THE OHIO STATE UNIVERSITY

COLLEGE OF VETERINARY MEDICINE

COLLEGE OF VETERINARY MEDICINE RESEARCH DAY

4 APRIL 2019

BOOK OF ABSTRACTS

PROGRAM

April 4, 2019

POSTER JUDGING

Graduate Student Posters
8:00 am – 11:00 am
(closed session – only open to those being judged)

AWARDS PRESENTATION

Dunlap Auditorium
12:00 pm

GRADUATE STUDENT PLATFORM PRESENTATIONS

Stasia Sullivan
Jack Wellmerling

KEYNOTE SPEAKER

Dunlap Auditorium
immediately following the awards and platform presentations

DR. Nicole Ehrhart

Professor
Colorado State University

"Limb Salvage in the Age of Regenerative Medicine: Pitfalls, Potential and Solutions"

POSTER SESSION

1st and 2nd Floors – Vet Med Academic Building
11:00 am – 4:00 pm

CHAIRED BY

Dr. Stephen Jones

ORGANIZED BY

Michele Morscher

Special thanks to Marc Hardman in the College's Technology Services for printing the posters

POSTER JUDGING SESSIONS

Wednesday, April 3, 2019
2:00 – 5:00 pm
Undergraduate and
Veterinary Student Poster Judging

Thursday, April 4, 2019
8:00 – 11:00 am
Graduate Student and PostDoc Poster Judging

Thank you to the following faculty and guests for taking time out of their busy schedules to judge 104 posters.

Andreia Goncalves Arruda
John Bartlett
Estelle Cormet-Boyaka
Nicole Ehrhart
Joelle Fenger
Rebecca Garabed
Alison Gardner
Vanessa Hale
Rebecca Jackson
Stephen Jones
Sanggu Kim
Bill Kisseberth
Krista La Perle Antoinette
Namal Liyanage
Marsh
Eric Miller
Sarah Moore
Georgina Newbold
Stefan Niewiesk
Mike Oglesbee
Gary Pierzynski
Yasuko Rikihisa
Ramiro Toribio
Christopher Weghorst

College of Veterinary Medicine

Research Day

Awards Presentation, Graduate Student Platforms, and Keynote Address

Thursday, April 4, 2019

Noon – 2:00 pm Dunlap Auditorium

"Limb Salvage in the Age of Regenerative Medicine: Pitfalls, Potential and Solutions"

Nicole Ehrhart, VMD, MS, DACVS

Professor, Surgical Oncology

Colorado State University

Poster Judging:

April 3rd, 2 – 5 pm for professional students

April 4th, 8 – 11:00 am for graduate students

THE OHIO STATE UNIVERSITY
COLLEGE OF VETERINARY MEDICINE

Office of Research and Graduate Studies

MCB – 17
Platform Presentation

Title of abstract:	**COMPARITIVE EFFECTS OF METHYLPREDNISOLONE AND TRIAMCINOLONE ON ENDOGENOUS DEEP DIGITAL FLEXOR TENDON AND NAVICULAR FIBROCARTILAGE CELLS**
Authors	S. Sullivan*, S. Cole+, M. Brokken*, S. Durgam* * Dept. of Veterinary Clinical Sciences, +Campus Microscopy Imaging Facility
Abstract	Navicular disease is a common cause of lameness in athletic horses where clinical signs are largely associated with pathologies in 'deep digital flexor tendon' (DDFT) and apposing 'navicular bone fibrocartilage' (NB). Although intrasynovial corticosteroids are widely used in navicular disease due to their anti-inflammatory properties, their effect on endogenous cells present in DDFT and NB is unknown. The objective of these experiments was to evaluate the effect of triamcinolone acetonide (TA) and methylprednisolone acetate (MPA) on metabolic activity and viability of DDFT and NB cells in an ex-vivo explant culture model. Explants from DDFT and NB were harvested sterilely from freshly euthanized adult horses (n=4). Explants were equilibrated in-vitro for 24-48 hours prior to culture with TA (0, 0.6 and 6mg/mL) and MPA (0, 0.5 and 5mg/mL). Metabolic activity of explants was measured using Alamar Blue assay at 6h and 24h of culture. Similarly, live-dead assay was conducted with Calcein-Sytox staining followed by fluorescent confocal microscopy. Quantitative image analysis for live-dead cells was conducted with Imaris Software. Data was analyzed with repeated measures two-way ANOVA (significance set at $p<0.05$). High dose (5mg/mL) MPA significantly reduced the metabolic activity of NB cells alone (38%, <0.003) at 6h, and DDFT (52%, <0.001) and NB cells (59%, <0.001) at 24h compared to untreated controls (Figure 1). In contrast, TA (both doses) did not significantly affect the metabolic activity of DDFT and NB cells at either timepoints. These findings were corroborated by live-dead confocal images (Figure 2). This in-vitro data demonstrates that MPA is more toxic to DDFT and NB cells than TA. Our current experiments are focused on assessing corticosteroids' effects on transcriptional activities of these cells. Accepting that these are in-vitro experiments, they serve as a guideline for future in-vivo work to determine the optimal intrasynovial corticosteroid for horses with navicular disease.
Keywords for abstract:	Navicular disease - Horse chondro-/teno-toxicity corticosteroids

MCB – 18
Platform Presentation

Title of abstract:	**TARGETING THE EGFR-ERK AXIS TO STABILIZE CFTR IN CYSTIC FIBROSIS**
Authors	J. Wellmerling, S. Chang, and E. Cormet-Boyaka Department of Veterinary Biosciences, Ohio State University
Abstract	Cystic Fibrosis (CF) is a life-limiting autosomal recessive disorder associated with chronic lung infection and inflammation caused by mutation in the gene encoding the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR). CFTR is a chloride channel responsible for maintaining adequate airway hydration. The most common CFTR mutation, F508del, results in severely reduced CFTR activity through impaired protein trafficking, channel gating, and plasma membrane stability. CFTR modulators and potentiators, which address trafficking and gating, respectively, have been developed. However, membrane stability of F508del CFTR remains an issue. Our laboratory has previously demonstrated that activation of Extracellular-Regulated Kinase (ERK) leads to CFTR degradation. We report that ERK signaling is constitutively active in CF airway epithelial cells due to signaling by the Epidermal Growth Factor Receptor (EGFR). Compared to controls, CF cells produce and shed the EGFR ligand Transforming Growth Factor-Alpha in excess. Our data show that this axis plays a role in regulation of F508del-CFTR. Next, we assessed the feasibility of improving CFTR membrane stability with the osmoprotectant ectoine. Ectoine stabilizes macromolecules through the biophysical principle of preferential exclusion, and has previously been shown to attenuate EGFR signaling by preventing its loss from lipid rafts and subsequent intracellular translocation. We show that ectoine suppresses ERK signaling in primary human airway epithelial cells from F508del-homozygous CF donors. Using cycloheximide chase, we show that ectoine increases the membrane half-life of pharmacologically rescued CFTR in a human CF bronchial epithelial cell line by 122%. Finally, we show by trans-epithelial short-circuit current measurements that ectoine increases CFTR-mediated chloride transport beyond what is accomplished by modulator alone, suggesting it may be beneficial for CF patients on modulator therapy.
Keywords for abstract:	Cystic Fibrosis EGFR ERK

CLINICAL RESEARCH

CR - 1

Title of abstract:	**FISH SPERM PHYSIOLOGY AND ITS IMPLICATIONS FOR CRYOPRESERVATION'S IMPACT ON FERTILIZATION IN THE SAUGER (*SANDER CANADENSIS*)**
Authors	Blawut, B., Wolfe, B., Schuenemann, G., Premanandan, C., Ludsin, S.A., Coutinho da Silva, MA. Depts. Of Veterinary Preventive Medicine, Veterinary Clinical Sciences, and Ecology, Evolution, and Organismal Biology.
Abstract	Previous attempts to cryopreserve sauger (*Sander canadensis*) milt for long-term storage to minimize yearly variability in saugeye (*S. vitreus x S. canadensis*) production have resulted in poor fertilization (< 15%) despite seemingly high post-thaw motility (60-70%) and viability (80%). This lack of fertility is the primary factor preventing hatchery-level application of cryopreserved sauger sperm. Unlike fish species, mammalian sperm cryopreservation been elevated to large-scale application via freezing media that conserves the ability of sperm to undergo a well-documented series of physiological changes leading to fertilization, known as capacitation. **Currently, it is not known whether fish sperm undergo a process similar to capacitation preceding fertilization or how cryopreservation might impact this process.** Therefore to address this question, we aim to compare sauger sperm physiological traits related to mammalian sperm maturation and capacitation among different sperm types and activation statuses during the spring of 2019. *Our central hypothesis* is that freshwater fish sperm physiology progresses to a peak fertile state as a result of maturation within the main testicular duct and motility activation via hyposmotic shock and that cryopreservation will negatively affect this status. Fist, we will assess *in vivo* maturation by comparing the male reproductive tract structure, seminal plasma composition, and sperm ultrastructure at different locations within the tract using histology and electron microscopy. Secondly, we will compare physiology traits among three different types of spermatozoa (**testicular, ejaculated, cryopreserved**) in two different states (**inactive, activate**) based on: glycocalyx characteristics, plasma membrane characteristics, and intracellular signaling using standard fluorescent microscopy, flow cytometry, and proteomic methods. We believe our research will help to better understand normal fish sperm physiology, its development, and mechanisms by which freezing impact those traits. The results of which are likely to advance cryomedia's ability to boost fertility to a level acceptable for large-scale application of frozen fish sperm.
Keywords for abstract:	**Spermatozoa, Capacitation, Fish, Physiology, and Cryopreservation**

CR – 2

Title of abstract:	**A NOVEL TECHNIQUE TO QUANTIFY SPASTICITY IN DOGS WITH SPINAL CORD INJURY**
Authors	Lane Bookenberger, Josey Sobolewski, Sarah Moore
Abstract	Spasticity is an important long-term complication of spinal cord injury (SCI) in people, resulting in increased muscle tone and painful spasms which negatively impact everyday life. There is little published information on the prevalence of spasticity in dogs with SCI and techniques to measure canine spasticity are limited. The aim of this study is to develop a novel technique to objectively quantify spasticity using a hand-held dynamometer, a device that measures resistance to passive muscle movement. The objective of this study is to evaluate reliability of a hand-held dynamometer and to assess its utility to quantify spasticity in dogs. We hypothesize that measures of muscle resistance obtained using the hand-held dynamometer will be reliable across testing sessions in normal dogs and will differ between normal and SCI-affected dogs. Ten clinically normal dogs will be initially enrolled. Dogs will be evaluated in both lateral recumbency and standing positions, and passive resistance to flexion and extension of several joints will be recorded in triplicate then averaged to produce a single value for each measure. Normal dogs will undergo two testing sessions separated by one hour and results compared between sessions. Once reliability of the technique has been established in normal dogs, SCI-affected dogs will be enrolled for comparison. The results of this study will provide partial-validation of a novel approach to measure one aspect of spasticity in dogs with SCI and will serve as preliminary data for future projects further evaluating the utility of SCI-affected dogs as a translational model of spasticity and for projects evaluating novel therapies to treat spasticity in SCI-affected individuals across species.
Keywords for abstract:	Spasticity Spinal cord injury

CR - 3

Title of abstract:	**RETROSPECTIVE EVALUATION OF CATARACTS AND LONG-TERM VISION OUTCOME FOLLOWING PHACOEMUSIFICATION IN A POPULATION OF AMERICAN COCKER SPANIELS: 186 CASES**
Authors	C. Brines, A. Gemensky-Metzler, T Wickware, E Miller, G Mitchell, and H Chandler. Departments of Veterinary Clinical Sciences and The College of Optometry
Abstract	**Purpose.** To determine clinical features and outcome in American Cocker Spaniels (ACS) diagnosed with cataracts. **Methods**. Medical records of ACS that presented for cataract evaluation between 1998-2015 were reviewed (n=182). Concurrently, a random sample of non-ACS undergoing phacoemulsification (n=105) in one or both eyes was evaluated as a comparison population. Data was analyzed via descriptive statistics, student's t-test and chi-square analysis with a p-value <0.05 considered significant. **Results.** American Cocker Spaniels most commonly presented with hypermature cataracts (40.98%); 61.33% (n=92) of these underwent phacoemulsification to restore vision. Younger ACS were significantly more likely to undergo phacoemulsification than older ACS (median age 5.0 vs. 8.6 years). American Cocker Spaniels undergoing phacoemulsification had a significantly lower prevalence of diabetes mellitus (n=7; 7.78%) compared to the sample population (n=54; 51.4%). At the last post-phacoemulsification examination, significantly fewer ACS remained visual compared to non-ACS dogs (72.2% vs. 85.7%) with a similar median follow-up time (415 days vs. 422 days). The most common reasons for vision loss in the ACS included glaucoma (19.1%), severe keratitis (3.37%), and retinal detachment (2.25%). Glaucoma developed post-phacoemulsification more commonly in ACS compared to non-ACS (19.1% vs. 12%, p<0.05). **Conclusions.** American Cocker Spaniels that presented for phacoemulsification were younger with hypermature inherited cataracts compared to non-ACS which were older, more frequently diabetic and most commonly presented with mature cataracts. For both groups, the most common reason for vision loss post-phacoemulsification was glaucoma with a higher prevalence in ACS dogs. **None.**
Keywords for abstract:	American Cocker Spaniel Phacoemulsification Cataract Glaucoma Canine

CR - 4

Title of abstract:	**METHODS TO IMPROVE AND MONITOR INTRAOPERATIVE THERMOREGULATION IN RODENT SURGERY**
Authors	N. Celeste, D. Mackessy, N. Burkey, K. Emmer, M. Perret-Gentil, R. Malbrue University Laboratory Animal Resources, Department of Veterinary Preventive Medicine
Abstract	General anesthesia induces many systemic effects, which notably includes thermoregulatory impairment and subsequent perioperative hypothermia. Due to their small size, monitoring and maintaining body temperatures in rodents and other small companion mammals during procedures is critical for successful surgical outcomes and prompt anesthetic recovery. Draping materials have the potential to aid in thermal support during surgical procedures requiring anesthesia. In this study, core (rectal) and surface (infrared) temperatures were measured every 5 min. for the duration of a 35 min. simulated surgery in C57BL/6 mice using isoflurane anesthesia. Mice were draped with commercial cling film (Press'n Seal®; CF), conventional paper drape (PD), or no drape (ND) during surgery (n = 6/group). Results indicated that CF-draped animals had higher rectal temperatures than both paper-draped (p = 0.0351) and non-draped animals (p < 0.0001). Furthermore, CF-draped infrared temperatures were also significantly higher than both paper-draped (p < 0.0001) and non-draped temperatures (p < 0.001). These data suggest that cling film is able to maintain body temperature better than other draping options; thus, it is an effective thermal support aid for small mammals requiring general anesthesia.
Keywords for abstract:	Mice, Body Temperature, Thermoregulation, Hypothermia, Rodent Surgery, Surgical Drape

CR - 5

Title of abstract:	**C-REACTIVE PROTEIN IN HYPERTENSION AND IMMUNE-COMPLEX GLOMERULAR DISEASE**
Authors	W. Cole, C. Langston, J. Hokamp, R. Cianciolo. Departments of Veterinary Clinical Sciences and Veterinary Biosciences
Abstract	Approximately half of dogs undergoing renal biopsy for proteinuria have immune-complex glomerulonephritis (ICGN). Preliminary data suggests that hypertension may be more common with ICGN. CRP elevations have been shown to correlate with hypertension in people. We hypothesized that CRP would be associated with hypertension and with a diagnosis of ICGN in dogs. The International Veterinary Renal Pathology Service database of previously obtained renal biopsies was used to select patients with documented systolic blood pressure measurement who also had stored serum samples for CRP measurement. Normotension was defined as </= 150 mmHg systolic blood pressure, while dogs with a documented systolic blood pressure >150 mmHg were classified as hypertensive. Groups were compared using a t-test. Thirty-nine dogs meeting our criteria have been evaluated. They have been categorized as non-ICGN normotensive (n=10), non-ICGN hypertensive (10), ICGN normotensive (7) and ICGN hypertensive (12). Comparison of CRP concentrations amongst these four categories did not show statistically significant correlations. However, CRP concentration was higher in hypertensive dogs (median 27.65 mg/L) compared to normotensive dogs (median 3.65 mg/L, $p<0.01$). A similar correlation was not identified between ICGN and non-ICGN groups, but the study was underpowered to detect a difference. The correlation between hypertension and an inflammatory biomarker such as CRP supports a role for hypertension in inducing inflammatory vascular lesions.
Keywords for abstract:	C-Reactive Protein Hypertension Canine Dog Glomerular Disease Immune-Complex Glomerular Nephritis

CR - 6

Title of abstract:	**RADIOGRAPHIC TRACHEAL DIMENSIONS AND TRACHEAL LUMEN TO VERTEBRAL RATIOS IN THE NORMAL AMERICAN MINIATURE HORSE**
Authors	Every LJ, Hostnik ET, Dunbar L, Yardley J Department of Veterinary Clinical Sciences
Abstract	Literature describing tracheal collapse in the American Miniature Horse is limited to severe cases. This study aimed to describe radiographic parameters for tracheal luminal diameter in clinically normal American Miniature Horses, report the prevalence of tracheal collapse in a population of subclinical American Miniature Horses, and fluoroscopically assess the variation in tracheal luminal diameter throughout the respiratory cycle. Thirty-four American Miniature horses were recruited. The prevalence of subclinical tracheal collapse within this study population was 14.7% (5/34), higher than previously reported. Lateral radiographic and fluoroscopic images were obtained for 29 normal horses followed by sedated tracheoscopy. Horses with tracheal collapse identified on tracheoscopy were excluded. A subset of the population statistics including the mean tracheal diameter (Tr) to vertebral body height (H) ratios, 95% confidence interval, and a bootstrapped 95% reference interval are: C4Tr:C4H 1.23 (+/- 0.109)(0.61-1.82), C6Tr:C6H 1.01 (+/-0.086)(0.52 – 1.47), T1Tr:T1H 0.75 (0.059)(0.42 – 1.07), and T3Tr:T3H 0.90 (0.076)(0.46 – 1.31). The mean tracheal diameter (Tr) to vertebral body length (L) ratios, 95% confidence interval, and a bootstrapped 95% reference interval are: C4Tr:C4L 0.40 (+/-0.033)(0.22-0.58), C6Tr:C6L 0.40 (+/- 0.033)(0.21-0.58), T1:T1L 0.57 (+/- 0.042)(0.32 – 0.79), and T3:T3L 0.71 (0.056)(0.43 – 1.04). There was no statistically significant difference in tracheal luminal diameter on video fluoroscopy during respiration, suggesting phase of respiratory cycle need not be a significant consideration when obtaining lateral tracheal radiographs. To the authors' knowledge, this is the first study to describe radiographic tracheal luminal dimensions in the American Miniature Horse.
Keywords for abstract:	American Miniature Horse Trachea Radiograph Ratio

CR - 7

Title of abstract:	**FEMORAL REMODELING IN DOGS WITH LUXATED DYSPLASTIC HIPS. A COMPLICATING FACTOR FOR TOTAL HIP REPLACEMENT**
Authors	Mariana Fernandez, Jonathan Dyce. Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio.
Abstract	Hip dysplasia is one of the most common orthopedic diseases in dogs. If the condition is refractory to medical management, the preferred treatment for this condition can be total hip replacement (THR). In young dogs, chronic luxation of the dysplastic hip (luxoid conformation) is associated with remodeling changes within the femur. One characteristic of luxoid hip conformation is the lateral migration of the proximal medial femoral cortex. The resultant narrowing of the proximal femur encroaches on an appropriate envelop of femoral broaching. The goal of the study is to identify specific patterns of femoral remodeling in the luxoid situation. Radiographs of the last 200 cases of THR performed at the OSU Veterinary Hospital were grouped into luxoid and uncomplicated hip dysplasia. The age, weight, breed, sex of the patient was recorded. It was identified that 31% of dogs undergoing a THR had a luxoid hip. It was recognized that Golden Retrievers are 4 times more likely to have luxoid hips compared to German Shepherds (OR = 4.06, P = 0.017). German Shepherds are also less likely to have luxoid hips compared to the remaining breeds. CT Scans in record were categorized into luxoid and normal. These studies were used to create 3D models to study differences in cross sectional area (CSA) throughout the proximal femur in the region of stem insertion. To compare CSA in a normalized fashion, the femurs were calibrated by length. The goal is to prove that the CSA of the femoral canal of the luxoid hip is significantly different to that of a normal femur. Defining the pattern of femoral remodeling in the luxoid hip and publicizing this data should reduce the risk of surgical complication, in particular femoral fissure and fracture.
Keywords for abstract:	Hip Dysplasia Total Hip Replacement Luxoid Conformation Femur remodeling THR Luxation Luxated femur Luxated hip

CR - 8

Title of abstract:	**EVALUATION OF BIOFILM PRODUCTION BY *ESCHERICHIA COLI* ISOLATED FROM CLINICAL CASES OF CANINE PYOMETRA**
Authors	T.E. Fiamengo,[a] E.E. Runcan,[a] C. Premanandan,[b] M.A. Coutinho-da Silva[a] [a]Department of Veterinary Clinical Sciences; [b]Department of Veterinary Biosciences
Abstract	Many *Escherichia coli* strains produce biofilm that confers antimicrobial resistance, and is suspected to result in recurrent canine pyometria. This study aimed to investigate biofilm production by *E. coli* in pyometra by: 1) assessing the ability of *E. coli* to produce biofilm *in vitro,* and 2) confirming biofilm *in situ*. We hypothesized that most *E. coli* strains from canine pyometra produce biofilm *in vitro* and *in vivo.* Samples were obtained from clinical cases of pyometra during ovariohysterectomy; a uterine swab sample was collected and submitted for aerobic culture and uterine segments were preserved for microscopic analysis (n=23). Isolated bacteria were identified by MALDI. Samples with confirmed *E. coli* were evaluated further. Optical densities from biofilm assay were compared by ANOVA, using StatPlus software. Significance was set at $P<0.05$. Histopathology, FISH and SEM were all used to evaluate the endometrium for the presence of bacteria and/or a fibrous matrix. Seventy percent of cases (16/23) resulted in pure growth of one or two *E. coli*, totaling 20 isolates. Fifteen isolates (15/20, 75%) had higher optical densities then negative controls ($P<0.05$). On histopathology, all tissues exhibited endometrial inflammation and mucus was located within cystic endometrial glands and/or overlying epithelium on 14 slides (14/16, 88%). Bacteria was noted in 50% of slides (8/16). During FISH, acellular debris within the uterine lumen consistent with biofilm formation was noted on 94% of samples (15/16) and *E coli* was positively identified on all samples. Areas suggestive of biofilm were observed on all samples on SEM; but, bacteria consistent with *E. coli* were only visualized in nine samples (9/16, 56%). In conclusion, we demonstrated that relevant strains of *E. coli* produce biofilm *in vitro* and *in vivo,* rejecting the null hypothesis. Development of new pyometra treatments aimed at disrupting *E. coli* biofilms may enhance therapeutic efficacy.
Keywords for abstract:	*Escherichia coli* Biofilm Canine pyometra

CR - 9

Title of abstract:	**COMPUTED TOMOGRAPHIC ATTENUATION VALUES CAN HELP DIFFERENTIATE BETWEEN DOGS WITH AND WITHOUT GALLBLADDER MUCOCELES**
Authors	J. Fuerst, E. Hostnik
Abstract	Gallbladder mucoceles are a potentially fatal biliary disease in dogs. The study aimed to describe the imaging characteristics of the canine gallbladder in three conditions: no sludge, sludge occupying ≥ 25% of the lumen, and mucoceles using computed tomography. Twenty dogs with normal hepatobiliary bloodwork and no gallbladder sludge, 13 dogs with normal bloodwork and ≥ 25% sludge in the gallbladder lumen, and 18 dogs with histologically confirmed gallbladder mucoceles underwent abdominal CT angiography. Three regions of interest (ROI) were stratified within the gallbladder and a single ROI within adjacent hepatic parenchyma. Mean attenuation in each ROI and presence of mineral were recorded. Average Hounsfield units (HU) were recorded for pre-contrast, arterial, portovenous, and late venous phases. The overall median HU value for dogs with no sludge, dogs with sludge, and gallbladder mucoceles in pre-contrast images was 35.8 HU, 39.7 HU, and 49.3 HU, respectively ($p<0.000004$). Mineral was seen in 4 (20%) dogs with no sludge, 7 (56%) dogs with sludge, and 9 (50%) dogs with mucoceles. Mineral in the dogs with mucoceles was suspended within the central aspect of the gallbladder lumen in a majority of dogs (67%) while this pattern was not seen in any dog without a mucocele. Computed tomography can differentiate gallbladder mucoceles from dogs with and without sludge, especially in the pre-contrast series. Though ultrasound is likely to remain the diagnostic of choice, a hyperattenuating gallbladder on pre-contrast images and corresponding hepatobiliary bloodwork abnormalities could be used to screen for gallbladder mucoceles.
Keywords for abstract:	CT Microlithiasis Canine

CR - 10

Title of abstract:	**EX VIVO BIOMECHANICAL EVALUATION OF TISSUE CONSTRUCT STRENGTH IN EQUINE COLOPEXY USING DIFFERENT SUTURING TECHNIQUES**
Authors	H.M. Gaitan, M.C. Mudge, A.S. Litsky, and A.K. Gardner. Depts of Veterinary Clinical Science and Biomedical Engineering
Abstract	Large colon volvulus and displacement are life-threatening conditions observed in horses. Colopexy is a surgical technique where the lateral band of the left ventral colon is sutured to the abdominal wall. Unfortunately, the colopexy may dehisce from the abdominal wall, predisposing the horse to loss of colopexy if failure is at the body wall or death if the colon ruptures at the colopexy site. Differing techniques for colopexy have been performed, but research on best practices is scarce. The aim of our study was to evaluate the strength of a tissue construct composed of the abdominal wall and lateral band of the colon at the colopexy site utilizing biomechanical testing. A colopexy was performed by the same surgeon in six equine cadavers euthanized for reasons separate from gastrointestinal pathology. Animals selected were between 2 and 25-years-old, had no known history of colic, and a body condition score >2. Distance between suture bites, suture knots, and colopexy distance from ventral midline were standardized, as well as suture material used. The order from cranial to caudal of our two variables, which included suture pattern (horizontal vs cruciate) and incorporation of solely dorsal sheath of the rectus abdominus muscle vs incorporation of both dorsal and ventral sheath were randomized. Load to failure and failure mode were assessed by testing the construct strength. Descriptive data indicated failure at body wall for 4/6 of samples in which a cruciate suture pattern and partial thickness colopexy were performed, while all other failure modes were at the colon. Regardless of mode to failure, the strength of the construct from cranial to caudal was not significantly different ($p=0.34$), nor was pexy strength between variables studied ($p=0.29$). Colopexy techniques such as suture pattern and depth of suture bite may impact failure mode but not strength of the tissue construct.
Keywords for abstract:	equine colopexy tissue construct strength biomechanical techniques suturing techniques

CR - 11

Title of abstract:	**MECHANICAL QUANTITATIVE SENSORY TESTING IN A CANINE TRANSLATIONAL MODEL OF NEUROPATHIC PAIN: DESCRIPTION AND PILOT INVESTIGATION**
Authors	A. Hechler, E. Hostnik, L. Cook, L. Cole, S. Moore
Abstract	Syringomyelia (SM) occurs commonly in pet Cavalier King Charles Spaniel (CKCS) dogs, causes behaviors suggestive of neuropathic pain, and may serve as a spontaneous pain model for translational studies; however, quantitative measures of sensory dysfunction in affected dogs have not been previously documented. The aim of this study was to compare mechanical sensory threshold (ST) in CKCS with and without SM and to assess the relationship between ST, severity of SM on MRI, and pain scores obtained from a previously validated owner-derived pain scale. We hypothesized that SM-affected dogs would have lower ST than controls and that ST in affected dogs would inversely correlate with syrinx size and with owner-derived pain scores. CKCS with (n=19) and without (n=10) SM had ST measured by electronic von Frey anesthesiometer. Groups were compared using Wilcoxin rank-sum. Associations between ST, pain score, and MRI findings were evaluated by linear regression. Median ST (range) in thoracic limbs was 184.1 grams (120.9-552) for control, and 139.9 grams (52.6-250.9) for SM-affected dogs. Median ST in pelvic limbs was 164.9 grams (100.8-260.3) for control, and 129.8 grams (57.95-168.4) for SM-affected dogs. ST for thoracic and pelvic limbs was lower in SM-affected dogs ($p=0.027$; $p=0.0396$), suggestive of hyperesthesia. Pelvic limb ST was inversely correlated with owner-derived pain scores, where dogs with lower ST displayed more severe pain signs ($r=-0.657$; $p=0.022$). Our results suggest that VFA may offer an objective assessment of neuropathic pain CKCS with SM and could be useful in future translational pain therapy studies.
Keywords for abstract:	Quantitative sensory testing Neuropathic pain Syringomyelia Chiari-like malformation Von Frey Anesthesiometry cavalier King Charles spaniel

