority of fecal microbes are unculturable, thus only a fraction of donor gut bacteria are represented here. Additionally, the CFU "dose" required to confer a clinical benefit in dogs and cats is unknown. Engraftment studies are needed to determine the optimal FMT preparation technique and dose in veterinary medicine.</p>
<p>Keywords for abstract:</p>	<p>Fecal microbiota transplant Canine microbiome Feline microbiome Gut bacterial viability</p>

Title of abstract:	EFFICACY OF THE TOPICAL ANTIHISTAMINE OLOPATADINE IN DOGS WITH EXPERIMENTALLY INDUCED ALLERGIC CONJUNCTIVITIS
Authors:	<u>E. Mamo</u> , G. Newbold. Department of Veterinary Clinical Sciences
Abstract:	<p>Allergic conjunctivitis is a common condition in dogs and can be associated with environmental allergens. Topical corticosteroids the basis of treatment, although there are contraindications that may limit their use. This creates a need for evaluation of alternative treatment options. There is currently little research assessing the use of topical antihistamines in dogs for treatment of allergic conjunctivitis. The purpose of this study was to evaluate the efficacy of a once a day, over the counter topical antihistamine 0.7% olopatadine hydrochloride in treating or preventing experimentally induced clinical signs of allergic conjunctivitis in dogs. Twelve healthy student/staff-owned dogs with no history of allergies or atopic dermatitis were randomly assigned to two groups: "Treatment" (n = 9) which received the topical antihistamine and "Control" (n = 3) which received artificial tears. The study involved two phases with dogs receiving the antihistamine eye drops before (Phase 1) or after (Phase 2) receiving the histamine eye drops. Conjunctival hyperemia, chemosis, follicles, ocular discharge and ocular pruritus were graded, and photographs were used to document the response to the antihistamine. Preliminary results suggest dogs receiving the antihistamine eye drops, 0.7% olopatadine hydrochloride, had lower conjunctivitis scores when compared to the control group ($P < 0.05$). When comparing treatment groups from Phase 1 and 2, dogs receiving the antihistamine eye drops prior to development of conjunctivitis (Phase 1) showed less severe clinical signs ($P < 0.05$). Early indications show that antihistamines may not only be beneficial in the treatment of allergic conjunctivitis but also in prophylaxis.</p>
Keywords for abstract:	<p>Allergic conjunctivitis Olopatadine Antihistamine</p>

**EPIDEMILOGY
AND
APPLIED RESEARCH**

EAR - 1

Title of abstract:	A REVIEW OF ANIMAL CRUELTY LEGISLATION ACROSS STATES IN THE UNITED STATES OF AMERICA
Authors:	<u>Virginia Behmer, Jeanette O'Quin</u> Department of Veterinary Preventative Medicine, College of Veterinary Medicine, Ohio State University, Columbus, Ohio
Abstract:	Every state in the US has laws against animal cruelty, abuse, and neglect. However, the regulations vary between states. There are major differences in definitions, penalties and even the type of events that are illegal. For example, animal hoarding is specifically addressed in some states but not in others. Other differences include who is required to report and who investigates suspected acts of cruelty. With the demonstrated link between animal cruelty and other forms of domestic abuse, some states have mandated cross-reporting of human and animal abuse. Humane investigators may be civilian or sworn officers depending on the state. To date, no review of animal cruelty regulations across all of the states has been conducted. This project aims to fill this gap by assessing the landscape of animal cruelty classification, investigation, and reporting regulations across the US. This will be conducted using a systematic review of the revised and administrative codes for each state. Specific factors will be evaluated, including: 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 will be described and compared to identify trends across states or regions. 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 State Policy Animal Welfare One Welfare Veterinary Public Health The Link

EAR - 2

Title of abstract:	UTILIZATION OF ARTIFICIAL INTELLIGENCE TO BETTER UNDERSTAND BEHAVIOR IN AFRICAN WILD DOGS (<i>LYCAON PICTUS</i>)
Authors:	<u>B. Braasch</u> ¹ , M. Flint ¹ , K.A. George ² ¹ Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio ² Zoological Association of America
Abstract:	<p>Advancements in technology have proven to benefit animal industries across multiple dimensions, including animal welfare and behavior, which impacts animal management decisions. These advancements have proliferated in scientific literature, particularly in animal health and management. Yet, to date, there is no study which examines the use of advanced machine learning in individual and social wild animal behavior. This study utilizes behavioral data collection and individual identification using advanced technology. The goal of this study is to determine how advancements in technology can enhance our understanding of animal behavior, specifically in African wild dogs, to influence management decisions at The Wilds in Cumberland, OH. Video cameras will be placed around the perimeter of the dog enclosure at The Wilds. Video feed will then be analyzed using artificial intelligence (AI) software. The first objective of this study is to determine individuals and basic behaviors within a managed pack of African wild dogs using AI. The second objective is to 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 animal care staff. The third objective of this study is to test if AI can be used to assess identification of individual personalities when presented with novel enrichment items that may change pack order.</p> <p>The significance of this study is a further exploration of technological advancements, which allows for the further understanding of the individuality of each animal in human care, which can then be used to determine the best methods for care regarding enrichment and space. The importance of this study to the field of zoological sciences is to better understand individual behaviors and sociality of a large carnivore, which can allow for better management of these animals in human care.</p>
Keywords for abstract:	African wild dog artificial intelligence machine learning animal behavior animal welfare animal management sociality

EAR - 3

Title of abstract:	EVALUATION OF DISINFECTION METHODS FOR AQUATIC ARTIFICIAL PLANTS IN ZEBRAFISH RECIRCULATING SUPPORT SYSTEMS
Authors:	<u>C. Camson</u> ^{1,2} , J. Palillo ³ , A. Adekanye ¹ , L. Fehrenbach ¹ , R. Malbrue ^{1,2} ¹ Animal Resources Core, Abigail Wexner Research Institute at Nationwide Children's Hospital, Columbus, OH ² Department of Veterinary Preventative Medicine, The Ohio State University, Columbus, OH ³ Data Management, Sean M. Healey and MAG Center for ALS & The Neurological Clinical Research Institute, Massachusetts General Hospital, Boston, MA
Abstract:	<p>The use of aquatic artificial plants as environmental enrichment for zebrafish in biomedical research facilities has been proven to reduce stress, anxiety, and improve overall animal well-being. Despite the benefits they provide for zebrafish welfare, some research facilities are hesitant to begin implementing them into their routine husbandry practices due to concerns for disease transmission and lack of guidance on most effective disinfection practices between tanks. There have been few publications on ways to adequately disinfect aquatic artificial plants as they are commonly reused between tanks within the life support system. Investigating proper sanitation and disinfection methods for these enrichment items are crucial to preventing the spread of pathogens within the aquatic life support system. Two disinfection methods, a commercial grade laboratory glassware dishwasher and an ethylene oxide sterilizer (ETO), were evaluated using ATP detection and bacterial culture of aquatic artificial plants pre- and post- disinfection process. Plants were placed in the dirty sump of two separate recirculating life support systems (2,500-3,000 fish/system) for two weeks before the start of the study. The commercial grade laboratory glassware dishwasher and ETO sterilizer reduced ATP levels by 100% and 97.19%, respectively. Both methods resulted in complete eradication of live bacteria present pre-treatment. This study demonstrates two effective methods for disinfecting artificial aquatic plants in zebrafish facilities.</p>
Keywords for abstract:	Zebrafish Aquatics Husbandry Enrichment Welfare

EAR - 4

Title of abstract:	EFFECT OF BENCHMARKING REPORTS ON THE TRANSFER OF PASSIVE IMMUNITY, NAVEL HEALTH, AND HYDRATION IN SURPLUS DAIRY CALVES
Authors:	<u>T.-Y. Cheng</u> , J. Pempek, S. Locke, D. Renaud, K. Proudfoot, K. George, D. Wilson, and G. Habing. Depts. Of Veterinary Preventive Medicine and Animal Sciences at the Ohio State University, Depts. Of Population Medicine at University of Guelph, Depts. Of Health Management and Companion Animals at University of Prince Edward Island, and Livestock Behavior Research Unit at USDA-ARS.
Abstract:	Surplus dairy calves that cannot be used to replace the milking cows provide limited profit to dairy producers and are often marketed within the first two weeks post-birth. Thus, they may receive suboptimal on-farm early-life care and subsequently have high morbidity and mortality on grower farms. Improved early-life care may be motivated by delivering the health data collected from calves at calf dealers back to the source dairy farms. Thus, this study aimed to test the hypothesis that benchmarking reports would improve the metrics for the transfer of passive immunity (TPI), navel health, and hydration of calves delivered to calf dealers. Overall, 13 dairy farms were recruited and randomly assigned to intervention (n = 6) and control (n = 7) groups. Two calf dealers were visited in May 2021 – June 2022 for health assessment in calves recruited farms. Six months after the study initiation, farm-wise benchmarking reports were generated for intervention farms containing metrics for passive transfer (total serum protein ≥ 5.1 g/dL), navel health, and hydration. De-identified results from other farms were reported to provide additional motivation to farmers. Changes in these metrics by the effect of benchmarking report reception were investigated using 3 calf-level logistic mixed models with “farm” as the experimental unit. A total of 653 calves were sampled from 6 intervention (n = 282) and 7 control (n = 371) farms. Model estimates for the overall probability of failure of TPI and navel infection were 21.4% (95% CI = [13.9, 31.6]) and 20.5% [15.5, 26.5], respectively. Dehydration was marginally less likely from intervention farms compared to control farms after receiving the benchmarking reports (OR = 0.29, [0.07, 1.13], p = 0.07). The results suggest the incidence of calf dehydration may decrease by delivering benchmarking reports back to dairy producers.
Keywords for abstract:	Benchmarking Calf health Surplus calves

EAR - 5

Title of abstract:	PUBLIC AQUARIA AND ONE WELFARE: A SYSTEMATIC APPROACH
Authors:	<u>B. Fischer</u> , J. Pempek, K. George, J. Flint, T. Wittum, and M. Flint. Department of Veterinary Preventive Medicine, College of Veterinary Medicine and Department of Animal Sciences, College of Food, Agricultural, and Environmental Sciences
Abstract:	Public aquariums are organizations that offer the public an opportunity to engage with, gain knowledge of, and contribute to the conservation of species and ecosystems. Aquatic ecosystems are currently facing a multitude of stressors from anthropogenic impacts, such as pollution, climate change, and overfishing. Public aquariums positively contribute to ecosystems through conservation, education, and scientific advancement; but may negatively detract through wild collection and sourcing from commercial suppliers. Changes within the industry have occurred, although the need for a holistic approach to quantify the impacts of aquarium population management is needed. The objective of this study was to implement a developed One Welfare-Based Ecosystem Model to predict impacts of aquarium population management on humans, animals, and the environment. Ecosystem indicators were selected and then grouped into physical-chemical, biological, and socio-economic categories. Data included measurements of environmental and animal indicators at wild collection field sites, aquarium visitor surveys, and publicly available data. Model development included comparing field data to reference ranges, assigning weightings based on indicator significance and beta testing of the model, and then assigning each institution a One Welfare status at completion. Confidence rating of measured indicator and reference data were performed for each field site to determine appropriateness of use of the model for each aquarium. Findings included a positive One Welfare status for each collaborating institution (81.15/100 and 91.71/100). Confidence ratings showed positive results (62/100 and 75/100) for model applicability for the field sites studied as well as future use by other institutions moving forward.
Keywords for abstract:	One Welfare, Ecosystem Health, aquarium, aquaculture

EAR - 6

Title of abstract:	EVALUATION OF A SWINE OUTREACH PROGRAM DIRECTED TO SMALL PRODUCERS
Authors:	<u>J. Hernández Cuevas</u> , and A. Arruda. Of Veterinary Preventative Medicine
Abstract:	<p>The emergence and rapid appearance of Foreign Animal Diseases (FADs) are a constant threat to animal and human health. The swine industry specifically is under constant threat of introduction of diseases including African Swine Fever (ASF), Foot and Mouth Disease, and Classical Swine Fever. Even though several national and local efforts occurred in the past years to support swine producers in preventing and detecting these diseases, the focus has been mostly on large commercial production, but not in small-scale production. The main objective of this study was to use data collected from small producer outreach sessions to identify potential knowledge gaps within this population and assess the program's effectiveness in educating about FADs and biosecurity concepts. A total of 31 participants attended five sessions, the average (\pmSD) age of participants was 43.36 (19.62), and the mean number of pigs owned by participants was 51.2 (126.61). Approximately 48% of participants reported having a veterinarian-client relationship, but only called the veterinarian as needed. A total of 97% of participants indicated they had heard of ASF, however, only 29% of participants felt that they understood important aspects of the disease. This is a concern for the US swine industry because it indicates that there could be potential delays in early identification of the disease and timely implementation of control measures in an outbreak situation. After the seminar, 71% of participants reported that they understood a lot about ASF, which indicates a possible positive impact of the outreach program in the small producer and non-swine veterinarian community.</p>
Keywords for abstract:	Foreign Animal Diseases (FADs) Threat Prevention Knowledge Biosecurity small producers.

