THE OHIO STATE UNIVERSITY

COLLEGE OF VETERINARY MEDICINE

# COLLEGE OF
# VETERINARY MEDICINE
# RESEARCH DAY

## 2021

# BOOK OF
# ABSTRACTS

THE OHIO STATE UNIVERSITY
COLLEGE OF VETERINARY MEDICINE

Office of Research
and Graduate Studies

Due to the COVID-19 pandemic, the College of Veterinary Medicine Research Day, the keynote lecture, and PowerPoint presentations, are taking place virtual in 2021. Abstracts and presentations can be found on the College's Research Day website, along with this book of abstracts.

The following pages contain 90 abstracts submitted by 57 graduate students, resident/graduate students and interns, 30 professional DVM students, 1 undergraduate student, 1 staff member and 1 faculty member in the categories of:

- Immunology and Infectious Diseases
- Molecular and Cellular Biology
- Structure/Function
- Epidemiology and Applied Research
- Clinical Research
- Educational

We hope you enjoy perusing through the book and learning more about the exciting research performed in our College. We look forward to hosting an in-person Research Day again in April of 2022.

Patrick Green

Patrick L. Green, PhD
Professor and Associate Dean for Research and Graduate Studies
Robert H. Rainier Chair in Industrial Veterinary Medicine and Research
Director, Center for Retrovirus Research
Associate Director for Basic Sciences, Comprehensive Cancer Center

THE OHIO STATE UNIVERSITY
COLLEGE OF VETERINARY MEDICINE

# Research Keynote Address

Thursday
**April 8, 2021**
**9:00 – 10:00 am**

Join Zoom Meeting
https://osu.zoom.us/j/96029621298?pwd=clpYTlZ3ckl1ejNwZlhFSzZKREVWQT09
Meeting ID: 960 2962 1298
Password: 623029

## "Flavivirus infections of Human Stem Cell-Derived Cerebral Organoids"

Presented by:

***Dr. Lee Gehrke***

*Hermann L.F. von Helmholtz Professor of Health Sciences and Technology, Massachusetts Institute of Technology, Boston, MA*
*Professor of Microbiology, Harvard Medical School, Cambridge, MA*

*Dr. Gehrke's research interests center on molecular aspects of host-pathogen interactions and on the pathogenesis of RNA viruses. Current experimental work focuses on understanding how viruses that are closely related in genetic sequence cause highly variable disease outcomes.*

# POWERPOINT JUDGES

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

Estelle Cormet-Boyaka

Sushmitha Durgam

Jiwoong Her

Sanggu Kim

Wendy Lorch

Georgina Newbold

Mike Oglesbee

Anastasia Vlasova

Teresa Burns

Rebecca Garabed

Scott Kenny

Krista La Perle

Margaret Mudge

Stefan Niewiesk

Gustavo Schuenemann

Jenessa Winston

A very special **Thank You** to Jeff Workman, Department of Veterinary Preventive Medicine, for his assistance in creating and uploading the webpage for the Abstracts and PowerPoints!

2021 Faculty Chair:
Dr. Jianrong Li
*Professor, Veterinary Biosciences*

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

# INDEX OF ABSTRACTS

| ABSTRACT # | PRESENTER | STATUS | ADVISOR(S) |
|---|---|---|---|
| **CLINICAL RESEARCH** | | | |
| CR – 1 | ALLEN, BRITTANY | VME | EVANS, SAMANTHA |
| CR – 2 | APLASCA, ANDREA | RESIDENT | FLINT, MARK |
| CR – 3 | BELACIC, ZARAH | UNDERGRADUATE | DURGAM, SUSHMITHA |
| CR - 4 | BENDLIN, ASHLEY | RESIDENT | METZLER, ANNE |
| CR – 5 | BOWLBY, CHARLES | GRAD STUDENT | DURGAM, SUSHMITHA |
| CR – 6 | CASHMAN, CONNOR | VME | HOWARD, JAMES |
| CR – 7 | CHEN, CAROLYN | INTERN | SELMIC, LAURA |
| CR – 8 | COOK, MATTHEW | RESIDENT | KISSEBERTH, WILLIAM |
| CR – 9 | DOYLE, CRYSTAL | RESIDENT | RICCO-PEREIRA, CAROLINA |
| CR – 10 | FARBER, BRIANNA | VME | HOSTNIK, ERIC |
| CR – 11 | HEINZ, JESSICA | RESIDENT | FLINT, MARK |
| CR – 12 | JACHEC, EMILY | VME | WINSTON, JENESSA |
| CR – 13 | JOHNSON, LAURA | RESIDENT | HOSTNIK, ERIC |
| CR – 14 | JOHNSON, ALEXIS | VME | KISSEBERTH, WILLIAM; LAPSLEY, JANIS; SELMIC, LAURA |
| CR – 15 | KINSELLA, HANNAH | RESIDENT | HOSTNIK, LAURA |
| CR – 16 | LAGES, MAISA | VME | SELMIC, LAURA |
| CR – 17 | LOEWEN, KELLY | VME | DIAZ-CAMPOS, DUBRA |
| CR – 18 | MCBRIDE, REBECCA | RESIDENT | MOORE, SARAH |
| CR – 19 | MILLER, MATTHEW | RESIDENT | PARKER, VALERIE |
| CR – 20 | MORENO, ADAM | VME | BERRIAN, AMANDA |
| CR – 21 | MUIR, ANDREW | RESIDENT | DURGAM, SUSHMITHA; NIEHAUS, ANDREW |
| CR – 22 | O’BRIAN, MAGGIE | RESIDENT | AARNES, TURI |
| CR – 23 | OU, TINGWEI | RESIDENT | HOSTNIK, ERIC |
| CR – 24 | PECK, CHANERA | VME | KIEFFER, JUSTIN; MOELLER, STEVEN |
| CR – 25 | PENNINGTON, ANNA | VME | HOSTNIK, LAURA |
| CR – 26 | SEELEY, KATHRYN | RESIDENT | FLINT, MARK |
| CR – 27 | TEN CATE, SOSCHA | RESIDENT | COOPER, EDWARD |
| CR – 28 | TIMKO, KATHRYN | RESIDENT | BURNS, TERESA |
| CR – 29 | URION, REBECCA | RESIDENT | HOSTNIK, ERIC |
| CR – 30 | VIOLETTE, NATHANIEL | RESIDENT | NEWBOLD, GEORGINA |
| CR – 31 | WANG, MUNING | VME | QUIMBY, JESSICA |
| CR – 32 | WILLETTE, CRAIG | RESIDENT | AARNES, TURI |
| CR – 33 | CARAMAGNO, LAUREN | VME | SELMIC, LAURA |
| CR – 34 | ZANN, GEOFFREY | | JONES, STEPHEN |
| **EPIDEMIOLOGY AND APPLIED RESEARCH** | | | |
| EAR – 1 | ALMEIDA, BREANNA | VME | HABING, GREGORY |
| EAR – 2 | ARCHIBALD, WILEY | VME | PESAPANE, RISA |
| EAR – 3 | BALLASH, GREGORY | GRAD STUDENT | WITTUM, THOMAS |

| | | | |
|---|---|---|---|
| EAR – 4 | BLACK, NICHOLAS | GRAD STUDENT | ARRUDA, ANDREA; WITTUM, THOMAS |
| EAR – 5 | COLLINS, TOI | RESIDENT | BLASER, BRADLEY |
| EAR – 6 | FISCHER, BRITTANY | GRAD STUDENT | FLINT, MARK; WITTUM, THOMAS |
| EAR – 7 | GREENBERG, JI ANN | VME | BOWMAN, ANDREW |
| EAR – 8 | HENNING, JED | VME | O'QUIN, JEANETTE |
| EAR – 9 | HUTCHINSON, DERMOT | VME | FLINT, JAYLENE |
| EAR – 10 | LOCKE, SAMANTHA | GRAD STUDENT | HABING, GREGORY |
| EAR – 11 | MCBRIDE, DILLON | GRAD STUDENT | BOWMAN, ANDREW |
| EAR – 12 | MENICHETTI, BERNARDO | GRAD STUDENT | SCHUENEMANN, GUSTAVO |
| EAR – 13 | MORAN, MEGAN | VME | HABING, GREGORY |
| EAR – 14 | OVERCAST, MACON | VME | GARABED, REBECCA |
| EAR – 15 | PORILLO-GONZALEZ, RAFAEL | GRAD STUDENT | HABING, GREGORY |
| EAR – 16 | SALERNO, MATTHEW | VME | GARABED, REBECCA |
| EAR – 17 | VESPRANI, LAUREN | VME | PESAPANE, RISA |
| EAR – 18 | WALKER, HEATHER | VME | POMEROY, LAURA |
| EAR – 19 | YEE, HEATHER | VME | MARSH, ANTOINETTE |
| EAR – 20 | THEILE, CHERYL | VME | FLINT, MARK |
| EAR – 21 | BAUTISTA, JESSE | VME | DENNIS, PAM |
| **IMMUNOLOGY AND INFECTIOUS DISEASE** | | | |
| IMID – 1 | BAEK, ALICE | GRAD STUDENT | KIM, SANGGU |
| IMID – 2 | BRAKEL, KELSEY | GRAD STUDENT | NIEWIESK, STEFAN |
| IMID – 3 | CHIEN, RORY | GRAD STUDENT | RIKIHISA, YASUKO |
| IMID – 4 | EL MUSA, HASAN | VME | DAVIS, IAN |
| IMID – 5 | GUNASENA, MANUJA | GRAD STUDENT | LIYANAGE, NAMAL |
| IMID – 6 | HARDER, OLIVIA | STAFF | NIEWIESK, STEFAN |
| IMID – 7 | JOLDRICHSEN, MARIELLA | GRAD STUDENT | RIKIHISA, YASUKO |
| IMID – 8 | KIM, SHIHYOUNG | GRAD STUDENT | KIM, SANGGU |
| IMID – 9 | LEE, GABBY | GRAD STUDENT | KIM, SANGGU |
| IMID – 10 | MESTRES-VILLANUEVA, MARIELLA | GRAD STUDENT | RIKIHISA, YASUKO |
| IMID – 11 | SMITH, ANNA | GRAD STUDENT | SHARMA, AMIT |
| IMID – 12 | SMITH, SUSAN | GRAD STUDENT | PANFIL, AMANDA |
| IMID – 13 | SNELL, CHLOE | RESIDENT | RUDINSKY, ADAM |
| IMID – 14 | YADAV, KUSH | GRAD STUDENT | KENNY, SCOTT |
| IMID – 16 | EVANS, JACK | GRAD STUDENT | LIU, SHAN-LU |
| **MOLECULAR AND CELLULAR BIOLOGY** | | | |
| MCB – 1 | CANNON, TESSA | GRAD STUDENT | HALE, VANESSA; MCGRAW, SCOTT |
| MCB – 2 | GOLCONDA, SARAH | GRAD STUDENT | KIM, SANGGU |
| MCB – 3 | KOREC, DANIELA | RESIDENT | HUSBANDS, BRIAN |
| MCB – 4 | MAKSIMOVA, VICTORIA | GRAD STUDENT | PANFIL, AMANDA |
| MCB – 5 | MEYERSON, JEREMY | VME | DAVIES, ALEXANDER |
| MCB – 6 | MROFCHAK, RYAN | GRAD STUDENT | HALE, VANESSA |

| | | | |
|---|---|---|---|
| MCB – 7 | MURTHY, VAIBHAV | GRAD STUDENT | DAVIES, ALEXANDER |
| MCB – 8 | PINNELL, ERIN | RESIDENT | BURNS, TERESA |
| MCB – 9 | SHUSTERMAN, LAUREN | VME | MARSH, ANTOINETTE |
| MCB – 10 | SLOAN, SHELBY | GRAD STUDENT | BAIOCCHI, ROBERT |
| MCB – 11 | SOARES, KILMER | GRAD STUDENT | HALE, VANESSA |
| MCB – 12 | WALKER, MARY | RESIDENT | POWELL, HEATHER |
| MCB – 13 | WANG, LIDAN | GRAD STUDENT | RIKIHISA, YASUKO |
| MCB – 14 | ZHANG, QIAN | GRAD STUDENT | RIKIHISA, YASUKO |
| **STRUCTURE/FUNCTION** | | | |
| SF – 1 | KIEFER, CAITLIN | VME | HOSTNIK, ERIC |
| SF – 2 | LONG, MACKENZIE | GRAD STUDENT | BAIOCCHI, ROBERT |
| SF – 3 | MEIHLS, MATTHIEU | VME | HORVATH, STEPHEN |
| SF – 4 | PASCHALL, RENE | INTERN | QUIMBY, JESSICA |
| SF – 5 | WINANS, MADELINE | GRAD STUDENT | GEORGE, KELLY; FLINT, MARK |
| **EDUCATIONAL** | | | |
| EDU – 1 | YARDLEY, JONATHAN | FACULTY | |

# CLINICAL
# RESEARCH

# CR – 1

| | |
|---|---|
| Title of abstract: | **DIAGNOSTIC ACCURACY OF CYTOLOGY FOR THE DIAGNOSIS OF BACTERIAL SEPSIS IN FLUID SAMPLES FROM VETERINARY PATIENTS** |
| Authors | B. Allen, S.J.M. Evans. Department of Veterinary Biosciences |
| Abstract | Bacterial sepsis is a relatively common, life-threatening condition with a high case-fatality rate. The current primary diagnostic tools for septic effusions in animal patients are bacterial culture and fluid cytology. While culture is the gold standard, it can take up to several days for results to be made available to clinicians, which can negatively impact a septic patient's chance at survival. The aim of this study was to evaluate the diagnostic accuracy of cytology for detecting bacterial sepsis in body fluids. We retrospectively reviewed 10 years of medical records at the Ohio State University's Veterinary Medical Center for mammalian patients with both cytology and bacterial culture of fluid samples, including body cavity fluids (peritoneal and thoracic effusion), blood, joint fluid, and CSF. The overall sensitivity and specificity of cytology relative to the reference method of bacterial culture was recorded, as well as among the subcategories of fluid type and species. The overall sensitivity and specificity of cytology for the diagnosis of sepsis were 42.6% and 93.0% respectfully. Separate sensitivities and specificities were also calculated for each fluid type. Thoracic fluid cytology had a high sensitivity and a low specificity, which was the inverse of all the other fluid types analyzed. Overall, cytology is poorly sensitive but highly specific for the detection of bacterial sepsis in fluid samples. The results from this study will allow better comparison between diagnostic accuracy of cytology and emerging diagnostic tests for the detection of bacterial sepsis in mammalian patients. |
| Keywords for abstract: | Canine<br>Culture<br>Equine<br>Sensitivity<br>Specificity |

# CR - 2

| | |
|---|---|
| Title of abstract: | **PATHOLOGIC FINDINGS AND SKIN MICROBIOME STRUCTURE OF JUVENILE EASTERN HELLBENDERS (CRYPTOBRANCHUS ALLEGANIENSIS ALLEGANIENSIS) UNDER HUMAN CARE DURING A HIGH MORTALITY EVENT** |
| Authors | A.C. Aplasca[1], M.E. Martinez[2], C. Madden[1], K. Soares[1], V.L. Hale[1], R.E. Junge[3], and M. Flint[1].<br>Depts. Of [1]Veterinary Preventive Medicine, [2]Veterinary Biosciences, and the [3]Columbus Zoo and Aquarium |
| Abstract | Amphibian population declines have occurred across a diverse range of geographic regions, and of approximately 7900 described amphibian species, an estimated 40% are threatened. Various factors, including disease and habitat degradation, have been linked to population declines. The Eastern hellbender (*Cryptobranchus alleganiensis alleganiensis*) is classified as endangered in the state of Ohio. To increase Ohio populations, conservation programs collect eggs from the wild and thousands of hellbenders have been successfully captive-reared and reintroduced to wild sites. However, mortality rates in captive hellbenders are highly variable and causes of mortality are poorly understood. Over a five-month period (November 2019 through March 2020), a high mortality rate (14%, 50/353) was observed in a captive population of hellbenders. Gross necropsies of 44 individuals revealed 86% (38/44) had cutaneous lesions (e.g. thick mucus layers, ulcerations, or white cottony aggregates). Histopathologic examination revealed cutaneous erosion, ulceration, or necrosis in 93% (41/44) of individuals. Bacteria was seen in 77% (34/44) and fungal hyphae were seen in 68% (30/44) of individuals. Based on the presence of severe cutaneous disease in a large number of animals, we used 16S rRNA sequencing to assess the cutaneous bacterial microbiota of 116 live hellbenders from the same cohort group-housed in multiple tanks. We found variation in skin microbial diversity based on animal weight and tank location. This suggests that local conditions influence skin microbial communities in hellbenders and that animals of different body weights exhibit microbial differences that may influence susceptibility to cutaneous and systemic disease. Future research should investigate the influence of husbandry practices on the skin microbiome of hellbenders under human care and how skin microbiome is related to the presence of cutaneous and systemic disease. Ultimately, this research can be used to identify risk factors for disease development in order to prevent morbidity and mortality in Eastern hellbenders. |
| Keywords for abstract: | Amphibians<br>Eastern hellbender<br>Captive-rearing<br>Pathology<br>Microbiome<br>Head-start programs |

# CR - 3

| | |
|---|---|
| Title of abstract: | **METHYPREDNISOLONE DIFFERENTIALLY DOWN-REGULATES NAVICULAR FIBROCARTILAGE CELL BIOACTIVITY COMPARED TO DEEP DIGITAL FLEXOR TENDON CELLS UNDER IN-VITRO IL-1β INFLAMMATORY STIMULUS** |
| Authors | Z. Belacic, S. Sullivan, S. Durgam |
| Abstract | Navicular bone fibrocartilage (NBF) and opposing deep digital flexor tendon (DDFT) lesions/degeneration represent the most common sources of lameness in horses afflicted with navicular disease, a debilitating disorder characterized by chronic inflammation. Methylprednisolone acetate (MPA) is a popular corticosteroid administered into the navicular bursa for its potent anti-inflammatory properties, however the effect on resident cells that maintain tissue extracellular matrix (ECM) is underdetermined. Our objective was to examine MPA effects on NBF- and DDFT-cell bioactivities exposed to interleukin-1β (IL-1β) in-vitro and to test the hypothesis that MPA effects on NBF- and DDFT-cells are equivalent.<br>Non-adherent aggregate cultures established from third passage NBF- and DDFT-cells (n=4; healthy donor horses' undergoing euthanasia navicular tissues) over 72-96 hours were treated with MPA (0, 0.05 and 0.5mg/mL) and 10ng/mL IL-1β. Tendon and cartilage ECM mRNA, cell aggregate and culture medium glycosaminoglycan (GAG) contents, culture medium MMP-3 and -13 concentrations were quantified. NBF/DDFT-cell type and treatment effects were analyzed via two-way ANOVA with significance at $p \leq 0.05$.<br>Both IL-1β and MPA treatments significantly down-regulated tendon (COL1A1, COL3A1, COMP 5-20, 3-8, 3-20 folds, respectively; $p<0.001$) and cartilage (SOX9, ACAN, COL2A1, COLXA1 5-10, 40-60, 80-110, 2-5 folds, respectively; $p<0.001$) mRNA in NBF-cells compared to the untreated control. In contrast, both IL-1β alone and MPA combinations did not affect DDFT mRNA, with the exception of ACAN (3-20 fold down-regulation; $p=0.002$). Both IL-1β and MPA up-regulated MMP-3 and GAG secretion in DDFT-cells, and similar analyses in NBF-cells are ongoing. We demonstrate that IL-1β and MPA treatments differentially down-regulated ECM mRNA in NBF- compared to DDFT-cells and both tested MPA doses improved IL-1β-induced down-regulation. Accepting the in-vitro nature, these foundational results serve as a guideline for future in-vivo work to establish optimal intrasynovial corticosteroid regimens to modulate inflammation, as well as promote tissue healing in horses with navicular disease. |
| Keywords for abstract: | navicular disease- horse<br>deep digital flexor tendon<br>navicular fibrocartilage<br>methylprednisolone acetate (MPA)<br>tendon ECM<br>cartilage ECM<br>glycosaminoglycan (GAG) |

# CR - 4

| | |
|---|---|
| Title of abstract: | **DIAGNOSING INFECTIOUS ULCERATIVE KERATITIS: THE USE OF NEXT-GENERATION SEQUENCING IN VETERINARY OPHTHALMOLOGY PATIENTS** |
| Authors | A. Bendlin, A.J. Gemensky-Metzler, D. Diaz-Campos, G. Newbold, E.J. Miller, H.L. Chandler. Depts. Of Veterinary Clinical Sciences and College of Optometry |
| Abstract | Objectives: To compare Next-Generation Sequencing (NGS) to corneal cytology and culture for identification of causative organisms in veterinary patients presenting for infectious ulcerative keratitis (IUK).<br>Procedure: Corneal culture swabs for aerobic and fungal cultures and swabs for NGS were submitted for canine and equine normal controls (n=11 and n=4, respectively) and IUK patients (n=22 and n=8, respectively) for which microbrush cytology specimens confirmed the presence of infectious organisms. The sensitivity of NGS was compared to bacterial and fungal culture results. Concordance between NGS and culture results was determined.<br>Results: NGS was positive for bacterial and fungal organisms in 5 and 1 normal and 18 and 1 IUK cases, respectively. Bacterial and fungal cultures were positive for 7 and 2 normal and 20 and 5 IUK cases, respectively. Sensitivity of NGS was 82.14% (95% confidence interval (CI), 63.11% to 93.94%) and specificity was 76.47% (95% CI, 50.10% to 93.19%). Concordance (complete and partial) between identified bacterial and fungal organisms was found in 79% and 100% of cases, respectively. NGS identified organisms in 3 culture-negative samples.<br>Conclusion: NGS may be useful in identification of causative agents in IUK cases with a sensitivity greater than the sensitivity previously reported for aerobic culture. Further testing is needed to determine the clinical significance of additional organisms isolated by NGS from infected cases, as well as organisms isolated from normal corneas. |
| Keywords for abstract: | infectious ulcerative keratitis<br>next-generation sequencing<br>sensitivity<br>bacterial culture<br>fungal culture |

# CR – 5

| | |
|---|---|
| Title of abstract: | **INTERLEUKIN-6 UP-REGULATES CHONDROGENIC PHENOTYPE OF EQUINE TENDON PROGENITOR CELLS AND IS MEDIATED BY TGFB1** |
| Authors | C. Bowlby, N. Altmann, H. Coughlin, Z. Belacic, S. Sullivan, S. Durgam, Department of Veterinary Clinical Sciences |
| Abstract | INTRODUCTION: Chronic inflammation and tendon tissue degeneration characterizes tendon healing. Delineating the impact of inflammatory cytokines on the phenotype of tendon cells (tenocytes and tendon progenitor cells; TPC) that maintain tendon structure is vital to improve tendon injury outcomes. This study evaluates the impact of interleukin-6 (IL-6) on equine superficial digital flexor tendon (SDFT)-derived TPC to test the hypothesis that - IL-6 upregulates the chondrogenic phenotype of TPC and is mediated by prochondrogenic, transforming growth factor β (TGFβ) signaling.<br>MATERIALS & METHODS: Passage 3 forelimb SDFT TPC (n=5) were exposed to 0, 1, 5 or 10ng/mL rEqIL-6 to assess TPC proliferation, migration, and tendon and chondrogenic marker mRNA, and TGFβ1 culture medium concentration (ELISA). TPC were also cultured with TGFβ type I receptor inhibitor (SB431542; 0 or 2 uM) in the presence of IL-6 and gene expression analyses were repeated. Data were analyzed with one-way ANOVA ($p \leq 0.05$).<br>RESULTS: IL-6 at 1, 5 and 10 ng/mL significantly reduced TPC proliferation and migration during monolayer culture. Both TPC tenogenic (SCX:15.1-fold, COL1A1:5.2-fold, COL3A1:5.3-fold) and chondrogenic (SOX9:4.8-fold, COL2A1:3.9-fold, ACAN:5.4-fold) mRNA were upregulated. IL-6 (10 ng/mL IL-6 only) significantly induced TPC TGFβ1 mRNA (7-fold) and TGFβ1 secretion in culture medium. SB431542 normalized IL-6-induced gene up-regulation. IL-6 also significantly upregulated MMP 1, 3, and 13 (~3-5-fold); however, SB431542 did not normalize MMP mRNA upregulation.<br>DISCUSSION/CONCLUSION: We establish that IL-6, an inflammatory and immunomodulatory cytokine, upregulated both tenogenic and chondrogenic gene expression, induces TGFβ1 mRNA, and were attenuated by TGFβ1 receptor inhibitor without impacting the basal TPC phenotype. TGFβ1, a critical growth factor maintaining tendon homeostasis, is also implicated in tendon fibrosis. Tendon degeneration during healing is a complex process, and dissecting the biological mechanisms linked to consequent tendon structural deterioration due to aberrant TPC phenotypes is critical for enhancing tendon healing. |
| Keywords for abstract: | Tendon Progenitor cell (TPC)<br>Interleukin-6 (IL-6)<br>Transforming Growth factor β 1 (TGFβ1)<br>Matrix Metalloproteinase (MMP) |

# CR – 6

| | |
|---|---|
| Title of abstract: | **COMPARISON BETWEEN ENERGY INTAKE AND ENERGY EXPENDITURE ESTIMATED BY THE FITBARK HEALTH MONITOR** |
| Authors | C. Cashman, J. Howard, DVM, MS, V. Parker, DVM, A. Rudinsky, DVM, MS, J. Winston, DVM, PhD. Department of Veterinary Clinical Sciences |
| Abstract | Animal activity monitors are becoming prevalent within the veterinary community and many pet owners are pushing for individualized medicine that has become the standard in human medicine. FitBark is a canine activity monitor with the ability to monitor activity, sleep, mobility, pain, stress, anxiety, and even skin itching. The purpose of this study is to test the efficacy and validity of the FitBark activity monitor as it relates to nutritional recommendations when used by veterinarians for treating and preventing certain conditions. Currently the study has 25 dogs enrolled and is on-going. The FitBark device is worn continuously for 4 weeks while the owner keeps an accurate daily diet log. This information will be used confirm the efficacy of the FitBark activity tracker so it can be confidently used in disease diagnosis, treatment and prevention, as well as help develop new weight-loss protocols for the ever-growing pet obesity crisis our society is experiencing. |
| Keywords for abstract: | FitBark<br>Activity monitor<br>Nutrition<br>Energy expenditure<br>Energy intake<br>Obesity |