CR - 12

Title of abstract:	**SERUM ALUMINUM CONCENTRATIONS IN HEALTHY CATS AND CATS WITH CHRONIC KIDNEY DISEASE**
Authors	C. Johnson and C. Langston (of the Ohio State University College of Veterinary Medicine, Columbus, OH) and C. Bloom (of the Animal Medical Center, New York, NY)
Abstract	The use of aluminum-containing phosphate binders in humans with chronic kidney disease (CKD) has been discontinued due to documented aluminum toxicity. Aluminum hydroxide is a first-line treatment in cats with CKD and hyperphosphatemia, but serum aluminum levels have not been investigated in these cats. The purpose of this s tudy was to compare serum aluminum levels between healthy cats, cats in various stages of CKD, and those taking aluminum-containing phosphate binders (aluminum hydroxide). Inductively coupled plasma mass spectrometry was used to measure serum aluminum concentrations. Serum samples were collected prospectively from healthy cats presented to the clinic for wellness evaluation or routine follow-up for cats with chronic kidney disease. 23 healthy cats, 41 cats with CKD not receiving aluminum hydroxide (20 with IRIS stage II, 12 with IRIS stage III, and 7 with IRIS stage IV), and 9 cats with CKD receiving aluminum hydroxide were included. No significant difference in serum aluminum concentration was found when comparing healthy cats (median 0.061, interquartile range [IQR] 0.034-0.132) to cats with IRIS stage II CKD (median 0.041, IQR 0.031-0.047), stage III CKD (median 0.033, IQR 0.029-0.044), stage IV CKD (median 0.032, IQR 0.028-0.050) and cats taking aluminum hydroxide (median 0.038, IQR 0.033-0.044). Administration of aluminum hydroxide to cats with CKD does not appear to result in statistically significant increases in serum aluminum concentration.
Keywords for abstract:	Chronic kidney disease Aluminum hydroxide Hyperphosphatemia

CR - 13

Title of abstract:	**COMPUTED TOMOGRAPHY TO EVALUATE HEPATIC ATTENUATION IN THREE SPECIES OF FRESHWATER TURTLES**
Authors	Emily M. King, Eric T. Hostnik, Randall Junge, Michael Adkesson, Erin Newman, Matt Allender Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH (King, Hostnik); Columbus Zoo and Aquarium (Junge); Chicago Zooogical Society/Brookfield Zoo (Adkesson); Department of Veterinary Clinical Medicine, College of Veterinary Medicine, University of Illinois, Urbana, IL (Newman, Allender).
Abstract	Freshwater turtle species are suffering from anthropocentric-caused population declines, making preservation of managed populations increasingly important. Turtles under human care have an increased risk to develop hepatic lipidosis, potentially resulting in early death. Computed tomography (CT) provides a more reliable and detailed approach to screen disease and provide antemortem diagnosis of increased fatty liver composition. Hepatic attenuation values (measured as Hounsfield units (HU)) of Vietnamese Pond turtles (10) and Northern Snake-Necked turtles (6) under human care and wild Blanding's turtles (95) were measured and recorded using CT studies. There were significant differences in hepatic attenuation between Vietnamese Pond, Northern Snake-Necked, and Blanding's turtles, with median HU values (95% confidence interval) of 5.39 HU (-6.45-61.50), 71.74 HU (59.44-94.49) and 95.42 HU (78.55-116.37), respectively. Bloodwork was performed in the two species under human care. The AST values were significantly higher in Vietnamese Pond turtles, and the HU were significantly lower. The lower attenuation values negatively correlated to higher AST. Blanding's turtles undergoing folliculogenesis presented with higher HU, suggesting a potential use of hepatic lipid stores for egg production. Overall, the findings demonstrate species variation, with CT analysis that demonstrated a negative correlation of HU and AST in two managed species; CT can therefore be used as a screening tool for hepatic lipidosis. Moreover, the results indicate further need to assess natural species variation on CT, which will aid in more accurate diagnosis.
Keywords for abstract:	Radiology Computed Tomography Chelonians Zoo Medicine Hepatic lipidosis Folliculogenesis

Title of abstract:	**FIELD USE OF ALFAXALONE IN MALLARD DUCKS (ANAS PLATYRHYNCHOS) AND POTENTIAL COMPLICATIONS**
Authors	T. Kruse, M. Flint, K. Messenger, J. Lorbach, A. Bowman, T. Aarnes, and T. Wittum. Depts. of Molecular Biomedical Sciences, Preventative Veterinary Medicine, and Veterinary Clinical Sciences at The Ohio State University and North Carolina State University
Abstract	Inhalant anesthetic agents are the most common in-hospital method for anesthetizing waterfowl. However, the cumbersome equipment and fluctuating anesthetic depth seen are confounding factors for field-based projects. Investigators performed a pharmacokinetics and pharmacodynamics study of injectable alfaxalone in a 2-hydroxypropyl-beta-cyclodextrin formulation (Alfaxan®) as a potential field anesthetic in juvenile and adult mallard ducks. A pilot study was performed to assess the safety of this drug administered IV and IM on six ducks from Northern Ohio at concentrations of 2.5 and 5 mg/kg IV. Then a randomized cross-over study was performed on ten separate ducks administered concentrations ranging from 10 to 15 mg/kg IV and IM. Plasma alfaxalone concentrations, heart and respiratory rates, and sedative effects were recorded to objectively assess plane of anesthesia at each pre-determined blood collection times following injection (0, 5, 10, 30, 60, and 90 minutes). Three out of 16 ducks died after being administered varying concentrations of alfaxalone. On gross necropsy all of them were found to have a persistent foramen ovale (PFO). In the literature on domestic chickens, embryos have two PDAs as a normal occurrence but constricts once hatching begins to allow increase blood flow through the arteries to the lungs. Persistance to adulthood was theorized to be a congenital anomaly that may negatively influence the use of alfaxalone as a safe field anesthetic in mallard ducks. In collaboration with Winous Point Conservancy, investigators are pursuing a field-based study to determine the true prevalence of PFOs in mallard ducks from this migratory region as a key factor in determining the suitability of Alfaxan as a field anesthetic. If this anomaly is found to be prevalent in this population, alternatives to Alfaxan will be examined in an attempt to eliminate the need for field inhalation anesthetics in waterfowl.
Keywords for abstract:	Alfaxalone Ana platyrhynchos Mallard duck Persistent foramen ovale Pharmacokinetics Pharmacodynamics

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Title of abstract:	**ASSESSING ACCURACY OF POST-MORTEM URINALYSES IN DOMESTIC SPECIES**
Authors	V. Lama, J. Hokamp
Abstract	Background: Urinalysis (UA) allows minimally invasive evaluation of local and systemic diseases. When UA cannot be performed pre-mortem, clinicians might evaluate post-mortem UA results. Studies have not determined the accuracy of post-mortem UA. Objective: Determine if post-mortem UA is an accurate substitute for pre-mortem UA. Hypothesis: Pre- and post-mortem urine protein and sediment will differ significantly. Methods: Urine was collected by cystocentesis between 0.5 to 48 hours post-mortem from animals submitted for necropsy to The Ohio State University College of Veterinary Medicine. When possible, urine was collected within 1 hour post-mortem (early post-mortem) and during full necropsy (late post-mortem) for serial comparison of post-mortem UA changes. Medical records were reviewed to determine if animals had pre-mortem UA(s) within 48 hours of death. Complete post-mortem UA was performed within 30 minutes of collection. Post-mortem and pre-mortem UA and early and late post-mortem UA were compared. Results: UAs from 90 animals were performed (predominantly dogs and cats). 12 had pre-mortem UAs; 7 had early- and late post-mortem UAs. Post-mortem urine protein consistently increased from pre-mortem protein. Late post-mortem urine protein increased from early post-mortem protein. Post-mortem urine specific gravity (USG) was often the same as pre-mortem USG, but infrequently increased or decreased slightly. pH and ketones were stagnant or increased in post- versus pre-mortem UA and in late versus early post-mortem UA. Exfoliated urothelial cells increased markedly from pre- to post-mortem and from early to late post-mortem. Erythrocytes and leukocytes consistently decreased from pre- to post-mortem. Conclusions and Discussion: Pre and post-mortem UA results differ markedly, as do early and late post-mortem UA results. In particular, urine protein concentration and number of urothelial cells appear to progressively increase over time after death. Post-mortem UA results do not appear to be accurate, with increasing inaccuracy with increased length of time after death.
Keywords for abstract:	Urine, urinalysis, post-mortem

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Title of abstract:	**UTILIZATION OF ADVANCED DIAGNOSTIC TECHNIQUES FOR DETECTION OF A UNIQUE STRAIN OF ADENOVIRUS IN A PARROTLET**
Authors	S. Linn[1], J. Hokamp[1], C. Gregory[2], B. Ritchie[2], R. Nilsen[2], R. Cianciolo[1] 1 – Department of Veterinary Biosciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH 2 – Infectious Diseases Laboratory, College of Veterinary Medicine, University of Georgia, Athens, GA
Abstract	A young adult male Pacific parrotlet (*Forpus coelestis*) rescued from a backyard breeder became acutely lethargic and huddled at the bottom of the cage approximately 4 months post adoption. Within 24 hours of the development of initial clinical signs and in spite of supportive care, the bird developed seizure activity and was humanely euthanized. Gross autopsy findings showed mild to moderate coelomic effusion and a diffusely pale tan liver. Histopathology was performed and showed that the hepatocytes of the liver and histiocytes of the spleen contained large, homogenous, amphophilic to eosinophilic, intranuclear inclusion bodies. Additionally, there was marked lymphocytolysis within the spleen. Electron microscopy (EM) on formalin-fixed liver that was post-fixed in 3% glutaraldehyde revealed numerous, small, round to polyhedral, electron-dense viral particles ranging in size from 58 to 74 nm in diameter within the hepatocyte nuclei. In situ hybridization (ISH) was performed at the Infectious Diseases Laboratory at University of Georgia on liver and spleen utilizing standard viral probes and was negative for avian adenovirus, Pacheco's disease virus, generic and psittacine circovirus, and polyomavirus. Tissue deep sequencing was performed for detection of viral DNA and revealed adenoviral DNA not typically detected by standard adenovirus probes and similar to an adenovirus detected in budgerigars (budgies) and a sun conure. A ISH probe developed from this similar adenovirus strain was positive in this parrotlet. This is the first report of this variant of avian adenovirus within the parrotlet genus. To date, the three other birds (another parrotlet and two budgies) in the household are clinically healthy.
Keywords for abstract:	Avian adenovirus Parrotlet *Forpus coelestis* In-situ hybridization Electron microscopy Liver

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Title of abstract:	**SYMMETRIC DIMETHYLARGININE (SDMA) AS A MARKER FOR RENAL INSUFFICIENCY IN CAPTIVE CHEETAHS (*ACINONYX JUBATUS)***
Authors	N. Lordi[1], P. Bapodra-Villaverde[2], and M. Flint[1]. [1]Department of Veterinary Preventative Medicine and [2]Columbus Zoo and Aquarium.
Abstract	Over 80% of cheetahs (Acinonyx jubatus) in captivity develop some degree of chronic renal disease, which shortens and impacts their quality of life. To mitigate the negative impacts of this insidious disease, early diagnosis is a key factor in management. Symmetric dimethylarginine (SDMA) is a naturally occurring renal biomarker, specific to kidney function in cats and dogs that elevates earlier than serum creatinine and blood urea nitrogen (BUN) in diseased kidneys. SDMA is often reported on non-domestic animal reference laboratory blood work panels but has not yet been appropriately validated in cheetahs. In assessing renal function, the gold standard is to measure glomerular filtration rate (GFR) and ultimately correlate this rate with the marker to be tested. GFR is often measured using contrast agents such as iohexol, which is a radiolucent intravenous marker that can be measured at various time points post-administration in order to determine the clearance rate. In this study, 9 cheetahs that presented voluntarily for blood draws were serially sampled to determine the clearance rate of iohexol (Time 0 [presumed 0], 120 minutes and 240 minutes) and compared with the corresponding SDMA level at Time 0. The iohexol clearance test provided GFR values that allowed for SDMA levels to be interpreted in light of appropriately assessed kidney function. SDMA results at this time suggest that cheetahs likely have their own reference interval apart from the previously hypothesized range that also included humans, cats, and dogs (0-14 µg/ml). Based on these findings, incorporating real-time SDMA analysis and urinalysis with known renal function profiles from individuals at other institutions is currently being carried out to advance our understanding of this potentially valuable biomarker.
Keywords for abstract:	Cheetahs SDMA Iohexol GFR Renal biomarker Renal dysfunction Chronic renal disease

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Title of abstract:	**EFFECTS ON EQUINE NEONATES OF EXOGENOUS PROGESTOGENS GIVEN TO LATE GESTATION MARES**
Authors	Rachel McAuley, Jacob Swink, Hailey Snyder, Annie Showers, Ramiro Toribio
Abstract	Mares with high-risk pregnancies (e.g., placentitis) are often given exogenous progestogens (progesterone, altrenogest) to maintain pregnancy. Although the use of these steroids in some mares is justified, for many of them their use lacks rationale. Progestogens cross the placental barrier and can potentially affect the health of the fetus and newborn foal. This study measured selected hormones in foals [progesterone, 17α-hydroxyprogesterone, and dehydroepiandrosterone (DHEA)] and included 45 sick-non-septic, septic, healthy, and dummy foals. Foals whose mare's were and weren't on exogenous progestogens were both included. Results showed that endogenous progestogens (progesterone, 17α-hydroxyprogesterone) are associated with disease severity in critically ill foals. High progesterone concentrations were associated with maladjustment syndrome. Therefore, it is reasonable to assume that progestogen treatment to pregnant mares can lead to perinatal diseases.
Keywords for abstract:	Horses Foaling Foal Hormones Sepsis Foal Progestogens

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Title of abstract:	**A TECHNIQUE TO PREPARE BOVINE PLATELET-RICH PLASMA – AN ADJUNCT THERAPY FOR SEPTIC ARTHRITIS**
Authors	A. Muir, A. Niehaus, J. Lozier, S. Durgam Dept. of Veterinary Clinical Sciences
Abstract	Septic arthritis in cattle is a common source of lameness that results in economic losses to the producer. Currently, medical and surgical treatment consists of arthroscopy- or arthrotomy-assisted joint lavage, and systemic and intra-articular (IA) antimicrobial administration. Recent studies have explored the immune-metabolic effects and antimicrobial properties of platelet-rich plasma (PRP). Accepting the restrictions associated with systemic and intra-articular antimicrobials in food-producing species, autogenous PRP offers a unique solution to this common orthopedic problem in cattle. In this technical report, we describe a 2-step, centrifugation protocol to prepare autogenous PRP for clinical use. Bovine whole blood mixed with heparin/ACD (6:1 ratio) was centrifuged first at 2500rpm for 3 minutes to separate red cells from plasma fraction. The plasma fraction was transferred to fresh centrifuge tubes and spun at 2500 rpm for an additional 3 minutes to obtain a platelet-rich pellet. The 'platelet' pellet was resuspended in 5-8 mLs of platelet poor plasma (PPP). The platelet count and differential WBC in whole blood and PRP was manually estimated. Manual estimates on 6 bovine whole-blood samples confirmed that our 2-step centrifugation procedure enriched platelet count by >5-fold compared to whole blood. On average, the platelet counts in PRP and whole blood were $11.1\pm0.5X10^6$ cells/uL, and $1.1\pm0.3X10^6$ cells/uL, respectively. Our results so far indicate that these PRP preps are leucocyte-poor platelet concentrates (average WBC $1.8\pm0.8X10^3$ cells/uL). Among the WBCs, lymphocytes were most predominant in this bovine PRP product. Our current efforts are focused on recruiting clinical cases of bovine septic arthritis presented to OSU VMC for a randomized-controlled study to evaluate the benefit of autogenous PRP as adjunct therapy for naturally-occurring bacterial septic arthritis. In addition, we aim to test the anti-cytotoxic effects of PRP in an in-vitro model of bovine septic arthritis.
Keywords for abstract:	Septic Arthritis Platelet-Rich Plasma Bovine Intra-articular

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Title of abstract:	**PHARMACODYNAMIC EFFECTS OF INTRAMUSCULAR ALFAXALONE-BUTORPHANOL COMBINED WITH ACEPROMAZINE, MIDAZOLAM, OR DEXMEDETOMIDINE IN DOGS**
Authors	MA. Murdock, CH. Ricco Pereira, TK. Aarnes, J. Cremer, P. Lerche, and R. Bednarski. Department of Veterinary Clinical Sciences.
Abstract	**Objective** To evaluate the cardiorespiratory and sedative effects of IM alfaxalone (2 mg/kg) and butorphanol (0.4 mg/kg) combined with either 0.02 mg/kg acepromazine (AB-ace), 0.2 mg/kg midazolam (AB-midaz), or 0.005 mg/kg dexmedetomidine (AB-dex) in dogs. **Animals** Six young, healthy, large mixed breed hound dogs. **Procedures** Each dog received each of three IM protocols once in a randomized, blinded, crossover trial with one week between treatments. Sedation scores and cardiorespiratory variables were recorded prior to treatment (T0), at 5 and 10 minute time points, then every 10 minutes up to 180 minutes, or until sedation score returned to baseline. Data were analyzed with mixed-model ANOVA with Holms-Tukey adjustments and linear generalized estimating equations with Tukey-Kramer adjustments. Significance was set at $P < 0.05$. **Results** All three protocols resulted in deep sedation by 5 minutes. A sedation score over 15 (out of 21) was considered deep sedation. Sedation scores did not differ between groups until 40 minutes. Protocol AB-dex resulted in deep sedation for longer, bradycardia, and an overall 41% decrease in cardiac output. Respiratory variables remained within clinically acceptable limits in all protocols. Recoveries were agitated in four dogs in AB-midaz, and smooth in AB-ace and AB-dex. Four dogs in AB-dex required atipamezole administration by 180 minutes. **Conclusions and clinical relevance** All protocols produced reliable deep sedation. In young, healthy dogs, AB-midaz protocol may result in undesirable recovery characteristics. Cardiorespiratory variables remained clinically stable for AB-midaz and AB-ace. Protocol AB-dex resulted in significant cardiovascular depression, however, it was well tolerated in all dogs.
Keywords for abstract:	Alfaxalone Sedation Cardiac output Dexmedetomidine Butorphanol Acepromazine Midazolam

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Title of abstract:	**A NOVEL PRESENTATION OF MAST CELL TUMOR IN A SHAR PEI.**
Authors	A.Mustonen, R. Jennings
Abstract	An 8-year-old spayed female Shar Pei presented to the Ohio State University applied veterinary pathology service following excision of a right axillary cutaneous mast cell tumor of unknown histologic grade 4 months prior. The patient was also diagnosed with chronic renal failure at that time. Gross examination revealed necrotizing dermatitis and fasciitis at the region of the right axilla, right thorax, and right lateral pelvic limb. Marked lymphadenopathy and bilateral renal cortical atrophy and fibrosis were also observed. Following gross examination, the primary differential diagnosis was bacterial necrotizing fasciitis. On histologic examination, disseminated mast cell tumor was observed throughout the dermis and subcutis in affected regions of skin, liver, and peripheral lymph nodes. The diagnosis of disseminated mast cell tumor was confirmed with toluidine blue staining and immunohistochemistry for c-kit. In addition, amyloidosis was noted within the adrenal glands, renal medullary interstitium, glomeruli, and liver. The renal and hepatic amyloidosis was confirmed with Congo red staining and was interpreted as a breed-associated condition, unrelated to the disseminated mast cell disease. Mast cell tumors in dogs typically present as focal skin masses and tend to be more aggressive in Shar Peis. The atypical presentation of canine mast cell tumor as a regionally diffuse and necrotizing skin disease provided a clinical and diagnostic challenge in the absence of an obvious mass effect.
Keywords for abstract:	Disseminated mast cell tumor Breed-related amyloidosis

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Title of abstract:	**COMPLICATIONS AND OUTCOME FOLLOWING VAGINECTOMY AND VULVOVAGINECTOMY IN 21 DOGS**
Authors	J. Ogden, L. Selmic, V. Wavreille
Abstract	Vaginectomy and vulvovaginectomy are surgical procedures employed for resection of neoplasia in the caudal reproductive or urinary tracts of female dogs. There is a paucity of literature regarding complications or risk factors in patients undergoing these procedures, and oncologic outcomes regarding disease recurrence and survival time remain undetermined. The purpose of this multi-institutional retrospective case series was: 1) to determine the nature and frequency of peri- and post-operative complications in dogs undergoing vaginectomy or vulvovaginectomy for neoplastic conditions, and 2) to describe the oncologic outcome of dogs undergoing these procedures. Dogs undergoing subtotal vaginectomy, complete vaginectomy, or vulvovaginectomy in the past 15 years with complete medical records and a minimum of 60 days follow up were included. Medical record review was performed to acquire pre-, intra-, and postoperative data, including occurrence of urinary incontinence, disease recurrence, metastatic disease, and death or euthanasia. Twenty-one dogs were included in the final analysis. Mean age at time of surgery was 9.2 years old (range 3.5-13.9), and 11/21 females were intact at the time of presentation. Smooth muscle tumors were the most common (leiomyoma: 10 dogs and leiomyosarcoma: 4 dogs). Urinary incontinence occurred in 6/21 dogs, of which all but one resolved within 60 days of surgery. Only one dog had major complications. Median time to follow up was 520 days (range 71-1955). Two dogs had disease recurrence. Information on complications and outcome following surgery of the female caudal reproductive tract is needed to ensure accurate communication of risks and expectations to clients.
Keywords for abstract:	Surgical oncology Vulvovaginectomy Perineal urethrostomy Urinary incontinence

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Title of abstract:	**INTER- AND INTRA-RATER RELIABILITY OF COMPUTED TOMOGRAPHIC MEASUREMENT OF FELINE EPAXIAL MUSCLE AREA**
Authors	L. Rayhel, J. Quimby, E. Green, V. Parker, S. Bai
Abstract	Non-invasive, objective measures of lean body mass in animals are needed in clinical and research settings. This retrospective study evaluated intra- and inter-rater reliability of normalized epaxial muscle cross-sectional area measurement on feline CT images, and evaluated this measure's relationship to muscle condition. 102 feline abdominal and thoracic CT images from the Ohio State University Veterinary Medical Center from 2005-2017 were retrospectively reviewed. The average of three measurements of transverse right and left epaxial muscle area over vertebral body height was calculated at the thirteenth thoracic vertebra, giving the overall epaxial area to vertebral height ratio (OAH). Measurements were performed twice by three observers (EG, LR, JQ), one month apart. OAH intra- and inter-rater reliability were assessed with a concordance correlation coefficient (CCC). Bias and limits of agreement (LoA) between and within observers were assessed with Bland-Altman analysis. OAH was compared between cats with subjectively severe vs. none – moderate muscle atrophy with a Wilcoxon Rank Sum test. Intra-rater reliability for OAH was good – excellent (CCC 0.889 to 0.989), bias was minimal (-0.09 to 0.035), and 95% LoA were narrow within observers [EG (-1.009, 0.930), JQ (-0.646, 0.466), LR (-0.287, 0.356)]. Inter-rater reliability for OAH was also good – excellent (CCC 0.865 to 0.940), but bias was larger (-0.447 to 0.618) between observers. 95% LoA were wider between observers [EG vs. JQ (-1.160, 0.266), EG vs. LR (-0.509, 0.850), JQ vs. LR (0.195, 1.042)]. Mean OAH was lower in cats with severe muscle atrophy (2.7072) than none – moderate atrophy (4.2831) ($p < 0.001$). In conclusion, OAH showed good – excellent inter- and intra-rater reliability, and mean OAH was lower in cats with severe muscle atrophy. Bias and 95% LoA were larger between observers than within observers. Prospective studies are needed to OAH with other subjective and objective measures of lean body mass.
Keywords for abstract:	cat lean body mass cachexia sarcopenia computed tomography

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Title of abstract:	**EVALUATION OF THE ENTEROINSULAR AXIS RESPONSE OF HEALTHY AND HOSPITALIZED EQUINE NEONATES**
Authors	L. Rings[1], J. Swink[1], K. Dembek[2], B. Barr[3], L. Dunbar[1], R. Toribio[1] The Ohio State University College of Veterinary Medicine – Columbus, OH[1] Iowa State University College of Veterinary Medicine – Ames, IA [2] Rood and Riddle Equine Hospital – Lexington, KY[3]
Abstract	The enteroinsular axis (EIA) comprises incretins that promote insulin secretion in response to the oral intake of nutrient. Glucose-dependent insulinotropic polypeptide (GIP) and Glucagon-like peptide-1 (GLP-1) are the main incretins. Alterations in the EIA may contribute to energy dysregulation in critically ill. Disorders of energy regulation are common in hospitalized equine neonates. Incretin information is lacking in sick foals. The aim of this study was to evaluate dynamic concentrations of GIP, GLP-1 and insulin in healthy and hospitalized foals. Blood samples were collected at admission (0) and then 24, 48 and 72 hours into hospitalization from 32 septic, 25 sick nonseptic (SNS) and 13 healthy foals, < 7 days of age. Disease severity was classified based on clinical and hematologic findings. On admission, septic foals had lower insulin and GIP and higher GLP-1 concentrations than healthy foals ($P < 0.05$). Insulin concentrations were lower in septic and SNS foals compared to healthy foals at 0, 48 and 72 hours. GIP and insulin concentrations did not differ significantly over time within groups. GIP concentrations in hospitalized foals (septic and SNS) were significantly lower when compared to healthy foals at all time points. GLP-1 decreased significantly in hospitalized foals at 48 and 72 hours when compared to admission. A positive correlation was noted in healthy foals between insulin and GLP-1 at 0, 24 and 72 hours. No correlation existed between these hormones in hospitalized foals. Hospitalized foals had elevated GLP-1 concentrations; while, insulin concentrations remains lower. This finding may reflect a disconnect between insulin production and GLP-1 in critically ill foals.
Keywords for abstract:	Enteroinsular, incretin, insulin, foal, equine

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Title of abstract:	**DETECTION OF CONGESTIVE HEART FAILURE BY DOPPLER ECHOCARDIOGRAPHY IN CATS WITH HYPERTROPHIC CARDIOMYOPATHY**
Authors	M. Rohrbaugh, KE. Schober, J. Rhinehart, J. Bonagura, A. Habing
Abstract	Left-sided congestive heart failure (CHF) is characterized by elevated filling pressures and related Doppler echocardiography (DE) filling patterns. This study addresses the general hypothesis that DE can be used to predict CHF in cats with hypertrophic cardiomyopathy (HCM). Prospective clinical cohort study with client-owned cats. Cats underwent physical examination, thoracic radiography, analysis of NT-proBNP, and echocardiography and were divided into three age-matched groups: G-1 (control), G-2 (preclinical HCM), and G-3 (HCM and CHF). Measured and calculated variables included respiratory rate, DE estimates of filling pressure using transmitral, pulmonary venous, and tissue Doppler variables, serum NT-proBNP, and a radiographic CHF score. Cats were examined twice, at baseline and 5-14 days later. Groups were compared using ANOVA, and presence of CHF was predicted using receiver-operating characteristic curve (ROC) and multivariate and logistic regression analyses. A total of 47 cats were enrolled: G-1 (n=15), G-2 (n=17), and G-3 (n=15). The E/A ratio (AUC 1.00, diagnostic cut-off 1.74, $P = 0.005$), diastolic functional class (AUC 0.97, cut-off class 2, $P = 0.006$), left atrial diameter (AUC 0.89, cut-off 19 mm, $P < 0.001$), E:E' (AUC 0.84, cut-off 12.7, $P = 0.014$), and rate of respiration (AUC 0.81, cut-off 43/min, $P = 0.004$) predicted presence of CHF best. Summation of diastolic filling waves in cats with CHF represents a relevant obstacle in the DE prediction of CHF. IVRT, E:IVRT and pulmonary vein AR duration were less useful in differentiating occult disease from those with congestive heart failure. Various DE variables can be used to predict CHF in cats with HCM. Determination of the clinical benefit of such variables in initiating treatments and assessing treatment success need further study.
Keywords for abstract:	Feline Hypertrophic cardiomyopathy Diastolic dysfunction Respiratory rate Echocardiography NT-proBNP