EAR - 7

Title of abstract:	UNLEASHING EARLY DETECTION: A NOVEL INFECTIOUS DISEASE SCREENING TOOL AND PROTOCOL FOR COMPANION ANIMALS AT THE OSU VMC
Authors:	<p><u>C. King</u>¹, L. Montgomery², J. Winston³, K. Norris², J. Nerswik², E. Cooper³, J. Stull¹, D. Diaz-Campos³, T. Wittum¹</p> <p>Department of Veterinary Preventive Medicine, The Ohio State University¹</p> <p>Veterinary Operations and Services, The Ohio State University²</p> <p>Department of Veterinary Clinical Sciences, The Ohio State University³</p>
Abstract:	<p>In veterinary healthcare settings, disease prevention and treatment are critical to the success of patient care and owner satisfaction. In addition, the risk of infectious disease transmission to other patients and humans is an ongoing concern that all veterinary hospitals encounter. Infection control and prevention measures have been developed at The Ohio State University Veterinary Medical Center (VMC) to address this concern that are documented in an infection control manual. This format, although published online, is not easily accessible and is cumbersome to find specific protocols on how to handle admission, examination, transportation, and hospitalization of infectious patients. In addition, key personnel have noted a lack of consistency of protocol compliance as well as poor communication between services to ameliorate this problem. In response to this concern, a novel graphic summary chart was created that displays information on management of companion animal patients with specific infectious conditions in the VMC. The American Animal Hospital Association phone triage checklist was also implemented to rapidly identify potentially infectious patients when scheduling an appointment or during patient admission. A coordinated effort between reception staff, the infection control committee, specialists in internal and emergency medicine, veterinary technicians and assistants, and the hospital information management team has allowed for the creation of a new intake and identification process for potentially infectious companion animals. The expected outcome of implementing this process is that we will identify infectious patients quickly and effectively using the AAHA checklist. By using color-coded identification bands, creating warning labels in the electronic medical record, and then referring to the summary graphic chart, we will more appropriately handle these patients in the hospital. This new system will create consistency in how patients with infectious conditions are identified and managed, effectively reducing the spread of infectious disease to other patients, owners, and veterinary personnel.</p>
Keywords:	Infection Control and Prevention, Infectious Disease, Hospital Epidemiology

EAR - 8

Title of abstract:	WATER-BASED FOAM DEPOPULATION IN SWINE: THE EFFECT OF WEIGHT AND SEX ON TIME TO UNCONSCIOUS AND BRAIN DEATH
Authors:	<p><u>Jack Korenyi-Both</u>, Magnus R. Campler, Ting-Yu Cheng, Andrew S. Bowman & Andréia G. Arruda Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, 43215, USA</p> <p>Jorge Vidaurre & Tim Held Pediatric Neurology Department, Nationwide Children's Hospital, Columbus, OH, 43205, USA</p> <p>Justin Kieffer & Steven J. Moeller Department of Animal Sciences, The Ohio State University, Columbus, OH, 43215, USA</p>
Abstract:	<p>The food animal industry is constantly challenged with disease outbreaks. An outbreak with a foreign animal disease (FAD) can be detrimental for animal health, the food supply, public health (especially if zoonotic), and the economy. Depopulation plans are needed when FADs are introduced into the food supply. This project further studied the use of water-based foam as a depopulation method in swine. Even though this method is currently approved for poultry, it is not approved for swine use due to lack of research on this species. The main goal was to further our understanding of using water-based foam as a depopulation method by describing the effect of weight and sex on time to loss of consciousness and brain death during water-based foam depopulation in nursery pigs. Data for this project was collected from a completed project supported by the National Pork Board, the Ohio Pork Council, and the USDA. During the field phase of this project, 12 pigs were depopulated using water-based foam, and EEGs were taken from each animal. Impact of weights and sex on time to unconsciousness and/or brain death will be analyzed using a multivariable linear regression model with the potential for further statistical analyses. The results of Part 2 showed that there was no effect of sex on time to unconsciousness ($p= 0.733$) or brain death ($p= 0.611$); and no effect of weight on time to unconsciousness ($p= 0.358$) or brain death ($p= 0.694$). The results of this project in its entirety will help the swine industry be better prepared for foreign animal disease outbreak as we improve, modify, and add to depopulation knowledge and techniques.</p>
Keywords for abstract:	depopulation, preparedness, biosecurity, outbreak, foam, swine

EAR - 9

Title of abstract:	BIOCIDE TOLERANCE OF <i>SALMONELLA</i> ISOLATES RECOVERED FROM CATTLE
Authors:	<u>S.R.Locke</u> and G. Habing
Abstract:	<p>Cleaning and disinfection protocols have had varied effectiveness against <i>Salmonella</i> in farm environment, and residual contamination is often reported. Choice of biocide is critical when designing effective cleaning and disinfection protocols, yet little is known regarding <i>Salmonella</i> susceptibility to commercial products. Our objective was to determine the minimum bactericidal concentration (MBC), defined as ≥ 3 log reduction, of 6 biocides commonly used in agriculture. We hypothesized that some biocide label guidelines would not be effective at eliminating <i>Salmonella</i>. To assess this, a 48 well assay was developed that included two-fold serial dilutions of Clorox® Germicidal Bleach, Chlorine Dioxide, Chlorhexidine Gluconate, KennelSol™, Rescue™, and VirkonS®, with the lowest concentration tested being the label guideline for preparation. A neutralizer was used to simulate 10 minutes of contact between bacteria and biocide. Six isolates each from <i>Salmonella</i> serovar Dublin, Newport, and Typhimurium recovered from cattle were tested in duplicate. Bacteria were enumerated to determine the log reductions after biocide exposure. The dilutions specified on the label of KennelSol™ and VirkonS® resulted in a complete kill (no bacterial growth) for all isolates after 10 minutes of contact. Chlorhexidine gluconate was biocidal (≥ 3 log reduction) at the labeled concentration for <i>S. Typhimurium</i> isolates, but Newport and Dublin isolates required 2- to 4-fold higher concentrations to achieve a biocidal effect. For all isolates, Clorox® was effective at either 625 or 1250 parts per million (ppm), while Rescue™ required a 2- to 4-fold concentration above label suggestion to achieve biocidal effects within 10 minutes. Chlorine dioxide had limited effectiveness in the timeframe, with only 2 isolates susceptible at 3000 ppm, far above suggested use guidelines. Results from this assay identified rapidly effective biocides and may be useful in guiding biocide choice in agricultural environments</p>
Keywords for abstract:	<i>Salmonella</i> Biocides

EAR - 10

Title of abstract:	NEUTRALIZING ACTIVITY OF UNITED STATES HUMAN YOUTH SWINE EXHIBITOR SERUM AGAINST ZONOTIC H1V AND H3V CANDIDATE VACCINE VIRUSES
Authors:	<u>DS McBride</u> ¹ , EE Stevens ¹ , D Huey ¹ , JM Nolting ¹ , AS Bowman ¹ ¹ Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, Ohio
Abstract:	<p>Zoonotic influenza A virus (IAV) remains a primary concern for pandemic IAV emergence. In the USA, most reported interspecies IAV transmission occurs at swine exhibitions, and little is known about zoonotic IAV in the high-risk human exhibitors who interact closely with these swine hosts. WHO coordinates selection of candidate vaccine viruses (CVVs) for zoonotic IAV based on swine IAV surveillance and human cases of swine origin IAV (designated as variant H1v and H3v viruses) to ensure pandemic preparedness for novel IAV spillovers. Because swine exhibitors have the highest risk of variant IAV cases, we assessed the neutralizing protection of this host group against the variant CVVs recommended by WHO. We tested the neutralizing activity of serum from 400 youth (aged 4 to 21 years) swine exhibitors against H1v and H3v CVVs using microneutralization assays. Preliminary analysis showed exhibitors had high mean titers against both 3.2010.1 viruses tested - 1:111 and 1:416 indicating relatively high seroprotection against this HA lineage, which has caused the most recent H3 variant outbreaks. This is also a potential indicator of underreporting of 3.2010.1 variant cases in swine exhibitors. In contrast, the mean titer was only 1:37 against NYMC X-203 (3.1990.4.A). This could reflect a gap in immunity at the human-animal interface for swine origin zoonotic IAV in the USA. Interestingly, 3.1990.4.A was the dominant HA lineage in exhibition swine surveillance for 2020 (over 80% of sequenced IAVs), but this increase has not corresponded with increased reporting of variant cases from this H3 lineages or neutralizing titers against the CVV in the exhibitors during the same timeframe. This warrants further investigation of factors that have limited the zoonotic transmission of 3.1990.4.A viruses in recent years and evaluation of for zoonotic risk for future fair seasons due to lower seroprotection.</p>
Keywords for abstract:	Influenza A virus Zoonoses Public health Exhibition swine

EAR - 11

Title of abstract:	ZOONOTIC SPILLOVER, WIDESPREAD GEOGRAPHIC DISTRIBUTION, AND INTERSPECIES TRANSMISSION OF SARS-COV-2 IN FREE RANGING WHITE-TAILED DEER IN OHIO
Authors:	<u>S. Overend</u> , D. McBride, J. Nolting. A. Bowman. Dept. of Veterinary Preventive Medicine
Abstract:	<p>Over the course of the COVID-19 pandemic, there has been much research into the origins and future evolution of SARS-CoV-2. Many animal species have been implicated as susceptible to infection with SARS-CoV-2, mainly due to ACE-2 homology with humans. White-tailed deer (<i>Odocoileus virginianus</i>) are one who have been proven experimentally and naturally capable of infection and transmission with SARS-CoV-2. To further examine the threat of white-tailed deer as a wildlife reservoir for SARS-CoV-2, 1,522 nasal swabs were collected statewide (83/88 counties) in Ohio from November 2021 to March 2022. This resulted in 10.7% of nasal swabs testing positive for SARS-CoV-2 viral RNA via rRT-PCR. There was a widespread geographic distribution of the virus across the state with estimated prevalence ranging from 1-100% and over half of the counties sampled having one or more positive samples. Whole-genome sequencing of isolated viruses revealed that the majority of samples were delta variant virus, which was the prevalent variant in human populations in the 2021 hunting season. However, nine alpha variant viruses were isolated which were introduced due to spillover from human populations but displayed evidence of further sustained within-deer transmission. This study supports and adds to the current knowledge base that white-tailed deer are a threat to public health by having the ability to serve as a reservoir for SARS-CoV-2. More research in this species is needed to determine if the virus will continue to be transmitted and evolve in deer leading to potential spillback into humans.</p>
Keywords for abstract:	SARS-CoV-2 Pandemic Reverse Zoonosis Animal Reservoir One Health

EAR - 12

Title of abstract:	COMPARISON OF TWO METHODS FOR COLLECTING ANTIMICROBIAL USAGE IN LARGE DAIRY FARMS IN OHIO AND CALIFORNIA
Authors:	<u>R. Portillo-Gonzalez</u> ¹ , A. Garzon ² , R.V.V. Pereira ² , G.G. Habing ¹ ¹ Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, OH, USA ² Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, Davis, CA, USA
Abstract:	<p>Quantification of on-farm antimicrobial use (AMU) is critical to correlate with patterns of antimicrobial resistance, surveillance programs, and formulate interventions to optimize its on-farm use. Prior studies have used the empty drug container (EDC) method to quantify AMU; however, the method is labor-intensive and time-consuming. Therefore, this study aimed to compare it against farm treatment records (FTR) as a reliable method to collect on-farm AMU. We hypothesized a low level of agreement in the farm treatment incidence (TI) obtained between these two different collection methods. The study was conducted as a part of a quasi-experimental field trial that included thirteen conventional dairy farms located in Ohio and California. On-farm AMU was quantified for six months by assessing the on-farm treatment records and by counting the number of used antibiotic packages discarded in containers provided by the research team. TI was calculated using animal daily doses (ADD) and expressed by 1,000 cow-days. Wilcoxon signed-rank test and Pearson correlation were calculated to analyze the TI data. The mean TI obtained from FTR was 10.4 ADD/1,000 cow-days and not significantly different compared to the mean TI of 13.4 ADD/1,000 cow-days obtained from the EDC inventory ($p= 0.95$). Similarly, the mean TI for dry-cow therapy obtained from FTR was 1.6 ADD/1,000, and not significantly different from the mean TI of 1.5 ADD/1,000 cow-days obtained from the EDC inventory ($p= 0.48$). The Pearson test showed a strong positive significant correlation between FTR and EDC inventory ($Rho= 0.80$, $p= 0.009$) as well as, for the dry-cow therapy ($Rho= 0.62$, $p=0.02$). Results demonstrated that the enrolled dairy farms have shown significant consistency in antimicrobial records collected between these two different methods for systemic and intramammary therapies. However, future efforts should be oriented to standardize on-farm antimicrobials collection methods to facilitate their application and improve data accuracy.</p>
Keywords for abstract:	Antimicrobial use Farm treatment records Empty drug container inventory Antimicrobial resistance Dairy cattle

EAR - 13

Title of abstract:	EFFECTS OF CONFINED DISPOSAL FACILITIES ON PAINTED TURTLES (CHRYSEMYS PICTA) BLOOD LACTATE AND WBC COUNTS
Authors:	<u>F. Satern</u> , E. Vincent, B. Fischer, J. Flint, M. Flint
Abstract:	<p>Dredging is commonly used to maintain navigational channels, and in Lake Erie, dredged material is often dumped into upland or in-water “confined disposal facilities” (CDFs). The long-term health implications for wildlife species living in the wetland habitats created by confined disposal facilities remain largely unknown. Due to their site fidelity, longevity, and propensity to accumulate environmental toxins, freshwater turtles can serve as sentinel species to evaluate the overall health of localized freshwater ecosystems. Lactate is an underutilized tool in chelonian health, providing information about physiologic stress that can be measured in the field. We compared painted turtle (<i>Chrysemys picta</i>) health assessments at two sites on Lake Erie: a managed coastal wetland and a confined disposal facility. Health assessments were performed on 51 painted turtles including physical examinations, estimated total white blood cell counts and differentials, and blood lactate levels. We hypothesized that turtles from the confined disposal facility would have higher blood lactate levels and estimated total white blood cell counts caused by anthropogenic stressors when compared to the managed wetland. With statistical analysis, we found no difference in overall lactate levels by site ($p=0.245$). Overall male turtles had a higher blood lactate level than the female turtles, mostly influenced by males at the confined disposal facility with 1.7 times higher lactate than females ($p=0.036$). This could indicate a unique physiologic or behavioral difference in male turtles that causes a more robust response to environmental stress. Further data analysis will explore an association between WBC count and blood lactate levels, investigating an immune response to environmental stress.</p>
Keywords for abstract:	Painted turtle Dredging Environmental stress Blood lactate