# CR - 7

| | |
|---|---|
| Title of abstract: | **A MODIFIED APPROACH TO CLOSED ANAL SACCULECTOMY IN THE DOG FOR ANAL SAC NEOPLASIA TREATMENT: 16 CASES (2018-2020)** |
| Authors | C.L. Chen, J.M. Lapsley, L.E. Selmic. Dept of Veterinary Clinical Sciences |
| Abstract | **Objective:** To describe the surgical technique and report the short-term outcomes of dogs with anal sac neoplasia that underwent a modified closed anal sacculectomy surgery.<br>**Animals:** 16 client-owned dogs referred to the authors' institution for anal sac neoplasia between January 1st, 2018, and September 30th, 2020.<br>**Procedures:** A single-institution retrospective case series was performed. Medical records were reviewed, and data collected included preoperative, intraoperative, and postoperative data, such as any complications, disease recurrence, and death/euthanasia.<br>**Results:** Neoplastic diagnoses were apocrine gland adenocarcinoma (n=15) and collision tumor (n=1). None of the dogs had intraoperative complications, and one dog had a minor postoperative complication that resolved. One dog had confirmed local recurrence of disease 290 days after surgery, and another dog had suspected local recurrence of disease 203 days after surgery. The median duration of follow up was 286 days postoperatively (range 67-777).<br>**Conclusions and Clinical Relevance:** The modified closed anal sacculectomy is a well-tolerated procedure with minimal short-term complications. This study provides evidence to justify performing this procedure in larger numbers of dogs to evaluate the effect of procedural modifications on postoperative complication rates and time to local recurrence. |
| Keywords for abstract: | Anal sacculectomy<br>Neoplasia<br>Surgery |

# CR - 8

| | |
|---|---|
| Title of abstract: | **A RETROSPECTIVE ANALYSIS OF 13 DOGS WITH SURFACE OSTEOSARCOMA.** |
| Authors | M.R. Cook, J Lorbach, W.C. Kisseberth, S. Samuels, C. Silveira, B. Wustefeld-Janssenss, R. Wouda, S. Keepman, M. Oblak, and L.E. Selmic. Departments of Veterinary Clinical Sciences and Veterinary Biosciences. |
| Abstract | While the majority of canine osteosarcoma (OSA) arises from the medullary cavity, a rare subset arises from the surface of bone. In humans, surface OSA often has a more indolent disease course with significantly better outcomes. The two most reported surface OSAs in the dog are periosteal (arising from under the periosteum) and parosteal (arising from the surface of the bone). The aim of this retrospective case series was to evaluate the clinical course and potential prognostic factors of dogs with surface OSA. Medical records from 13 dogs with surface OSA were identified and reviewed from 5 academic institutions. The histopathology of all cases was evaluated by two veterinary anatomic pathologists. For the estimation of median progression free interval (PFI) and median survival time (ST), the Kaplan-Meier method was utilized. Log-rank analysis was used to compare PFI and ST between groups. Ten dogs were given a diagnosis of periosteal OSA and 3 dogs were given a diagnosis of parosteal OSA. Overall, 7/13 cases of surface OSA went on to develop metastatic disease with a median time to metastasis of 350 days (range 0-497 days). The median PFI and median OST for all dogs with surface OSA was 456.5 and 540.5 days, respectively. The 10 dogs diagnosed with periosteal OSA (PFI 416 days, OST 555 days) had similar outcomes to the three dogs diagnosed with parosteal OSA (PFI not reached, OST 526 days). Multiple prognostic factors (excisional surgery, systemic adjunctive therapy, elevated ALP at baseline, appendicular vs axial location) were evaluated and none were found to be prognostic with regards to PFI or OST. The outcomes reported here for dogs with surface OSA appear to be have prolonged PFI and OST, consistent with human studies of surface OSA. |
| Keywords for abstract: | Canine<br>Osteosarcoma<br>Periosteal osteosarcoma<br>Parosteal osteosarcoma |

# CR - 9

| | |
|---|---|
| Title of abstract: | **EVALUATION OF PERFUSION INDEX AS A NON-INVASIVE TOOL TO DETERMINE EPIDURAL ANESTHESIA EFFECTIVENESS IN DOGS.** |
| Authors | C. Doyle, C. Ricco Pereira, A. Wanstrath, P. Lerche, T. Aarnes, R. Bednarski and S. Were. Dept. of Veterinary Clinical Science (The OSU-VMC) and Dept. of Population Health Sciences (Virginia-Maryland CVM) |
| Abstract | Epidural anesthesia is a well described technique for pain management in human medicine as well as in veterinary medicine. It can reduce the amount of required inhalant anesthesia and increase the duration of post-operative analgesia. Opioids are commonly administered in combination with local anesthetics for epidural injection, as it has been shown to increase the duration of analgesia when compared to either medication administered alone.<br>Perfusion index (PI) is a non-invasive measure of peripheral perfusion that can be used to monitor vascular tone. In human medicine, the PI increases after the vasodilation that occurs following epidural injection of local anesthetics. Our objective in this study was to determine if PI was an accurate tool to determine effectiveness and onset of epidural anesthesia in adult dogs undergoing stifle surgery.<br>Twenty-one dogs were sedated with acepromazine and morphine and placed under general anesthesia. A probe was secured to the base of the tail to monitor PI and an arterial catheter was placed for invasive blood pressure monitoring. A lumbosacral epidural was performed in each dog while in sternal recumbency. Dogs were randomly assigned to receive morphine (control) or morphine and lidocaine (treatment). The PI was recorded at baseline and every 10 minutes for 30 minutes and before and after the surgical skin incision and before and after completion of the osteotomy.<br>Physiological parameters were recorded at the same time points.<br>There was no significant difference in PI between the control and treatment group at any time point following epidural injection prior to surgical stimulation. There was also no significant difference in PI between the two groups following skin incision or osteotomy. In conclusion, the PI did not provide an objective means for determining onset or effectiveness of epidural anesthesia in anesthetized dogs and additional studies are recommended to determine alternative methods. |
| Keywords for abstract: | Lidocaine<br>Dogs<br>Perfusion index<br>Epidural anesthesia<br>Morphine<br>Oximetry |

# CR - 10

| | |
|---|---|
| Title of abstract: | **OPTIC NERVE SHEATH SIZE IN NORMAL STANDARDBRED FOALS** |
| Authors | R. Urion, H. Kinsella, B. Farber, L.D. Hostnik, E.T. Hostnik. |
| Abstract | Neonatal encephalopathy causes a variety of neurologic signs in neonatal foals, on which presumptive diagnosis is based. As timely intervention reduces morbidity, an objective diagnostic measurement may aid in earlier recognition. Increased intracranial pressure is a presumed component of this syndrome but direct measurement is impractical and invasive. Due to extension of the subarachnoid space surrounding the optic nerves, increased optic nerve sheath (ONS) diameter in humans and dogs correlates with intracranial pressure, serving as a non-invasive indicator of increased intracranial pressure. Prior investigation of this technique in foals is limited. The goals of this prospective, observational, cross-sectional study were 1) establish an expected range of ultrasonographic ONS measurements in a homogeneous population of neonatal foals and 2) determine intra- and inter-observer variation in ultrasonographic measurement of ONS size. Fourteen clinically normal Standardbred foals <14 days of age underwent non-sedated bilateral transpalpebral ocular ultrasound exams either while standing or in lateral recumbency. Optic nerve height (superior-inferior dimension) and width (nasal-temporal dimension) were measured by two independent examiners, with each examiner performing measurements successively in triplicate. Average ONS width was 4.2 ± 0.24 mm and average height was 2.7 ± 0.05 mm with average height being smaller than previously reported. Using paired analysis, no significant differences were found between measurements of left versus right eyes or between observers. Intraclass correlation coefficient inter-rater agreement measures were moderate for right eye height (0.62) and width (0.50), as well as for left eye height (0.54) and width (0.59). Results suggest ultrasonographic measurement of ONS size is easily and repeatably performed in clinically normal, non-sedated neonatal foals and expected values in the superior-inferior dimension may be smaller than previously reported. The established expected values may be applied to future studies investigating the difference in ONS size between normal foals and foals affected by neonatal encephalopathy. |
| Keywords for abstract: | Foal<br>Ultrasound<br>Optic nerve sheath<br>Neonatal encephalopathy<br>Intracranial pressure |

# CR - 11

| | |
|---|---|
| Title of abstract: | **METAL ACCUMULATIONS IN WETLAND-DEPENDENT SPECIES** |
| Authors | J. Heinz, M. Flint. Dept. Veterinary Preventive Medicine |
| Abstract | Heavy metal toxicity can be found as a pollutant after human disturbance of the land and has detrimental effects on the health of animals. Wetlands are concentrators of these heavy metals and serve to help sequester and clean waters. Two locations were evaluated, one impacted by previous strip-mining which results in acid mine drainage and metal contamination, the other a wetland of Lake Erie which was impacted by industrial pollutants and human disturbance. Three species were evaluated: painted turtles (*Chrysemys picta*), channel catfish (*Ictalurus punctatus*) and bluegill fish (*Lepomis macrochirus*). Twenty animals of each species were collected, ten for each site. Liver samples were analyzed on each animal for cobalt, copper, iron, manganese, molybdenum, selenium, zinc, arsenic, cadmium, lead, and thallium. In livers, some metals showed species differences --bluegill had higher levels of zinc (Av. 168.73 ± Std Dev 39.30µg/g), cobalt (3.05±2.87µg/g), and arsenic (0.67±0.75µg/g); cadmium was more commonly found in catfish and bluegill at Lake Erie than turtles (50%, 60% vs 10% respectively), lead more commonly found in catfish (50% vs 15% and 0% in turtles and bluegills resp); turtles had higher copper (21.78±13.0µg/g) levels but lower selenium (4.77±2.14µg/g). Metals varied between location as well --the strip-mine site had higher cobalt in catfish (4.78±3.0µg/g) and bluegill (1.32±0.29µg/g); higher iron (8659.47±4196µg/g), molybdenum (2.16±1.93µg/g) and lead (0.71±0.45µg/g) in catfish, while the Lake Erie site had arsenic more commonly in bluegill fish (100% vs 20% at strip-mine site), and cadmium across all species (10-60% vs none at strip-mine site). Blood was collected on turtles for metal comparison but did not show correlation to liver metal analysis. These differences in metal levels between species and locations demonstrate differences in accumulations likely due to exposure and physiology. These measures may be important in tracking the health of wetland ecosystems and species impacts. |
| Keywords for abstract: | Heavy metals<br>Wetland<br>Bluegill fish<br>Channel Catfish<br>Painted Turtle |

# CR - 12

| | |
|---|---|
| Title of abstract: | **CLINICAL UTILITY OF SCORING CANINE FECES** |
| Authors | E. Jachec, A. Rudinsky, V. Parker, J. Howard, J. Winston<br>Department of Veterinary Clinical Sciences |
| Abstract | Various fecal scoring systems exist to characterize canine bowel movements in clinical settings. The most common have been developed by Nestle Purina PetCare Company and The Waltham Petcare Science Institute. These scoring systems categorize feces based on several characteristics. Data from these systems can assist in monitoring gastrointestinal disease and therapeutic responses. The use of these scoring systems requires accurate in-person scoring, limiting the potential for use in clinical trials. Therefore, this study aims to determine if a digital photo can be scored in place of an in-person fecal score.<br><br>A collection of 113 bowel movements were scored in person by two veterinarians using both the Purina and Waltham scoring systems. Digital images were obtained during the in-person scoring. These images were randomized and scored by three veterinarians. Scores were analyzed using Cohen's and Fleiss' kappa statistics and Bland-Altman agreement plots. Kappa scores can be interpreted as: <0 indicates poor agreement, 0.0 to 0.2 indicates slight agreement, 0.21 to 0.41 indicates fair agreement, 0.41 to 0.60 indicates moderate agreement, 0.61 to 0.80 indicates substantial agreement and 0.81 to 1.0 indicates almost perfect agreement.<br><br>The results demonstrated agreement between in-person scoring and image scoring, using Bland-Altman plots, with more than 50% of the data falling within the interquartile ranges along the mean. Moderate to substantial agreement between veterinarian raters and the in-person scores among both scoring systems based on kappa statistics was observed. The Purina scoring system showed higher agreement when compared to the Waltham scoring system (Cohen's kappa 0.54-0.73 and 0.40-0.43 respectively).<br><br>Overall, these findings support the scoring of digital fecal images in lieu of in-person fecal scoring in dogs. This provides proof of concept that artificial intelligence could be used to automatically perform fecal scoring using a digital fecal image, which is directly applicable to clinical and research settings. |
| Keywords for abstract: | fecal scoring<br>Purina<br>Waltham<br>clinical trials<br>gastrointestinal disease<br>artifical intelligence |

# CR - 13

| | |
|---|---|
| Title of abstract: | **HIGH-VOLUME COMPARATIVE ANALYSIS (HVCA) AND RECORD** |
| Authors | L. Johnson, Department of Veterinary Clinical Sciences, E. Hostnik, Department of Veterinary Clinical Sciences, G. Habing, Department of Veterinary Preventive Medicine |
| Abstract | A novel educational technique (high volume comparative analysis, HVCA) is compared to an existing technique (recorded descriptive rounds, RDR) to see which most improves the ability of veterinary students to recognize normal and diseased canine thoracic radiographs. One-hundred forty-seven (147) student volunteers representing 14 veterinary schools are randomly assigned to HCVA or RDR groups by a URL allocator. In HVCA (65 students), students evaluate slides of side-by-side lateral images, one normal, one diseased (pulmonary nodules), and identify normal images on a web-based survey. Each image set is presented for 10 seconds, then the normal image is highlighted for 5 seconds. In HVCA, students evaluate 240 images over 30 minutes. RDR (82 students) consists of five three-view thoracic cases, one normal and four abnormal (pulmonary nodules, left-sided congestive heart failure, pleural effusion, and aspiration pneumonia), discussed by an instructor in an approximately 30-minute recorded online presentation. In RDR, students evaluate 15 images over 30 minutes. Before and after instruction, subjects must diagnose 50 lateral thoracic images (pulmonary nodules, left-sided congestive heart ailure, pleural effusion, and aspiration pneumonia). Students record their perceived ability pre- and post-instruction, previous experience with making/interpreting radiographs, and satisfaction with the method of instruction. Data was analyzed using a generalized linear mixed model with the student score as the dependent variable. For students exposed to RDR, there is significant post-test improvement, and for students exposed to HVCA, there is significant post-test worsening. For students with a higher level of pre-test confidence in their radiographic interpretation ability, the positive effect of RDR and the negative effect of HVCA were significantly attenuated. Results support the utility of RDR and refute the efficacy of HVCA as instructional tools for rising, current, and recently-graduated veterinary students. |
| Keywords for abstract: | radiology<br>education<br>instruction<br>student |

# CR - 14

| | |
|---|---|
| Title of abstract: | **SURVIVAL IMPACT OF CERVICAL LYMPHADENECTOMY COMBINED WITH SURGICAL EXCISION OF ORAL MALIGNANT MELANOMA IN DOGS** |
| Authors | A.Johnson, L. Selmic, J. Lapsley, W. Kisseberth, W. Dirksen.<br>Department of Veterinary Clinical Sciences |
| Abstract | Given the local invasiveness and high metastatic potential of oral malignant melanoma (OMM), surgical excision of the primary tumor combined with lymphadenectomy and adjuvant therapy is considered the standard of care. Currently, there is a lack of information concerning the therapeutic and survival benefit that cervical lymphadenectomy provides for dogs with OMM. This multi-institutional retrospective cohort study aims to compare the outcome of dogs that have received surgery as treatment for OMM with or without lymphadenectomy. The criteria for inclusion were: (1) diagnosis of OMM was confirmed with histopathology; (2) surgical excision of the primary tumor was performed with curative intent. The criteria for inclusion for cases with cervical lymphadenectomy in addition to surgical excision was that both procedures were performed concurrently. Cases where surgery of the primary tumor was palliative in intent were excluded. Data reviewed included information on signalment, staging, local disease therapy, adjuvant therapy, histopathology, and disease progression. The study group consists of 104 confirmed OMM patients retrospectively identified from Alta Vista Animal Hospital,The Ohio State University Veterinary Medical Center, and University of Guelph Ontario Veterinary College medical records. Of these 104 cases collected, 54 had lymphadenectomy performed concurrently with surgery of their primary tumor. Kaplan-Meier survival analyses of the overall survival time and disease-progression free interval were not significant at p-values of 0.15 and 0.38 respectively. The overall incidence of surgical complications was 72% in the dogs treated with concurrent surgical excision and lymphadenectomy, and 18% in those treated with surgical excision alone. Further data analysis is still ongoing. |
| Keywords for abstract: | Melanoma<br>Oncology<br>Lymphadenectomy |

# CR - 15

| | |
|---|---|
| Title of abstract: | **THE INSULIN-MODIFIED FREQUENTLY SAMPLED INTRAVENOUS GLUCOSE TOLERANCE TEST IN HEALTHY NEONATAL FOALS AND HORSES** |
| Authors | H. Kinsella, L. Hostnik, S. Mazur, H. Snyder, T. Burns, R. Toribio |
| Abstract | The equine neonate is considered insulin resistant in the first days of life due to delayed maturation of the hypothalamic-pituitary-adrenal axis and pancreatic endocrine system. Few studies have investigated insulin sensitivity in newborn foals using dynamic testing methods. In order to investigate insulin sensitivity in the healthy newborn foal, the objective of this study was to compare the insulin-modified frequently sampled intravenous glucose tolerance test (I-FSIGTT) between neonatal foals and horses.<br>The I-FSIGTT was performed on healthy neonatal foals (n=12), 24-60 hours of age, and adults (n=8), 3-14 years of age, using dextrose (300 mg/kg/IV) and insulin (0.02 IU/kg/IV). Insulin sensitivity (SI), acute insulin response to glucose (AIRg), glucose effectiveness (Sg), and disposition index (DI) were calculated using minimal model analysis. Data was tested for normality with the Shapiro Wilk normality test. Minimal model parameters were compared between foals and horses using Mann Whitney U test.<br>SI (median, interquartile range [IQR]) was significantly higher in foals (18.3 L·min$^{-1}$·mU$^{-1}$ [13.4-28.4]) compared to horses (0.9 L·min$^{-1}$·mU$^{-1}$ [0.5-1.1]); ($p < 0.0001$). DI (median, IQR) was significantly higher in foals (12 x 10$^{3}$ [8 x 10$^{3}$-14 x 10$^{3}$]) compared to horses (4 x 10$^{2}$ [2 x 10$^{2}$-7 x 10$^{2}$]); ($p < 0.0001$). AIRg and Sg were not significantly different between foals and horses.<br>While the acute insulin response to glucose (AIRg) and ability of glucose to mediate its own disposal (Sg) were not different between foals and horses, insulin had a higher capacity to promote glucose disposal and inhibit endogenous glucose production (SI) in foals versus adults. These results suggest that healthy neonatal foals may not be insulin resistant as previously proposed, but insulin sensitive in the first days of life. Foals are born with minimal energy reserves, and these findings could be an adaptation to conserve energy throughout the transition to extrauterine life. |
| Keywords for abstract: | Foal<br>Pancreas<br>Endocrine<br>Insulin<br>Glucose |

# CR - 16

| | |
|---|---|
| Title of abstract: | **EXPLORING OPTICAL COHERENCE TOMOGRAPHY IMAGING DEPTH TO DIFFERENTIATE TISSUES AT SURGICAL MARGINS** |
| Authors | M. Lages, L. Selmic. Dept. of Veterinary Clinical Sciences, The Ohio State University College of Veterinary medicine |
| Abstract | Optical coherence tomography (OCT) is an imaging modality that provides real-time visualization of tissue microstructure. The goal of this study was to assess OCT image tissue depths (TD) and other objective characteristics of tissue types at surgical margins in canine soft tissue sarcoma (STS). In this study, a single observer reviewed 248 images of four predominant tissue types (sarcoma, skeletal muscle, adipose and fascia) collected from 25 dogs with STS. The observer evaluated for tissue characteristics and measured TDs utilizing ImageJ software. Images were evaluated in normal, Threshold and Binary conditions. Measurements were repeated one week later to evaluate for intra-observer variability. In all three image processing conditions, the order of TD from greatest to least light penetration was adipose, skeletal muscle, fascia and sarcoma tissue. Neovascularization was observed in 53.2% sarcoma, and lines of fascia surrounding muscle bundles was present in 93.5% of skeletal muscle images. These observed differences between tissue types in OCT images can be utilized to improve observer evaluation, aid in development of algorithms, and improve the accuracy of surgical margin assessment. |
| Keywords for abstract: | Optical coherence tomography<br>Soft tissue sarcoma<br>Tissue depth<br>Surgical margin |

# CR - 17

| | |
|---|---|
| Title of abstract: | **DETECTING BACTEREMIA IN VETERINARY SPECIES THROUGH A COMPARISON OF BLOOD CULTURE AND 16S RRNA SEQUENCING** |
| Authors | K. Loewen[1], M. Moran[1], J. van Balen[2], G. Habing[3], J.Winston[2], D. Diaz-Campos[2]<br>Departments of [2]Clinical Sciences, [3]Veterinary Preventive Medicine, [1]College of Veterinary Medicine, The Ohio State University, Columbus, Ohio |
| Abstract | Culture-based diagnosis of septicemia in veterinary patients can require up to a week or more and it is impractical when rapid treatment decisions are needed. In most cases, antibiotics are given empirically without confirmation of sepsis or identification of the causative agent, raising concerns over unnecessary or suboptimal antibiotic administration. The objective of this study is to investigate the use of next-generation (NGS) and 16s rRNA gene sequencing in cases of septicemic and healthy veterinary patients compared to blood culture. We hypothesize that these alternative methods will demonstrate more rapid results for detecting bacteremia than traditional culture-based methods. Samples will be collected from calves on a dairy farm, a veal barn, and from suspected septicemia cases in a veterinary teaching hospital. Three to ten mL of blood will be inoculated in a blood culture bottle (BCB) with an indicator top from a syringe. Bottles will be incubated at 35˚C and monitored for 5 days following inoculation to assess turbidity and fluid translocation into the indicator top, which defines a plausible positive BCB. Blood culture fluid from positive BCBs will be processed following established protocols for traditional culture. At 24 hours post inoculation, 13 mL will be collected from the BCB, homogenized, and aliquoted in -80˚C for further testing. Three ml of blood will be aseptically collected on Vacutainer glass collection tubes with K2EDTA, and one aliquot of one mL will be submitted to a private laboratory for NGS. Some potential limitations to this study are the collection of aseptic samples outside of a hospital setting, sensitivity of the gold standard (BCB), and potentially the number of samples able to be collected from each patient. With this study, we hope to determine the realistic potential for the two methods as an alternative for the diagnosis of septicemia in veterinary patients. |
| Keywords for abstract: | Septicemia<br>blood culture<br>infection<br>animals<br>NGS<br>culture |

# CR - 18

| | |
|---|---|
| Title of abstract: | **DEVELOPING A PREDICTIVE MODEL FOR SPINAL SHOCK IN DOGS WITH ACUTE SPINAL CORD INJURY** |
| Authors | McBride, R[1]; Parker E[2]; Garabed R[3]; Olby NJ[4]; Tipold A[5]; Stein VM[6]; Granger N[7]; Hechler AC[1]; Yaxley PE[1]; CANSORT-SCI; Moore SA[1].<br>[1]Department of Veterinary Clinical Sciences, The Ohio State University College of Veterinary Medicine, Columbus, Ohio, USA. [2]Department of Animal Science, The Ohio State University, Columbus, Ohio, USA. Department of Preventative Veterinary Medicine, The Ohio State University, Columbus, Ohio, USA. [4]Department of Clinical Sciences, College of Veterinary Medicine, North Carolina State University, Raleigh, North Carolina, USA. [5]Department of Small Animal Medicine and Surgery, University of Veterinary Medicine, Hannover, Germany. [6]Department of Clinical Veterinary Sciences, University of Bern, Bern, Switzerland. [7]School of Veterinary Sciences, University of Bristol Department of Small Animal Clinical Sciences, Bristol, UK. |
| Abstract | Acute spinal cord injury is common in dogs, where reduced pelvic limb reflexes typically suggest a lesion of the L4-S3 spinal cord segments. However, pelvic limb reflexes may also be reduced in dogs with a T3-L3 myelopathy and concurrent spinal shock, which can lead to clinical confusion. In order to help distinguish between these two localizations, we compared clinical and demographic factors in a large, prospectively identified cohort of 59 dogs with T3-L3 myelopathies and spinal shock and a group of 11 dogs with L4-S3 myelopathies. A univariable logistic regression was performed to assess influence of clinical factors on the odds of spinal shock. Independent variables were selected for a multivariable logistic regression model if they had a significant effect ($p > 0.100$) on the odds of spinal shock in univariable logistic regression. When other independent variables are held constant, the odds of spinal shock increased with decreasing weight, decreasing duration of clinical signs, presence of a cutaneous trunci cut-off, and severity of neurologic deficits (presence of paraplegia). The odds of spinal shock in paraplegic dogs is 7.87 times greater than dogs with paraparesis ($p= 0.041$). The odds of a L4-S3 myelopathy is 8.57 and 5.63 times greater in dogs with decreased pelvic limb tone and decreased patellar reflex, respectively ($p= 0.004$; $0.013$). A predictive formula, as developed by the present study and using these criteria, can be useful for assisting the clinician in determining the likelihood of spinal shock in various clinical scenarios and aid clinicians in diagnostic planning. |
| Keywords for abstract: | canine<br>spinal shock<br>acute spinal cord injury<br>intervertebral disc disease<br>reflex |