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Title of abstract:	**PHARMACOKINETIC AND PHARMACODYNAMICS CHANGES ASSOCIATED WITH EXPERIMENTALLY INDUCED HYPERMAGNESEMIA IN HORSES**
Authors	S. Schumacher, R. Toribio, B. Scansen, J. Lakritz, and A. Bertone Of Veterinary Clinical Sciences
Abstract	The objectives of this study were to describe the pharmacokinetic and pharmacodynamic changes as a result of the intravenous administration of a single bolus of magnesium sulfate ($MgSO_4$). $MgSO_4$ is a magnesium salt that has been used to calm horses in equestrian competition and is difficult to regulate because magnesium is an essential constituent of all mammals and there are many forms. Ionized Mg (Mg^{2+}) is the active form of magnesium in the body and the focus for regulatory purposes. Six healthy adult female horses were administered a single bolus of $MgSO_4$ at a dose of 60 mg/kg of body weight. Blood, urine, and cerebrospinal fluid (CSF) was collected, and cardiovascular parameters were monitored and echocardiograms performed at predetermined times. Noncompartmental pharmacokinetic analysis was applied to plasma concentrations of Mg^{2+}. Objective data were analyzed using the Wilcoxon Rank-Sum test with $P < 0.05$ used as a determination for significance. Plasma concentrations of ionized magnesium (Mg^{2+}) increased nearly 5-fold, and the ionized calcium (Ca^{2+}) to Mg^{2+} ratio declined more than 3.5-fold and remained different than baseline until 24 hours. Changes in the fractional excretion of electrolytes included a 6-fold change for Mg^{2+} and a 3-fold change for Ca^{2+}. Left ventricular function increased evidenced by increases in percent ejection fraction (%EF), percent fractional shortening (%FS), the velocity of systolic contractions (S'), and cardiac output (CO). A significant decrease in mean arterial pressure (MAP) was observed, along with an initial increase in heart rate (HR). There were significant changes in plasma concentrations of calcitonin and parathyroid hormone (PTH); closely related to the changes in plasma Ca^{2+} concentrations. No changes were detected in the electrolyte concentrations of the CSF. Alterations detected in plasma electrolyte concentrations, fractional excretion and hormone concentrations may serve as biomarkers for regulatory control for the nefarious administration of $MgSO_4$.
Keywords for abstract:	$MgSO_4$ Mg^{2+} Ca^{2+} Fractional Excretion

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Title of abstract:	**SEX STEROIDS IN HEALTHY AND HOSPITALIZED NEONATAL FOALS**
Authors	Swink JS[1], Rings LM[1], McAuley RC[1], Dembek KA[2], Reed SM[3], Bozorgmanesh R[4], Toribio RE[1] The Ohio State University College of Veterinary Medicine[1], Iowa State University College of Veterinary Medicine[2], Rood and Riddle Equine Hospital[3], Hagyard Equine Medical Institute[4]
Abstract	Sepsis is a leading cause of mortality in neonatal foals. Critical illness alters multiple endocrine systems in foals. Little is known regarding estrogen and androgen production in healthy and sick neonatal foals. The effect of exogenous progestogens on steroidogenesis in newborn foals is unknown. We hypothesized that sex steroids would mimic changes seen for other steroids during disease. We proposed that foals born to progestogen-treated mares would have abnormal sex steroid profiles compared to unexposed foals. Blood samples were collected on admission (0) and at 24, 48, and 72 hours from 40 healthy, 61 septic, and 54 sick-nonseptic (SNS) foals of < 7 days of age. Clinicopathologic data and history were used to classify disease severity (healthy, SNS, septic) and survivorship. Serum steroids were measured using radioimmunoassays. At admission, septic foals had higher progesterone and testosterone concentrations than SNS and healthy foals ($P < 0.05$). All three hormones declined in healthy and SNS compared to septic foals. Nonsurvivors had higher estradiol, testosterone, and progesterone (all $P < 0.05$) at admission compared to survivors. Dummy foals had higher estradiol ($P < 0.001$) and progesterone ($P = 0.026$), but not testosterone, at admission compared to healthy foals. Sick foals born to progestogen-treated mares did not exhibit a decline in hormone concentrations over time as non-exposed sick foals did. Sex steroids were associated with disease severity and may play a role in or reflect a response to illness. In utero exposure to exogenous progestagens may influence the postnatal endocrine maturation in sick foals.
Keywords for abstract:	Foal Sepsis Progestagen Estrogen Androgen

Title of abstract:	**EVALUATION OF CARDIAC CYCLE LENGTH AND STROKE VOLUME IN DOGS WITH ATRIAL FIBRILLATION**
Authors	R. Van Zile, J. Rhinehart, and J. Bonagura. Dept of Veterinary Clinical Sciences
Abstract	The optimal heart rate (HR) in atrial fibrillation (AF) remains unknown. In people with AF and heart failure, stroke volume (SV) variability might be more dependent on HR than ventricular contractile function. This study aimed to identify the influence of preceding cardiac cycle length on SV in dogs with spontaneous AF. We hypothesized that SV varies significantly with instantaneous HR and a "threshold" for optimal SV might be evident. Echocardiograms were retrospectively evaluated from 25 dogs associated with AF and cardiomyopathy (12), valvular disease (9), or structurally normal hearts (4). Preceding cycle length and SV were determined from five cardiac cycles per dog. Aortic cross-sectional area (CSA) was calculated from maximum systolic valve diameter and aortic velocity-time integral (VTI) was recorded. Stroke volume index (SVI) was calculated as CSA*VTI, indexed to bodyweight. Correlations between cycle length and SVI were determined by multiple linear regression accounting for repeated measurements. The HR associated with optimal SVI was evaluated by receiver operating characteristic curve (ROCC) analysis. SVI was significantly correlated with cycle length ($p < 0.0005$), with zero, partial- and part-correlations of 0.67, 0.87, 0.60. ROCC analysis (Youden) showed a HR< 145/minute was associated with a 70% sensitivity and 78% specificity for SVI≥ 1mL/beat/kg (AUC 0.77); additionally this "threshold" produced the highest average SVI/dog. Preceding cycle length explained ~40-50% of accounted unique variation in SVI. This study shows preceding cycle length impacts SVI in canine AF and is probably optimized by an instantaneous HR <145/minute. Additional prospective studies are indicated.
Keywords for abstract:	Atrial fibrillation Stroke volume Stroke volume index Preceding cardiac cycle length Instantaneous heart rate Heart rate threshold

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Title of abstract:	**CEREBROSPINAL FLUID MIRNA PROFILING OF DOGS WITH AND WITHOUT OSSEOUS-ASSOCIATED CERVICAL SPONDYLOMYELOPATHY**
Authors	Daniella P. Vansteenkiste, Joelle M. Fenger, Paolo Fadda, Paula Martin-Vaquero, Ronaldo C. da Costa**.** Department of Veterinary Clinical Sciences, The Ohio State University, College of Veterinary Medicine.
Abstract	Osseous associated cervical spondylomyelopathy (OA-CSM) is a degenerative condition of the cervical vertebral column that affects mainly giant dog breeds. microRNAs (miRNA) are small RNAs that play important gene-regulatory roles and recent data suggest that circulating miRNAs present in biological fluids may serve as potential biomarkers of neurodegenerative disease. The miRNA profile of normal canine cerebrospinal fluid (CSF) and OA-CSM has not been previously described; therefore, the overarching goal of this study was to characterize the expression levels of miRNAs present in the CSF of Great Danes and identify differentially expressed miRNAs present in the CSF of dogs clinically affected with OA-CSM. Global CSF miRNA expression levels were evaluated in twelve clinically normal dogs and 12 OA-CSM affected dogs using the NanoString nCounter platform. We identified eight miRNAs showing differential expression in OA-CSM dogs compared to clinically normal dogs. MiR-299-5p and miR-765 were upregulated in the OA-CSM affected dogs and miR-494, miR-612, miR-302-d, miR-4531, miR-4455 and miR-6721-5p were upregulated in the clinically normal group. qRT-PCR was performed to validate the expression levels of two miRNAs (miR-494 and miR-612) and we found that miR-494 expression was increased by 1.5 fold in the OA-CSM affected dogs and the expression of miR-612 was decreased by 1.15 fold in the OA-CSM affected group (*p*-value= 0.41 and 0.89 respectively). Data generated from our study represent an initial characterization of the global miRNA profile of canine CSF and suggest that a distinct CSF miRNA expression profile is associated with OA-CSM in dogs.
Keywords for abstract:	Cervical Spondylomyelopathy Wobbler syndrome cerebrospinal fluid microRNA

CR - 30

Title of abstract:	**DEFINITIVE-INTENT INTENSITY-MODULATED RADIATION THERAPY IN THE TREATMENT OF CANINE PROSTATE CARCINOMA: A MULTI-INSTITUTIONAL RETROSPECTIVE STUDY**
Authors	JZ Walz[a], N Van Asselt[b], V Poirier[c], K Hansen[d], N Desai[a] *[a]OSU-CVM Dept of Veterinary Clinical Sciences, [b]University of Wisoconsin-Madison, [c]University of Guelph, [d]University of California-Davis*
Abstract	No standard of care is currently recognized for the treatment of canine prostate carcinoma. Local disease is a common cause of morbidity and euthanasia in these patients. The aim of this retrospective study was to assess the outcome following definitive-intent radiation therapy (RT) in dogs with prostate carcinoma. Medical records of dogs that received definitive-intent radiation therapy for treatment of prostatic neoplasia were reviewed. Sixteen patients from four institutions were included. Diagnosis was incidental in 6 patients. Evidence of metastasis to loco-regional lymph nodes was identified in 5 dogs (31%) at the time of diagnosis. All patients were treated with intensity-modulated radiation therapy. Fifteen patients received concurrent nonsteroidal anti-inflammatory drugs. Chemotherapy was administered in 15/16 patients; chemotherapy protocols and timing of administration varied. Total prescribed radiation dose ranged from 48-54Gy delivered as daily doses of 2.5-2.8Gy. One patient was euthanized prior to completion of RT. Acute toxicity was observed in 8 of the surviving patients (53%) consisting of VRTOG Grade 2-3 diarrhea in 6/8 patients (75%). Late toxicity (urethral stricture, ureteral stricture, and hindlimb edema) was observed in 3 patients (20%). Measurable PR was documented in 5 dogs (31%). Clinical benefit (PR+SD) was observed in 100% of cases evaluated following RT (n=15). Median event-free survival following radiation therapy was 220 days, median overall survival was 431 days. Local progression was documented in 40% of patients at a median of 192 days. Metastatic progression was documented in 9 patients (60%); metastatic sites included regional lymph nodes (n=2), pulmonary (n=2), bone (n=2), body wall (n=2), and popliteal lymph node (n=1). Definitive-intent radiation therapy is a viable treatment option for canine prostatic neoplasia. Toxicity was moderate. Clinical benefit was observed in most patients and prolonged survival is possible.
Keywords for abstract:	Radiotherapy Definitive radiation therapy Canine prostate carcinoma Intensity modulated radiation therapy

Title of abstract:	**A CADAVERIC EVALUATION OF PIN AND TENSION BAND CONFIGURATION STRENGTH FOR TIBIAL TUBEROSITY OSTEOTOMY FIXATION**
Authors	A.N. Zide, S.C. Jones, A.S. Litsky, N.R. Kieves. Department of Veterinary Clinical Sciences and Department of Biomedical Engineering
Abstract	Objective: The purpose of this study was to compare the load at failure and mode of failure of four constructs used to stabilize a tibial tuberosity (TT) osteotomy; including two vertically aligned pins (V), two horizontally aligned pins (H), two vertically aligned pins with a tension band wire (V-TB), and two horizontally aligned pins with a tension band wire (H-TB). Study Design: Eighteen pairs of cadaveric tibiae were randomized to receive a tension band or not, with one limb being randomized to be in the H or V group. The contralateral limb was then assigned to the remaining configuration (H or V). One pair of limbs was used as a control. A tensile force was applied to the patellar ligament until construct failure occurred. Results: There was no significant difference between the mean load at failure of the H (595 N) and V (556 N) groups or between H-TB (1032 N) and V-TB groups (1034 N) ($p = 0.487$ and $p = 0.238$, respectively). The TB constructs were significantly stronger than the pin only constructs ($p < 0.001$). The mode of failure was similar for the pin only constructs, regardless of pin orientation. The TB constructs and control tibias failed at similar loads, most commonly by patellar ligament rupture. Conclusion: The use of vertically aligned pins versus horizontally aligned pins does not affect construct strength when stabilizing a TT osteotomy. These results support the placement of pins in a vertically aligned fashion when horizontally aligned pin placement cannot be accomplished. When performing a TT osteotomy, the addition of a TB adds significant strength to the construct.
Keywords for abstract:	Tibial tuberosity transposition Patellar luxation Mechanical testing

EPIDEMILOGY
AND
APPLIED RESEARCH

EAR - 1

Title of abstract:	**INTRAUTERINE ANTIBIOTIC INFUSION INCREASES ANTIMICROBIAL RESISTANCE IN THE REPRODUCTIVE MICROBIOTA OF MARES**
Authors	R. Adams[1], D. Mollenkopf[1], E. Sechrist[1], M. Coutinho da Silva[2], T. Wittum[1] Depts. of Veterinary Preventive Medicine[1] and Veterinary Clinical Sciences[2]
Abstract	In the thoroughbred racing industry, prophylactic intrauterine infusion with extended-spectrum cephalosporin (ESC) antibiotics after breeding to improve conception is a common practice, though efficacy has not been established. There is also anecdotal evidence of carbapenem antibiotics used for this purpose. We measured the impact of intrauterine infusion of ESC and carbapenem antibiotics on the recovery of antimicrobial resistant bacteria from the reproductive and fecal microbiota of mares. We hypothesized that intrauterine infusion would increase the recovery of β-lactam resistant uterine, vaginal, and fecal *Enterobacteriaceae*. Seven mares were infused after estrous cycle synchronization; 4 received 1 gram of meropenem and 3 received 2 grams of ceftiofur sodium. Fecal, vaginal, and uterine samples were collected prior to and after infusion and later processed using selective media to identify ESC and carbapenem resistant bacteria. Resistant bacteria were not recovered from vaginal or uterine samples prior to infusion. An increase in the recovery of fecal microbiota resistant to both antimicrobials occurred at 24 hrs post-infusion and remained elevated until 25 days post-infusion. In vaginal samples, ESC and carbapenem resistant organisms were first observed 24 hrs and 48 hrs post-infusion, respectively; in uterine samples, resistance was observed at 72 hrs post-infusion. The highest prevalence of resistant bacteria from vaginal and uterine samples occurred at 72 and 96 hrs post-infusion, respectively. These data suggest that intrauterine antibiotic infusion transiently selects for the recovery of resistant bacteria from the enteric and reproductive systems of mares. Our preliminary data support the need for additional field studies to evaluate post-breeding antibiotic infusion efficacy and its impact on antimicrobial resistant bacteria to improve the welfare and reproductive success of thoroughbred mares.
Keywords for abstract:	antimicrobial resistance equine intrauterine infusion mare antibiotics

EAR - 2

Title of abstract:	**EVALUATION OF THE EFFECTS OF ENVIRONMENTAL CONTAMINANTS AND HUSBANDRY ON THE LARVAL DEVELOPMENT IN THE ENDANGERED EASTERN HELLBENDER (*CRYPTOBRANCHUS ALLEGANIENSIS ALLEGANIENSIS*)**
Authors	AC Aplasca and M. Flint. Dept of Veterinary Preventive Medicine
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 overharvesting, disease, habitat loss and degradation, and environmental contamination have been linked to amphibian population declines. The Eastern hellbender (*Cryptobranchus alleganiensis alleganiensis*) is a salamander native to areas of the Northeast, Mid-Atlantic, and Midwest United States and is classified as endangered in the state of Ohio. Population declines and low numbers of juveniles, suggesting poor recruitment, have been documented in many areas. To increase Ohio populations, several collaborative programs formed to collect eggs from the wild and captive-rear individuals until they are released to the wild as juveniles. These head-start programs have reintroduced hundreds of hellbenders into the wild, however, mortality rates are highly variable and observed occasional gross morphological abnormalities are poorly understood. Our research aims to investigate major factors that impact larval development and mortality in hellbenders. Our first major objective is to investigate husbandry factors commonly controlled in captive-rearing programs and our second major objective is to evaluate the impact of yolk quality on larval development and mortality. Eggs will be collected from the wild and reared under controlled egg densities, water flow velocities, temperatures, and dissolved oxygen levels. Growth patterns, gross abnormalities, and mortality rates will be monitored. Gross and histopathologic examination will be performed on individuals that fail to survive. The yolk content of these individuals will be tested for environmental contaminants such as heavy metals and other commercial waste compounds. We will identify factors that have direct and indirect adverse impacts on hellbender populations, and ultimately, this information can be used to improve captive-rearing practices and identify major risk factors for free-ranging populations.
Keywords for abstract:	Amphibians, Eastern hellbender, Toxicology Husbandry, Captive-rearing, Pathology Head-start programs, Ecosystem Health

EAR - 3

Title of abstract:	**RECOVERY OF BETA-LACTAMASE PRODUCING *ENTEROBACTERIACEAE* IN FREE-RANGING WHITE-TAILED DEER IN NORTHEAST OHIO**
Authors	G Ballash, P Dennis, D Mollenkopf and T Wittum
Abstract	The dissemination of antimicrobial resistant (AMR) bacteria and their genes from clinical and hospital settings to the environment is a significant One Health concern. Wildlife species, particularly herbivorous wildlife, are often used as sentinels for environmental dissemination of AMR bacteria because they are not exposed to antimicrobials providing direct selection pressure. The objective of this study is to recover and estimate the occurrence of beta-lactamase mediated antimicrobial resistance in *Enterobacteriaceae* from white-tailed deer (WTD). A total of 414 individual WTD fecal samples were collected from WTD harvested as part of an annual deer management program in Cleveland, Ohio from January 2018 to March 2018. Four gram fecal aliquots were mixed with 36ml of MacConkey broth containing 2ug/ml of cefotaxime to select for AmpC, ESBL, and carbapenem-resistant *Enterobacteriaceae*. The broth was incubated for 18-24 hours and subsequently inoculated on MacConkey agar containing 8ug/ml of cefoxitin to select for AmpC phenotypes, 4ug/ml cefepime for ESBL phenotypes and 1ug/ml of meropenem and 70ug/ml of ZnSO4 for carbapenem-resistant phenotypes and incubated for 24 hours. Positive isolates were further characterized for the prevalence of *bla*$_{\text{CMY-2}}$, *bla*$_{\text{CTX-M}}$ and *bla*$_{\text{KPC}}$ by PCR. Approximately 10% (40/414) of fecal samples had isolates expressing the AmpC phenotype with the corresponding *bla*$_{\text{CMY}}$ genotype, and 0.4% (2/414) of the fecal samples harbored isolates expressing the ESBL phenotype with the corresponding *bla*$_{\text{CTX-M}}$ genotype. Approximately 7% (13/414) of the fecal samples had carbapenemase-producing bacteria. These results suggest there is significant dissemination of beta-lactamase producing *Enterobacteriaceae* into the environment. In addition, WTD may serve as a wildlife reservoir furthering the dissemination of these clinically relevant AMR bacteria and their genes.
Keywords for abstract:	Antimicrobial resistance, Enterobacteriaceae, wildlife

EAR - 4

Title of abstract:	**ENVIRONMENTAL SURVEILLANCE OF SALMONELLA, EXTENDED-SPECTRUM CEPHALOSPORIN RESISTANT- AND CARBAPENEM RESISTANT-ENTEROBACTERIACEAE AT THE OHIO STATE UNIVERSITY'S VETERINARY MEDICAL CENTER**
Authors	R. Bates and T. Wittum
Abstract	There is a great need for understanding the extent of resistant bacteria present in the hospital environment that could pose a risk to humans and animals. Antibiotic resistance lowers clinical outcomes and increases healthcare costs. Salmonella, extended-spectrum beta-lactamase (ESBL)-producing *Enterobacteriaceae*, and carbapenem-resistant *Enterobacteriaceae* (CRE) were targeted for active surveillance in the Ohio State University Veterinary Medical Center (OSU-VMC) in order to make recommendations for infection control in the hospital and understand the baseline levels of potentially pathogenic and medically important antibiotic-resistant bacteria. Environmental samples were collected from the OSU-VMC at 1-month intervals from January 2018 through June 2018. Isolates were cultured and selected for resistance phenotypes. Salmonella was more often found in the Equine hospital, and ESBL *Enterobacteriaceae* was more often found in the Large Animal and Equine areas compared to the small animal area. The Equine ICU had more positive Salmonella samples than any other section with a difference between the sections (p-value<0.05). The later months of the year (May and June) had more Salmonella and ESBL *Enterobacteriaceae* (p-value<0.05). ESBL *Enterobacteriaceae* was found on animal contact surfaces more often than on human contact surfaces (p-value<0.05). In the Equine hospital, the countertop/cabinets and stalls had the most Salmonella and ESBL *Enterobacteriaceae*. The Equine ICU should increase hand hygiene awareness and offer more sanitizing dispensers near the equipment carts and cabinets. Footbaths should be used before moving between the Large and Small Animal hospitals. Countertops and cabinets in the Equine hospital and all Cubex machines should be regularly cleaned with disinfectants close by.
Keywords for abstract:	Epidemiology Zoonosis Salmonellae Diagnostics Enterobacteriaceae

EAR - 5

Title of abstract:	**DISSECTING A LONG-STANDING DOG-MAINTAINED RABIES EPIZOOTIC AND DISCOVERY OF A RABIES CYCLE IN WILDLIFE IN ETHIOPIA: A MOLECULAR EPIDEMIOLOGY APPROACH TO MONITOR PROGRESS ON RABIES CONTROL AND ELMINATION EFFORTS**
Authors	Laura Binkley, Jeanette O'Quin, Wondwossen Gebreyes and Getnet Yimer. The Ohio State University Global One Health initiative (GOHi). Miriam Shiferaw, Emily G. Pieracci, Mary Reynolds, Yoshinori Nakazawa and Andrés Velasco-Villa. Centers for Disease Control and Prevention. Asefa Deressa and Ebba Abate. The Ethiopian Public Health Institute.
Abstract	Ethiopia has long been among the most rabies-affected countries on the African continent with a national annual incidence rate of 1.6/100,000 population rabies deaths. However, little information exists regarding the genetic diversity of rabies viruses (RABV) circulating in dogs or the existence of alternative rabies cycles maintained by other mammalian species. This study encompasses 230 samples obtained from wild and domestic animals collected throughout Ethiopia during the period 2010-2017. We sequenced partial nucleoprotein genes from 187/230 samples, and obtained complete sequences for 43/230 samples. We then compared sequences against references representing current RABV variants across Africa. Results identified a complex assemblage of co-circulating dog RABV variants throughout Ethiopia with detection of geographical pockets, suggesting multiple historic dissemination events across regions from an epicenter in Oromia. There was no evidence of dog-maintained rabies imported from other African countries. Finally, we identified a RABV variant apparently established in side-striped jackals. This investigation provides necessary baseline data to monitor progress on RABV control and elimination efforts in Ethiopia.
Keywords for abstract:	Rabies Virus Disease Ecology Molecular Epidemiology Ethiopia Wildlife Surveillance Side-Stripped Jackals Virus Assemblage Phylogenetic Analysis

EAR - 6

Title of abstract:	**ASSESSMENT OF INTERNAL BIOSECURITY IN U.S. SWINE FARMS USING INNOVATIVE TECHNOLOGY**
Authors	N. Black, A. G. Arruda. Dept. of Veterinary Preventive Medicine
Abstract	Porcine reproductive and respiratory syndrome (PRRS) is one of the most costly infectious diseases that the swine industry faces today. Within-farm PRRS virus (PRRSv) transmission via fomite plays a major role for the spread and persistence of the virus in the herd. This study aims to utilize beacon-sensing technology to describe between-room movements of farm workers within U.S. swine farms and to investigate whether an increase in "risky" movements is associated with production parameters of interest. Three commercial farrow-to-wean farms with a history of PRRS outbreaks located in the states of Indiana (n=2) and Iowa (n=1) were enrolled in this project. Wireless internet services were optimized throughout the farms and sensors were placed in each room. These sensors were set up to detect Bluetooth-based beacon devices, which were individually distributed to farm employees. A movement was defined when an employee spent at least two minutes in one room from another room in the farm. A "risky" movement was defined when an employee moved from a shipping point or a nursery to other parts of the farm. Statistical analysis was performed in STATA-IC 14. Preliminary analysis included 14 weeks (Mar-Jul 2018) of movement data from a 4,400 sow farm located in a swine dense area. During this period, there was an average of approximately 1,841 (SD: 352.4) total movements per week with "risky" movements occurring on average approximately 176 (SD: 74.4) times per week. Analysis of data from this farm also showed a tendency for an increase in "risky" movements in a previous week to increase pre-weaning mortality in the current week by approximately 3% (P = 0.052). Furthermore, an increase in "risky movements" tended to decrease the number of piglets per litter by 0.37 (P = 0.09).
Keywords for abstract:	PRRS Biosecurity Epidemiology

EAR - 7

Title of abstract:	**ANTIMICROBIAL STEWARDSHIP IN THE OSU VETERINARY MEDICAL CENTER: ENVIRONMENTAL SURVEILLANCE FOR METHICILLIN RESISTANT STAPHYLOCOCCUS SPP.**
Authors	L. Brady
Abstract	Antimicrobial stewardship is a growing area of focus in the veterinary world that protects both human and animal health. The Antimicrobial Stewardship Program at the OSU Veterinary Medical Center (VMC) has utilized environmental surveillance to detect pathogens of interest, including methicillin-resistant Staphylococcus (MRS) species. This research project focuses on determining the prevalence and contamination patterns in the small animal hospital at the VMC for MRS species and looking at the resistance patterns. Sampling was performed once a month on predetermined sites that stayed consistent (N=111) throughout the study period. After the collection of 6 months of data, it is clear that contamination is significantly associated with both the season of the year and the hospital service. In contrast, there were no associations seen among presence of MRS and human-only or human and animal contact surfaces. These results indicate that much of the current contamination levels at the VMC are likely due to transient carrier states on the hands of veterinary faculty. Based on this, an improvement in hand hygiene and glove usage could lead to lower environmental contamination levels, further reducing the risk for nosocomial infections.
Keywords for abstract:	Antimicrobial Stewardship, Methicillin Resistant Staphylococcus, Hand Hygiene, Environmental Surveillance

EAR - 8

Title of abstract:	**THE EFFECT OF RIDLEY SOW BLOCKS ON LACTATING SOWS AND LITTER**
Authors	M. Brake, J. Kieffer, M. Pairis-Garcia, T. Parker The Ohio State University Department of Animal Science and Department of Veterinary Preventive Medicin
Abstract	The use of farrowing crates is ethically contentious in the swine production industry. Although the crates are restrictive of movement and prevent the sow from turning around, the use of gestation crates reduces the mortality rates of litters by minimizing the risk of a piglet being crushed by the sow. Nesting is an important pre-farrowing behavior in sows. Previous studies have shown that the inability for a sow to nest causes stress; stress can be manifested in stereotypical behaviors such as bar biting. Encouraging natural behavior and minimizing stress are important aspects in promoting animal welfare in agriculture. This project centers on the creation of an enrichment device that can be placed in a farrowing crate. We hypothesize that sows with the enrichment device will spend different amounts of time eating, lying down, bar biting, and rooting compared to sows without the enrichment device. Initial results have shown that behavioral observation in this study accurately recorded pre-farrowing and post-farrowing changes in sow behavior. The data showed that the behaviors of eating, bar biting, rooting, and lying down were more likely to be observed pre-farrowing than post-farrowing. A higher activity level pre-farrowing likely reflects nesting behavior of pigs. At this time, no difference was seen in overall behavior between sows with enrichment and sows without enrichment. In addition, there was no difference in behavior between sows with enrichment and sows without enrichment at the same stage of gestation. Further studies using 24/7 video surveillance are needed to elucidate the sows' use of the enrichment device and its effects on behavior.
Keywords for abstract:	Enrichment, Sow, Farrowing, Gestation Crat

EAR - 9

Title of abstract:	**WHOLE GENOME SEQUENCING BASED ANALYSIS AND DETECTION OF ANTIMICROBIAL RESISTANCE DETERMINANTS IN DRUG RESISTANT *SALMONELLA* DUBLIN ISOLATES ORIGINATING FROM CATTLE.**
Authors	B. Byrne, Y. Zhang, G. Habing. Dept. of Veterinary Preventative Medicine.
Abstract	Multidrug-resistance (MDR) in *Salmonella enterica* is a threat to public health, in part due to a broad spectrum of resistance to antimicrobials, making severe infections especially difficult to treat. *Salmonella* Dublin is a bovine adapted *S. enterica* serotype. Human cases tend to manifest in a more invasive manner and are often associated with a high prevalence of antimicrobial resistance (AMR). The aim of this study was to genetically characterize components of AMR features in MDR *S*. Dublin isolates from cattle in Ohio, assess the capacity of whole-genome sequencing (WGS) to predict AMR phenotypes, and characterize the genetic relatedness of the strains. Twenty-four *S*. Dublin isolates submitted to the Ohio Department of Agriculture by veterinarians from sick cattle were selected for WGS with Illumina MiSeq. Genotypic analysis of AMR determinants and plasmid replicons in each assembly was performed through Center for Genomic Epidemiology (https://cge.cbs.dtu.dk/services/) and nucleotide BLAST analyses. Cohen's kappa coefficient of agreement between phenotypic and genotypic AMR was calculated. CSI Phylogeny was used for phylogenetic reconstruction to determine *S*. Dublin relatedness. Average genotype and phenotype agreement for characterization of AMR was 94.8%. Identification of a resistance gene correlated with an 84.2% mean specificity and 88.9% sensitivity to identify the corresponding resistance phenotype. Resistance genes were located on plasmid incompatibility group IncA/C2. IncFII(S) and IncX1 replicon groups were also present. WGS was able to identify chromosomal point mutations conferring resistance to quinolones. All isolates were found to be MLST ST10 and showed close clustering in SNP phylogenetic analyses. Results indicate that WGS is a robust method to accurately detect comprehensive AMR determinants in MDR *S*. Dublin isolates from bovine sources. WGS could also simultaneously generate additional molecular epidemiologic data from isolates, including identification of MLST type and plasmid replicons, making this method a fast and inexpensive alternative to conventional phenotyping.
Keywords for abstract: Please list your keywords – one per line	Salmonella Whole Genome Sequencing Plasmids Antimicrobial Resistance

