

COLLEGE OF VETERINARY MEDICINE RESEARCH DAY

2020

BOOK OF ABSTRACTS



Office of Research and Graduate Studies

Due to the COVID-19 pandemic and the stay-at-home orders issued just prior to our scheduled 2020 College of Veterinary Medicine Research Day, the keynote lecture, platform presentations, and poster sessions were cancelled. However, to showcase the amazing research efforts of the CVM faculty, staff, and the graduate and professional students a Book of Abstracts was compiled.

The following pages contain 105 abstracts submitted by 56 graduate and resident/graduate students, 40 professional DVM students, 7 post docs, 1 visiting scholar and 1 faculty member in the categories of:

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

We hope you enjoy perusing through the book and learning more about the exciting research performed in our College. We look forward to hosting an in-person Research Day again in April of 2021.

Patrick L. Green, PhD

Artick Steen

Professor and Associate Dean for Research and Graduate Studies

Robert H. Rainier Chair in Industrial Veterinary Medicine and Research

Director, Center for Retrovirus Research

Associate Director for Basic Sciences, Comprehensive Cancer Center

IMMUNOLOGY AND INFECTIOUS DISEASE

IMID – 1	IDENTIFICATION OF THE ROLE OF CFTR (CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR) IN LYSOSOMAL ACIDIFICATION, AUTOPHAGY PROCESS, AND BACTERIAL CLEARANCE IN MACROPHAGES. A. Badr ^{1,2} , K. Krause ¹ , M. Anne ¹ , C. Carafice ¹ , E. Cormet-
	Boyaka ² and A. O. Amer ¹ . ¹ Department of Microbial Infection and Immunity, Infectious Diseases Institute, Ohio State University. ² Department of Veterinary Biosciences, Ohio State University
IMID – 2	IDENTIFYING EPITRANSCRIPTOMIC MODIFICATIONS IN HIV-1 gRNA BY NANOPORE SEQUENCING. A. Baek*, G. Lee*, O. Zablocki*, S. Chen*, N. Tirumuru*, W. Lu*, M. Sullivan*, L. Wu*, and S. Kim*. *Department of Veterinary Biosciences, *Department of Microbiology
IMID – 3	HUMAN RESPIRATORY SYNCYTIAL VIRUS ENVELOPE PROTEINS EXPRESSED IN A VESICULAR STOMATITIS VIRUS VECTOR SYSTEM. K. Brakel, B. Binjawadagi, S. Niewiesk, Department of Veterinary Biosciences.
IMID – 4	ROTAVIRUS C: PREVALENCE IN SUCKLING PIGLETS AND DEVELOPMENT OF VIRUS-LIKE PARTICLES TO ASSESS THE INFLUENCE OF MATERNAL IMMUNITY ON THE DISEASE DEVELOPMENT. J. Chepngeno, A. Diaz, F.C. Paim, L.J. Saif, A.N. Vlasova
IMID – 5	EFFECTS OF CD3E-IMMUNOTOXIN TREATMENT ON MURINE LYMPHOID TISSUE T-LYPHOCYTES. S. Kim, L. Smith, R. Shukla, A. Kim, N. Liyanage, S. Cressman, and S. Kim. Depts. Of Veterinary Biosciences and Microbial Infection and Immunity.
IMID – 6	PRIMATE TIM-1 ORTHOLOGS: RESTRICTION OF LENTIVIRAL INFECTION AND ANTAGONISM BY NEF. J.P. Evans, P.S. Mitchell, H.S. Malik, and S.L. Liu. Molecular, Cellular, and Developmental Biology Program, Dept. of Veterinary Biosciences, and Div. of Basic Sciences, Fred Hutchinson Cancer Research Center.
IMID – 7	GENERATING VESICULAR STOMATITIS VIRUS RECOMBINANT VACCINE CANDIDATES FOR HUMAN RESPIRATORY SYNCYTIAL VIRUS. K. French-Kim, K. Brakel, S. Niewiesk. Dept. of Veterinary Biosciences, The Ohio State University College of Veterinary Medicine
IMID – 8	USING MINIMUM INHIBITORY CONCENTRATION VALUES OF COMMON TOPICAL ANTIBIOTIC RESISTANCE: A RETROSPECITVE STUDY OF 134 DOGS AND 20 HORSES WITH ULCERATIVE KERATITIS. M. Jinks†, E. iller†, D. Diaz-Camos†, D. Mollenkpf*, G. Newbold†, A. Gemensky-Metzler†, H. Chandler‡. †Department of Veterinary Clinical Sciences, The Ohio State University, Columbus, OH; *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH; ‡College of Optometry, The Ohio State University, Columbus, OH.
IMID – 9	MECHANISMS OF INTERFERON GAMMA RESISTANCE OF EHRLICHIA CHAFFEENSIS. A. Johnson, O. Teymournejad, M. Lin, Y. Rikihisa
IMID – 10	PANETH CELLS REGULATE DIET-INDUCED OBESITY AND TRAFFICKING OF INFLAMMATORY IMMUNE CELLS INTO ADIPOSE TISSUES. M.R. Joldrichsen, E. Kim, E. Cormet-Boyaka, P.N. Boyaka. Department of Veterinary Biosciences
IMID – 11	ANTIBODY AND IMMUNOTOXIN COMBINATION THERAPY TARGETING HIV LYMPHOID RESERVOIR IN THE MURINE MODEL. S. Kim*, R. Shukla, L. Smith, S. Cressman, A. Kim, A. Tracey, N. Liyanage, and S. Kim. Depts. Of

	Veterinary Biosciences and Microbial Infection and Immunity, The Ohio State
IMID 40	University, Columbus, OH.
IMID – 12	IDENTIFICATION OF NOVEL HTLV-1 ENV BINDING PARTNERS AND THEIR ROLE IN CELLULAR TRANSFORMATION TROPISM. E.M. King, A.R.
	Panfil, & P.L. Green
IMID – 13	VACCINATION OF SWINE TO REDUCE RISK OF ZOONOTIC INFLUENZA
	A VIRUS TRANSMISSION. J.N. Lorbach ¹ , S.W. Nelson ¹ , S.E. Lauterbach ¹ ,
	J.M. Nolting ¹ , E. Kenah ² , D. McBride ¹ , C. Goodell ³ , and A.S. Bowman ¹
	¹ Department of Veterinary Preventive Medicine, ² Biostastics, The Ohio State
	University, ³ Boerhinger Ingelheim Vetmedica, Inc.
IMID – 14	THE ROLE OF HBZ MRNA IN HTLV-1 PATHOBIOLOGY. M. Martinez 1,2, W.
	Dirksen ² , A. Panfil ^{1,2} , S. Bonifati ^{1,2} , 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
IMID – 15	INHIBITION OF EHRLICHIA CHAFFEENSIS INFECTION BY
	INTRACELLULAR NANOBODY TARGETING A REQUIRED TYPE IV
	SECRETION EFFECTOR. Mestres-Villanueva, M., Lin, M., and Rikihisa, Y.
IMID – 16	INHIBITION OF OXIDATIVE PHOSPHORYLATION BUT NOT GLYCOLYSIS
	ATTENUATES LUNG INJURY CAUSED BY H1N1 INFLUENZA A VIRUS
	INFECTION. K. Nolan, L. Baer, A. Nelson, K. Stanford, L. Doolittle, L. Rosas,
	J. Hickman-Davis, and I. Davis.
IMID – 17	INACTIVATED INFLUENZA VIRUS AND POLY (I:C) ADSORBED CORN
	BASED NANOVACCINE ELICITED CELL MEDIATED IMMUNE RESPONSE
	IN MATERNAL ANTIBODY POSITIVE NURSERY PIGS. V Patil ¹ , S Renu ¹ , N
	Feliciano-Ruiz ¹ , Y Han ¹ , J Schrock ¹ , A Ramesh ¹ , GJ Renukaradhya ¹ ¹ Food
	Animal Health Research Program, The Ohio State University, Wooster, OH,
	USA
IMID – 18	INTRANASAL DELIVERABLE MANNOSE SURFACE CONJUGATED
	CHITOSAN-BASED INFLUENZA NANOVACCINE FOR NURSERY PIGS. S.
	Renu, N. Feliciano-Ruiz, A. Ramesh, V. Patil, Y. Han, J. Schrock, and G.J.
	Renukaradhya. Food Animal Health Research Program and Department of
	Veterinary Preventive Medicine.
IMID – 19	INVESTIGATING INTRANASAL VACCINATION STRATEGIES TO
	IMPROVE PROTECTION AGAINST RESPIRATORY PATHOGENS. J.C.
	Rowe, R.M. Woodfint, Z. Attia, E. Kim, E. Cormet-Boyaka, P.N. Boyaka
IMID – 20	ADAPTIVE CHANGES IN VIRAL ENVELOPE RESULTING FROM
	ADAPTATION OF SIMIAN-TROPIC HIV-1 TO MACAQUES CONFERS
	RESISTANCE TO INTERFERON. A.C. Smith ¹ , H. Weight ² , J. Overbaugh ² , and
	A. Sharma ¹ . ¹ Depts. Of Veterinary Biosciences and Microbial Infection &
	Immunity. ² Division of Human Biology, Fred Hutchinson Cancer Research
	Center.
IMID – 21	BROAD-SPECTRUM AND GRAM NEGATIVE-TARGETING ANTIBIOTICS
	DIFFERENTIALLY REGULATE IMMUNE RESPONSE TO NON-
	ADJUVANTED VACCINE ANTIGENS. R.M. Woodint, A. Haile, M.R.
	Joldrichsen, and P.N. Boyaka
IMID – 22	RNA INTERNAL N6-METHYLADENOSINE MODIFICATION MODULATES
	INNATE AND ADAPTIVE IMMUNE RESPONSES TO VIRUS INFECTION. M.
	Xue1, M. Lu1, A.Li1, Z. Zhang2, P. Boyaka1, S. Niewiesk1, C. He2, J. Li1*.
	1Department of Veterinary Biosciences, College of Veterinary Medicine; The
	Ohio State University, Columbus, OH 43210, USA. 2Department of Chemistry,

	Department of Dischargistm, and Malagulan Dislam, and Institute for
	Department of Biochemistry and Molecular Biology, and Institute for
	Biophysical Dynamics, The University of Chicago, Chicago, IL 60637, USA
IMID – 23	SERINC PROTEINS POTENTIATE ANTIVIRAL TYPE I IFN INDUCTION AND
	PROINFLAMMATORY SIGNALING PATHWAYS. C. Zeng ^{1,2} , A. Waheed ³ , T.
	Li ⁴ , J. Yu ^{1,2} , Y. Zheng ^{1,2} , J. Yount ⁴ , H. Wen ⁴ , E. Freed ³ , S. Liu ^{1,2,4,5}
	¹ Center for Retrovirus Research, The Ohio State University, Columbus, OH.
	² Department of Veterinary Biosciences, The Ohio State University, Columbus,
	OH. ³ Virus-Cell Interaction Section, HIV Dynamics and Replication Program,
	National Cancer Institute-Frederick, Frederick, MD. ⁴ Department of Microbial
	Infection and Immunity, The Ohio State University, Columbus, OH. 5Viruses
	and Emerging Pathogens Program, Infectious Diseases Institute, The Ohio
	State University, Columbus, OH.

MOLECULAR AND CELLULAR BIOLOGY

MCB – 1	CHARACTERIZING REEN EXPRESSION IN CANINE OCTEOGARCOMA
MCB – 1	CHARACTERIZING PTEN EXPRESSION IN CANINE OSTEOSARCOMA CELL LINES. K. Bick, J.M. Fenger
MOD	
MCB – 2	THE SELECTIVE INHIBITOR OF NUCLEAR EXPORT VERDINEXOR
	EXHIBITS BIOLOGICAL ACTIVITY AGAINST CANINE OSTEOSARCOMA
	CELL LINES. J.T. Breitbach, D.S. Louke, M.R. Watts, S.J. Tobin, A.E.
	Davies, J.M. Fenger. Departments of Veterinary Biosciences and Veterinary
	Clinical Sciences
MCB – 3	INFLUENZA A VIRUS EFFECT ON ALVEOLAR FLUID CLEARANCE AND
	CDP-CHOLINE AS POTENTIAL TREATMENT FOR ARDS IN MICE. <u>El</u>
	Musa H, Davis IC, Rosas L, Nelson A, Doolittle LM, Joseph L. Department of
	Veterinary Biosciences, College of Veterinary Medicine, The Ohio State
	University, Columbus, OH.
MCB – 4	EVALUATING THE ROLE OF INTERFERON STIMULATED GENE CMPK2
	IN RESTRICTION OF PRIMATE LENTIVIRUSES. J. Garcia, A. Sharma
MCB - 5	RECEPTOR TYROSINE KINASE DYSREGULATION AND BIOLOGICAL
	ACTIVITY OF TOCERANIB AND CANINE UROTHELIAL CARCINOMA
	CELL LINES. D. Korec, D.S. Louke, J.M. Fenger. Department of Veterinary
	Clinical Sciences
MCB – 6	INTERROGATING THE ROLE OF WWOX IN CANINE MAST CELL
	TUMORS & CELL LINE. R. Makii, H. Cook, D. Louke, J.M. Fenger.
	Department of Veterinary Clinical Sciences, College of Veterinary Medicine,
	The Ohio State University.
MCB – 7	THE MOLECULAR DETERMINANT OF HTLV TRANSFORMATION
	TROPISM. V.V. Maksimova, E.M. King, P.L. Green, and A.R. Panfil
MCB – 8	INVESTIGATING LORIKEET ENTERITIS: IS CLOSTRIDIUM
	PERFRINGENS THE CULPRIT? D. Minich, C. Madden, G.A. Ballash, R.
	Junge, V.L. Hale
MCB – 9	EXTRACTION METHODS FOR OBTAINING MICROBIAL DNA IN
	HEALTHY CANINE URINE. R. Mrofchak, C. Madden, and V. Hale
MCB - 10	CONTRIBUTION OF FGF/FGFR SIGNALING TO SUSTAINED ERK
	ACTIVATION, A DRIVER OF CELLULAR HETEROGENEITY AND DRUG
	RESISTANCE. V. Murthy, A.E. Davies
MCB - 11	EX VIVO CYSTIC FIBROSIS 3D CULTURE LUNG MODEL
	DIFFERENTIATED FROM EXPANDED PRIMARY CF PATIENT-DERIVED
	LUNG CELLS. R.E. Rayner, J. Wellmerling, W. Osman, S. Honesty, M.E.
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	Peeples, and E. Cormet-Boyaka. Depts. Of Veterinary Biosciences, The Ohio State University; and Center for Vaccines Immunity, Abigail Wexner Research Institute at Nationwide Children's Hospital, Columbus, OH
MCB – 12	EVALUATIONG MKLP2 INHIBITION AS A NOVEL ANTIMITOTIC FOR HUMAN AND CANINE GLIOBASTOMA. M.S. Schrock, P. Dickinson, M. Venere, and M.K. Summers
MCB - 13	TARGETING PRMT5 TO OVERCOME IBRUTINIB RESISTANCE IN HUMAN MANTLE CELL LYMPHOMA. S. Sloan ^{1,2} , F. Brown ¹ , M. Long ^{1,2} , A. Prouty ¹ , E. Brooks ¹ , J. Chung ¹ , Y. Youssef ¹ , X. Zhang ³ , A.S. Yilmaz ³ , H.G. Ozer ³ , J.C. Byrd ¹ , R. Lapalombella ¹ , R.A. Baiocchi ¹ , and L. Alinari ¹ . ¹ Department of Internal Medicine, Division of Hematology, College of Medicine, The Ohio State University, Columbus, OH. ² Department of Veterinary Biosciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH. ³ Department of Biomedical Informatics, College of Medicine, The Ohio State University, Columbus, OH
MCB – 14	CONTRIBUTIONS OF HBZ INTERACTING PROTEINS, TOP1 AND YBX1, TO HTLV-1 PATHOBIOLOGY. R. Stahl, A. Panfil, P. Green. Depts of Veterinary Biosciences, Center for Retrovirus Research, Comprehensive Cancer Center and Solove Research Institute, Department of Cancer Biology and Genetics
MCB – 15	CFTR DYSFUNCTION AND COPD: DNA DAMAGE AS A POTENTIAL LINK. J. Wellmerling, S. Change, E. Kim, W. Osman, P. Boyaka, M. Borchers, and E. Cormet-Boyaka. Depts of Veterinary Biosciences, Ohio State University, and Internal Medicine, University of Cincinnati
MCB – 16	INTRACELLULAR BACTERIA SUBVERSION OF IRON SEQUESTRATION BY TYPE IV SECRETION SYSTEM. Q. Yan, O. Teymournejad, M. Lin, Y. Rikihisa. Department of Veterinary Biosciences

STRUCTURE/FUNCTION

SF – 1	IMMUNOLOCALIZING LUBRICIN IN NORMAL AND EXPERIMENTALLY-INJURED INTRASYNOVIAL DEEP DIGITAL FLEXOR TENDON. N.
	Altmann, S Durgam
SF – 2	MOTILITY ACTIVATION AND ASSISTED REPRODUCTION TECHNIQUES
	ALTER THE SPERMATOZOA GLYCOCALYX OF THE FRESHWATER
	FISH, SAUGER (SANDER CANADENSIS). B. Blawut, B. Wolfe, G.
	Scheunemann, C. Premanandan, S.A. Ludsin, M.A. Coutinho da Silva. Depts
	of Veterinary Clinical Sciences, Preventive Medicine, and Ecology, Evolution,
	and Organismal Biology
SF – 3	OPTIMIZING FOOD ACCESSIBILITY DURING ZEBRAFISH REARING
	IMPROVES GROWTH, SURVIVAL, AND BREEDING PERFORMANCE. \underline{T} .
	Collins, S. Cabrera, E. Teets, J. Shaffer, and B. Blaser. Office of Research,
	University Laboratory Animal Resources and College of Medicine, Division of
	Hematology, and Comprehensive Cancer Center
SF – 4	VARIABILITY IN HATCHING RATES OF THE AMERICAN ALLIGATOR
	(ALLIGATOR MISSISSIPPIENSIS). S. Dampney, J. Flint, M. Flint.
	Department of Veterinary Preventive Medicine, College of Veterinary
	Medicine
SF – 5	PHARMACOKINETICS AND PHARMACODYNAMIC EFFECTS OF ORAL
	TRANSMUCOSAL AND INTRAVENOUS ADMINISTRATION OF