# CR - 19

| | |
|---|---|
| Title of abstract: | **THE EFFECTS OF CALCIFEDIOL SUPPLEMENTATION ON THE RENIN-ANGIOTENSIN-ALDOSTERONE SYSTEM IN DOGS WITH CHRONIC KIDNEY DISEASE** |
| Authors | M. Miller, J. Quimby, C. Langston, V. Parker<br>Department of Veterinary Clinical Sciences, The Ohio State University College of Veterinary Medicine, Columbus, OH |
| Abstract | Chronic kidney disease (CKD) leads to decreased serum concentrations of vitamin D metabolites. Vitamin D metabolites have been shown to negatively affect mediators of the renin-angiotensin-aldosterone system (RAAS). Increased RAAS metabolite concentrations can lead to pro-fibrotic and pro-inflammatory changes within the kidney, potentially leading to worsening CKD. We hypothesize that supplementation with calcifediol (25-hydroxyvitamin D) will decrease circulating RAAS mediators in dogs with CKD.<br>Six dogs with IRIS Stage 2 and 3 CKD were prospectively enrolled and supplemented with calcifediol for 3 months. Dogs were evaluated at baseline (day 0), month 3, and month 5 (2 months after discontinuation of calcifediol). Vitamin D metabolites (25-hydroxyvitamin D, 1,25 hydroxyvitamin D, 24,25 hydroxyvitamin D), parathyroid hormone (PTH), and RAAS mediators (angiotensin I/II/III/IV/1-5/1-7, and aldosterone) were evaluated at all time-points, as well as calculated angiotensin converting enzyme (ACE) activity (by performing the ratio of angiotensin II to angiotensin I). RAAS mediators were evaluated using a novel liquid-chromatography-tandem mass spectroscopy assay (RAS Fingerprint).<br>Calculated ACE activity was significantly decreased at month 3 compared to baseline (P = 0.01). There were no significant differences in any of the evaluated RAAS metabolites at any other time-point. In conclusion, short-term calcifediol supplementation is this small subset of CKD dogs appeared to decrease calculated ACE activity, as calculated by the ratio of angiotensin II to angiotensin I. |
| Keywords for abstract: | RAAS<br>ACE<br>calcifediol<br>Vitamin D |

# CR - 20

| | |
|---|---|
| Title of abstract: | **ANESTHETIC MANAGEMENT AND PHYSIOLOGIC EFFECTS IN PANGOLINS: A SYSTEMATIC LITERATURE REVIEW** |
| Authors | A. Moreno, A. Berrian |
| Abstract | Pangolins are underrepresented in the scientific veterinary literature. While anesthetic procedures have been performed successfully on pangolins, little information is known about their physiology while under anesthesia and comparative efficacy and safety studies of different anesthetic protocols have not been published and remain anecdotal in nature. Pangolins' unique, specialized morphology and physiology necessitate a much more species-specific approach to anesthetic procedures and monitoring. A variety of injectable anesthetic protocols have been used in pangolins; however, the use of gas anesthesia using chamber induction and maintenance using a fitted face mask is the preferred method of immobilization for minimally invasive procedures. Anesthetic monitoring can be especially challenging for pangolins, necessitating systematic evaluation of their physiological response while under anesthesia in order to empower clinicians to provide best-practices and evidence-based care for these animals during veterinary procedures. Given their conservation status and possible significance in the transmission and evolution of SARS-CoV-2, maximizing pangolin health while under human care is critically important. This review provides a foundation for wildlife and zoological centers to develop informed anesthetic protocols and highlights gaps in existing published reports where there is a need for future research. |
| Keywords for abstract: | Pangolin<br>Anesthesia<br>literature review<br>*Manis*<br>Wildlife immobilization |

# CR - 21

| | |
|---|---|
| Title of abstract: | **AUTOGENOUS PLATELET-RICH PLASMA FOR BOVINE SEPTIC ARTHRITIS TREATMENT: IN-VITRO CHONDROPROTECTIVE EFFICACY AND CLINICAL CASE SERIES** |
| Authors | A. Muir, A. Niehaus, J. Lozier, Z. Belacic, G. Ballash, S. Durgam<br>Dept. of Veterinary Clinical Sciences |
| Abstract | Septic arthritis is an important cause of debilitating/fatal lameness in cattle. The lack of antimicrobials labeled for regional use, and the stringent regulatory restrictions associated with antimicrobial use in cattle, renders PRP as an effective therapeutic option for bovine septic arthritis treatment, and is supported by evidence demonstrating the immune-metabolic effects and antimicrobial properties. Our objective was to evaluate the chondroprotective effects of autogenous PRP, ampicillin/sulbactum (AmpS) and PRP+AmpS in an explant model of bovine Staphylococcus aureus-induced septic arthritis. We hypothesized that the chondroprotective effects of PRP and PRP+AmpS are similar to that of AmpS. We evaluated the feasibility, safety and outcomes of PRP as an adjunct therapy in clinical septic arthritis cases.<br>Autogenous PRP was prepared, prior to euthanasia and cartilage explant collection from the stifle joints (n=6). Explants were incubated in synovial fluid (SF), *Staphylococcus aureus*-inoculated synovial fluid (SA; 1x$10^5$CFU/mL), or SA with treatments PRP (25% volume), AmpS (50mg/mL), or PRP+AmpS. Explant chondrocyte viability, metabolic activity and glycosaminoglycan (GAG) content were measured via confocal live-dead microscopy (24-hour), Alamar-blue (24-hour) and dimethylmethylene blue assays (48-hour), respectively. Data were analyzed with one-way-ANOVA ($p \leq 0.05$). Septic arthritis clinical cases that received 'gold-standard' treatment and post-operative intraarticular PRP were reviewed.<br>PRP (26±2.8%), AmpS (25±10.6%) and PRP+AmpS (22±4%) treatments significantly ($p=0.01$) decreased chondrocyte death compared to *SA* (64±10.5%), and was not different among treatments ($p=0.3$). The live- dead assay corroborated with explant metabolic activity results. Explant GAG content was similar in SA, SF and treatment groups. Intraarticular PRP for 3 consecutive days post-operatively was safe in all 5 cases. All were discharged, and objective efficacy evaluation compared to control cases are ongoing. The chondrocyte viability effects of autogenous PRP is similar to AmpS; our collective results highlight the therapeutic potential of PRP in bovine septic arthritis treatment and warrants further in-vivo investigation. |
| Keywords for abstract: | Autogenous bovine PRP<br>Septic arthritis<br>Explant model<br>Live-dead<br>Ampicillin/sulbactum |

# CR - 22

| | |
|---|---|
| Title of abstract: | **DEVELOPMENT AND PROGRESSION OF COGNITIVE DYSFUNCTION SYNDROME IN SENIOR DOGS AND THE EFFECTS OF A WEEKLY GROUP CLASS ON THEIR BEHAVIOR** |
| Authors | M. O'Brian, M. Herron, A. Smith, T. Aarnes. Dept. Of Veterinary Clinical Sciences |
| Abstract | Cognitive dysfunction syndrome (CDS) is a neurodegenerative disorder that is characterized by behavioral changes as well as neurodegenerative markers in senior dogs. Despite the high prevalence of CDS and the range of interventions available, many owners remain unaware of the disease and the available supportive measures. The objective in this study was to assess for changes in behavior consistent with CDS in senior dogs and to determine if a weekly group training class led to fewer such changes.<br>Eighty-six owners whose dogs were aged 8 years and older completed the study, 20 of whom attended 4 weekly classes with their dogs. All participants completed a CDS baseline survey that was subsequently scored 3, 6 and 12 months after the baseline survey. Twenty-two participants attended 4, weekly dog classes that addressed common senior dog behavior problems and offered training and enrichment activities.<br>There was a significant association between age and CDS score ($P<0.001$), where higher age groups had higher impairment levels of CDS. Scores for dogs who attended the class showed no significant change in CDS scores from 3 months to 12 months ($P = 0.0670$), where dogs who did not attend the class had a significant increase in CDS scores from 3 months to 12 months ($P = 0.0016$).<br>The prevalence of CDS in dogs increases with advanced age. Results suggest senior dog classes reduce clinical signs of CDS and may thereby improve senior dog's qualify of life. |
| Keywords for abstract: | behavior<br>cognitive dysfunction syndrome<br>aging<br>dogs |

# CR - 23

| | |
|---|---|
| Title of abstract: | **COMPUTED TOMOGRAPHIC EVALUATION OF PULMONARY VASCULATURE IN DOGS WITH MYXOMATOUS MITRAL VALVE DISEASE AND PULMONARY HYPERTENSION** |
| Authors | T. Ou, E. Hostnik, J. Rhinehart, T. Aarnes, K. Schober. Dept of Veterinary Clinical Sciences |
| Abstract | Myxomatous mitral valve disease (MMVD) is most common heart disease in dogs. A pathophysiologic sequela to the progression of MMVD is pulmonary hypertension (PH). Transthoracic echocardiography (TTE) has been traditionally used to diagnose PH in dogs but is incapable of characterizing pulmonary vascular remodeling secondary to PH. It is unknown if pulmonary vascular remodeling is detectable on computed tomography angiography (CTA) in dogs with PH secondary to MMVD. The goal of this study is to characterize pulmonary vascular changes on CTA in dogs with PH secondary to MMVD.<br>Fifteen geriatric small breed dogs with MMVD and PH were prospectively recruited. Dogs were categorized into groups of none to mild PH (tricuspid regurgitant pressure gradient (TRPG) <36 mmHg), moderate PH (36<TRPG <60 mmHg), and severe PH (TRPG > 60 mmHg). ECG-gated and non-gated thoracic CTA measurements included pulmonary arterial tapering percentages, peripheral pulmonary vascular densities, and pulmonary trunk to aorta ratio (Pa/Ao). There was no difference in pulmonary arterial tapering, peripheral vascular density, and Pa/Ao between PH severity groups. Dogs with severe PH had a larger vertebral heart scale.<br>In conclusion, pulmonary arterial tapering, peripheral vascular density, and Pa/Ao on ECG-gated and non-gated CTA are not reliable parameters for diagnosing PH secondary to MMVD in this population of dogs. Future research may be directed to expand sample population. Alternative means of quantifying pulmonary vascular changes secondary to PH on CTA in dogs is warranted. In the meantime, TTE should remain the diagnostic of choice for characterizing PH in dogs. |
| Keywords for abstract: | Canine<br>Pulmonary hypertension<br>Pulmonary artery<br>ECG-gating<br>Computed tomography |

# CR - 24

| | |
|---|---|
| Title of abstract: | **THE EFFECT OF ENVIRONMENTAL ENRICHMENT ON STRESS, BEHAVIOR, AND PRODUCTION IN GESTATING AND FARROWING SUS SCROFA SOWS** |
| Authors | CD Peck1, JD Kieffer2,3, SJ Moeller3<br>1College of Veterinary Medicine, 2University Laboratory Animal Resources, and 3Department of Animal Sciences |
| Abstract | The materials of confinement housing limit periparturient behaviorial expression, which may increase stress. Increased stress has been shown to negatively influence parturition, which can impact production. Natural fiber cloth or rope may allow natural behaviors with little concern for digestibility. However, there is a lack of enrichment protocols for gestating and farrowing sows. This study aims to assess the impact of a natural fiber cloth on gestating and farrowing sow stress, behavior, and production. The purpose is also to evaluate appropriate provision criteria for future implementation of environmental enrichment in commercial settings. We hypothesized that enriched sows will display more natural behaviors and have lower cortisol levels, resulting in faster farrowing and fewer stillborn piglets. Sus scrofa sows were randomly divided into two groups (n=6 per group): enriched and control. Burlap cloth was secured with twine in enriched sow pens 6 days before the expected farrowing date and removed 24 hours post-farrowing. Salivary cortisol was measured to evaluate stress level 6 days and 2 days before the expected farrowing date, 24 and 48 hours after environmental enrichment, daily until farrowing, and at the beginning and end of farrowing. Video surveillance was used evaluate piglet (n=208) and sow behavior. Preliminary results demonstrate that, on average, enriched sows produce more live piglets (avg=17.67) and fewer stillborns (avg=3.17), than controls (avg live=17, avg SB=5.17). No differences in salivary cortisol were observed between groups (p=0.78). As expected, salivary cortisol in all sows increased ($p<0.05$) when farrowing began and remained elevated when the last piglet was farrowed ($p<0.05$). 24 hours post-farrowing, salivary cortisol levels decreased to a level similar to what they measured 24 hours pre-farrowing ($p<0.05$) in both groups. The current study results will facilitate the determination of an enrichment protocol and additional housing criteria to increase sow production and profit for swine farmers. |
| Keywords for abstract: | Farrowing<br>Behavior<br>Enrichment<br>Swine<br>Parturition<br>Housing |

# CR - 25

| | |
|---|---|
| Title of abstract: | **Comparison of Proxy Measurements of Insulin Sensitivity and Insulin Secretion Between Foals and Adult Horses** |
| Authors | A. Pennington, H. Kinsella, L. Hostnik, L. Rings, S. Mazur, H. Snyder, K. Timko, T. Burns, R. Toribio |
| Abstract | While reference intervals for adult horses are vital in a clinical setting, they are often inappropriately extrapolated to neonates. The objectives of this investigation were to establish normal ranges for proxy measurements of insulin sensitivity, blood glucose (BG), and insulin concentrations in healthy foals, determine correlation with minimal model analysis, and differences between horses and neonatal foals. Blood samples were collected from healthy neonatal foals less than 72 hours in age and healthy adult horses. Reference intervals were calculated from BG and insulin concentrations while nursing and after a 1-hour fast. Proxies were calculated after a 1-hour fast in neonates and 12-hour fast in adults. Proxies were compared between foals and horses, and neonatal proxies were correlated with minimal model analysis in foals. Data was tested for normality using the Shapiro Wilk normality test. Proxy measurements were compared between foals and horses using Mann Whitney U test, and correlations were performed using Spearman's correlation coefficient.<br>BG concentrations in nursing foals and after a 1-hour fast were 209-236.3 mg/dL and 153.8-169.5 mg/dL, respectively. Insulin concentrations before and after fasting were 0 to 102.91 µIU/ml and 0 to 33.60 µIU/ml, respectively. Insulin to BG ratio (IG) and Modified Insulin-to-Glucose Ratio (MIRG) were significantly lower ($P<0.0001$), and BG to Insulin Ratio (FGIR) was significantly higher ($P=0.0007$) in foals compared to adults. Proxy measurements did not correlate to calculated indices of minimal model analysis (insulin sensitivity and acute insulin response to glucose) in neonatal foals, in contrast to studies in humans and horses.<br>Results of this study show dramatic differences in energy regulation in neonatal foals. Neonatal foals appear to have decreased insulin secretory ability relative to elevations in blood glucose, based on low MIRG values. Our findings contradict previous conclusions on insulin sensitivity and dysregulation in newborn foals, and further investigation is warranted. |
| Keywords for abstract: | foal<br>proxies<br>insulin<br>glucose<br>minimal model analysis |

# CR - 26

| | |
|---|---|
| Title of abstract: | **VALIDATING THE USE OF ALLOSTATIC LOAD INDEX IN RING-TAILED LEMURS (*LEMUR CATTA*): A PILOT STUDY** |
| Authors | K.E. Seeley, K. Proudfoot, B. Wolfe, and D.E. Crews. Depts of Veterinary Preventive Medicine and Anthropology |
| Abstract | Stress is unavoidable and can be an adaptive mechanism for survival. However, chronic stress has been linked to poor health outcomes and increased morbidity. The concept of allostasis describes the physiologic dysregulation that occurs when an organism is exposed to chronic stressors. An allostatic load index (ALI) composed of six biomarkers was used to evaluate the relationship between stressors and allostasis in a population of ring-tailed lemurs (*Lemur catta*) under human care. Any biomarker that fell within the high risk quartile was given a score of 1. The allostatic load index for each animal was the summation of all of the high risk biomarkers. Using linear regression statistically significant associations were found between ALI and stressors. There were negative associations between average group size and ALI suggesting that smaller groups resulted in chronic stress. The amount of time spent indoors was positively associated with ALI. The number of group composition changes was negatively associated with ALI, but only in females. This pilot study illustrates that several social and husbandry variables were associated with increases in allostasis. Allostatic load index may be a useful tool in assessing the health and welfare of lemurs in human care. |
| Keywords for abstract: | Allostasis<br>Prosimians<br>Stress<br>Welfare |

# CR - 27

| | |
|---|---|
| Title of abstract: | **ASSESSMENT OF CHANGES IN PULMONARY FUNCTION ASSOCIATED WITH BODY POSITIONING IN DOGS WITH ASPIRATION PNEUMONIA.** |
| Authors | S. Ten Cate, R. Urion, E. Hostnik, P. Yaxley, E. Cooper. The Ohio State University, Columbus, Ohio, USA. |
| Abstract | *Objective* – To evaluate the variability in arterial blood gas (ABG) assessment of pulmonary function with different body positioning in canine patients with aspiration pneumonia and correlation to radiographic changes.<br>*Design* – Prospective, randomized, case series conducted over 8-months.<br>*Setting* – University teaching hospital, Emergency Room or Intensive Care Unit<br>*Animals* – Fourteen dogs diagnosed with aspiration pneumonia based on clinical signs and radiographic interpretation. Exclusion criteria were patients <5 kg or age < 6 months or intolerance of arterial sampling on room air.<br>*Interventions* – Patients were randomized to start in left or right lateral recumbency. After equilibration on room air, an ABG was obtained. This was repeated with the patient in sternal and then the opposite lateral recumbency. All ABG's were analyzed within 3 minutes. Thoracic radiographs and airway scores were assigned to each patient as a means of quantifying disease severity using a novel scoring system.<br>*Measurements and Main Results* – The median partial pressure of oxygen ($P_aO_2$) in left lateral recumbency was 75.5 mmHg (IQR 18.5mmHg), 77.8 mmHg (IQR 19 mmHg) in right lateral recumbency and 79.4 mmHg (IQR 11.9 mmHg) in sternal recumbency across all patients. The median change in $P_aO_2$ between sternal and left lateral and right lateral were 1.15mmHg (IQR 9.4 mmHg) and 5 mm Hg (IQR 4.5 mmHg). The median A-a difference between sternal and left lateral and right lateral were 5.2 mmHg (IQR 7.86 mmHg) and 5.12 mmHg (IQR 4.8175 mmHg). Radiographic severity scores did not correlate to a lower $P_aO_2$ or to a higher A-a gradient.<br>*Conclusions* – There were no significant difference in A-a gradient or $P_aO_2$ values within an individual in different positions, or across the study population, regardless of which side was more affected. This suggests that positioning of patients is not an important consideration when attempting arterial blood sampling. |
| Keywords for abstract: | Aspiration pneumonia<br>arterial blood gas<br>Alveolar-arterial gradient<br>hypoxemia<br>recumbency<br>radiographs |

# CR - 28

| | |
|---|---|
| Title of abstract: | **EFFECT OF AMPK AGONISTS ON INCRETIN HORMONE SECRETION IN HORSES WITH EXPERIMENTALLY-INDUCED INSULIN DYSREGULATION** |
| Authors | KJ Timko, LD Hostnik , MR Watts, C Chen , A Bercz, RE Toribio, JK Belknap, TA Burns |
| Abstract | Insulin dysregulation (ID) in horses increases the risk of endocrinopathic laminitis. The enteroinsular axis is comprised of the incretin hormones glucagon-like peptide-1 (GLP-1) and glucose-dependent insulinotropic peptide (GIP), which plays a significant role in insulin secretion after meal feeding. Adenosine 5' monophosphate-activated protein kinase (AMPK), a highly conserved enzyme involved in energy regulation, is a therapeutic target in humans with metabolic syndrome. The objective of this study was to investigate the response of GIP, GLP-1, and active GLP-1 (GLP-1a) to an oral sugar test (OST) before and after the induction of ID and in response to AMPK agonist combination therapy with metformin and aspirin. Insulin dysregulation was induced in 7 light-breed horses with dexamethasone (0.08 mg/kg PO q24h) for 7 days. Then, horses received metformin (30 mg/kg PO q12h) and aspirin (10 mg/kg PO q24h) for 7 days in addition to dexamethasone. An OST was performed at baseline, ID, and ID + combination therapy timepoints, and serum incretin hormones were measured at 0, 30, 60, 90, 120, and 150 minutes. The $AUC_{GIP0-150}$ and $AUC_{GLP-1a0-150}$ were significantly increased at the ID (P=0.005, 0.05) and ID + combination therapy (P=0.006, 0.004) time points compared to baseline. The $AUC_{GLP0-150}$ was significantly increased at ID + combination therapy compared to baseline and ID (P=0.03, 0.03). We have shown that incretin hormone secretion is altered following the induction of ID with dexamethasone. Previous work from our lab has shown that metformin/aspirin combination treatment significantly increased baseline serum insulin concentration, insulin concentration at 60 minutes during an OST, and insulin concentration and 45 minutes during a CGIT. The administration of metformin and aspirin enhances the secretion of GLP-1 in response to enteral carbohydrate, leading to increased insulin secretion, thus providing a plausible explanation for the enhanced ID observed following metformin/aspirin administration in our previous work. |
| Keywords for abstract: | Insulin dysregulation<br>laminitis<br>AMPK<br>incretin<br>metformin<br>aspirin |

# CR - 29

| | |
|---|---|
| Title of abstract: | **DIFFUSION WEIGHTED TENSOR IMAGING AND TRACTOGRAPHY OF EQUINE SUPERFICIAL DIGITAL FLEXOR TENDONS** |
| Authors | R. Urion, S. Durgam, E. T. Hostnik |
| Abstract | Tools to assess in-vivo tendon functionality in horses are limited. The ability to characterize tendon functionality facilitates accurate injury identification and prognostication as well as guides rehabilitation. Diffusion weighted tensor imaging (DWTI) is an adjunctive MRI technique that can generate fiber tracts representing water proton movement within tissue. It can also calculate apparent diffusion coefficient (ADC) and fractional anisotropy (FA) values, quantifying the amount and directionality of proton movement, respectively. The objectives of this prospective, proof of concept study were to 1) co-evaluate computer-generated fiber tracts of mid-metacarpal superficial digital flexor tendon (SDFT) and histological tendon hierarchical structure and 2) establish a normal range of ADC and FA values for equine forelimb SDFT. Disarticulated forelimbs of freshly euthanized (<6 hours) sound horses underwent metacarpal 3T MRI exams, including standard pulse sequences and diffusion weighted sequences. Longitudinal and cross-sectional histological (SHG and light microscopy) images were compared to the MRI-derived images. The average ADC values were 0.725 ± 0.344 $10^{-3}$ mm$^{2}$/s and the average FA values were 0.458 ± 0.077. Computer-generated fiber tracts were reliably produced between individual horses but did not correspond to tendon fascicles on histology. Computed generated fibers may represent proton movement within the interfascicular matrix rather than within tendon fascicles themselves. The established normal ranges of ADC and FA values will serve as a foundation for future studies investigating SDFT injury severity and determining healing response within tendons. |
| Keywords for abstract: | MRI<br>Equine<br>Tendon<br>Diffusion weighting<br>Tractography |

# CR - 30

| | |
|---|---|
| Title of abstract: | **EFFECTS OF GABAPENTIN AND TRAZODONE ON ELECTRORETINOGRAMS RECORDED IN NORMAL DOGS** |
| Authors | N. Violette, G. Newbold, C. Chen, E. Miller, A. Gemensky-Metzler<br>Department of Veterinary Clinical Sciences |
| Abstract | **Objective** — To compare electroretinogram (ERG) responses obtained in normal dogs before and after administration of oral gabapentin, trazodone and a combination of both medications.<br>**Animals studied —** Twelve normal dogs<br>**Procedures —** A short protocol scotopic ERG with 20 min dark adaption was performed on both eyes of all dogs to establish individual baseline ERG recordings. Dogs then received the oral study medication, ~30 mg/kg of gabapentin, and the same ERG protocol was recorded 2 hours later. Dogs were given a washout period of a least 1-week duration. This protocol was repeated three times, substituting the study medication with ~20 mg/kg of trazodone, ~5 mg/kg of trazodone and a combination of ~20 mg/kg of gabapentin and ~5 mg/kg of trazodone. Effect of study medication on signal amplitudes and implicit times were analyzed with repeated measures ANOVA.<br>**Results —** The b-wave amplitudes were decreased after 20 mg/kg of trazodone ($P = 0.006$) and the combination of 20 mg/kg of gabapentin and 5 mg/kg of trazodone ($P = 0.002$). The a-wave amplitudes were decreased after the combination of 20 mg/kg of gabapentin and 5 mg/kg of trazodone ($P = 0.018$). Heavier dogs that received higher total doses of trazodone had additional decreases in a- and b-wave amplitudes. Differences in a- and b-wave implicit times were not significant after any study medications.<br>**Conclusions —** High doses of trazodone and the combination of gabapentin and trazodone significantly decreases the amplitudes of both a-waves and b-waves in normal dogs. However, these effects on retinal responses have little clinical significance. |
| Keywords for abstract: | dog<br>electroretinogram<br>gabapentin<br>trazodone |