EAR - 10

Title of abstract:	**COMPARISON OF UROPATHOGENIC ESCHERICHIA COLI ISOLATES FROM HUMAN AND COMPANION ANIMAL PATIENTS**
Authors	L. Courtney, D. Mollenkopf, D. Diaz-Campos, P. Pancholi, T. Wittum Department of Veterinary Preventive Medicine (Courtney, Mollenkopf, Wittum), Department of Veterinary Clinical Sciences (Diaz-Campos), Department of Clinical Microbiology (Pancholi)
Abstract	Urinary tract infections are often caused by extraintestinal uropathogenic E. coli (UPEC) strains. Past studies have found similarities between companion animal and human UPEC strains, but the significance of this overlap and the potential for cross-species transmission are not understood. An overlap may indicate that the patients were infected from a common reservoir. In this study, we ran minimum inhibitory concentration (MIC) assays using the NARMS gram negative panel to determine the lowest concentration of antimicrobial necessary to inhibit growth. There were 34 isolates collected and analyzed with a panel of 11 antimicrobial agents of differing concentrations. Isolates with resistant and intermediate MICs are as follows (human isolates in parenthesis): Amoxicillin/Clavulanic Acid: 3(3)=R, 1(6)=I; Ampicillin: 7(12)=R; Ceftoxitin: 3(2)=R, 1(6)=I; Chloramphenicol: 1(1)=R, 8(8)=I; Ciprofloxacin: (6)=R, (2)=I; Naladixic Acid: 2(8)=R; Streptomycin: 3(6)=R; Sulfisoxazole: 22(29)=R; Tetracycline:1(8)=R, (1)=I; Trimethoprim/Sulfamethoxazole: 4(5)=R. While 19 isolates were resistant to the penicillin-type antibiotic Ampicillin, only 13 had reduced susceptibility to Amoxicillin/Clavulanic Acid. Further, while there was resistance to the second-generation cephalosporin, Ceftoxitin, there was no bacterial growth in the third-generation cephalosporins, Ceftiofur and Ceftriaxone. The greatest resistance was to Sulfisoxazole, with 76% of the isolates showing resistance. It is important to note that only human isolates expressed resistance to Ciprofloxacin. Additionally, PFGE analysis of 24 isolates was used to separate DNA fragments and look for genotypic clustering. Our findings indicated that the isolates were very diverse. This study shows that understanding the resistance mechanisms of each strain will help select appropriate treatments. Moreover, comparing the UPECs will help predict the zoonotic potential and identify a common reservoir.
Keywords for abstract:	Uropathogenic E. coli (UPEC) Antimicrobial resistance

EAR - 11

Title of abstract:	**EFFECT OF STOCKING DENSITY AND A BARRIER IN A GROUP CLOSE-UP PEN ON THE ODDS THAT DAIRY COWS DEVELOP METRITIS AFTER CALVING**
Authors	K. Creutzinger[1], H. M. Dann[2], L. Moraes[1], P. Krawczel[3], K. Proudfoot[1] *[1]Ohio State University, Columbus, Ohio, USA.* *[2]William H. Miner Agricultural Research Institute, Chazy, New York, USA.* *[3]University of Tennessee, Knoxville, Tennessee, USA.*
Abstract	Many dairy cows succumb to disease after calving, and the social environment before calving may affect the disease risk. This study objective was to determine the effect of stocking density and the provision of a barrier in group close-up pens on the likelihood that cows developed metritis after calving. Holstein dairy cows (n=319, primiparous=113, multiparous=206) that were part of a larger experiment were included in the study. Cows were enrolled 21±3 d before their expected calving date and removed immediately after calving. At enrollment, cows were assigned randomly to one of four treatments using a 2×2 factorial arrangement including 1) high vs. low stocking density (9.7 to 12.9m^2 vs. 19.4 to 25.8m^2 lying space /cow), and 2) presence of a barrier (yes vs. no). The barrier was designed using two road Jersey barriers and plywood (3.6×0.6×1.5m). Pens were created using gates separating four areas within a large sawdust bedded pack and were replicated four times at 4 different periods so that all treatments were in all positions in the larger pack. Vaginal discharge was scored on 3, 7, 10, 14d after calving to diagnose subclinical and clinical metritis. Data describing metritis (healthy, subclinical, clinical) were analyzed with a multinomial proportional odds mixed model. Random effects for period, pen and pen×period×treatment were included in the model. Fixed effects describing the factorial arrangement of treatments as well as parity, calving assistance, and retained placenta were included in the model. Calving assistance ($P<0.0001$) and retained placenta ($P<0.0001$) significantly affected the odds of metritis severity. Stocking density and the presence of barrier did not affect the odds of developing metritis. No significant interactions were detected. Results suggest that moderate increases in stocking density and a physical barrier in a group bedded-pack for close-up cows did not affect the odds of developing metritis after calving.
Keywords for abstract:	Stocking density transition

EAR - 12

Title of abstract:	**THE EFFECTS OF FATTY ACID SUPPLEMENTATION AND PROVISION OF A DRY TEAT ON DISEASE IN VEAL CALVES**
Authors	L. L. Deikun[1,2], G. G Habing[1], J. D. Quigley[2], and K. L. Proudfoot[1]
Abstract	Veal calves are at a high risk of disease early in life. Research is needed to determine interventions that reduce disease. The aim of this study was to determine the effects of fatty acid supplementation (NeoTec5g®, Provimi) and the provision of a dry teat on bovine respiratory disease (BRD), navel inflammation, and diarrhea. A total of 240 Holstein bull calves from 2 cohorts were randomly assigned to 4 treatments using a 2x2 factorial design (n=60/treatment): control, NeoTec5g, NeoTec5g+Teat, and Teat upon arrival to a commercial veal facility (d 0). Milk replacer (MR) was fed twice daily using a proprietary step-up program. NeoTec5g was added to MR at a feeding rate of 0.5g/kg of BW/hd/day for NeoTec5g groups. Serum IgG was determined using radial immunodiffusion assays on d 1; 33% of the calves had failure of passive transfer (<10 mg of IgG/mL.) Health exams were conducted twice weekly for 6 wk to diagnose BRD (UC Davis scoring system: 0=total score for all clinical signs < 5, 1=total score ≥ 5), navel inflammation (0=no or mild inflammation, 1=moderate or severe inflammation) and diarrhea (0=normal feces, 1=loose or watery feces). Health data were analyzed using logistic regression (PROC GENMOD in SAS) using calf as the experimental unit; the model included IgG, disease at arrival, cohort, NeoTec5g, Teat, and NeoTec5g*Teat. Data is reported as odds ratios (OR). There was no effect of NeoTec5g (OR=1.0; *P*=0.86), Teat (OR=1.1; *P*=0.57) nor their interaction (*P*=0.48) on the odds of BRD. There was no effect of NeoTec5g (OR=1.3; *P*=0.18), Teat (OR=1.2; *P*=0.33) nor their interaction (*P*=0.64) on the odds of diarrhea. There was no effect of NeoTec5g (OR=0.4; *P*=0.14) or Teat (OR=1.2; *P*=0.63) on the odds of navel inflammation. We saw no effect of our interventions on calf health.
Keywords for abstract:	Calf BRD Diarrhea Navel inflammation

EAR - 13

Title of abstract:	**PYRROLIDINLYL BASED SMALL MOLECULE THERAPEUTIC TO CONTROL AVIAN PATHOGENIC ESCHERICHIA COLI (APEC) INFECTION IN POULTRY**
Authors	D. Kathayat, Y. A. Helmy, L. Deblais, V. Srivastava, G. Closs Jr, and G. Rajashekara. Dept. of Veterinary Preventive Medicine
Abstract	Avian pathogenic *E. coli* (APEC), an extra-intestinal pathogenic *E. coli* (ExPEC), is a causative agent of avian colibacillosis. Further, recent report has suggested APEC as a foodborne human uropathogen transmitted through consumption of contaminated poultry products. Currently, APEC infections in poultry are controlled by antibiotic medication and vaccination. However, APEC resistant to multiple antibiotics has been reported worldwide and the available vaccine does not confer protection against heterologous APEC serotypes. Therefore, new and improved anti-APEC therapeutics are critically needed. To this end, we screened a small molecule (SM) library, and identified 11 SMs bactericidal to multiple APEC serotypes including those resistant to antibiotics. Eight SMs, that are non-toxic and effective in cultured cells (Caco-2, HD11 and THP-1) and wax moth larvae, were tested in one-week-old commercial broiler chickens. Chickens were infected subcutaneously (s/c) with rifampicin resistant (Rif^r) APEC O78 (1 x 10^7 CFU/chicken) and SMs were orally gavaged (1 mg/kg body weight) twice a day starting one day prior to infection to three days post-infection. Four SMs (GI-7, GI-10, GI-6 and GI-2) reduced the mortality (42.8 to 71.42%), APEC load (1.3 to 2.6 logs) and APEC lesions severity (13.5 to 62%) in chickens. Further, GI-7, a most effective SM, administration in drinking water (40 mg/L and 60 mg/L), for seven days, also reduced the chicken's mortality (83.34 to 84.84%), APEC load (2.0 to 2.5 logs) and APEC lesions severity (13.63 to 36.36%). Preliminary study showed GI-7 downregulated the expression of LptD (outer membrane lipopolysaccharide transporter) in APEC. Our results demonstrate that the GI-7 containing pyrrolidinyl moiety can represent a novel anti-APEC therapeutic.
Keywords for abstract:	Drug discovery APEC Poultry Colibacillosis Pyrrolidinyl

EAR - 14

Title of abstract:	**GUIDING ANTIMICROBIAL THERAPY: PREVALENCE OF BACTEREMIA IN DAIRY CALVES WITH DIARRHEA**
Authors	Jessica Garcia, Miranda Hengy, Jessica Pempek, Austin Hinds, Dubra Diaz-Campos, Gregory Habing; Depts. Of Veterinary Preventative Medicine and Veterinary Clinical Science
Abstract	Calfhood diarrhea is the most common cause of mortality in dairy calves. Septicemia is an important sequela of diarrhea, and the primary justification for antimicrobial treatment for diarrhea. Farm workers make routine decisions regarding antimicrobial therapy based on clinical signs, yet there is a lack of criteria associated with bacteremia. The prevalence of bacteremia in diarrheic calves has been estimated to be 30%; however, this estimate included calves presented to a veterinary hospital or raised for veal, and may not reflect the prevalence in calves on commercial dairy operations. Thus, our objective was to determine the prevalence of bacteremia in diarrheic dairy calves and identify clinical signs associated with bacteremia. We hypothesized the prevalence of bacteremia would be less than 30% in diarrheic calves, and clinical signs would be accurate predictors of bacteremia. Calves (≤ 21 days old) were enrolled across two dairy farms into a diarrheic or clinically healthy group (control to assess aseptic technique). Diarrheic calves enrolled presented with loose to watery stool, dehydration (assessed by skin tent) or depression (assessed by suckle reflex and standing ability), and were not previously treated with antibiotics. Clinical signs assessed included respiratory signs, joint inflammation, navel score, temperature, and heart and respiratory rate. Aseptic blood samples were collected and cultured to determine any bacterial species present using mass spectrometry. The prevalence of bacteremia in diarrheic calves was 15.3% (17/111) and 18.5% (5/27) in clinically healthy calves. There was no association between clinical signs and bacteremia. The prevalence of bacteremia in the diarrheic group was significantly lower than previous estimates, indicating a potential opportunity to reduce antimicrobial use in calves with diarrhea that are not septicemic. Future studies should investigate the prevalence of bacteremia in clinically healthy calves to determine if there are intermittent bouts of bacteremia in venous blood.
Keywords for abstract:	Calves Diarrhea Bacteremia

EAR - 15

Title of abstract:	**DEVELOPMENT OF MULTILOCUS SEQUENCE TYPING (MLST) ASSAY FOR *MYCOPLASMA GALLISEPTICUM (MG)***
Authors	M. Ghanem[a], W. Gebreyes[a], and M.El-Gazzar[c,] [a] Departs of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, OH 43210, USA; Veterinary Diagnostics and Production Animal Medicine, Iowa State University, Ames, IA 50011, USA.
Abstract	Mycoplasma gallisepticum (MG) is the most pathogenic avian mycoplasma species. It affects commercial, non-commercial poultry and wild birds. Current MG sequence typing methods rely on the partial sequence of one or more surface antigen genes. Mulitocus Sequence Typing (MLST), a widely used typing method for many human and animal pathogens relies on conserved housekeeping genes. Recently, MLST assays have been developed for M. synoviae and M. iowae. Additionally, a whole genome based, core genome MLST (cgMLST) assay has been developed for MG and MS. However, cgMLST cannot be applied to clinical samples. Here, we have developed 7-loci based MLST scheme for MG that can be applied directly on clinical samples without the need for isolation. These seven loci were selected out of 425 genes recently used for cgMLST assay. A total of 101 diverse MG samples, including isolates and clinical samples, were typed using the newly developed 7-loci MLST. The phylogeny and discriminatory power of this 7-loci MLST were evaluated and compared to cgMLST and compared to surface antigens genes currently used for MG sequence typing. The 7-loci MLST provided optimum discriminatory power and congruent phylogeny to cgMLST. Additinally, a database for MG MLST was created and is currently available for public use https://pubmlst.org/mgallisepticum/. This assay will increase the accessibility to MG sequence typing and provide a stable and expandable nomenclature that is compatible with cgMLST. This assay represents an important tool for epidemiological investigation of MG that can contribute to better control and eradication efforts.
Keywords for abstract:	MLST; *Mycoplasma gallisepticum*; Poultry; Molecular typing

EAR - 16

title of abstract:	**THE POTENTIAL USE OF MALDI SEPSITYPER™ TECHNOLOGY FOR RAPID DIAGNOSIS OF BACTEREMIA IN DAIRY CALVES**
Authors	Miranda H. Hengy, Jessica D. Garcia, Jessica A. Pempek, Dubraska Diaz-Campos, C. Austin Hinds, Gregory G. Habing
Abstract	Culture-based diagnosis of septicemia in veterinary patients can require a week or more and is therefore 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. A recent alternative method for diagnosing bacteremia involves utilization of a Sepsityper™ kit in conjunction with matrix-assisted laser desorption/ionization (MALDI) mass spectrometry, which is capable of detecting and speciating bacterial growth within 30 min of a positive blood culture bottle. The objective of this study was to investigate the use of Sepsityper with MALDI to detect bacteremia in diarrheic dairy calves. We hypothesized that this method would demonstrate more rapid and sensitive results for detecting bacteremia than traditional culture-based methods. Aseptic blood samples were collected from diarrheic calves, and 10mL of blood was inoculated in a blood culture bottle (BCB) with indicator top. Bottles were incubated at 35˚C and monitored for 5 d following inoculation to assess turbidity and fluid translocation into the indicator top, which defined a positive BCB. Blood culture fluid from positive BCBs was analyzed by Sepsityper with MALDI and traditional culture to media-based isolation and identification methods. Preliminary results show that the Sepsityper method identified bacteria in 50% (n=11/22) of cases positive on BCB, while the culture-based method identified bacteria in 82% (n=18/22). Despite a potentially lower sensitivity, results from Sepsityper method were available at least 24 h sooner than traditional methods, and may therefore play an important role when rapid treatment decisions are required.
Keywords for abstract:	Neonatal Calf Diarrhea, Bacteremia, Sepsityper, MALDI-TOF, Blood Culture

EAR - 17

Title of abstract:	**YEAR-ROUND INFLUENZA A VIRUS SURVEILLANCE IN WILD MALLARDS, *ANAS PLATYRHYNCHOS*, USING THE MARSHES OF THE SOUTHWEST LAKE ERIE BASIN.**
Authors	S.E. Lauterbach[1], M.A. Piccutio[2], B.T. Shirkey[2], J.M. Nolting[1], and A.S. Bowman[1]. [1]The Ohio State University, Department of Veterinary Preventive Medicine [2]Winous Point Marsh Conservancy
Abstract	As the primary reservoir of influenza A viruses (IAV), the study of wild waterfowl is vital to describing the epidemiology and natural history of IAVs as a whole. Active IAV surveillance in waterfowl in the United States has largely been conducted during hunter-harvest in autumn and winter when birds are most accessible for sample collection. This has resulted in gaps in surveillance during spring and summer. Therefore, IAV surveillance, though extensive, has yet to document IAV transmission patterns in waterfowl on a continuous timeline. Substantial historical surveillance data has been reported for mallards, *Anas platyrhynchos,* as they account for over one-quarter of all waterfowl surveillance samples in the United States. We initiated an active IAV surveillance study in mallards continually over two years using marshes of a wetland conservancy in the southwest Lake Erie basin, a historically successful surveillance site. To date, we have collected 789 cloacal swabs of mallards from January through August 2018 using live-trapping collection methods. All samples have been tested for IAV by RNA extraction and real-time reverse transcription polymerase chain reaction (rRT-PCR). No ducks were captured during winter. During spring, 713 samples were collected, 75 (10.5%) were positive with rRT-PCR, and five viral isolates were recovered. During summer, 76 samples were collected, 22 (28.9%) were positive using rRT-PCR and two viral isolates were recovered. Live-trapping proved labor-intensive and yielded fewer birds than predicted, despite being performed by experienced wildlife technicians using historically productive methods. Estimated viral prevalence during spring was much higher than previously reported (by about 9.0%), but this estimate may be artificially high due to cross-contamination during trapping. Estimated viral prevalence during summer was similar to historical estimates. Conducting IAV surveillance in waterfowl outside the convenience of hunter-harvest sample collection requires extensive effort but may reveal new information about IAV epidemiology in waterfowl.
Keywords for abstract:	influenza A virus ducks prevalence

EAR - 18

Title of abstract:	**SEROLOGIC IMMUNITY AGAINST CONTEMPORARY SWINE-ORIGIN INFLUENZA A VIRUSES IN A COHORT OF HEALTHY INDIVIDUALS**
Authors	J. N. Lorbach[1], T. Fitzgerald[2], C. Nolan[2], J. M. Nolting[1], J. J. Treanor[2], D. J. Topham[2], and A. S. Bowman[1] [1]Department of Veterinary Preventive Medicine, The Ohio State University [2]Department of Microbiology and Immunology, University of Rochester Medical Center
Abstract	Diverse influenza A viruses (IAVs) are maintained in swine populations, with occasional bidirectional transmission between swine and humans. IAVs established in swine can persist relatively unchanged while the same IAVs circulating in humans mutate via genetic drift. With the vast majority of swine-to-human IAV transmission occurring in children, it is likely that immunologic gaps exist and may permit novel viruses to become established following zoonosis. To characterize human immunity against swine-origin IAVs (swIAV), we performed a cross-sectional analysis of sera from 153 healthy human donors. Serum antibody (Ab) titers were measured by hemagglutination inhibition assay (HAI) against two human seasonal IAV vaccine-strains and 11 swIAV strains representing distinct genetic lineages of H1 and H3 IAVs currently circulating in swine. Endpoints were selected according to industry standard IAV vaccine effectiveness guidelines, and age groups were binned by decade of birth (n=8). Individual seroprotection status (HAI $\geq$ 40, corresponding with 50% reduction in individual disease risk), group seroprotection rate (SPR; proportion with HAI $\geq$ 40), and geometric mean titer (GMT; natural log-transformed) were determined. Adequate protection (overall or by group) was defined as SPR $\geq$ 70%. The GMT was <40 for 6 swIAVs, including 3 H1 and 3 H3 swIAVs. In the youngest age group (donors born 2004-2013), the SPR was <70% for 10 swIAVs and 0% for 5 swIAVs. There were 3 swIAVs with an SPR $\geq$70% in donors born 1974-1983 and <70% in all other age groups. No swIAVs were associated with adequate protection in all age groups. One human-lineage H1N2 (H1-δ1 clade) swIAV introduced into the swine population in the early 2000s was associated with inadequate protection in all age groups. Overall, there are insufficient immunologic barriers to prevent spillover of swIAVs into humans and youth are particularly predisposed to infection with swIAVs.
Keywords for abstract:	influenza zoonotic serology virology swine

EAR - 19

Title of abstract:	**EFFECT OF PREPARTUM LYING TIME AND ENERGY BALANCE ON STILLBIRTH IN TRANSITION DAIRY HEIFERS AND COWS**
Authors	B.T. Menichetti, Piñeiro, J.M., A.A. Barragan, A. Relling, S. Bas, and G.M. Schuenemann. Depts. of Veterinary Preventive Medicine and Animal Sciences
Abstract	The objective was to assess the effect of pre-partum lying time (LT) and non-esterified fatty acids (NEFA) on stillbirth in transition dairy heifers and cows. A total of 1051 Holstein dairy cows (401 PRIM and 650 MULT) from 3 commercial dairy herds were enrolled at 14 d before calving until 14 d post-calving. Weekly, a cohort of 10 to 15 cows was enrolled at each farm and electronic data loggers (IceQube, IceRobotics, Edinburgh, UK) were fitted to the hind leg of individual cows to assess their lying time. All heifers and cows were housed in similar prepartum free-stall barns and moved into a contiguous individual maternity pen for parturition. Stillbirth was defined as a calf born dead or died within 24 h after birth, and with normal gestation length. Blood samples were collected at 7 d prior to (dpp) and at calving to assess NEFA and calcium, respectively. Data were analyzed using MIXED procedure of SAS. MULT cows had greater ($P < 0.05$) LT prior to parturition compared with PRIM cows. MULT cows with a stillborn calf had reduced pre-partum LT ($P < 0.05$), increased NEFA 7 dpp and decreased calcium at calving compared with cows with a calf born alive. PRIM cows with stillborn calf had reduced calcium at calving ($P < 0.05$) but NEFA and LT did not differ compared with PRIM cows with a calf born alive. These results suggest that LT, energy status of prepartum dams and calcium at calving are critical for calf survival.
Keywords for abstract:	Stillbirth, Lying time, NEFA, Dairy cattle

EAR - 20

Title of abstract:	**FMDV CONTAMINATION OF THE ENVIRONMENT SURROUNDING CATTLE HERDS IN CAMEROON**
Authors	S.R. Mielke, R. B. Garabed, Dept of Veterinary Preventive Medicine
Abstract	Foot-and-Mouth Disease virus has been shown to persist in the environment dependent upon a range of pH, relative humidity (RH), and temperature. A recent analysis of available survival data showed that viral persistence is likely affected in diverse ways from interactions between RH, temperature, and matrix (i.e. soil, water, or air). In endemic regions disentangling these relationships will aid efforts to eliminate FMD, which devastates economies and destabilizes food security. Cameroon, in West Africa, has a unique livestock mobility network consisting of mobile herds, transboundary trade herds, and sedentary herds. The potential for environmental transmission of FMDv is exacerbated by the presence of these groups and range of environmental conditions in Cameroon. To understand this potential, I hypothesize that: (A)**Detection of FMDv is inversely related to distance from the center of the herd,** (B) **Detection of FMDv is inversely related to time from index case,** and (C) **The rate of decline for environmental FMDv is related directly with decreasing relative humidity (RH)**. To investigate viral contamination, soil, fomite, and air samples were collected from three sedentary herds beginning on day one of reported FMD outbreaks and ending by day 30. Soil and air were sampled along three pathways at 0, 50, 75, and 100 meters from the center of the herd, representing high, medium, and low cattle presence. Fomite sampling was completed by swabbing vehicle tires and the soles of shoes from herders and researchers. rRT-PCR was used to test for the 3D RNA polymerase gene, which indicates presence of viral RNA. Preliminary results suggest that increasing RH is associated with increased detection of FMDv and that increasing distance from the center of the herd is associated with decreased detection of FMDv. Initial analysis of time suggests that over time detection of FMDv will decrease.
Keywords for abstract:	Spatial and Temporal Analysis Logistic Regression FMDv Viral Persistence Environment

EAR - 21

Title of abstract:	**SURVEILLANCE AND GENOMIC CHARACTERIZATION OF AMR *E. COLI* AND SALMONELLA FROM AN OVINE COLONY ON NAVAJO NATION**
Authors	M. Overcast, S. Bender, G. Daye, D. Mollenkopf, T. Wittum, A. Arruda
Abstract	Antimicrobial resistance has emerged as a threat to global health in recent decades. It is necessary to quantify the prevalence of antimicrobial resistant (AMR) bacteria in various contexts so that methods of reducing risk contributing to its dissemination may be identified. Few studies offer insight into resistant populations in food production sheep. Sheep living on Navajo Nation typically grow up in a pastoral setting, and enteric AMR bacteria dissemination amongst ovine with this context has not been reported. Antimicrobial use is infrequent in the flock we tested at Navajo Technical University due to low risk of infection; but, breeding rams are leased to various shepherds during breeding season and have unknown exposure to sheep and environments potentially harboring AMR bacteria during breeding season. To investigate, we gathered fecal and environmental samples from this flock and its housing unit during non-breeding season to establish a baseline prevalence of enteric *Salmonella spp*., extended spectrum beta-lactamase gene *bla*$_{\text{CTX-M}}$, and AmpC gene *bla*$_{\text{CMY}}$. We predicted that antimicrobial resistance patterns found in sheep isolates will be the same as resistance patterns from environmental isolates taken from housing surfaces. Selective media using antimicrobial drugs cefoxitin and cefepime were used to isolate colonies. We discovered that 1.79% of samples showed phenotypic resistance indicating *bla*$_{\text{CMY}}$, and 0% of samples showed phenotypic resistance indicating *bla*$_{\text{CTX-M}}$. Environmental samples showed no phenotypic resistance. Altogether resistance was low in both the environment and fecal samples, so comparison between groups couldn't be made with statistical significance. Using minimum inhibitory concentration plates and Poisson and exact logistical regression, we found that adult isolates harbored resistance to more antimicrobial classes than did lamb isolates. These data could be used as the basis for further inquiry regarding food animal production style and antimicrobial resistance, and more data about resistance in various sheep populations is needed.
Keywords for abstract:	Epidemiology Sheep Antimicrobial resistance Salmonella Extended Spectrum Beta Lactamase

EAR - 22

Title of abstract:	**UTILIZATION OF SERVICES AND PET OWNERSHIP AMONG INDIVIDUALS EXPERIENCING HOMELESSNESS IN COLUMBUS, OHIO**
Authors	P. Rullan-Oliver & J. O'Quin.
Abstract	Background: Approximately 40,648 individuals experience homelessness in Ohio every year, with an estimated 1,691 people in Columbus without a place to live on any given night. Many have pets that provide mental health benefits including emotional support and safety. This study aims to assess the utilization of available services and the impact pet ownership may have. Methods: A survey was conducted at six locations in Columbus selected to allow targeting of those who own pets and those who do not. Demographics were collected as well as information on homelessness, pet ownership, and use of shelters and public transportation. Results: The survey was administered to 57 people: 24 pet owners and 33 non-pet owners. The majority of the participants were between the ages of 48 and 57 (40.35%) and experienced homelessness for <1 year (61.82%). Most of them reported living "on the land" (59.65%), of which 66.67% and 54.55% were pet owners and non-pet owners, respectively. Among pet owners, the majority (28/31,90.32%) reported that their pet played a primary role in companionship and emotional support; however, 32.26%(10/31) of individuals also reported that their pet was a barrier for housing assistance. Discussion: A key factor for prevention of homelessness is accessible and affordable housing. While many reasons were given for not using shelters, those owning pets (1/21) were far less likely to use them than those without pets (8/23). Of those that owned pets, 45.45% owned them before they became homeless. With pet restrictions on most government-subsidized housing, it is possible that some pet owners will elect homelessness over giving up their pet. Addressing barriers to housing, such as pet ownership, is essential for preserving the human-animal bond and reducing rates of homelessness.
Keywords for abstract:	Homelessness Pet Ownership Human-animal bond

EAR - 23

Title of abstract:	**THE RELATIONSHIP BETWEEN ALLOSTATIC LOAD INDEX AND STRESSORS IN RING-TAILED LEMURS (*LEMUR CATTA*)**
Authors	K.E. Seeley, K. Proudfoot, B. Wolfe, and D.E. Crews. Depts of Veterinary Preventive Medicine and Anthropology
Abstract	Stress is an unavoidable part of life and can often be an adaptive mechanism for survival. However, chronic stress has been linked to poor health outcomes and increased morbidity. The concept of allostasis has been used to describe the physiologic dysregulation that occurs when an organism is exposed to chronic stressors. This study utilized an allostatic load index (ALI) composed of six biomarkers to evaluate the relationship between stressors and allostasis in a population of thirty-eight captive ring-tailed lemurs (*Lemur catta*). Biomarkers were measured in serum obtained during either anesthetic events or manual restraint. Any biomarker noted to fall 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 work illustrates that several social and husbandry variables were associated with increases in allostasis and indications that allostatic load index may be a useful tool in assessing the health and welfare of lemurs in human care.
Keywords for abstract:	Allostasis Prosimians Stress Welfare