	DEXMEDETOMIDINE IN DOGS. BT Dent ¹ , TK Aarnes ¹ , VA Wavreille ¹ , J Lakritz ¹ , P Lerche ¹ , B KuKanich ² , CH Ricco Pereira ¹ , RM Bednarski ¹ . ¹ Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State University. ² Department of Anatomy and Physiology, Institute of Computational Comparative Medicine, College of Veterinary Medicine, Kansas State University.
SF – 6	REPLACEMENT OF FISH OIL WITH HIGH-OLEIC ACID SOYBEAN OIL IN ONCORYHYNCHUS MYKISS DIETS, AND ASSOCIATED PATHOLOGIES.
	A. Feinzig ¹ , J. Grayson ² , and K. Dabrowski ³ . College of Veterinary Medicine ¹ , School of Environmental and Natural Resources ^{2,3}
SF – 7	DEVELOPMENT OF AN EVIDENCE-BASED WELFARE APPROACH FOR
	CHEETAHS (ACINONYX JUBATUS) IN HUMAN CARE. B. Fischer, M. Flint, K. Cole, and K.A. George. Department of Animal Sciences, College of Food, Agriculture, and Environmental Sciences, and Department of Veterinary
	Preventive Medicine, College of Veterinary Medicine
SF – 8	COMPREHENSIVE EVALUATION OF KIDNEY TISSUE FROM YORKSHIRE TERRIERS WITH RENAL DISEASE. M. Klein, N. Etedali, R. Cianciolo. Department of Veterinary Biosciences and the Animal Medical Center
SF – 9	EXPRESSION OF CD31 IN FELINE KIDNEYS TO CHARACTERIZE PERITUBULAR CAPILLARY DENSITY IN CKD. R. Paschall, J. Quimby, R. Cianciolo
SF – 10	HAIR CORTISOL AND BEHAVIOR: A NOVEL APPROACH TO MEASURING CALIFORNIA SEA LION (ZALOPHUS CALIFORNIANUS) WELFARE. M. Winans, M. Flint, K. Cole, K. George. College of Veterinary Medicine, Department of Veterinary Preventive Medicine, and College of Food, Agriculture, and Environmental Sciences, Department of Animal Sciences

EPPIDEMIOLOGY AND APPLIED RESEARCH

EAR – 1	IDENTIFICATION OF ENVIRONMENTAL SURFACE RESERVOIRS FOR
	THE PERSISTENCE OF SALMONELLA IN THE OSU GALBREATH
	EQUINE CENTER. R. Adams, D. Mollenkopf, G. Ballash, T. Wittum. Dept. of
	Veterinary Preventive Medicine
EAR – 2	UTILIZING PATIENT AND CLINICAL-BASED RISK FACTORS TO
	PREDICT RESISTANT UROPATHOGENIC E. COLI URINARY TRACT
	INFECTIONS. G. Ballash, D. Mollenkopf, D. Diaz-Campos, T. Wittum. Depts
	of Veterinary Preventive Medicine and Veterinary Clinical Sciences
EAR – 3	PERCEIVED RISKS AND BENEFITS FOR PARTICIPATION IN POULTRY
	DISEASE MONITORING PROGRAMS IN THE UNITED STATES: A
	CLUSTER ANALYSIS. T.J. Beyene ^a , G. Lossie ^b , C-W Lee ^a , A.G. Arruda ^a .
	^a Department of Veterinary Preventive Medicine, The Ohio State University,
	Columbus, OH, 43210; Department of Comparative Pathobiology, Purdue
	University College of Veterinary Medicine, West Lafayette, IN, 47907
EAR – 4	PIGS, PATHOGENS AND PEOPLE: A NOVEL APPROACH TO
	MONITORING INTERNAL BIOSECURITY IN SWINE PRODUCTION. N.J.
	Black, L.E. Moraes, A.G. Arruda. Depts of Veterinary Preventive Medicine and
	Animal Sciences

EAR – 5	STOCKING DENSITY IMPACTS GROUP-HOUSED COWS' ABILITY TO SEEK SECLUSION BEFORE CALVING. K. Creutzinger ¹ , H. Dann ² , P.
	Krawczel ³ , G. Habing ¹ , and K. Proudfoot ⁴ . ¹ Veterinary Preventive Medicine,
	² William H. Miner Agriculture Research Institute, ³ University of Helsinki,
	⁴ University of Prince Edward Island
EAR – 6	DRIVERS AND BENEFITS OF CANINE LYME BORRELIOSIS
	PREVENTION METHODS I A LYME-ENDEMIC AREA. L. Giralico, T.
	Wittum, A. Smith, J. Stull. Department of Veterinary Preventive Medicine,
	College of Veterinary Medicine, The Ohio State University, Columbus, Ohio
EAR – 7	PREGNANCY DIAGNOSIS IN SOUTHERN WHITE RHINOCEROS
	(CERATOTHERIUM SIMUM SIMUM) BY NASAL SECRETION AND
	SERUM. D. Guzman, P. Joyner, M. Stoops, M. Flint. The Ohio State
	University College of Veterinary Medicine, The Wilds, Omaha Henry Dooly
	ZOO
EAR – 8	A SURVEY STUDY OF PROPHYLACTIC RABIES VACCINATION REGULATIONS FOR COMPANION ANIMALS IN OHIO. A. Jokerst, and J.
	O'Quin. Dept. of Veterinary Preventive Medicine
EAR – 9	IDENTIFYING MEMBRANE-ACTIVE NEXT GENERATION
LAIX — 9	ANTIMICROBIALS EFFECTIVE AGAINST AVIAN PATHOGENIC
	ESCHERICHIA COLI (APEC). D. Kathayat, G. Closs Jr, Y.A. Helmy, L.
	Deblais, and G. Rajashekara. Food Animal Health Research Program,
	Department of Veterinary Preventive Medicine
EAR - 10	YEAR-ROUND INFLUENZA A VIRUS SURVEILLANCE IN ANAS
2,	PLATYRHYNCHOS REVEALS GENETIC PERSISTENCE DURING THE
	UNDER-SAMPLED SPRING SEASON. S.E. Lauterbach ¹ , D.S. McBride ¹ ,
	J.M. Schmit ² , M.A. Piccutio ² , B.T. Shirkey ² , J.M. Nolting ¹ , A.S. Bowman ¹ . ¹ The
	Ohio State University Department of Veterinary Preventive Medicine. ² Winous
	Point Marsh Conservancy
EAR – 11	ENVIRONMENTAL SOURCES OF LYMPH NODE INFECTIONS WITH NON-
	TYPHOIDAL SALMONELLA IN CALVES. S. Locke ¹ , N. Aulik ² , D. Sockett ² ,
	R. Meyer ² , J. Pempek ¹ , R. Portillo-Gonzalez ¹ , G. Habing ¹ . ¹ The Ohio State
	University College of Veterinary Medicine, Department of Veterinary
	Preventive Medicine, Columbus, Ohio. ² Wisconsin Veterinary Diagnostic
	Laboratory, Madison, Wisconsin
EAR – 12	MINDING THE GAP: INFLUENZA A VIRUS IN UNIQUE SEA DUCK HOST
	SPECIES. D.S. McBride, S.E. Lauterbach, J.M. Nolting, A.S. Bowman.
EAD 42	Department of Veterinary Preventive Medicine
EAR – 13	CO-OCCURRENCE OF CAMPYLOBACTER SPECIES IN CHILDREN FROM EASTERN ETHIOPIA, AND THEIR ASSOCIATION WITH
	ENVIRONMENTAL ENTERIC DYSFUNCTION, DIARRHEA AND HOST
	MICROBIOME. Y Terefe ^{1,2,3} , L Deblais ^{1,3} , M Ghanem ^{1,3} , YA Helmy ¹ , B
	Mummed ² , D Chen ⁴ , N Singh ⁴ , V Ahyong ⁵ , K Kalantar ⁶ , G Yilmer ^{1,3} , JY
	Hassen ² , A Mohammed ² , SL McKune ³ , MJ Manary ⁷ , W Gebreyes ^{1,3} , AH
	Havelaar ⁴ , G Rajashekara ^{1,3}
	¹ The Ohio State University, Columbus, OH, USA
	² Haramaya University Dire Dawa, Ethiopia
	³ Global One Health Initiative, The Ohio State University, Addis Ababa,
	Ethiopia
	⁴ University of Florida, Gainesville, FL, USA
	⁵ Chan Zuckerberg Biohub, San Francisco, CA, USA

	⁶ Chan Zuckerberg Initiative, Redwood City, CA, USA
	⁷ Washington University, St. Louis, USA
EAR – 14	CONSISTENCY OF LYING TIME IS ASSOCIATED WITH REDUCED
	SERUM NON-ESTERIFIED FATTY ACIDS OF PREPARTUM DAIRY
	HEIFERS AND COWS. B.T. Menichetti, J.M. Piñeiro, A. Garcia-Guerra, A.E.
	Relling, W.P. Weiss, and G.M. Schuenemann. Depts. Of Veterinary
	Preventive Medicine and Animal Sciences
EAR – 15	THE PRACTICAL APPLICATION OF ENVIRONMENTAL SURVEILLANCE
LAIX - 13	AS A COMPONENT OF A COMPREHENSIVE VETERINARY ASP. E.E.
	Feyes, D.F. Mollenkopf, G.A. Ballash, J.C. Van Balen, A.E. Hoet, D.V.
	Diaz-Campos, ² T.E. Wittum ¹
	¹ Dept. of Veterinary Preventive Medicine, and ² Dept. of Veterinary Clinical
	Sciences
EAR – 16	INFLUENCE OF SOCIODEMOGRAPHIC FACTORS ON INFECTIOUS AND
LAIX - 10	ZOONOTIC PATHOGEN RISK IN A RESOURCE-LIMITED COMMUNITY AT
	THE LIVESTOCK-WILDLIFE INTERFACE, MPUMALANGA, SOUTH
	AFRICA. P. Oruganti ¹ , A. Berrian ¹ , E. Root ² , and I. van Wyk ³
	¹ The Ohio State University College of Veterinary Medicine, Department of
	Veterinary Preventive Medicine; ² The Ohio State University College of Public
	Health; ³ University of Pretoria, Pretoria, South Africa
EAR – 17	LANDSCAPE ECOLOGY AS AN APPROACH TO UNDERSTANDING
	ANTIMICROBIAL RESISTANCE ACROSS COMMUNITIES. M. Overcast, S.
	Mielk, R. Garabed, D. Jackson-Smith, S. Matthews, C. Brock. Dept. of
	Veterinary Preventive Medicine and School of Environmental and Natural
	Resources
EAR – 18	HOUSING, HUSBANDRY AND CLINICAL TECHNIQUES IN THE
LAIX - 10	LABORATORY CRAYFISH (PROCAMBARUS CLARKII). M. Palillo, J.
	Palillo, M. Glon, L. Pintor, W. Bidot, M. White, and R. Malbrue
EAR – 19	HIERARCHICAL SURVEY OF VETERINARIAN AND DAIRY FARM
2,414	WORKER ANTIMICROBIAL USE PRACTICES. R. Portillo-Gonzalez, J.
	Pempek, S. Locke, G. Habing
EAR - 20	THE EFFECT OF STOCKING DENSITY AND A BLIND ON THE SOCIAL
L/ II Zo	BEHAVIOR OF PREPARTURIENT DAIRY CATTLE. J. Rose ¹ , K.C.
	Creutzinger ¹ , and K.L. Proudfoot ² . ¹ Veterinary Preventive Medicine, College of
	Veterinary Medicine, Ohio State University, Columbus, Ohio. ² Atlantic
	Veterinary College, University of Prince Edward Island, Charlottetown,
	Canada
EAR – 21	TONSIL SCRAPINGS FOR PORCINE REPRODUCTIVE AND
2,414 21	RESPIRATORY SYNDROME VIRUS DETECTION. H.L. Walker ¹ ; A.S.
	Bowman ¹ ; J.B. Ferreira ² ; S.W. Nelson ¹ ; A.G. Arruda ¹ . ¹ Department of
	Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio
	State University, Columbus, OH; ² Department of Population Health and
	Pathobiology, College of Veterinary Medicine, North Carolina State University,
	Raleigh, NC
EAR – 22	ORGANIC DAIRY FARMER HERD HEALTH DECISIONS ON TREATMENT
	AND PREVENTION OF DISEASE. K. Weaver, J. Pempek, C. Brock, D.
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	Junge ³ , and M. Flint ¹ . Depts. Of ¹ Veterinary Preventive Medicine, ² Veterinary
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	Campos ¹ . Department of Veterinary Clinical Sciences ¹ and Department of
	Veterinary Preventive Medicine ² , The Ohio State University College of
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	and Surgery ³ , University of Missouri Veterinary Health Center, Columbia, MO;
	Department of Microbiology and Clinical Pathology ⁴ , University of Wisconsin-
	Madison Veterinary Care, Madison, WI; Department of Bacteriology and
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	^a The Ohio State University College of Veterinary Medicine, Columbus, Ohio
	b University of Florida College of Veterinary Medicine, Gainesville, Florida
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	Adams, S. Summers, A. Rudinsky. Department of Veterinary Clinical
	Sciences, College of Veterinary Medicine, The Ohio State University,
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	Midlothian; Innovation Centre, Edinburgh, United Kingdom (Caney); Colorado
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	V.A. Wavreille ¹ , DVM, MS, MRCVS, DACVS, ACVS Fellow Surgical
	Oncology; J.M. Fenger ¹ , DVM, PhD, ACVIM; R.N. Jennings ² , DVM, PhD,
	DACVP; L.E. Selmic1, BVetMed (Hons), MPH, DACVS-SA, DECVS, ACVS
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	¹ College of Veterinary Medicine, The Ohio State University, USA
	² Nationwide Children's Hospital, Columbus, Ohio USA
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	Slovis NM 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
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	CARBOPLATIN CHEMOTHERAPY. K. Taikowski ¹ , A.J. Rudinsky ^{1,2} , D.S.
	Louke ¹ , E. Warry ³ , J.M. Fenger ¹ .
	¹ Department of Veterinary Clinical Sciences, College of Veterinary Medicine,
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	College of Veterinary Medicine, The Ohio State University, Columbus, OH
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	³ Department of Small Animal Clinical Sciences, College of Veterinary
	Medicine, Texas A&M University, College Station, TX 77843
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	Department of Veterinary Clinical Sciences.