EAR - 14

Title of abstract:	DESCRIPTION OF CALF PRODUCTION SYSTEMS AND NETWORK PATTERNS TO IMPROVE DISEASE SURVEILLANCE
Authors:	<u>Sequeira S</u> ¹ , Habing, G ¹ Arruda, A. G. ¹ ¹ Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio, United States
Abstract:	<p>Dairy-beef and veal calf production systems are underrecognized and important sources of antimicrobial resistance, which impacts human health. A considerable number of surplus calves are born on dairy farms and sold within the first weeks through a complex production and distribution network. Several studies have recognized the role of animal movements in disease spread. However, capture of this data is not standardized across regions in the United States which limits our understanding on the magnitude of disease transmission. The objective of this study was to characterize calf production systems' animal movement patterns in the state of Ohio.</p> <p>A survey study was developed and interstate calf movement records from June-2021 to June-2022 were collected in collaboration with the Ohio Department of Agriculture. Records included Interstate Certificates of Veterinary Inspection (ICVIs) and Owner Shipper Statements (OSSs). Animal imports and exports were analyzed along with shipment descriptive information using R software.</p> <p>A total of 1,475 shipments were obtained, including 52.5% ICVIs and 47.5% OSSs. Animal imports represented the majority (77.3%) of the state's recorded movements. Shipments varied from one to 696 animals, and movements recorded through OSSs showed larger (82.2 ± 70.6) loads of animals compared to ICVIs (64.4 ± 74.0). Even though states located closer to Ohio exhibited higher frequency of movements, distances ranged up to 2,097 miles. Pennsylvania and Indiana represented the largest exporter and importer of calves, respectively, within the network. Ohio sites receiving calf loads were concentrated in the western region, while sites sending loads had a wider distribution. Most shipments included mixed sex loads (60.0%), dairy breeds (81.6%) and animals up to one week old (74.1%).</p> <p>Preliminary results suggest highly heterogeneous patterns of calf movements in Ohio. The network shaped by calf movements connects distant regions, which supports the potential for disease spread.</p>
Keywords for abstract:	Calf Production and Distribution Network Shipments Interstate Certificates of Veterinary Inspection Owner Shipper Statement

EAR - 15

Title of abstract:	CONTRASTING PRRSV-2 TEMPORAL LINEAGE PATTERNS AT THE INDIVIDUAL FARM, PRODUCTION SYSTEM, AND REGIONAL LEVELS
Authors:	Y.F. Shen, T.Y. Cheng, M. Prarat, A.G. Arruda. Department of Veterinary Preventative Medicine, College of Veterinary Medicine, The Ohio State University, Columbus OH; Animal Disease Diagnostic Center, Ohio Department of Agriculture, Reynoldsburg, OH
Abstract:	<p>Porcine reproductive and respiratory virus (PRRSV), a significant disease in the swine industry, has been challenging to control due to its high mutation rate. The objective of this retrospective study was to describe and compare the temporal patterns of PRRSV lineages obtained from individual swine farms, production systems, and at the regional level.</p> <p>PRRSV sequences from Ohio swine farms during 2017 – 2021 were obtained from one private swine production system (n = 138) and Ohio Department of Agriculture, Animal Disease Diagnostic Center (ODA-ADDL, n = 652). The MUSCLE algorithm on Geneious Prime® was used to align the ORF5 region along with vaccine strains (n = 6) and lineage anchors (n = 169). Unknown sequences were classified into the most identical lineage anchor sequences. Results were compared to PRRSV lineages from Midwest states reported by the Swine Disease Reporting System (SDRS).</p> <p>At the regional level, L1A, L5, L1H, L1C, and L8, were the most identified lineages, similar to that reported by the SDRS. L1A was the most identified in 2017 (52.9%), 2018 (59.1%), 2020 (72.6%), and 2021 (74.1%). Similar distributions of L1A (42.5%) and L5 (41.0%) were found in 2019. A smaller proportion (<14.5%) of L1H, L1C, and L8 were identified. In three production systems, while L1A and L5 were dominant across 5 years, one production system had a greater proportion of L1C. At three individual farms, we found less lineage diversity with only L1A and L5 in circulation.</p> <p>Our results show that at the farm and production system levels, PRRSV lineage temporal patterns do not necessarily correspond to the regional level, confirming the importance of farm and production systems in shaping PRRSV spread, and highlighting the crucial goal of timely communication for accurate knowledge on PRRSV occurrence and spread within a region.</p>
Keywords for abstract:	Porcine reproductive and respiratory virus Temporal patterns Lineage classification

EAR - 16

Title of abstract:	INSULIN RESISTANCE AND ACYCLICITY IN AFRICAN ELEPHANTS AT CMZ
Authors:	<u>C. Stewart</u> , K. Tennant, L. Amendalogine, P. Dennis Department of Veterinary Preventive Medicine
Abstract:	<p>In AZA (Association of Zoos and Aquariums) zoos housing African elephants over 54% of the females show a lack of normal reproductive cycles. This is a huge conservation concern because this could lead to a completely reproductively dead population of North American African elephants in a few decades. We currently do not know what is causing the lack of reproductive cyclicity, but previous studies have found acyclic elephants to be hyperprolactinemic and have cystic ovaries. In other species cystic ovaries have been linked to insulin resistance and systemic health issues. The objective of this study is to determine the association of insulin levels with ovarian activity in four African elephants housed at Cleveland Metroparks Zoo. We found no difference in serum insulin concentration ($V=6365.5$, $p=0.3108$) in cyclic versus acyclic periods for any of the females. There was a statistical difference in serum glucose concentration in one elephant. Insulin resistance does not seem to be associated with reproductive acyclicity in Cleveland Metroparks zoo's African elephants.</p>
Keywords for abstract:	zoo African elephants Acyclicity Reproduction Insulin resistance

EAR - 17

Title of abstract:	COMPARISON OF PAINTED TURTLE (<i>CHRYSEMYS PICTA</i>) HEALTH ASSESSMENTS AT A CONFINED DISPOSAL FACILITY AND A MANAGED COASTAL WETLAND IN SOUTHWESTERN LAKE ERIE, OHIO
Authors:	<u>E. Vincent</u> , J. Flint, A. Bowman, M. Flint, Dept of Veterinary Preventive Medicine
Abstract:	<p>The harbors of Lake Erie on the northern coast of Ohio must be routinely dredged to maintain shipping channels, and the dredged sediments are commonly placed into “confined disposal facilities” (CDFs) designed to contain contaminated materials. Confined disposal facilities often become wildlife habitats, but the long-term health and welfare implications of exposure to dredged materials are largely unknown. Freshwater turtle species may serve as sentinels of ecosystem health due to their longevity, tendency to bioaccumulate environmental contaminants and pathogens, and relative site fidelity. Painted turtles (<i>Chrysemys picta</i>) were sampled from two sites in southwestern Lake Erie: a confined disposal facility (CDF) in Lorain, Ohio (n=27) and a managed coastal wetland (WPMC) in Port Clinton, Ohio (n=24). Health assessments were performed including physical examinations, morphometrics, hematology, and plasma biochemistry profiles. Oral and cloacal swabs were tested for <i>Chlamydia</i>, <i>Mycoplasma</i>, ranaviruses, and herpesviruses through polymerase chain reaction. Six turtles were positive for <i>Chlamydia</i> (11.8%), and one of these turtles was coinfecting with herpesvirus (2.0%). Ranavirus and <i>Mycoplasma</i> were not detected. <i>Chlamydia</i>-positive turtles had significantly higher lymphocyte percentages ($p=0.028$) and significantly lower calcium:phosphorus ratios ($p=0.036$) than <i>Chlamydia</i>-negative turtles. There was no significant difference in pathogen prevalence by site. Turtles from the CDF had significantly higher heterophil percentages ($p=0.004$), heterophil:lymphocyte ratios ($p=0.028$), and glucose levels ($p<0.001$), but significantly lower total protein ($p=0.015$), lymphocyte percentages ($p=0.024$), eosinophil percentages ($p=0.011$), and calcium:phosphorus ratios ($p=0.015$) than turtles from WPMC. These results suggest that painted turtles living in the confined disposal facility may experience higher stress levels than conspecifics found in a more pristine wetland ecosystem, potentially due to exposure to contaminants or environmental disturbances related to dredge activity. Further research into the long-term impacts of confined disposal facilities on freshwater ecosystem health is warranted.</p>
Keywords for abstract:	Wildlife health Dredging Freshwater turtles

EAR - 18

Title of abstract:	VACCINE OPINIONS AND PRACTICES IN PEOPLE AND ANIMALS
Authors:	<u>E. Welker</u> , J. O'Quin, R. Garabed, J. Nolting, A. Calinger-Yoak. Depts. Of Veterinary Preventative Medicine, Ohio State University, and Biology & Earth Science, Otterbein University
Abstract:	<p>Vaccinations are important tools to prevent and reduce disease in people and animals. Numerous diseases have been eliminated or nearly eliminated through vaccination programs saving millions of lives. Despite this, it seems that vaccine hesitancy continues to rise over the past few decades. More recently, vaccine hesitancy has spilled over into vaccination decisions for pets and livestock. It is currently unknown how common vaccine hesitancy is and what factors play a role in vaccine decision making. Further, false information regarding Covid-19 vaccine risks may be fueling some of these concerns. The purpose of this study was to gain a better understanding of vaccine perceptions and how attitudes and practices regarding vaccines are correlated in people and animals. To investigate this, a survey was developed, piloted, and found to be exempt by IRB. The survey was conducted online using Qualtrics software and distributed to adults in the general population of the United States using paid Facebook advertising. Specifically, this study aims to 1) identify factors associated with individual perceptions on core and optional vaccines; 2) identify preferred sources of vaccine information; 3) determine the association between the way people vaccinate themselves, their children, and their animals; and 4) investigate whether individual views on vaccines changed during the pandemic. Data is currently being analyzed using descriptive and comparative analysis using commercial software programs. The results of this research will help identify the determinants of vaccine decision making. This knowledge is important as it could be used to tailor educational efforts aimed at increasing vaccination. By meeting people where their concerns lie, vaccine information will be more accessible across educational and socioeconomic levels. Ultimately, this may provide individuals with the tools to protect their own health through vaccine practices as well as their children and animals by making informed vaccine decisions on their behalf.</p>
Keywords for abstract:	Vaccination, Vaccine, Vaccine hesitancy, Animal vaccine, Human vaccine, Vaccine survey

EAR - 19

Title of abstract:	PREVALENCE OF <i>BRUCELLA</i> SPECIES IN SMALL CETACEAN PULMONARY NEMATODES ALONG THE COAST OF CALIFORNIA
Authors:	<u>M. Shields</u> , R. Pesapane, M. Martinez, and S. Roger Williams Veterinary Preventive Medicine, College of Veterinary Medicine, Ohio State University, Columbus, OH (Shields, Pesapane), The Marine Mammal Center, Sausalito, CA (Martinez), The National Marine Life Center, Bourne, MA (Roger Williams).
Abstract:	Brucellosis is a zoonotic disease caused by <i>Brucella</i> spp., an intracellular bacteria affecting mammals, including humans. Brucellosis occurs in several marine mammals, including cetaceans, with infection often resulting in abortion, meningoencephalitis, and pneumonia. Marine <i>Brucella</i> strains can also cause human disease and there is concern over zoonosis amid populations in contact with cetaceans. A potential route of <i>Brucella</i> infection is by pulmonary nematode infection. <i>Halocercus</i> and <i>Pseudalius</i> , common cetacean nematodes, harbor <i>Brucella</i> and cause disease, however their vector potential is unknown and cetacean brucellosis remains understudied. To determine the prevalence of <i>Brucella</i> in cetacean nematodes, as well as their vector potential, nematodes from small cetaceans with and without clinical brucellosis stranded over a five year period off the coast of California were collected and identified by pathologists with The Marine Mammal Center. These nematodes were archived at the National Marine Life Center and then shipped to Ohio State where RT-PCR was used to detect the presence of <i>Brucella</i> spp. within each nematode sample. Results are still ongoing for this study. It is the hope that study results may be used to explore vector-borne transmission of marine brucellosis and provide background for future studies in order to determine the impact of <i>Brucella</i> on vulnerable cetaceans as well as potential public health risks.
Keywords for abstract:	One Health Brucellosis Pulmonary Nematodes Cetaceans

**IMMUNOLOGY
AND
INFECTIOUS DISEASES**

IMID - 1

Title of abstract:	DEVELOPMENT OF BROADLY PROTECTIVE INTRANASAL MULTIVALENT SARS-COV-2 VACCINE CANDIDATES BASED ON A MMR VACCINE PLATFORM
Authors:	<u>Michelle Chamblee</u> ¹ , Yuexiu Zhang ¹ , Jiayu Xu ¹ , Cheng Chih Hsu ¹ , Sung J. Yoo ¹ , Panke Qu ¹ , Jack Misny ² , Mohamed M. Shamseldin ³ , Ilada Thongpan ² , Mahesh KC ² , Jesse M. Hall ³ , John P. Evans ¹ , Mijia Lu ¹ , Xueya Liang ¹ , Prosper N Boyaka ^{1,5} , Shan-Lu Liu ^{1,3,5} , Purnima Dubey ^{3,5} , Mark E. Peeples ^{2, 4, 5} , Jianrong Li ^{1,5}
Abstract:	<p>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.</p>
Keywords for abstract:	Vaccine SARS-CoV-2 Coronavirus