# CR - 31

| | |
|---|---|
| Title of abstract: | **ASSESSMENT OF ERYTHROCYTE FRAGILITY IN CATS WITH CHRONIC KIDNEY DISEASE** |
| Authors | M.Wang, J. Quimby, J. Hokamp. Depts of Veterinary Clinical Science. Assessment of Erythrocyte Fragility in Cats with Chronic Kidney Disease |
| Abstract | Chronic kidney disease (CKD) constitutes one of the most common diseases in cats. The aim of this study was to explore the effect of azotemia on the fragility of feline erythrocytes using an osmotic fragility assay. We hypothesized that erythrocyte fragility would be increased in cats with CKD in comparison to healthy cats. The increase in RBC fragility among feline CKD patients has clinical implications for the successful management of this condition as anemia is common in these patients. To further explore the association between azotemia and RBC fragility, samples from 21 feline CKD patients (11 IRIS Stage 2, 5 IRIS Stage 3, 1 IRIS Stage 4, and 4 acute on chronic uremic crisis) and 12 healthy feline patients were collected and processed within one hour of collection using a conventional osmotic fragility assay. Osmotic fragility curves were plotted and the percent hemolysis at each NaCl concentration in the curve was compared between groups using a Mann Whitney test. There was no statistically significant difference in the percentage of hemolysis between normal cats and cats with CKD at any NaCl concentration. However, three individual CKD cats displayed much higher percent hemolysis (beyond the standard deviation of the rest of the group at 0.65 and 0.70 NaCl concentration). One of these cats was an Abyssinian with CKD that was used as a positive control, but the other two CKD cats had stable IRIS Stage 3 CKD and no known other cause for RBC fragility. The conclusion drawn from this study is that erythrocyte fragility does not appear to be common in this population of patients, however individual cases of RBC fragility can occur under clinical setting. |
| Keywords for abstract: | Erythrocyte Fragility<br>Chronic Kidney Disease<br>Feline |

# CR - 32

| | |
|---|---|
| Title of abstract: | **EVALUATION OF INTRAMUSCULAR ANESTHETIC PROTOCOLS IN HEALTHY DOMESTIC HORSES** |
| Authors | C. Willette, T.K. Aarnes, P. Lerche, C.H. Ricco-Pereira, G.A. Ballash, and R.M. Bednarski. Depts. of Veterinary Clinical Sciences and Veterinary Preventive Medicine. |
| Abstract | **Introduction:** The objectives were to assess anesthetic induction, recovery quality, and describe cardiopulmonary parameters after intramuscular injection of three different drug combinations for immobilization of horses.<br><br>**Methods:** Eight healthy horses were enrolled in a randomized, prospective, blinded three-way-crossover study, with a minimum one-week washout period. Intramuscular combinations were: 1) tiletamine-zolazepam (1.2 mg/kg), ketamine (1 mg/kg), and detomidine (0.04 mg/kg) (TKD); 2) ketamine (3 mg/kg) and detomidine (0.04 mg/kg) (KD); and 3) tiletamine-zolazepam (2.4 mg/kg) and detomidine (0.04 mg/kg) (TD). Time to event data, blood gas, and cardiorespiratory data were analyzed using mixed model linear regression. Induction, muscle relaxation and recovery scores, and number of attempts to stand were compared using a Skillings-Mack test. $p < 0.05$ was considered statistically significant.<br><br>**Results:** All horses administered TD became recumbent. One horse administered KD and one administered TKD remained standing. PaO$_2$ at T$_{15}$ was significantly higher after administration of KD than TD ($p < 0.0005$) and TKD ($p = 0.001$). Horses administered KD had faster time to first movement (25 ± 15 minutes) ($p < 0.0005$, $p = 0.005$) and time to sternal recumbency (55 ± 11 minutes) ($p = 0.001$, $p = 0.021$) than horses administered TD and TKD, respectively. There were no differences in induction quality, muscle relaxation score, number of attempts to stand or recovery quality.<br><br>**Conclusion:** In domestic horses, intramuscular injections of tiletamine-zolazepam combined with detomidine resulted in more reliable recumbency despite an overall longer duration when compared with combinations of ketamine-detomidine and tiletamine-zolazepam-ketamine-detomidine. Recoveries were comparable between protocols. |
| Keywords for abstract: | Detomidine<br>Horse<br>Injectable anesthesia<br>Intramuscular<br>Ketamine<br>Tiletamine-zolazepam |

# CR - 33

| | |
|---|---|
| Title of abstract: | **CASE-CONTROL STUDY OF NON-PULMONARY SOFT TISSUE METASTATIC DISEASE IN DOGS WITH APPENDICULAR OSTEOSARCOMA** |
| Authors | L. Caramagno, C. Matthew, L. Selmic, K.Curran, K. Bourne, S. Keepman, B. Wusterfeild-Jassens |
| Abstract | Osteosarcoma (OSA) is both the most common primary bone tumor in dogs and highly metastatic. Metastases into the non-pulmonary soft tissues are the least common observed at time of death and therefore less is known about their pathogenesis. This study seeks to understand how treatments for OSA affect the development of non-pulmonary soft tissue metastases in dogs with appendicular OSA. Using a medical record search we identified 34 cases where dogs developed soft tissue metastases (atypical) and 124 where dogs developed metastases in lungs or bones (control). Information about the treatments administered and pathogenesis in these cases were collected to create profiles that describe the relationship of treatment routes with development of metastases over time. Our study found that the pathogenesis of metastases follow a distinct timeline, where soft tissue metastases develop after pulmonary metastases, indicating that the soft tissues are a late-stage target of disease progression. Additionally, we discovered that subcutaneous and cutaneous tissue are the most common soft tissues to develop metastases and that while chemotherapy was the most common treatment for OSA patients, differences in what treatments were used had no effect on where metastases developed. In the future, clinicians should carefully monitor any new skin or subcutaneous masses that arise following treatment of appendicular OSA. |
| Keywords for abstract: | Osteosarcoma<br>Metastasis<br>Soft tissues |

# CR - 34

| | |
|---|---|
| Title of abstract: | **LONG TERM OUTCOME OF DOGS TREATED BY SURGICAL DEBRIDEMENT OF SHOULDER OSTEOCHONDRITIS DISSECANS** |
| Authors | G. Zann, S. Jones, L. Selmic, A. Wanstrath, S. Tinga, N. Kieves,<br>Department of Veterinary Clinical Sciences |
| Abstract | Shoulder osteochondondritis dissecans (OCD) represents a disruption in the orderly process of endochondral ossification, commonly affecting the caudal humeral head. Comprehensive outcome analysis in patients receiving surgical debridement of shoulder OCD is lacking in the veterinary literature. The aim of our study was to evaluate the long-term outcomes of dogs surgically treated for shoulder OCD via lesion debridement. We hypothesized that shoulder lameness and osteoarthritis would be documented in the majority (>50%) of patients and that clinical outcomes would not be as favorable as previously reported. Dogs treated with debridement of shoulder OCD lesions >12 months prior were enrolled. Orthopedic examination, kinetic gait analysis, shoulder radiographs, shoulder CT, and shoulder arthroscopy were performed. Twenty dogs were enrolled; n=13 unilateral, n=7 bilateral. Brachial circumference (p=0.004) and shoulder extension angle (p=0.007) were significantly decreased and shoulder flexion angle (p=0.015) was significantly increased in the OCD limb versus the contralateral limb in unilaterally-affected dogs. Patients with unilateral disease also demonstrated a 4.4% decrease in load distributed to the operated limb. Osteoarthritis was present in all shoulders with OCD lesions. Degree of osteoarthritis in OCD-affected shoulders was significantly increased compared to the contralateral on both CT (p=0.005) and radiography (p=0.0001). Moderate-severe synovitis was seen in all OCD-affected joints. Arthroscopically, all lesions were noted to have patchy, incomplete cartilaginous infilling; average cartilage infilling was 37.4%. Dogs receiving surgical debridement of shoulder OCD lesions have evidence of persistent orthopedic disease. These patients demonstrated osteoarthritis, impoverished range of motion, asymmetric forelimb loading, synovitis, and incomplete articular cartilage lesion infilling. Long-term clinical outcomes do not seem as favorable as previously reported in the scientific literature. |
| Keywords for abstract: | Shoulder<br>osteochondritis dissecans<br>kinetics |

# EPIDEMILOGY
# AND
# APPLIED RESEARCH

# EAR - 1

| | |
|---|---|
| Title of abstract: | **QUANTITATIVE ESTIMATES OF ANTIMICROBIAL USE IN VEAL CALVES** |
| Authors | B. Almeida, J. Pempek, G. Habing. Depts. of Veterinary Preventative Medicine and Department of Animal Sciences |
| Abstract | Antimicrobial are necessary for the treatment of bacterial infections in food animals, but may result in emergence of antimicrobial-resistant bacteria that are a critical threat to animal and public health. Antimicrobial use in neonatal veal calves is frequent due to the inherent susceptibility of young calves to bacterial diseases. The objective of the study was to quantify and describe the use of antimicrobials on veal farms within a single production system. The antimicrobial treatment incidence (TI) was estimated by collecting used antimicrobial containers, producer-recorded treatment records, and nutrition records from calf arrival through slaughter at approximately 23 weeks for 8 cohorts of calves located across 7 premises. The total mg of active substance per total kg of animal body weight and defined daily doses (DDD) per 100 days were calculated for each farm, based on the labeled dosage for each antimicrobial and the standardized weight. Treatment incidence for group therapy ranged from 6.5 to 16 doses per 100 calf-days across cohorts. For parenteral (individual) treatment, calves received a range of 6.4 to 19.8 doses of antimicrobials in 100 calf-days. There was 1.8 times more group oral antimicrobial usage than individual parenteral usage, and there was 1.9 times more antimicrobial usage during the first three weeks compared to the rest of the entire grow. The first three weeks after arrival a calf received an average of 0.71 doses of antimicrobials per day. The study provides the first estimates for quantified antimicrobial use for veal calves in the United States. Group oral medications represented the largest amount of usage compared to individual parenteral treatments. Group oral antimicrobial usage was highest during weeks 1-3 after arrival. These data will be useful to monitor usage or set benchmarks for continued improvement in antimicrobial stewardship in veal production. |
| Keywords for abstract: | Antimicrobial resistance<br>Antimicrobial stewardship<br>Veal calves<br>Antimicrobial usage<br>Defined daily dose |

# EAR - 2

| | |
|---|---|
| Title of abstract: | **PREVALENCE OF NASOPULMONARY MITES AMONG SEA OTTERS AND HARBOR SEALS SHOW DISTINCT GEOGRAPHIC HOTSPOTS** |
| Authors | W. Archibald, D. Monson, K. Worman, M. Miller, T. Norris, C. Fontaine, and R. Pesapane. Dept of Preventive Veterinary Medicine (Archibald, Pesapane), College of Veterinary Medicine, Ohio State University, Columbus, OH; USGS (Monson), Anchorage, AK; USFWS Service (Worman), Anchorage, AK; CDFW (Miller), Santa Cruz, CA; The Marine Mammal Center (Norris, Fontaine), Sausalito, CA |
| Abstract | Regional infestation hotspots of the nasopulmonary mite Halarachne halichoeri have been demonstrated within the southern sea otter (Enhydra lutris nereis; SSO) population. However, the prevalence and geographic distribution of nasopulmonary mites within the northern sea otters (E.l. kenyoni; NSO) and within harbor seals (Phoca vitulina), remain poorly understood. In this study, we determined mite infestation prevalence and assessed potential mite hotspots using necropsy data for harbor seals and both live-capture and necropsy data for NSO. Among 1,765 live-capture records of NSO from 1986 through 2012, 69 (3.91%, 95% CI 3.1-4.9%) were infested. Mite-positive otters were found at 2 of 3 northern Pacific regions sampled, but at specific capture locations with mites prevalences ranged from 4.35%-72.13%. In contrast, NSO necropsy data from 2004-2015 showed just 1 of 220 (0.45%, 95% CI 0.08-2.53%). Among 105 harbor seals necropsied between 2016 and 2019 in California, 21 (20.0%, 95% CI 13.47-28.65%) were infested, which is not significantly different from the reported SSO rate of 25.6% ($p=0.19$). However, the distribution of infested seals differs from that of otters. While the prevalence within harbor seal and SSO populations is similar, factors such as host density, behavior, and susceptibility should still be taken into consideration when examining otters for translocation and rehabilitation. The significant discrepancy between NSO prevalence generated from live-capture and necropsy data ($p<0.05$) emphasizes the importance of utilizing multiple surveillance methods for population health. Future studies should screen for nasopulmonary mites to develop an accurate understanding of their range-wide prevalence and epidemiology. |
| Keywords for abstract: | nasopulmonary<br>mite<br>infestation<br>sea otter<br>harbor seal<br>hotspot<br>live capture<br>necropsy |

# EAR - 3

| | |
|---|---|
| Title of abstract: | **BIOFILM FORMATION AMONG CANINE UROPATHOGENIC *ESCHERICHIA COLI* IS INDEPENDENT OF PATHOGEN AND HOST FACTORS** |
| Authors | G. Ballash, D. Mollenkopf, J. Van Balen Rubio, D. Diaz-Campos, T. Wittum, Depts. Of Veterinary Preventive Medicine and Clinical Sciences |
| Abstract | Uropathogenic *Escherichia coli* (UPEC) is the most common etiology of urinary tract infections (UTI) in dogs and humans. Biofilm formation among UPEC is thought to predispose patients to chronic urinary tract infections, either by recurrence with different strains or persistence of a single strain. However, factors associated with biofilm formation among urinary isolates are unclear and not well understood in canine patients. The objective of this study was to evaluate the biofilm capacity of canine UPEC and identify patient and pathogen characteristics that may influence their formation. Here we collected 104 *E. coli* isolates from dogs diagnosed with a clinical UTI. Isolates were tested for their capacity to form biofilms using a crystal violet staining assay. Biofilm capacity was investigated for an association with phenotypic resistance, patient factors, phylogroups and pathogenome using minimum inhibitory concentration antimicrobial susceptibility testing, retrospective record review and in-silico gene identification from whole genome sequencing data, respectively. A total of 83 isolates (79.8%) were able to form a biofilm, with 58 (55.8%) forming weak biofilms, 18 (17.3%) forming moderate biofilms and 7 (6.7%) forming strong biofilms. Biofilm formation was present among both pathogenic (82.6%; 71/86) and commensal phylogroups (66%; 12/18). Biofilm formation was not associated with patient factors including comorbidities, active recurrent infection, age, sex or previous antimicrobial use. Isolates with phenotypic antimicrobial resistance were at marginally lower odds (P = 0.08) of developing a biofilm, especially those resistant to tetracyclines, fluoroquinolones and gentamicin. There was no association between the presence of specific virulence genes related to colonization and adhesion and biofilm formation. Our data show that biofilm formation is a relatively common feature of UPEC and not necessarily related to the isolate's pathogenic or resistance profile, or to patient factors. |
| Keywords for abstract: | UPEC<br>Biofilm<br>antimicrobial resistance<br>Virulence<br>UTI |

# EAR - 4

| | |
|---|---|
| Title of abstract: | **TURNOVER OF ANIMAL CARETAKERS AND PRODUCITIVITY IN OHIO SWINE FARMS** |
| Authors | N.J. Black and A.G. Arruda. Dept. of Veterinary Preventive Medicine |
| Abstract | Attracting and retaining quality animal caretaking personnel is one of most pressing issues the US swine industry currently faces. The primary objectives of this study were to describe the amount of animal caretaker turnover events that occur in a single year and to investigate associations between employee turnover events and two subsequent production parameters of interest: number of pigs weaned per sow (PWS) and pre-weaning mortality (PWM). A retrospective cohort study was conducted with eleven commercial farrow-to-wean swine farms belonging to two production systems enrolled. Human resources and production data for the year of 2019 were obtained monthly from each farm. The primary predictor of interest was the occurrence of an employee turnover event, defined as 'voluntary' (employee decided to leave or quit) or involuntary (employee was terminated by company decision). The primary outcomes of interest included the monthly average PWS and PWM. These associations were assessed with 1-, 2-, 3-, and 6-months between the turnover events and the outcome. Linear mixed effects models were fit in STATA 15, with system and farm included as random effects. To account for temporal and seasonal trends of production, season and the monthly production were included in the models. There were a total of 152 turnover events, with 4 and 148 turnover events in systems 1 and 2, respectively. The average turnover, as percent of total turnover among full time employee positions, was 92% (SD = 62%; Range = 0.08-2.17). Both monthly PWS ($p = 0.01$) and PWM ($p = 0.02$) were significantly associated with the occurrence of an involuntary turnover event 2-months prior, after controlling for season, previous month production, farm, and system. For the PWS outcome, there was a significant interaction between an involuntary turnover event 2-months prior and monthly county-level unemployment rate ($p = 0.02$). |
| Keywords for abstract: | Pigs<br>Farm<br>Turnover<br>Production |

# EAR - 5

| | |
|---|---|
| Title of abstract: | **OPTIMIZING FOOD ACCESSIBILITY DURING ZEBRAFISH REARING IMPROVES GROWTH, SURVIVAL, AND BREEDING PERFORMANCE** |
| Authors | T. Collins[1], S. Cabrera[1], E. Teets[2], J. Shaffer[2], BW. Blaser[2]<br>[1]University Laboratory Animal Resources, Ohio State University, Columbus, OH<br>[2]College of Medicine, Division of Hematology, and Comprehensive Cancer Center |
| Abstract | Setting feeding standards for larval zebrafish (Danio rerio) that maximize growth, survival and reproductive success is challenging. We hypothesized that by increasing nutrient availability through continuous delivery of live food or high-nutrient density pelleted food, larval zebrafish would experience faster growth, better survival and better reproductive success. Gemma Micro 75 pelleted diet and live type L rotifers (Brachionus plicatilis), were compared in 3 feeding regimens starting at 9 days post-fertilization (dpf): bolus feeding of live diet (BL), continuous feeding of live diet (CL), and pelleted diet (PD). Animals in the PD and CL groups were longer than the BL group at 4-5 weeks post fertilization with the PD group also being greater in height than both the CL and BL groups. There was no significant difference in weight between any of the 3 groups. This suggest that the both the continuous live rotifer system and pelleted diet increase growth rates of juvenile zebrafish compared to standard feeding with live rotifer boluses. There were also no significant differences noted in fecundity parameters or sex distribution between the 3 feeding groups indicating that all feeding methods successfully promote a useful sex distribution while maintaining reproductive capability. In addition, we quantified the equipment, consumable and labor costs associated with these methods, compared to providing intermittent boluses of live feed and found that both the CL and PD regimens are attractive alternatives for nursery care that reduce labor as well as costs. The CL and PD regimens promoted growth, survival and reproductive success when compared with the standard live diet boluses indicating that both the CL and PD diets could serve as adequate replacement feeding methods for rearing larval and juvenile zebrafish. |
| Keywords for abstract: | zebrafish<br>zebrafish husbandry<br>zebrafish feeding<br>feeding larval zebrafish<br>rearing larval zebrafish |

# EAR - 6

| | |
|---|---|
| Title of abstract: | **NOVEL ECOSYSTEM HEALTH AND WELFARE APPROACH TO ASSESSING SUSTAINABILITY OF WILD COLLECTION FOR PUBLIC AQUARIUMS** |
| Authors | B. Fischer, T. Wittum, and M. Flint |
| Abstract | Zoos and aquariums play a vital role in the conservation, education, and scientific advancement of species and ecosystems represented within their institutions. Many advances over the last forty years have led to reintroduction programs and reduction of collection from the wild. However, due to challenges of husbandry requirements, many marine fishes are annually sourced from the wild for aquariums. Although attitudes and industry have shifted, impacts of refined practices on globally stressed marine environments remains to be elucidated. The sustainability of wild collection of marine species can be measured using ecosystem health assessments of collection sites. Objectives of this study include: 1) assessment of ecosystem health of sites using chemical, biological, and physical indicators; 2) evaluation of welfare of species collected upon arrival at aquarium and then reevaluation annually for determination of longevity and frequency of demand for collection; and 3) industry level determination of proportion of animals within the Association of Zoos and Aquariums' (AZA) member institutions which were wild-sourced, aquarium bred or commercially acquired through survey distribution. Methodology is divided into three sections: 1) ecosystem health assessments of collection sites using water quality parameters, repeated surveying and sampling, and complete health exams of representative wild species; 2) welfare and longevity evaluation of species acquired for aquariums based on the Five Domains Model; and 3) proportion of origin survey distribution to institutions using Qualtrics software. To our knowledge, this study will be the first of its kind to demonstrate ecosystem impact of wild collection for AZA aquaria. Completion of this study will help to fill this important gap within the literature and promote sustainability within institutions. An ecosystem-based approach to measure sustainability of wild collection is critical for a healthy, functioning, biological community. Through this study, we hope to influence ecosystem health assessments at collection sites in the future. |
| Keywords for abstract: | Animal welfare<br>Aquarium<br>Ecosystem Health<br>Fish<br>Marine<br>Sustainability |

# EAR - 7

| | |
|---|---|
| Title of abstract: | **ASSESSING THE RISK FACTORS ASSOCIATED WITH PRESENCE OF INFLUENZA A VIRUS IN EXHIBITION SWINE AT COUNTY FAIRS.** |
| Authors | J. Greenberg, D. S. McBride, A. S. Bowman. Department of Veterinary Preventive Medicine |
| Abstract | Influenza A virus (IAV) infections amongst the swine population have been commonly reported in association with county fairs where many pigs are brought together to be shown. The numerous amounts of swine and humans present at the fairs, presents a public health risk for not only intra-species transmission but also inter-species transmission of IAV. We investigated risk factors that may contribute to the presence and transmission of IAV in swine at county fairs from 2013-2019. The presence of IAV at a fair was determined by the PCR testing using nasal swab and snout wipes samples at 633 individual fair events in the United States. Chi square tests were used to test the association of potential risk factors with IAV status of fairs. We found that whether the fair had a breeding show in addition to a market swine show (p=0.000), if the fair held an open show in addition to the junior show (p=0.004), if pigs were removed due to illness prior to sampling (p=0.002), if pigs showed any signs of respiratory disease at the time of sampling (p=0.000), and if the fair had a primary tagin prior to the show (p=0.031) were significantly associated with the presence of IAV. Furthermore, it was found using Kruskal-Wallis tests that factors such as whether pigs were removed prior to show due to illness (p=0.0195) and if pigs showed signs of respiratory disease (p=0.0001) have significantly affected the prevalence of IAV among positive fairs. These findings can assist in improving protocols in efforts to decrease the presence and prevalence of IAV in swine at county fairs amongst the swine population. This can also help improve public health associated with this variant IAV at agricultural fairs. |
| Keywords for abstract: | Swine<br>Influenza A virus<br>Epidemiology<br>County Fairs |

# EAR - 8

| | |
|---|---|
| Title of abstract: | **MOLECULAR AND SEROLOGIC SURVEYS OF SHELTER DOGS FOR TICK-BORNE DISEASE IN OHIO** |
| Authors | J. Henning, J. O’Quin, C. Shockling, R. Pesapane<br>College of Veterinary Medicine, The Ohio State University, Columbus, OH (Henning)<br>College of Veterinary Medicine, Department of Veterinary Preventative Medicine, The Ohio State University, Columbus, OH (O’Quin, Pesapane) Gigis’s Shelter for Dogs, Columbus, Ohio (Shockling) |
| Abstract | Tick-borne disease (TBD) in domestic dogs is on the rise in the United States. Determining the prevalence of canine infection, exposure, or coexposure, to Anaplasma spp., Ehrlichia spp., spotted fever group rickettsiae, and Borrelia burgdorferi is of great importance to veterinary medicine and public health. Due to their increased environmental exposure risks, shelter dogs can be effective sentinel animals for TBD risk and geographic distribution. This study assessed infection prevalence among 26 shelter dogs from southern Ohio using molecular and/or serological assays. A total of 65 ticks representing four tick species were collected (range 1-16). Serology was performed on 26 dogs, 14 of which were seropositive (53%), including three that did not have an active tick infestation. Eight dogs were seropositive for multiple TBD (32%). Only one seropositive dog had related clinical symptoms and one additional dog had hematological results suggestive of illness. Real-time PCR was performed on blood from 24 dogs and 64 ticks to determine the prevalence of active infection. No dogs were PCR-positive, but ticks were positive for B. burgdorferi, A. phagocytophilum, and spotted fever group rickettsiae. Our results underscore the emerging threat of TBD in Ohio and highlight the need for routine screening of dogs even in absence of observed ticks. With the relatively recent invasion of the blacklegged tick (Ixodes scapularis) in Ohio, the prevalence and distribution of TBD in canines in Ohio is an important step in mitigating health complications for canines as well as humans. Further this study identified the first evidence of Asian Longhorned tick (Haemaphysalis longicrnis) invasion in Ohio, highlighting the importance of multi species tick surveillance programs and the role of veterinarians on the front lines of emerging disease identification and control. |
| Keywords for abstract: | Tick-Borne<br>Asian Longhorned<br>Shelter dogs<br>Canine infection |

# EAR - 9

| | |
|---|---|
| Title of abstract: | **ENVIRONMENTAL AND GENETIC EFFECTS ON EMBRYOLOGIC DEVELOPMENT OF THE AMERICAN ALLIGATOR (*ALLIGATOR MISSISSIPPIENSIS*)** |
| Authors | D. Hutchinson, J. Flint, M. Flint |
| Abstract | “A is for alligator.” a phrase taught in grade schools across the nation, and although many people could recognize an alligator, information about the growth and development of *A. mississippiensis* has yet to be discovered. As a multi-million dollar enterprise, alligator farms aim to rear large alligators with blemish free hides as these animals are highly sought after in the luxury leather market. Many methods of environmental control are currently used during alligator incubation to increase animal size and decrease unwanted scaring, with genetics now under consideration as well. Interestingly, alligators in Louisiana (LA) are known for their large size, whereas alligators in Florida (FL) are smaller but known for their hide quality. Whether these differences are related to environmental factors or genetics has yet to be studied. It is concluded from past studies that environmental exposures during embryonic development influence the presence of umbilical scaring and animal size. The aim of this study is to evaluate genetic and environmental effects on umbilical scaring and size of animals from both LA and FL. To test this, 12 incubators were set up with 6 containing eggs from LA and 6 containing eggs from FL. Three incubators from each state were provided supplemental oxygen increasing atmospheric oxygen concentration from 20.9% to 27% to determine the effects of oxygen on embryo growth and umbilical scarring prevalence. Umbilical scarring were scored by an experienced assessor at 12 weeks post hatch. Results from this study suggest that supplemental oxygen had no influence on umbilical scars, but decreased incubation time and trended towards larger animals. Umbilical scaring differed between clutches and between states suggesting that genetics may play a role in scar development. |
| Keywords for abstract: | Alligator<br>Umbilical Scar<br>Environment<br>Genetics<br>Oxygen |