EDUCATIONAL

EDU – 1	SPECTRAL FLOW CYTOMETRY FOR VETERINARY DIAGNOSTICS AND
	RESEARCH AT OSU CVM. S. Evans. Dept. of Veterinary Biosciences

IMMUNOLOGY AND INFECTIOUS DISEASES

Title of abstract	IDENTIFICATION OF THE ROLE OF CFTR (CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR) IN LYSOSOMAL ACIDIFICATION, AUTOPHAGY PROCESS, AND BACTERIAL CLEARANCE IN MACROPHAGES
Authors	A. Badr ^{1, 2} , K. Krause ¹ , K. Hamilton ¹ , M. Eltobgy ¹ , S. Estfanous ¹ , K. Daily ¹ , A. Abu Khweek ¹ , M. Anne ¹ , C. Carafice ¹ , E. Cormet-Boyaka ² , and A. O. Amer ^{1*} . ¹ Department of Microbial Infection and Immunity, Infectious Diseases Institute, Ohio State University. ² Department of Veterinary Biosciences, Ohio State University.
Abstract	Cystic fibrosis (CF) is the most common autosomal recessive disease in Caucasians with no available cure. CF is caused by mutation in (CFTR), in which the most common mutation is F508del. F508del CFTR is misfolded and malfunctioning. CFTR is a chloride channel transporting chloride across cell membranes of epithelial cells, however its function in macrophages is unclear. F508 del (CF) macrophages are defective in their bacterial killing activity, causing some bacteria as <i>Burkholderia cenocepacia</i> (<i>B. c.</i>) to cause fatal respiratory infections. Furthermore, the autophagy process, by which cells deliver unwanted materials and pathogens to lysosomes for degradation, is defective. Lysosomal high luminal acidity is important for proteolytic enzymes activity and can be maintained by transporting anions inside lysosomes. CFTR modulators were recently approved for treating CF patients, via correction of misfolded CFTR, and improving its function. Our hypothesis is that CFTR is responsible for lysosomal acidification in macrophages, hence, lysosomes are dysfunctional in CF macrophages. We further hypothesize that CFTR modulators will correct lysosomal dysfunction, improve autophagy, and enhance bacterial clearance. Experimental design: Murine bone marrow derived CF macrophages were used to identify lysosomal acidification, degradative function, and enzymes activity in comparison to WT macrophages. CF macrophages were treated with CFTR modulators and lysosomal function, autophagy process and bacterial clearance were assessed. In our results, we found that CF macrophages had defective lysosomal acidification and decreased degradative function. CFTR modulators treatment restored the acidification and degradative capacity of lysosomes. Furthermore, they enhanced autophagy and increased <i>B.c.</i> clearance. We concluded that, CFTR plays an important role in acidifying lysosomes and regulating lysosomal function as well as autophagy process in CF macrophages. CFTR correction in CF macrophages confers a hope to CF patients thro
Keywords for abstract	CFTR, Lysosomal acidification, Autophagy, Cystic fibrosis, CFTR modulators

Title of abstract	IDENTIFYING EPITRANSCRIPTOMIC MODIFICATIONS IN HIV-1 gRNA BY NANOPORE SEQUENCING
Authors	A.Baek*, G.Lee*, O.Zablocki*, S.Chen*, N.Tirumuru*, W.Lu*, M.Sullivan*, L.Wu*, and S.Kim*. *Departments of Veterinary Biosciences, *Departments of Microbiology
Abstract	Recent studies have shown that HIV-1 genomic RNA (gRNAs) contains different types of epitranscriptomic modifications that have important biological and pathogenic functions in the host. Our understanding of HIV-1 gRNA modifications, however, remains poor because even the state-of-the-art, RNA-modification analysis tools only read short, fragmented RNA around the modification sites. This only allows partial information that lacks both precise base positions of modified nucleotides and ensembles of different modifications over the whole gRNA. Our hypothesis is that epitranscriptomic modification patterns present in full-length HIV-1 gRNAs are not all identical; there are heterogenous populations of HIV-1 gRNAs with distinct modification patterns, that will have differential biological functions during the infection cycle. We have employed Nanopore MinION direct RNA sequencing methods to address the hypothesis. Unlike other sequencing platforms, Oxford Nanopore sequencing can directly read modified nucleotides of native RNA by measuring unique electric signal differences between modified and unmodified RNAs passing through a small protein pore. We mapped epitranscriptomic modifications of full-length HIV-1 gRNA from purified virions by comparing the electric signals of HIV-1 gRNA with those of <i>in vitro</i> transcribed HIV-1 RNA. We found several prominent modification sites correlated with m ⁶ A predicted motifs that matched with previous studies. These results were reproducible in three independent experiments. All the major modification sites aligned with m ⁶ A motifs were disappeared when HIV-1 gRNA was treated with a known m ⁶ A modification eraser, fat mass and obesity-associated protein (FTO). Single RNA molecule level analysis revealed that there are heterogeneous populations of HIV-1 gRNA with distinct methylation patterns. The major modification sites and their relative abundance will be further confirmed with LC-MS/MS and reverse-transcription assays. This study demonstrated the potential of Nanopore seque
Keywords for abstract	RNA m ⁶ A modification Nanopore sequencing direct RNA sequencing

Title of abstract	HUMAN RESPIRATORY SYNCYTIAL VIRUS ENVELOPE PROTEINS EXPRESSED IN A VESICULAR STOMATITIS VIRUS VECTOR SYSTEM
Authors	K. Brakel, B. Binjawadagi, S. Niewiesk, Dept. of Veterinary Biosciences
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, the immune response is short-lived, and antibodies produced after natural infection do not elicit long-term immunity. We have created recombinant vesicular stomatitis virus (rVSV) vectors expressing RSV-F (the fusion envelope glycoprotein), RSV-G (the attachment envelope glycoprotein), or both the G and F protein (RSV-G-2A-F). Cotton rats were inoculated either subcutaneously or intranasally with recombinants expressing RSV-G, RSV-F, or RSV-G-2A-F, and then challenged with RSV-A2 after either 56 days or 80 days, to test the strength and longevity of the immune response. Animals immunized subcutaneously with rVSV-G-2A-F and challenged after 56 days were not significantly more protected in the lung than those that received rVSV-G or rVSV-F. After 12 weeks, all groups were completely protected in the lung, and no groups were protected in the nose. Neutralizing antibodies were initially high for rVSV-F and rVSV-G-2A-F, but both groups had low levels after 12 weeks, while rVSV-G had low levels for all 12 weeks. When immunized intranasally with rVSV-G-2A-F and challenged after 56 days, cotton rats were less protected in the lungs than those that received rVSV-F or rVSV-G, and there was no significant difference in protection in the nose between rVSV-G-2A-F and rVSV-G. This trend continued after 80 days. Neutralizing antibody levels generated by rVSV-F were initially highest, but steadily declined over the course of 12 weeks. rVSV-G generated low levels of RSV neutralizing antibodies. rVSV-G-2A-F neutralizing antibody levels were significantly higher than either rVSV-F or rVSV-G alone by week 12. This study suggests that combining G and F into the same vaccine may not improve protection from RSV challenge, but may produce longer-lasting antibodies.
Keywords for abstract	Respiratory syncytial virus Vaccines Vesicular stomatitis virus Cotton rats

Title of abstract	ROTAVIRUS C: PREVALENCE IN SUCKLING PIGLETS AND DEVELOPMENT OF VIRUS-LIKE PARTICLES TO ASSESS THE INFLUENCE OF MATERNAL IMMUNITY ON THE DISEASE DEVELOPMENT
Authors	J. Chepngeno, A. Diaz, F. C. Paim, L. J. Saif, A. N. Vlasova
Abstract	Rotavirus C (RVC) has been detected increasingly in humans and swine in different countries, including the US. It is associated with significant economic losses due to diarrheal disease in nursing piglets. In this study we aimed: (1) to determine the prevalence of RVC in healthy and diarrheic suckling piglets on US farms; and (2) to evaluate if maternal antibody (Ab) levels were associated with protection of newborn suckling piglets against RVC. There was a significantly higher prevalence (p = 0.0002) of litters with diarrhea born to gilts compared with those born to multiparous sows. Of 113 nursing piglet fecal samples tested, 76.1% were RVC RNA positive. Fecal RVC RNA was detected in significantly (p = 0.0419) higher quantities and more frequently in piglets with diarrhea compared with healthy ones (82.5 vs. 69.9%). With the exception of the historic strain Cowden (G1 genotype), field RVC strains do not replicate in cell culture, which is a major impediment for studying RVC pathogenesis and immunity. To circumvent this, we generated RVC virus-like particles (VLPs) for Cowden (G1), RV0104 (G3) and RV0143 (G6) and used them as antigens in ELISA to detect swine RVC Abs in serum and milk from the sows. Using RVC-VLP Ab ELISA we demonstrated that sows with diarrheic litters had significantly lower RVC IgA and IgG Ab titers in milk compared to those with healthy litters. Thus, our data suggest that insufficient lactogenic protection provided by gilts plays a key role in the development of and the increased prevalence of clinical RVC disease.
Keywords for abstract	Rotavirus pigs Maternal immunity VLPs

Title of abstract	EFFECTS OF CD3E-IMMUNOTOXIN TREATMENT ON MURINE LYMPHOID TISSUE T-LYMPHOCYTES
Authors	S. Kim, L. Smith, R. Shukla, A. Kim, A. Tracey, N. Liyanage S. Cressman and S. Kim. Depts. Of Veterinary Biosciences and Microbial Infection and Immunity
Abstract	Adoptive T-cell gene therapy, including Chimeric Antigen Receptor (CAR) T-cell therapy, is a new treatment method being investigated as a potential cure for certain cancers and other previously incurable diseases like HIV/AIDS. Therapy efficacy can be significantly improved by preconditioning patients before cell transplantation. During preconditioning, lymphodepletion treatment ablates lymphoid cells to create a favorable "space" for transferred cells. Current lymphodepleting preconditioning methods, however, rely on high doses of toxic and non-specific chemotherapies which often result in variable therapeutic efficacy and adverse, sometimes deadly, side effects. The Kim lab is testing murine CD3e-immunotoxin (CD3e-IT) — anti-CD3e-antibody conjugated with saponin — as a safer and viable preconditioning method. Preliminary studies found that CD3e-IT can specifically and effectively ablate total systemic murine T-cells, except CXCR5+ follicular T-helper cells (Tfh). Tfh in germinal centers (GC) are important in lymphomas of GC origin and HIV infection as they remain a reservoir for neoplasia or HIV such that disease can persist after chemotherapy or anti-retroviral therapy. We hypothesize that the anatomic structure of lymphoid follicles protects Tfh from CD3e-IT-mediated killing but that administration of anti-CD40L monoclonal antibody (CD40L-mAb) followed by CD3e-IT will effectively dissociate the follicle to allow CD3e-IT penetration for Tfh killing. Preliminary immunohistochemical analysis of CD3e-IT will effectively dissociate the follicle to allow CD3e-IT penetration for Tfh killing. Preliminary immunohistochemical analysis of CD3e-IT treated murine lymphoid tissue revealed reduction in CD3+ T-cell populations surrounding B-cell follicles but no change to populations within follicles when compared to PBS treated controls. These results demonstrate the potential of CD3e-IT/CD40L-mAb combination treatment as a specific and effective preconditioning protocol for T-cell depletion. To further investigate CD3e-I
Keywords for abstract	Adoptive immunotherapy Lymphodepleting preconditioning CD3e-immunotoxin Follicular T cells Immunohistochemistry

Title of abstract	PRIMATE TIM-1 ORTHOLOGS: RESTRICTION OF LENTIVIRAL INFECTION AND ANTAGONISM BY NEF
Authors	J.P. Evans, P.S. Mitchell, H.S. Malik, and S.L. Liu. Molecular, Cellular, and Developmental Biology Program, Dept. Of Veterinary Biosciences, and Div. Of Basic Sciences, Fred Hutchinson Cancer Research Center.
Abstract	The T-cell immunoglobulin and mucin domain (TIM) family of phosphatidylserine (PS) receptors are known for their role in enhancing entry of enveloped viruses. Interestingly, we have demonstrated that TIM proteins restrict virion release of HIV in a PS-binding dependent manner (Li et al. PNAS 2014), and that TIM protein surface expression is reduced by HIV-1 Nef-mediated internalization as well as sequestration in intracellular, autophagy-related compartments (Li, Waheed, Yu et al. PNAS 2019). However, the impact of the Nef-TIM interplay on the transmission and spread of lentiviruses within and across primate species remains unclear. To determine the evolutionary relationship between TIM proteins and primate lentiviruses, we examined the anti-viral function of a panel of primate TIM-1 orthologs from apes, old world monkeys, and new world monkeys against representative lentiviruses. The production and infectivity of HIV-1 virions in the presence of each TIM-1 ortholog was determined by anti-p24 immunoblot, and infection of HeLa-TZM-bI reporter cells. Restriction of HIV-1 release was conserved across all primate TIM-1 orthologs, with monkey orthologs being modestly less potent. We also examined virion release of WT and ΔNef molecular clones for HIV-1, HIV-2, and SIVmac in the presence of primate TIM-1 orthologs, For all viruses, TIM-1 orthologs restricted ΔNef virion release with more potency relative to that of wildtype, indicating that TIM-1 restriction of virion release, as well as its antagonism by Nef, are evolutionarily conserved among primate lentiviruses. Further experiments showed that SIVmac Nef antagonism of TIM-1 is more efficient than that of HIV-1 Nef, suggesting that productive HIV-1 replication in humans can occur with less antagonism of TIM-1 by Nef. The interplay between TIM orthologs and primate lentivirus Nef proteins may play a role in driving HIV-host co-evolution and viral pathogenesis.
Keywords for abstract	HIV Restriction Factor Virus-Host TIM-1 Nef

Title of abstract	GENERATING VESICULAR STOMATITIS VIRUS RECOMBINANT VACCINE CANDIDATES FOR HUMAN RESPIRATORY SYNCYTIAL VIRUS
Authors	K. French-Kim, K. Brakel, S. Niewiesk Dept. of Veterinary Biosciences, The Ohio State University College of Veterinary Medicine
Abstract	Respiratory syncytial virus (RSV) causes significant respiratory disease leading to high morbidity and mortality in infants, the elderly, and immunosuppressed individuals. There are currently no licensed vaccines or antiviral therapeutics for RSV. In the present study, vesicular stomatitis virus (VSV) was used as a vector system to express various forms of RSV glycoproteins to generate vaccine candidates. The two glycoproteins are the target of neutralizing antibodies: the fusion protein (RSV-F) mediates fusion of the virus with a cell and the attachment protein (RSV-G) binds to the cellular receptor. It has been discussed whether antibody production might be limited by the amount of protein expressed as well as the shielding of the receptor-binding site on the G protein by O-linked glycans. In order to address these questions, we incorporated the codon optimized RSV-F and RSV-G gene, and a RSV-G gene with the deletion of 9 O-linked glycans near its receptor binding site (RSV-G- Δ -9O), into individual VSV vectors. Presently, the codon optimized F and G, and the G- Δ -9O genes have been incorporated into separate VSV plasmids. Plasmids for the viral genome will be transfected into BSRT7 cells to recover a recombinant VSV virus, followed by plaque purification and sequencing to confirm the presence of the genes. The virus will then be amplified and titered via plaque assay. Western blot will be used to determine protein expression, and flow cytometry will be used to determine protein quantity and level of expression on the cell surface. Lastly, the VSV recombinants will be tested in cotton rats for immunogenicity.
Keywords for abstract	Human respiratory syncytial virus Vesicular stomatitis virus recombinant vaccine Immunology

Title of abstract	USING MINIMUM INHIBITORY CONCENTRATION VALUES OF COMMON TOPICAL ANTIBIOTICS TO INVESTIGATE EMERGING ANTIBIOTIC RESISTANCE: A RETROSPECTIVE STUDY OF 134 DOGS AND 20 HORSES WITH ULCERATIVE KERATITIS
Authors	M. Jinks†, E. Miller†, D. Diaz-Campos†, D. Mollenkopf*, G. Newbold†, A. Gemensky-Metzler†, H.Chandler‡ †Department of Veterinary Clinical Sciences, The Ohio State University, Columbus, OH; *Department of Veterinary Preventative Medicine, The Ohio State University, Columbus, OH; ‡College of Optometry, The Ohio State University, Columbus, OH
Abstract	Objectives: To identify the minimum inhibitory concentration (MIC) distribution for commonly used topical antibiotics from isolates of dogs and horses with ulcerative bacterial keratitis, and to investigate changes in MIC values over time or following treatment with fluoroquinolones. Animals studied: 134 client owned dogs and 20 client owned horses with bacterial ulcerative keratitis. Procedure: MIC values for 14 antibiotics were reported for canine and equine cases of bacterial ulcerative keratitis between 2013-2018. Changes in MIC values over time and after treatment with topical fluoroquinolones were reported. Results: The three most common bacterial genera isolated from the site of infection were Staphylococcus, Streptococcus, and Pseudomonas. Together, these represented 79.4% of canine cases and 77.4% of equine cases. Overall, isolates from horses tended to have lower MIC values, as did Pseudomonas isolates from both dogs and horses, compared to other bacterial genera, especially Staphylococcus spp. The MIC values of erythromycin and trimethoprim sulfa for Staphylococcus spp., and the MIC value of moxifloxacin for Pseudomonas significantly increased over time. Previous fluoroquinolone use was associated with a significant increase in the MIC value of ofloxacin in Staphylococcus isolates and current fluoroquinolone use was associated with significant increases in the MIC values of ciprofloxacin, moxifloxacin and ofloxacin in canine Staphylococcus isolates. Conclusion: Patients previously or currently treated with topical fluoroquinolones, particularly in Staphylococcus infections, may require alternative antibiotics or additional antibiotic classes other than fluoroquinolones. Bacterial culture with MIC susceptibility testing should be highly recommended when a Staphylococcal infection is suspected.
Keywords for abstract	Fluoroquinolones MIC Antibiotic resistance Ulcerative keratitis

IMID - 9

Title of abstract	MECHANISMS OF INTERFERON GAMMA RESISTANCE OF EHRLICHIA CHAFFEENSIS
Authors	A. Johnson, O. Teymournejad, M. Lin, Y. Rikihisa
Abstract	Ehrlichia chaffeensis is a gram-negative obligatory intracellular bacteria that is transmitted to humans by the tick, Amblyomma americanum. It is the causative agent of human monocytic ehrlichiosis (HME), a severe and sometimes fatal disease. The broad-spectrum antibiotic doxycycline is currently the only available treatment. We know that <i>E. chaffeensis</i> uses the c-terminus of the ehrlichial surface protein EtpE to bind the host cell surface protein, DNaseX. This triggers bacterial entry and infection. It has been shown that interferon gamma (IFN-γ), a cytokine, added to monocytes at the early stage of infection inhibits E. chaffeensis infection, but after 24 hours IFN-γ has no anti-ehrlichial effect. Further confirmation that it is the binding of EtpE to DNase X that promotes host cell infection through immunosuppression could mark EtpE as an effective target for the development of more specific treatments or vaccines of Ehrlichial diseases. <i>E. Chaffeensis, Arkansas</i> organisms were used to challenge macrophages derived from the progenitor cells from the bone marrow (BMDMs) of either wild-type or DNase X knockout C57BL/6J mice and treated with IFN-γ. After treatment, the BMDMs were lysed, and the samples run on 10% SDS-Page followed by Western Blot to evaluate the presence of Stat-1 and Stat-3 which are downstream activators of transcription in the IFN-γ signaling pathway. Total Stat1 bands were detected in both DNase X KO and wild-typeBMDMs challenged with THP-1 lysate indicating no IFN-γ inhibition. Total Stat3 and Stat3-P bands were detected in both DNase X KO groups indicating DNase X has no influence on Stat3. Total Stat3 was detected in wild-type BMDMs challenged with THP-1 cells This study is ongoing with detecting Stat1-P in both wild-type and DNase X KO BMDMS challenged with <i>E. chaffeensis</i> .
Keywords for abstract	Ehrlichia Tick-borne Interferon Gamma