IMID - 2

Title of abstract:	MECHANISM OF ACTION OF AN <i>IN VIVO</i> VIRULENCE FACTOR OF <i>EHRlichia</i>
Authors:	<u>R.C. Chien</u> , M. Lin, Y. Rikihisa. Department of Veterinary Biosciences
Abstract:	<p>Infection with <i>Ehrlichia</i> species, blood-borne obligate intracellular bacteria, potentially causes life-threatening disease collectively called “Ehrlichiosis” such as human monocytic ehrlichiosis (HME). To overcome the complex mammalian immune system, establish infection, and cause diseases within the host, <i>Ehrlichia</i> needs to utilize additional strategies (e.g. <i>in vivo</i> virulence factors) to those required to infect eukaryotic cells in culture. Our laboratory developed a mouse model of ehrlichiosis using <i>Ehrlichia japonica</i> (<i>Eja</i>) which causes overwhelming infection and fatal disease in mice. We created a library of <i>Eja</i> mutants by using Himar1 transposon mutagenesis system that randomly inserts transposon into the <i>Eja</i> genome. Using this mutant library, we found that <i>EHF0962</i> is required for fatal infection in mice but is dispensable for infection of cultured cell lines such as canine macrophages (DH82), monkey endothelial cells (RF/6A), and tick embryo-derived cells (ISE6). <i>EHF0962</i> encodes a unique hypothetical protein EHF0962 (~13.5 kDa) that is conserved among <i>Ehrlichia</i> spp. We have cloned <i>EHF0962</i> and obtained the recombinant EHF0962 protein and the protein-specific antiserum. We verified the presence of native EHF0962 protein in wild-type (WT) <i>Eja</i> and the absence of this protein in the mutant H59 that has an Himar1 insertion in <i>EHF0962</i>. <i>EHF0962</i> mRNA is highly upregulated immediately prior to exponential growth of WT <i>Eja</i>. Obligatory intracellular bacteria have a short extracellular stage in order to spread infection. Compared to WT <i>Eja</i>, H59 rapidly lost infectivity at the extracellular stage. Thus, our hypothesis is that EHF0962 mediates <i>Ehrlichia</i> resistance at the extracellular stage. To test this, we aim to investigate mechanisms by which EHF0962 confers extracellular resistance. We also aim to test whether the infectivity loss of H59 can be restored by <i>EHF0962</i> molecular complementation and whether WT <i>Eja</i> infection can be blocked by targeting EHF0962. The results will provide critical knowledge of treating and preventing severe ehrlichiosis.</p>
Keywords for abstract:	<p><i>Ehrlichia chaffeensis</i> Human monocytic ehrlichiosis <i>Ehrlichia japonica</i> Virulence factor <i>EHF0962</i></p>

IMID - 3

Title of abstract:	NOVEL HIGH-FIDELITY TARGET SEQUENCING AND ABSOLUTE QUANTIFICATION ENABLES HIV-1 DRUG RESISTANCE SURVEILLANCE
Authors:	<u>S. Golconda</u> , H. Yu, A. Baek, G. Lee, and S. Kim
Abstract:	<p>Human Immunodeficiency Virus Type-1 (HIV-1) genotyping and drug-resistance surveillance have been limited by erroneous sequencing and HIV-1's high mutation rate. Due to frequent viral genetic recombination, diverse variants can rapidly evolve within patients infected with HIV-1. A high degree of genetic diversity of these viruses enables them to adapt to changes in the host, including those under effective combination antiretroviral therapy (cART) which target different stages of the viral replication cycle. This viral evolution necessitates sensitive detection of drug-resistant mutants for effective patient care. However, current genotyping methods are limited by their inability to detect low-frequency, minority variants and may overestimate them due to sequencing errors. To address this, we have established an approach to analyze each individual HIV-1 genome separately and accurately for sensitive detection and quantification of viral subpopulations without bias. We have recently developed a novel self-error-correction barcoding method utilizing a library of Tandem Twin-barcode linkers (TTB) that each contain two consecutive identical barcodes in the same direction. Our TTB approach can eliminate barcode read errors by enabling cross-comparison of 4 identical barcodes in the same read (2 in the sense strand and 2 in the anti-sense strand) for self-error correction. This accurate barcode reading will thereby enable the effective application of barcoding-mediated error correction of the target DNA, radically reducing template read errors. Our preliminary data showed that we can sequence up to 99.9% accuracy. This current study targets drug-resistant mutation sites through viral specific reverse transcription primers followed by TTB linker ligation, amplification, and sequencing. The sensitivity and fidelity of new TTB-mediated HIV-1 sequencing will be demonstrated. Furthermore, this technical advancement will have a broad impact on diverse areas of biomedical sequence analysis.</p>
Keywords for abstract:	Drug Resistance Surveillance, HIV-1/AIDS, Next Generation Sequencing, Barcoding-Mediated Error Correction

IMID - 4

Title of abstract:	IN VITRO GROWTH OF ANCYLOSTOMA CANINUM SUPPORTED BY HEAT-INACTIVATED BACTERIA
Authors:	<u>S. Hegde</u> and A. Marsh. Department of Veterinary Preventive Medicine
Abstract:	<p><i>Ancylostoma caninum</i>, an intestinal hookworm nematode of dogs, is demonstrating anthelmintic resistance. Hence, <i>in vitro</i> studies are needed to evaluate new drugs. The study hypothesis was that heat-inactivated bacteria would support the development of <i>in vitro</i> stages of <i>A. caninum</i>. The study aims also included different culture conditions to evaluate the development of <i>A. caninum</i> from eggs through to infective larval stages. Study conditions included using Slide-A-Lyzer Dialysis Cassette, cell culture flasks, varying concentrations of amphotericin B, Super Optimal Broth, low melt agar with porcine-derived gelatin, and antibiotic-antimycotic solutions in the presence and absence of heat-inactivated <i>E. coli</i>. Cultures were observed microscopically for larvae development, movement, and viability. Larvae do develop in the presence of heat-inactivated <i>E. coli</i>. In addition, dialysis cassettes larvae were more active than flask cultures. In the substrate support media, larvae were predominantly found in the air pockets. These results suggest that the larvae will migrate towards areas of greater gas exchange. Furthermore, the optimal larvae temperature development was 27°C. Additionally, the low antimycotics concentration cultures experienced increased fungal growth, resulting in larvae trapping and death. The higher amphotericin B concentrations suppressed the growth of the fungus without affecting the development of <i>A. caninum</i>. These outcomes provide information on the supplements and conditions for <i>in vitro</i> cultivation of <i>A. caninum</i>.</p>
Keywords for abstract:	<p><i>Ancylostoma caninum</i> Heat-inactivated <i>E. coli</i> <i>In vitro</i> growth Dialysis cassettes Amphotericin B concentrations</p>

IMID - 5

Title of abstract:	LOSS OF PANETH CELLS ALTERS THE GUT INNATE LYMPHOID CELLS SUBSETS AND INCREASES B1 CELL POPULATIONS
Authors:	<u>M.R. Joldrichsen</u> , E. Kim, S.J. Yoo, R. Rayner, Cormet-Boyaka, P.N. Boyaka. Department of Veterinary Biosciences
Abstract:	<p>Paneth cells are a subset of small intestinal epithelial cells specialized in the production of antimicrobial products and cytokines with the purpose to maintain gastrointestinal homeostasis. While a loss of functional Paneth cells is known to cause dysbiosis with the loss of anti-microbials, the effects of a loss of the cytokines on the gastrointestinal immune environment remain elusive. Using mice with no functional Paneth cells (Sox9^{ΔIEC} mice) we were able to explore the immune environment in the intestines and distant immune sites to analyze the effects of a loss of these cytokines. We found that a loss of Paneth cells leads to a significant decrease in ILC3s in the lamina propria and an increase in ILC2s in naïve mice when compared to wild-type mice. We also see in the intestines a significant increase in the visible Peyer's patches leading to a significant increase in the immune cells present. When we analyzed the immune cells in the lamina propria and the Peyer's Patches we see a significant increase in CD11b⁺Ly6G⁺ neutrophils in both tissues. We also see an increase in CD19⁺IgA⁺ B cells and CD19⁺CD5⁺ B-1a cells. Finally, when we look at other distant tissues, we also see a significant increase in B-1a cells in the Mesenteric lymph node, bone marrow and in the lungs. With the increase in B-1a cells seen in many different tissues it suggests that B-1a cells have an important function in the immune system when there is a loss of Paneth cells. This research also shows the importance of Paneth cells and what happens when they are gone.</p>
Keywords for abstract:	Paneth cells Gastrointestinal immune system B cells

IMID - 6

Title of abstract:	FULL-LENGTH, SINGLE-RNA-LEVEL ANALYSIS REVEALS EPITRANSCRIPTOMIC RISK-SPREADING BY HIV-1
Authors:	<u>G. Lee</u> , A. Baek, S. Golconda, A. Manganaris, and S. Kim. Depts. Of Veterinary Biosciences
Abstract:	<p>HIV-1 exploits every aspect of RNA, a versatile macromolecule that undergoes various post-transcriptional modifications, to maximize its replication. Although the importance of chemical modifications on RNA has been recognized, their evolutionary benefits for HIV-1 remain unclear. Most studies have relied on indirect analyses of the phenotypic effects of perturbing host effectors, showing inconsistent results depending on the viruses and replication stages, and have provided only population-averaged values of modifications for fragmented RNAs at low resolution. Here, we developed a new RNA-library-preparation method for full-length direct RNA sequencing and analyzed HIV-1-specific modifications at the single-RNA level. Our analysis revealed that the HIV-1 modification landscape is unexpectedly simple, showing three predominant N6-methyladenosine (m6A) modifications near the 3' end. More densely installed in viral mRNAs than in genomic RNAs, these m6As play a crucial role in maintaining normal levels of RNA splicing and translation. We also discovered that HIV-1 generates diverse RNA subspecies with distinct ensembles of the m6As and that these m6As regulate splicing independently of each other. Our single-RNA-level study demonstrates that HIV-1 tolerates functionally redundant m6As to provide stability and resilience to viral replication while minimizing the risk of unpredictable mutagenesis – a novel strategy similar to bet-hedging in evolutionary biology.</p>
Keywords for abstract:	Human immunodeficiency virus Viral epitranscriptome RNA modifications Viral survival strategy Direct RNA sequencing

IMID - 7

Title of abstract:	CLINICAL AND PATHOLOGIC FEATURES OF FELINE INFECTIOUS PERITONITIS (FIP) IN SENIOR CATS
Authors:	<u>B. Li</u> , M.E. Schreeg, Department of Veterinary Biosciences
Abstract:	<p>Feline infectious peritonitis (FIP) has a reported bimodal age distribution with a second peak in senior cats. However, variability in disease manifestation, comorbidities, and higher-ranked differentials complicates diagnosis in seniors. Currently, reported clinical, clinicopathologic, gross, and histological features of FIP+ senior cats is lacking.</p> <p>We hypothesized that FIP+ seniors would have unique characteristics compared to FIP+ younger cats.</p> <p>Cases were identified via retrospective search of the OSU-CVM Applied Pathology archives. Cats were considered FIP+ if pathognomonic lesions were noted in reports; confirmatory histologic review and immunohistochemistry (IHC) staining was performed on a sub-set; IHC-negative cases with a high suspicion of FIP were submitted for PCR testing to help rule out FIP, resulting in 243 FIP+ cases.</p> <p>Patient signalment, presence/location(s) of effusion, tissues affected, and gross/histologic features were analyzed.</p> <p>Kittens were more often affected (n=120), than young adults (n=88), mature adults (n=21), seniors (n=9) or cats of unknown ages (n=5). Trends in senior cats were similar to the other age groups, including over-representation of males and mixed-breed cats with enrichment in the population by purebred cats.</p> <p>The majority of senior (n=8/9) and younger cats (n=154/234) had effusions. Grossly, the liver was most frequently affected tissue in both senior (n=5/9) and younger cats (n=103/234). Gross renal involvement was more common in younger cats (n=96/234) than in seniors (n=2/9). Histologically, hepatitis was common in seniors (n=8/9), and across all tissues, pyogranulomatous inflammation and vasculitis were consistently present.</p> <p>No unique features have been identified in FIP+ seniors. Gold standard testing via FIP IHC for the senior cats revealed that all nine tested positive on IHC. Additional research to discuss the common comorbidities present in senior cats with FIP+ is ongoing.</p>
Keywords for abstract:	<p>Feline infectious peritonitis FIPv Coronavirus FCoV Feline enteric coronavirus FECV Hepatitis Pyogranulomatous Vasculitis Pleuritis Senior Geriatric</p>

IMID - 8

Title of abstract:	DELAYED CD8 T CELL RESPONSES IMPAIR RESPIRATORY SYNCYTICAL VIRUS CLEARANCE IN GERIATRIC COTTON RATS
Authors:	<u>J. Miller</u> , C. Leedale, O. Harder, S. Niewiesk Department of Veterinary Biosciences
Abstract:	Elderly individuals are at increased risk of severe disease and mortality resulting from respiratory syncytial virus (RSV) infection. RSV clearance is delayed in adults over 65 years of age, a finding that is mirrored in geriatric cotton rats. Treatment with pan-cyclooxygenase (COX) and COX-2-specific inhibitors eliminates this delay in cotton rats, implicating the arachidonic acid cascade as a contributor to impaired RSV clearance. We show that prostaglandin D ₂ (PGD ₂), a downstream product of COX activity, is elevated in airways of RSV-infected cotton rats. Administration of PGD ₂ to adult cotton rats delays RSV clearance as observed in geriatric animals, while treatment of geriatric animals with a PGD ₂ synthase inhibitor improves clearance, indicating that age-associated PGD ₂ prolongs RSV infection. Cytotoxic T cells are key mediators of virus clearance and restoration of RSV clearance in geriatric animals by COX inhibitors is abolished by CD8 T cell depletion. This indicates that the therapeutic effect of COX inhibition is related to restoring cell-mediated immunity. We measured IFN γ induction in CD8 T cells from lung and mediastinal lymph nodes after <i>ex vivo</i> stimulation with immunodominant RSV epitope peptides. Compared to adult cotton rats, geriatric animals exhibit a delay in induction of a robust RSV-specific CD8 T cell response, which correlates with delayed viral clearance. Future studies will examine the mechanism by which age-associated elevation in COX activity and PGD ₂ levels delay CD8 T cell responses to RSV.
Keywords for abstract:	Respiratory syncytial virus Aging Cotton rat Prostaglandin D ₂