EAR - 24

Title of abstract:	**DESCRIPTIVE AND SPATIO-TEMPORAL ANALYSES OF 45 CANINE LEPTOSPIROSIS CASES FROM CHICAGO, ILLINOIS (2015 – 2018)**
Authors	A. Smith[a], J. Hinrichs[b], A. Arruda[a], T. Wittum[a], and J. Stull[a] [a] College of Veterinary Medicine, Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, Ohio, United States [b]MedVet Chicago, Chicago, Illinois, United States
Abstract	Canine leptospirosis is a reemerging zoonotic disease of concern, and Chicago has been identified as a high-risk area for canine leptospirosis. The objectives of this study were to describe the signalment, vaccination history, treatment, and outcome of canine leptospirosis cases, and to investigate the presence of spatio-temporal clusters. Data (signalment, vaccination history, clinical signs, treatment, outcome, and home zip code) from 45 dogs diagnosed with leptospirosis between January 2015 and December 2018 were collected from medical records from a private small animal hospital (4 cases) and an emergency referral hospital (41 cases) in Chicago. Descriptive statistics were used to describe the cases, and spatial coordinates of home zip code were analyzed visually using mapping tools; and statistically using a space-time Poisson scan statistic. The majority of the cases were young (median: 3 years; range: 8 weeks – 11 years), small (median: 17.5 lbs; range: 2.9 – 74 lbs), and male (55%). None of the cases were fully immunized against leptospirosis according to AAHA vaccination guidelines. Clinical signs were first observed a median of 2 days before presentation to the clinic (range 0 - 20 days), and vomiting (84% of cases), anorexia (78%), and depression (76%) were the most common clinical signs. PCR testing (67% of cases) and MAT (31%) were used for diagnosis. Intravenous fluids (82% of cases) and antiemetics (84%) were commonly used, and all cases received antimicrobial treatment. Thirteen cases (29%) were euthanized or died. Most of the cases were in northern Chicago, and a significant space-time cluster was identified from August 2017 through November 2017 in the north-central region. These results highlight the epidemiology of canine leptospirosis cases in a previously identified high-risk area for the disease in the United States and demonstrate the need for increased awareness of the benefits of canine leptospirosis vaccination in Chicago.
Keywords for abstract:	Leptospirosis Canine Zoonotic

ED - 1

Title of abstract:	**EVALUATION OF BEHAVIOR KNOWLEDGE IN FIRST YEAR VETERINARY STUDENTS BEFORE AND AFTER AN INTRODUCTION TO ANIMAL BEHAVIOR COURSE**
Authors	ML Lilly, A. Gonçalves Arruda, K. Proudfoot Depts of Veterinary Clinical Sciences and Veterinary Preventive Medicine
Abstract	**OBJECTIVES** 1) To measure incoming veterinary students' knowledge of behavior and pop-culture behavior myths regarding companion animal (dog, cat, horse) body language, motivation, and learning. 2) To identify which sources of prior behavior knowledge predicted pre-course knowledge. 3) To evaluate the survey as predictor of the course' final exam score. **SAMPLE** First year veterinary students at the Ohio State University. **PROCEDURE** An anonymous electronic survey was given before (Pre-Class) and after (Post-Class) the semester long, 2-credit, animal behavior course. Sources of incoming knowledge were evaluated as predictors of knowledge score Pre-Class. Post-Class survey scores were evaluated as predictive of Final Exam scores as a measure of validity. **RESULTS** Incoming veterinary students (n=152) performed poorly Pre-Class (M= 48.99%, Std. Dev= 12.73). Reporting "peer-reviewed journals" as a source of incoming knowledge predicted 9.03% higher scores, whereas reporting "magazines and pop-culture literature" as a source of incoming knowledge predicted 7.57% lower scores compared to students not reporting those sources. Companion animal ownership was not predictive of scores. Students' knowledge improved dramatically (M=84.3%, Std. Dev= 8.01) Post-Class and these scores were predictive of Final Exam score.
Keywords for abstract:	Veterinary behavior Behavior knowledge Behavior education Veterinary students Clinical competency

IMMUNOLOGY
AND
INFECTIOUS DISEASES

IMID - 1

Title of abstract:	**ROLE OF CASPASE-1-DEPENDENT AND -INDEPENDENT PATHWAYS IN THE ADJUVANT ACTIVITY OF ALUM.**
Authors	Zayed Attia, Amal Amer, and Prosper N. Boyaka.
Abstract	Aluminum salts or alum are the most widely used adjuvants in human and veterinary vaccines. This group of adjuvants has been approved by FDA since the early sixties but mechanisms underlying their adjuvanticity are not fully understood. For example, it remains unclear whether alum enhance immune responses to co-administered vaccine antigens in a Nodes like receptors 3 (NLRP3)-inflammasome dependent or independent fashion. Another well-established feature of injected vaccines containing alum as adjuvant is the induction of Th2-type responses, which support production of antibody isotypes (i.e., IgE and no- complement fixing IgG subclasses) more effective for protections against extracellular pathogens. Stimulation of NLRP3 leads to the activation of Caspase 1, which leads to the maturation of interleukin 1 beta (IL-1β), a chemoattractant for myeloid cells. To gain a better understanding of the role played by NLRP3 inflammasome in the adjuvant activity of alum, we compared systemic (bloodstream) and mucosal antibody responses of control wild-type and Caspase 1 KO mice immunized with an alum-adsorbed anthrax protective antigen (PA) vaccine. Our data show that the absence of caspase-1 does affect the overall ability of alum to enhance antibody responses. However, the development of PA-specific IgG1 was slower in Caspase 1 KO mice. We also found that Caspase 1 KO mice develop higher levels of the complement fixing IgG2c subclasses suggesting that higher levels of Th1 responses developed in the absence of Caspase 1. Finally, like their wild-type counterpart, Caspase 1 KO mice failed to develop PA-specific serum or mucosal IgA responses. Taken together, our data show that Caspase 1-dependent and -independent pathways differentially regulate the profile of T helper cell and immunoglobulin isotype responses to alum-based vaccines and thus, potential protection against intracellular or extracellular pathogens.
Keywords for abstract:	Adjuvants, Alum, Caspase-1, Th2 responses.

IMID - 2

Title of abstract:	**HIGHLY SENSITIVE SEQUENCING METHOD FOR INTEGRATED PROVIRAL HIV-1 DNA ANALYSIS**
Authors	A.Baek*, H.Yu*, S.Golconda , S.H.Kim , L.Smith and S.Kim
Abstract	HIV/AIDS remains a global epidemic. The genetic diversity and continual hyper-evolution of HIV-1 have presented major challenges in controlling the epidemic. Meanwhile, HIV genotyping has been hampered by the short-read length (100-800bp) and frequent errors (1/100~1/1000) of current sequencing platforms. Nanopore sequencing (Oxford Nanopore Technologies), a 3rd generation sequencing platform, has several revolutionary features, including an extremely long-read length (up to 350kb), real-time data output, and pocket-size mobility. However, its application is significantly limited by its high error rates (1/20~1/10). We have developed a novel Tandem Twin barcode (TTB) method that can eliminate read errors in Nanopore single-molecule target sequencing. Our method can correct read errors by labeling individual target DNA uniquely with a TTB, PCR amplifying the TTB-labeled DNA, and high-throughput sequencing of the PCR products followed by correction of read errors via cross-comparison of sequences sharing identical barcodes. We have successfully generated a high-quality TTB library specific to HIV-1 sequenced 24 TTB-labeled, clonal HIV-1(NL4.3) plasmid DNA molecules and integrated proviral DNA with an accuracy as high as 99.99%. To sequence integrated HIV-1 proviral DNA in patients, however, sensitivity is a major hurdle, given approximately 1-10^4 proviral DNA present in 1 million cells in patients. Two different approaches were tested: the PCR mediated sequencing and the CRISPR/Cas9 mediated sequencing methods. CRISPR/Cas9 approach showed several folds higher efficiency than PCR mediated sequencing method. The sensitivity and fidelity of new CRISPR/Cas9-mediated HIV-1 sequencing will be demonstrated. The development of this new long-range sequencing method will enable high-fidelity genotyping of full-length HIV DNA in a high-throughput fashion. This technical advancement will have a broad impact on diverse areas of biomedical sequence analysis.
Keywords for abstract:	HIV/AIDS Tandem twin-barcode(TTB) library long-read sequencing barcoding-mediated error correction CRISPR/Cas9 Nanopore sequencing

IMID - 3

Title of abstract:	**RANDOM MUTAGENESIS OF *EHRLICHIA* SP. HF STRAIN FOR IDENTIFICATION OF VIRULENCE GENES**
Authors	H. Bekebrede, M. Lin, Y. Rikihisa
Abstract	*Ehrlichia* spp. (*E. canis, E. ruminantium, E. ewingii*, and *E. chaffeensis*) are tick-borne obligatory intracellular bacteria that infect a variety of mammals including dogs, ruminants, deer, and humans, causing severe and sometimes fatal systemic disease. Research to identify *in vivo* virulence factors of *Ehrlichia* spp. is hampered by the lack of small laboratory animal models. The Rikihisa laboratory culture isolated and completed whole genome sequencing on a novel *Ehrlichia* species named “HF strain” from *Ixodes ovatus* ticks in Japan. The HF strain is most closely related to *E. chaffeensis* human isolates in the US, and kills laboratory mice within 10 days. My research seeks to analyze *in vivo* virulence factors of the HF strain using Himar transposon mutagenesis. Our hypothesis is that some genes of HF strains are not required in cell culture infection so knocked-out mutants can be recovered in cell culture system, but are required for mouse infection. Mutant HF strains are being cloned, and genomic loci of transposon insertion are being identified by semi random two-step PCR (ST-PCR). Mutants are used to infect mice; mutated genes in mutants that cannot infect mice are *in vivo* virulence factors. I have so far isolated 158 stable mutants expressing mCherry fluorescence as an indication of transposon insertion. 61 inserts are intragenic affecting 49 distinct ORFs and 107 inserted intragenically, including 30 close (<200 bp) to the ORF potentially disrupting expression of 29 ORFs. Out of eleven mutants tested, two mutants reduced infection and delayed disease progression in mice. While this suggests that they are virulence factors, these genes are not required for *Ehrlichia* to overcome host immune defense and kill mice. *In vivo* testing of more mutants is in progress. Because *Ehrlichia* spp. share homologus genes, the proposed study will help understanding virulence factors of other *Ehrlichia* spp. as well.
Keywords for abstract:	Ehrlichia HF strain obligate intracellular bacteria virulence mutagenesis

IMID - 4

Title of abstract:	**HUMAN RESPIRATORY SYNCYTIAL VIRUS FUSION PROTEINS EXPRESSED IN A VESICULAR STOMATITIS VIRUS VECTOR SYSTEM**
Authors	K. Brakel, B. Binjawadagi, and S. Niewiesk
Abstract	Human respiratory syncytial virus (RSV) is a leading cause of respiratory disease in infants, the elderly, and immunocompromised individuals. There is no approved vaccine, and antibodies produced after natural infection do not elicit long-term immunity. Both the F (fusion) and G (attachment) envelope glycoproteins have been used in vaccine development, with monoclonal antibodies produced against the F protein showing more effective neutralization properties than those against the G protein. The F protein has both a pre-fusion and a post-fusion conformation, and protein subunit vaccines against the pre-F are more effective than those against the post-F. In this project, we have created recombinant vesicular stomatitis virus (rVSV) vectors expressing the pre-fusion F (pre-F), a pre-fusion form of F derived from a clinical isolate of RSV (HEK-pre-F), the post-fusion F (post-F), or the native F. After confirming successful recovery of all recombinants via sequencing, flow cytometry, and Western blot, cotton rats were inoculated intranasally with recombinants. Only the native F provided complete protection in the lungs and partial protection in the nose, although HEK-pre-F provided partial protection in the lung and nose. The native F also generated significantly more neutralizing antibodies than other recombinants. This indicates that in the VSV system, the native F is more protective and immunogenic than pre-F or post-F alone, unlike in protein-based systems.
Keywords for abstract:	Cotton rat Human respiratory syncytial virus Immunology Virology Vaccines

IMID - 5

Title of abstract:	**EVALUATION OF A COMMERCIAL *HAEMONCHUS CONTORTUS* VACCINE IN NON-DOMESTIC HOOFSTOCK**
Authors	M. Carman, D. Love, P. Bapodra-Villaverde, J. Ramer, R. Junge, and A.E. Marsh. Dept. of Veterinary Preventive Medicine (Carman, Marsh), Center for Conservation of Tropical Ungulates (Love), Columbus Zoo and Aquarium (Bapodra-Villaverde, Junge), The Wilds (Ramer)
Abstract	Similar to small ruminant populations, non-domestic hoofstock in human care facilities face significant challenges with parasite management. *Haemonchus contortus* (the Barber's pole worm) is of particular concern, causing significant morbidity and mortality in non-domestic ungulates within the United States and abroad, and management of this nematode is often complicated by the high stress nature, unique social structures and behavior, and particular habitat requirements of these non-domestic hoofstock species. This study utilized Barbervax®, a vaccine that has shown efficacy in sheep, goats, and, more recently, alpacas at producing antibodies against the gastrointestinal intraluminal membrane protease complex, H11/H-gal-GP, responsible for nutrient metabolism within *H. contortus*. This vaccine is further effective in sheep and goats at reducing fecal egg counts (FEC) and lowering mortality associated with infection. Specific aims of this study were to determine the safety of Barbervax® administered to Chinese gorals (*Nemorhaedus griseus*) (n=4) and pronghorns (*Antilocapra americana*) (n=3) and determine if vaccination would result in antibody production directed to the protease complex of the parasite that, under normal infection conditions, is not detected by the host's immune system. All animals involved were vaccinated at regular intervals and exposed to parasite challenge on existing *H. contortus* contaminated pastures during the summer months. Serum was collected to evaluate antibody production. The animals showed no detectable local or systemic indications of an adverse vaccine reaction. One pronghorn developed lameness following intramuscular vaccine injection. We also investigated appropriate secondary antibodies for optimization of the non-domestic hoofstock ELISA assay to detect the H11/H-gal-GP specific antibodies. The gorals and pronghorns developed antibodies following vaccination. These results demonstrate potential for Barbervax® to be a beneficial adjunct for *H. contortus* management in non-domestic hoofstock in human care.
Keywords for abstract:	*Haemonchus contortus* Barbervax® Non-domestic hoofstock

IMID - 6

Title of abstract:	**TESTING VESICULAR STOMATITIS VIRUS RECOMBINANT VACCINES EXPRESSING THE F, G, M2-1, AND N, PROTEINS OF HUMAN RESPIRATORY SYNCYTIAL VIRUS IN THE COTTON RAT MODEL (*SIGMODON HISPIDUS)***
Authors	K. French-Kim, K. Brakel, O. Harder, S. Niewiesk
Abstract	Human respiratory syncytial virus (HRSV) causes severe lower respiratory disease and even mortality in pediatric, geriatric and immunocompromised individuals. HRSV infection does not provide life-long immunity, and there is no licensed vaccine or antiviral therapeutic drugs available. Recent efforts in HRSV vaccine development are centered primarily on the fusion protein (F glycoprotein) of the virus. However, the focus on one protein may be suboptimal as a vaccine. This study utilized four HRSV proteins: the fusion protein (F) and the attachment protein (G glycoprotein) which are mainly antibody targets, in addition to two nucleocapsid proteins (M2-1 and N) which are T-cell targets. The purpose was to see if immunizing with a combination of proteins provided better protection against HRSV than immunizing with the F protein alone. Vesicular stomatitis virus (VSV) was used as the vector system due to recent success with the recombinant VSV (rVSV) Ebola vaccine, and cotton rats were used as the animal model to better simulate infection in humans. Protection was seen after immunization with all rVSV candidates. The rVSV-M2-1 and rVSV-N showed reduced viral titer of 0.5-0.75 log, rVSV-F and rVSV-G showed reduced titer of about 2 log (in the lung), and rVSV-G-F-M-N and rVSV-G-2A-F showed reduced titer over 2 log. All VSV recombinants induced T-cell and antibody responses, with the protection level correlating with the degree of the neutralizing antibody response. In conclusion, the combination vaccines yielded similar protective capacity to the individual F and G vaccines, while the nucleocapsid-associated proteins did not provided an added advantage.
Keywords for abstract:	Human respiratory syncytial virus Vesicular stomatitis virus recombinant vaccine Immunology Cotton rats

IMID - 7

Title of abstract:	**THE USE OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS TO RESTORE IMMUNE FUNCTION OF GERIATRIC COTTON RATS DURING RESPIRATORY SYNCYTIAL VIRUS INFECTION.**
Authors	O. Harder and S. Niewiesk. Department of Veterinary Biosciences
Abstract	Human respiratory syncytial virus (RSV) is the leading cause of respiratory disease in infants and young children worldwide. RSV is also the second most common cause of pneumonia in the elderly. We investigated in cotton rats (*Sigmodon hispidus*) how age affected viral clearance and immune responses and whether pharmacological intervention was possible. Our results demonstrated that virus grew to similar titers in the geriatric cotton rats as in adult rats, but had prolonged clearance rates in geriatric rats. After immunization with RSV, the geriatric cotton rats were not fully protected and had minimal neutralizing antibody titers. Geriatric rats had significantly fewer RSV specific B cells when compared to adult rats and B cells did not respond to co-immunization with toll-like receptor agonists. Antibody-mediated depletion of cytotoxic lymphocytes (CTL) delayed RSV clearance, indicating the role of CTL which, however, do not function as well as in an adult rat. Published literature suggests that the inflammatory state of the lungs, which increases with age, can contribute to the increased susceptibility of the elderly to various diseases. Pharmacological suppression of inflammation through nonsteroidal anti-inflammatory ibuprofen resulted in faster viral clearance and complete protection after immunization. Depletion of CTL during infection, in the presence of ibuprofen, indicated the restoration of CTL functionality. These results suggest that anti-inflammatory therapy acts on cytotoxic lymphocytes to restore their function. It appears that in geriatric animals, the immune system works similarly as in adults animals, but not as effectively and that anti-inflammatory therapy may restore immune function.
Keywords for abstract:	Respiratory Syncytial Virus Virology Immunology Cotton Rat

IMID - 8

Title of abstract:	**SHIFTING IN SEROTYPES OF NEISSERIA MENINGITIS FOLLOWING THE INTRODUCTION OF MENAFRIVAC IN ETHIOPIA**
Authors	Rajiha Abubeker1, Biruk Yeshitela2, Surafel Fentaw1, Hannah Joan Jørgensen3, Bente Børud3, Dominique Caugant3, Melaku Ydinekachew2, Negga Asamene1, Elias Seyum1, Amete Mihret1, Degefu Beyene1, Adugan Woyessa1 1Ethiopian Public Health Institute (EPHI), Addis Ababa, Ethiopia; 2Armauer Hansen Research Institute (AHRI), Addis Ababa, Ethiopia; 3Norwegian Institute of Public health (NIPH), Oslo, Norway.
Abstract	**Back ground**: Neisseria *meningitis* represents one of the major causes of morbidity and mortality in Ethiopia. Between 2013 and 2015, a vaccine called MenAfriVac(or with only serotype A) was introduced to protect persons with age 1-29 years old. Subsequently, a passive surveillance network among various institutions including the Ethiopian Public Health Institute (EPHI), Armauer Hansen Research Institute (AHRI) and Norwegian Institute of Public Health (NIPH) was established comprising seven hospitals. The intervention using a vaccine is expected to reduce the predominant serotype A and emergence of others. This study is aimed at investigating the distribution of various serotypes of *Neisseria meningitis* in seven hospitals for the year 2015. **Methods:** This study used data from the surveillance performed in seven hospitals that used cerebrospinal fluids (CSF) analysis by applying WHO recommended procedures and case definition Gram stain, culture and Real Time PCR were processed to identify the serotypes. **Results:** Real time PCR identified a total of 8.5% (26) strains of *N. meningitis* were detected among 307 CSF samples. Of those, 13 *N. meningitis* serotype C, three *N. meningitis* sero type A and three *N. meningitis* W 135 were detected. Various serotypes were identified in various surveillance sites. Previously, both serotypes W135 and B were not common in Ethiopia. **Conclusion:** This study revealed that *N. Meningitis serotype* has shown a shifting in trends of the common serotype A and wider appearance of other serotypes such as W135 and B. It is recommendable to expand the surveillance to wider geographical areas of the country and use longitudinal data in comparison with vaccine coverage.
Keywords for abstract:	Neisseria *meningitis* meningitis serotype

IMID - 9

Title of abstract:	**SOX9 DELETION IN THE INTESTINAL EPITHELIUM INCREASES HOUSE DUST MITE INDUCED ALLERGIC ASTHMA SYMPTOMS IN MICE**
Authors	M.R. Joldrichsen, E. Kim, Z. Attia, I.C. Davis, E. Cormet-Boyaka, and P.N. Boyaka. Department of Veterinary Biosciences
Abstract	Paneth cells regulate many key aspects of gastrointestinal health through the antimicrobial products and cytokines they produce. Loss or defective Paneth cell functions leads to dysbiosis and is one of the causes of Inflammatory Bowel Disease (IBD). Mice with Sox9 gene deletion within the intestinal epithelium ($Sox9^{\Delta IEC}$ mice) lack Paneth cells making these mice a great model for the study or IBD and other consequences of dysbiosis. Our separate studies have shown that dysbiosis of the gut microbiota could enhance allergic sensitization in the gut and subsequent allergic responses to nasal allergen challenge. We investigated whether dysbiosis caused by a Sox9 deletion in the intestinal epithelium of mice could affect allergic sensitization in the airway and development of asthma responses. For this purpose, control wild-type and $Sox9^{\Delta IEC}$ mice were sensitized to house dust mite (HDM) by daily intranasal administration over two weeks period. Upon nasal HDM challenge, $Sox9^{\Delta IEC}$ mice showed more severe signs of allergic asthma than wild-type C57 BL/6 mice as indicated by their higher hypothermia. We also established that the increased allergic symptoms in $Sox9^{\Delta IEC}$ mice correlated with higher IgE levels in serum and bronchoalveolar lavage fluid, and higher frequency of HDM-specific Th2 cells but no difference in Th1 or Th17 responses. These results further illustrate that the gut immune homeostasis plays an important role in allergic responses at distant mucosal sites.
Keywords for abstract:	Intestinal Epithelium Gut Dysbiosis Allergic Asthma

IMID - 10

Title of abstract:	**EVALUTATION OF EFFECT OF CD3E-IT TREATMENT ON MULTIPLE ORGANS AND OF THE FUNCTION AND SURVIVAL OF TRANSPLANTED T CELLS AFTER CD3E-IT TREATMENT.**
Authors	S. Kim, L. Smith, R. Shukla, A. Kim, A. Tracey, N. Liyanage and S. Kim. Depts. Of Veterinary Biosciences and Microbial Infection and Immunity
Abstract	T-cell gene therapy has proven to be an advanced and potentially critical application for treating cancers and other previously incurable diseases, such as HIV/AIDS. Preconditioning with chemotherapy regimens, such as Cyclophosphamide (CTX) and fludarabine, has often been used to enhance the repopulation and function of transferred T cells. The risk of applying such toxic chemotherapy prematurely, however, has unfortunately been demonstrated in recent CD19 CAR T-cell therapy clinical trials. CD3e-immunotoxin (CD3e-IT), an anti-CD3e monoclonal antibody conjugated with diphtheria toxin, is a potentially useful preconditioning regimen for T-cell therapy. CD3e-IT, currently under clinical trial for cutaneous lymphoma, has been shown to specifically ablate T-cells in vivo and promote T-cell recovery through peripheral T-cell expansion; but it has not been tested as a preconditioning regimen for adoptive T-cell therapy. In order to evaluate the safety and efficacy of CD3e-IT in mice, we have developed a murine version CD3e-IT. Unlike CTX treatment – which non-specifically deplete total lymphocytes – 4-day CD3e-IT treatment in mice resulted in specific ablation of T cells in all organs tested, including peripheral blood, spleen, bone marrow, thymus, lymph nodes, Peyer's Patches, liver, and lung. Interestingly, we found the surviving CD4+ T-cells were enriched with CXCR5+ (PD-1^{high}) follicular T helper cells in all organs tested. Lymphocytes were fully recovered by 12 weeks post-CD3e-IT-treatment. Transplantation of spleen and lymph node cells at 5 day post-CD3e-IT showed a transient but sharp increase in T cells for the first 2 weeks, especially in effector CD4+ and CD8+ lymphocytes, followed by gradual decrease of transferred T-cells - a typical pattern seen in adoptive T-cell transplant. The transferred T-cells remained detectable until the endpoint (12 weeks). Our data thus support the use of CD3e-IT as a lymphodepletion regimen that can potentially enhance the survival and function of transferred T cells safely and effectively in adoptive immunotherapy settings.
Keywords for abstract:	T-cell gene therapy Adoptive immunotherapy Lymphodepleting preconditioning CD3e-immunotoxin Cyclophosphamide Fludarabine Follicular T cells

IMID – 11

Title of abstract:	**PERSISTENT DYSBIOSIS AND ENHANCED SUSCEPTIBILITY TO DSS-INDUCED COLITIS OCCUR LONG AFTER CHRONIC INGESTION OF CADMIUM**
Authors	E. Kim, E. Cormet-Boyaka, S. O. Opiyo, and P. N. Boyaka
Abstract	Most studies have addressed the toxicity of high doses of heavy metals. However, most people will more likely be exposed to subtoxic doses of heavy metal pollutants and their effects on the gut immune homeostasis is poorly understood. Furthermore, it is unknown whether the effects of chronic exposure to sub-toxic doses of heavy metal pollutants persist after the end of exposure. We report that in mice, chronic ingestion of subtoxic doses of cadmium (Cd), a heavy metal found in contaminated food and water, does not impair the barrier function of the intestine. However, chronic exposure to subtoxic doses of Cd stimulates the growth of intestinal epithelial cells, including Paneth cells, and production of anti-microbial peptides and proteins by Paneth cells. We also found that subtoxic doses of Cd induce a dysbiosis of the gut microbiota that persist along after the end of the exposure. Interestingly, 12-14 months after exposure to Cd, the Cd-treated mice weighted more and had more fat content than age-matched controls. Furthermore, post-menopausal mice previously exposed to Cd showed more severe signs of DSS (Dextran sodium sulfate)-induced colitis including weight loss and shortening of large intestine. Analysis of T cell responses associated with the increased colitis in Cd-treated mice showed enhanced Th17 responses (i.e., expression of RORγt and secretion of IL-17) in aged Cd-exposed mice. Our results provide new insights into the alteration of gut immune homeostasis by chronic exposure to environmentally relevant subtoxic doses of cadmium, which may have important implication for the pathogenesis of colitis or colon cancer.
Keywords for abstract:	Cadmium Dysbiosis Colitis Th17

IMID - 12

Title of abstract:	**ANTIBODY MEDIATED PROTECTION AGAINST RSV AFTER IMMUNIZATION WITH A VSV-G AND F RECOMBINANT**
Authors	C.Lewis, K.Brakel, O.Harder, and S.Niewiesk. Dept. Of Veterinary Bioscience
Abstract	Respiratory Syncytial Virus (RSV) is an enveloped ssRNA virus that causes severe upper respiratory tract disease in young, immunocompromised, and geriatric patients. While this disease has a high mortality rate in these demographics, there is no licensed RSV vaccine available. Previous studies have shown that the fusion (F) glycoprotein is a potential vaccine target as it is necessary for infectivity. This study aims to explore whether or not a combination of two glycoproteins would confer protection, and whether or not this protection was B cell or T cell mediated. The fusion glycoprotein and the attachment glycoprotein (G) were utilized because they are both envelope proteins, and are the target for neutralizing antibodies and T cells. A recombinant vesicular stomatitis virus was generated which expressed both the F and the G protein, and tested in cotton rats which display increased susceptibility to RSV compared to mice. Cotton rats were inoculated with the recombinant VSV twice, and then challenged with RSV. Immunization with the VSV recombinant lead to the induction of antibody and a reduction in viral titer of l.5 log. Even groups in which CD4+ T cells or CD8+ T cells, or both CD4+ and CD8+ T cells were depleted by antibody treatment were protected against infection with RSV. These findings indicated that the RSV-specific antibodies were the main correlate of protection against challenge with RSV. In summary, our study found that VSV-G and F recombinants are protective and able to induce an antibody response.
Keywords for abstract:	Respiratory Syncytial Virus Immunization