Title of abstract	PANETH CELLS REGULATE DIET-INDUCED OBESITY AND TRAFFICKING OF INFLAMMATORY IMMUNE CELLS INTO ADIPOSE TISSUES
Authors	M.R. Joldrichsen, E. Kim, E. Cormet-Boyaka, 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). The prevalence of obesity is growing in the general population and among recently diagnosed IBD patients, leading to the speculation that obesity increases IBD incidence, but the underlying mechanisms remain to be elucidated. We addressed whether Paneth cells of the small intestine play a role in the development of obesity. For this purpose, control wild-type C57BL/6 and Sox9 ^{ΔIEC} mice, which lack Paneth cells due to Sox9 gene deletion within the intestinal epithelium (Sox9 ^{ΔIEC} mice), were fed a high fat diet for 13 weeks. Though the consumption of food was similar between the 2 groups, weekly measurement of body weight showed that Sox9 ^{ΔIEC} mice gained weight much faster and ultimately became more obese than the wild-type mice. The Sox9 ^{ΔIEC} mice also developed larger abdominal fats, which included increased numbers of inflammatory macrophages (p<0.05), neutrophils (p<0.05). Interestingly, B cells were the most increased (p<0.01) immune cells population in white fat tissues of Sox9 ^{ΔIEC} mice. When compared to control mice, the Sox9 ^{ΔIEC} mice displayed impaired glucose tolerance (p<0.0001) indicating that these mice also developed a metabolic disorder. Finally, the <i>in vivo</i> FITC-dextran permeability assay showed that Sox9 ^{ΔIEC} mice on high-fat diet have increased intestinal permeability (p<0.05). These results suggest a new role for Paneth cells as regulators of diet-induced obesity via their impact on gut immune homeostasis and recruitment of immune cells into omental fat tissues.
Keywords for abstract	Paneth cell deficiency Gastrointestinal dysbiosis Diet-induced obesity

Title of abstract	ANTIBODY AND IMMUNOTOXIN COMBINATION THERAPY TARGETING HIV LYMPHOID RESERVOIR IN THE MURINE MODEL
Authors	S. Kim*, R. Shukla, L. Smith, S. Cressman, A. Kim. A. Tracey, N. Liyanage and S. Kim. Depts. Of Veterinary Biosciences and Microbial Infection and Immunity, The Ohio State University, Columbus OH
Abstract (300 word limit)	A highly potent and specific CD3e-immunotoxin (CD3e-IT) has been studied <i>in vivo</i> as a potential treatment for previous incurable disease, such as HIV/AIDS. Surprisingly, we found that CD3e-IT treatment is not efficient in depleting follicular helper T-cells (T _{FH}) – a major target of HIV/AIDS cure strategies – due likely to the protective effects of the lymphoid follicles where T _{FH} reside. Here, using a murine-version CD3e-IT developed in our lab, we demonstrate that pretreatment with CD40L monoclonal antibody (mAb) – which dissociates the B-cell follicular structure by blocking essential CD40-CD40L interactions – significantly improves CD3e-IT-mediated T-cell depletion in mice. The CD40L-mAb and CD3eIT combination treatment effectively ablated T _{FH} , in all organs tested, including spleen, multiple lymph nodes, Peyer's Patches and the peripheral blood. CD3e-IT monotherapy, by contrast, resulted in similar CXCR5+ T _{FH} enrichment we observed in our nonhuman primate studies. The CD40L-mAb and CD3e-IT combination treatment was well tolerated in mice; there was no notable organ damage, and body weight loss was similar to that associated with CD3e-IT monotherapy. This study demonstrates a novel means of ablating T _{FH} in vivo, which could prove useful in treating HIV/AIDS and T-cell malignancies
Keywords for abstract	CD3e-Immunotoxin (CD3e-IT) CD40L monoclonal antibody HIV lymphoid reservoir T follicular helper cells

Title of abstract	IDENTIFICATION OF NOVEL HTLV-1 ENV BINDING PARTNERS AND THEIR ROLE IN CELLULAR TRANSFORMATION TROPISM
Authors	E. M. King, A. R. Panfil, & P. L. Green
Abstract	Human T-cell leukemia virus type 1 (HTLV-1) is a deltaretrovirus infecting approximately 20 million people worldwide (Kazanji, 1996), causing adult T-cell leukemia/lymphoma (ATL) and HTLV-associated myelopathy/tropic spastic paraparesis (HAM/TSP) (Gonçalves et al., 2010). While less than 10% of infected individuals develop disease, the virus exhibits a clinical latency period of several decades (Yasunaga, 2007), making early viral detection an important component of disease prevention. While HTLV-2 exhibits similar genetic organization and expression patterns to HTLV-1, it has not been linked to disease (Ciminale et al., 2014). This may be attributed to the distinct transformation tropism of the viruses; HTLV-1 transforms CD4+ T lymphocytes, while HTLV-2 transforms CD8+ T lymphocytes. The genetic determinant of this transformation tropism and selective clonal expansion has been mapped to the viral envelope (Env-1/Env-2) (Kannian, 2012). We therefore hypothesize that differences in interaction between Env-1 and Env-2 and a cellular receptor/protein will induce unique downstream signaling events, leading to this distinct transformation tropism. In this study, we identified and characterized 19 Env-interacting proteins that may serve as both screening markers and therapeutic targets for HTLV-1.
Keywords for abstract	HTLV Retrovirus Transformation tropism Viral envelope

Title of abstract	VACCINATION OF SWINE TO REDUCE RISK OF ZOONOTIC INFLUENZA A VIRUS TRANSMISSION
Authors	J.N. Lorbach ¹ , S.W. Nelson ¹ , S.E. Lauterbach ¹ , J.M. Nolting ¹ , E. Kenah ² , D. McBride ¹ , C. Goodell ³ , and A.S. Bowman ¹ ¹ Department of Veterinary Preventive Medicine, ² Biostatistics, The Ohio State University; ³ Boerhinger Ingelheim Vetmedica, Inc.
Abstract	Strategies to reduce the public health threat posed by influenza A virus (IAV) in swine (IAV-S) at the swine-human interface include reducing the prevalence of IAV in swine at agricultural exhibitions. Multiple IAV vaccine products are available for use in swine, however no studies have examined the ability of pre-exhibition vaccination of swine to reduce risk of zoonotic IAV transmission. We vaccinated swine and assessed post-challenge virus shedding and transmission to ferrets serving as surrogates for humans exposed to infected swine.
	Groups of 5 pigs were vaccinated (live-attenuated influenza virus, LAIV; killed influenza virus, KV; sham vaccine, NV) prior to intranasal challenge with 1x10 ⁶ TCID ₅₀ H3N2 human-like (3.2010.1) IAV-S mismatched to the LAIV and KV vaccine strains. Six naïve ferrets were exposed to each swine group following IAV challenge (indirect contact, IC; simulated direct contact, DC). Detection and quantification of IAV in serial nasal and air samples were performed by rRT-PCR and TCID ₅₀ assay. Intergroup comparisons were used to assess impact of vaccine treatment group on shedding and infection parameters.
	Virus shedding was significantly lower in LAIV and KV swine (LAIV vs. naïve, p=0.0088; KV vs. naïve, p=0.0090). Peak shedding was reduced in LAIV (mean, 4.55 logTCID ₅₀ /mL) and KV swine (mean, 4.53 logTCID ₅₀ /mL) and occurred two days before peak shedding in naïve swine (mean, 6.40 logTCID ₅₀ /mL). LAIV and KV group study room air contained lower IAV levels compared to the naïve group. Time to infection was significantly delayed among LAIV ferrets (LAIV vs. naïve, p=0.028). Clinical sign duration and peak nasal shedding were lower in LAIV group ferrets (mean, 2.43 logTCID ₅₀ /mL) compared to KV (mean, 5.61 logTCID ₅₀ /mL) and naïve groups (mean, 5.53 logTCID ₅₀ /mL). These findings support the use of LAIV or KV in swine to mitigate risk of zoonotic IAV transmission at agricultural exhibitions.
Keywords for abstract	influenza vaccines prevention & control swine zoonoses transmission

Title of abstract	THE ROLE OF HBZ mRNA IN HTLV-1 PATHOBIOLOGY
	M. Martinez ^{1,2} , W. Dirksen ² , A. Panfil ^{1,2} , S. Bonifati ^{1,2} , and P. Green ^{1,2,3}
Authors	¹ Center for Retrovirus Research, ² Department of Veterinary Biosciences, and ³ Comprehensive Cancer Center, The Ohio State University, Columbus, OH, USA
Abstract	Human T-cell leukemia virus type 1 (HTLV-1) is the etiologic agent of adult T-cell leukemia/lymphoma (ATL) and the neurological disorder HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP). Treatment options for ATL and HAM/TSP are limited and both conditions carry a poor prognosis. For reasons unknown, only a small proportion of infected individuals will go on to develop one of the aforementioned HTLV-1 associated diseases. The HTLV-1 antisense transcript HTLV-1 bZIP factor (Hbz) protein is well documented as a regulator of <i>Tax</i> , the primary oncogenic transcript of HTLV-1, and is the only constitutively expressed HTLV-1 transcript in ATL cells. This constitutive expression suggests that <i>Hbz</i> plays a critical role in the development and maintenance of virus-induced leukemic cells. Hbz protein has been shown to be dispensable for immortalization in vitro, but is required for efficient HTLV-1 viral persistence in the New Zealand White (NZW) rabbit, an established model of HTLV-1 persistence. We have made the observation, through alterations in <i>Hbz</i> mRNA secondary structure, that <i>Hbz</i> mRNA alone can drive cellular proliferation in vitro. I hypothesize that <i>Hbz</i> mRNA contributes to the immortalization capacity of HTLV-1 in cell culture and viral persistence in vivo. To test this hypothesis several HTLV-1 proviral clones will be created that generate <i>Hbz</i> mRNA with intact or altered <i>Hbz</i> mRNA secondary structure in the presence or absence of Hbz protein. Each clone will be assessed for in vitro immortalization capacity and in vivo persistence using the NZW rabbit model. The ultimate goal of this research is to dissect the mechanisms by which <i>Hbz</i> mRNA and protein contribute to HTLV-1 pathobiology.
Keywords for abstract	HTLV-1 Hbz mRNA ATL

Title of abstract	INHIBITION OF EHRLICHIA CHAFFEENSIS INFECTION BY INTRACELLULAR NANOBODY TARGETING A REQUIRED TYPE IV SECRETION EFFECTOR
Authors	Mestres-Villanueva, M., Lin, M., and Rikihisa, Y.
Abstract	Ehrlichia chaffeensis (Ech) is the causative agent of Human Monocytic Ehrlichiosis (HME), a severe, influenza-like illness. The preferred treatment available is the broad-spectrum antibiotic Doxycycline (Dox), which must be given early to avoid severe, late-stage illness or death. There is no vaccine available to prevent ehrlichiosis. Ech produces unique proteins that allow for the avoidance of host immune responses, replication, and spread of infection. These proteins include Ehrlichia translocated factor 2 (Etf-2). Single-domain antibodies, which lack a light chain, are naturally produced by Camelids. Nanobodies are the variable antigen-binding component of these peculiar antibodies. Nanobodies are proteolytically stable and of a small molecular weight, allowing for their use in an intracellular environment and for binding with epitopes that a conventional antibody could not access. The first aim is to test if mammalian expression plasmids encoding Etf-2-binding nanobodies delivered into human cells by transfection can express nanobodies and effectively block Ech infection in culture. The plasmid iAb-47 encodes for a nanobody against human heterogeneous nuclear ribonucleoprotein K (hnRNP-K) that is known to block Ech infection and is used as a positive control. A plasmid encoding an unrelated nanobody is used as negative control. A total of 10 plasmids encoding Etf-2-binding nanobodies have been purified and chemical transfection of 3 plasmids showed significant intracellular nanobody protein expression by Western Blot (WB) analysis. No significant toxic effects were detected. After evaluating expression by WB, quantitative reverse transcription polymerase chain reaction (qRT-PCR) will be carried out to quantitate the Etf-2-binding nanobodies' ability to inhibit Ech infection. Based on this data, the best candidate will be recloned for E. coli expression and purification. The generation of inhibitory nanobodies, such as the one in development, will lead to the development of a specific treatment against HME.
Keywords for abstract	Ehrlichia Obligatory intracellular bacteria Nanobody
	Type IV Secretion System

Title of abstract	INHIBITION OF OXIDATIVE PHOSPHORYLATION BUT NOT GLYCOLYSIS ATTENUATES LUNG INJURY CAUSED BY H1N1 INFLUENZA A VIRUS INFECTION
Authors	K. Nolan, L. Baer, A. Nelson, K. Stanford, L. Doolittle, L. Rosas, J. Hickman-Davis and I. Davis
Abstract	Despite availability of vaccines and antiviral drugs, seasonal influenza A virus (IAV) epidemics cause >300,000 deaths/year worldwide. IAV infection alters lung epithelial cell metabolism. This promotes a shift towards glycolysis and away from oxidative phosphorylation (OXPHOS) for ATP production. We hypothesized that this shift benefits the virus rather than the host and that inhibition of glycolysis would improve infection outcomes. C57BL/6 mice (n=5-6/group) were intranasally inoculated with mouse influenza A/WSN/33 (H1N1). To inhibit glycolysis, mice were treated daily from 1 day post-infection (dpi) with 1g/kg 2-deoxy-D-glucose (2-DG). To block OXPHOS, mice were injected every other day from 1 dpi with 0.8 mg/kg rotenone (ROT). Carotid arterial oxygen saturation (SaO2) was measured using the MouseOx system at 2, 4 and 6 days post inoculation (d.p.i). Open circuit calorimetry and measurement of mouse activity were performed simultaneously using the Oxymax/CLAMS metabolic chambers from 5-6 d.p.i. On day 6, mice were euthanized and lungs harvested. Viral replication was quantified by TCID50. Whole lung wet:dry weight ratios were calculated as an index of intrapulmonary fluid accumulation. Relative to controls, IAV infection induced severe hypoxemia and pulmonary edema at 6 dpi. There was a significant decline in nocturnal activity and a decrease in the respiratory exchange ratio (RER), indicating a shift towards increased lipid catabolism for ATP generation. Treatment of IAV-infected mice with 2-DG and ROT did not alter lung IAV titers; however, 2-DG significantly worsened IAV-induced hypoxemia and further decreased nocturnal activity. In contrast, ROT treatment restored SaO2 to normal levels, normalized RER, and significantly attenuated IAV-induced pulmonary edema. OXPHOS blockade with ROT improves outcomes in IAV-infected mice while glycolysis may be protective in influenza and suggests that OXPHOS may be a therapeutic target in this disease.
Keywords for abstract	Influenza A virus Alveolar type II epithelial cells Mitochondrial dysfunction Oxidative phosphorylation Glycolysis

Title of abstract	INACTIVATED INFLUENZA VIRUS AND POLY (I:C) ADSORBED CORN BASED NANOVACCINE ELICITED CELL MEDIATED IMMUNE RESPONSE IN MATERNAL ANTIBODY POSTIVE NURSERY PIGS
Authors	V Patil ¹ , S Renu ¹ , N Feliciano-Ruiz ¹ , Y Han ¹ , J Schrock ¹ , A Ramesh ¹ , Renukaradhya GJ ¹ . ¹ Food Animal Health Research Program, The Ohio State University, Wooster, OH, USA
Abstract	There is a need to develop an effective killed vaccine against Swine Influenza A virus (SwIAV) infection in pigs. Maternal antibody interference to commercial injectable SwIAV vaccination in grower pigs is a problem. We designed and tested the response of intranasally administered killed/inactivated H1N2 SwIAV antigen (KAg) loaded Nano-11 (Nano-11-KAg) delivered with Poly (I:C) against a heterologous H1N1 SwIAV challenge and compared to a commercial KAg vaccine.
	In tracheobronchial lymph node (TBLN) cells of pigs restimulated with a H1N2 SwlAV observed an increased frequency of cytotoxic lymphocytes (CTLs) and T-helper/Memory cells in Nano-11-KAg+ Poly(I:C) vaccinates compared to commercial vaccine; and Nano-11-KAg+ Poly(I:C) also increased the frequency of T-helper cells compared to Nano-11-KAg vaccinates. There was an increased frequency of IFN- γ^+ CTLs, T-helper/memory cells and T-helper cells in Nano-11-KAg+Poly(I:C) group. However, there was a decrease in the frequency of IL-17A+ CTLs and T-helper cells in Nano-11-KAg+Poly(I:C) group, while there was an increased frequency of IL-17A+, TNF α^+ and TNF α^+ IFNY+T-helper/memory cells were detected in that group. Furthermore, there was an increase in central memory and effector memory T-helper/memory cell frequencies in Nano-11-KAg+Poly(I:C) group; and the frequencies of effector memory T-helper cells were reduced while TNF α^+ and TNF α^+ IFN- γ^+ T-helper cell frequencies were enhanced. Similar effects were observed in case of H1N1 SwIAV restimulated TBLN cells.
	In H1N2 SwIAV restimulated peripheral blood mononuclear cells (PBMCs) of pigs receiving Nano-11-KAg+Poly (I:C) there was an increased T-helper cell frequency and TNF α ⁺ CTLs. In H1N1 SwIAV restimulated PBMCs, Nano-11-KAg+Poly (I:C) increased the T-helper cells, IFN- γ ⁺ CTLs, IL-17A ⁺ T-helper/memory cells. Overall, adjuvant Poly (I:C) enhanced the antigen-specific cell mediated immune response of intranasally co-delivered Nano-11-KAg vaccine (but not commercial SwIAV vaccine) at both mucosal and systemic sites of maternal antibody positive pigs.
Keywords for abstract	Nanovaccine maternal antibody inactivated SwIAV antigen