IMID - 9

Title of abstract:	PREVALENCE OF <i>P. TENUIS</i> (MENINGEAL WORM) IN INVERTEBRATE VECTORS FROM OHIO COUNTIES WITH CLINICAL DISEASE IN CAMELIDS
Authors:	<u>Annaliese Schrandt</u> , Antionette Marsh, Nathan Shoobs, Richard Gerhold Jr., Eryn Watson, Jeffery Lakritz Department of Veterinary Clinical Sciences (Lakritz, Marsh), Museum of Biological Biodiversity (Shoobs), The Ohio State University, Columbus, OH; Department of Diagnostic & Biomedical Sciences (Gerhold Jr.), Department of Forestry Wildlife & Fisheries (Watson), University of Tennessee, Knoxville, TN.
Abstract:	Parasites pose a significant public health and animal welfare concern globally. The purpose of this study is to investigate the prevalence and transmission of meningeal worm (<i>Parelaphostrongylus tenuis</i>), a neurotropic nematode, in domestic ungulate species in Ohio counties. This will provide critical information for parasite management to reduce infection in domestic camelid and other susceptible species. It is hypothesized that there is another route of transmission, involving the shedding of infective L3 larvae from terrestrial gastropod intermediate hosts via slime trails into the environment rather than direct ingestion of infected gastropods by vulnerable hosts. This would lead to the contamination of grasses, hay, and other feedstuff by the gastropod intermediates. Collected gastropods from camelid farms in different counties (Madison, Perry, Warren, Portage, Lawrence so far) were identified for genus and species based on microscopy. Slime trails were collected for nematode larvae detection followed by analysis of nematode stages in the gastropod tissues. Gastropods were humanely euthanized with 5% MgSO ₄ solution and digested using acid-pepsin solution with larvae detected via microscopy. Larvae recovered were further processed for molecular analysis. Ohio lacks a contemporary terrestrial snail inventory which this study initially addresses. To date, the total number of gastropods collected is 138. Nematodes were visually detected in 4% of the slugs/snails and are undergoing molecular characterization. GIS mapping was used to visualize the environmental factors present on Ohio properties with clinical <i>P. tenuis</i> cases in livestock.
Keywords for abstract:	<i>P. tenuis</i> , nematode, larvae, lifecycle, gastropod, morphology

IMID - 10

Title of abstract:	CAMPYLOBACTER PREVALENCE AND ANTIMICROBIAL RESISTANCE IN ANIMAL SHELTERS
Authors:	<u>S. Strader</u> , D. Mollenkopf, M. Herron, T. Wittum
Abstract:	<p><i>Campylobacter</i> is a zoonotic pathogen that can easily spread to susceptible individuals, including children. <i>Campylobacter</i> is one of the most common causes of bacterial enteritis in humans and is associated with direct animal contact. The prevalence of animal shelter dogs shedding <i>Campylobacter</i> was previously estimated between 50-73%. Potential adopters should be aware of the risks of <i>Campylobacter</i> and the symptoms associated. The purpose of this study was to determine asymptomatic shedding of <i>Campylobacter</i> by dogs in animal shelters and the risk of zoonotic disease transmission to new pet owners. Shelter dogs in central Ohio were screened for the presence of <i>Campylobacter</i> in fresh feces. At each shelter twenty fecal samples were collected from the ground. One shelter was sampled weekly and other shelters were sampled cross-sectionally throughout the summer. For <i>Campylobacter</i> culture, each 1g fecal sample was mixed with 9 mL of supplemented Bolton broth and incubated at 42°C in microaerophilic conditions. After 24 hours, samples were plated on CVA and Campy-Cefex and again incubated overnight. Isolated colonies were grown on TSA blood agar and speciated using MALDI-TOF. A total of 158 samples were collected with two samples (2%) positive for <i>Campylobacter</i> spp.</p>
Keywords for abstract:	Campylobacter Antimicrobial Resistance

IMID - 11

Title of abstract:	EVALUATION OF <i>PASTEURELLA MULTOCIDA</i> ANTIBODY TITERS IN FREE-RANGE BROWN LAYING HENS.
Authors:	<u>L. Trimble</u> , J. Higgins, D. Huey, A. Bowman. The Ohio State University College of Veterinary Medicine (Trimble), Department of Veterinary Preventive Medicine (Bowman, Huey), Kalmbach Feeds (Higgins)
Abstract:	<p><i>Pasteurella multocida</i> (<i>PM</i>) vaccines are a valuable disease prevention tool for the organic, free-range layer industry due to restricted antibiotic use. Industry standard is to vaccinate at 8 and 12 weeks of age for <i>PM</i> with expectation that protection lasts the duration of a hen's life at 75 weeks. However, <i>PM</i> remains a concern in late production among vaccinated hens. It is unclear what this is due to since antibody baselines for <i>PM</i> are rarely established. We hypothesized that antibodies would decrease with age and be unprotected at 65 weeks of age. In this cross-sectional study, antibody titers for 1140 commercially owned free range Bovan and Hyline brown laying hens were measured using an IDEXX <i>PM</i> enzyme-linked immunosorbent assay (ELISA). Hens were vaccinated at 8 and 12 weeks of age with one of two prime-boost protocols. One group was primed with a commercial killed <i>PM</i> vaccine (Avipro[®]108 FC3 Platinum) and boosted with a modified live <i>PM</i> vaccine (Poulvac[®]Cholera PM-1). The other group was primed with a modified live <i>PM</i> (Poulvac[®]Cholera PM-1) and boosted with killed <i>PM</i> autogenous vaccine (Ceva). Age points for sampling in flocks occurred at 15, 40, 45, 50, 55, 60, 65 or 70 weeks of age and was done by collecting 1.5 mL of blood from 30 hens per flock. In total, 20 flocks; 5 at each age point were sampled. The current study found a killed vaccine used to prime and a modified live vaccine used to boost, provided hens with better antibody protection and duration then a modified live vaccine used to prime hens and a killed vaccine to boost, this contrasts with conventional immunology principles. This study will help vaccination strategies for <i>PM</i> and an understanding of antibody levels at different ages allowing for insight where minimum protection occurs during late production.</p>
Keywords for abstract:	<p><i>Pasteurella multocida</i> Vaccination Chickens Antibodies</p>

IMID - 12

Title of abstract:	DEVELOPMENT OF A HUMAN T-CELL LEUKEMIA VIRUS TYPE 1 MRNA VACCINE
Authors:	<p><u>Joshua J. Tu</u>¹, Victoria Maksimova¹, Susan Smith¹, Emily King¹, Ramon Macias², Lianbo Yu¹, Xiaogang Cheng³, Lee Ratner³, Patrick L. Green¹, Stefan Niewiesk¹, Justin Richner⁴, <u>Amanda R. Panfil</u>¹</p> <p>¹Center for Retrovirus Research, Department of Veterinary Biosciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH USA</p> <p>²Cellular and Molecular Biology Graduate Program, The Ohio State University, Columbus, OH USA</p> <p>³Department of Medicine, Washington University, St. Louis MO USA</p> <p>⁴Department of Microbiology and Immunology, University of Illinois-Chicago, Chicago, IL USA</p>
Abstract:	<p>Human T-cell leukemia virus type 1 (HTLV-1) is an oncogenic human retrovirus which causes a lifelong infection. An estimated 5-10 million persons are infected worldwide and while HTLV-1 is normally asymptomatic in infected individuals, 5-10 percent will develop an aggressive CD4+ T-cell malignancy called adult T-cell lymphoma (ATL) or a progressive neurodegenerative disease known as HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP). Despite this, no preventative vaccine has been tested in clinical trials to date. In this study, we developed a mRNA lipid nanoparticle (mRNA-LNP) vaccine encoding for a codon optimized HTLV-1 envelope (Env) and evaluated its efficacy as a vaccine candidate in New Zealand white rabbits. Rabbits (n=6) were vaccinated with 2 doses of either Env mRNA-LNP or control GFP mRNA-LNP, then challenged with cell-associated HTLV-1. All rabbits were rechallenged 15 weeks after initial virus challenge to evaluate the durability of vaccine immune responses. We detected anti-Env antibody responses by western blot in all Env-vaccinated rabbits after the booster dose. Anti-Env antibody responses in Env mRNA-LNP rabbits were also quantitatively measured using infected cell binding assays. 3/6 Env mRNA-LNP vaccinated rabbits had no detectable proviral load after first virus challenge, and 2 of these rabbits had no detectable proviral load after rechallenge. Proviral loads were significantly lower in Env mRNA-LNP rabbits compared to GFP mRNA-LNP rabbits. HTLV-1 <i>tax</i> and <i>hbz</i> expression was significantly lower at peak timepoints for Env mRNA-LNP rabbits compared to GFP mRNA-LNP rabbits. Cell-associated syncytia inhibition assays and cell-free viral infectivity assays detected significantly more neutralizing antibody activity in Env-vaccinated rabbits compared to GFP control vaccinated animals. In conclusion, our Env mRNA-LNP vaccine was immunogenic and provided protection against HTLV-1 challenge in rabbits. Current studies are focused on immune correlates (T-cell responses) of vaccine protection and antigen optimization.</p>
Keywords for abstract:	<p>HTLV-1 Vaccines mRNA Lipid Nanoparticle Envelope Cancer Virus Retrovirus</p>

IMID - 13

Title of abstract:	<i>IN VITRO GROWTH OF ANCYLOSTOMA CANINUM SUPPORTED BY HEAT-INACTIVATED BACTERIA</i>
Authors:	<u>J. Xu</u> , Y. Zhang, P. Qu, M. Shamseldin, S. Yoo, J. Misny, I. Thongpan, M. KC, J. Hall, J. Evans, m. eltoigy, M. Lu, C. Ye, M. Chamblee, X. Liang, L. Martinez-Sobrido, A. Amer, J. Yount, P. Boyaka, M. Peoples, S. Liu, P. Dubey, J. Li. Department of Veterinary Biosciences.
Abstract:	<p>As SARS-CoV-2 variants of concern (VoCs) that evade immunity continue to emerge, next generation adaptable COVID-19 vaccines which protect the respiratory tract and provide broader, more effective, and durable protection are urgently needed. Here, we have developed one such approach, a highly efficacious, intranasally delivered, trivalent measles-mumps-SARS-CoV-2 spike (S) protein (MMS) vaccine candidate that induces robust systemic and mucosal immunity with broad protection. This vaccine candidate is based on three components of the MMR vaccine, a measles virus Edmonston and the two mumps virus strains [Jeryl Lynn 1 (JL1) and JL2] that are known to provide safe, effective, and long-lasting protective immunity. The six proline-stabilized prefusion S protein (preS-6P) genes for ancestral SARS-CoV-2 WA1 and two important SARS-CoV-2 VoCs (Delta and Omicron BA.1.) were each inserted into one of these three viruses which were then combined into a trivalent "MMS" candidate vaccine. Intranasal immunization of MMS in IFNAR1^{-/-} mice induced a strong SARS-CoV-2-specific serum IgG response, cross-variant neutralizing antibodies, mucosal IgA, and systemic and tissue resident T cells. Immunization of golden Syrian hamsters with MMS vaccine induced similar high levels of antibodies that efficiently neutralized SARS-CoV-2 VoCs and provided broad and complete protection against challenge with any of these VoCs. This MMS vaccine is an efficacious, broadly protective next generation COVID-19 vaccine candidate which is readily adaptable to new variants, built on a platform with a 50-year safety record that also protects against measles and mumps</p>
Keywords for abstract:	SARS-CoV-2 Intranasal trivalent vaccine MMR vaccine

IMID - 14

Title of abstract:	5-METHYLCYTOSINE (m5C) RNA MODIFICATION CONTROLS THE INNATE IMMUNE RESPONSE TO VIRUS INFECTION BY REGULATING TYPE I INTERFERONS
Authors:	<u>JY. Zhang</u> , L. Zhang, Q. Dai, P. Chen, M. Lu, E. Kairis, V. Murugaiah, J. Xu, R. Shukla, X. Liang, Z. Zou, E. Boyaka, J. Qiu, M. Peeples, A. Sharma, C. He, and J. Li. Department of Veterinary Biosciences, College of Veterinary Medicine
Abstract:	5-methylcytosine (m5C) is one of the most prevalent modifications of RNA, playing important roles in RNA metabolism, nuclear export, and translation. However, the potential role of RNA m5C methylation in innate immunity remains elusive. Here, we show that depletion of NSUN2, an m5C methyltransferase, significantly inhibits the replication and gene expression of a wide range of RNA and DNA viruses. Notably, we found that this antiviral effect is largely driven by an enhanced type I interferon (IFN) response. The antiviral signaling pathway is dependent on the cytosolic RNA sensor RIG-I but not MDA5. Transcriptome-wide mapping of m5C following NSUN2 depletion in human A549 cells revealed a marked reduction in the m5C methylation of several abundant noncoding RNAs (ncRNAs). However, m5C methylation of viral RNA was not noticeably altered by NSUN2 depletion. In NSUN2-depleted cells, the host RNA polymerase (Pol) III transcribed ncRNAs, in particular RPPH1 and 7SL RNAs, were substantially up-regulated, leading to an increase of unshielded 7SL RNA in cytoplasm, which served as a direct ligand for the RIG-I -mediated IFN response. In NSUN2-depleted cells, inhibition of Pol III transcription or silencing of RPPH1 and 7SL RNA dampened IFN signaling, partially rescuing viral replication and gene expression. Finally, depletion of NSUN2 in an ex vivo human lung model and a mouse model inhibits viral replication and reduces pathogenesis, which is accompanied by enhanced type I IFN responses. Collectively, our data demonstrate that RNA m5C methylation controls antiviral innate immunity through modulating the m5C methylome of ncRNAs and their expression.
Keywords for abstract:	5-methylcytosine innate immune response virus infection interferon

IMID - 15

Title of abstract:	NEUTRALIZATION AND FUSOGENICITY OF SARS-COV-2 OMICRON XBB SUBVARIANT
Authors:	<u>J.N. Faraone</u> , P. Qu, J.P Evans, Y.M. Zheng, C. Carlin, M. Anghelina, P. Stevens, S. Fernandez, D. Jones, G. Lozanski, A. Panchal, L.J. Saif, E.M. Oltz, R.J. Gumina, S.L. Liu
Abstract:	<p>The emergence of the Omicron variant of SARS-CoV-2 in 2021 caused widespread concern due to its large amount of spike mutations. These spike mutations have since demonstrated marked effects on the binding of neutralizing antibodies, attenuating the efficacy of mRNA vaccines. Since the variant's initial emergence, several new Omicron subvariants have continued to emerge throughout the world, posing further challenges to current vaccination strategies. In particular, the XBB subvariant, which is a recombinant virus between BA.2.10.1.1 and BA.2.75.3.1.1.1, as well as the BA.2.3.20 and BR.2 subvariants that contain mutations distinct from BA.2 and BA.2.75, have been increasing in proportion of variants sequenced. Here we show that antibodies induced by 3-dose mRNA booster vaccination as well as BA.1 and BA.4/5 wave-infection effectively neutralize BA.2, BR.2, and BA.2.3.20, but had significantly reduced efficiency against XBB. This escape by XBB could be partially recovered by the administration of a bivalent booster mRNA vaccine. XBB also demonstrates modest increases in fusogenicity and spike processing relative to BA.2, though infectivity in both human lung epithelial cell line Calu-3 and HEK293T-ACE2 cells remains comparable to BA.2. Notably, the BA.2.3.20 subvariant exhibits enhanced infectivity in the lung-derived CaLu-3 cells and in 293T-ACE2 cells and increased fusogenicity and spike processing relative to BA.2. Overall, our results demonstrate that the XBB subvariant is highly neutralization resistant, and that newly emerged Omicron variants have altered fusogenicity and infectivity, highlighting the need for continued monitoring of the immune escape and tissue tropism of emerging Omicron subvariants.</p>
Keywords for abstract:	SARS-CoV-2 COVID-19 XBB Viral Neutralization Neutralizing Antibodies mRNA Vaccination Vaccine Efficacy