# EAR - 10

| | |
|---|---|
| Title of abstract: | **ENVIRONMENTAL SOURCES OF LYMPH NODE INFECTION WITH NON-TYPHOIDAL *SALMONELLA* IN VEAL CALVES** |
| Authors | S. Locke[1], N. Aulik[2], D. Sockett[2], R. Meyer[2], J. Pempek[1], R. Portillo-Gonzalez[1], G. Habing[1]<br>[1]The Ohio State University College of Veterinary Medicine, Department of Veterinary Preventive Medicine, Columbus, Ohio,<br>[2]Wisconsin Veterinary Diagnostic Laboratory, Madison, Wisconsin. |
| Abstract | The inclusion of peripheral lymph node (LN) tissue in ground beef contributes to contamination and foodborne transmission of non-typhoidal *Salmonella* (NTS). However, the source and timing of LN infections in cattle are unclear. Previously, our lab recovered multi-drug resistant NTS serovars in the LN tissue of 20-week old veal calves, despite a low prevalence in on-farm samples, suggesting other exposures were responsible for infections. Therefore, the objective of this prospective cohort study was to assess the prevalence and strain types of NTS at additional points in veal production. We hypothesized that NTS strains present in LNs would be indistinguishable from strains present in trailer or lairage environments. Ten cohorts of roughly 82 calves each were enrolled between November 2018 and October 2019. Environmental swabs were taken in the source barn (n=6), livestock trailer used to haul calves to the harvest facility (n=8), and harvest facility holding pens (n=8). Trailer and pen samples were collected before and after calf entry. We collected mesenteric LNs from 35 calves and pooled prefemoral LNs from 25 calves per cohort. Sample enrichment, culture, and analysis were conducted by Wisconsin Veterinary Diagnostic Laboratory. In general, environments were highly contaminated with NTS isolated from 73.8% (59/80) of trailer and 92.5% (74/80) of holding pen samples. NTS was confirmed in 29.7% (98/330) of mesenteric LNs and in the prefemoral LNs of three cohorts. NTS prevalence in LNs was variable between cohorts, ranging from 0% to 80%. In four cohorts matching serovars (Agona, Muenster, Give) were recovered from trailer and pen environments and calf LNs. Whole genome sequencing of the matching serovars confirmed lymph node strains were indistinguishable from trailer or holding pen strains within the same cohort, suggesting that mitigation of these exposures could be used to reduce the transmission of NTS through ground beef. |
| Keywords for abstract: | Salmonella<br>Lymph Nodes<br>Veal Calves |

# EAR - 11

| | |
|---|---|
| Title of abstract: | **GENOMIC EVIDENCE FOR SEQUESTRATION OF INFLUENZA A VIRUS LINEAGES IN SEA DUCK HOST SPECIES** |
| Authors | D.S. McBride1, S.E. Lauterbach1, Y.T. Li2, G.J.D. Smith2, M.L. Killian3, J.M. Nolting1, Y.C.F. Su2 and A.S. Bowman1<br>1. Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, OH 43210, USA.<br>2. Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore 169857, Singapore.<br>3. Diagnostic Virology Laboratory, National Veterinary Services Laboratories, APHIS, USDA, 1920 Dayton Avenue, Ames, IA 50010, USA. |
| Abstract | Wild birds are considered the natural reservoir of influenza A viruses (IAVs) making them critical for IAV surveillance efforts. While sea ducks have played a role in novel IAV emergence events that threatened food security and public health, very few surveillance samples have been collected from sea duck hosts. From 2014–2018, we conducted surveillance focused in the Mississippi flyway, USA at locations where sea duck harvest has been relatively successful compared to our other sampling locations. Our surveillance yielded 1662 samples from sea ducks, from which we recovered 77 IAV isolates. Our analyses identified persistence of sea duck specific IAV lineages across multiple years. We also recovered sea duck origin IAVs containing an H4 gene highly divergent from the majority of North American H4-HA with clade node age of over 65 years. Identification of IAVs with long branch lengths is indicative of substantial genomic change consistent with persistence without detection by surveillance efforts. Sea ducks play a role in the movement and long-term persistence of IAVs and are likely harboring more undetected IAV diversity. Sea ducks should be a point of emphasis for future North American wild bird IAV surveillance efforts. |
| Keywords for abstract: | influenza A virus<br>ducks<br>birds<br>genomics<br>prevalence<br>United States<br>Great Lakes region |

# EAR - 12

| | |
|---|---|
| Title of abstract: | **ASSOCIATION OF PREPARTUM LYING TIME WITH COLOSTRUM IMMUNOGLOBULINS AND CORTISOL CONCENTRATIONS AT CALVING AND MILK YIELD IN HOLSTEIN DAIRY COWS** |
| Authors | B.T. Menichetti, A. Garcia-Guerra, J. Lakritz, W.P. Weiss, J.S. Velez, H. Bothe, D. Merchan, and G.M. Schuenemann<br>Deps. Of Veterinary Preventive Medicine, Veterinary Clinical Sciences, Animal Sciences and Aurora Organic Dairy |
| Abstract | The objective was to assess the association of the coefficient of variation of lying time (CV of LT) within 7 d prior to parturition (dpp) with colostrum immunoglobulin G (IgG), cortisol concentrations at calving, and milk yield at first DHIA test in Holstein dairy cows. Pregnant cows (n=292) were enrolled at 35±3 dpp and fitted with an electronic data logger (IceQube, IceRobotics, Edinburgh, UK) to assess their LT. The within cow CV of LT was computed by dividing the standard deviation of LT over the mean for the last 7 dpp and reposted as an absolute ratio. Cows were then classified into 1 of 3 groups based on their CV of LT using the 50th (0.13) and 95th (0.24) percentile: <0.13 (n=154), from 0.13 to 0.24 (n=125), and ≥0.25 (n=13). Colostrum samples were collected within 1 h following parturition. Data were analyzed using MIXED or CORR procedures of SAS (SAS Institute Inc., Cary, NC). The CV of LT within 7 dpp was significantly associated (P<0.05) with colostrum IgG concentrations and milk yield at first DHI test but was not associated with colostral cortisol at calving (P=0.26). Cows with a CV of LT of ≥0.25 (116 g/L) within 7 dpp had 43 g/L less colostrum IgG concentrations at calving compared with cows having a CV of LT of <0.13 (159 g/L) or from 0.13 to 0.24 (157 g/L; P=0.006). Cows having a CV of LT ≥0.25 (31.9 kg/d) within 7 dpp had 5.8 kg/d less milk yield compared with cows having a CV of LT <0.13 (37.7 kg/d) or from 0.13 to 0.24 (37.6 kg/d; P=0.03). These findings suggest that prepartum pregnant cows with inconsistent LT within the last 7 dpp, defined as CV of LT ≥0.25, was detrimental for colostrum quality at calving and milk yield in early lactation. |
| Keywords for abstract: | lying time consistency<br>immunoglobulins<br>dairy cattle |

# EAR - 13

| | |
|---|---|
| Title of abstract: | **PREVALENCE OF BACTEREMIA IN CLINICALLY HEALTHY DAIRY CALVES** |
| Authors | M. Moran, K. Loewen, D. Diaz-Campos, J. van Balen, and G. Habing. Depts. of Veterinary Preventive Medicine and Veterinary Clinical Sciences |
| Abstract | Diarrhea is a leading cause of death in pre-weaned dairy calves, which is often a result of intermittent bouts of septicemia. In preliminary research focusing on heifer calves with diarrhea, 9.3% (10/108) of diarrheic calves and 14.8% (4/27) of clinically healthy calves were bacteremic. This finding may suggest that clinically healthy calves experience intermittent bouts of bacteremia due to high intestinal permeability early in life. Currently, there is no available research on the prevalence of bacteremia in healthy calves. The objective of this study is to determine if clinically healthy neonatal calves experience bouts of bacteremia. We hypothesized that younger calves would be more likely to experience bouts of bacteremia due to higher intestinal permeability when compared to older calves. Healthy calves were enrolled based on health scoring criteria including temperature, dehydration, navel score, fecal score, and depression. Aseptic jugular and saphenous venous blood samples were collected from the same calves at 2-7 days of age and again at 21-27 days of age. Isolates from positive blood culture bottles were evaluated with mass spectrometry to determine bacterial species. Our preliminary results show that the prevalence of bacteremia in healthy calves at 2-7 days of age is 22.2% (10/45) and at 21-27 days of age is 14.3% (5/35). We continue to expect that there will be a higher prevalence of bacteremia when calves are at 2-7 days of age when compared to 21-27 days of age, due to a higher likelihood of intestinal permeability. The significance of this potential outcome can lead to novel approaches for treatment and prevention of unrecognized bouts of bacteremia in calves. |
| Keywords for abstract: | Calf<br>Neonate<br>Bacteremia<br>Blood culture |

# EAR - 14

| | |
|---|---|
| Title of abstract: | **LANDSCAPE ECOLOGY AS AN APPROACH TO UNDERSTANDING ANTIMICROBIAL RESISTANCE ACROSS COMMUNITIES** |
| Authors | M. Overcast, S. Mielke, D. Jackson-Smith, C. Brock, S. Matthews, R. Garabed |
| Abstract | Having risen as a global concern, characterization of antimicrobial resistant (AMR) bacteria within different farming landscapes is essential to recognize and mitigate AMR associated global health risks (1). Barn type, housing density, temperature, pH, soil carbon, and proximity to municipal and agricultural run-off sites are environmental and spatial factors shown to impact environmental AMR prevalence (2, 3). Landscape ecology has been posed as a method to dissect the complexity of AMR (4), as it allows us to characterize various environmental relationships. The confluence of variables impacting AMR necessitates interpretation using tools with more appropriate scope and specificity in addition to traditional statistical methods.<br>Our study targets beef and dairy cattle farms from three counties across Ohio with varying landscape and production styles. County 1 represents homogeneous large operations; county 2 represents homogeneous small operations; and county 3 represents heterogeneous operations of different sizes. Using publically available data on land-use and simulated farm locations, we made different summary measures of local landscape heterogeneity. From each site, we compare proportions of *Enterobacteriaceae*in cattle and deer feces resistant to beta-lactams and fluoroquinolones to these measures of diversity. We also assessed the resistance data for spatial clustering using Ripley's K function.<br>We predicted that antimicrobial resistance would be higher in counties of low spatial heterogeneity and farms near other farms of similar types would have more resistant bacteria.<br>Our study team is still gathering field data, but preliminary analysis will be presented. |
| Keywords for abstract: | Antimicrobial Resistance<br>Infectious Disease Epidemiology<br>Landscape Ecology<br>ArcGIS<br>Remote Sensed Data |

# EAR - 15

| | |
|---|---|
| Title of abstract: | **INTER-OBSERVER AGREEMENT BETWEEN VETERINARIANS AND FARM-CARETAKERS: A HIERARCHICAL SURVEY OF ANTIMICROBIAL USE** |
| Authors | R. Portillo-Gonzalez,[1]; J. A. Pempek,[1]; S. Locke[1]; A. M. Dietsch,[2]; R. V. V. Pereira,[3]; G. G. Habing,[1] |
| Abstract | Antimicrobial use in food-producing animals may contribute to the development of drug-resistant bacterial infections in humans. Veterinarians prescribe and dispense antimicrobials, but farm caretakers are responsible for judging disease severity and initiating on-farm treatments. The objective of this study was to estimate the level of agreement on initiating on-farm antimicrobial treatment between farm caretakers and the respective farm veterinarian at different levels of disease severity. This was a cross-sectional study that used hierarchical surveys and clinical case vignettes to collect information from farm caretakers and veterinarians on their dairy farm clients. The survey included vignettes of mild, moderate, and severe cases of metritis, lameness, and mastitis. In 2019, we received responses from 35 veterinarians and 66 farm-matched caretakers in Ohio. Cohen's Kappa coefficients (k) were applied to the matching farm caretakers and farm veterinarian responses to evaluate the level of agreement for treating hypothetical but routine cases with antimicrobials. The results suggested that little agreement was reached on cases that require local or systemic antimicrobial therapy for severe (k= -0.010) and moderate (k= -0.053) cases of metritis. Additionally, there was only slight agreement on antimicrobial use between veterinarians and farm caretakers on local (k= 0.016, 0.017) and systemic (k= 0.019, 0.052) moderate digital dermatitis and mild interdigital pododermatitis respectively. Also, slight agreement between veterinarians and farm caretakers was reached on intramammary antimicrobial on mild (k= 0.055) and severe (k= 0.026) cases of mastitis. This study demonstrates that the level of agreement on initiating on-farm antimicrobial treatment at different levels of disease severity between veterinarians and farm caretakers is weak. Therefore, attention should be paid to implement on-farm educational campaigns to improve the criteria for initiation of on-farm antimicrobial treatment therapies. |
| Keywords for abstract: | Antimicrobial<br>hierarchical survey<br>dairy cattle<br>antimicrobial use |

# EAR - 16

| | |
|---|---|
| Title of abstract: | **RISK OF INFECTIOUS DISEASE IN UNIVERSITY DAYCARE CENTERS** |
| Authors | M. Salerno, R. Garabed. Department of Veterinary Preventive Medicine. |
| Abstract | The aim of this study was to better understand the relationship between daycare environments and infant disease exposure. An extensive literature review was performed, and retrospective analysis of exposure reports and disease events were collected and analyzed from three daycare rooms at The Ohio State University. A total of 33 exposure notices and 189 total fever or diarrheal disease events were observed. Day care census data was also collected from January 1, 2018 to July 14, 2020. 20 exposure notices and 131 total fever or diarrheal disease events were observed between this time. Results demonstrated a consistent increase in disease reporting in January, with lower numbers being reported in the summer months. The most common diseases reported from exposure notices were conjunctivitis (6) followed closely by hand-foot-and-mouth disease, influenza, and roseola (5 each). In the future, these findings will be supplemented with longitudinal stool collection and microbiome analysis, guardian surveys, and environmental sampling from multiple daycare locations at The Ohio State University. |
| Keywords for abstract: | Daycare<br>Exposure<br>Disease<br>Infant |

# EAR - 17

| | |
|---|---|
| Title of abstract: | **CULTURALLY APPROPRIATE TICK BITE PREVENTION RECOMMENDATIONS FOR AMISH COMMUNITIES** |
| Authors | L. Vesprani , R. Pesapane Department of Preventive Medicine (Vesprani, Pesapane), The Ohio State College of Veterinary Medicine; School of Environment and Natural Resources, College of Food, Agriculture, and Environmental Sciences (Pesapane), The Ohio State University, Columbus, OH |
| Abstract | In 2010, blacklegged ticks (Ixodes scapularis), the primary vector for Lyme disease in the eastern United States, were determined to be established in Tiverton Township, Ohio, and in subsequent years, there has been an increase in the reported number of cases of Lyme disease and other tick-borne zoonoses in Ohio. Tiverton Township is in Coshocton County, one of several counties in Ohio that are home to over 76,000 Amish members. The Amish community are a high-risk group due to their heavy use of outdoor spaces for recreation, farming, and other outdoor occupations. Due to the large population of Amish in Ohio and their increased risk, culturally appropriate tick bite prevention methods are important to help protect this community. After reviewing the CDC's "Tick Management Handbook" for recommended tick bite and Lyme disease prevention methods, and literature on Amish history and culture, we compiled prevention methods understood to align with Amish cultural practices. These recommendations will be reviewed by Amish families in Ohio to assure their cultural acceptability within Amish communities. While some methods such as tick checks, landscape modifications, and discouraging rodent activity were deemed culturally appropriate other common methods such as deer management, tick habitat avoidance, and protective clothing were not. In particular, Amish are unlikely to use methods requiring synthetic chemicals such as repellents and acaricides but may be receptive to the use of EPA-approved, plant-based products. Our culturally appropriate tick bite prevention methods, in conjunction with tick education, may increase compliance and reduce tick-borne disease among Amish communities. |
| Keywords for abstract: | Lyme Disease<br>Amish<br>ticks<br>prevention<br>culturally appropriate |

# EAR - 18

| | |
|---|---|
| Title of abstract: | **MODELING AVIAN INFLUENZA VIRUS TRANSMISSION DYNAMICS IN MIGRATORY WATERFOWL TO ASSESS RISK TO PIG POPULATIONS** |
| Authors | H. L. Walker, A. S. Bowman, A. G. Arruda, L. W. Pomeroy. (HLW, ASB, AGA) Department of Veterinary Preventative Medicine; (LWP) Division of Environmental Health Sciences, College of Public Health and Translational Data Analytics Institute |
| Abstract | Infectious avian influenza has the potential to influence more than just bird health; this disease can have rippling effects on biodiversity, livestock, public health, and create significant economic losses worldwide. Migratory waterfowl (MWF) are the wildlife reservoir for avian influenza virus and the source of spillover events that can infect other wildlife and susceptible livestock. However, influenza dynamics in MFW remain unquantified and routes of transmission to livestock remain unidentified. Here, we use a long-term dataset that describes influenza seroprevalence in avian wildlife in Ohio from 1976 to 2015 to quantify transmission among mallards (*Anas platyrhynchos*) and other MWF. We also quantify the risk of transmission from avian wildlife to swine. We fit age-structured catalytic and reverse catalytic transmission models to serological data to estimate the time-varying force of infection and the rate of waning immunity. The models indicated varying transmission rates based on the sample year, sample month, and mallard age (mature or immature). Additionally, they suggest that immunity can wain, allowing for possibility for re-infection of avian influenza within the same year. From this, we simulated a model to determine the probability of swine influenza infection from MFW during the fall and validated our final model with data that describes swine influenza infections from 2015 to 2019. Our computational tools, calibrated with timeseries prevalence data, quantify reservoir dynamics of influenza and identify how migration contributes to cross-species transmission. This work can improve disease surveillance in both bird and swine populations and contribute to more accurate disease risk assessment among swine production. |
| Keywords for abstract: | Avian influenza<br>Swine influenza<br>Disease modeling<br>Disease transmission |

# EAR - 19

| | |
|---|---|
| Title of abstract: | **RISK FACTORS OF GASTROINTESTINAL PARASITES IN CENTRAL OHIO DOGS, A RETROSPECTIVE STUDY** |
| Authors | H. Yee, A. Arruda, A. Rudinsky, C. Bremer, C. Iazbik, L. Millward, and A. Marsh. Depts. Of Veterinary Preventive Medicine (Yee, Arruda, Bremer, Marsh), Department of Veterinary Clinical Sciences (Rudinsky, Millward), Veterinary Medical Center (Iazbik) |
| Abstract | Infections with endoparasites, especially gastrointestinal helminths, are a common finding in client-owned dogs. The Community Practice (CP) section at the Ohio State University College of Veterinary Medicine (OSU-CVM) follows Companion Animal Parasite Council (CAPC), American Animal Hospital Association (AAHA), and American Veterinary Medical Association (AVMA) guidelines for parasitology by recommending annual fecal analyses of dogs and prescribing year-round, broad-spectrum parasite preventatives. There is increasing interest in determining if drug resistant helminths are present in canine populations as there are reports of greyhounds with drug resistant hookworms. Our 2019 study retrospectively analyzed the fecal analysis results from varying dog breeds. We report 891 total canine fecal samples submitted during 2019 from 681 dogs of varying breeds. Of the 891 canine fecal samples, 190 (21.32%) of these samples had a positive fecal analysis for gastrointestinal parasites. We included in this analysis 130 fecal samples derived from 63 greyhounds. To determine if COVID-associated hospital restrictions impacted the fecal examinations performed, data from January to July, 2020, was compared to the same period in 2019. The age of dog, time of year, reproductive status, purpose of fecal examination, gastrointestinal signs, and type of parasite preventives were assessed as potential risk factors of gastrointestinal parasite infection in dogs. Identifying such risk factors in dogs will guide veterinarians to advise annual fecal examinations more strongly to clients with high risk dogs or when routine health visits are postponed for an extended period. |
| Keywords for abstract: | canine<br>gastrointestinal parasites<br>prevalence<br>epidemiology |

# EAR - 20

| | |
|---|---|
| Title of abstract: | **PHYSIOLOGICAL RESPONSE TO WATER CONTAMINATION BY STRIP MINED LANDS AS MEASURED BY LEUKOGRAMS IN TWO SPECIES OF FISH** |
| Authors | C. Theile, J. Heinz, and M. Flint Department of Veterinary Preventive Medicine, College of Veterinary Medicine |
| Abstract | Coal mining has previously been shown to pollute surrounding water systems by leaching in metal contaminants that impact water quality and build up in the tissues of aquatic animals. Currently a study is underway comparing the leukograms of fish caught in two water sheds. The first is located within The Wilds, currently a conservation area in Cumberland, Ohio with a previous history of land use for strip mining, while the second, a control site, is located in Port Clinton, Ohio. Two species of fish have been selected for this study: bluegill (Lepomis macrochirus) and channel catfish (Ictalurus punctatus). This is because of the contrasting niches they inhabit and their differing lifespans. The fish have been collected by rod and reel, weighted, measured, euthanized, and necropsied. Additionally, blood was drawn for smears and age was being determined by otolith analysis. White blood cell counts have been determined by manually reading the blood smears and compared between both sites, while controlling for possible variations in fish age. This study will hopefully demonstrate how metal contaminants remaining from past mining may influence the immune systems of aquatic animals within the affected region. |
| Keywords for abstract: | Aquatic medicine<br>Wildlife medicine<br>Strip mining<br>Leukograms<br>Water contamination |

# EAR - 21

| | |
|---|---|
| Title of abstract: | **CHARACTERIZING THE MICROBIOME OF ZOO HOUSED AFRICAN (AFRICANA LOXODONTA) AND ASIAN (ELEPHAS MAXIMUS) ELEPHANTS** |
| Authors | J. Bautista, A. London, and P. Dennis. Dept of Veterinary Preventative Medicine and Cleveland Metroparks Zoo |
| Abstract | The microbiome is a community of intrinsic microbes that includes viruses, fungi, bacteria, and other protozoa. These microbe communities are found on and inside the body, with the largest microbiome community inhabiting the digestive tract of its host. The gut microbiome is associated with several metabolic processes, including food digestion, vitamin metabolism, and initiating an immune response.<br><br>To date, there is deficient data outlying the composition of the gut microbial community of elephants under human care. The goal of our project is to characterize the gut microbiome of the Asian elephant (*Elephas maximus*) and the African elephant (*Loxodonta africana*) in relation to diet fed in zoos. Since the gut microbial community is influenced by diet, we expect the gut microbiome to be similar amongst animals offered similar dietary fibers. Furthermore, we are invested in investigating the gut microbiome variability between these species and the possible associated with susceptible to elephant endotheliotropic herpes virus (EEHV), a deadly herpes virus affecting young elephants in human care. Asian elephants are thought to be more susceptible to EEHV infection, though fatal infections are also described in African elephants in zoos. While it is currently unknown whether the gut microbiome influences immunity or susceptibility towards EEHV, comparing the gut microbiome of Asian and African elephants is a first step towards understating a potential influence on EEHV infections. |
| Keywords for abstract: | microbiome<br>African elephant<br>Asian elephant |

# IMMUNOLOGY
# AND
# INFECTIOUS DISEASES

# IMID - 1

| | |
|---|---|
| Title of abstract: | **INVESTIGATING THE EPIGENETIC MODIFICATION LANDSCAPE OF THE HIV-1 RNA GENOME AT THE SINGLE-VIRUS LEVEL** |
| Authors | A.Baek*, G.Lee*, S.Golconda*, O.Zablocki[+], S.Chen*, N.Tirumuru*, W.Lu*, M.Sullivan[+], L.Wu*, and S.Kim* |
| Abstract | Recent studies have shown that HIV-1 genomic RNA (gRNAs) contains different types of epitranscriptomic modifications that have important biological and pathogenic functions in the host. Our understanding of HIV-1 gRNA modifications, however, remains poor because even the state-of-the-art, RNA-modification analysis tools only read short, fragmented RNA around the modification sites. This only allows partial information that lacks both precise base positions of modified nucleotides and ensembles of different modifications over the whole gRNA. Our hypothesis is that epitranscriptomic modification patterns present in full-length HIV-1 gRNAs are not all identical; there are heterogenous populations of HIV-1 gRNAs with distinct modification patterns, that will have differential biological functions during the infection cycle. We have employed Nanopore MinION direct RNA sequencing methods to address the hypothesis. Unlike other sequencing platforms, Oxford Nanopore sequencing can directly read modified nucleotides of native RNA by measuring unique electric signal differences between modified and unmodified RNAs passing through a small protein pore. We mapped epitranscriptomic modifications of full-length HIV-1 gRNA from purified virions by comparing the electric signals of HIV-1 gRNA with those of *in vitro* transcribed HIV-1 RNA. We found several prominent modification sites correlated with $m^6A$ predicted motifs that matched with previous studies. These results were reproducible in three independent experiments. All the major modification sites aligned with $m^6A$ motifs were disappeared when HIV-1 gRNA was treated with a known $m^6A$ modification eraser, fat mass and obesity-associated protein (FTO). Single RNA molecule level analysis revealed that there are heterogeneous populations of HIV-1 gRNA with distinct methylation patterns. The identified sites will be confirmed by several orthogonal assays including mass spectroscopy, positive synthesized RNA oligo sequencing, and bisulfite sequencing. This study will establish an innovative assay to study RNA modifications and reveal novel insights into the biology of epigenetic modification in HIV-1 pathogenesis. |
| Keywords for abstract: | HIV-1<br>RNA $m^6A$ modification<br>Nanopore sequencing<br>direct RNA sequencing |