Title of abstract	INTRANASAL DELIVERABLE MANNOSE SURFACE CONJUGATED CHITOSAN-BASED INFLUENZA NANOVACCINE FOR NURSERY PIGS
Authors	S. Renu, N. Feliciano-Ruiz, A. Ramesh, V. Patil, Y. Han, J. Schrock, and G.J. Renukaradhya. Food Animal Health Research Program and Department of Veterinary Preventive Medicine
Abstract	Virulent swine influenza A virus (SwIAV) infection causes acute febrile respiratory disease in pigs of all ages. The triple reassortant 2009 pandemic SwIAV-H1N1 spillover to humans is evidence that pig can act as a mixing vessel for mammalian and avian influenza viruses. The commercial inactivated SwIAV vaccine is a multivalent formulation administered by intramuscular (IM) injection. It induces systemic IgG with poor induction of mucosal secretory IgA (SIgA) antibody response. The SIgA antibody is important because SwIAV enters the body through airways and replicates primarily in the respiratory tract epithelial cells. Therefore, intranasal (IN) vaccination is the ideal approach to mimic the natural virus infection-induced mucosal immunity. However, IN delivered antigens are poorly immunogenic, and they need a suitable adjuvant and vaccine delivery system to trigger mucosal immune response. Thus, we conjugated a ligand mannose on natural mucoadhesive chitosan nanoparticles (CS NPs), which helps in recognizing and uptake of particle antigens by dendritic cells. IN delivery of killed/inactivated SwIAV antigen (KAg) loaded mannose-conjugated CS NPs (mCS NPs-KAg) in pigs was shown to be internalized by mucosal immune cells in nasal turbinate and lymph nodes germinal center compared to unmodified CS NPs. Similarly, <i>in vitro</i> treated pig immune cells with mCS NPs-KAg was found internalized. Maternally derived antibodies carrying nursery pigs vaccinated IN with mCS NPs-KAg induced significantly increased SIgA antibodies and reduced heterologous challenge virus load in the nasal passage and lung airways compared to commercial vaccine. In conclusion, mannose modified influenza nanovaccine delivered IN in pig targets immune cells in the airways and elicits antibody response which mediates cross-protection.
Keywords for abstract	Swine influenza virus Mannose Chitosan nanoparticle Intranasal delivery Pigs Secretory antibody

Title of abstract	INVESTIGATING INTRANASAL VACCINATION STRATEGIES TO IMPROVE PROTECTION AGAINST RESPIRATORY PATHOGENS
Authors	J. C. Rowe, R. M. Woodfint, 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, safety issues were reported after intranasal immunization with vaccine adjuvants that can be retrograde transported into the brain or those which induce strong inflammatory responses in the nasal cavity. Alum is a safe and widely used injectable adjuvant. The mechanisms underlying the adjuvant activity of Alum are believed to include stimulation of NLRP3 inflammasome and recruitment of neutrophils. Previous studies in our lab have shown that recruitment of neutrophils in sublingual tissues and cervical lymph nodes of mice immunized sublingually 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 containing Alum as adjuvant. Utilizing a bivalent vaccine model containing an inactivated H1N1 influenza A virus and protective antigen (PA) of <i>Bacillus anthracis</i> , we tested the adjuvant effect of a low dose of alum (20 µg) in the presence and absence of a neutrophil elastase inhibitor. Preliminary results center on systemic serum and mucosal surface antibody 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 or influenza.
Keywords for abstract	Mucosal Vaccination Intranasal IgA Neutrophil

	ADAPTIVE CHANGES IN VIRAL ENVELOPE RESULTING
Title of abstract	FROM ADAPTATION OF SIMIAN-TROPIC HIV-1 TO
	MACAQUES CONFERS RESISTANCE TO INTERFERON
Authors	A. C. Smith ¹ , H. Weight ² , J. Overbaugh ² , and A. Sharma ¹ . ¹ Depts of Veterinary Biosciences and Microbial Infection & Immunity. ² Divison of Human Biology, Fred Hutchinson Cancer Research Center.
Abstract	HIV-1 does not persistently infect macaques due to restriction by several type-I interferon (IFN)-induced host-factors. Therefore, chimeric SIV/HIV-1 viruses (SHIVs) encoding the SIV antagonists of restrictive host-factors and HIV-1 Envelope glycoprotein (Env), are used to infect macaques to model HIV-1 infection. A major limitation of the SHIV/macaque model is that SHIVs generated <i>in vitro</i> replicate poorly in macaques. A small subset of SHIVs has been successfully adapted for high-level replication through serial passage in macaques. We have previously identified that serial macaque-passage selects for IFN-resistant SHIV variants that have higher replication in macaque lymphocytes. The viral determinant(s) contributing to increased replication and IFN resistance in macaque-passaged SHIVs have not been examined.
	In order to identify the viral determinant(s) of macaque-passaged SHIVs that confer resistance to IFN, we generated SHIV infectious molecular clones (IMCs) encoding the parental <i>env</i> and representative <i>env</i> clones from sequential macaque-passaged viruses. We found that the unpassaged, parental SHIV IMC is potently inhibited by IFN (mean IC50 range 1.9 to 54.6 U/ml), whereas the SHIV IMCs encoding macaque-passaged <i>envs</i> are resistant to IFN inhibition (mean IC50 >5000 U/ml). In addition, we found that SHIV IMCs encoding macaque-passaged <i>envs</i> have high replication capacity and most, but not all, have more virion Env content. Next, we took a gain-of-function approach and generated chimeras that introduce portions of <i>env</i> gene from IFN-resistant SHIV IMC into the parental IFN-sensitive SHIV IMC. Using this approach, we mapped the determinant of IFN resistance and high replication capacity to the gp120 subunit of HIV-1 Env.
	In conclusion, the adaptive changes in HIV-1 <i>env</i> resulting from serial macaque-passage of SHIVs are sufficient to increase resistance to IFN, replication capacity, and virion Env content. Thus, the host IFN response serves as a strong selective pressure during the process of adaption of SHIV to macaques.
Keywords for abstract	HIV-1 SHIV IFN

Title of abstract	BROAD-SPECTRUM AND GRAM NEGATIVE-TARGETING ANTIBIOTICS DIFFERENTIALLY REGULATE IMMUNE RESPONSE TO NON-ADJUVANTED VACCINE ANTIGENS
Authors	R. M. Woodfint, A. Haile, M. R. Joldrichsen, and P. N. Boyaka
Abstract	Commensal microbes are increasingly recognized as playing a vital role in human health including immune responses. Antibiotics are widely used to limit the growth of microbial pathogens. However, oral antibiotic treatments also alter the gut microbiome. We address whether antibiotic-induced dysbiosis effects host responses to injected vaccines. For this purpose, antibiotics targeting grambacteria (neomycin), or a broad-spectrum antibiotic cocktail (neomycin, vancomycin, metronidazole, and penicillin) were orally administered to groups of mice. Mice were then immunized, via the intraperitoneal route, with non-adjuvanted mixture of vaccine antigens [i.e., protective antigen (PA) of Bacillus anthracis, the B subunit of <i>vibrio cholera</i> toxin B (CTB), and ovalbumin (OVA)], and antibody responses assessed in the serum, mucosal secretions (fecal extracts) and mucosal tissues (intestinal lamina propria). Our results show that gram-negative-targeting antibiotic and broadspectrum antibiotics differentially affect antigen-specific serum IgG and IgA responses. Interestingly, mucosal IgA responses were induced in gut tissues and intestinal contents (fecal extract) of mice that received a specific oral antibiotic treatment. In summary, our study suggests that antibiotic treatment should be a considered parameter when designing vaccine formulations or vaccination schedules.
Keywords for abstract	Vaccine Antibiotics Immunology

Title of abstract	RNA INTERNAL Nº-METHYLADENOSINE MODIFICATION MODULATES INNATE AND ADAPTIVE IMMUNE RESPONSES TO VIRUS INFECTION
Authors	M. Xue1, M. Lu1, A. Li1, Z. Zhang2, P. Boyaka1, S. Niewiesk1, C. He2, J. Li1* 1Department of Veterinary Biosciences, College of Veterinary Medicine; The Ohio State University, Columbus, OH, 43210, USA 2Department of Chemistry, Department of Biochemistry and Molecular Biology, and Institute for Biophysical Dynamics, The University of Chicago, Chicago, IL 60637, USA;
Abstract	Internal N6-methyladenosine (m6A) modification is one of the most prevalent and abundant modifications of RNA. The m6A methylation is catalyzed by host methyltransferases (METTL3 and METTL14) and can be reversibly removed by host demethylases (FTO and ALKBH5). Recent studies have revealed that RNA of many DNA and RNA viruses contains m6A methylation and that viral m6A can play a pro-viral or anti-viral role. However, the biological functions of viral RNA m6A methylation remain poorly understood. In this study, we found that genome and antigenome of human respiratory syncytial virus (RSV), a non-segmented negative-sense (NNS) RNA virus, are m6A methylated and that viral m6A methylation positively regulates RSV replication and gene expression. Interestingly, virion RNAs purified from RSV grown in METTL3-knockout cells induced significantly higher type I interferon responses than virion RNAs purified from RSV grown in wild type cells, demonstrating that viral RNA m6A methylation inhibits innate immunity. Similarly, inactivation of m6A methylation in RSV genome and/or antigenome by site-directed mutagenesis induced significantly higher innate immune responses than wild type RSV RNA. Mechanistically, these m6A-unmodified or m6A-deficient RSV RNAs trigger a higher expression of pattern recognition receptors (such as RIG-I and MDA5), enhance their binding affinity to the innate immune RNA sensors, facilitate the RIG-I conformational changes, and enhance the phosphorylation of downstream transcription factor IRF3, leading to an enhanced activation of type I interferon signaling pathway. We further demonstrated that this novel function of viral RNA m6A methylation is universally conserved in other NNS RNA viruses such as human metapneumovirus, Sendai virus, measles virus, and vesicular stomatitis virus. Importantly, these m6A-deficient recombinant RSVs also induced significantly higher antibody and T cell immunity compared to the parental virus, and provided complete protection against RSV infection. Taken together, our
Keywords for abstract	N ⁶ -methyladenosine (m6A) Respiratory syncytial virus (RSV) Innate and adaptive immunity

IMID - 23

Title of abstract	SERINC PROTEINS POTENTIATE ANTIVIRAL TYPE I IFN INDUCTION AND PROINFLAMMATORY SIGNALING PATHWAYS
Authors	C. Zeng ^{1,2} , A Waheed ³ , T. Li ⁴ , J. Yu ^{1,2} , Y. Zheng ^{1,2} , J. Yount ⁴ , H. Wen ⁴ , E. Freed ³ , S. Liu ^{1,2,4,5} ¹Center for Retrovirus Research, The Ohio State University, Columbus, OH, ²Department of Veterinary Biosciences, The Ohio State University, Columbus, OH, ³Virus-Cell Interaction Section, HIV Dynamics and Replication Program, National Cancer Institute-Frederick, Frederick, MD, ⁴Department of Microbial Infection and Immunity, The Ohio State University, Columbus, OH, ⁵Viruses and Emerging Pathogens Program, Infectious Diseases Institute, The Ohio State University, Columbus, OH
Abstract	SERINC proteins are recently identified human immunodeficiency virus (HIV) restriction factors that diminish viral infectivity by incorporating into virions. Here we provide evidence that SERINC3 and SERINC5 enhance the type I interferon and NF-kB signaling pathways, thus exhibiting additional antiviral activities. Mechanistically, we find that SERINC5 interacts with the mitochondrial antiviral-signaling protein (MAVS) and promotes MAVS aggregation. Upon stimulation by Sendai virus, SERINC5 is recruited to mitochondria, become oligomerized, and co-localizes with MAVS. SERINC5 also interacts with and stabilizes TNF receptor associated factor 6 (TRAF6), likely by suppressing a K48-linked but increasing a K63-linked polyubiquitination. Notably, knockdown of SERINC5 in PMA-treated THP-1 cells, as well as human primary monocyte-derived macrophages (MDMs), increased the single-round HIV-1 infection, suggesting that SERINC5 has direct antiviral effects against HIV-1. While knockdown of SERINC5 in mouse embryonic fibroblasts (MEFs) enhances infection by recombinant vesicular stomatitis virus (rVSV) bearing VSV-G or Ebola virus (EBOV) glycoprotein (GP), as well as by the prototype and endemic Zika virus (ZIKV) strains, depletion of SERINC5 in STAT1-deficient MEFs fails to further boost viral infection, suggesting that the antiviral activity executed by SERINC5 is type I IFN dependent. Altogether, our work uncover a new function of SERINC proteins that promotes the type I IFN and NF-kB inflammatory signaling, thus contributing to the antiviral activities.
Keywords for abstract	SERINC NF-kB type I IFN TRAF6 MAVS

MOLECULAR AND CELLULAR BIOLOGY

Title of abstract	CHARACTERIZING PTEN EXPRESSION IN CANINE OSTEOSARCOMA CELL LINES
Authors	K. Bick, J. M. Fenger
Abstract	Osteosarcoma (OS) is the most common malignant bone tumor in dogs & adolescents. Despite treatment, 30-40% of children & 90% of dogs die due to metastatic disease. Genomic analyses of canine & human OS revealed aberrations of the PI3K/mTOR pathway in approximately 70% of OS. PTEN is a tumor suppressor that negatively regulates signaling through the PI3K/AKT/mTOR pathway — its loss is thought to be involved in metastatic lung colonization. The goal of this study was to characterize PTEN expression in canine OS cell lines & primary tumors & assess the consequence of PTEN loss on the AKT/mTOR pathway. We hypothesize that loss of PTEN is a common event in canine OS cell lines & tumors & that PTEN knockdown will result in activation of downstream AKT/mTOR signaling, thereby enhancing OS cell growth. PTEN mRNA & protein expression was assessed in canine osteoblasts (Ob; Cell Applications, Inc.), OS cell lines (Kerafast Inc.; ATCC) & primary OS tumors by qRT-PCR & Western blotting. PTEN mRNA & protein levels were reduced in 65% of cell lines & the majority of primary tumors compared to normal Obs. Cell lines deficient in PTEN exhibited increased phospho-AKT independent of serum-starved media conditions. To assess the consequences of PTEN loss on AKT/mTOR signaling & cell growth, lentiviral shRNA constructs targeting PTEN were generated — studies are ongoing to assess the impact of PTEN knockdown. These data demonstrate that PTEN expression is frequently reduced in OS cell lines & tumors & suggest that loss of PTEN is associated with enhanced activation of AKT signaling. With a lack of clinically active agents in OS, inhibition of PI3K/AKT/mTOR represents a potential therapeutic vulnerability that warrants further investigation.
Keywords for abstract	Osteosarcoma PTEN

Title of abstract	THE SELECTIVE INHIBITOR OF NUCLEAR EXPORT VERDINEXOR EXHIBITS BIOLOGICAL ACTIVITY AGAINST CANINE OSTEOSARCOMA CELL LINES
Authors	J. T. Breitbach, D. S. Louke, M. R. Watts, S. J. Tobin, A. E. Davies, J. M. Fenger. Departments of Veterinary Biosciences and Veterinary Clinical Sciences
Abstract	Osteosarcoma (OS) is the most common malignant bone tumor in dogs. Despite aggressive surgical management and systemic chemotherapy, 90% of dogs still die due to chemotherapeutic-resistant metastatic disease. As chemotherapy remains the backbone for treatment of OS metastases, the development of combinational treatments with novel targeted molecular therapeutics and conventional chemotherapy represents a potential strategy to enhance therapeutic response. Exportin 1 (XPO1, also known as CRM1) is a chaperone protein responsible for the export of >200 target proteins out of the nucleus. Dysregulation of XPO1 activity is documented in a number of human cancers and XPO1 expression has been associated with the development of chemotherapy resistance. Prior studies in canine melanoma and mammary carcinoma cell lines have demonstrated that XPO1 is a relevant target for therapeutic intervention and recent phase I and II clinical trials evaluating a novel, orally bioavailable Selective Inhibitor of Nuclear Export (SINE) Verdinexor in dogs with spontaneous cancer demonstrate anti-tumor activity against non-Hodgkin lymphoma. In the present study, we sought to characterize the expression of XPO1 in primary canine OS tumor samples, OS cell lines and normal osteoblasts and evaluate the <i>in vitro</i> efficacy of Verdinexor alone or in combination with doxorubicin in canine OS cell lines. Real time PCR and Western blotting was performed to assess XPO1 transcript and protein expression in normal canine osteoblast cells, canine OS cell lines and primary OS tumors had increased expression of XPO1 mRNA and protein compared to normal canine osteoblasts. All canine OS cell lines exhibited dose-dependent growth inhibition and increased caspase 3,7 activity in response to low nanomolar concentrations of Verdinexor (ICS0 concentrations ranging from 21-74 nM). Notably, growth inhibition of normal canine osteoblast cell lines treated with Verdinexor was only observed at high micromolar concentrations (ICS0 = 21 μM). The combination of Verdi
Keywords for abstract	Dog Cancer Doxorubicin Osteosarcoma XPO1 Verdinexor