IMID - 13

Title of abstract:	**ZIKA VIRUS NONSTRUCTURAL PROTEIN 1 (NS1) ALONE INDUCES PROTECTIVE IMMUNITY AGAINST ZIKA VIRUS INFECTION IN THE ABSENCE OF NEUTRALIZING ANTIBODY**
Authors	Anzhong Li[1], Miaoge Xue[1], Zayed Attia[1], Mijia Lu[1], Jingyou Yu[1,3] Xueya Liang[1], Thomas Z Gao[1], Shan-Lu Liu[1,2,3,4], Mark E Peeples[5,6], Prosper N Boyaka[1,2], Jianrong Li[1,2]* [1]Department of Veterinary Biosciences, [2] Infectious Diseases Institute, [3]Center for Retrovirus Research, and [4]Department of Microbial Infection and Immunity, The Ohio State University, 1925 Coffey Road, Columbus, OH, 43210, USA; [5]Center for Vaccines and Immunity, The Research Institute at Nationwide Children's Hospital, 700 Children's Drive, Columbus, OH, 43205, USA; [6]Department of Pediatrics, College of Medicine, The Ohio State University, 370 W. 9th Ave., Columbus, OH, 43210, USA. *Corresponding author
Abstract	The nonstructural protein 1 (NS1) of several flaviviruses including West Nile virus, Dengue virus, and yellow fever virus is capable of inducing sufficient protection against flavivirus infection in animal models. However, the protection efficacy of Zika virus (ZIKV) NS1 protein remains poorly understood. Here, we showed that ZIKV NS1-based vaccine candidates only provided partial protection against ZIKV-induced viremia in immunocompetent mice and lethal ZIKV challenge in immunodeficient mice. By optimizing the signal peptide, we showed that ZIKV NS1 was highly expressed by methyltransferase-defective recombinant VSV (mtdVSV) and DNA vaccine platforms. A single dose of mtdVSV-NS1-based vaccine or two doses of DNA vaccine provided partial protection against ZIKV-induced viremia in BALB/c mice despite the fact that they triggered a high level of NS1-specfic antibody and T cell immune response. Using the highly susceptible A129 mouse model, we found that NS1-based vaccine candidates were not sufficient to provide protection against lethal ZIKV challenge. Collectively, we found that, unlike NS1 of other flaviviruses, ZIKV NS1 alone only conferred partial protection against ZIKV infection. However, incorporation of NS1 with prM-E may have synergetic effects against ZIKV infection.
Keywords for abstract:	Zika virus NS1 MTase-defective rVSV

IMID - 14

Title of abstract:	**IMMUNE RESPONSE TO RESPIRATORY SYNCYTIAL VIRUS ATTACHMENT PROTEIN**
Authors	Martinez, ME; Niewiesk, S. Department of Veterinary Biosciences
Abstract	Human respiratory syncytial virus (RSV) is a leading cause of lower respiratory tract infection in infants and young children worldwide, with no current vaccine. The receptor-binding attachment (G) protein has two forms, a membrane bound (mG) and secreted form (sG), with a distinct CX3C motif. Similarly fractalkine, an endogenous chemokine, has a similar structure with a CX3C motif and two forms: membrane bound and secreted. Previous studies suggest that the G protein increases pulmonary inflammation through cytokine mimicry via the interaction of the G protein with CX3CR on immune cells. However, these studies ablated the G protein from RSV or used a monocloncal antibody, which does not account for the essential receptor-binding function of the G protein for *in vivo* replication. Our lab used the established RSV small animal model of the cotton rat, as well as a vector system, adenovirus associated virus (AAV), to express the G protein (both forms), sG or mG. Also, the sG was produced via protein expression and purification. Our goal was to determine the role of the various forms of the G protein on the immune system independent of its receptor binding function. We found no significant difference in pulmonary inflammation as determined by histology and bronchoalveolar lavage after inoculation of AAV-G or with the secreted G protein. No neutralizing antibodies were produced from inoculation with AAV-G, AAV-mg, or AAV-sG. There was partial protection from challenge with RSV when cotton rats were inoculated with AAV-G, which was mostly attributed to a CD8 T cell response. Complete protection was accomplished with the combination therapy of AAV-INFa and AAV-G. This was not due to neutralizing antibodies or CD8 T cells. Therefore, the G protein was not found to be inflammatory, and in fact induced partial protection which was enhanced with the addition of type I interferon.
Keywords for abstract:	respiratory syncytial virus Adenovirus associated virus vector attachment protein inflammation interferon alpha

IMID - 15

Title of abstract:	**HTLV-1 CTCF-BINDING SITE IS DISPENSABLE FOR *IN VITRO* IMMORTALIZATION AND EARLY VIRUS REPLICATION *IN VIVO***
Authors	M. Martinez[1,2], J. Al-Saleem[1,2], A. Panfil[1,2], W. Dirksen[1,2], X. Cheng[4], L. Ratner[4], and P. Green[1,2,3] *[1]Center for Retrovirus Research, [2]Department of Veterinary Biosciences, and [3]Comprehensive Cancer Center, The Ohio State University, Columbus, OH, USA; [4]Division of Oncology, Washington University, St Louis, MO, USA*
Abstract	Human T-cell leukemia virus type 1 (HTLV-1) is the retroviral etiologic agent of adult T-cell leukemia/lymphoma and the neurological disorder HTLV-1-associated myelopathy/tropical spastic paraparesis. The exact mechanisms through which latency and disease progression are regulated are not fully understood. CCCTC-binding factor (CTCF) is an 11-zinc finger, sequence-specific, DNA-binding protein that plays a major role in organization of mammalian higher-order chromatin structure, gene expression, chromatin insulation, and genomic imprinting through homodimer formation. A CTCF-binding site was identified within the HTLV-1 genome (vCTCF). Therefore, HTLV-1 integration randomly inserts a vCTCF into the host genome. CTCF-mediated interactions between proviral and host CTCF-binding sites have been shown to alter host chromatin structure and flanking host gene expression. This study examines the effects of the vCTCF on HTLV-1-induced *in vitro* immortalization and *in vivo* persistence. First, an HTLV-1ΔCTCF proviral mutant was generated via mutation of the vCTCF to abolish CTCF binding. Then an LTR-based reporter gene assay and an ELISA for HTLV-1 Gag were used to compare *in vitro* LTR-transactivation and virion production. *In vitro* HTLV-1-induced PBMC immortalization capacity was then evaluated via co-cultivation assay. Lastly, New Zealand White rabbits were inoculated with irradiated viral producer cell clones followed by serial blood collection over a twelve-week period. Collected samples were used to assess HTLV-1-specific antibody response, proviral load, gene expression, and total lymphocyte count. HTLV-1 and HTLV-1ΔCTCF *in vitro* immortalization capacity was comparable. HTLV-1-specific antibody response was significantly decreased in HTLV-1ΔCTCF-inoculated rabbits. Proviral load, gene expression, and total lymphocyte count were not significantly different. The mechanism through which abrogation of CTCF binding alters antibody response in the absence of significant proviral load changes remains unclear. Future studies will explore the mechanism through which CTCF binding alters the HTLV-1-specific host antibody response during early infection and the effects of vCTCF binding on HTLV-1-induced tumorigenesis.
Keywords for abstract:	HTLV-1 CTCF ATL

IMID - 16

Title of abstract:	**INHIBITION OF *EHRLICHIA CHAFFEENSIS* INFECTION BY INTRACELLULAR NANOBODY TARGETING HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN-K**
Authors	M. Mestres-Villanueva, M. Lin, and Y. Rikihisa
Abstract	Human Monocytic Ehrlichiosis (HME) is an emerging zoonotic disease, first discovered in 1986. The Center for Disease Control and Prevention reports a steady increase in the number of cases with more than 1,427 confirmed cases reported in the U.S. in 2018. HME is a severe influenza-like illness. The causative agent is the tick-borne and obligatory intracellular bacteria *Ehrlichia chaffeensis* (*Ech*). Currently, the only recommended treatment is the broad-spectrum antibiotic doxycycline, and early treatment is required to avoid severe disease or death. There are no vaccines against *Ech* infection. Previous research carried out in the Rikihisa lab has led to the discovery of several human and unique *Ech* proteins that may function as targets to inhibit infection. Camelids produce single-domain antibodies (nanobodies), which lack a light chain. The VHH is the antigen-binding component of these single-domain antibodies. Nanobodies are stable and small (~15 kDa), allowing for their use in an intracellular environment and for binding with antigens that a conventional antibody could not access. The application of intracellular nanobodies (iAbs) are an innovative tool we can use to carry out functional interference against *Ech* infection. My hypothesis is that iAbs can neutralize *Ech* infection and neutralizing iAbs can be isolated, cloned, and be intracellularly delivered conjugated to cell-penetrable peptides (CPPs). Published works from Rikihisa laboratory indicate the mammalian expression plasmid encoding iAb that binds human heterogeneous nuclear ribonucleoprotein-K (hnRNP-K) (Inoue et al., 2007) effectively inhibits ehrlichial entry into the host cell, thus blocks infection. To test my hypothesis, my first project is to clone recombinant anti-hnRNP-K iAb and conjugate it with CPP to determine its effectiveness in blocking *Ech* infection in cell culture and in our mouse model of infection.
Keywords for abstract:	Ehrlichia Obligatory intracellular bacteria Nanobody Cell-penetrable peptide

IMID - 17

Title of abstract:	***EXAMINING ROUTES OF PRION ENTRY INTO THE GUT OF WHITE-TAILED DEER, Odocoileus virginianus***
Authors	David Minich, Christopher Madden, Eunsoo Kim, Prosper Boyaka, Patricia M. Dennis, Vanessa L. Hale The Ohio State University College of Veterinary Medicine, Columbus, OH (Minich) Veterinary Biosciences, The Ohio State University College of Veterinary Medicine, Columbus, OH (Kim, Boyaka) Veterinary Preventative Medicine, The Ohio State University College of Veterinary Medicine, Columbus, OH (Madden, Dennis, Hale)
Abstract	Chronic wasting disease (CWD) is a fatal, contagious, neurodegenerative prion disease of cervids and is documented in 25 states in the United States. Transmission of CWD is poorly understood but has been linked to exposure to infectious material, including bodily fluids, feces, contaminated water, soil, or food. Studies in cervids demonstrate oral exposure to infectious material can result in CWD infection. Prions are thought to enter the gastrointestinal tract, undergo transcytosis via microfold cells (M-cells), and subsequently move from the blood to the brain. M-cells are gut epithelial cells specialized for the transport of molecules from the gut lumen to the host immune system. M-cells can be found in the follicle associated epithelium overlying Peyer's patches in the small intestine and in the villi throughout the GI tract. Research has shown links between oral prion disease susceptibility and M-cell abundance. In this study, our goal was to optimize a stain that allowed us to identify M-cells in white-tailed deer, *Odocoileus virginianus*. We obtained small intestinal and rectal samples from 30 CWD-negative deer harvested from urban and suburban Cleveland Metroparks in 2018. We then tested M-cell targeting lectin [i.e., Ulex europaeus agglutinin (UEA-1)] or antibodies –for visualization by immunofluorescence. Optimizing this technique will allow us to compare M-cell abundance in deer with and without CWD or from different environments – with the ultimate goal of understanding how M-cells or other cells in the gut epithelium influence CWD susceptibility. As M-cell abundance is influenced by the gut microbiota, ongoing work also includes characterizing the gut microbiota of urban, suburban, and CWD-positive deer.
Keywords for abstract:	Chronic wasting disease White-tailed deer M cells Prions Gut microbiome *Odocoileus virginianus*

IMID - 18

Title of abstract:	**ASSESSMENT OF *Haemonchus contortus* BURDEN IN A CAPTIVE PRONGHORN (*Antilocapra americana)* POPULATION AT A ZOO**
Authors	Daniela Monje, MPH, CPH,[1*] Antoinette E. Marsh, MS, PhD[1], Randall Junge, MS, DVM, Dipl ACZM, Dipl ACAW,[2] Nicholas A. Lordi,[1] and Mark Flint, BVSc, BSc(hons), MApplSc, MPhil, PhD[1] *[1] The Ohio State University College of Veterinary Medicine (OSU CVM),[2] Columbus Zoo and Aquarium*
Abstract	*Haemonchus contortus* is the most economically significant parasite in small ruminants worldwide due to the severity of parasitism and the emergence of anthelmintic resistance.[1-4] The highly pathogenic, blood-feeding nature of this parasite is an important catalyst in the morbidity and mortality of many exotic ruminant species. Pronghorn can be especially susceptible to heavy parasitism. In certain captive populations, gastrointestinal nematode burden will cause mortality or be a key player in the mortality of pronghorn, and thus prevention and treatment becomes critically important for their management.[5-6] Most prevention practices derive from the husbandry of sheep and often times these practices are not feasible nor validated for captive non-domestic ruminants. Current gastrointestinal nematode recommendations for exotic ruminants under human care suggest performing monthly fecal egg counts (FEC) and using anthelmintic treatments, but offers no recommendation on the appropriate FEC threshold to initiate anthelmintic treatment. Our study's pronghorn population, housed in a mixed-species exhibit at the Columbus Zoo and Aquarium, historical FEC data demonstrated that monthly testing lead to potential delays in treatment. This was due to sharp, acute fluctuations of FEC parasite loads occurring within the monthly testing times. Thus, this study's objectives aimed to evaluate daily FEC to further describe trends in gastrointestinal nematode worm burden in each pronghorn (n=3) during the summer months, and to use lectin-based staining and DNA analysis to identify *H. contortus* in this population. The study also evaluated the FEC of bison (n=2) housed within the same enclosure as the pronghorn to determine if *Haemonchus* species were potentially shared between hoof stock within this exhibit. The results of this study showed that each individual pronghorn's and Bison's eggs per gram of feces (EPG) varied significantly regardless of sharing the same environment (FEC's range: Pronghorn 1 [229-9150], Pronghorn 2 [1060-5400], Pronghorn 3 [nod-243], Bison 1 [nod], Bison 2 [nod-10]). These unique findings showed that monthly FEC testing of these pronghorn is not enough to predict a large *Haemonch*us worm burden or potential Heamonchosis-morbidity. **LITERATURE CITED** 1. Charlier J, van der Voort M, Kenyon F, Skuce P, Vercruysse J. Review: Chasing helminths and their economic impact on farmed ruminants. Trends in Parasitology. 2014;30:361-367. 2. Lane J, Jubb T, Shephard R, Webb-Ware J, Fordyce G. Report: Priority List of Endemic Diseases for the Red Meat Industries. Meat and Livestock Australia. https://www.mla.com.au/download/finalreports?itemId=2877. Published March 20, 2015. Accessed November 17, 2018. 3. Qamar MF, Maqbool A, Ahmad N. Economic losses due to haemonchosis in sheep and goats. 2011; Scie. Int (Lahore) 23: 321-324. 4. Taylor MA, Learmount J, Lunn E, Morgan C, Craig BH. Multiple resistance to anthelmintics in sheep nematodes and comparison of methods used for their detection. Small Ruminant Research. 2009;86:67-70. 5. Young KE, Craig TM, Jensen JM. Evaluation of anthelmintic activity in captive wild ruminants by fecal egg reduction tests and a larval development assay. Journal of Zoo and Wildlife Medicine.2000;3:348-352. 6. Martinez M, Seeley K, Zimmerman D, Bapodra P, Cianciolo R. Systemic amyloidosis in a captive population of pronghorn antelope (*Antilocapra americana*). Poster presented at 2017 Annual Meeting of the American College of Veterinary Pathologists and the American Society of Veterinary Clinical Pathology; November 4-7, 2017; Vancouver, BC, Canada
Keywords for abstract:	*Antilocapra americana*, fecal egg count, *Haemonchus contortus*, nematode, Pronghorn

IMID - 19

Title of abstract:	**COMPLEX I INHIBITION DECREASES OXYGEN CONSUMPTION IN MURINE MODEL OF ACUTELY LETHAL INFLUENZA INFECTION**
Authors	Katherine E. Nolan, Lauren, M. Doolittle, Lucia E. Rosas, Lisa M. Joseph, Ian C. Davis
Abstract	Alveolar type II epithelial cells synthesize and recycle lipid-rich surfactant and are the primary site of influenza A virus (IAV) infection and replication. ATII cell infection impairs synthesis of cytidine 5'-diphosphocholine (CDP-CHO), which is a primary lipid precursor and surfactant component. This phospholipid synthesis impairment causes mitochondrial dysfunction and contributes to an energy crisis that results in decreased alveolar fluid clearance and progression to acute respiratory distress syndrome (ARDS). Supplementation of CDP-CHO to influenza-infected mice increases arterial oxygenation, reduces inflammation and increases ATII surfactant content, however the mechanism by which this occurs is unclear. It is hypothesized that the beneficial effects of liponucleotide treatment are due to the improved ATII cell oxidative phosphorylation in influenza-infected mice. C57BL/6 mice were inoculated with 50 ul of saline or mouse-adapted influenza (A/WSN/33, H1N1) on day 0. Rotenone (0.8 mg/kg), a complex I inhibitor, was administered intraperitoneally (IP) on days 1, 3 and 5 and the liponucletotide treatment (CDP-CHO, 100 ug) was administered IP daily from days 1 to 5. At day 5 post-infection, mice were placed in the Comprehensive Laboratory Animal Monitoring System (Columbus Instruments) for whole body metabolism analysis. At day 6, physiologic data was collected and ATII cells were isolated for Seahorse XF Cell Mito Stress Test Profile (Agilent). Arterial oxygen saturation was decreased in rotenone-treated mice receiving liponucleotide treatment compared to liponucleotide-treated mice that did not receive rotenone. Whole body metabolism data revealed decreased oxygen consumption in combined rotenone and CDP-CHO treated mice compared to CDP-CHO-treated mice. These data suggest that in the presence of complex I inhibition, the beneficial effects of liponucleotide treatment is lost in influenza-infected mice. Although further investigation is required, these data help support the hypothesis that impaired oxidative phosphorylation may play a contributory role in pathogenesis of influenza virus infection and IAV-induced ARDS.
Keywords for abstract:	Influenza A virus Acute respiratory distress syndrome Alveolar type II epithelial cells Oxidative phosphorylation Mitochondrial dysfunction

IMID - 20

Title of abstract:	**BREED ASSOCIATION OF NATURAL KILLER (NK) CELL NUMBER AND FUNCTION IN DOGS**
Authors	C. Peck, M. Naeimi Kararoudi, E. Elmas, J.A. Foltz, W.C. Kisseberth, and D.A. Lee
Abstract	Unlike T-cells, natural killer (NK) cells do not require antigen specificity or priming to kill tumor targets and are not implicated in graft-vs-host disease or cytokine release syndrome. However, evaluating novel NK cell-based therapies is difficult due to an inability to expand mouse NK cells for doing so. In contrast, canine NK cells can be expanded and canines spontaneously develop several cancers homologous to humans. However, it is difficult to predict which canine breeds will have higher NK cell numbers and be better donors for testing NK cell therapies in canine cancer patients. The purpose of this study is to determine canine inter-donor variability in number of NK cells in four dog breeds (Greyhound, Labrador Retriever, Golden Retriever, and Staffordshire Terrier) and produce enough adoptively transferred NK cells to conduct a clinical trial in dogs with cancer. It has been shown that NK cell numbers vary substantially between donors. Flow cytometry will be used to determine number of NK cells (identified by NKp46 antibody) after red blood cell lysis of heparinized blood from 10 dogs each of the four specified breeds from The Ohio State University Veterinary Medical Center Canine Blood Bank donors and healthy individuals; NK cell expansion will be conducted using a feeder-cell system developed by the Lee Laboratory at Nationwide Children's Hospital for human NK cells. We expect inter-donor variability in number of NK cells (approximately 2-3% of lymphocytes) to be partially breed-associated. We also expect absolute NK cell numbers to be lower in Greyhounds since they are known to have lower lymphocyte counts. These results will facilitate the selection of ideal canine NK cell donors for cancer immunotherapy.
Keywords for abstract:	Natural killer cells NK cell therapy Canine cancer Cancer immunotherapy Adoptive cell therapy

IMID - 21

Title of abstract:	**THE dNTPASE ACTIVITY OF SAMHD1 IS REQUIRED FOR ITS SUPPRESSION OF INNATE IMMUNE RESPONSES IN DIFFERENTIATED MONOCYTIC CELLS**
Authors	Z. Qin[1], S. Bonifati[1], C. St. Gelais[1], T. Li[1], S. Kim[1], B. Mahboubi[2], B. Kim[2], L. Wu[1] [1]The Ohio State University, Depts. Of Veterinary Biosciences Center for Retrovirus Research, Center for RNA Biology, Columbus, OH; [2]Emory University School of Medicine, Center for Drug Discovery, Department of Pediatrics, Atlanta, GA
Abstract	Sterile alpha motif and HD domain-containing protein 1 (SAMHD1) is a deoxynucleoside triphosphohydrolase (dNTPase) with a nuclear localization signal (NLS). We reported that SAMHD1 suppresses innate immune responses to viral infection and inflammatory stimuli by inhibiting the NF-κB and type I interferon (IFN-I) pathways. However, whether the dNTPase activity and nuclear localization of SAMHD1 are required for its suppression of innate immunity remains unknown. To address this question, we compared monocytic U937 cell lines stably expressing wild-type (WT) SAMHD1 or mutants defective for dNTPase activity (HD/RN) or nuclear localization (mNLS). Expression of WT SAMHD1 in differentiated U937 cells significantly inhibited mRNA levels of *TNF-*α and *IL-6* induced by lipopolysaccharide (LPS) treatment, as well as *IFN-*α, *IFN-*β and *TNF-*α mRNA levels induced by Sendai virus (SeV) infection. In contrast, expression of the HD/RN mutant did not show the inhibition. Consistent results were also observed in SAMHD1-knockout THP-1 cells after re-expressing the HD/RN mutant, suggesting that the dNTPase activity of SAMHD1 is required for suppressing NF-*k*B activation and IFN-I induction by inflammatory stimuli or viral infection. However, expression of the mNLS mutant or WT SAMHD1 similarly reduced *TNF-*α or *IFN-*β mRNA levels in LPS-treated or SeV-infected U937 cells, suggesting that cytoplasmic SAMHD1 inhibits innate immune responses to inflammatory stimuli and viral infection. Our data demonstrated that the dNTPase activity, but not nuclear localization of SAMHD1, is required for its suppression of innate immune responses in differentiated monocytic cells. This study further defines the role and mechanism of SAMHD1 in suppressing innate immunity.
Keywords for abstract:	SAMHD1 dNTPase activity Innate immune responses Monocytic cells

IMID - 22

Title of abstract:	**USER-FRIENDLY *SALMONELLA* NANOVACCINE FOR POULTRY DELIVERABLE BY FEED AND DRINKING WATER**
Authors	S. Renu, Y. Han, Y. S. Lakshmanappa, S. Dhakal, N. Feliciano-Ruiz, S. Ghimire, R. Selvaraj and G.J. Renukaradhya. Food Animal Health Research Program and Department of Veterinary Preventive Medicine
Abstract	*Salmonella* contamination in poultry meat and eggs causes severe economic impact and human health problems. Oral delivery of inactivated/subunit *Salmonella* vaccine targeting the intestinal lymphoid tissues is ideal, as it induces robust mucosal immunity and overcomes injection stress. Soluble antigens delivered oral gets degraded in stomach, thus identifying a suitable vaccine carrier is essential. A mucoadhesive chitosan nanoparticles (CS-NPs) based subunit *Salmonella* vaccine (nanovaccine) containing outer membrane proteins and flagellar (F) protein loaded and F-protein surface coated was formulated for oral delivery in poultry. *Salmonella* nanovaccine was formulated using the ionic gelation method, and characterized by analytical techniques, biocompatibility and pH stability by hemolysis and turbidity assays. We found F-protein surface coated CS-NPs (CS-NPs-F) targeted to chicken intestinal Peyer's patch sites by *in vivo* and *ex vivo* analyses by microscopy. Vaccinated layer chickens with nanovaccine by mixing in drinking water or feed challenged with live *Salmonella* were examined for induction of immune response and efficacy. *Salmonella* nanovaccine particles were spherical with average particle size 398 nm, and monodispersed with a high surface positive charge. Spectroscopic analyses showed CS-NPs compatible with chicken RBCs and stable in acidic pH condition. Fluorescent microscopy and F-protein specific immunostaining analysis confirmed the oral delivered CS-NPs-F specifically targeted to intestinal Peyer's patches and up taken by chicken immune cells. *Salmonella* nanovaccine treated chicken immune cells upregulated the mRNA expression of TLR, Th1 and Th2 immune markers. In *Salmonella* nanovaccine immunized layer chickens, administered through drinking water and feed induced secretory IgA antibody response. Notably, drinking water and feed mixed nanovaccine induced significant and non-significant reduction in challenge bacterial load in the ceca of chickens, respectively. Needle-free oral immunization of nanovaccine enhanced the local immune response associated with reduced bacterial load, thus likely be a potential alternate to injectable *Salmonella* vaccine for poultry.
Keywords for abstract:	*Salmonella* Subunit antigen Chitosan nanoparticles Oral delivery Layer birds Mucosal immunity

IMID - 23

Title of abstract:	**AN INTRANASAL VACCINATION STRATEGY TO IMPROVE PROTECTION AGAINST RESPIRATORY PATHOGENS**
Authors	J. C. Rowe, Z. Attia, E. Kim, E. Cormet-Boyaka, P. N. Boyaka
Abstract	Intranasal vaccination is an alternative route of vaccine administration that is needle-free and which, in addition to inducing systemic immunity in the bloodstream, has the potential of promoting immunity at the mucosal surfaces of the airways. However, most licensed vaccines against respiratory pathogens are injected vaccines that often require multiple doses in order to achieve protective immunity. However, in times of a crisis, it may be necessary to have readily available and easy administer vaccine that can provide expedited protection. Previous studies in our lab have shown that recruitment of neutrophils in sublingual tissues and cervical lymph nodes of mice immunized by the sublingual route blunts the subsequent immune responses and prevents the development of mucosal IgA responses. We also found that supplementation of a sublingual vaccine with a neutrophil elastase inhibitor helps the development of mucosal IgA, but also regulates the kinetic of antibody responses. In this study, we tested whether pharmacological inhibitors of neutrophil elastase can regulate the immune responses to an intranasal vaccine. Our preliminary results show that a single intranasal vaccination of C57BL/6J mice in the presence of a neutrophil elastase inhibitor results in high titers of antigen specific systemic IgG1. The complete profile of B and T cell responses induced by intranasal immunization of wild-type C57BL/6J mice in the presence of a neutrophil elastase inhibitor is being characterized. This work is expected to demonstrate that the efficacy of current experimental intranasal vaccines can be regulated to quickly provide protection against infection with a respiratory pathogen such as anthrax.
Keywords for abstract:	Mucosal vaccination Intranasal IgA Neutrophil

IMID - 24

Title of abstract:	**TOLC AND OTHER *EHRLICHIA HF* VIRULENCE FACTORS IN VIVO**
Authors	Anthony Smith, Hannah Bekebrede, Yasuko Rikihisa
Abstract	*Ehrlichia* spp. are obligate intracellular bacteria that infect monocytes, macrophages, and epithelial cells. *Ehrlichia chaffeensis* is the causative agent of human monocytic ehrlichiosis (HME) but does not induce disease in immunocompetent mice, which generally precludes this species from being used in investigating pathogenesis factors. *Ehrlichia HF* was previously determined to contain 16S rRNA sequences that are 98.2% similar to *E. chaffeensis*, and unlike *E.chaffeensis* will induce a fatal dose-dependent disease in mice. C57BL/6J mice (5-8 weeks old, male and female, 5 mice per strain) were intraperitoneally inoculated with 0.5 ml of select mutant *Ehrlichia HF* strains from a random mutagenesis library (due to Himar1 transposon insertion) and compared to wild type HF. Mice were euthanized by CO_2 and cardiac puncture and spleens were aseptically excised, weighed, and then stored at -80°C. Sections of spleens were frozen in RNAlater for cDNA synthesis and qPCR analysis of bacterial load. Other spleen sections were used for DNA purification and PCR for confirmation of transposon insert**.** Two individual mutants and one mutant mixture were tested including a TolC type I secretion system outer membrane protein, a hypothetical protein, a type IV secretion system needle protein, and a ComEC family protein. The type I and hypothetical protein mixture showed significant reductions in spleen bacterial load when compared to wild type HF. TolC and hypothetical proteins may function as pathogenesis factors in *Ehrlichia HF* and may be implicated in HME. These proteins could potentially be targets for vaccine development or other treatment options.
Keywords for abstract:	Ehrlichia C57BL/6J PCR qPCR Virulence

IMID - 25

Title of abstract:	**EFFECTS OF CTX-IMMUNOTOXIN TREATMENT ON TISSUE LYMPHOCYTES**
Authors	Amahdi Tracey, Shihyoung Kim, Lauren Smith, Rajni Shukla, Namal Liyanage, Sanggu Kim
Abstract	Gene therapy is a new treatment model that may provide lifelong protection against human immunodeficiency virus type 1 (HIV-1) infection. Genetically modifying hematopoietic stem cells (HSC) and/or T-cells using lentiviral vectors expressing anti-HIV genes produces cells resistant to HIV-1 infection. Recent clinical successes with Chimeric Antigen Receptor (CAR) T-cell therapy has generated hope for incurable diseases as such. Lymphodepletion preconditioning is a proven technique to increase the survival and function of the transferred CAR-T cells in patients, but the potential toxicity of the procedure justifies a careful risk-vs-benefit analysis. Also, the inefficiency of removing HIV-1 infected T cells and replacing them with “genetically protected” ones remains a barrier. In this study, as an effort to optimize lymphodepletion preconditioning procedures for the treatment of HIV/AIDS, we evaluated and compared two lymphodepleting agents, cyclophosamide (CTX) and anti-CD3-epsilon-immunotoxin (CD3e-IT), for their effect on various organs using the mouse as our model. CTX is a chemotherapy agent commonly used in clinic and CD3e-IT is a new and potentially safe and efficacious agent currently under evaluation. In this study, mice were treated with different doses of CTX or CD3e-IT and evaluated for the effects of the treatment on various T-cell and B-cell lineages, NKs, monocytes, and granulocytes in different body organs. We particularly focused on evaluating the depletion of follicular helper T-cells (Tfh), a known major HIV-1 reservoir. CD3e-IT and CTX showed distinct killing efficiencies; CD3e-IT were highly specific in killing T cells, whereas CTX significantly reduced total lymphocytes, primarily killing B cells. Both CTX and CD3e-IT led to varying levels of lymphodepletion among the different body organs examined. Interestingly, both treatments were limited in killing Tfh. This study provides detailed and important insights into the effects of two different lymphodepleting agents on various tissue lymphocytes, useful in the development future anti-HIV gene therapy.
Keywords for abstract:	Gene therapy for HIV/AIDS