# IMID - 2

| | |
|---|---|
| Title of abstract: | **RSV GLYCOPROTEINS EXPRESSED IN A VESICULAR STOMATITIS VIRUS VECTOR SYSTEM PROTECT AGAINST RSV INFECTION IN A COTTON RAT MODEL** |
| Authors | K. Brakel, O. Harder, B. Binjawadagi, S. Niewiesk |
| Abstract | Respiratory syncytial virus (RSV) is one of the most important causes of respiratory disease in infants and the elderly. Natural infection does not result in long-term immunity, and there is no licensed vaccine. Vesicular stomatitis virus (VSV) is a commonly used vaccine vector platform against infectious diseases, and has been used as a vector for a licensed Ebola vaccine. In this study, we expressed the unmodified RSV fusion (F) protein, or RSV F protein stabilized in either a pre-fusion or a post-fusion configuration, the attachment (G) protein, as well as the G and F proteins of RSV in combination in a VSV vector. Cotton rats were immunized with these recombinants intranasally or subcutaneously to test their immunogenicity. RSV F stabilized in either a pre-fusion or a post-fusion configuration proved to be poorly immunogenic and protective when compared to unmodified F. RSV G provided partial protection and moderate levels of neutralizing antibody production, both of which improved with intranasal administration compared to subcutaneous inoculation. The most successful vaccine vector was VSV expressing both the G and F proteins after intranasal inoculation. Immunization with this recombinant induced neutralizing antibodies and provided protection from RSV challenge in the upper and lower respiratory tract for 80 days. |
| Keywords for abstract: | Respiratory syncytial virus<br>Cotton rat<br>Vesicular stomatitis virus<br>Vaccine vector |

# IMID - 3

| | |
|---|---|
| Title of abstract: | **THE MOLECULAR PATHOGENESIS OF *EHRLICHIA CHAFFEENSIS*-MEDIATED INTERFERON-GAMMA SIGNALING ABROGATION** |
| Authors | R.C. Chien, M. Lin, Y. Rikihisa. Department of Veterinary Biosciences. |
| Abstract | Human monocytic ehrlichiosis (HME) is an emerging disease caused by infection of *Ehrlichia chaffeensis*, a tick-borne, obligate intracellular bacterium. Host monocytes and macrophages are the primary targets of *E. chaffeensis*. The pathogenesis of HME, specifically host-pathogen interactions and evasion of host immunity, is not fully understood. Interferon-gamma (IFN-γ) is known to activate macrophages via Jak-Stat signal transduction, which is an important immune response against invading pathogens. Previous studies have shown that *Ehrlichia* binding alone blocks Jak-Stat signaling induced by IFN-γ. The study also indicated that a surface protein of *E. chaffeensis* is likely involved in the abrogation of host IFN-γ signaling. However, the bacterial surface protein as well as the interacting host surface molecules remain unknown. Recently, our laboratory identified the entry-triggering protein of *Ehrlichia* (EtpE), an invasin from the bacterial outer membrane, directly binds to the mammalian cell surface DNase X molecule, a GPI-anchored protein, which triggers internalization of *E. chaffeensis*. Thus, our hypothesis is that the EtpE-DNase X interaction is involved directly or indirectly in the *E. chaffeensis*-mediated inhibition of IFN-γ signaling. To test this hypothesis, bone marrow-derived macrophages (BMDMs) from both wild-type and DNase X knockout mice were incubated with *E. chaffeensis* followed by IFN-γ treatment. The BMDMs were subject to Western-blot analysis for Stat1 phosphorylation to evaluate IFN-γ signaling. Understanding the IFN-γ-resistant mechanisms of *E. chaffeensis* help developing more effective therapy for HME. |
| Keywords for abstract: | *Ehrlichia chaffeensis*<br>Interferon-γ<br>STAT1<br>DNase X<br>EtpE<br>Monocyte/macrophage |

# IMID - 4

| | |
|---|---|
| Title of abstract: | **INFLUENZA A VIRUS EFFECT ON ALVEOLAR FLUID CLEARANCE AND CDP-CHOLINE AS POTENTIAL TREATMENT FOR ARDS IN MICE.** |
| Authors | H. El Musa, I. Davis, L. Rosas, L. Joseph, A. Nelson, LM. Doolittle<br>Department of Veterinary Biosciences |
| Abstract | The bronchoalveolar epithelium clears excess fluid by an active, ATP-dependent $Na^+$ transport process, which can be measured across the whole lung as alveolar fluid clearance (AFC). Maintenance of AFC is important to alveolar gas exchange. Impaired AFC has been shown to correlate with worse outcomes in patients who develop Acute Respiratory Distress Syndrome (ARDS). We have shown that ARDS development in mice infected with influenza A virus (IAV) is associated with impaired AFC. IAV infection also reduces mitochondrial function in alveolar type II (ATII) cells and inhibits synthesis of the liponucleotide CDP-choline (CDP-CHO), which is a precursor for the phospholipid phosphatidylcholine. We have shown that treatment of IAV-infected mice with CDP-CHO significantly attenuates IAV-induced hypoxemia and improves mitochondrial function in ATII cells. Since AFC is highly dependent on ATP, and mitochondrial function is dependent on normal phospholipid metabolism, we hypothesized that IAV-infected mice treated with CDP-CHO will have increased AFC when compared to untreated infected mice. To test this hypothesis, we mock-infected or infected C57BL/6 mice intranasally with 10,000 pfu/mouse influenza A/WSN/33. At 6 days post-infection (dpi), mice were anesthetized and intubated to measure AFC. 300µL of 5% BSA/saline solution was instilled into the lungs via the tracheal cannula, followed by 200µL of air. Mice were then mechanically ventilated on 100% $O_2$ for 30 minutes, with a tidal volume of 0.2 ml and 18cm$H_2O$ PEEP. Following ventilation, fluid was aspirated back from the lungs. Protein concentration was quantified with a BCA assay. AFC rate was calculated from the ratio of initial (instillate) to final protein concentration. |
| Keywords for abstract: | Influenza A virus<br>Alveolar Fluid Clearance<br>ARDS<br>ATII |

# IMID - 5

| | |
|---|---|
| Title of abstract: | **MONOCYTES DYSREGULATION DURING COVID-19 MAY INCREASES CARDIOVASCULAR RISK** |
| Authors | M Gunasena[1], Y Wijewantha[1], E Bowman[1], J Gabriel[1], A Kumar[1], A Kettelhut[1], A Ruwanpathirana[1], K Weragalaarachchi[1], D Kasturiratna[2], A Vilgelm[1], J Bednash[1], T Demberg[3], N Funderburg[1], N Liyanage[1]<br>[1]The Ohio State University, Columbus, OH, USA, [2]Northern Kentucky University, Highland Heights, KY, USA, [3]Marker Therapeutics, Inc, Houston, TX |
| Abstract | Covid-19, caused by SARS-CoV-2 infection, has resulted in millions of deaths leading to a global pandemic. An effective and appropriate immune response is essential to control and eliminate viral infections whereas dysregulated immune responses may lead to immunopathology in viral infections. SARS-CoV-2 can lead to excessive immune activation, inflammation and multi-organ damage. Clinical data showed that COVID-19 may promote the development of cardiovascular disorders. However, the exact mechanism associated with CVD risk in COVID-19 patients is currently unknown. Monocytes play a major role against many infections while it is also associated with development of CVDs. In this study we investigated the role of monocytes in severe SARS-CoV-2 infection associated CVDs. We studied functional and phenotypic changes in monocyte subsets in whole blood and plasma biomarkers of cardiovascular disease using flowcytometry and immune biomarker assays, in healthy donors (n=17), severe-COVID-19 patients (n=20) admitted to the ICU at OSU medical center and COVID-19 recovered individuals after 2-3 months of the infection (n=30). Multiple group comparisons were analyzed by running both parametric (ANOVA) and non-parametric (Kruskal–Wallis) statistical tests with Dunn’s and Tukey’s post hoc tests. Multiple correlation analysis was performed by computing Spearman’s coefficients. Our data showed an elevation of intermediate monocytes and MCP-1, one of the most important chemokines that regulates migration and infiltration of monocytes to the subendothelial space, where they may become foam cells. We found a significant decrease in CCR7+ and CXCR3+ monocytes in the blood indicating possible migration of those cells to the site of infection. Spearman correlation network analysis showed a strong correlation between intermediate monocytes and plasma cardimetabolic biomarkers such as FABP-4, C-reactive protein, soluble CD14 and LPS binding protein in ICU patients. Our data show for the first time, the possible role of monocytes in the development of CVDs in severe COVID-19 patients. |
| Keywords for abstract: | Monocytes<br>Covid-19<br>Cardiovascular risk<br>Biomarkers<br>Flowcytometry |

# IMID - 6

| | |
|---|---|
| Title of abstract: | **NONSTEROIDAL ANTI-INFLAMMATORY DRUGS RESTORE IMMUNE FUNCTION TO RESPIRATORY SYNCYTIAL VIRUS IN GERIATRIC COTTON RATS (*SIGMODON HISPIDUS*)** |
| Authors | O. Harder and S. Niewiesk. Department of Veterinary Biosciences |
| Abstract | Respiratory syncytial virus (RSV) infection is not only a childhood disease, but also a serious health risk for adults and the elderly. RSV is a common cause of viral pneumonia in the elderly. The cotton rat (*Sigmodon hispidus*) is an excellent small animal model for infection with RSV due to its susceptibility to infection and similarities to the pathogenesis in humans. We investigated in cotton rats how age affected viral clearance and immune responses. Our results demonstrated that in geriatric animals, virus grew to similar titers, but was cleared with delayed kinetics, compared to adult animals. After primary infection with RSV, geriatric animals developed, in contrast to adult animals, a very low humoral immune response and were susceptible to secondary RSV infection. In the elderly and geriatric animals, chronic inflammation has been observed to be the cause of many disease conditions. In geriatric cotton rats, treatment with nonsteroidal anti-inflammatory ibuprofen resulted in faster viral clearance and complete protection after immunization, comparable to adult animals. However, humoral immune response was not restored. Cytotoxic T lymphocyte (CTL) responses play a crucial role in viral clearance and therefore the CTL response in the presence of ibuprofen seemed to be restored. Antibody-mediated depletion of CTL in ibuprofen-treated animals reversed treatment benefits, indicating the importance of ibuprofen in restoring CD8 T cell response. It appears that in geriatric animals, the basic immune functions do not act as effectively as in adult animals and that anti-inflammatory therapy may restore effective immune function. |
| Keywords for abstract: | Respiratory Syncytial Virus<br>Virology<br>Immunology<br>Cotton Rat |

# IMID - 7

| | |
|---|---|
| Title of abstract: | **GASTROINTESTINAL DYSBIOSIS CAUSED BY A LACK OF PANETH CELLS PROMOTES DIET-INDUCED OBESITY AND TRAFFICKING OF INFLAMMATORY IMMUNE CELLS INTO ADIPOSE TISSUES** |
| Authors | M.R. Joldrichsen, E. Kim, E. Cormet-Boyaka, and P.N. Boyaka.<br>Department of Veterinary Biosciences |
| Abstract | Paneth cells regulate many aspects of gastrointestinal health through the antimicrobial products and cytokines they produce. Loss or defective Paneth cell function leads to dysbiosis and is one of the causes of Inflammatory Bowel Disease (IBD). The prevalence of obesity is growing in the general population and among recently diagnosed IBD patients, leading to the speculation that obesity increases IBD incidence, but the underlying mechanisms remain to be elucidated. We address whether gastrointestinal dysbiosis caused by a lack of Paneth cells influences obesity. Analysis of their fecal bacterial composition showed that $\text{Sox9}^{\Delta \text{IEC}}$ mice, which lack Paneth cells due to Sox9 gene deletion within the intestinal epithelium, have more Firmicutes bacteria ($p<0.001$) in their feces. These mice were then fed a high fat diet for 13 weeks. When $\text{Sox9}^{\Delta \text{IEC}}$ mice were fed a high-fat diet, they exhibited increased bacterial dysbiosis. Furthermore, intestinal permeability measured by FITC-dextran absorption *in vivo* was increased ($p<0.05$) in $\text{Sox9}^{\Delta \text{IEC}}$ mice. Finally, $\text{Sox9}^{\Delta \text{IEC}}$ mice gained weight faster and ultimately became more obese than the wild-type mice and displayed impaired glucose tolerance ($p<0.0001$) indicating the presence of metabolic disorder. The $\text{Sox9}^{\Delta \text{IEC}}$ mice developed larger abdominal fats, which included increased numbers of inflammatory immune cells such as macrophages ($p<0.05$), neutrophils ($p<0.05$), and T cells ($p<0.05$). Interestingly, B cells were the most increased ($p<0.0001$) immune cell population in abdominal fat tissues. These results suggest a new role for Paneth cells as regulators of diet-induced obesity via their effect on gastrointestinal dysbiosis and immune cell infiltration of omental fat tissues. |
| Keywords for abstract: | Diet-induced obesity<br>Inflammatory Bowel Disease<br>Gastrointestinal dysbiosis<br>Immune cell trafficking |

# IMID - 8

| | |
|---|---|
| Title of abstract: | **A NEW TREATMENT RESISTANCE MECHANISM OF ANTIBODY-BASED T CELL DEPLETION BY FOLLICULAR STRUCTURE IN T-CELL LYMPHOMA AND HIV/AIDS** |
| Authors | S. Kim*, R. Shukla, S. Cressman, A. Kim, A. Tracey, N. Liyanage and S. Kim<br>Depts. Of Veterinary Biosciences and Microbial Infection and Immunity, The Ohio State University, Columbus, OH |
| Abstract | Antibody-based T-cell depletion agents - such as immunotoxins and T-cell depleting antibodies - have been developed to treat various diseases, including T-cell lymphomas, HIV/AIDS, allograft rejection and graft-versus-host disease. 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 B-cell follicles 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 diptheria toxin)-mediated T-cell killing. We found that both anti-CD3e mAb and CD3e-IT are effective and specific in depleting T cells *in vivo*. Remarkably, however, a small number of CXCR5+ T cells survived the treatment. CXCR5+ T cells, including CD4+ T follicular helper cells (TFH), are an important therapeutic target in HIV/AIDS and T-cell lymphoma therapy. CXCR5+ T cells were enriched in both our monkey and mice studies after intensive CD3e-IT treatment. Our immunohistochemistry analysis showed that CD3e-IT efficiently depleted T cells in the T cell zone outside the B follicles, whereas T cells within the follicles 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. Lastly, using CD4/iDTR transgenic mice that expressed Diphtheria toxin receptors on the surface of 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 B-follicles protect their resident CXCR5+ T cells from all these different sizes and types of protein agents. Our findings, therefore, suggest a potentially a new treatment resistance mechanism mediated by the normal lymphoid B-cell follicles against T-cell depletion protein agents. |
| Keywords for abstract: | A new treatment resistance mechanism<br>B-cell follicular structure<br>CXCR5+ T cells<br>CD3e-IT<br>CD3e monoclonal Ab<br>Diphtheria toxin<br>T-cell lymphoma<br>HIV/AIDS |

# IMID - 9

| | |
|---|---|
| Title of abstract: | **MULTI-PRONGED TRANSCRIPTOME ANALYSIS OF HIV-1 EPIGENETIC MODIFICATIONS** |
| Authors | G.Lee[1], A.Baek[1], S.Golconda[1], O.Zablocki[2], S.Chen[1], N.Tirumuru[1], W.Lu[1], M.Sullivan[2], L.Wu[1], and S.Kim[1].<br>[1]Departments of Veterinary Biosciences<br>[2]Departments of Microbiology |
| Abstract | HIV-1 RNA epigenetics has recently become a subject of intense interest in light of the critical roles of epigenetic modification in virus and cell biology. Our group has adapted Nanopore sequencing technology – a new 3rd generation sequencing platform that identifies both nucleotide sequences and epigenetic modifications by direct sequencing of native RNA molecules – to study HIV-1 RNA epigenetic modifications. Here, I introduce a new Nanopore data analysis pipeline that analyzes multiple important biological events simultaneously using a single Nanopore RNA sequencing run data. This pipeline performs four major RNA analyses, including (i) identification of epigenetic modification sites on the full-length HIV-1 RNA genome, (ii) quantification of viral RNA production in cells, (iii) HIV-1 RNA splicing variant analysis, and (iv) cellular gene expression analysis. As a proof-of-concept study, we analyzed how over-expression (OE) or knockout (KO) of three RNA modification genes, including FTO, ALKBH5, and NSUN2, would affect HIV-1 RNA production, viral transcripts regulation, and epigenetic modifications. The OE or KO of FTO, ALKBH5, or NSUN2 in 293T cells resulted in perturbation of a group of host genes specifically involved in "RNA modification" and the total HIV-1 RNA produced in these cells was significantly lower than that in unmodified 293T. The viral transcript splicing patterns in these cells were distinct from one another and the patterns reflected those observed in previous studies. Interestingly, however, the six major modification sites of the HIV-1 RNA genome we identified in WT 293T cells were not affected by OE or KO of these genes, suggesting target-specific modification controls by these genes. This multi-pronged data analysis pipeline enables comprehensive and simultaneous analysis of four key aspects of viral production in host cells using only a single Nanopore sequencing run, potentially replacing the multiple other laboratory experiments that would otherwise be required to produce similar results. |
| Keywords for abstract: | Human immunodeficiency virus<br>Viral epigenetics<br>Direct RNA sequencing<br>Transcriptome analysis<br>RNA modifications |

# IMID - 10

| | |
|---|---|
| Title of abstract: | ***EHRLICHIA* SP. HF OUTER MEMBRANE PROTEINS AS VACCINE CANDIDATES IN A FATAL HUMAN MONOCYTIC EHRLICHIOSIS MOUSE MODEL** |
| Authors | M. Mestres-Villanueva, K. Budachetri, M. Lin, and Y. Rikihisa.<br>Dept. of Veterinary Biosciences |
| Abstract | *Ehrlichia* spp. are emerging tick-borne obligatory intracellular bacteria that cause human monocytic ehrlichiosis (HME), a potentially fatal and severe, influenza-like illness. The only treatment available is the broad-spectrum antibiotic Doxycycline, and there is no vaccine available. *Ehrlichia* lack conventional pathogen-associated molecular patterns (PAMPS), but surface proteins and virulence factors have been identified and their roles in infection have been studied. Entry-triggering protein of *Ehrlichia* (EtpE) is an invasin required for bacterial entry into human cells; the C-terminal (EtpE-C) binds DNase-X for receptor-mediated endocytosis. Outer membrane protein 1B (Omp-1B/P28) is an immunodominant outer membrane protein and porin required for intracellular survival. *Ehrlichia* spp. possess Type IV secretion system (T4SS) and VirB2 proteins function as major pilus subunits, thus playing an important role in the secretion of T4S effectors into the host cell cytoplasm. Our hypothesis is that immunization with EtpE-C, Omp-1B, and VirB2-4 prevents *Ehrlichia* infection, thus HME. The objective of this study is to determine the vaccine potential of these three proteins using *Ehrlichia* HF in the mouse model of acute fatal HME. Each protein sequence has been cloned from the *Ehrlichia* HF genome into a protein expression vector, followed by expression and purification of the recombinant proteins. Four groups of immunocompetent mice will be immunized with rEtpE-C, rOmp-1B, rVirB2-4, or sham-immunized and challenged with *Ehrlichia* HF. Mouse survival curves will be generated. At euthanasia, blood, spleen, and liver samples will be collected for analysis of bacterial load and cytokine expression, via quantitative reverse transcriptase polymerase chain reaction (qRT-PCR). Cytokine mRNA levels and the immune cell population in liver and spleen will be analyzed by qRT-PCR and flow cytometry, respectively. This project will lead to a better and more thorough understanding of the pathogenicity and immunological response in fatal ehrlichiosis patients, and of the vaccination potential of these antigens. |
| Keywords for abstract: | Ehrlichia<br>Obligatory intracellular bacteria<br>Immunization |

# IMID - 11

| | |
|---|---|
| Title of abstract: | **ADAPTIVE CHANGES IN VIRAL *ENVELOPE* RESULTING FROM ADAPTATION OF SIMIAN-TROPIC HIV-1 TO MACAQUES CONFERS RESISTANCE TO INTERFERON** |
| Authors | A. C. Smith[1], H. Weight[2], J. Overbaugh[2], and A. Sharma[1]. [1]Depts of Veterinary Biosciences and Microbial Infection & Immunity. [2]Divison of Human Biology, Fred Hutchinson Cancer Research Center. |
| Abstract | HIV-1 does not persistently infect macaques due to restriction by several type-I interferon (IFN)-induced host-factors. Therefore, chimeric SIV/HIV-1 viruses (SHIVs) encoding the SIV antagonists of restrictive host-factors and HIV-1 Envelope glycoprotein (Env), are used to infect macaques to model HIV-1 infection. A major limitation of the SHIV/macaque model is that SHIVs generated *in vitro* replicate poorly in macaques. A small subset of SHIVs has been successfully adapted for high-level replication through serial passage in macaques. We have previously identified that serial macaque-passage selects for IFN-resistant SHIV variants that have higher replication in macaque lymphocytes. The viral determinant(s) contributing to increased replication and IFN resistance in macaque-passaged SHIVs have not been examined.<br>In order to identify the viral determinant(s) of macaque-passaged SHIVs that confer resistance to IFN, we generated SHIV infectious molecular clones (IMCs) encoding the parental *env* and representative *env* clones from sequential macaque-passaged viruses. We found that the unpassaged, parental SHIV IMC is potently inhibited by IFN (mean $IC_{50}$ range 1.9 to 54.6 U/ml), whereas the SHIV IMCs encoding macaque-passaged *envs* are resistant to IFN inhibition (mean $IC_{50}$ >5000 U/ml). In addition, we found that SHIV IMCs encoding macaque-passaged *envs* have high replication capacity and most, but not all, have more virion Env content. Next, we took a gain-of-function approach and generated chimeras that introduce portions of *env* gene from IFN-resistant SHIV IMC into the parental IFN-sensitive SHIV IMC. Using this approach, we mapped the determinant of IFN resistance and high replication capacity to the C2 region of the gp120 subunit of HIV-1 Env.<br>In conclusion, the adaptive changes in HIV-1 *env* resulting from serial macaque-passage of SHIVs are sufficient to increase resistance to IFN, replication capacity, and virion Env content. Thus, the host IFN response serves as a strong selective pressure during the process of adaption of SHIV to macaques. |
| Keywords for abstract: | Human immunodeficiency virus<br>Simian-human immunodeficiency virus<br>Type-I interferon |

# IMID - 12

| | |
|---|---|
| Title of abstract: | **THE EFFECTS OF M6A RNA MODIFICATIONS ON HUMAN T-CELL LEUKEMIA VIRUS TYPE 1 PATHOGENESIS** |
| Authors | S.M. Smith, P.L. Green, A.R. Panfil. Department of Veterinary Biosciences. |
| Abstract | Human T-cell leukemia virus type 1 (HTLV-1) can lead to a variety of debilitating diseases, including adult T-cell leukemia/lymphoma and neurodegenerative disorders. Successful regulation of HTLV-1 gene expression allows the virus to immortalize infected target cells, establish latent infection, and evade immune detection. While gene regulation is crucial, epigenetic modifications that control post-transcriptional gene regulation in HTLV-1 have yet to be fully evaluated. Methylation of the N6 position of adenine (m$^6$A) is the most abundant RNA modification in eukaryotes and plays essential roles in post-transcriptional gene regulation. These dynamic modifications are regulated by several host proteins including methyltransferases (writers), demethylases (erasers), and m$^6$A-binding proteins (readers). Although RNA m$^6$A modifications have been shown to play a critical role in several RNA and DNA viral lifecycles, the presence and role of m$^6$A in viral oncogenesis has not been well studied. We hypothesize that m$^6$A modifications have an impact on HTLV-1 RNA gene regulation and are crucial for viral persistence and pathogenesis. Our preliminary data demonstrate that HTLV-1 virions contain m$^6$A-modified RNA. Cross-linking immunoprecipitation experiments in HTLV-1 transformed cells have shown that several viral transcripts (*tax, hbz, gag*) contain m$^6$A modifications. In addition, a variety of m$^6$A-binding proteins (YTHDC1-2, YTHDF1-3) have been found to interact with these viral transcripts. shRNA-mediated knockdown of YTHDF2 in JET-ACH (an HTLV-1 latently infected T-cell line) induced viral gene expression further confirming the role of m$^6$A in regulation of HTLV-1 gene expression. Future experiments will be to map the m$^6$A modifications in HTLV-1 RNA and determine their effects on HTLV-1 RNA structure. We will also further elucidate the effects of m$^6$A modifications on viral gene expression/function and determine their effect(s) on viral persistence and disease development. By understanding the role of m$^6$A modifications, new insights into disease development and disease progression may reveal targets for novel HTLV-1 treatments. |
| Keywords for abstract: | HTLV-1<br>N6-methyladenosine (m6a) modification<br>epigenetics |