Title of abstract	INFLUENZA A VIRUS EFFECT ON ALVEOLAR FLUID CLEARANCE AND CDP-CHOLINE AS POTENTIAL TREATMENT FOR ARDS IN MICE.
Authors	El Musa H, Davis IC, Rosas L, Nelson A, Doolittle LM, Joseph L Department of Veterinary Biosciences, College of Veterinary Medicine, The Ohio state University, Columbus, OH.
Abstract	The bronchoalveolar epithelium clears excess fluid by an active, ATP-dependent Na ⁺ transport process, which can be measured across the whole lung as alveolar fluid clearance (AFC). Maintenance of AFC is important to alveolar gas exchange. Impaired AFC has been shown to correlate with worse outcomes in patients who develop Acute Respiratory Distress Syndrome (ARDS). We have shown that ARDS development in mice infected with influenza A virus (IAV) is associated with impaired AFC. IAV infection also reduces mitochondrial function in alveolar type II (ATII) cells and inhibits synthesis of the liponucleotide CDP-choline (CDP-CHO), which is a precursor for the phospholipid phosphatidylcholine. We have shown that treatment of IAV-infected mice with CDP-CHO significantly attenuates IAV-induced hypoxemia and improves mitochondrial function in ATII cells. Since AFC is highly dependent on ATP, and mitochondrial function is dependent on normal phospholipid metabolism, we hypothesized that IAV-infected mice treated with CDP-CHO will have increased AFC when compared to untreated infected mice. To test this hypothesis, we mock-infected or infected C57BL/6 mice intranasally with 10,000 pfu/mouse influenza A/WSN/33. At 6 days post-infection (dpi), mice were anesthetized and intubated to measure AFC. 300μL of 5% BSA/saline solution was instilled into the lungs via the tracheal cannula, followed by 200μL of air. Mice were then mechanically ventilated on 100% O ₂ for 30 minutes, with a tidal volume of 0.2 ml and 18cmH ₂ O PEEP. Following ventilation, fluid was aspirated back from the lungs. Protein concentration was quantified with a BCA assay. AFC rate was calculated from the ratio of initial (instillate) to final protein concentration.
Keywords for abstract	Influenza A Virus Acute Respiratory Distress Syndrome

Title of abstract	EVALUATING THE ROLE OF INTERFERON STIMULATED GENE CMPK2 IN RESTRICTION OF PRIMATE LENTIVIRUSES
Authors	J. Garcia, A. Sharma
Abstract	Macaque model systems are critical for preclinical studies of Human Immunodeficiency Virus-1 (HIV-1). However, HIV-1 does not persistently infect macaques due to several restrictions by macaque-specific host factors. Chimeric Simian Immunodeficiency Virus (SIV)/HIV-1 viruses (SHIVs) are used as challenge viruses to infect macaques to model HIV-1 infection. The host interferon (IFN) response is the first line of defense against viral infections. IFN upregulates IFN-stimulated genes (ISGs), which encode proteins that block viral replication. In our recent study, we performed RNA-Seq in macaque lymphocytes and identified Cytidine MonoPhosphate Kinase 2 (CMPK2) as the highest upregulated (~900 fold) ISG. The potential of CMPK2 to restrict lentiviral replication is yet-to-be explored. Comparative analysis shows CMPK2 is conserved in most vertebrate animals, excluding non-jawed species, and is 97% similar in humans and macaques. The specific aim of this study is to evaluate the contribution of CMPK2 in restriction of HIV-1 and SHIVs. To this end, CRISPR sgRNA guides were created to knockout human and macaque CMPK2. CRISPR ribonucleoproteins were assembled using the recombinant Cas9 and sgRNA guides, which were electroporated into the cells. Ongoing experiments are verifying the extent of knockout and their functional relevance in inhibiting HIV-1/SHIVs. If CMPK2 contributes to the IFN-induced inhibition of HIV-1 or SHIVs, then CMPK2 knockout will result in recovery of viral replication to levels observed in non-IFN treated cells. Accomplishment of these goals may help improve the SHIV/macaque models by rationally designing SHIVs to avoid key macaque restriction factors such as CMPK2.
Keywords for abstract	Human Immunodeficiency Virus-1 Simian Immunodeficiency Virus (SIV)/HIV-1 Viruses (SHIVs) CRISPR-Cas9 Interferon Response Cytidine MonoPhosphate Kinase 2 (CMPK2)

Title of abstract	RECEPTOR TYROSINE KINASE DYSREGULATION AND BIOLOGICAL ACTIVITY OF TOCERANIB AND CANINE UROTHELIAL CARCINOMA CELL LINES
Authors	D. Korec, D.S. Louke, J. M. Fenger, Department of Veterinary Clinical Sciences
Abstract	Transition cell carcinoma (TCC) accounts for >90% of canine malignant tumors occurring in the urinary bladder with few available effective therapies. Toceranib phosphate (Palladia) is a multi-target receptor tyrosine kinase (RTK) inhibitor that exhibits potent activity against members of the split kinase family of RTKs, including vascular endothelial growth factor receptor, platelet-derived growth factor receptor, Kit, and Flt-3, resulting in both direct antitumor and antiangiogenic activity. The purpose of this study was to evaluate normal canine bladder tissues, primary bladder TCC tumors, and established TCC cell lines for the expression and activation of VEGFR1, VEGFR2, PDGFRα, PDGFRβ, and KIT to assess whether dysregulation of these RTKs may contribute to the biological activity of TOC. Real Time PCR was performed on primary TCC tissue samples (N=10) and TCC cell lines (N=5) to detect VEGFR2, PDGFRα, PDGFRβ, and KIT mRNA. Transcript for VEGFR2, PDGFRα, and PDGFRβ was detected in all TCC tissue samples and TCC cell lines; however, mRNA for KIT was not detectable in any samples. The Proteome Profiler TM Human Phospho-RTK Array Kit (R & D Systems) was used to assess phosphorylation of 42 different RTKs in primary TCC tissue specimens using the available flash frozen tumor specimens and TCC cell lines. PDGFRα and PDGFRβ were found to be phosphorylated in all tumor samples and cell lines but KIT activation was not observed on the arrays. While mRNA for VEGFR2 was identified in all tumor samples and cell lines all samples exhibited low phosphorylation levels of this RTK. Studies are ongoing to evaluate the <i>in vitro</i> activity of TOC on cell viability, apoptosis, and VEGFR, PDGFRα, and PDGFRβ phosphorylation in TCC cell lines. Our findings demonstrate that known targets of TOC are expressed/activated in primary TCC tumors and TCC cell lines and merit further investigation.
Keywords for abstract	Canine Urogenital Carcinoma Receptor Tyrosine Kinase Toceranib

	INTERROGATING THE ROLE OF WWOX IN CANINE MAST
Title of abstract	CELL TUMORS & CELL LINE
	R. Makii, H. Cook, D. Louke, J. M. Fenger
	TX. Wakii, TI. Gook, D. Louke, G. W. Tenger
Authors	Department of Veterinary Clinical Sciences, College of Veterinary
	Medicine, The Ohio State University
Abstract	Mast cell tumors (MCT) are the most common skin tumor in dogs with behavior varying from benign to aggressive, metastatic disease. While cKIT mutations are present in 30% of high grade MCTs, the genetic alterations driving tumorigenesis in the 70% of MCTs that do not possess cKIT mutations remains unclear. The WW domain-containing oxidoreductase (WWOX) tumor suppressor is frequently lost in cancer and plays a role in regulating DNA damage repair (DDR). The overarching hypothesis of this study is that loss of WWOX impairs DNA damage response and repair pathways, thereby contributing to genomic instability in MCs. qRTPCR and Western blotting showed that WWOX is decreased in MC lines and primary MCTs compared to bone marrow-cultured MCs, suggesting that loss of WWOX is a frequent event in this disease. To better define the functional consequences of WWOX loss on MC behavior, BR cells were transduced with empty vector or WWOX and C2 cells expressing scramble control or shRNAs targeting WWOX were treated with ionizing radiation and cell survival/viability was assessed by MTT & clonogenicity assays. Overexpression of
	WWOX in the BR MC line did not alter DDR or cell viability, however, further decreasing expression of WWOX in the C2 MC line conferred a survival advantage post-irradiation. These findings provide insight
	into the functions of WWOX in MCs with the ultimate goal of
	identifying novel targets for therapeutic intervention.
Keywords for abstract	Mast cell tumors WWOX Cancer Mast cells

Title of abstract	THE MOLECULAR DETERMINANT OF HTLV TRANSFORMATION TROPISM
Authors	V.V. Maksimova, E.M. King, P.L. Green, and A.R. Panfil
Abstract	Human T-cell leukemia virus type 1 (HTLV-1) is the only oncogenic human retrovirus and is the causative infectious agent of both adult T-cell leukemia/lymphoma (ATL), an aggressive and fatal CD4+ T-cell malignancy, and chronic neurological disease. HTLV-2 is closely related to HTLV-1 in its genomic features and capacity to transform T-cells but is non-pathogenic. <i>In vitro</i> , HTLV-1 transforms CD4+ T-cells while HTLV-2 transforms CD8+ T-cells. These observations are clinically relevant as both ATL and neurological disorders caused by HTLV-1 are CD4+ T-cell-dependent. However, the molecular mechanism(s) underlying preferential transformation of CD4+ T-cells and HTLV-1-mediated disease development remain unknown. The genetic determinant for the divergent transformation tropism of HTLV-1/2 has been mapped to the viral envelope (Env). During early infection <i>in vivo</i> , HTLV-1 and -2 proviruses can be detected in both CD4+ and CD8+ T-cells. Further, <i>in vitro</i> studies have shown that early proliferation of both T-cell types occurs during infection with either virus, and the preferred transformation target emerges during selective clonal expansion over time. These data suggest that postentry mechanisms are responsible for the distinct pathogenesis of these viruses and have led us to hypothesize that HTLV-1 Env (Env-1) interacts with a cellular signaling pathway in certain cell environments and modulates downstream signaling events, which drive HTLV-1-mediated CD4+ T-cell transformation tropism. In this study, we created chimeric mutants of HTLV-1/2 to test the contribution of Env surface or transmembrane domains on transformation tropism <i>in vitro</i> . Treatment with the integrase inhibitor Raltegravir was used to determine whether transformation preference is due to initial infection or continual re-infection of cells. Our study will define new roles for Env beyond initial viral entry and evaluate the cellular factors that participate in the differential transformation processes of HTLV-1/2, thus improving our understand
Keywords for abstract	HTLV Envelope Transformation CD4+ T-cell

Title of abstract	INVESTIGATING LORIKEET ENTERITIS: IS CLOSTRIDIUM PERFRINGENS THE CULPRIT?
Authors	D. Minich, C. Madden, G. A. Ballash, R. Junge, V. L. Hale
Abstract	Since 2012, the Columbus Zoo and Aquarium (CZA) lorikeet flock has been challenged with recurrent outbreaks of enteritis despite extensive diet, husbandry, and exhibit modifications. In 2018, lorikeet morbidity and mortality events spiked as a result of enteritis. Necropsy reports consistently identify severe enteritis in the lorikeets, but enteric cultures yield negative or inconsistent results. We employed culture-free 16S rRNA sequencing to characterize the cloacal microbiota associated with lorikeet enteritis and identify potential etiologic agents. We obtained cloacal swabs from 48 healthy lorikeets across two seasons (Fall 2018, Winter 2019) and opportunistically collected cloacal swabs from 20 lorikeets that presented with enteritis during this period. We also swabbed lorikeet water and feed. Using QIME 2 for analysis, we identified a significant difference in healthy lorikeet cloacal microbial composition across seasons but no differences based on sex. We also detected reduced microbial richness and evenness and significantly higher levels of <i>Clostridium perfringens</i> in lorikeets with enteritis as compared to healthy lorikeets and to the same birds at previously healthy timepoints. No <i>C. perfringens</i> was found in water or feed samples. <i>C. perfringens</i> is a common avian gut microbe that can potentially cause necrotizing enterocolitis. As such, we characterized the toxin and antimicrobial susceptibility profiles of lorikeet <i>C. perfringens</i> . These results have guided changes in the clinical management of lorikeets with enteritis to include medications with activity against <i>Clostridial</i> pathogens.
Keywords for abstract	Clostridium perfringens Enteritis Lorikeet Microbiota

Title of abstract	EXTRACTION METHODS FOR OBTAINING MICROBIAL DNA IN HEALTHY CANINE URINE
Authors	R. Mrofchak, C. Madden, and V. Hale
Abstract	The microbiome is the collection of microbes and their associated genomes present in a habitat. Recent studies have revealed how host-associated microbiomes can play in a role disease susceptibility an progression. Alterations in the urine or bladder microbiome have been associated with diseases such as urinary incontinence, interstitial cystitis, and bladder cancer. Studying the relationship between disease and the urine microbiome is difficult because urine is a low biomass sample. It is important, therefore, to establish an efficient method to maximize DNA isolation from urine samples. The purpose of this project was to test five different methods for extracting DNA from canine urine. Urine samples were collected from eleven healthy dogs and divided into five 3 ml aliquots. The five extraction methods we tested included the following kits: QlAamp PowerFecal DNA Kit, QlAamp BiOstic Bacteremia DNA Kit, DNeasy Blood and Tissue, QlAamp PowerFecal Pro DNA Kit (Qiagen, Germany) and extraction using magnetic beads. We used a Qubit _{TM} 4.0 fluorometer to record the DNA concentration of each sample. Because the fluorometer measures both host and microbial DNA, we further quantified the microbial DNA abundance in each sample by performing qPCR using universal 16S rRNA (Bacteria/Archaea) primers and probe (Thermo Fisher Scientific). DNA was then sequenced on an Illumina Miseq at Argonne National Laboratories. Sequences were filtered using QIIME2 and taxonomy was assigned using the SILVA database (version 132 99% ID classifier). Microbial community diversity and composition were compared across extraction methods using QIIME2 (2020.2) and R (3.5.2). These results will help identify the most effective method(s) for microbial DNA extraction from canine urine as well as the potential strengths and weaknesses of each method. This work will inform our future studies focused on understanding if and how microbial communities in urine play a role in urogenital diseases like bladder cancer.
Keywords for abstract	Canine DNA extraction Urine microbiome

Title of abstract	CONTRIBUTION OF FGF/FGFR SIGNALING TO SUSTAINED ERK ACTIVATION, A DRIVER OF CELLULAR HETEROGENEITY AND DRUG RESISTANCE
Authors	V. Murthy, A. E. Davies
Abstract	The complexity of extracellular signaling cues from the tumor microenvironment gives rise to a phenotypically heterogeneous population of tumor cells. In triple negative breast cancer (TNBC), intratumoral heterogeneity is associated with aggressive disease, therapeutic resistance, and poor patient outcomes. ERK/Akt signaling pathways are often upregulated in TNBCs. These pathways integrate microenvironment signaling cues which contribute to tumor heterogeneity, making them an attractive target for anti-cancer therapies. However, inhibitors of ERK and Akt signaling demonstrate poor efficacy in patients indicating a level of intrinsic resistance to these drugs. Our preliminary data exploring resistance has identified fibroblast growth factor/receptor (FGF/FGFR) signaling as a possible mechanism. Using live-cell fluorescence microscopy with single cell resolution, we determined that erlotinib (inhibitor of epidermal growth factor receptor [EGFR]) potently inhibits ERK signaling in cancer cells, but this is rapidly overcome by FGF2. However, this activity is independent of FGFR signaling. These results suggest that dual inhibition of EGFR/FGFR signaling, may overcome intrinsic resistance, improve efficacy, and reduce microenvironmental contributions to intratumoral heterogeneity.
Keywords for abstract	Drug resistance Cellular heterogeneity ERK signaling Tumor microenvironment

Title of abstract	EX VIVO CYSTIC FIBROSIS 3D CULTURE LUNG MODEL DIFFERENTIATED FROM EXPANDED PRIMARY CF PATIENT-DERIVED LUNG CELLS
Authors	R. E. Rayner, J. Wellmerling, W. Osman, S. Honesty, M.E. Peeples and E. Cormet-Boyaka. Depts. of Veterinary Biosciences, The Ohio State University; and Center for Vaccines Immunity, Abigail Wexner Research Institute at Nationwide Children's Hospital, Columbus OH
Abstract	Cystic fibrosis (CF) is currently an incurable, ultimately fatal genetic disease in humans due to mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) gene. Multiple organs are affected, however damage to the lungs are often the cause of death. The CF airway epithelium has reduced CFTR channel function, increased mucus production and impaired mucociliary clearance (i.e. reduced ciliary beat frequency). Therefore, airway models are crucial to understand the mechanisms and consequences of this disease, as well as assess the efficacy of current/potential CF drugs. Due to limited access to primary CF airway cells, the aim of this study was to investigate the expansion and differentiation of primary CF human bronchial epithelial cells (CF-HBEC), which represent the gold standard for pre-clinical studies. Here we describe new culture conditions to expand primary CF-HBEC using PneumaCult-Ex Plus (StemCell Technologies) medium that does not require addition of Rho kinase inhibitor (ROCK) or feeder cells (often used to expand primary cells). Primary CF-HBEC from 3 CF donors F508del homozygous, grown at air-liquid interface, were characterized phenotypically and functionally in response to the CFTR corrector drug VX-661 (Tezacaftor). Optimal CF-HBEC 3D epithelia were achieved from cells expanded up to at least five passages (~20 population doublings), as evidenced by trans-epithelial electrical resistance (TEER) >400 Ohms·cm², presence of ciliated pseudostratified columnar epithelium with goblet cells, and increased CFTR channel function when treated with VX-661 corrector drug. Ciliary beat frequency also increased with VX-661 corrector to the level of normal cells. In conclusion, CF patient-derived airway cells can be expanded without the use of feeder cells or ROCK inhibitor, and still achieve optimal 3D epithelial cultures. These cultures can be used to assess responses to CF drugs and help guide the selection and choice of drugs to help treat CF patients.
Keywords for abstract	Cystic fibrosis Ex vivo In vitro Cell culture Lung