IMID - 16

Title of abstract:	LYMPHOID GERMINAL CENTERS PROTECT THEIR RESIDENT T CELLS FROM ANTIBODY-BASED T-CELL-TARGETING REAGENTS
Authors:	<p><u>S. Kim*</u>, R. Shukla, S. Cressman, A. Kim, A. Tracey, N. Liyanage and S. Kim</p> <p>Depts. Of Veterinary Biosciences and Microbial Infection and Immunity, The Ohio State University, Columbus, OH</p>
Abstract:	<p>Antibody and immunotoxin-mediated therapeutic T-cell depletion have become increasingly useful in T cell lymphoma, HIV/AIDS, allograft rejection, and transplant medicine. Despite the tremendous hope generated by these new agents, their treatment outcomes have often been limited and inconsistent for unclear reasons. Here, we demonstrate that germinal centers in secondary lymphoid organs protect their resident T cells (CXCR5+ T cells) against anti-CD3e monoclonal antibody (mAb) or CD3e-immunotoxin (CD3e-IT: anti-CD3e mAb conjugated with saporin or diphtheria toxin)-mediated T-cell killing in various organs. We found that both anti-CD3e mAb and CD3e-IT are effective and specific in depleting T cells in vivo. Remarkably, however, we found that CD3e-IT was inefficient at killing a subset of T-cell populations that express CXCR5, including follicular T-helper cells (TFH), are an important therapeutic target in HIV/AIDS and T-cell lymphoma therapy. Immunohistochemistry analysis showed that CD3e-IT efficiently depleted T cells in the T cell zone outside the B follicles, whereas T cells within the GCs were enriched. When CXCR5(+) and CXCR5(-) T-cell killing efficiency was compared in vitro, there was no notable difference between these two cell types, indicating that CXCR5+ T cells are not intrinsically resistant to CD3e-IT. Our short-term in vivo CD3e-IT binding assay – where CD3e-IT was retro-orbitally injected 8 minutes prior to euthanasia – also showed that, in spleen, CD3e-IT binds to CXCR5(-) T cells with a significantly better efficiency than to CXCR5(+) T cells. Lastly, using CD4/iDTR transgenic mice that expressed Diphtheria toxin receptors on T cells, we compared in vivo T-cell depletion by three different protein reagents, including Diphtheria toxin, CD3e mAb and CD3e-IT, and the results showed that GCs protect their resident CXCR5+ T cells from all these protein agents. Our findings, therefore, suggest a potentially a new treatment resistance mechanism mediated by the normal lymphoid GCs against T-cell depletion protein agents.</p>
Keywords for abstract:	<p>A new treatment resistance mechanism Germinal Centers CXCR5+ T cells CD3e-IT CD3e monoclonal Ab Diphtheria toxin T-cell lymphoma HIV/AIDS</p>

IMID - 17

Title of abstract:	BCG INDUCED NK CELL DYNAMICS AND TARGETS FOR ENHANCED VACCINE EFFICACY.
Authors:	<u>Manuja Gunasena</u> , Richard Robinson, Namal Liyanage
Abstract:	<p>Bacillus Calmette-Guerin (BCG), a live attenuated strain of the cattle Tuberculosis (TB) pathogen, Mycobacterium bovis is currently being used throughout the world as a preventive neonatal vaccine against Mycobacterium tuberculosis (MTB). Administration of BCG is considered safe for neonates, infants, and adults. There have been reports supporting the fact that BCG vaccine can induce innate memory in monocytes. Newborns vaccinated with BCG have been found to have reduced mortality rates and enhanced innate immune responses, not only against MTB, but also against other microorganisms such as Candida albicans and Staphylococcus aureus. However, the role of NK cells following BCG vaccination and its ability to generate memory-like NK cell subsets are understudied.</p> <p>We studied phenotypic and functional changes of splenic NK cells using cells of BCG-vaccinated (n= 4) and wildtype control C57BL/6 (n=4) mice. High dimensional flowcytometry was carried out on isolated splenic cells as well as on cells restimulated with BCG lysate for 24 hours invitro.</p> <p>NK cell frequency (NK1.1+ cells) was reduced in the spleen following BCG vaccination (p<0.05). However, NK cell functionality (TNFα IFNγ and IL1β production) and a mature phenotype of NK cells (KLRG1+) were both enhanced following vaccination (p<0.05). When restimulated with BCG lysate, it was observed that a memory like NK cell phenotype (NK1.1+ Ly49H+) was induced in the spleen (p<0.05). Also, during recall responses to BCG lysate, we observed a significant elevation in cytotoxic responses (granzyme B production) compared to cytokine production among memory NK cells (p<0.05). These data suggest an induction of mature and cytotoxic memory like NK cell subsets during BCG recall responses.</p> <p>We plan to explore the possibility of targeting the NK cell component for protection against MTB infection and increase BCG vaccine efficacy. Further studies will be carried out to study genomic and epigenetic alternations in NK cells in response to BCG vaccination.</p>
Keywords for abstract:	BCG NK cells Mycobacterium Tuberculosis

IMID - 18

Title of abstract:	ENHANCED NEUTRALIZATION ESCAPE AND FUSOGENICITY OF NEWLY EMERGING OMICRON SUBVARIANTS INCLUDING BQ.1.1, BQ.1 AND XBB.1.5
Authors:	<u>P. Qu</u> , J.P. Evans, J.N. Faraone, Y.M. Zheng, C. Carlin, M. Anghelina, P. Stevens, S. Fernandez, D. Jones, G. Lozanski, A.R. Panchal, L.J. Saif, E.M. Oltz, K. Xu, R.J. Gumina, and S.L. Liu. Depts. Of Veterinary Biosciences.
Abstract:	Since its emergence in late 2021, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has evolved into numerous subvariants. Most recently, the BQ.1 and BQ.1.1 (derived from BA.4/5), BA.2.75.2 (derived from BA.2.75), as well as the XBB and XBB.1.5 subvariants have emerged and are causing serious concern about further immune escape and potentially varied pathogenicity. Therefore, it is important to understand the cell tropism, fusogenicity, and immune resistance of these variants. We first examined the infectivity of newly emerging Omicron subvariants but found no differences between these variants and corresponding parental subvariants except XBB and XBB.1.5, which exhibited increased titer, especially in human lung epithelial cell line Calu-3. We next determined the propensity for the Omicron subvariant spike-mediated cell-cell fusion and found that enhanced fusogenicity in most of Omicron subvariants relative to BA.2, consistent with their enhanced S processing. More importantly, we observed enhanced neutralization resistance in all new subvariants to sera from BA.1-wave patients, BA.4/5-wave patients, vaccinated healthcare workers including those receiving 3-dose monovalent mRNA vaccines and those receiving one additional bivalent hybrid mRNA vaccine. The neutralization resistance in BQ.1 and BQ.1.1 subvariants is driven largely by a N460K mutation, whereas in the BA.2.75.2 subvariant it is driven largely by a signature F486S mutation. In contrast, resistance by XBB.1.5 subvariant is driven by F486P, while the CH1.1 and CA.3.1 subvariants is dictated by K444T/M and L452R mutations. Altogether, these findings uncover key biological features of Omicron subvariants, including enhanced transmissibility and potentially altered pathogenicity, and support the need for administration of the bivalent mRNA vaccine and the need for continued surveillance of Omicron subvariants.
Keywords for abstract:	Omicron subvariants Neutralization escape Fusogenicity

**MOLECULAR
AND
CELLULAR BIOLOGY**

MCB - 1

Title of abstract:	THE PRMT5 INHIBITOR EPZ015666 DEMONSTRATES EFFICACY AGAINST HTLV-1 T-CELL LINES IN VITRO AND IN VIVO
Authors (see example above for format)	<u>K. Ernzen</u> , C. Melvin, L. Yu, C. Phelps, S. Niewiesk, P. Green, and A. Panfil. Depts. of Veterinary Biosciences and Biomedical Informatics.
Abstract (300 word limit)	<p>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 highly aggressive and 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 demonstrated 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 goal of this study was to assess how PRMT5 activity impacts HTLV-1 infected cell viability, transformation, and disease pathogenesis. Small molecule-mediated inhibition of PRMT5 enzymatic activity with a commercially available inhibitor (EPZ015666) resulted in selective <i>in vitro</i> toxicity of actively proliferating and transformed T-cells. Compared to uninfected Jurkat cells, EPZ015666-treatment also led to a dose-dependent increase in apoptosis in HTLV-1-transformed and ATL-derived cell lines. Using a co-culture model of infection and immortalization, we identified that 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 <i>in vitro</i>. To determine the importance of PRMT5 activity <i>in vivo</i>, 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 survival, transformation, and pathogenesis of HTLV-1, demonstrating the potential utility of this cellular enzyme as a therapeutic target for the treatment of ATL.</p>
Keywords for abstract: Please list your keywords – one per line	HTLV-1 ATL PRMT5 Transformation EPZ015666

MCB - 2

Title of abstract:	CHARACTERIZING THE ROLE OF N-6-METHYLADENOSINE (M6A) IN HTLV-1 PATHOBIOLOGY
Authors:	<u>E. King</u> , A. Midkiff, A. Panfil. Dept. of Veterinary Biosciences.
Abstract:	<p>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. Patient prognosis is poor and there are few effective therapeutic options available for patients with HTLV-1-mediated diseases. Two viral genes, <i>tax</i> and <i>hbz</i>, have been previously identified as critical to viral persistence and pathogenesis. Methylation of the N6 position of adenine (m⁶A) 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 m⁶A modifications and regulate target gene expression. Recent data from our lab using cross-linking and immunoprecipitation (CLIP) assays has found both <i>tax</i> and <i>hbz</i> mRNAs contain m⁶A modifications and reader protein YTHDC1 binds the viral transcripts <i>tax</i> and <i>hbz</i>. Sites of m⁶A modification were also mapped within the HTLV-1 genome using methylated RNA immunoprecipitation sequencing (MeRIP-seq). We identified 3 major peaks, the largest of which localizes to the regulatory pX region of the genome encoding both <i>Tax</i> and <i>Hbz</i> genes. Over-expression of YTHDC1 causes a decrease in both spliced and unspliced viral transcript level, viral transcription, and p19 gag release into the supernatant. Conversely, shRNA-mediated knockdown of YTHDC1 increases viral transcript levels, viral transcription, and p19 gag release. Finally, HTLV-1-infection of primary CD4⁺ T-cells induces a significant increase in total m⁶A levels within the cell as early as two weeks post-infection. Given our current understanding of HTLV-1 and m⁶A, we hypothesize that the m⁶A modification of <i>tax</i> and/or <i>hbz</i> regulates viral gene expression and thus subsequent viral-mediated cellular proliferation and pathogenesis.</p>
Keywords for abstract:	retrovirus, HTLV-1, m ⁶ a, epigenetics, pathogenesis

MCB - 3

Title of abstract:	URINE LIMBO: DETERMINING MINIMUM URINE VOLUME FOR EFFECTIVE CHARACTERIZATION OF CANINE URINARY TRACT MICROBIOTA
Authors:	<u>Z. Lewis</u> , C. Madden, S. Justice, A. Rudinsky, J. Hokamp, and V. Hale. Depts. Veterinary Preventive Medicine, College of Nursing, Veterinary Clinical Sciences, and Veterinary Biosciences
Abstract:	<p>Until recently, the urinary tracts of healthy individuals were thought to be sterile. However, culture-independent methods have since revealed a distinct and diverse urinary microbiome (“urobiome”). Early studies of the urobiome in humans and dogs have demonstrated important correlations between urobiome composition and disease states such as bladder cancer and incontinence. However, these studies work with urine volumes ranging from 0.5mL to 50mL. Despite growing awareness of the importance of the urobiome, standardized, uniform sampling and analysis pipelines have not been well established for the study of urinary microbiota. Factors like disease states, breed/age, and species may limit available urine for analysis, but it is unknown if there is a minimum volume needed for effective urobiome profiling. That urine is a low-biomass substrate ($<10^5$ CFU/mL), making it particularly vulnerable to contamination and introduced community stochasticity, compounds this issue. To determine whether a minimum volume of urine is necessary to obtain consistent urobiome profiles from 16S rRNA gene sequencing, we collected urine from five healthy dogs and fractionated the samples into 0.1, 0.2, 0.5, 1.0, 3.0, and 5.0 mL aliquots before extraction and sequencing. We show that the microbial composition of samples with <1 mL is highly subject to stochastic variability, while samples ≥ 1 mL qualitatively show consistent clustering within dogs. Sample volume negatively correlated with the percent of sequencing reads identified as contaminants ($r = -0.43$, $p = 0.02$) and positively correlated with total reads ($r = 0.63$, $p = 0.0008$) within each sample. Samples ≥ 1 mL tended to have greater microbial diversity than samples with <1 mL starting volume ($p = 0.14$). Overall, results indicate that urine samples of <1 mL are unlikely to be representative of the urobiome within a dog, while samples ≥ 1 mL show consistent community composition.</p>
Keywords for abstract:	Canine urinary microbiome Microbiota Urobiome Urinary tract Urine volume