# IMID - 13

| | |
|---|---|
| Title of abstract: | **CHARACTERIZATION AND *IN VITRO* SUSCEPTIBLITY OF FELINE *UPEC* ISOLATES TO A NOVEL *E. COLI* PROBIOTIC** |
| Authors | C. Snell[1], J. Gibson[1], C. Zumpetta[1], J. Byron[1], J. Quimby[1], A. Harrison[1], S. Justice[2], A. Rudinsky[1]<br>[1] College of Veterinary Medicine, The Ohio State University, Columbus, Ohio, USA<br>[2] Nationwide Children's Hospital, Columbus, Ohio, USA |
| Abstract | The rise in antibiotic resistance amongst urinary tract infections (UTIs) in both cats and dogs underscores the need for non-antibiotic approaches to UTIs. The probiotic *Escherichia coli* Nissle-1917 (EcN) has many benefits including the ability to outcompete and produce antibiotic like substances (microcins) against *E. coli* that can cause UTIs, also known as uropathogenic *E. coli* (UPEC). The aim of this study was to genetically characterize (serogroup and clade) UPEC in feline UTI cases and investigate the susceptibility of these isolates to EcN outside the body in a laboratory setting (*in vitro*).<br>Forty-one cats with positive *E. coli* urine cultures were included in the study. Samples used in this study were obtained from surplus urine collected for evaluation of possible UTIs. Genetic characterization of UPEC isolates was performed by clade and serotyping analysis using PCR testing. EcN effectiveness against UPEC isolates was tested *in vitro* using microcin plate analysis.<br>The serogroups and clades found were similar to previous findings in human UPEC studies, however a higher proportion of clade A was noted in feline samples. The most common clades were A (41.4%), B2 (39%), and D (14.6%). Fifty-nine percent of isolates were found to be resistant to antibiotics with 29.2% of those being multi-drug resistant. Eighty percent of UPEC isolates were susceptible to the EcN probiotic *in vitro,* with 83.3% of the antimicrobial resistant isolates also showing susceptibility. The median zone of UPEC growth inhibition noted was 3.33 mm with a range of 1.67-10.67 mm. Thirteen isolates showed inhibition via EcN competitive growth and 28 via microcin production.<br>In conclusion, UPEC isolates from feline patients were similar in genetic background to isolates found in human patients. Additionally, the analyzed UPEC samples were highly susceptible to EcN suggesting its potential use as a novel therapeutic to treat feline UTIs. |
| Keywords for abstract: | Urinary tract infection<br>Probiotic<br>Antibiotic resistance<br>Uropathogen<br>Nissle<br>*E. coli*<br>EcN |

# IMID - 14

| | |
|---|---|
| Title of abstract: | **EVALUATION OF COMPOUND “X” AS A PROPHYLACTIC FOR COVID-19 IN A SYRIAN HAMSTER MODEL** |
| Authors | K.K. Yadav[1], P. Boley[1], J. Hanson[2], C. Lee[1], R. Gourapura[1], S.P. Kenney[1]. [1]Center for Food Animal Health [2]Plant and Animal Agrosecurity Research Facility |
| Abstract | SARS-CoV-2, the causative agent of COVID-19, caused an unprecedented global public health threat, spreading rapidly with significant morbidity and limited FDA approved drugs for treatment. This scenario required rapid screening of already approved drugs for repurposing against SARS-CoV-2. Repurposing established medications, with excellent human safety profiles, is a viable approach for treating the disease. We tested an available FDA approved drug (named compound “X”, due to nondisclosure agreements) to combat the virus. We present the in vivo antiviral effectiveness of compound “X” after it was shown to kill SARS-CoV-2 in vitro within 24 hours. In this study, we utilized the hamster model known to be naturally susceptible to SARS-CoV-2 infections with similar pathophysiology to humans for studying the efficacy of compound “X”. We hypothesized that hamsters given compound “X” intranasally every 12 hours would be resistant to infection when caged together in direct contact with SARS-CoV-2 infected hamsters. Four hamsters from infected and treated groups were necropsied on day 3 and day 7. Blood, nasal wash, lung lavage, nasal turbinate, lung tissue, spleen, kidney, brain, and intestine samples were harvested at necropsy. We found that contrary to our hypothesis, SARS-CoV-2 was transmitted from inoculated hamsters to naive compound “X” treated hamsters. Inoculated and exposed drug treated hamsters showed weight loss until day 7 (last day of experiment) post inoculation or post contact. Significant differences in temperature between groups was noted only on day 1 and day 3. Although fatalities were not observed, SARS-CoV-2 was shed in nasal washes, lung lavage, and tracheal tissues in both groups measured via tissue culture infectious dose (TCID50 per ml). Viral RNA was determined in all extracted tissues from both groups. Our results suggest that compound “X” failed to protect in vivo under continuous contact conditions while cohoused with SARS-CoV-2 infected hamsters. |
| Keywords for abstract: | SARS-CoV-2<br>hamsters<br>direct contact<br>infection<br>in vivo |

# IMID - 16

| | |
|---|---|
| Title of abstract: | **TIM-1 RESTRICTION OF LENTIVIRUS RELEASE IS CONSERVED ACROSS PRIMATE ORTHOLOGS** |
| Authors | J. Evans, P. Mitchel, C. Ross, H. Malik, and S.L. Liu. Dept. of Veterinary Biosciences and Center for Retrovirus Research, OSU and Basic Science Division, Fred Hutch Cancer Research Center. |
| Abstract | Human immunodeficiency virus (HIV) has entered the human population at least 5 times in the past 150 years. Opposing these transmission events are host “restriction factors” which disrupt viral replication. The ability of a virus to evade host restriction factors, typically mediated by a viral protein, is critical to both the cross-species transmission of a virus and the subsequent within-species spread. This virus-host interaction leads to an evolutionary arms-race where restriction factors evolve to evade viral antagonism and viral factors evolve to recapitulate this antagonism, producing the high degree of positive selection characteristic of many restriction factors. We previously demonstrated that the T-cell immunoglobulin and mucin domain type 1 (TIM-1) protein restricts HIV-1 particle release and is antagonized by the HIV Nef. Additionally, several positively selected amino acid residues have been identified on TIM-1. In light of this, we investigated TIM-1 as a possible barrier to cross-species transmission of lentiviruses by characterizing TIM-1 orthologs from various primate species and Nef orthologs from various HIV/SIV strains. We demonstrated conserved restriction of HIV-1 release for TIM-1 orthologs as well as TIM-1 ortholog restriction of other lentiviruses. Finally, alanine-scanning mutations in positively selected TIM-1 orthologs potentially appeared to enhance TIM-1 restriction of lentivirus release. Together these results highlight the importance of TIM-1 in primate and lentivirus interactions. |
| Keywords for abstract: | HIV-1<br>SIV<br>Lentivirus<br>TIM-1<br>Restriction Factor |

# MOLECULAR
# AND
# CELLULAR BIOLOGY

# MCB - 1

| | |
|---|---|
| Title of abstract: | **GUT MICROBIOTA SHAPED BY DIET AND PHYLOGENY IN SEVEN CERCOPITHECIDS FROM TAI FOREST, IVORY COAST.** |
| Authors | T. H. Cannon; L. Fannin; W. S. McGraw; V. Hale; Departments of Anthropology and Veterinary Preventive Medicine, The Ohio State University and Department of Anthropology, Dartmouth College |
| Abstract | Gut microbiota fundamentally contribute to an animal's overall health and immune function. Current evidence indicates that host-microbe interactions have very likely influenced primate evolution, so the determinants of gut microbial composition and diversity, including diet, phylogeny, habitat disturbance, strata use, and social interaction, continue to be actively investigated. Here, we report results from an analysis of the gastrointestinal microbial communities derived from fecal samples of seven cercopithecid species living sympatrically in the Ivory Coast's Tai Forest. Study taxa are *Cercocebus atys* (Sooty mangabey), *Cercopithecus campbelli* (Campbell's monkey), *Cercopithecus diana* (Diana monkey), *Cercopithecus petaurista* (Lesser spot-nosed monkey), *Colobus polykomos* (Western black and white or King colobus), *Piliocolobus badius* (Western red or Bay colobus), and *Procolobus verus* (Olive colobus). We extracted microbial DNA from fecal samples (n=138) from the seven study taxa using QIAamp® PowerFecal® Pro DNA Kit. Raw, paired-end sequence reads were processed using QIIME2 v. 2020.11. Alpha and beta diversity indices, and an analysis of composition of microbes, were analyzed in QIIME 2. Distinct microbial signatures were evident within each primate species (PERMANOVA, $p < 0.001$), with the greatest similarities in microbiota observed between closely related taxa. Preliminary analyses reveal beta diversity clustering associated with phylogenic relationship and percent folivory, with variation noted between young-leaf and mature-leaf specialists. Additionally, both alpha and beta diversity metrics were associated with diet and strata use. Study of gut microbial diversity and composition in the Tai monkeys presents an excellent opportunity to decipher the interactive effects and relative contributions of diet, habitat use, and evolutionary lineage on the gut microbiome in an ecologically complex community of primates. |
| Keywords for abstract: | Gut microbiome<br>Primate<br>Microbial ecology<br>Diet<br>Phylogeny |

# MCB - 2

| | |
|---|---|
| Title of abstract: | **DEVELOPMENT OF HIGH FIDELITY NANOPORE LONG-READ SEQUENCING METHODS FOR METAGENOMIC ANALYSIS OF OCEAN RNA VIRUSES** |
| Authors | S. Golconda, H. Yu, D. Xue, G Dominguez Huerta, A. Baek, G. Lee, S. Kim, C. Kimmel, C. Viola, J. Guo, M. Sullivan, and S. Kim.<br>Depts. of Veterinary Biosciences and Microbiology |
| Abstract | Metagenomic analysis of RNA viruses has been hindered by the limited amount of available RNA in test samples, the low sensitivity of current assays, and the limitations of current short read shotgun sequencing and targeted analysis approaches. We are developing a novel high-fidelity (HiFi), long-read sequencing methods for metagenomic RNA virus analysis using so-called “3rd generation” Nanopore sequencing technology. Here we demonstrate three major technical innovations that enabled us to achieve sensitive HiFi sequencing for metagenomic RNA virus analysis. First, we maximized cDNA length by optimizing the reverse-transcription step via testing different combinations of “high processivity” reverse transcriptases, including Super Script IV, Marathon, TIGRTIII. Secondly, we significantly improved sequencing sensitivity by employing a new hairpin-mediated cDNA amplification method; the new hairpin method enabled more than 97% detection of cDNA in the sample. Lastly, we employed rolling-circle-amplification (RCA) methods to correct the intrinsic read errors of Nanopore sequencing. Our RCA-mediated error correction enabled HiFi sequencing at >99.9% (QV30) level accuracy when the reference was available and >99% (QV20) without reference. A pilot-scale sequencing run on ocean RNA samples (non-detectable RNA concentration, complex backgrounds, after processing over 2 liters of seawater) resulted in more than 4.8K different RNA molecules, including thousands of identifiable novel RNA viruses, such as Barns Ness breadcrumb sponge aquatic picorna-like virus, Chaetoceros species RNA virus, *Guinardia delicatula* RNA virus, and Wenzhou picorna-like virus. Furthermore, matched long-read sequences up to 5 kb and 6 kb sequences were mapped to viruses *Dicistroviridae* sp. isolate and Beihai picorna-like virus, respectively. HiFi long-read data can also significantly improve the assembly step as shown in recent studies. Our HiFi long-read sequencing method is the first to achieve >QV30 accuracy using the portable Nanopore sequencing platform and, thus, has the great potential to improve RNA metagenomics as well as many other sequencing-based genomics studies. |
| Keywords for abstract: | Metagenomics<br>Nanopore<br>RNA Virus<br>Viral Detection |

# MCB - 3

| | |
|---|---|
| Title of abstract: | **RECEPTOR TYROSINE KINASE ACTIVATION AND IN VITRO ACTIVITY OF TOCERANIB PHOSPHATE IN CANINE UROTHELIAL CARCINOMA CELL LINES.** |
| Authors | Korec, D.I.1, Louke, D.1, Fenger, J., M.1 Department of Veterinary Biosciences and Veterinary Clinical Sciences |
| Abstract | Urothelial carcinoma (UC) accounts for >90% of canine malignant tumors occurring in the urinary bladder. Toceranib phosphate (Palladia) is a multi-target receptor tyrosine kinase (RTK) inhibitor that exhibits potent activity against members of the split kinase family of RTKs. The purpose of this study was to evaluate normal canine bladder tissues, primary bladder UC tumors, and established UC cell lines for the expression and activation of VEGFR2, PDGFRα, PDGFRβ, and KIT to assess whether dysregulation of these RTKs may contribute to the biological activity of TOC. Real Time PCR was performed on primary UC tissue samples (N=9) and UC cell lines (N=5) to detect VEGFR2, PDGFRα, PDGFRβ, and KIT mRNA. Transcript for VEGFR2, PDGFRα, PDGFRβ, and KIT was detected in all UC tissue samples and UC cell lines. The Proteome Profiler™ Human Phospho-RTK Array Kit (R & D Systems) provided a platform to assess phosphorylation of 42 different RTKs in primary UC tissue specimens using the available tumor specimens and UC cell lines. PDGFRα, and PDGFRβ were found to be phosphorylated in all tumor samples and cell lines and KIT activation was not observed on the arrays. While message for VEGFR2 was identified in all tumor samples and cell lines, all samples exhibited low basal phosphorylation levels of this RTK. The the in vitro activity of TOC on cell viability, apoptosis, and VEGFR, PDGFRα, and PDGFRβ phosphorylation in UC cell lines was evaluated. Treatment with TOC did not lead to appreciable cell death in UC cell lines compared to mast cell line controls. Taken together, our findings demonstrate that known targets of TOC are expressed/activated in primary UC tumors and UC cell lines. Given the observed phosphorylation of PDGFRα and PDGFRβ, these RTKs merit further investigation as to their role in mediating the biology of UC and their contribution to TOC's activity. |
| Keywords for abstract: | toceranib phosphate<br>canine urothelial carcinoma<br>receptor tyrosine kinase<br>phosphorylation |

# MCB - 4

| | |
|---|---|
| Title of abstract: | **THE MOLECULAR DETERMINANT OF HTLV TRANSFORMATION TROPISM** |
| Authors | V.V. Maksimova, E.M. King, P.L. Green, and A.R. Panfil |
| Abstract | Human T-cell leukemia virus type 1 (HTLV-1) is the only oncogenic human retrovirus and the causative infectious agent of both adult T-cell leukemia/lymphoma (ATL), an aggressive and fatal CD4$^{+}$ T-cell malignancy, and chronic neurological disease. HTLV-2 is closely related to HTLV-1 with ~70% nucleotide similarity and several overlapping gene functions; however, HTLV-2 is not associated with disease. *In vitro*, HTLV-1 transforms CD4$^{+}$ T-cells while HTLV-2 transforms CD8$^{+}$ T-cells. These observations are clinically relevant as both ATL and neurological disorders caused by HTLV-1 are CD4$^{+}$ T-cell-dependent. Our lab has previously mapped the genetic determinant for transformation tropism to the viral envelope protein (Env). However, transformation tropism is not solely conferred at the level of entry, as our previous *in vivo* studies have detected HTLV-1 and HTLV-2 proviruses early after infection in *both* CD4$^{+}$ and CD8$^{+}$ T-cells. Importantly, a late selection and outgrowth of the preferred T-cell type was observed several weeks after infection using *in vitro* immortalization assays. These data suggest T-cell tropism ensues during the cellular transformation process that occurs over several weeks. We hypothesize that HTLV-1 Env (Env-1) interacts with a cellular signaling pathway or protein in certain cell environments and modulates downstream signaling events, leading to the distinct transformation tropism. In this study, we created chimeric mutants of HTLV-1/2 to test the contribution of Env surface or transmembrane domains on transformation tropism *in vitro*. Using a proteomics approach, we have identified 13 unique cellular binding partners of Env-1 and have confirmed the interactions in HTLV-1-positive cells. Our experiments will expand on the role of Env after initial viral entry into the cell and inform the field of key pathways that are regulated by Env-1 during the establishment of viral persistence in an infected host. This will lead to new diagnostic markers for HTLV-1-associated disease development or therapeutic targets. |
| Keywords for abstract: | HTLV<br>Envelope<br>Transformation<br>CD4$^{+}$ T-cell |

# MCB - 5

| | |
|---|---|
| Title of abstract: | **CHARACTERIZATION OF SPATIO-TEMPORAL RESISTANCE TO EGFR-TARGETED THERAPY IN TRIPLE NEGATIVE BREAST CANCER** |
| Authors | J. Meyerson, A. Davies. Dept. Of Veterinary Biosciences |
| Abstract | Epidermal Growth Factor Receptor (EGFR) overexpression is a common feature in aggressive cancers, such as triple negative breast. EGFR overexpression and hyperactivation of the downstream MAP Kinase (MAPK) pathway can lead to uncontrolled cell proliferation, making this pathway a promising therapeutic target. Although EGFR-targeted therapies, such as erlotinib, are effective at inhibiting signaling through EGFR and MAPK, resistance inevitably develops in a population of cells. However, it remains unknown 1) whether resistance arises in single cells, groups of cells, or if single resistant cells can influence the response of neighboring cells to EGFR inhibitors, and 2) if growth factors present in the tumor microenvironment, such as IGF, HGF, and FGF, exacerbate resistance. To this end, we used live single cell imaging techniques to monitor activation of signaling through EGFR-MAPK in breast cancer cells using a reporter for MAPK signaling pathway component, ERK. By monitoring ERK activity we were able to track the activity of single cells within a population and perform spatio-temporal analysis of signaling in the presence or absence of EGFR inhibitor. Using this approach, we find that groups of cells exhibit resistance with similar ERK pulse magnitude and duration. These affects result in activation of downstream ERK target genes such as Fra-1 and Egr1 which are associated with proliferation, altered DNA damage response, and metastasis. Cells treated with FGF, HGF, and IGF exhibited minimal difference in pulsatility at their current dose rate compared to the Erlotinib-treated control wells, therefore, the tumor microenvironment may contribute less to resistance of EGFR inhibitors as compared to tumor-derived paracrine signals. |
| Keywords for abstract: | Epidermal Growth Factor Receptor<br>EGFR<br>Tumor Microenvironment<br>Erlotinib<br>Breast Cancer<br>Single cell imaging |

# MCB - 6

| | |
|---|---|
| Title of abstract: | **EVALUATING EXTRACTION METHODS TO STUDY CANINE URINE MICROBIOTA** |
| Authors | R. Mrofchak, C. Madden, M.V. Evans, V.L. Hale |
| Abstract | The urinary microbiota is the collection of microbes present in urine that may play a role in host health. Studies of urine microbiota have traditionally relied upon culturing methods aimed at identifying pathogens. However, recent culture-free sequencing studies of the urine microbiota have determined that a diverse array of microbes is present in health and disease. To study these microbes and their potential role in diseases like bladder cancer or interstitial cystitis, consistent extraction and detection of microbial DNA from urine is critical. However, urine is a low biomass substrate, requiring sensitive methods to capture DNA and making the risk of contamination high. To address this challenge, we collected urine samples from ten healthy dogs and extracted DNA from each sample using five different commercially available extraction methods. Extraction methods were compared based on total and bacterial DNA concentrations and microbial community composition and diversity assessed through 16S rRNA gene sequencing. Significant differences in the urinary microbiota were observed by dog and sex but not extraction method. The Bacteremia Kit yielded the highest total DNA concentrations (Kruskal-Wallis, $p = 0.165$, not significant) and the highest bacterial DNA concentrations (Kruskal-Wallis, $p = 0.044$). Bacteremia also extracted bacterial DNA from the greatest number of samples. Taken together, these results suggest that the Bacteremia kit is an effective option for studying the urine microbiota. This work lays the foundation to study the urine microbiome in a wide range of urogenital diseases in dogs and other species. |
| Keywords for abstract: | extraction methods<br>microbiota<br>urine<br>dog<br>16S sequencing |

# MCB - 7

| | |
|---|---|
| Title of abstract: | **COMBINATION INHIBITORS TARGETING EGFR-RAS-ERK AND IGF-1 SIGNALING PREVENTS DRUG ESCAPE IN TRIPLE NEGATIVE BREAST CANCERS** |
| Authors | V. Murthy, D. Louke, A. Davies<br>Department of Veterinary Bioscience, College of Veterinary Medicine, The Ohio State University, Columbus, OH 43210, USA |
| Abstract | The majority of breast cancer (BC) mortalities can be attributed to metastasis to distant organs. The overall survival for BCs is about 90% but decreases to less than 30% in cases of metastasis to distant sites. In triple negative breast cancer (TNBC), an aggressive subtype of BCs, metastasis to the lung results in the poorest clinical outcomes, with an overall 5-year survival rate of about 10%. Genetically, TNBCs lack the expression of classical estrogen and progesterone hormone receptors, and human epidermal growth factor 2 receptor, making cytotoxic chemotherapy the only treatment option. However, TNBCs overexpress epidermal growth factor receptor (EGFR), a central molecule in numerous cancers. Targeted therapies against EGFR, or its downstream effectors, have shown success in some cancers, but are largely ineffective in TNBCs. Here we show that insulin-like growth factor-1 (IGF-1) secreted from the tumor microenvironment overcomes EGFR inhibition by activating parallel non-EGFR receptors and their signaling cascade. Using single live-cell imaging we show that IGF-1 stimulation re-wires downstream pathways to provide compensatory signals that result in tumor proliferation. Combination treatment with small molecule inhibitors of JAK/STAT signaling (ruxolitinib) and downstream EGFR effectors such as MEK (mirdametinib) abrogates IGF-1 signaling. Our data demonstrate that selective inhibition of certain target pathway proteins is sufficient to prevent drug escape in TNBCs. Taken together, these results offer promising rationale for combination therapy in drug resistant TNBCs. |
| Keywords for abstract: | Triple Negative Breast Cancer<br>EGFR<br>ERK<br>Microenvironment<br>MAPK |

# MCB - 8

| | |
|---|---|
| Title of abstract: | **LAMELLAR RIBOSOMAL PROTEIN S6 ACTIVATION IN THREE FORMS OF EXPERIMENTALLY INDUCED EQUINE LAMINITIS** |
| Authors | E. Pinnell, M. Watts, O. Hegedus, S. Eades, A. Van Eps, J. Belknap, T. Burns. |
| Abstract | A comprehensive research effort has revealed signaling pathways contributing to lamellar stretching, failure, and laminitis in experimental models. However, pathophysiological mechanisms common to all forms of laminitis have remained elusive. Ribosomal protein S6 (RPS6) is activated downstream of insulin-like growth factor-1 receptor and is active within the lamellae during laminitis. The objectives of this study were 1) determine the concentration of phosphorylated-RPS6 (pRPS6 240-244 and 235-236) following experimentally-induced endocrinopathic (euglycemic-hyperinsulinemic clamp model [EHC]), sepsis-associated (carbohydrate overload [CHO]), and supporting-limb laminitis models (SLL), and 2) evaluate the effect of distal limb cryotherapy (CRYO) on pRPS6 concentrations. Healthy adult light-breed horses were used for three different laminitis models (CHO n=6, control n=6), (EHC n=8, control n=8), (SLL n=7, control n=7). Additionally, CRYO was applied to one forelimb while the other forelimb remained at ambient temperature (AMB) in CHO and EHC models. Digital lamellar tissue was collected following humane euthanasia and the concentrations of p-RPS6, total RPS6, and β-actin were determined using western immunoblotting. Lamellar [p-RPS6] was significantly increased in all models of equine laminitis at the time of onset of clinical signs (CHO p =0.0006, 0.05; EHC p=0.0002, <0.0001; SLL p=0.0005, 0.0017 [235-236 and 240-244, respectively]). Cryotherapy significantly attenuated RPS6 activation in the CHO and EHC models (p=<0.0001 and p=0.0078). RPS6 appears to play a role in the pathophysiology of all three forms of laminitis and is attenuated by a practice is known to prevent disease in high-risk individuals. Evaluation of pharmacological inhibition of RPS6 for laminitis prophylaxis and treatment is warranted. |
| Keywords for abstract: | Laminitis<br>Cryotherapy<br>Equine Metabolic Syndrome<br>Carbohydrate overload<br>Sepsis<br>RPS6<br>Insulin-like growth factor-1 |

# MCB - 9

| | |
|---|---|
| Title of abstract: | ***TRICHURIS* DETECTION IN GIRAFFE (*GIRAFFA CAMELOPARDALIS*) AT MULTIPLE ZOOS** |
| Authors | L. Shusterman, A. Marsh, P. Joyner, and G. Habing. Depts. Of Veterinary Preventive Medicine (Shusterman, Marsh, Habing). The Wilds (Joyner) |
| Abstract | *Trichuris* spp. are parasites infecting domestic and wild ruminants at The Wilds in Cumberland, Ohio; White Oak Conservation Center in Yulee, Florida; Fossil Rim Wildlife Center in Glen Rose, Texas and Binder Park Zoo in Battle Creek, Michigan, as well as many other zoological institutions worldwide. These helminths can cause significant morbidity in giraffe (*Giraffa camelopardalis*) and other hoofstock. However, relative to domestic species, little is known about parasitism in giraffes in human care. Using giraffe fecal and soil-inhabited samples, this study documented the *Trichuris* species relationships in giraffe populations at these locations using targeted sequence PCR and compared genetic sequences. The study also investigated free ranging white-tailed deer (*Odocoileus virginianus*) at The Wilds as potential reservoir hosts. Additionally, to support routine monitoring of zoo populations and wildlife, protocol optimization for detection of fecal and soil derived *Trichuris* eggs is described. Detection of eggs requires optimization of solutions used to float the eggs using a Modified Stoll's method and solutions used to liberate the eggs from soil. Previous studies have used a variety of flotation and egg liberating methods. We identified solutions with specific gravity of ≥ 1.27 yielded more eggs on flotation as compared to lower specific gravity solutions. Also 0.1 N NaOH and 0.9% w/v NaCl water-based solutions were successful in liberating eggs from soil. The results of this study will provide insight for both zoo and wildlife management in routine detection and potential *Trichuris* spp. present in giraffe. |
| Keywords for abstract: | *Trichuris*<br>Giraffe<br>Nematode<br>Feces<br>Soil<br>Genetic sequence<br>Modified Stoll's<br>Specific gravity |