IMID - 26

Title of abstract:	**VIRAL N^6-METHYLADENOSINE UPREGULATES REPLICATION AND PATHOGENESIS OF HUMAN RESPIRATORY SYNCYTIAL VIRUS**
Authors	Miaoge Xue, Boxuan Zhao, Zijie Zhang, Mijia Lu, Olivia Harder, Phylip Chen, Zhike Lu, Anzhong Li, Yuanmei Ma, Xueya Liang, Stefan Niewiesk, Mark E. Peeples, Chuan He, Jianrong Li
Abstract	N^6-methyladenosine (m6A) is the most prevalent internal modification of mRNAs in most eukaryotes. RNAs produced in these cells during virus replication may also acquire m6A methylation. Here we show that RNAs of human respiratory syncytial virus (RSV), a medically important non-segmented negative-sense (NNS) RNA virus, are modified by m6A within discreet regions and that these modifications enhance viral replication and pathogenesis. Overexpression of m6A binding proteins significantly enhanced RSV replication and gene expression. Knockdown of m6A methyltransferases decreased viral replication and gene expression whereas knockdown of m6A demethylases had the opposite effect. The G gene transcript contained the most m6A modifications. Recombinant RSV variants expressing G transcripts that lack particular clusters of m6A displayed reduced replication in A549 cells, primary well differentiated human airway epithelial (HAE) cultures, and the upper and lower respiratory tracts of cotton rats. These RSV variants also displayed reduced pathogenesis in the lungs of cotton rats. One of the m6A-deficient variant, rgRSV-G12, was highly attenuated yet retained high immunogenicity in cotton rats. Collectively, our results demonstrate viral m6A methylation upregulates RSV replication and pathogenesis and identify viral m6A methylation as a target for rational design of live attenuated vaccine candidates for RSV and perhaps other NNS RNA viruses.
Keywords for abstract:	N^6-methyladenosine Respiratory syncytial virus (RSV) Vaccine

IMID - 27

Title of abstract:	**GENOTYPE-1 HEPATITIS E VIRUS ORF4 PROTEIN ENHANCES GENOTYPE-3 HEV REPLICATION**
Authors	K. Yadav, P. Boley and S. Kenney.
Abstract	Hepatitis E Virus (HEV) is one of the major concern causing acute viral hepatitis worldwide. HEV genotypes (g), g-1 and g-2 are strictly limited to human infections and g-3 and g-4 are zoonotic, infecting animals (pigs, rabbits and deer) and humans. Typically, HEV causes less than 1% mortality in otherwise healthy individuals but the mortality rate for pregnant women can increase by up to 30%. Different factors been proposed for HEV mortality during pregnancy but none have been shown to be the definitive mechanism to enhanced mortality. This is further complicated by the lack of animal model system and difficulty to culture the virus. Increased pregnancy mortality is generally observed in geographical regions in which genotype 1 HEV is the predominant circulating strain, suggesting it may possess unique attributes contributing to pregnancy mortality. Recently, a novel fourth open reading frame (ORF4) was discovered overlapping ORF1 in g-1 HEV. The expression of this ORF4 protein is regulated via an IRES-like RNA element that is upregulated via endoplasmic reticulum stress. As such, ORF4 has been suggested to play a role in enhanced pregnancy mortality. In this study, we utilized lentivirus transduction of Huh7 cells to create cell lines expressing genotype 1 ORF4 protein. Utilizing these cell lines, we asked whether genotype 1 HEV ORF4 protein provided in trans is capable of enhancing the replication of g-3 HEV. We demonstrate that despite not encoding ORF4 within its genome, g-3 HEV replication is enhanced in the presence of ORF4. This study has important implications towards the development of the g-1 / g-3 chimeric virus. In addition, the chimeric virus if formed would lead to develop pig model system for HEV that would ease our way to understand virus growth kinetics and virus-host interactions highlighting high virulence reasons in pregnant woman.
Keywords for abstract:	hepatitis E ORF4 (Open Reading Frame 4) pregnancy genotypes IRES (Internal Ribosome Entry Site)

MOLECULAR
AND
CELLULAR BIOLOGY

MCB - 1

Title of abstract:	**HTLV-1 TAX-1 INTERACTS WITH SNX27 TO REGULATE CELLULAR LOCALIZATION OF THE HTLV-1 RECEPTOR MOLECULE, GLUT1**
Authors	J. Al-Saleem[1,2], W. Dirksen[1,2], M. Martinez[1,2], N. Shkriabai[4], M. Kvaratskhelia[4], L. Ratner[5], and P. Green[1,2,3]
Abstract	HTLV-1 and HTLV-2 are highly related viruses, with differential pathogenic outcomes in humans. While HTLV-1 is associated with several diseases, such as adult T cell leukemia, HTLV-2 is not associated with disease. The trans-activator of HTLV-1, Tax-1, has higher transforming potential then its HTLV-2 homolog, Tax-2. It is believed that this difference in transforming capacity plays a pivotal role in HTLV-1 pathogenesis. We propose that Tax-1 interacts with cellular gene products via domains lacking in Tax-2, and that these interactions contribute to pathogenesis. We performed proteomic screens of Tax-1 binding partners utilizing Tax-1 mutants to identify these interactions. Novel interactions were confirmed and mapped by co-immunoprecipitation studies and further characterized by biochemical and biologic assays. We identified a novel interacting partner of Tax-1, Sorting Nexin 27 (SNX27). SNX27 regulates the localization and expression of transmembrane proteins via interactions with its PDZ domain. SNX27 has been demonstrated to regulate glucose transporter 1 (GLUT1), and SNX27 knock down in HeLa cells results in a dramatic redistribution of GLUT1 from the cell surface to the lysosome. GLUT1 serves as one of three receptor molecules for HTLV-1. We proposed that Tax-1 alters GLUT1 localization post-infection via its interaction with SNX27. We confirmed that Tax-1 and SNX27 interact via their PDZ domain binding motif and PDZ domains, respectively. We then show GLUT1 localization is altered by Tax-1 overexpression, a result similar to when SNX27 is knocked down with siRNA. We demonstrate that Tax-1 expression causes an increase of GLUT1 co-localization with LAMP1, indicating transfer to the lysosome. Lastly, we demonstrate that SNX27 knockdown causes an increase in HTLV-1 virion release, but surprisingly resulted in a decrease in HTLV-1 infectivity. This work demonstrates a novel mechanism by which HTLV-1 regulates a surface receptor molecule post-infection and this interaction could serve as a therapeutic target to inhibit viral spread.
Keywords for abstract:	HTLV, SNX27, GLUT1

MCB - 2

Title of abstract:	**INSULIN INCREASES THE IN-VITRO OSTEOGENIC CAPACITY OF FLEXOR TENDON PROGENITOR CELLS**
Authors	N. Altmann, L. Dunbar*, H. Coughlin, A. Rollins, S. Durgam*. *Dept. of Veterinary Clinical Sciences
Abstract	Calcific tendinopathy from aberrant differentiation of endogenous tendon progenitor cells (TPCs) has been reported in naturally-occurring and experimental tendinopathy. There is minimal knowledge about pathogenesis and molecular mechanisms of tendinitis/tendinopathy, a common musculoskeletal disease in diabetic patients. Exogenous insulin is used in diabetes treatment and systemic hyperinsulinemia can occur during early diabetes mellitus. This in-vitro study investigates the effect of exogenous insulin on osteogenic capacity of TPCs. Tendon progenitor cells were isolated from flexor tendons of 3 normal horses. Third passage TPCs were cultured as monolayers in osteogenic medium with and without insulin (0,10, 100 μU/mL) for up to 14 days. Similar cultures were also maintained with 100 nM picropodophyllin (PPP), a selective IGF-I receptor antagonist. Osteogenic differentiation was assessed with osteogenic mRNA expression, Alizarin Red Staining, and alkaline phosphatase activity analyses. Data was analyzed with one way-ANOVA (significance set at $p \leq 0.05$). Insulin supplementation markedly enhances the in-vitro osteogenic capacity of flexor TPCs. At day 14, in osteogenic cultures treated with 100 μU/mL insulin, Runx2 (7-fold), alkaline phosphatase (4.5-fold) and osteonectin (5.2-fold) mRNAs were significantly elevated compared to untreated osteogenic controls. Alkaline phosphatase activity in osteogenic cultures treated with 10 (8-fold) and 100 (25-fold) μU/mL insulin was significantly increased compared to untreated controls. These findings were corroborated by Alizarin red staining (*Figure 1*). At day 14, osteogenic cultures treated with 100 μU/mL insulin and PPP mitigated the enhanced osteogenic capacity (mRNA, alkaline phosphatase activity) of TPCs seen with insulin supplementation. These results demonstrate that insulin markedly increased the in-vitro osteogenic capacity of TPCs. Additionally, our data suggests this enhanced osteogenic capacity of TPCs with exogenous insulin is mediated by IGF-I signaling. Given the significance of calcific tendinopathy and prevalence of diabetes in people, further investigation on molecular mechanisms mediating aberrant phenotypes of TPCs is warranted.
Keywords for abstract:	Calcific tendonitis/tendinopathy Tendon-progenitor cells Insulin IGF-1 signaling

MCB - 3

Title of abstract:	**CHARACTERIZING THE BIOLOGICAL AND MOLECULAR CONSEQUENCE OF PTEN LOSS IN CANINE OSTEOSARCOMA**
Authors	Natalie Boisvert, Joelle M. Fenger
Abstract	Osteosarcoma (OS) is the most common bone malignancy in dogs and adolescent children. Early micrometastatic disease commonly occurs in both species and despite aggressive therapy, approximately 30% of children and 90% of dogs will succumb to this disease. The marked chromosomal heterogenicity of OS has hindered progress to identify molecular drivers for targeted therapies. However, a growing number of studies have identified alterations in the PTEN/PI3K/Akt signaling pathway in canine and human OS suggesting this pathway may play a critical role in mediating OS biology. Tumor suppressor phosphatase and tensin homolog deleted from chromosome 10 (PTEN) functions as a phosphatase and through its activity antagonizes the PI3K/Akt pathway. Loss of PTEN and subsequent activation of the PI3K/Akt signaling pathway is a common event in OS. The objective of this study was to characterize the biological consequence of PTEN loss in normal and malignant canine osteoblasts (Ob). PTEN transcript and protein expression was evaluated in 8 canine OS cell lines and normal canine Ob via Western blotting and Real time PCR. PTEN expression was significantly reduced or absent in 50% of canine OS cell lines compared to normal Ob. Concordantly, loss of PTEN correlated with an increase in Akt phosphorylation and activation. To define the role of PTEN in canine OS cell behavior, we are currently generating canine OS cell lines expressing lentiviral PTEN constructs or shRNAs for PTEN to evaluate the effect of PTEN loss on OS cell biology. Data generated from this study will aid in characterizing the role of PTEN in canine OS cell behavior with the ultimate goal of developing therapeutic strategies against the PI3K/AKT signaling pathway.
Keywords for abstract:	Osteosarcoma Canine PTEN Akt signaling

MCB - 4

Title of abstract:	**CHARACTERIZING THE ROLE OF WWOX DYSREGULATION IN CANINE OSTEOSARCOMA**
Authors	J Breitbach, B Makii, J Walz, N Desai, F Xu, J Fenger Departments of Veterinary Biosciences and Veterinary Clinical Sciences
Abstract	Osteosarcoma (OS) is the most common primary bone tumor in humans and canines. Tumor location, chemotherapy resistant metastases, and overlapping transcription profiles are similar in both species supporting the notion that canine osteosarcoma serves as a relative model to the human disease. Additionally, genomic instability is a well-recognized feature of OS and suggests that early oncogenic events in this cancer may result from alterations in DNA repair and sensing mechanisms, leading to an accumulation of mutations and tumorigenic qualities. The WW domain-containing oxidoreductase (WWOX) is a tumor suppressor gene that is commonly attenuated or deleted in a variety of human cancers. Specifically, Wwox expression is reduced in 60% of human OS tumors. Wwox is implicated in the DNA damage response as an important binding partner of ATM in response to double stranded DNA breaks. We *hypothesize that WWOX depletion impairs DNA damage repair and cell cycle checkpoint activation, thereby contributing to genomic instability in osteosarcoma.* Preliminarily, we have found that Wwox is frequently down-regulated in canine osteosarcoma cell lines and primary and metastatic tumors. In addition, attenuation of WWOX with shRNA constructs in canine OS cell lines confers resistance to ionizing radiation. These data provide support for our hypothesis that loss of WWOX contributes to genomic instability as a result of ineffective DNA damage repair. This study serves as a foundation by which potential novel targets for therapeutic intervention can be identified, with the ultimate goal of improving outcomes in dogs and children.
Keywords for abstract:	Osteosarcoma WWOX DNA damage repair Canine

MCB - 5

Title of abstract:	**ACUTELY LETHAL INFLUENZA INFECTION TRUNCATES THE CITRIC ACID CYCLE IN MURINE ALVEOLAR TYPE II EPITHELIAL CELLS**
Authors	L. Doolittle, L. Rosas, P. Woods, L. Joseph, and I. Davis
Abstract	Mitochondria-rich alveolar type II (ATII) cells are the primary site of influenza A virus (IAV) replication within the distal lung. Acutely lethal IAV infection of mice alters ATII cell mitochondrial (mito) structure and reduces mito energy production. The citric acid cycle (CAC) occurs in the mito matrix and generates electron carriers critical to oxidative phosphorylation. We therefore hypothesized that changes in the CAC may contribute to reduced mito energy production by ATII cells after infection. C57BL/6 mice were inoculated intranasally with 10,000 p.f.u. influenza A/WSN/33 (H1N1), which induces acute respiratory distress syndrome (ARDS) in mice by 6 days post-inoculation (dpi). Controls were mock-infected with virus diluent. ATII cells were isolated at 6 dpi. UHPLC/MS was used to measure levels of metabolites following methanol extraction. Live cell metabolism was measured using the Biolog platform. Gene and protein expression were quantified by qRT-PCR and Western blotting respectively. Relative to mock-infected controls, ATII cells contained normal levels of succinate but significantly reduced levels of fumarate and malate at 6 dpi. The ability of live ATII cells from IAV-infected mice to metabolize succinate was also reduced. Succinate dehydrogenase (SDH) oxidizes succinate to fumarate using FAD as an electron carrier, and the IAV-induced block in succinate metabolism was associated with decreased ATII cell FAD content and reduced SDH subunit gene and protein expression at 6 dpi. We concluded that following IAV infection, the CAC is truncated in ATII cells, as a result of reduced SDH activity. Truncation of this essential biochemical pathway will reduce the amount of the electron carriers available for mito oxidative phosphorylation and energy production. Changes in mito energy production in ATII cells may negatively impact cell processes which help maintain normal lung function, potentially contributing to the development of ARDS following IAV infection.
Keywords for abstract:	Influenza Pulmonary Mitochondria Metabolism Citric acid cycle

MCB - 6

Title of abstract:	**MAMMARY TUMOR AND MASTECTOMY SYNERGISTICALLY PROMOTE NEUROINFLAMMATION IN A BREAST CANCER SURVIVOR MODEL**
Authors	K.M. Emmer, W.H. Walker II, N. Zhang, A.C. DeVries. Depts. of Veterinary Preventive Medicine and Neuroscience
Abstract	Understanding why breast cancer survivors are at an increased risk for cognitive and affective disorders is essential for developing targeted treatment plans and improving quality of life. Microglia priming results in chronic neuroinflammation and can contribute to neuronal degeneration and dysfunction, thereby offering a potential mechanism for altered brain function that persists after tumor removal. This study examined whether mammary tumors alter microglia and augment the inflammatory profile and behavior of mice. To test this, non-metastatic mammary tumor cells (67NR) were injected orthotopically into the mammary glands of BALB/c mice, allowed to grow for 16 days, and then the tumors were removed via mastectomy. Following a 14-day surgical recovery, the mice were challenged with lipopolysaccharide (LPS), and then central and peripheral inflammation, anxiety, and depressive-like behavior were evaluated. Here we show that major central and peripheral inflammatory markers were not altered by tumor growth nor mastectomy surgery alone. However, hippocampal mRNA expression of major proinflammatory cytokines IL-1β and TNFα was increased in tumor removal animals, persisting past surgical recovery. Nonetheless, the immune and behavioral responses following LPS administration were comparable among groups. In sum, these data demonstrate that the combination of tumor and mastectomy promotes neuroinflammation; however, immune challenge did not elucidate this inflammation as maladaptive for the host.
Keywords for abstract:	Breast cancer Mastectomy Microglia Neuroinflammation Priming

MCB - 7

Title of abstract:	**GENETIC COMPARISON OF CARBAPENEMASE PRODUCING BACTERIA FROM FARM AND WATERWAY SAMPLES**
Authors	S.V. Grooters, D. Mollenkopf, T.E. Wittum. Dept. of Veterinary Preventive Medicine
Abstract	Antimicrobial resistance is a critical public health threat. In the U.S., regulations require that certain antibiotics be preserved only for use in human medicine. Carbapenems are a class of drugs with such restriction. As such, bacteria possessing resistance to carbapenems are not expected in a livestock environment, without selective pressure from these drugs. Under a One Health paradigm, environmental, livestock, and human health are all interconnected. Isolates of carbapenemase-producing bacteria were found in three different farm environments, a food producing facility, and local waterway. Phenotypic evidence from 14 isolates tested suggested resistance to meropenem, and imipenem, two carbapenem drugs. Initial genetic screening by PCR was conducted which confirmed in 10 of the isolates, the presence of blaIMP, the gene cassette known for translating a carbapenemase. To correctly identify the genes responsible for phenotypic antimicrobial resistance, and to accurately annotate chromosomes, mobile genetic elements, plasmids, transposons, and integrons, we utilized whole genome sequencing on the miSeq platform, and utilized a variety of bioinformatic tools. Short-read sequences were assembled and annotated, with eight isolates showing significant similarities in the type2 integron and gene cassette structure. Four isolates contained the blaIMP-64 gene cassette, two isolates a blaIMP-27 gene cassette contained within slightly different integron structure. Dairy, swine, and waterway samples were associated by genetic characteristics surrounding the blaIMP cassettes. The integron surrounding gene cassettes allows a platform for gene transcription. Further analysis of genetic characteristics surrounding the integron structure allow prediction of transposition events. Functional transposase genes allow vertical as well as horizontal gene transfer among bacteria. Transposons can relocate integrons from chromosome to plasmid, and plasmid to chromosome, through a replicative or a cut and paste mechanism. Our study highlights the use of genomic epidemiologic tools to analyze the public health threat and dissemination of antimicrobial resistance within a One Health framework.
Keywords for abstract:	Antimicrobial Resistance Integron Transposon Plasmid Bacterial Genomics

MCB - 8

Title of abstract:	**CHARACTERIZATION OF CIRCULATING EXOSOMAL MICRORNA EXPRESSION IN CANINE OSTEOSARCOMA**
Authors	E. Kuerbitz, A. Repasy, J. Fenger, and E. Warry
Abstract	Osteosarcoma (OS) is the most common primary bone tumor in children and dogs. Despite aggressive therapy, 90% of dogs and 30% of children die of chemotherapy-resistant metastatic disease. MicroRNAs (miRs) are noncoding RNAs that post-transcriptionally regulate gene expression and are frequently dysregulated in OS. Exosomes are 40-150nm vesicles that contain proteins and nucleic acids, including miRs. They are secreted by several cell types, including tumor cells, and are thought to mediate cell-to-cell communication through transfer of their cargo. The objective of this study is to characterize the expression of exosomal miRs in serum from dogs with OS and determine the prognostic significance of circulating miRs in canine OS. We hypothesize that dogs with OS will possess a unique serum exosome miR expression signature distinct from that found in healthy dogs. We further predict that circulating miRs detected in canine OS patients will be associated with disease outcome. Exosomes were isolated from the serum of dogs with OS (N=12) and age-matched healthy dogs (N=12) and exosome purity was validated using NanoSight imaging and Western blotting. RNA was isolated and global miRNA expression was performed using the NanoString platform. The expression of candidate miRs associated with OS was validated using real-time PCR. Studies are ongoing to identify circulating miRs associated with outcome in dogs with OS and determine their utility as noninvasive biomarkers to predict prognosis. This study will generate important new data characterizing circulating miR expression in canine OS. These data will lay the foundation for the identification of potential therapeutic targets and prognostic biomarkers in both human and canine OS.
Keywords for abstract:	Osteosarcoma Exosomes MicroRNA

MCB - 9

Title of abstract:	**INVESTIGATING THE ROLE OF WWOX IN DNA DAMAGE REPAIR AND RADIOSENSITIVITY OF CANINE OSTEOSARCOMA CELL LINES**
Authors	Rebecca Makii, Justin Breitbach, Joelle M. Fenger
Abstract	Osteosarcoma (OS) is the most common form of malignant bone cancer in both dogs and children. Despite aggressive treatment, up to 30-40% of children and >90% of dogs die due to multi-drug resistant metastatic disease. WW domain-containing oxidoreductase (WWOX) is a tumor suppressor gene that is frequently deleted in many human cancers, including OS. WWOX has been shown to play a major role in regulating DNA damage repair responses in human cell lines, in part through its interaction with ATM and ATR. Our laboratory has been studying canine OS, a well-established large animal model of the human disease and found that similar to human OS tumors, loss of WWOX is a frequent event in canine OS cell lines and OS tumors. We hypothesize that loss of WWOX in canine OS cell lines impairs DNA damage repair and cell cycle checkpoint activation, thereby contributing to the genomic instability of OS. The canine OSA8 and Abrams OS cell lines which express low basal levels of WWOX were transduced with empty vector or canine WWOX lentiviral constructs and flow-sorted to generate cells stably overexpressing WWOX. WWOX overexpression was validated using qRTPCR and Western blotting. OSA8 and Abrams cell lines expressing either empty vector or WWOX were treated with aphidicolin (0.5, 1 uM) or ionizing radiation (IR, 0, 5, 10 Gy) to induce DNA replication stress, and the effects of WWOX overexpression on cell survival and viability were assessed by CyQuant Cell Proliferation Assays and clonogenicity assays. We found that enforced WWOX expression in the canine Abrams OS cell line significantly decreased colony formation following IR. Interestingly, overexpression of WWOX did not affect the survival of OS cell lines following treatment with Aphidicolin, suggesting that WWOX does not play a significant role in mediating single-stranded DNA damage repair pathways in canine OS cell lines. Studies are underway to better characterize the role of WWOX in regulating cell cycle checkpoint activation and repairing radiation-induced DNA damage. This study will provide important new data regarding the role of WWOX in canine OS cell biology with the ultimate goal of identifying novel targets for therapeutic intervention in OS.
Keywords for abstract:	Osteosarcoma, radiation, WWOX, tumor suppressor gene, DNA damage

MCB - 10

Title of abstract:	**ASTHMA – NOT JUST AN AIRWAY DISEASE**
Authors	Andrew Nelson, Lauren Doolittle, Katherine Nolan, Lindsey Jiron, Lisa Joseph, Lucia Rosas, and Ian Davis. Department of Veterinary Biosciences.
Abstract	Asthma is a common chronic disease of the lungs that is characterized by airway inflammation and narrowing, together with abnormal bronchoconstriction in response to specific allergens. Current treatments focus on mitigating and/or preventing bronchoconstriction and inflammation of the conducting airways. However, chronic allergic asthma can result in airway remodeling, decreased lung compliance and an overall decrease in pulmonary function, which may be related to decreased production of pulmonary surfactant. Given that the Alveolar Type II (ATII) pneumocyte is responsible for the production of surfactant, we hypothesized that chronic asthma results in abnormal ATII cell function and metabolism. To test this, we used the well-established murine DRA (Dermatophagoides [dust mite]/ragweed/Aspergillus fumigatus) asthma model. 8-12 week old, female BALB/c mice were sensitized by i.p. injection of DRA + Alum on Days 0 and 5, then challenged with intranasal DRA on days 12, 13 and 14. Control mice received PBS at all timepoints. On Day 15 airway resistance was measured following administration of increasing doses of the muscarinic agonist methacholine. Airway resistance results indicate increased airway hyperresponsiveness in the DRA group. Bronchoalveolar lavage fluid was collected and analyzed for total and differential cell counts. The DRA group exhibited significant eosinophilia. Finally, lungs were removed and ATII cells were isolated. We measured changes in expression of genes associated with allergy, the electron transport chain, and glycolysis using Qiagen RT2 Profiler PCR Arrays, as well surfactant protein C (SFTPC). The DRA group had an increase in expression of certain immunomodulatory genes associated with allergy and epithelial repair and fibrosis with concurrent changes in the expression of genes associated with metabolism. Additionally, expression of SFTPC was decreased by 50%. These findings suggest that the allergic environment in the distal lung of asthmatics may attenuate the ATII cell's ability to produce surfactant.
Keywords for abstract:	asthma alveolar Type II pneumocyte allergy airway hyperresponsiveness metabolism

MCB - 11

Title of abstract:	**EFFECTS OF LEPTIN ON EQUINE LAMELLAR KERATINOCYTES: POTENTIAL ROLE IN ENDOCRINOPATHIC LAMINITIS**
Authors	Eline Nijveldt, Mauria Watts, James Belknap, Teresa Burns
Abstract	Equine metabolic syndrome (EMS)-associated laminitis (EMSAL) is currently the most common cause of equine laminitis, a devastating orthopedic condition of equids. Serum [leptin] is commonly increased in horses with EMS, as many are overweight; however, its role in EMSAL has not been well characterized to date. Leptin exerts mitogenic effects on keratinocytes and can regulate the pro-inflammatory response of human epidermal keratinocytes. In addition, the euglycemic hyperinsulinemic clamp (EHC) model can acutely increase circulating [leptin] in healthy adult humans. The aim of this study is to investigate the roles of leptin and leptin receptor (lepR) in EMSAL. Healthy Standardbred horses (n=16) were randomly assigned to receive either 1) an EHC for 48h (or until signs of lameness developed; EHC, n=8) or 2) a saline infusion for 48h (CON, n=8). Real-time PCR analysis of lamellar tissue revealed significant downregulation of leptin and lepR gene expression in response to the EHC (P= 0.0002 and 0.0158, respectively). Lamellar immunohistochemistry (IHC) showed diffuse expression of lepR within keratinocytes of the primary and secondary epidermal lamellae in both groups. These results suggest that lamellar keratinocytes appear capable of responding to circulating leptin, as well as that leptin does not appear to be locally produced within the lamellae. Measurement of serum leptin concentrations revealed that 5/8 of the EHC horses had acutely increased leptin levels at 6h in response to the model. Further clarification of the role of leptin in EMSAL is warranted given these results and the prevalence of hyperleptinemia in EMS patients.
Keywords for abstract:	Equine Metabolic Syndrome Laminitis Leptin EMSAL

MCB = 12

Title of abstract:	**PRTM5 INHIBITOR, EPZ015666, HAS ANTI-PROLIFERATIVE AND ANTI-TUMOR ACTIVITY *IN VITRO* AND *IN VIVO***
Authors	A.R. Panfil, D.D. Huey, N.B. Rushlow, M.P. Martinez, J. Al-Saleem, W.P. Dirksen, S. Niewiesk, and P.L. Green. Department of Veterinary Biosciences
Abstract	Human T-cell leukemia virus type 1 (HTLV-1) is the causative infectious agent of various diseases, including an aggressive $CD4^+$ T-cell malignancy called adult T-cell leukemia (ATL). ATL is chemotherapy-resistant with a median survival time of <1 year. The current lack of effective therapies for ATL patients indicates a need for innovative clinical approaches. Recently, PRMT5 over-expression has been identified to be relevant to the pathogenesis of both hematologic (lymphoma) and solid tumors (melanoma, astrocytomas). PRMT5 is a type II PRMT enzyme that silences the transcription of key regulatory genes by symmetric di-methylation of arginine residues on histone proteins. Previously, we found PRMT5 is upregulated in leukemia/lymphoma cell lines and negatively regulates HTLV-1 viral gene expression *in vitro*, indicating that PRMT5 could be an important cellular regulator of the viral transformation process. Additionally, inhibition of PRMT5 in HTLV-1-positive cell lines reduces cell survival; therefore, PRMT5 may represent an important therapeutic target for ATL. In this study, we tested if an orally available, commercial PRMT5 selective inhibitor, EPZ015666, has anti-proliferative and/or anti-tumor effects on HTLV-1-transformed cells *in vitro* and *in vivo*. EPZ015666 treatment of HTLV-1-transformed and ATL-derived T-cell lines decreased cellular proliferation and led to cell death, while HTLV-1-negative T-cell lines and primary human T-cells were less affected. NSG mice were inoculated with 10^7 HTLV-1-transformed cells. Eight days after transplant, the mice were orally administered 25 mg/kg or 50 mg/kg EPZ015666, twice daily for twenty-one days. Blood was collected weekly and tumor size and weight were measured biweekly. Treatment with 50 mg/kg EPZ015666 in the HTLV-1 NSG tumor transplant mice had anti-tumor and anti-proliferative effects due to the increased survival and decreased tumor growth rate. In summary, our work here suggests PRMT5 is a key cellular player involved in ATL development and represents a viable target to treat patients with ATL.
Keywords for abstract:	T-cell Lymphoma Leukemia HTLV-1 PRMT5