MCB - 4

Title of abstract:	HTLV-1 HBZ PROTEIN, BUT NOT HBZ RNA SECONDARY STRUCTURE, IS CRITICAL FOR VIRAL PERSISTENCE AND DISEASE DEVELOPMENT
Authors:	<u>V. Maksimova</u> , T. Wilkie, S. Smith, C. Phelps, C. Melvin, L. Yu, S. Niewiesk, P.L. Green, and A.R. Panfil
Abstract:	<p>Human T-cell leukemia virus type 1 (HTLV-1) is the etiologic cause of adult T-cell leukemia/lymphoma (ATL) and encodes a viral oncoprotein on the antisense strand of the proviral genome (Hbz) that is consistently expressed in asymptomatic carriers and ATL patients, suggesting its importance in the development and maintenance of HTLV-1 leukemic cells. Our previous work found Hbz protein is dispensable for virus-mediated T-cell immortalization but enhances viral persistence. We and others have also shown that hbz mRNA promotes T-cell proliferation. In our current studies, we evaluated the role of hbz mRNA on HTLV-1-mediated immortalization in vitro as well as in vivo persistence and disease development. We generated mutant proviral clones to examine the individual contributions of hbz mRNA, hbz mRNA secondary structure (stem-loop), and Hbz protein. Wild-type (WT) and all mutant viruses produced virions and immortalized T-cells in vitro. Viral persistence and disease development were also evaluated in vivo by infection of a rabbit model and humanized immune system (HIS) mice, respectively. Proviral load and sense and antisense viral gene expression were significantly lower in rabbits infected with mutant viruses lacking Hbz protein compared to WT or virus with an altered hbz mRNA stem-loop (M3 mutant). HIS mice infected with Hbz protein-deficient viruses showed significantly increased survival times compared to animals infected with WT or M3 mutant virus. Altered hbz mRNA secondary structure, or loss of hbz mRNA or protein, has no significant effect on T-cell immortalization induced by HTLV-1 in vitro; however, the Hbz protein plays a critical role in establishing viral persistence and leukemogenesis in vivo.</p>
Keywords for abstract:	HTLV Hbz Immortalization Persistence Leukemogenesis

MCB - 5

Title of abstract:	THE LONG-TERM <i>IN VITRO</i> BACTERIAL VIABILITY OF LYOPHILIZED AND FROZEN CANINE AND FELINE FECAL MICROBIAL TRANSPLANTATION PRODUCTS
Authors:	Nina Randolph ^{1,2} , Dubra Diaz-Campos ¹ , Joany van Balen ¹ , Nora Jean Nealon ^{1,2} , John Rowe ^{1,2} , Jenessa A. Winston ^{1,2} ¹ Department of Veterinary Clinical Sciences. The Ohio State University, College of Veterinary Medicine. Columbus, Ohio. 43210. ² Comparative Hepatobiliary and Intestinal Research Program, The Ohio State University, College of Veterinary Medicine. Columbus, Ohio. 43210.
Abstract:	Fecal microbiota transplantation (FMT) is the transfer of feces from a healthy donor into a diseased recipient to confer a health benefit. The precise mechanism in which FMT confers a health benefit is unknown but is linked to the viability and engraftment of microbes. Our study aims to quantitate the colony forming units (CFUs) of microbes within canine and feline FMT products using culture-based techniques in aerobic and anaerobic environments. Three screened canine and feline fecal donors each provided three separate fresh fecal samples for processing. Fecal processing techniques include unprocessed (raw) 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 (immediately following processing), 1 month, 3, 6, and 12 months. At the 3-month timepoint, canine and feline lyophilized products preserved with M:D yielded significantly greater total CFUs compared with other lyophilized products (dogs, $p < .0001$; cats, $p < .0005$). For canine and feline samples frozen at -20C, feces preserved with glycerol and M:D yielded significantly more CFUs than other products (dogs, $p < .0057$; cats, $p < .0022$), with no significant difference between glycerol and M:D (dogs, $p = .6115$; cats, $p = 0.999$). In canine and feline samples stored at -80C, 10% glycerol yielded the most CFUs at the 3-month timepoint, however this was not significantly different from samples stored with saline or 25% M:D (dogs, $p > 0.1547$; cats, $p > 0.999$). One limitation of this study is the unculturability of most fecal microbes. Additionally, the clinical relevance of viability and the CFU/gram "dose" required to confer a benefit for the recipient is unknown. Further research is needed to determine whether increased CFUs translates to microbe engraftment and thus additional clinical benefit.
Keywords for abstract:	Fecal microbiota transplant Canine microbiome Feline microbiome Gut bacterial viability

MCB - 6

Title of abstract:	REGULATION OF HTLV-1 TRANSCRIPTION BY THE CELLULAR FACTOR YBX1
Authors:	<u>Susan M. Smith</u> , Jaideep Seth, Amanda K. Midkiff, Patrick L. Green, and Amanda R. Panfil. Dept. of Veterinary Biosciences.
Abstract:	<p>Human T-cell leukemia virus type 1 (HTLV-1) is a retrovirus and the etiologic agent of the highly aggressive adult T-cell leukemia/lymphoma (ATL) malignancy. Studies have shown two viral genes, <i>Tax</i> and <i>Hbz</i>, are linked to oncogenic transformation and are critical for the pathogenic process. <i>Tax</i> is the major driver of viral transcription and transformation, while <i>Hbz</i> supports proliferation of infected cells in both its protein and mRNA forms. <i>Hbz</i> is often the only viral gene consistently expressed in ATL patients. Consequently, regulation of HTLV-1 gene expression is a central feature in the viral lifecycle and directly contributes to its pathogenic potential. Our lab recently identified that <i>Hbz</i> interacts with the cellular protein YBX1 via mass spectrometry. YBX1 is a transcription factor involved in growth-associated gene expression. We hypothesize that the <i>Hbz</i>/YBX1 interaction plays a key role in viral gene expression and HTLV-1 pathobiology. Using reporter gene assays, we found YBX1 activates transcription from the viral promoter or LTR (long terminal repeat). Co-transfection of <i>Tax</i> and YBX1 enhances LTR transcriptional activation, while co-transfection of <i>Hbz</i> and YBX1 inhibits transcriptional activation. Previously, <i>Hbz</i> has been shown to repress <i>Tax</i>-mediated transcriptional activation, and we additionally found shRNA-mediated knockdown of YBX1 decreases <i>Tax</i> transcriptional activation of the LTR and decreases <i>Hbz</i> inhibition of <i>Tax</i>. Chromatin immunoprecipitation assays revealed that YBX1 associates with the viral LTR in HTLV-1-transformed T-cell lines. Immunoprecipitation experiments confirmed the YBX1/<i>Hbz</i> interaction in HTLV-1-transformed and ATL-derived T-cell lines. We also found that YBX1 is able to interact with <i>Tax</i> in HTLV-1-transformed T-cell lines and in Jurkat cells (HTLV-1-negative T-cell). Our data suggests YBX1 facilitates <i>Tax</i> recruitment to the viral LTR and the <i>Hbz</i>/YBX1 interaction prevents YBX1 transcriptional activation. Current experiments are underway to define the regions of <i>Tax</i>/<i>Hbz</i> protein interaction in YBX1. This work will further define HTLV-1 transcriptional regulation.</p>
Keywords for abstract:	HTLV-1 Human T-cell leukemia virus type 1 <i>Hbz</i> <i>Tax</i> Ybx1 Transcriptional Regulation

MCB - 7

Title of abstract:	ANALYSIS OF A NEW TYPE IV SECRETION SYSTEM EFFECTOR OF ANAPLASMA PHAGOCYTOPHILUM
Authors:	<u>L. Wang</u> , M. Lin, L. Hou, and Y. Rikihisa. Depts. Of Veterinary Biosciences
Abstract:	<p>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, <i>Anaplasma phagocytophilum</i> (<i>Aph</i>), is an obligatory intracellular bacterium that proliferates in the membrane bound compartment “inclusions” in the cytoplasm of neutrophils. Mechanisms by which <i>Aph</i> infects, survives, and proliferates in these host defensive cells remain mostly unknown. <i>Aph</i> has Type IV secretion system (T4SS) that can secrete effector molecules into human cells. We predicted the APH0874 protein is a new <i>Aph</i> T4SS effector using bacterial two-hybrid system analysis. To validate APH0874 as a bona fide T4SS effector, cellular localization of native APH0874 were examined by immunofluorescence labelling. In addition, <i>Aph</i> mutant expressing FLAG-tagged APH0874 with/without its C-terminal secretion signal were created by Himar1 transposon mutagenesis. Results showed that both native APH0874 and FLAG-APH0874 are secreted and localized to <i>Aph</i> inclusions, while the fragment without secretion signal localized within <i>Aph</i> inclusions. To determine roles of APH0874 in <i>Aph</i> infection, APH0874 was knocked down using anti-sense peptide nucleic acid (PNA) of APH0874. Results showed that APH0874 PNA knockdown significantly reduced <i>Aph</i> 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 <i>Aph</i> inclusion membranes in infected cells. Pulldown assay for proteomics analysis and yeast two-hybrid screening were used to identify the host target proteins of APH0874. Results showed that APH0874 interacts with Golgi-associated proteins SCFD1 and TANGO1. These results demonstrated APH0874 is a T4SS effector that plays an important role in <i>Aph</i> infection of human cells. The study also suggests APH0874 employs SCFD1 and/or TANGO1 to hijack Golgi-associated cellular functions to facilitate biogenesis of <i>Aph</i> inclusions. The findings will help uncovering molecular targets for HGA therapies alternative or adjunctive to doxycycline.</p>
Keywords for abstract:	<p><i>Anaplasma phagocytophilum</i> Human granulocytic anaplasmosis Type IV Secretion System effector Obligatory Intracellular bacteria <i>Anaplasma</i> inclusions Golgi apparatus</p>

MCB - 8

Title of abstract:	SRPK1 AND ANGEL2 INTERACT WITH THE HTLV-1 HBZ MRNA AND INFLUENCE CELLULAR PROLIFERATION
Authors:	<u>T. Wilkie</u> , S. Bonifati, J. Seth, PL. Green, AR. Panfil
Abstract:	<p>Adult T-cell leukemia/lymphoma (ATL) is a T-cell lymphoproliferative neoplasm caused by the oncogenic retrovirus human T-cell leukemia virus type 1 (HTLV-1). ATL develops in ~5% of HTLV-1-infected patients after a long clinical latency period and patients have poor prognosis. Our current understanding of the molecular events driving HTLV-1 disease development are still unclear. Among HTLV-1 encoded genes, Hbz is critical for ATL leukemogenesis. Hbz is encoded from the antisense strand of the integrated viral genome. Our presented data, as well as the work of others, show 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 <i>hbz</i> mRNA is expressed in all ATL tumor cells. We hypothesize cellular protein interaction with <i>hbz</i> mRNA secondary structure translates to cell signaling pathways important for viral persistence and cellular proliferation. Our new proteomics data identified SRPK1 and Angel2 as distinct cellular proteins that bind <i>hbz</i> RNA. We further validated interaction with <i>hbz</i> RNA using CLIP assays. SRPK1 regulates mRNA splicing and Angel2 was recently identified as a cyclic phosphatase. SRPK1 and Angel2 are also involved in cell cycle regulation via PHLIP and <i>p21</i> mRNA, respectively. Using <i>in vitro</i> proliferation assays, we found shRNA-mediated knockdown of SRPK1 or Angel2 in ATL cell lines decreased cellular proliferation. Importantly, in the immortalized human T-cell line Kit-225, we found that <i>hbz</i> mRNA alone can enhance cellular proliferation and that this proliferative effect is diminished by chemical inhibition or knockdown of SRPK1. <i>Hbz</i> mRNA proliferative abilities are dependent on its nuclear localization. Loss of SRPK1 expression resulted in <i>hbz</i> mRNA mislocalization, thus decreasing cellular proliferation. Further delineation of the <i>hbz</i> mRNA interaction with cellular SRPK1 and Angel2 will contribute to the understanding of ATL development.</p>
Keywords for abstract:	HTLV-1 Adult T cell leukemia (ATL) HBZ SRPK1 Angel2 proliferation

MCB - 9

Title of abstract:	RANDOM MUTAGENESIS OF <i>EHRlichia japonica</i> HF FOR IDENTIFICATION OF <i>IN VIVO</i> VIRULENCE FACTORS
Authors:	<u>T. Zhang</u> , R. Chien, K. Budachetri, M. Lin, and Y. Rikihisa. Dept of Veterinary Biosciences
Abstract:	<p><i>Ehrlichia</i> are tick-borne obligatory intracellular bacteria that cause emerging febrile and sometimes fatal diseases called Ehrlichiosis. Technical difficulties to employ forward genetics methods and lack of well-established small animal disease models of tick transmission have hampered Ehrlichiosis investigation. <i>Ehrlichia japonica</i> HF (<i>Eja</i> HF) isolated in Japan from <i>Ixodes ovatus</i> ticks, causes acute fatal infection in laboratory mice. Our lab has succeeded in stably culturing <i>Eja</i> HF in DH82 canine macrophage cell line, and obtained its whole genome sequence and annotation, making it possible to analyze <i>Ehrlichia in vivo</i> virulence factors in mouse disease model. Moving forward with forward genetics, we have created a Himar1 transposon random mutagenesis library of <i>Eja</i> HF. In addition to previous 158 published mutants, 249 new and distinct mutants were obtained. Total 183 transposon insertions were within 129 distinct protein-coding genes, potentially disrupting functions of these genes. Selected mutants were cloned and tested for mouse virulence and/or tick transmission. Our study found that a mutant that has the Himar1 insertion within the gene encoding 120-kDa Tandem Repeat Protein (TRP120) has negligible bacteremia despite of infection all other tissues examined, consequently reduced ability to transmit to blood-sucking ticks. Several other <i>Eja</i> mutants that lost potential <i>in vivo</i> virulence factors such as TRP75 and collagenase due to transposon insertion were investigated. We expect ehrlichial genes critical for virulence and tick transmission will be identified by further analysis of the current <i>Eja</i> HF mutant library, which will help develop effective therapeutic and preventative measures for ehrlichiosis.</p>
Keywords for abstract:	<i>Ehrlichia japonica</i> HF; Himar1 random transposon mutagenesis; obligatory intracellular bacteria; tick-borne disease; mouse virulence.