# MCB - 10

| | |
|---|---|
| Title of abstract: | **INHIBITION OF PRMT5 RESTORES REGULATORY ACTIVITY TO THE CELL CYCLE IN IBRUTINIB RESISTANT MANTLE CELL LYMPHOMA** |
| Authors | S. Sloan[1,2], F. Brown[1], M. Long[1,2], A. Prouty[1], J. Helmig-Mason[1], E. Brooks[1], J. Chung[1], Y. Youssef[1], J. C Byrd[1], R. Lapalombella[1], R. A. Baiocchi[1] and L. Alinari[1]<br>[1]Department of Internal Medicine, Division of Hematology, College of Medicine, The Ohio State University, Columbus, OH<br>[2]Department of Veterinary Biosciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH |
| Abstract | Mantle cell lymphoma (MCL) is characterized by dysregulation of the cell cycle driving uncontrolled B-cell proliferation and survival. Although the BTK inhibitor ibrutinib has achieved significant single-agent therapeutic activity in relapsed/refractory MCL (ORR=68%), all patients inevitably develop resistance characterized by compensatory signaling through sustained cell cycle progression with activation of PI3K-AKT and/or NF-kB pathways. Our publish work supports the oncogenic role of protein arginine methyltransferase 5 (PRMT5) in driving B-cell lymphomagenesis. Our published and preliminary work indicates that the inhibition of PRMT5 restores regulatory activity to the cell cycle (RB/E2F), tumor suppressors (p53), and PI3K/AKT and NF-kB signaling leading to lymphoma cell death. Given the overlap of identified mechanisms of resistance to ibrutinib and known target genes modulated by PRMT5 inhibition, we hypothesize that selective inhibition of PRMT5 with PRT382 will circumvent ibrutinib resistance in MCL through attenuation of the identified compensatory mechanism resulting in reduced proliferation and MCL cell death.<br>Comparing the MCL cell lines with primary ibrutinib-resistance (ic50>10uM), we found an inverse correlation between ibrutinib ic50s and PRT382 ic50s ($r=-0.94$, $p=0.0167$). In a treatment-naïve MCL patient derived xenograft (PDX), ibrutinib monotherapy provided no therapeutic benefit, whereas crossover to PRT382 after progression on ibrutinib provided a significant survival advantage ($p<0.05$) compared to ibrutinib alone. In a PDX derived from an ibrutinib-resistant MCL patient, treatment with PRT382 significantly prolonged survival ($p<0.01$), reduced systemic disease, and reduced spleen size compared to control or ibrutinib treatment ($p<0.0001$). In the ibrutinib relapsed MCL PDX, RNA-sequencing and gene set enrichment analysis (GSEA) identified cell cycle arrest with activation of p53, repression of E2F targets, and decreased G2M checkpoint as the top Hallmark gene sets modulated upon PRMT5 inhibition (NES=1.73, -2.51, -2.26). Pharmacologic inhibition of PRMT5 represents a novel therapeutic approach to circumvent ibrutinib resistance in MCL and merits further investigation in clinical trials. |
| Keywords for abstract: | PRMT5<br>MCL<br>Lymphoma<br>Ibrutinib<br>drug resistance<br>cell cycle |

# MCB - 11

| | |
|---|---|
| Title of abstract: | **GUT MICROBIOTA OF AFRICANIZED HONEY BEES IS AFFECTED BY TETRACYCLINE HYDROCHLORIDE EXPOSURE** |
| Authors | K. Soares1, C. Oliveira1,3, A. Evangelista-Rodrigues1, T. Rocha1, M. SANTOS1, P. Vasconcelos1, C. Madden2, V. Hale2<br>1 Department of Animal Science, College of Agricultural Sciences (CCA), Federal University of Paraíba (UFPB), 58397-000, Areia, Paraiba, Brazil<br>2 Department of Veterinary Preventive Medicine, Ohio State University, Columbus, OH, 43210<br>3 Global One Health initiative (GOHi), Ohio State University, 43210, Columbus, OH, USA |
| Abstract | Bees are one of the most important pollinators across Earth's habitats; however, recent human activities have threatened bee survival. While foraging, for example, honey bees can be exposed to antimicrobials commonly used in agriculture. These compounds can have direct or indirect effects on bee health by altering the gut microbiome. To understand the potential effects of tetracycline exposure on honey bee gut microbiota, approximately one thousand bees were collected from five hives, divided into two groups, and placed in an incubator. The control group was fed daily with 10g of sugar syrup and 10g of solid artificial protein diet. The tetracycline group was fed identically but with the addition of 0.045% tetracycline hydrochloride added to both types of food. We collected 100 bees from each group on days 0, 3, 6 and 9. Abdominal contents were removed and pooled (17-20 bees per pool) for DNA extraction using a Qiagen PowerSoil kit. Paired-end sequencing of the 16S rRNA gene (V3-V4 region) was performed on an Illumina MiSeq. Reads were filtered, denoised and parsed for non-chimeric sequences using DADA2. Alpha (Shannon and Pielou's index) and beta-diversity (Bray-Curtis and Jaccard) and differentially abundant taxa (ANCOM) were assessed using QIIME2-2020.2. Bee gut microbial composition and diversity differed significantly and increasingly over time and between the control and tetracycline groups. In the tetracycline group, we observed increased relative abundances of Lactobacillus, Bifidobacterium, and Idiomarina and decreased abundances of Gilliamella, Snodgrassella, Fructobacillus, Bombella, Rhizobiaceae and Enterobacteriaceae. As Bombella is associated with nutrient metabolism and Gilliamella and Snodgrassella play an important role in pathogen defense, decreases in these microbes in bees exposed to tetracycline suggest disturbances in the gut microbiota that could affect critical digestive and immune functions. Future work assessing bee survivorship and behavior can help examine the impacts of these gut microbial changes. |
| Keywords for abstract: | Africanized bees<br>antimicrobials<br>gut microbiota |

# MCB - 12

| | |
|---|---|
| Title of abstract: | **OPTIMIZATION OF BIOMIMETIC NANOFIBER SCAFFOLDS TO PROMOTE PERIOSTEAL EXPANSION** |
| Authors | M. Walker, M. Baumann, and H. Powell |
| Abstract | Traumatic injuries, neoplasia, and osteolysis can result in large segmental bone defects that present particular clinical challenges. Autogenous bone grafts, allografts, and synthetic bone implants have been used to manage large defects; due to poor incorporation with the patient's bone, however, complications such as nonunion, malunion, and infection are common. This project harnesses the osteogenic properties of periosteum to investigate its potential for segmental defect healing when used in conjunction with bioengineered nanofiber scaffolds. The periosteum provides vasculature, cytokines, proteins, and mesenchymal stem cells that are central to new bone formation. Biomimetic scaffolds act as a foundation on which periosteal cells can expand to incorporate with host tissue. The central objective of this investigation is to demonstrate that nanofiber scaffolds can promote the expansion of fresh persioteum in vitro and in vivo. Bovine-extracted collagen nanofiber scaffolds were created in either an aligned or random orientation. Half of the scaffolds were doped with hydroxyapatite (HA). Fresh porcine periosteum and isolated periosteum-derived stem cells were cultured on aligned collagen, aligned HA, random collagen, and random HA scaffolds for a duration of 5, 10, and 15 days. Immunohistochemical staining was used to determine the orientation (random v. aligned) and architecture (collagen v. HA-doped collagen) that resulted in maximum cellularity. ELISA will be used to assess synthesis of growth factors and cytokines, and PCR data will demonstrate expression of genes involved in healing and bone regeneration. Findings of this project will inform future trials in small and large animal models. In vivo implantation will consist of periosteal tissue on the optimized nanofiber scaffold, wrapped around a synthetic bone implant. This work will translate to the ultimate goal of clinical implementation of the tissue and bioengineered construct in human patients. |
| Keywords for abstract: | Biomedical engineering<br>Tissue engineering<br>Periosteum<br>Periosteal-derived stem cells<br>Bone/fracture healing<br>Osteogenesis |

# MCB – 13

| | |
|---|---|
| Title of abstract: | **FUNCTIONAL ANALYSIS OF NEW TYPE IV SECRETION SYSTEM EFFECTORS OF *ANAPLASMA SPECIES*** |
| Authors | L, Wang and Y. Rikihisa. Depts. Of Veterinary Biosciences |
| Abstract | *Anaplasma phagocytophilum* is a gram-negative obligatory intracellular bacterium that causes emerging infectious disease, human granulocytic anaplasmosis (HGA), potentially fatal severe influenza-like illness. An important virulence factor of *A. phagocytophilum* is the type IV secretion system (T4SS) that directly inoculates bacterial effector molecules into human cells. Our lab has identified two potential T4SS effectors in *A. phagocytophilum*, APH0641 and APH0874. Based on yeast two-hybrid analysis, I found APH0641 directly binds snapin that regulate lysosomal function. By transfecting APH0874-GFP into RF/6A, I found APH0874 localizes to Golgi apparatus. I will (1) determine molecular targets of APH0641 and APH0874 in human cells, (2) confirm the secretion of native APH0641 and APH0874 by *Anaplasma* in human cells, (3) determine the localization of APH0641 and APH0874 in *Anplasma*-infected cells, and (4) elucidate their roles in *Anaplasma* infection *in vitro*. Further studies on functions of *A. phagocytophilum* T4SS effector molecules and signaling pathways will advance our understanding of the complex interplay between obligatory intracellular pathogens and their hosts. |
| Keywords for abstract: | *A. phagocytophilum*,<br>T4SS effectors,<br>cellular localization,<br>molecular targets |

# MCB - 14

| | |
|---|---|
| Title of abstract: | **RANDOM MUTAGENESIS OF *EHRLICHIA* SP. HF FOR IDENTIFICATION OF *IN VIVO* VIRULENCE FACTORS** |
| Authors | Q. Zhang, R. Chien, K. Budachetri, M. Lin, and Y. Rikihisa. Dept. Of Veterinary Biosciences |
| Abstract | *Ehrlichia* spp. are Gram-negative, obligately intracellular bacteria that infect granulocytes, monocytes, macrophages, and platelets of domestic animals, wild animals, and humans using ticks as vectors. Human Monocytic Ehrlichiosis (HME) characterized by flu-like symptoms including fever, headache, myalgia, thrombocytopenia, leucopenia, and elevated liver enzyme levels can be fatal. However, *Ehrlichia* spp. lacks typical pathogen-associated molecules such as LPS or peptidoglycan. *Ehrlichia* sp. HF isolated in Japan from *Ixodes ovatus* ticks serves as a mouse disease model of fatal HME. Our lab has succeeded in stably culturing HF in DH82 canine macrophage cell line and completed the whole genome sequence with detailed annotations. To investigate *in vivo* virulence mechanisms and mechanisms of tick transmission of *Ehrlichia*, we have created a random transposon mutagenesis library of *Ehrlichia* sp. HF using Himar1 transposon-based mutagenesis procedure. Previously 158 mutants were obtained. Of total additional 63 insertional HF mutants which I have obtained, 25 insertions were in the coding regions of 21 distinct protein-coding genes. Using limited dilution methods, partial clonal TRP120 HF mutant is obtained and tested in mice. The results showed TRP120 mutant is as virulent as wild-type HF in mice but has restricted tissue distribution. We expect *Ehrlichia* genes critical for *in vivo* virulence and for tick transmission will be identified by further cloning of mutants and analysis of *in vivo* mouse virulence and tick transmission studies, which will help develop effective therapies and preventive measures for HME. |
| Keywords for abstract: | *Ehrlichia* HF<br>Himar1 transposon mutagenesis<br>Mouse virulence<br>Inflammatory cytokines<br>Obligatory intracellular bacteria |

# STRUCTURE/FUNCTION

# SF - 1

| | |
|---|---|
| Title of abstract: | **RADIOGRAPHIC ASSESSMENT OF APPENDICULAR SKELETAL PATHOLOGY IN STRANDED PINNIPEDS (2013-2019).** |
| Authors | C. J. Kiefer, E. T. Hostnik, C. Field. College of Veterinary Medicine (Kiefer,Hostnik), The Ohio State University, Columbus, Ohio; The Marine Mammal Center (Field), Sausalito, CA. |
| Abstract | The Marine Mammal Center (Sausalito, CA) rescues hundreds of ill and injured marine mammals throughout Northern and Central California each year. Stranded pinnipeds commonly present with trauma from human activity and predators are common. The severity of these wounds often necessitates rescue for further assessment and characterization of the wound to plan for treatment and rehabilitation.. Radiography is integral in the diagnostic work up to screen for osseous trauma. Records from 48 stranded pinnipeds (42 California sea lions (Zalophus californianus), three Pacific harbor seals (Phoca vitulina richardii), two Northern elephant seals (Mirounga angustirostris), one Guadalupe fur seal (Arctocephalus townsendi)) were reviewed for this retrospective study. Radiography was included if an abnormality of the appendicular skeleton or bone involvement was suspected. Of the 48 individuals, 47 (97.9%) within the subset of rescued pinnipeds that received radiographs were immature. Forty-five (93.75%) had some version of osseous pathology (acute fracture or osteomyelitis); 3 (6.25%) were only soft tissue pathology. Soft tissue and/or bony injuries of multiple limbs were common, affecting 87.5% (42/48). Polyostotic lesions were identified in 70.8% of individuals (34/48). Most common sites of bony pathology were phalanges (35.4%), radius (29.2%), and carpal bones (18.75%). Radiographic findings consistent with erosive arthropathy was found in 31.25% of individuals (15/48). Five individuals had a sequestrum (10.4%) associated with lytic bone disease. Bony pathology is common in young, stranded pinnipeds. Radiography can be incorporated in health assessments to identify injuries and guide treatment/ rehabilitation plans. |
| Keywords for abstract: | Pinniped<br>Radiology<br>Bony pathology |

# SF - 2

| | |
|---|---|
| Title of abstract: | **CHARACTERIZATION OF RESISTANCE TO PRMT5 INHIBITOR THERAPY IN MANTLE** |
| Authors | M. Long, S. Koirala, S. Sloan, F. Brown, K. Corps, J. Helmig-Mason, S. Beck, J. Chung, B. Blaser, A. Alinari, R. Baiocchi. Depts. Of Veterinary Biosciences and Internal Medicine (Wexner) |
| Abstract | Mantle cell lymphoma (MCL) is an incurable B-cell Non-Hodgkin's lymphoma with a median survival time of 8-12 years if treated aggressively. The vast majority of MCL patients eventually relapse and those with refractory disease or who relapse on targeted therapies have a particularly poor prognosis with short survival. Protein arginine methyltransferase 5 (PRMT5) is an enzyme that drives symmetric dimethylation of histone arginine residues and is over-expressed in MCL. PRMT5 has been associated with epigenetic silencing of tumor suppressor genes and supporting multiple oncogenic drivers. For this reason, PRMT5 has emerged as an attractive therapeutic target to inhibit MCL cell survival and proliferation. Our group in collaboration with Prelude Therapeutics has developed a small molecule PRMT5 inhibitor (PRT-382) that exhibits significant anti-tumor activity in MCL cell lines (low nM range) and primary *in vivo* preclinical MCL murine models (10 mg/kg). While the anti-tumor activity of PRMT5 inhibition is encouraging, we have observed some treated animals to develop drug resistance leading to rapid progression of MCL tumor burden. Multiple MCL cell lines also show primary resistance to PRMT5 inhibition based on their half maximal inhibitory concentrations (IC50s) for PRT-382. In addition, prolonged culture of MCL lines with drug escalation has produced acquired drug resistance in several cell lines that persists even after prolonged culture (30d) in the absence of drug. Utilizing next generation sequencing technologies (scRNA-seq, RNA-seq, WES), we are characterizing the epigenetic and genetic alterations that contribute to PRT-382 resistant phenotypes. Several potential markers of increased sensitivity to PRMT5 inhibitor therapy have and continue to be investigated including MTAP deletion, p53 mutation status, dependency on other dysregulated PRMTs, and mutations in spliceosome genes. We hypothesize that identifying and targeting compensatory prosurvival pathways overamplified with PRMT5 inhibitor resistance will lead to the development of rational therapeutic strategies to circumvent it. |
| Keywords for abstract: | PRMT5<br>Mantle cell lymphoma<br>resistance |

# SF - 3

| | |
|---|---|
| Title of abstract: | **AGE ESTIMATION IN GREYHOUNDS USING PULP CHAMBER TO TOOTH WIDTH RATIO** |
| Authors | M Meihls, S Horvath. Department of Veterinary Clinical Sciences, The Ohio State University |
| Abstract | In veterinary medicine, there is currently no accurate method for age determination of canine patients after adult tooth eruption. An accurate means to determining age in canines could significantly affect the health care future of many dogs of unknown age who are receiving dentals. The frequency and affordability of dentals are increasing rapidly, thus the number of dogs that could benefit from an equation which could yield age is suspected to be significant. The final adult teeth erupt at about 7 months of age, after which all age estimations are educated guesses at best. Kvaal's method has been determined a successful technique to estimate age in humans, this method utilizes the pulp chamber to tooth width ratio in dental radiographs. This method was successful as it operated under the anatomical understanding that the pulp chamber width decreases relative to total tooth width as humans age; the same is suspected in canine patients. A population of greyhounds was selected because the U.S. greyhound population has readily discoverable birthdates due to their racing history. The selection of one breed also allowed for limitation of variables that may be present between breeds. The pulp chamber to tooth width ratio of the mandibular canines and mandibular fourth premolars was then determined using the program J Image. The datum analysis is expected to yield a linear regression equation that will allow birthdate estimation after the eruption of adult teeth. An equation with any level of precision would provide the veterinary community with the only reliable mechanism to age adult canine patients. This study could then be expanded to other breeds to determine if accuracy of pulp chamber to tooth width ratio age estimation has species-wide efficacy. |
| Keywords for abstract: | Age estimation<br>Greyhounds<br>pulp chamber<br>tooth width ratio<br>ratio,<br>age<br>tooth<br>dentistry<br>dental<br>dental radiographs |

# SF - 4

| | |
|---|---|
| Title of abstract: | **ASSESSMENT OF CAPILLARY RAREFACITON IN CATS WITH AND WITHOUT CKD** |
| Authors | Paschall R, Quimby J, Cianciolo R, McLeland S, Lunn K, Elliott J |
| Abstract | Feline chronic kidney disease (CKD) is histologically characterized by tubulointerstitial inflammation, tubular atrophy and fibrosis. Hypoxia is a key driver of fibrosis in CKD and is associated with capillary rarefaction (reduction in vascular density) in humans. The purpose of this study was to determine if capillary rarefaction occurs in cats with CKD.<br>Seventy-eight formalin-fixed paraffin-embedded kidney tissues collected at autopsy from cats with CKD (16 IRIS Stage 2, 18 IRIS Stage 3, and 24 IRIS Stage 4) and without CKD (10 young cats (≤9 years old) and 10 geriatric cats (≥10 years old)) were assessed. Percentage glomerulosclerosis, inflammation and fibrosis were scored as absent, mild, moderate or severe. Vascular structures were identified with a combination of CD31 immunohistochemistry and visual assessment. Consecutive high-power fields (40x), ten from the cortex and five from the corticomedullary junction (CMJ) were examined and an observer (masked to clinical data) identified, counted and colored the capillary area. Image analysis of the colored capillaries was used to determine average capillary size, and average % capillary area (capillary area/total area)<br>Capillary size was significantly smaller in CKD cats than cats without CKD in both the cortex and CMJ. Percent capillary area was significantly smaller in CKD cats than cats without CKD in both the cortex and CMJ. Capillary size in the cortex and CMJ and % capillary area in the cortex were negatively correlated with creatinine levels. Capillary size in the cortex was negatively correlated with % global glomerulosclerosis, fibrosis, and inflammation within the cortex. The capillary size in the CMJ was negatively correlated with fibrosis and inflammation within the CMJ. The % capillary area in the cortex was negatively correlated with % global glomerulosclerosis, fibrosis, and inflammation within the cortex.<br>Capillary rarefaction was observed in cats with CKD and was associated with severity of disease. Further exploration of novel treatments directed towards ameliorating capillary rarefaction is warranted |
| Keywords for abstract: | capillary density<br>chronic renal disease<br>feline<br>CD31 |

# SF - 5

| | |
|---|---|
| Title of abstract: | **EVALUATING THE IMAPCT OF TRANSPORT AND RELOCATION ON MARINE MAMMAL WELFARE THROUGH MEASUREMENT OF HAIR AND SALIVARY CORTISOL** |
| Authors | M.M. Winans, K. Cole, M. Flint, and K.A. George. Depts. of Animal Sciences and Veterinary Preventive Medicine |
| Abstract | As the field of animal welfare science continues to grow, there is an increasing need for valuable welfare indicators. Among these is the study of glucocorticoids as potential indicators of \`stress,' measured through a variety of biomarkers. In this study, The Ohio State University's Center for Human-Animal Interactions Research and Education (CHAIRE) and the Columbus Zoo and Aquarium (CZA) partnered for a longitudinal study which aimed to assess the welfare of their California sea lions (Zalophus californianus) throughout relocation from a temporary facility to permanent habitat at CZA, by measurement of cortisol. Cortisol concentrations in hair (HCC) were evaluated throughout the duration of the study (28 months) using a shave/re-shave method, and salivary cortisol (SCC), collected via oral swab, was measured throughout the transport process itself (~1 week). In our assessment of the long-term relocation, we found mean HCC of the population to be 3.069 ± 1.792 pg/dL, and HCC was significantly lower during baseline (M = 2.9432, SD = 1.2174) than acclimation (t4 = -3.18, p = .0335). From analysis of salivary cortisol during transport, we found that SCC was highest post-transport (LSMean = .765 μg/dL, t74 = 6.23, p < .0001), although only significantly different from pre-transport (t74 = -3.84, p = .0003) not transport itself (t74 =-1.74, p = .0856). We also established a species-specific range of SCC for California sea lions to be .447 ± .68 μg/dL, a novel contribution to marine mammal physiology. These findings indicate transport and relocation may have implications on sea lions' welfare, although cautious interpretation is necessary given factors such as the animals' prior experiences and the delicate nature of interpreting cortisol concentrations. While somewhat preliminary, we hope these findings will contribute to the growing field of marine mammal welfare science, particularly regarding transport and relocation. |
| Keywords for abstract: | animal welfare<br>cortisol<br>transport<br>endocrinology<br>marine mammals<br>sea lions<br>zoo |

# EDUCATIONAL

# EDU - 1

| | |
|---|---|
| Title of abstract: | **CHANGING THE CULTURE OF A MEDICAL VETERINARY COLLEGE STEEPED IN ACADEMIC TRADITION** |
| Authors | Jonathan Yardley, Brenda Buffington, Amanda Fark |
| Abstract | Background/Significance of the Problem<br>Factors that affect wellbeing, including burnout, are on the rise among healthcare professionals.. In 2009, veterinarians had the highest incidence of death by suicide of medical professions and twice as high as human physicians and dentists. Students within their first and second years of traditional veterinary school curriculum report the greatest levels of emotional exhaustion during the spring semester. The literature has very little information on burnout scores in veterinary medical students in the US, hower every one study indicated that 32% of first year veterinary medical students experienced clinical levels of depressive symptoms and elevated anxiety levels compared to medical students (14.3%) and the US general population (6.7%). These results are similar to unpublished findings collected within the College of Veterinary Medicine.<br>Purpose<br>Two major crises occurred at the College of Veterinary Medicine during the 2015-2016 academic year that had a significant negative impact upon the entire College community. As a result, many began to first question and then examine the how the rigors of the College's academic curriculum and the "hidden curriculum" potentially attributed to these events. These tragedies served as catalysts for change as the process of the examination of the College's culture began to take place, both from a grassroots and systematic perspective.<br>Methods<br>The Dean initiated a task force to create an all-encompassing wellbeing plan that would address the needs of the entire College community. Three years later, with combined efforts of faculty, staff, and students, new programs have been implemented in efforts to increase our overall wellness score which is currently the second lowest of all colleges at The Ohio State University* (unpublished data). The implementations are below.<br>o Health Athlete One-Day Programs (50 CVM employees have completed HA in 2019):<br>o MINDSTRONG a cogitative behavior therapy for increasing resilience<br>o Health & Wellbeing Committee established<br>o Student Driven Wellbeing efforts – |

### Results

Anecdotally, we have received very positive feedback from staff and students. We came in 1st place overall for the University wide walking competition. First and second year students enjoy the reprieve the hands-on skills course provides, which decreases the amount of time they spend sitting in lecture halls. The 4th year students said they now look forward to snack cart on Friday and enjoy a few minutes to take a break from the high stress of veterinary clinics.

### Discussion

In the future we would like to collect quality improvement data to guide our implementation of interventions. In July of 2020 all first year veterinary medical students will take a seven-week on line evidence-based cognitive-behavioral skills building program with a goal of improving resiliency and self-protective factors for the overall wellbeing of students before starting the fall. In June of 2020 all house officers of the veterinary medical center will take the same program “MINDSTRONG” program in person.

Results: See Chart

### Implications for linking evidence to activation in the real world or in future research.

The College of Veterinary Medicine has a lower overall sense of well-being because of working at Ohio State compared to the rest of the university cohort. We need more descriptive data and qualitative data for faculty, staff, students and house officers to discovery why this is happening. We have attempted a two prong approach to change the culture within the College of Veterinary Medicine: curricular change and promotion of wellbeing as a fundamental aspect of campus culture. Please see additional posters for implementation.

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | |
| | | **Ohio State supports me in my efforts to** | | | **It is important for Ohio State to support my efforts** | | | **I have a substantially higher overall well-being** | | |

| | | **achieve a healthy lifestyle.** | | | **to achieve a healthy lifestyle.** | | | **because I work for Ohio State.** | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | 2018 | 2017 | 2016 | **2018** | 2017 | 2016 | **2018** | 2017 | 2016 |
| **Strongly Agree/Agree** | **OSU Main** | 78% | 78% | 77% | 85% | 85% | 85% | 58% | 58% | 55% |
| | **Veterinary Med** | 75% | 64% | 66% | 81% | 76% | 84% | 38% | 42% | 47% |
| **Disagree/Strongly Disagree** | **OSU Main** | 6% | 6% | 6% | 3% | 3% | 3% | 10% | 10% | 12% |
| | **Veterinary Med** | 7% | 11% | 10% | 4% | 6% | 5% | 19% | 22% | 17% |