Title of abstract	EVALUATING MKLP2 INHIBITION AS A NOVEL ANTIMITOTIC FOR HUMAN AND CANINE GLIOBLASTOMA
Authors	M.S. Schrock, P. Dickinson, M. Venere, and M.K. Summers
Abstract	Background: Inhibition of motor kinesins, proteins which travel along microtubules and perform specific mitotic, meiotic or cellular transport functions, is a growing area of cancer drug development. There are over 20 proteins in the kinesin superfamily and inhibition of kinesins with mitosis-specific functions have the potential to circumvent neurotoxicity associated with traditional anti-mitotics. We have preliminary data indicating a previously undescribed role for mitotic kinesin-like protein 2 (MKlp2) in early mitosis. The goal of this study is to further define this novel function of MKlp2 and to determine the efficacy of MKlp2 inhibition in decreasing canine and human glioblastoma cell growth.
	Methods: Applying cell synchronization techniques, we used live cell imaging to determine the effects of paprotrain, a commercially available MKlp2 inhibitor, on short-term cellular proliferation and duration of metaphase in canine and human glioblastoma cell lines. Results: Our data indicate that MKlp2 is overexpressed in human GBM cell lines. In addition, MKlp2 inhibition with paprotrain significantly decreased short-term and long-term survival in canine and human GBM cell lines. Our live cell imaging also revealed a serious chromosome congression defect in MKlp2 inhibitor-treated cells, confirming an MKlp2 function in early mitosis.
	Conclusions: Altogether our data reveals a novel function for MKlp2 in facilitating chromosome congression during metaphase. The observed decreases in short-term and long-term cellular proliferation upon treatment with paprotrain suggest MKlp2 inhibition could be an effective next-generation anti-mitotic for glioblastoma patients. However, more work is needed to determine the clinical relevance of the canine glioblastoma model for human glioblastoma, particularly in the context of MKlp2 expression.
Keywords for abstract	MKlp2 Mitotic kinesin Glioma glioblastoma

Title of abstract	TARGETING PRMT5 TO OVERCOME IBRUTINIB RESISTANCE
THO OT ADOLLADE	IN HUMAN MANTLE CELL LYMPHOMA
Authors	S. Sloan ^{1,2} , F. Brown ¹ , M. Long ^{1,2} , A. Prouty ¹ , E. Brooks ¹ , J. Chung ¹ , Y. Youssef ¹ , X. Zhang ³ , A. S. Yilmaz ³ , H. G. Ozer ³ , J. C Byrd ¹ , R. Lapalombella ¹ , R. A. Baiocchi ¹ and L. Alinari ¹ Department of Internal Medicine, Division of Hematology, College of Medicine, The Ohio State University, Columbus, OH Department of Veterinary Biosciences, College of Veterinary
	Medicine, The Ohio State University, Columbus, OH ³ Department of Biomedical Informatics, College of Medicine, The Ohio State University, Columbus, OH
Abstract	Mantle cell lymphoma (MCL) is an incurable subtype of B-cell Non-Hodgkin's lymphoma characterized by genetic and epigenetic dysregulation of the cell cycle driving uncontrolled B-cell proliferation and survival. Ibrutinib is a novel and irreversible inhibitor of Bruton's tyrosine kinase (BTK) with an unprecedented 68% overall response rate in relapsed/refractory MCL. Unfortunately, the majority of MCL patients progress and succumb to their disease highlighting the urgent need to develop novel therapeutic strategies. Identified mechanism of ibrutinibresistance include compensatory PI3K-AKT signaling and activation of the pro-survival B-cell receptor (BCR)-NFkB signaling or alternative NIK-NFkB pathways.
	Over the past decade extensive data has implicated the epigenetic dysregulation of protein arginine methyltransferase 5 (PRMT5) as a driver of tumorigenesis. In MCL the overexpression of PRMT5 drives the activity oncogenes and silences key tumor suppressors. Research conducted in our lab and others has validated the selective inhibition of PRMT5 as a rationale therapeutic strategy in MCL by restoring regulatory activity to cell cycle (cyclin D1 and RB/E2F), tumor suppressors (P53), signaling pathways (PI3K-AKT and BCR), and apoptotic programs (NFKB/p65).
	Given the overlap of identified mechanisms of resistance to ibrutinib and known target genes modulated with PRMT5 inhibition, we propose selective inhibition of PRMT5 as a novel therapeutic approach for patients with ibrutinib-resistant MCL. We have shown that treatment with the small molecule inhibitor of PRMT5 (PRT382) overcomes ibrutinib-resistance in human MCL cell lines resulting in enhanced cell death with 50% inhibitory concentrations (I _C 50s) in the low nM range. In a patient derived xenograft of ibrutinib-resistant MCL, mice treated with PRT382 showed significantly prolonged survival (median-survival = 83 days) compared to ibrutinib (median-survival = 54 days) (p-value = 0.0082). Whereas, in our ongoing immune-competent mouse model, mice receiving PRT382 (10 mg/kg) are showing an even greater survival advantage, demonstrating its single-agent therapeutic activity (p-value < 0.0001).
Keywords for abstract	Lymphoma, drug resistance, ibrutinib, PRMT5

Title of abstract	CONTRIBUTIONS OF HBZ INTERACTING PROTEINS, TOP1 AND YBX1, TO HTLV-1 PATHOBIOLOGY
Authors	R. Stahl, A. Panfil, P. Green. Depts of Veterinary Biosciences, Center for Retrovirus Research, Comprehensive Cancer Center and Solove Research Institute, Department of Cancer Biology and Genetics
Abstract	Human T-cell leukemia virus type 1 (HTLV-1) is a retrovirus which causes an aggressive CD4+ T-cell malignancy (ATL) and a neurodegenerative disease (HAM/TSP). The precise mechanisms of HTLV-1 pathogenesis remain poorly understood, but current models suggest the viral oncogene, Tax, initiates cellular transformation early in infection, while Hbz provides maintenance or cell survival signals for transformed cells later in infection when Tax is silenced. Our goal is to identify and characterize HBZ cellular binding partners and their effects on HTLV-1 pathobiology. Herein, we identified DNA Topoisomerase I (TOP1) and Y-Box Binding Protein 1 (YBX1) as HBZ-interacting partners using proteomics and colPs in both HEK293T and HTLV-1-transformed lymphoid cells. TOP1 is a cellular enzyme known to alter DNA topology during replication and transcription to reduce torsional stress in DNA. TOP1 is also involved in maintenance of genome stability by participating in DNA repair and chromosome condensation. Tax is able to bind TOP1 and inhibit its catalytic activity and subsequent DNA repair properties in cells. We hypothesize HBZ may also affect TOP1 activity – either by inhibiting Tax interaction with TOP1 or by inhibiting TOP1 itself. YBX1 is a cellular transcription factor previously suggested to bind to and activate transcription of the HTLV-1 promoter located in the 5' LTR. Our studies confirm YBX1 activates viral transcription and interestingly, we find a synergistic positive effect on transcription with both Tax and YBX1. However, in the presence of HBZ, YBX1-mediated transcription is repressed. Insights on the roles of TOP1 and/or YBX-1 will allow us to refine the role of HBZ in T-cell transformation and development of disease.
Keywords for abstract	YBX1 HTLV Transcription Tax HBZ

Title of abstract	CFTR DYSFUNCTION AND COPD: DNA DAMAGE AS A POTENTIAL LINK
Authors	J. Wellmerling, S. Chang, E. Kim, W. Osman, P Boyaka, M. Borchers, and E. Cormet-Boyaka. Depts of Veterinary Biosciences, Ohio State University, and Internal Medicine, University of Cincinnati
Abstract	Chronic obstructive pulmonary disease (COPD) is a lung disease representing the third leading cause of death worldwide. The two main COPD phenotypes are chronic bronchitis and emphysema. Chronic bronchitis is characterized by airflow limitation in the small airways. Emphysema encompasses cell death and tissue destruction in the alveoli, which leads to respiratory failure. Smoking is the primary cause of COPD, however age and genetics play a role. Evidence suggests the cystic fibrosis transmembrane conductance regulator (CFTR), an anion channel, is implicated in COPD. COPD shares many features with the autosomal-recessive disease cystic fibrosis (CF); caused by loss-of-function mutations in CFTR. Interestingly, cigarette smoke (CS) causes CFTR degradation; and CFTR expression is reduced in COPD lungs. Approximately 1 in 30 people in the U.S. is an asymptomatic CF carrier. Thus, it is important to determine whether CFTR haploinsufficiency promotes COPD susceptibility. To address this question, Cftr-// (WT), Cftr-//. (Het), and Cftr-// (KO) mice were subjected to CS and natural aging. Compared to controls, CS-exposed Het and KO mice displayed increased alveolar mean linear intercept (LM), indicative of emphysema. Upon aging, only KO mice displayed increased LM. Evidence suggests "accelerated aging," caused by DNA damage accumulation, may drive COPD. Thus, we hypothesized that CFTR dysfunction may lead to DNA damage accumulation. To determine whether CFTR is implicated in the DNA damage response, we utilized a human CF bronchial epithelial cell line (CFBE41o-) overexpressing either WT-CFTR, or the most common disease-causing mutant, F508del. Cells were exposed to two different DNA damagers- hydrogen peroxide or camptothecin. In response to either compound, cells expressing F508del-CFTR displayed increased phosphorylation of histone H2AX, a DNA damage marker often associated with double-strand breaks; which could be attenuated by intracellular calcium chelation. Ongoing efforts aim to understand the mechanisms behin
Keywords for abstract	COPD CFTR DNA Damage

Title of abstract	INTRACELLULAR BACTERIA SUBVERSION OF IRON SEQUESTRATION BY TYPE IV SECRETION SYSTEM
Authors	Q. Yan, O. Teymournejad, M. Lin, Y. Rikihisa. Department of Veterinary Biosciences
Abstract	Ehrlichia chaffeensis (E. chaffeensis) is anobligate intracellular Gram-negative bacterium which infects monocytes and macrophages, and causes human monocytic ehrlichiosis. During infection, E. chaffeensis acquires essential nutrients, such as iron, inside host cells. However, how Ehrlichia acquires intracellular iron is poorly understood. In this study, we found Ehrlichia translocated factor-3 (Eft-3), a previously predicted effector of the Ehrlichia type IV secretion system, directly binds ferritin light chain based on our yeast two-hybrid screening of human leukocyte cDNA prey library. Territin light chain is one of two subunits of ferritin which plays an important role in intracellular iron homeostasis. Therefore, our hypothesis is secreted Etf-3 participates in intracellular iron homeostasis in host-cell cytoplasm and facilitates iron acquisition by E. chaffeensis. The far-western blotting and immunoprecipitation assay confirmed that Etf-3 directly binds endogenous ferritin light chain. OpenSPR assay revealed Etf-3 has high affinity to human ferritin. Ehrlichial Etf-3 and recombinant Etf-3 (cloned into the Ehrlichia genome) are secreted into the host-cell cytoplasm and form small pucta. Ectopically expressed Etf-3-GFP co-localized with both ferritin light chain and LC3 (Autophagosome marker). Further experiments showed Etf-3-GFP can dramatically reduce ferritin light chain protein amount in host cells, but has no effect on ferritin light chain mRNA level. In addition, Etf-3-induced ferritin light chain degradation can be attenuated by autophagosome inhibitors and lysosome inhibitors. Thus, Eft-3 can induce ferritinophagy by helping delivery of ferritin light chain (ferritin) to ferritinophagosomes which are selective autophagosomes in iron homeostasis. Thereby ferritin is degraded and iron is released for Ehrlichia to acquire iron. Our study reveal a novel virulence mechanisms of E. chaffeensis to develop effective countermeasures to prevent and treat fatal or debilitating ehrlichiosis in humans and animal
Keywords for abstract	Ehrlichia chaffeensis T4SS effector Ferritin Light Chain Iron Acquisition Ferritinophagy

STRUCTURE/FUNCTION

Title of abstract	IMMUNOLOCALIZING LUBRICIN IN NORMAL AND EXPERIMENTALLY-INJURED INTRASYNOVIAL DEEP DIGITAL FLEXOR TENDON
Authors	N. Altmann, S. Durgam
Abstract	Adhesion formation is a significant clinical problem following intrasynovial flexor tendon injuries. Fibrous adhesions between the tendon and synovial sheath disrupt the gliding motion required for complete range of motion of the digit. Lubricin, encoded by proteoglycan 4 gene, is a mucinous glycoprotein in synovial joints and facilitates a gliding surface. As a corollary, the objective of this study is to immunolocalize lubricin in normal ovine intrasynovial deep digital flexor tendon (DDFT) and to assess its alteration following an excisional model of experimental injury. We hypothesize that lubricin can be immunolocalized to the intrasynovial surface of DDFT and will decrease following injury.
	Partial width excisional defects were surgically induced in both forelimb DDFTs within the digital flexor tendon sheath of 4 young-adult sheep. Sheep were euthanized 3 months following injury, and both injured forelimb and normal hindlimb DDFT were collected. Tendon samples were fixed in 4% paraformaldehyde for 1-hour and embedded in OCT. Ten micron-thick transverse and longitudinal sections were incubated overnight with mouse polyclonal anti-lubricin antibody (1:100) in 10% BSA. Sections were then incubated with Alexa546 goat anti-mouse IgG secondary antibody (1:500) in 10% BSA and mounted with DAPI. Nuclei (DAPI) and lubricin (Alexa Fluor 546) signals were captured using standard confocal imaging with 405 and 543nm excitation wavelengths, respectively. Additionally, second harmonic generation (SHG) signal was captured using a Ti:Sapphire laser at 950nm to visualize collagen structure.
	Our analyses thus far demonstrate that lubricin is largely localized to the intrasynovial surface [Figure 1] with small amounts located between collagen bundles. We are currently assessing if lubricin immunolocalization is altered following injury. Given that lubricin is a boundary lubricant, delineating the temporal and spatial distribution/regulation of lubricin in a clinically relevant large animal model is necessary for translating lubricin supplementation as an anti-adhesion therapy for intrasynovial tendon injuries.
Keywords for abstract	Lubricin/PRG4 Intrasynovial flexor tendon Immunostaining Second harmonic generation (SHG) microscopy

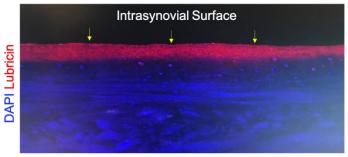


Figure 1: Confocal microscopy image depicting lubricin (red) immunolocalized at the intrasynovial surface (arrow) of DDFT

Title of abstract	MOTILITY ACTIVATION AND ASSISTED REPRODUCTION TECHNIQUES ALTER THE SPERMATOZOA GLYCOCALYX OF THE FRESHWATER FISH, SAUGER (SANDER CANADENSIS)
Authors	B. Blawut, B. Wolfe, G. Scheunemann, C. Premanadan, S.A. Ludsin, M.A. Coutinho da Silva. Depts. of Veterinary Clinical Sciences, Preventative Medicine, and Ecology, Evolution, and Organismal Biology
Abstract	The spermatozoa glycocalyx is a dynamic coating of extracellular glycoproteins known to facilitate fertilization in mammals. In contrast, the structure, function, and impact of assisted reproduction techniques on the glyocalyx in fish is still uncertain. The objective of this study was to describe and compare the glycocalyx among sperm types (stripped, testicular, and cryopreserved) and between activation statuses (inactive vs. activated) in the sauger (Sander canadensis). Additionally, the importance of GlcNAc to fertilization was investigated. Stripped, testicular, and cryopreserved sperm were prepared using currently available techniques. All sperm types were assessed in both the inactive and the activated state (dilution in hatchery water). Three fluorescent lectins commonly used in mammalian sperm analysis were used to evaluate the quantity and distribution of specific sugar moieties in the sperm membrane (N – acetyl glucosamine (GlcNAc), α -mannose, β -galactose, respectively) using flow cytometry and fluorescent microscopy. Fertilization was assessed in each sperm type and in stripped sperm pre-treated to block GlcNAc prior to insemination. Linear mixed models were used to compare staining patterns (%) and fluorescent intensity (a.u.) among sperm types and activation statuses (α = 0.05, n = 10 - 12). The sauger glycocalyx contained GlcNAc and α -mannose but lacked β - galactose. GlcNAc was the most dynamic moiety, displaying a 10 fold increase in apical staining after activation in testicular and stripped sperm (39.07% and 51.09 %, respectively). Cryopreserved sperm showed inhibited apical staining following activation (4.61 %). Furthermore, blocking GlcNAc availability prior to insemination reduced fertilization by 81% relative to the untreated control. These results support a dynamic sauger sperm glycocalyx which responds to motility activation and has a pivotal role in fertilization. Cryopreservation largely negated these changes, which may partially explain the reduced fertility observed in
Keywords for abstract	Milt Cryopreservation Aquaculture Physiology Glycocalyx

Title of abstract	OPTIMIZING FOOD ACCESSIBILTY DURING ZEBRAFISH REARING IMPROVES GROWTH, SURVIVAL, AND BREEDING PERFORMANCE
Authors	T. Collins, S. Cabrera, E.Teets, J. Shaffer, and B. Blaser. Office of Research, University of Laboratory Animal Resources and College of Medicine, Division of Hematology, and Comprehensive Cancer Center
Abstract	Zebrafish (<i>Danio rerio</i>) are the second most common animal used in biomedical research. Setting nutritional and feeding standards for larval and juvenile zebrafish that promote growth and survival, and enhance reproductive success is a challenge. We hypothesized that by increasing nutrient availability through continuous delivery of live food or high-nutrient density pelleted food, larval zebrafish will experience faster growth, better survival and better reproductive success. Gemma Micro 75 pelleted diet and live type L rotifers (<i>Brachionus plicatilis</i>) were compared in 3 feeding regimens: bolus feeding of live diet (BL), continuous feeding of live diet (CL), and pelleted diet (PD). Each was administered to zebrafish from 9 to 30 days post-fertilization (dpf). At 38 dpf, fork length was greater for PD and CL groups compared to BL (p = 0.001 and p = 0.0009, respectively, compared to BL). At 113 dpf, fork length was significantly greater in the PD group compared to BL (p = 0.03). Sexual maturity was assessed by external morphology by 3 independent observers and confirmed in breeding trials using validated breeding stock. Fish in the PD and CL groups were sexually mature by morphology at 55 dpf and 52 dpf respectively, while the BL feeding group was sexually mature at 118 dpf. The sex distribution was 67% male for the PD group and 69% male for the CL group. The age of successful spawning in more than 50% of breeding pairs was 93 dpf for the PD and CL groups and 118 dpf in the BL group. Our data suggest that the PD and CL feeding methods promote faster growth and decrease the age at sexual maturity while also maintaining a useful sex distribution. Pelleted diets also offer a clear advantage in labor cost and therefore represent an attractive option for zebrafish nursery care.
Keywords for abstract	zebrafish husbandry zebrafish rearing zebrafish growth zebrafish breeding feeding zebrafish zebrafish survival