MCB - 13

Title of abstract:	**ISOLATION AND CHARCTERIZATION OF EQUINE DEEP DIGITAL FLEXOR TENDON-DERIVED PROGENITOR CELLS**
Authors	V. Quam, N. Altmann, H. Coughlin, M. Brokken, S. Durgam Department of Veterinary Clinical Sciences
Abstract	Deep digital flexor tendon (DDFT) injuries seen in navicular syndrome are a common cause of lameness in the horse. These injuries can be career-ending as healing is limited. The DDFT at this intrasynovial location is heterogenous and consists of an avascular, dorsal fibrocartilaginous region. The objective of this study is to isolate and characterize progenitor cells from the frequently injured DDFT. Forelimb DDFT (1-2cm^2) adjacent to the navicular bone was harvested from two young-adult QH cadavers and digested in 0.2% collagenase. The resulting cell suspension was plated at low-density (2000 cells/cm^2) for colony formation and expanded in monolayers for two passages. Fluorescent activated cell sorting (FACS) was used to characterize the immunophenotype (CD29, CD44, CD90 and CD45) of cells at each passage. Trilineage differentiation assays (osteogenesis, chondrogenesis and adipogenesis) of third-passage cells were conducted. Cell cultures were stained with Alizarin Red and Oil-Red-O to assess osteogenic and adipogenic differentiation, respectively. Aggregate cultures were maintained in chondrogenic medium for 7 days. RNA was extracted to analyze lineage-specific gene expression by qPCR. Statistical analyses was carried out using one-way ANOVA, with significance set at $p \leq 0.05$. The population doubling time for second passage cells was 4.05 ± 0.21 days. Growth in osteogenic media resulted in Alizarin red positive nodules, however had minimal intensity (with reference to cardinal BM-MSCs) (Fig. 1). Osteogenic gene expression (Runx2, alkaline phosphatase mRNAs) and alkaline phosphatase activity increased 4-fold in end-point cultures, however was not significantly ($p=0.6$) from untreated controls. In contrast, chondrogenic markers, collagen II and aggrecan were significantly increased 10-fold ($p<0.01$) and 15-fold ($p<0.001$), respectively from untreated controls. Our preliminary findings suggest that the progenitor cells isolated from equine DDFT have a restricted osteogenic and marked chondrogenic potential. Characterization of resident progenitor cells is a necessary first-step to implement therapies that recruit endogenous progenitor cells.
Keywords for abstract:	Trilineage differentiation Progenitor cells Equine deep digital flexor tendon

MCB - 14

Title of abstract:	**S100A9 INHIBITOR TASQUINIMOD: A NOVEL STRATEGY TO INHIBOT SMALL CELL LUNG CANCER PROGRESSION AND METATASIS**
Authors	Salha Sassi [1, 3], Tasha wilki[1, 2] Ramesh K. Ganju *, [1,2] Department of Pathology and [2] The Comprehensive Cancer Center at, The Ohio State University (OSU), Wexner Medical Center 43210, USA. [3] Department of Pathology, Medical school, Benghazi University, Libya.
Abstract	Small cell lung cancer (SCLC) treatment is a major clinical challenge at present as it is highly refractory to available drugs. The MDSCs/macrophages are known to help SCLC develop resistant to available therapies. S100A9 (Migration inhibitory factor-related protein 14 (MRP14) is an EF-hand calcium-binding protein that has been involved in cell migration, invasion, proliferation, and tumor metastasis in various type of cancers, however not much is known about its role in SCLC. In this study, we found that S100A9 protein is highly up-regulated in various types of pulmonary neuroendocrine carcinomas (NEC) patient tissues compared to normal using tissue microarrays. We also observed that SCLC patients with higher S100A9 expression have significantly increased numbers of macrophage in the stroma. We have also shown that pre-treatment of the cells with S100A9 inhibitor (Tasquinimod) suppressed in-*vitro* cell migration, invasion, and colony formation. In addition, we analyzed the efficacy of S100A9 inhibitor against SCLC using *in vivo* mouse models. S100A9 inhibitor significantly reduces tumor growth and metastasis in SCLC in xenograft mouse models. We further observed that S100A9 inhibitor suppressed myeloid-derived suppressor cells (MDSC) populations and TAMs of the M2-polarized phenotype in SCLC. Moreover, we found myeloid cells sequestered from tumors of treated mice expressed were MI type as they showed higher levels of inducible nitric oxide synthase (iNos), and lower levels of arginase-1. Molecular analysis revealed that Tasquinimod decreases expression of IL6, IL10, and TGF-β1 in the cancer cells which helps inhibit macrophage activation to TAMs. Reduced proliferation and vascularization were observed in the tumors obtained from animals treated with S100A9 inhibitor. We also observed S100A9 inhibitor suppressed osteolytic bone formation in ex-vivo resorption assay. Overall, our studies, for the first time, show that Tasquinimod that targets S100A9 signaling could be used as a novel therapeutic strategy against SCLC.
Keywords for abstract:	S100A9, Small Cell Lung Cancer, Tasquinimod, Myeloid-derived Suppressor Cells, Macrophages, Metastasis.

MCB - 15

Title of abstract:	**EXPLORING PRMT5 AS A POTENTIAL THERAPEUTIC TARGET IN CANINE LYMPHOMAS**
Authors	K. Renaldo[1], S. Sloan[2], J. Chung[2], L. Courtney[1], K.Shilo[3], W. Kisseberth[1] and R. Baiocchi[1] [1]Department of Veterinary Clinical Sciences, The Ohio State University College of Veterinary Medicine, Columbus, OH; [2]Division of Hematology, Department of Internal Medicine, College of Medicine, The Ohio State University, Columbus, OH; [3]Department of Pathology, The Ohio State University, Columbus, OH
Abstract	Non-Hodgkin lymphoma (NHL) represents approximately 4 percent of all human cancer diagnoses in the United States, with diffuse large B-cell lymphoma (DLBCL) accounting for approximately 40 percent of all new cases. There are numerous histologic and genetic subtypes of DLBCL and the overall outcome of patients who receive standard therapy is heterogeneous. Lymphoma is also a common malignancy in dogs and while initially responsive to combination chemotherapy, remissions times are short and cures rare. Protein arginine methyltransferase 5 (PRMT5) is a type II protein arginine methyltransferase (PRMT) enzyme capable of driving the symmetric dimethylation of arginine residues on histone tails (H3R8 and H4R3) and other proteins such as P53. PRMT5, a master epigenetic regulator driving the activity of MYC, CYCLIND1 and NOTCH, is commonly overexpressed and dysregulated in both human solid and hematologic tumors. Here we characterized patterns of PRMT5 expression and correlated these with histologic subtype in canine lymphoma tissue microarrays (TMAs, n=337). We characterized expression of PRMT5 and key biomarkers in three canine lymphoma-derived cell lines (CLBL-1, 17-71, and OSW) and primary lymph node biopsies. We have demonstrated that PRMT5 inhibition leads to growth suppression and induction of apoptosis in CLBL-1, 17-71, OSW, and primary patient lymphoma cells in a time and/or dose-dependent manner, while selectively decreasing symmetric dimethylarginine (SDMA) marks on H4R3. We preformed gene expression microarrays showing whole transcriptome changes in canine lymphoma cell lines treated with PRMT5 inhibitors. We are currently exploring genome-wide recruitment of PRMT5 on chromatin and examining genome-wide changes in chromatin accessibility with PRMT5 inhibition. These findings provide justification for incorporating the spontaneously occurring canine lymphoma model into the preclinical development of PRMT5 inhibitors.
Keywords for abstract: per line	PRMT5 Canine Lymphoma DLBCL

MCB - 16

Title of abstract:	**ROLE OF HTLV-1 HBZ IN TRANSFORMATION AND DISEASE**
Authors	R. Stahl, A.R. Panfil, P.L. Green. Depts. Of Veterinary Bioscience and molecular virology, immunology, and medical genetics, Center for Retrovirus Research, Comprehensive Cancer Center and Solove Research Institute
Abstract	Human T-cell leukemia virus type 1 (HTLV-1) is a retrovirus that infects 10-20 million people worldwide. While most infections are asymptomatic, around 5% of patients will develop an aggressive T-cell malignancy called ATL or a neurodegenerative disease termed HAM/TSP over the course of their lifetime. The HTLV-1 protein HBZ is consistently expressed in HTLV-1 infected cells and provides cellular proliferative and tumor maintenance signals. Human T-cell leukemia virus type 2 (HTLV-2) is a closely related retrovirus to HTLV-1. While both viruses encode proteins with similar structure and function, they differ in pathogenicity. HTLV-2 is not associated with disease like HTLV-1. The HTLV-2 equivalent to HBZ is called APH-2. ***We hypothesize differences in cellular binding partners of HBZ and APH-2 will translate to differences in viral pathogenicity between HTLV-1 and HTLV-2.*** Using affinity capture coupled with shotgun proteomics, we identified and compared cellular binding partners of HBZ and APH-2. Potential HBZ binding partners were confirmed using S-tag pulldowns and coIP experiments. Based on these results, 6 cellular proteins that interacted with HBZ and displayed a connection to HTLV-1 biology or disease progression were selected for further analysis. Ongoing experiments using shRNA and/or over-expression vectors to determine the importance of each candidate HBZ interacting protein in the viral life cycle are in process. Through exploration of HBZ binding partners and their effects within T-cells, we hope to further refine the role of HBZ in T-cell transformation and development of disease. Insight of these roles will allow us to explore HBZ cellular targets as potential targets for disease prevention and treatment.
Keywords for abstract:	HTLV-1 ATL HBZ APH-2

MCB – 17
Platform Presentation

Title of abstract:	**COMPARITIVE EFFECTS OF METHYLPREDNISOLONE AND TRIAMCINOLONE ON ENDOGENOUS DEEP DIGITAL FLEXOR TENDON AND NAVICULAR FIBROCARTILAGE CELLS**
Authors	S. Sullivan*, S. Cole+, M. Brokken*, S. Durgam* * Dept. of Veterinary Clinical Sciences, +Campus Microscopy Imaging Facility
Abstract	Navicular disease is a common cause of lameness in athletic horses where clinical signs are largely associated with pathologies in 'deep digital flexor tendon' (DDFT) and apposing 'navicular bone fibrocartilage' (NB). Although intrasynovial corticosteroids are widely used in navicular disease due to their anti-inflammatory properties, their effect on endogenous cells present in DDFT and NB is unknown. The objective of these experiments was to evaluate the effect of triamcinolone acetonide (TA) and methylprednisolone acetate (MPA) on metabolic activity and viability of DDFT and NB cells in an ex-vivo explant culture model. Explants from DDFT and NB were harvested sterilely from freshly euthanized adult horses (n=4). Explants were equilibrated in-vitro for 24-48 hours prior to culture with TA (0, 0.6 and 6mg/mL) and MPA (0, 0.5 and 5mg/mL). Metabolic activity of explants was measured using Alamar Blue assay at 6h and 24h of culture. Similarly, live-dead assay was conducted with Calcein-Sytox staining followed by fluorescent confocal microscopy. Quantitative image analysis for live-dead cells was conducted with Imaris Software. Data was analyzed with repeated measures two-way ANOVA (significance set at $p<0.05$). High dose (5mg/mL) MPA significantly reduced the metabolic activity of NB cells alone (38%, <0.003) at 6h, and DDFT (52%, <0.001) and NB cells (59%, <0.001) at 24h compared to untreated controls (Figure 1). In contrast, TA (both doses) did not significantly affect the metabolic activity of DDFT and NB cells at either timepoints. These findings were corroborated by live-dead confocal images (Figure 2). This in-vitro data demonstrates that MPA is more toxic to DDFT and NB cells than TA. Our current experiments are focused on assessing corticosteroids' effects on transcriptional activities of these cells. Accepting that these are in-vitro experiments, they serve as a guideline for future in-vivo work to determine the optimal intrasynovial corticosteroid for horses with navicular disease.
Keywords for abstract:	Navicular disease - Horse chondro-/teno-toxicity corticosteroids

MCB – 18
Platform Presentation

Title of abstract:	**TARGETING THE EGFR-ERK AXIS TO STABILIZE CFTR IN CYSTIC FIBROSIS**
Authors	J. Wellmerling, S. Chang, and E. Cormet-Boyaka Department of Veterinary Biosciences, Ohio State University
Abstract	Cystic Fibrosis (CF) is a life-limiting autosomal recessive disorder associated with chronic lung infection and inflammation caused by mutation in the gene encoding the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR). CFTR is a chloride channel responsible for maintaining adequate airway hydration. The most common CFTR mutation, F508del, results in severely reduced CFTR activity through impaired protein trafficking, channel gating, and plasma membrane stability. CFTR modulators and potentiators, which address trafficking and gating, respectively, have been developed. However, membrane stability of F508del CFTR remains an issue. Our laboratory has previously demonstrated that activation of Extracellular-Regulated Kinase (ERK) leads to CFTR degradation. We report that ERK signaling is constitutively active in CF airway epithelial cells due to signaling by the Epidermal Growth Factor Receptor (EGFR). Compared to controls, CF cells produce and shed the EGFR ligand Transforming Growth Factor-Alpha in excess. Our data show that this axis plays a role in regulation of F508del-CFTR. Next, we assessed the feasibility of improving CFTR membrane stability with the osmoprotectant ectoine. Ectoine stabilizes macromolecules through the biophysical principle of preferential exclusion, and has previously been shown to attenuate EGFR signaling by preventing its loss from lipid rafts and subsequent intracellular translocation. We show that ectoine suppresses ERK signaling in primary human airway epithelial cells from F508del-homozygous CF donors. Using cycloheximide chase, we show that ectoine increases the membrane half-life of pharmacologically rescued CFTR in a human CF bronchial epithelial cell line by 122%. Finally, we show by trans-epithelial short-circuit current measurements that ectoine increases CFTR-mediated chloride transport beyond what is accomplished by modulator alone, suggesting it may be beneficial for CF patients on modulator therapy.
Keywords for abstract:	Cystic Fibrosis EGFR ERK

MCB - 19

Title of abstract:	**ROLE OF EHRLICHIA TRANSLOCATED FACTOR-3, A TYPE IV SECRETION EFFECTOR IN E. CHAFFEENSIS INFECTION**
Authors	Qi Yan, Mingqun Lin, Yasuko Rikihisa, Depeartment of Veterinary Biosciences, CVM, OSU
Abstract	Ehrlichia chaffeensis (E. chaffeensis) is an obligatory intracellular Gram-negative bacterium which infect human monocytes and macrophages, and causes Human monocytic ehrlichiosis (HME), a disease that can be fatal. E. chaffeensis has a type IV secretion system (T4SS). T4SS consists of a secretion apparatus and secreted effectors, which can interact with eukaryotic proteins to manipulate host cells to facilitate bacterial infection. The Rikihisa laboratory recently found three putative ehrlichial T4SS effectors by bacterial two-hybrid system, named E. chaffeensis translocated factor(Etf)-1, 2 and 3. Etf-1 and Etf-2 have been verified as T4SS effectors and facilitate E. chaffeensis proliferation by inducing autophagy (Etf-1), and blocking lysosomal fusion with Ech inclusions (Etf-2) and host cell apoptosis (Etf-1). However, host cell target and functions of Etf-3 remain unknown. My hypothesis is that Etf-3 is a true T4SS secretion effector of E. chaffeensis, and can faciliate E. chaffeensis infection by manipulating specific host cell functions. To test my hypothesis, I employed the Himar1 random mutagenesis system to insert a gene encoding FLAG-Etf-3 or FLAGEtf-3C into the E. chaffeensis chromosome. Results show that the E. chaffeensis Himar1 transposon mutants secrete both FLAG-Etf-3 and FLAG-Etf-3C into the host cell cytoplasm across the bacterial two membranes and the inclusion membrane. Secreted FLAG-Etf-3 and FLAG-Etf-3C proteins localized as numerous small puncta in the cytoplasm of host cells. Ectopically expressed Etf-3-GFP and RFP-LC3 in RF/6A cells revealed that Etf-3 is delivered to autophagosomes. Yeast two-hybrid screening of human leuckocyte cDNA prey library using Etf-3 as bait revealed several human proteins that bind Etf-3. Experiments to validate yeast two-hybrid analysis using human cells transfected with Etf-3, or infected with Ech are in progress to further analyzing the human cell target of Etf-3 and Etf-3 functions.
Keywords for abstract:	*Ehrlichia chaffeensis* T4SS effector Etf-3 Himar1 random mutagenesis system Yeast Two-Hybrid

STRUCTURE/FUNCTION

SF – 1

Title of abstract:	**COMPLICATIONS AND OUTCOME FOLLOWING SURGERY FOR TREATMENT OF GASTRIC CARCINOMA IN 40 DOGS (2004-2018): A VETERINARY SOCIETY OF SURGICAL ONCOLOGY RETROSPECTIVE STUDY.**
Authors	B. Abrams, V. Wavreille, B. Husbands, B. Matz, F. Massari, J. Liptak, M. Cray, C. Souza, B. Wustefeld-Janssens, M. Oblak, L. Su, L. E. Selmic
Abstract	Canine gastric carcinoma is a rare clinical entity, and information regarding clinical outcome following treatment with surgical excision is currently limited to case reports and small case series. The aim of this study was to report the complications and outcome in a larger cohort of dogs (n=40) receiving surgery for treatment of gastric carcinoma. Case accrual was solicited from Veterinary Society of Surgical Oncology members. Information gathered from retrospective medical record review included clinical presentation, results of tumor staging, tumor characteristics, surgical findings, histologic results, adjuvant therapy and oncologic outcome. The median progression free interval (PFI), median survival time (MST) and cause of death were recorded. Prognostic factors associated with outcome were evaluated using Cox proportional hazards regression analysis. The median PFI and MST were 54 and 178 days (range, 1-1902), respectively. Eight patients (20.0%) experienced major postoperative complications, including septic peritonitis secondary to dehiscence in 4 dogs (10.0%). Based on multivariable analysis, administration of adjuvant chemotherapy conferred a survival benefit and experiencing an intraoperative complication was associated with a poorer overall survival time. The findings from this study showed that dogs presenting with gastric carcinoma had a longer survival time following surgical resection than what has historically been reported, and that major postoperative complication rates were comparable to established literature. Although adjuvant chemotherapy was associated with an improved survival time in this study population, further investigation is warranted as no standardized chemotherapy protocols have been established.
Keywords for abstract:	Gastric Carcinoma Canine Oncology Stomach Cancer

SF – 2

Title of abstract:	**EFFECT OF ORAL TRAZODONE ON THE MINIMUM ALVEOLAR CONCENTRATION OF ISOFLURANE IN DOGS**
Authors	E.A. Hoffman, T.K. Aarnes, C.H. Ricco Pereira, P. Lerche, R.M. Bednarski & M.A. McLoughlin. Department of Veterinary Clinical Sciences
Abstract	Trazodone is used to facilitate handling and decrease signs of anxiety in hospitalized dogs. Premedication administered prior to inhalant anesthetic induction can facilitate patient handling and decrease the required dose of anesthetic agents. This study aimed to determine the effect of oral trazodone premedication on isoflurane minimum alveolar concentration (MAC). We hypothesized that trazodone premedication would decrease isoflurane MAC. Six dogs were anesthetized twice with a minimum of 7 days between anesthetic episodes. Dogs received no premedication or 8 mg/kg of trazodone orally two hours prior to anesthetic induction. Isoflurane MAC was determined using an iterative bracketing technique with electrodes placed in the buccal mucosa. Hemodynamic parameters were compared at the lowest end-tidal concentration at which each dog did not respond. Data were analyzed using statistical software with significance set to a value of $p < 0.05$. Data were normally distributed and reported as mean ± standard deviation. A paired *t* test was used to assess the effect of treatment on outcome variables. The mean isoflurane MAC in dogs receiving trazodone was 0.85% +/- 0.17% compared with 1.02% +/- 0.11% in the ISO treatment (p = 0.01, 95% confidence interval - 0.25 to -0.05) resulting in a mean isoflurane MAC reduction of 17% +/- 12%. There were no differences in hemodynamic parameters between treatments. Limitations include potential variability of oral trazodone absorption and plasma concentrations at the time of MAC determination. This study concluded that oral premedication with 8 mg/kg of trazodone decreases the MAC of isoflurane in dogs.
Keywords for abstract:	anesthesia, dog, isoflurane, minimum alveolar concentration, trazodone

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Title of abstract:	**EFFECT OF ORAL GABAPENTIN ON THE MINIMUM ALVEOLAR CONCENTRATION OF ISOFLURANE IN DOGS**
Authors	BA. Johnson, TK Aarnes, AW Wanstrath, CH Ricco Pereira, RM Bednarski, P Lerche, MA McLoughlin
Abstract	**Objective**: To determine the effect of 20 mg/kg oral gabapentin on the minimum alveolar concentration (MAC) of isoflurane in dogs. **Animals**: Six healthy adult dogs (three males, three females) with a mean ± SD body weight of 24.8 ± 1.3 kg. **Procedures**: Each dog was anesthetized twice with a minimum of 7 days between treatments. Each dog received both treatments. Dogs were randomly assigned to one of two treatments: one treatment, dogs received 20 mg/kg of gabapentin orally two hours prior to anesthesia induction (Gaba-Iso), the other treatment, dogs received isoflurane anesthesia alone (Iso). Isoflurane MAC was determined utilizing an iterative bracketing technique with stimulating electrodes placed in the maxillary buccal mucosa. Hemodynamic and vital parameters were recorded at the lowest end-tidal isoflurane concentration at which dogs had no gross purposeful movement. Effect of treatment group on outcome variables was analyzed using a paired t-test with significance set at $P < 0.05$. **Results**: Isoflurane MAC was significantly lower when dogs received oral gabapentin (0.71 ± 0.12%) compared with isoflurane alone (0.91 ± 0.26) ($P = 0.0229$). Mean isoflurane MAC reduction was 20 ± 14%. Hemodynamic parameters did not differ between treatments. Mean time to extubation was significantly shorter ($P = 0.0148$) in the Gaba-Iso group (6 ± 4 minutes) than the Iso Group (23 ± 15 minutes). **Conclusions and Clinical Relevance**: Gabapentin orally administered 2 hours prior to induction of isoflurane inhalant anesthesia had a MAC sparing effect with no effect on hemodynamic or vital parameters.
Keywords for abstract:	Anesthesia, analgesia, gabapentin, Isoflurane, MAC

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Title of abstract:	**ANTI-INFLAMMATORY CYTOKINE PROFILE OF SYNOVIUM CONSTRUCTS**
Authors	Michael Palillo, Nathalie A. Reisbig, Alicia L. Bertone
Abstract	Osteoarthritis (OA) is an irreversible degenerative joint disease affecting 30 million adults across the United States. Regenerative therapy approaches, such as injection of autologous mesenchymal stem cells (MSCs) into OA joints has shown transient efficacy. Surgical transplantation of a viable synovium extracellular matrix (sECM) seeded with synovium MSCs (sMSCs), termed synovium contructs (sConstructs) has been shown to stimulate chondrogenesis in vivo in rat stifle lesions. This novel approach may offer a longer term and broader delivery of chondrogenic proteins. Research in our laboratory has shown that sConstructs in culture produce a mild level of the pro-inflammatory cytokines (Il-1, Il-6 and TNF-α), whereas sConstructs co-cultured with peripheral blood mononuclear cells (PBMCs) have a dampened inflammatory response. sConstructs were produced from decellularized sECM seeded with sMSC, and co-cultured with PBMCs. Analysis of TGF-β, IL-1ra and Il-10 was performed on the co-culture media by ELISA. The anti-inflammatory cytokines TGF-β ($P<0.03$) and IL-1ra ($P< 0.013$) were increased (4- and 3-fold increase, respectively) in media from sConstruct-PBMC compared to sConstruct alone. IL-10 was below the level of detection in both the sConstruct-PBMC and sConstruct alone. In the presence of sConstructs, immune cells such as PBMCs, can improve the environment by reducing the inflammatory and increasing the anti-inflammatory cytokine profile. This modulatory effect of immune cells may be a mechanism for the benefits on cartilage identified with sConstruct in vivo and thereby support the efficacy of sConstruct as a novel treatment option for OA.
Keywords for abstract:	Osteoarthritis Regenerative therapy cytokine IL-10 TGF-B IL-ra

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Title of abstract:	**SECOND HARMONIC GENERATION (SHG) IMAGING OF EQUINE FLEXOR TENDON FASCICULAR STRUCTURE DURING HEALING**
Authors	B. Singh, S. Cole+, M. Brokken*, S. Durgam* * Dept. of Veterinary Clinical Sciences, +Campus Microscopy Imaging Facility
Abstract	Tendon injuries are amongst the most common musculoskeletal injuries. Tensile property of tendons is largely attributed to sliding between fascicles, in addition to elongation of collagen fiber crimp. Despite this, current histologic assessment of repair tendon is restricted to longitudinal collagen fiber alignment alone. The objective of our study was to evaluate the utility of Second Harmonic Generation (SHG) imaging, current standard for collagen orientation, to assess cross-sectional fascicle structure of normal and injured tendons. Secondly, we determined the feasibility of combining SHG with immuno-fluorescence to assess non-collagenous components of tendon. Normal and collagenase-injured superficial digital flexor tendon (SDFT) samples from 4 horses were used. Tendon specimens were paraffin-embedded, sectioned at 25 microns, immuno-stained with elastin and imaged through a confocal microscope (2-photon laser source) to generate SHG images. Serial sections were immuno-stained for elastin. Quantitative measurements of fascicle size, interfascicular matrix (IFM) thickness, elastin quantity were conducted with Imaris© and ImageJ©. Data was analyzed using a one-way ANOVA for repeated measures (significance set at $p \leq 0.05$). Cross-sectional SHG provides high resolution images of tendon hierarchical structure and can be combined with immuno-staining techniques. Fascicle size was significantly increased at 6- (2-fold) and 16-weeks (3.5-fold) following collagenase injection compared to normal tendon (0.22 ± 0.01 mm^2) (Fig 1). Our preliminary results indicate that elastin in IFM decreases during tendon repair (Fig 2). The current findings of incomplete fascicle pattern restoration, increased fascicle bundle size and reduced interfascicular matrix thickness at 16-weeks post-injury may explain the disconnect between longitudinal collagen alignment and lack of corresponding biomechanical strength in 'healed' tendon. Restricting assessment of tendon histology during healing to longitudinal collagen alignment and crimp restoration alone ignores the considerable importance of higher order re-organization. Understanding tendon hierarchical structure restoration following injury is critical for assessing therapeutic efficacy, and developing strategies for improving treatment.
Keywords for abstract:	Tendinitis SHG Collagen-Elastin

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Title of abstract:	**PHARMACOKINETICS AND PHARMACODYNAMICS OF INTRANASAL AND INTRAVENOUS NALOXONE HYDROCHLORIDE ADMINISTRATION IN HEALTHY DOGS**
Authors	BM Wahler, P Lerche, CH Ricco Pereira, RM Bednarski, B KuKanich, J Lakritz, TK Aarnes
Abstract	**OBJECTIVE** To evaluate the pharmacokinetics and pharmacodynamics of naloxone hydrochloride in dogs following intranasal (IN) and IV administration. **ANIMALS** 6 healthy adult mixed-breed dogs. **PROCEDURES** In a blinded crossover design involving 2 experimental periods, separated by a washout period (minimum of 7 days), dogs were randomized to first receive naloxone IN (4 mg via a commercially available fixed-dose naloxone atomizer; mean ± SD dose, 0.17 ± 0.02 mg/kg) or IV (0.04 mg/kg) and then the opposite treatment in the later experimental period. Plasma naloxone concentrations, dog behavior, heart rate, and respiratory rate were evaluated for 24 hours/period. **RESULTS** IN administered naloxone was well absorbed after a short lag time (mean ± SD, 2.3 ± 1.4 minutes). Mean maximum plasma concentration following IN and IV administration was 9.3 ± 2.5 ng/mL and 18.8 ± 3.9 ng/mL, respectively. Mean time to maximum concentration following IN administration was 22.5 ± 8.2 minutes. Mean terminal half-life after IN and IV administration was 47.4 ± 6.7 minutes and 37.0 ± 6.7 minutes, respectively. Mean bioavailability of IN administered naloxone was 32 ± 13%. There were no notable changes in dog behavior, heart rate, or respiratory rate following naloxone administration by either route. **CONCLUSIONS AND CLINICAL RELEVANCE** Use of a naloxone atomizer for IN naloxone administration may represent an effective alternative to IV administration in emergency situations involving opioid exposure. Future studies are needed to evaluate the efficacy of IN administered naloxone in dogs with opioid intoxication, including a determination of effective doses.
Keywords for abstract:	Pharmacokinetics Anesthesia