MCB - 10

Title of abstract:	SINGLE-RNA-LEVEL OF FULL-LENGTH HIV RNA ANALYSIS REVEALS FUNCTIONAL REDUNDANCY OF m⁶As
Authors:	A.Baek, G.Lee, S.Golconda, A.Rayhan, A.Manganaris, S.Chen, N.Tirumuru and S.Kim
Abstract:	<p>HIV-1 has evolved to become extremely efficient, exploiting every feature of its relatively small RNA genome (9.2 Kb) to encode all information necessary for its replication. Chemical modifications add another layer of functional regulation of viral RNAs, but the evolutionary benefits of these modifications remain unclear and often controversial. Most studies to date provide population-average values of modifications, neglecting the site-specificity and intra-RNA heterogeneity. Here, we present technical innovations enabling a full-length, single-molecule-level analysis of HIV-1 RNAs using nanopore direct RNA sequencing (DRS) and demonstrate a novel evolutionary strategy of HIV-1 minimizing the risks of losing a crucial modification by random mutagenesis. Our full-length DRS revealed an unexpected simplicity in the modification landscape, showing predominant site-specific modifications of three N6-methyladenosines (m⁶As) near the 3' end, important in maintaining regular splicing and translation. We found HIV-1 generates diverse RNA subspecies with distinct ensembles of the three m⁶As and fine-tunes them in viral mRNA and virion RNAs. The functional redundancy and intra-RNA diversity of these m⁶As helped viruses minimize the impact of mutagenesis that removes a major portion of m⁶As. HIV-1 invest in the stability and resilience of viral replication at the expense of tolerating the redundancy of these m⁶As. The novel insights into viral epitranscriptome and technological innovations presented here in will help guide future interrogations of RNAs of interest.</p>
Keywords for abstract:	HIV-1 RNA m6A modification Viral epitranscriptome Direct RNA sequencing

STRUCTURE/FUNCTION

SF - 1

Title of abstract:	APPLICATION OF EDNA METABARCODING TO ASSESS FISH BIODIVERSITY AT A LEGACY PAH-CONTAMINATED SITE
Authors:	<u>B. Graham</u> , J. Feller, R. Lanno
Abstract:	<p>Environmental DNA (eDNA) metabarcoding has emerged as a quick and cost-effective tool for monitoring biodiversity in aquatic systems. The high throughput nature of this technology and improved sample efficiency overall makes eDNA an ideal alternative to traditional, more labor-intensive environmental survey methods. eDNA metabarcoding can be used to simultaneously evaluate the effects of environmental stressors on the biodiversity of a wide variety of taxa and thus obtain proxy indicators of environmental and wildlife health. Polycyclic aromatic hydrocarbons (PAHs), a byproduct of fuel combustion and industrial manufacturing, are persistent carcinogens frequently found at contaminated sites. The objective of this study was to use eDNA metabarcoding to evaluate fish biodiversity in the Little Scioto River (Marion, OH), a creosote-contaminated site dating back to the 1800s. Extensive chemical and biological monitoring, in addition to several remediation efforts by the US EPA, have taken place at this site over the past several decades. Fish biodiversity was assessed at an upstream reference site and compared with biodiversity at the PAH remediation site and a downstream site to assess the impact of PAH contamination and the efficacy of remediation efforts (2002-2006) 15 years later. Water samples were taken in triplicate at three sites along the Little Scioto River and a secondary reference site along the Scioto River. Site samples were pooled and filtered through cellulose nitrate filters. eDNA was extracted from these filters and samples were sequenced using a 12S MiFish metabarcoding approach. The results of our study reflect higher biodiversity estimates than those detected previously at remediated sites, which may indicate improved aquatic health within the stream or reveal limitations of traditional sampling methods within stream segments with less-than-ideal topography. Significant overlap in beta diversity estimates between eDNA metabarcoding results and previous traditional biological surveys of upstream reference sites demonstrates the robusticity of our approach.</p>
Keywords for abstract:	environmental DNA metabarcoding polycyclic aromatic hydrocarbons beta diversity

SF - 2

Title of abstract:	EMBRYO SIZE CLASSIFICATION AT EGG COLLECTION AND ITS RELATIONSHIP TO HATCH SUCCESS AND UMBILICAL SCARRING IN BOTH FARMED AND WILD FLORIDA ALLIGATORS (<i>ALLIGATOR MISSISSIPPIENSIS</i>)
Authors:	N. Lordj, M. Flint, and J. Flint. Department of Veterinary Preventive Medicine
Abstract:	<p>The alligator industry is a multi-million dollar industry in Florida with the main source of revenue coming from harvesting hides. The presence of umbilical scars decreases the value of hides. Umbilical scarring or defects are caused by incomplete absorption of the yolk sac and/or incomplete healing of the navel. The exact mechanism of scarring contributed during incubation is not well understood. Prior experiments have examined how substrate type, oxygen supplementation, and temperature and humidity regimes may contribute to umbilical scarring and hatch success. Anecdotally, younger embryos from previous years appeared to have a higher chance of developing umbilical scar abnormalities. Our objectives include: 1) examining hatch success, hatchling size, and prevalence of American alligator (<i>Alligator mississippiensis</i>) umbilical scarring abnormalities in comparison to the embryo size classification at time of egg collection, and 2) developing a non-lethal staging scheme to determine stage of embryo development during field collection of eggs using commonly identified embryonic features. We hypothesize that a lower hatch success, in addition to abnormal umbilical scarring, would be more common in embryos that are at an earlier stage of development at time of collection. In the current study, 369 eggs from farmed and wild Florida alligators were incubated at constant temperature and humidity regimes. Each egg was candled at least once to estimate age, stage, and record any key anatomic features. Post-hatch data measurements included hatch success, umbilical score, length, and weight. The overall hatch success was 60.9%. The hatch success for farmed and wild eggs was 40.8% and 81.9% respectively. Hatch success for embryos based on their age category (undetermined, small, small-med, medium, med-large, and large) at time of collection appears to have a significant positive trend. Comprehensive data analysis, including the umbilical scoring in relation to embryo age, and development of the non-lethal field guide are underway.</p>
Keywords for abstract:	American Alligator Alligator Alligator farming Incubation Umbilical scarring Umbilical defect Hatch success

SF - 3

Title of abstract:	FASCICLE-INTERFASCICULAR MATRIX ADAPTATION TO ATHLETIC TRAINING IN THOROUGHBRED RACEHORSE SUPERFICIAL DIGITAL FLEXOR TENDON (SDFT)
Authors:	C. Moreno ¹ , S. Long ¹ , M. Samol ² , T. Garcia ³ , S. Stover ³ , S. Durgam ¹ ¹ Department of Veterinary Clinical Sciences, The Ohio State University, ² California Animal Health and Food Safety Laboratory System-San Bernardino, University of California-Davis, ³ JD Wheat Veterinary Orthopedic Laboratory, University of California-Davis
Abstract:	<p>The pathophysiological mechanisms responsible for superficial digital flexor tendon (SDFT) injuries in Thoroughbred (THB) racehorses are poorly understood. This research aims to determine if Thoroughbred SDFT fascicles and interfascicular matrix (IFM) undergo structure-function adaptations reflective of the racehorse's age and athletic training. Mid-metacarpal SDFT (n=50) from 2-, 3-, 4-yo Thoroughbred racehorses necropsied through CAHFS preserved within 48 hours of death/euthanasia were evaluated.</p> <p>Longitudinal and transverse histological sections were imaged via Picro-Sirius Red (fascicle CSA) and confocal microscopy (elastin immunofluorescence and SHG focused on collagen type I) for quantifying fascicle cross-sectional area (CSA) and IFM thickness. Biochemical total tendon elastin (FASTIN™), collagen (Sircol™) and proteoglycan (DMMB assay) contents were quantified. Load-to-failure whole tendon tensile biomechanical testing was conducted. The effect of THB racehorse age on histologic and biochemical variables was assessed using a mixed-model ANOVA and post-hoc pairwise comparisons. Interactions between SDFT histomorphometry and biochemical concentrations with biomechanical indices and exercise variables were evaluated via univariate linear regression. Significance was set at $p \leq 0.05$.</p> <p>Fascicle CSA ($p=0.005$), total tendon elastin ($p=0.019$), collagen ($p=0.002$), and proteoglycan content ($p=0.03$) decrease, while IFM thickness ($p=0.005$) increases with age, most significantly between 2- and 3-year-old racehorses. Yield stress ($r=0.36$) and pre-yield modulus ($r=0.46$), SDFT tensile strength indices, tended ($p \leq 0.05$) to increase with races per year. Yield torque, recovered stress, and recovered torque, SDFT torsional and recoil parameters, tended ($p \leq 0.05$) to be lower in younger and higher in older horses. The decrease in SDFT core fascicle CSA and total collagen provides a potential mechanistic explanation for core lesion predisposition in THB racehorses. Collective results of SDFT tensile-recoil properties suggest adaptive modeling of tendon fascicles and IFM in response to athletic training of racehorses. This research provides a foundation for delineating SDFT injury mechanisms, as well as identifying optimal athletic training and post-injury rehabilitation regimens in THB racehorses.</p>
Keywords for abstract:	Equine SDFT Fascicle-IFM Collagen Elastin Adaptation

SF - 4

Title of abstract:	ATHLETIC TRAINING INTENSITY IMPACTS THOROUGHBRED RACEHORSE SUPERFICIAL DIGITAL FLEXOR TENDON INTERFASCICULAR MATRIX ELASTIN AREA FRACTION AND TENSILE MECHANICAL PROPERTIES
Authors:	S. Seabeck ¹ , C. Moreno ¹ , S. Long ¹ , H. Rice ¹ , M. Samol ² , T. Garcia ³ , S. Stover ³ , S. Durgam ¹ ¹ Department of Veterinary Clinical Sciences, The Ohio State University, ² California Animal Health and Food Safety (CAHFS) Laboratory, San Bernardino, University of California-Davis, ³ JD Wheat Veterinary Orthopedic Laboratory, University of California-Davis
Abstract:	<p>Equine superficial digital flexor tendon (SDFT) possesses a specialized hierarchical structure consisting of type I collagen fibers bundled as fascicles and are interspersed by elastin- and proteoglycan-rich interfascicular matrix (IFM). The IFM facilitates overall extensibility and energy-storing function of SDFT via fascicle sliding ultimately supporting the maximal strains sustained during athletic training and racing. This research hypothesizes that IFM elastin content and tensile mechanical properties exhibit structure-function adaptations reflective of the racehorse's age and athletic training intensity.</p> <p>Mid-metacarpal SDFT (n=50) from 2-, 3-, 4-yo Thoroughbred racehorses necropsied through CAHFS preserved within 48 hours of death/euthanasia were evaluated. Confocal microscopy of longitudinal histological sections for elastin immunofluorescence and quantitative IFM %elastin area fraction (ImageJ) was performed. Replicate (n=3/horse) fascicle and IFM subunits were dissected (stereomicroscope) for load-to-failure tensile biomechanical analyses. The effect of THB racehorse age on IFM %elastin area fraction was assessed using a mixed-model ANOVA. Interactions between IFM elastin area fraction with whole tendon, fascicle and IFM biomechanical indices and athletic training variables were evaluated via univariate linear regression ($p \leq 0.05$).</p> <p>SDFT IFM elastin area fraction of 2-, 3-, 4-yo Thoroughbred racehorses were quantified as $15.4 \pm 1.8\%$, $12.3 \pm 2.1\%$ and $11.6 \pm 2.3\%$, respectively. These results corroborate with total tendon biochemical elastin content decrease ($p=0.019$) with THB racehorse age. At the whole tendon level, yield stress ($r=0.36$) and pre-yield modulus ($r=0.46$), SDFT tensile strength indices, tended ($p \leq 0.05$) to increase with races per year. Fascicle and IFM biomechanical analyses are currently underway. Results suggests that specific changes in elastin content occur with age and, paradoxically, biomechanical parameters improved even when elastin decreased. This research provides a foundation for delineating mechanisms linked to SDFT injury, a common cause of racehorse wastage and economic loss in the industry, as well as for identifying optimal athletic training and post-injury rehabilitation regimens in THB racehorses.</p>
Keywords for abstract:	Equine SDFT Fascicle-IFM Collagen Elastin Adaptation

SF - 5

Title of abstract:	COMPUTED TOMOGRAPHIC ANATOMY AND TOPOGRAPHY OF THE LOWER RESPIRATORY SYSTEM OF THE BLANDING'S TURTLE (EMYDOIDEA BLANDINGII).
Authors:	<u>J. Wichtel</u> , E. Hostnik. Department of Veterinary Clinical Sciences.
Abstract:	<p>Despite conservation efforts, semi-aquatic turtles experience population instability due to anthropocentric causes and often respiratory disease. Chelonians have unique airway anatomy dissimilar to mammals such that normal anatomy can easily be mistaken for pathology. The goal of this study was to provide objective computed tomographic anatomy parameters in a large population of wild Blanding's turtles (BT- <i>Emydoidea blandingii</i>). In this prospective analytical cross-sectional study, ninety-five wild BT were opportunistically collected and underwent full-body helical CT scans. Comprehensive airway measurements were obtained and morphometric ratios were reviewed to assess for allometric growth patterns. Tomographically, the lungs were finely reticulated and multicameral. The lungs decreased in size from cranial to caudal, thus occupying less overall coelomic height, caudally. The lungs of smaller turtles occupied a significantly smaller proportion of the coelom in the dorsoventral plane compared to larger turtles. The caudal central bronchus was dilated relative to the rest of the intrapulmonary bronchi and occupied the majority of the caudal lung. There was a bimodal distribution for carapace and plastron size; likely a reflection of age. The plastron length to coelomic height had the greatest correlation to allometric data ($R^2 = 0.96$); no significant difference was found between groups. Airway measurements between sides were symmetric. This study supports the use of CT in the antemortem assessment of chelonian respiratory anatomy where physical exam is limited and unique airway anatomy makes interpretation challenging.</p>
Keywords for abstract:	Emydoidea blandingii Chelonian Sem-aquatic turtle Air-way Computed tomography