Title of abstract	VARIABILITY IN HATCHING RATES OF THE AMERICAN ALLIGATOR (ALLIGATOR MISSISSIPPIENSIS)
Authors	S. Dampney, J. Flint, M. Flint. Department of Veterinary Preventive Medicine, College of Veterinary Medicine
Abstract	The American alligator is an endemic crocodilian species often commercially farmed to control wild alligator populations and produce a high quality hide product. Hatchery management of the American alligator relies heavily on the proper maintenance of eggs, including appropriate ambient temperatures, humidities, and substrates. Research on the efficiency and efficacy of standard hatchery conditions are limited and alternative options have yet to be identified. (1). The objectives of this study was to investigate the effects of varying substrates and temperature controls on hatchability. There were a total of 842 eggs, from 10 different laying farms, that were set in 12 incubators. Each incubator contained 3 trays filled with either vermiculite (V) or natural (N) nesting material, and then set to either a constant (C) or diurnal timed (T) temperature, with diurnal consisting of 14 hours on and 10 hours off. The current industry standard is Constant/Natural (CN). A subsection of the collected eggs were also subsequently enrolled in a Vetrap study. This study was designed to reduce umbilical scarring by promoting an increased pipping time. Hatchability was variable across the farms, ranging from 37.2% to 94.1% hatch success per farm. High success rate incubators (>80% hatchability) were incubators 5 (TN), 6 (TV), 7 (CV), and 9 (CN). The results from necropsy of the failed pips revealed dehydration as the primary cause of death (15.7%). Vetrap hatch success rates were very low and contributed 5.2% to the overall mortality of 27.3%; thus, it is encouraged to discontinue this practice. Our results indicate that the alligator hatching industry does not need to be confined to the current incubator standard parameters (CN) as any combination of incubator settings and substrates mentioned above can yield the same hatchability. 1. Shirley, M., Elsey, R. 2018.
Keywords for abstract	American, Alligator, Mississippiensis, Hatchability, Temperature, Diurnal, Vermiculite, Substrate, Incubator

Title of abstract	PHARMACOKINETICS AND PHARMACODYNAMIC EFFECTS OF ORAL TRANSMUCOSAL AND INTRAVENOUS ADMINISTRATION OF DEXMEDETOMIDINE IN DOGS
Authors	BT Dent ^{1,} TK Aarnes ¹ , VA Wavreille ¹ , J Lakritz ¹ , P Lerche ¹ , B KuKanich ² , CH Riccó Pereira ¹ , RM Bednarski ¹ ¹Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State University. ²Department of Anatomy and Physiology, Institute of Computational Comparative Medicine, College of Veterinary Medicine, Kansas State University.
Abstract	Fearful and aggressive behavior are the two most common behavioral complaints in veterinary practice. They represent a significant challenge for patient welfare, client satisfaction, and safety of the veterinary staff. These patients often require intravenous or intramuscular sedation to achieve safe examination, with α_2 -agonists such as dexmedetomidine representing the mainstay clinical sedative drugs. However, administration can pose risks to all involved and may negatively imprint on patients, which may make future evaluation more difficult. Alternative, pain-free routes of administration, such as the oral transmucosal (OTM) route, may make such interactions safer and better for patient welfare. The objectives of this study were to determine pharmacokinetic and pharmacodynamic properties of injectable dexmedetomidine administered via the oral transmucosal route to dogs. Dexmedetomidine was administered IV (5 µg/kg) or via the OTM route (20 µg/kg) in a blinded, single-observer, randomized crossover study. Dogs received dexmedetomidine and a sham treatment at each administration. Serial blood samples were collected from the saphenous vein. Heart rate, respiratory rate, and subjective sedation score were assessed for 24 hours. Plasma samples were analyzed for dexmedetomidine concentrations via ultraperformance liquid chromatography-tandem mass spectrometry. For the OTM route, the maximum plasma concentration was 3.8 \pm 1.3 ng/mL, which occurred at 73 \pm 33 minutes. The extrapolated maximum concentration for IV dosing at the time of administration was 18.6 \pm 3.3 ng/mL. The half-life was 152 \pm 146 minutes and 36 \pm 6 minutes for OTM and IV administration, respectively. Bioavailability for OTM administration was 11.2 \pm 4.5%. Peak sedation scores did not differ between routes. Decreases in heart rate, respiratory rate, and sedation score were evident sooner after IV administration. OTM administration of injectable dexmedetomidine resulted in similar sedation and prolonged duration of action, compared
Keywords for abstract	Dexmedetomidine Oral transmucosal Pharmacokinetics Pharmacodynamics

Title of abstract	REPLACEMENT OF FISH OIL WITH HIGH-OLEIC ACID SOYBEAN OIL IN ONCORYHYNCHUS MYKISS DIETS, AND ASSOCIATED PATHOLOGIES
Authors	A. Feinzig ¹ , J. Grayson ² , and K. Dabrowski ³ Depts. Of College of Veterinary Medicine ¹ , School of Environmental and Natural Resources ^{2,3}
Abstract	Fish require high dietary levels of omega-3 polyunsaturated fatty acids (PUFA) in order to achieve commercial standards of growth and survival. Omega-3 deficiencies have been associated with reduced growth and various deformities. Supplements of fish oils in fish diets are considered a necessary dietary ingredient for meeting the omega-3 PUFA requirement, which is derived primarily from wild marine fish. The demand for fish oil continues to grow, decimating the already over-harvested marine fish stocks. Thus, there is an interest in finding suitable plant-based replacements. Soybean products, particularly High-Oleic Soybean Oil (HOSBO), is one alternative of interest because of its high heat and oxidative stability for cooking uses, cost advantages due to the economy of scale of US soybean production, and health benefits. HOSBO is an enhanced soybean oil comprised of more than 70% oleic acid - an alternative for trans-fatty acid vegetable oils. The purpose of the proposed research is to investigate the replacement of fish oil with soybean oil (SBO) or HOSBO in the diet of rainbow trout (<i>Onchoryncus mykiss</i>). Past research has documented deleterious effects on the distal intestine and liver of
	rainbow trout fed soybean-based diets. However, this project will specifically investigate various pathologies associated with HOSBO diets enriched with PUFA supplementation. Pathologies will be analyzed via histology and radiology methods, as well as tracking trout growth rates. Major findings are: HOSBO may not be as available as other soy-based oils, which correspond to experimental diet growth rates; frequency of digestive tract pathologies did not differ amongst experimental diets. Therefore, HOSBO supplemented with PUFA may be a viable candidate for commercial fish diets.
Keywords for abstract	High-Oleic Acid Soybean Oil Oncoryhynchus mykis (Rainbow Trout) Feed Trial Gastrointestinal Pathologies

Title of abstract	DEVELOPMENT OF AN EVIDENCE-BASED WELFARE APPROACH FOR CHEETAHS (ACINONYX JUBATUS) IN
	HUMAN CARE
Authors	B. Fischer, M. Flint, K. Cole, and K.A. George. Department of Animal Sciences, College of Food, Agricultural, and Environmental Sciences and Department of Veterinary Preventative Medicine, College of Veterinary Medicine
Abstract	Animal welfare science is an expanding field in zoological institutions throughout the United States and the world. In 2017 the Association of Zoos and Aquariums (AZA) established a new accreditation standard requiring member organizations to have a formal animal welfare assessment process. As a result, the Animal Programs Department at the Columbus Zoo and Aquarium sought partnership with the Center for Human-Animal Interactions Research & Education (CHAIRE) to develop an assessment for the animals in their department using a focal species, the cheetah (<i>Acinonyx jubatus</i>). A multi-faceted approach was developed using the Five Domains Model as a framework for one-year, divided into six 60d periods, to measure the welfare of the cheetahs and determine influential factors. Species and individual histories including nutritional, environmental, and medical information, were acquired and combined with behavior observations and non-invasive physiological measurement of hair cortisol production. Behavior outputs were recorded using scan sampling for a total of six observations per period. One hair sample was collected from the same location at the beginning of each period. Participation in a cheetah run activity (P=<.0001), housing (P=0.0120), and period (P=<.0001) were found to influence behavior. Stereotypic behavior was positively correlated within individual cheetahs throughout our study (P=0.0026). No difference of hair cortisol was found for the population, but further analysis resulted in differences within individuals (P=0.0139). To our knowledge, this study was the first to measure cortisol production using hair sampling in cheetahs. Hair was the most appropriate biomarker due to its reflection of chronic cortisol production. Assessment using the Five Domains Model is necessary for a holistic view of welfare. This study demonstrates a foundation for welfare assessments and evidence-based management decisions of cheetahs as well as other species within zoological institutions in the future.
Keywords for abstract	Welfare Hair cortisol Five Domains Model Cheetah

Title of abstract	COMPREHENSIVE EVALUATION OF KIDNEY TISSUE FROM YORKSHIRE TERRIERS WITH RENAL DISEASE
Authors	M. Klein, N. Etedali, R. Cianciolo. Department of Veterinary Biosciences and the Animal Medical Center
Abstract	Comprehensive evaluation of kidney tissue from Yorkshire terriers with renal disease has revealed glomerular basement membrane (GBM) lesions. This retrospective study characterizes these lesions and associated clinical features. Eighty-six Yorkshire terriers (4% intact females, 49% spayed females, 4% intact males, and 44% castrated males), ranging in age from 8 to 198 months were included. Clinical parameters, including but not limited to: signalment, blood pressure, serum creatinine, serum albumin, and urine protein to creatinine ratio (UPC) were assessed by a board-certified veterinary internist. Median serum creatinine was 1.0mg/dL (range: 0.3 to 7.1mg/dL; n=77) and median UPC was 8.1 (range: 0.08 to 28.1; n=74). Light microscopy, transmission electron microscopy, and immunofluorescence assessed the presence and severity of glomerular, vascular and tubulointerstitial lesions. 33.3% of dogs were diagnosed with immune complex glomerulonephritis (ICGN), 21.0% with podocyte-driven disease (e.g. podocytopathy and focal segmental glomerulosclerosis), 30.9% with GBM-mediated disease, 3.7% had renal maldevelopment, and the remaining 11.1% had other lesions. No dogs were diagnosed with renal amyloidosis. In 90% of the cases, ultrastructural evaluation revealed one or more lesions in their GBM, independent of the primary disease process, including: multilamination, electron-lucent vacuoles in the GBM, and club-like projections toward the urinary space without associated immune complexes. Although the clinical significance and pathogenesis of these GBM lesions is unknown, these GBM abnormalities might be the sole diagnostic finding in Yorkshire terriers with renal disease. Also ICGN might be less prevalent in proteinuric Yorkshire terriers compared to previous reports of all dogs biopsied for proteinuric renal disease.
Keywords for abstract	Glomerular basement membrane Kidney Proteinuria Transmission electron microscopy Yorkshire terriers

Title of abstract	EXPRESSION OF CD31 IN FELINE KIDNEYS TO CHARACTERIZE PERITUBULAR CAPILLARY DENSITY IN CKD
Authors	R. Paschall, J. Quimby, R. Cianciolo
Abstract	Feline chronic kidney disease (CKD) is characterized by tubulointerstitial inflammation, tubular atrophy and fibrosis. Hypoxia is a key driver of fibrosis and is associated with capillary rarefaction (reduction in vascular density) in humans. It is unknown whether similar pathophysiologic mechanism occur in cats. CD31 immunohistochemistry was assessed in formalin-fixed paraffinembedded kidney tissue collected at autopsy from 21 CKD cats and 5 normal controls. Consecutive high power fields (40x), ten from the cortex and five from the corticomedullary junction (CMJ), were examined and an observer (blinded to clinical data) counted and colored capillary area. Image analysis was used to determine capillary number, average capillary area (ACA), and percent capillary area (PCA). Differences between normal and CKD cats were assessed with Mann-Whitney and correlation with serum creatinine was assessed with Spearman correlation. No significant difference in capillary number was found between normal and CKD cats in either region. No significant difference in ACA was found between normal and CKD cats in the CMJ region of the kidney, but CKD cats tended (p = 0.06) to have smaller ACA in the cortex than normal cats. ACA was significantly negatively correlated to serum creatinine (p=0.03, r=-0.42). There was no significant difference in PCA between normal and CKD cats in either region, but the lowest PCAs were found only in CKD cats (7/21 CKD cats versus 0/5 normal cats having a PCA <2%). Reduction in ACA and density may be present in later stages of CKD in cats.
Keywords for abstract	CD31 Feline Chronic Kidney Disease Peritubular Capillary Capillary Rarefaction

Title of abstract	HAIR CORTISOL AND BEHAVIOR: A NOVEL APPROACH TO MEASURING CALIFORNIA SEA LION (ZALOPHUS CALIFORNIANUS) WELFARE
Authors	M. Winans, M. Flint, K. Cole, K. George. College of Veterinary Medicine, Department of Veterinary Preventive Medicine, and College of Food, Agriculture, and Environmental Sciences, Department of Animal Sciences
Abstract	As the Columbus Zoo and Aquarium (CZA) prepares to acquire California sea lions, CZA and The Ohio State University have partnered to conduct a long-term welfare assessment of the focal population in response to relocation from temporary facilities in Myakka City, FL to a permanent habitat at CZA. The project phase presented here aimed to establish baseline measures of a novel biomarker, hair cortisol concentrations (HCC), and behavior whilst the sea lions were housed at their temporary facility. Data were analyzed using generalized liner mixed models. Results indicated mean HCC changed significantly across time periods (p = 0.0152) but found no effect of sex (p = 0.7888), and age was significant only between juvenile and adults (p = 0.0430). Additionally, training staff was significant with hair cortisol concentrations (p = 0.0295). The mean HCC for this sample population was determined to be (3.345 \pm 3.0624). Analysis of behavior through odds ratios indicated that time period (p < 0.0001) and training staff (p < 0.0001) significantly impacted the likelihood of performing inactive behaviors over active behaviors, while sex (p = 0.3865) had no effect. Our results suggest time period and change in training staff were primary predictor variables of both behavior and HCC. Additionally, our results provide novel information on the measurement of HCC in this species. These findings will allow for comparisons to be made against post-relocation measures to assess the impact of relocation on the welfare of zoo-housed animals. We aim to present the study's findings to-date and review methodology for upcoming phases. This unique opportunity for a long-term study will contribute to the growing body of literature on marine mammal behavior and welfare in human-care.
Keywords for abstract	Welfare California sea lions Hair cortisol Behavior Physiology

EPIDEMILOGY AND APPLIED RESEARCH

	IDENTIFICATION OF ENVIRONMENTAL SURFACE
Title of abstract	RESERVOIRS FOR THE PERSISTENCE OF SALMONELLA IN THE OSU GALBREATH EQUINE CENTER.
Authors	R. Adams, D. Mollenkopf ¹ , G. Ballash ¹ , T. Wittum ¹ . Dept. of
	Veterinary Preventive Medicine ¹
Abstract	Objective: Salmonellosis is a common infectious cause of diarrhea in horses ranging in severity from asymptomatic shedding to severe clinical disease and death. Cephalosporin-resistant Salmonella have been implicated in nosocomial outbreaks within equine facilities, with case fatality rates from 31.5-42%. Environmental contamination and persistence with Salmonella can pose an important health risk to hospitalized patients. In fall of 2018, the equine ICU of the OSU Galbreath Equine Center was closed due to the persistence of a clonal strain of multidrug resistant (MDR) Salmonella Newport in the hospital environment. Our objective was to identify surfaces serving as potential point sources of nosocomial infection risk. Methods: Hospital surface sampling included routine monthly surveillance and surfaces located within equine isolation, triage, ICU, surgery, breezeway, general purpose, theriogenology, and orthopedic wards, and ancillary areas. Six hospital sampling dates were included between May 13 and July 16, 2019. Samples were cultured to recover and identify Salmonella isolates. Results: Overall prevalence of Salmonella on surfaces was 2.88%. Contaminated surfaces included the isolation hallway floor and drains, the isolation outdoor concrete aisle, the fork-lift and skid steer, the compactor, the floor of the theriogenology ward, and the mulch carts. No single surface was repeatedly contaminated with Salmonella over sampling periods. Conclusions: We observed that infrequently used equipment such as the skid steer was contaminated with fecal matter from the outdoor compactor before traversing through the hospital. We recommended placement of a barrier around the compactor to decrease run-off during periods of rain. Since implementation, the hospital has not experienced additional clonal spread of MDR Salmonella. These results emphasize the value of surveillance in identifying problem areas within the hospital, thus allowing for control measures to be implemented before an outbreak occurs.
Keywords for abstract	Salmonella epidemiology environmental contamination nosocomial infection

Title of abstract	UTILIZING PATIENT AND CLINICAL-BASED RISK FACTORS TO PREDICT RESISTANT UROPATHOGENIC E. COLI URINARY TRACT INFECTIONS
Authors	G. Ballash, D. Mollenkopf, D. Diaz-Campos, T. Wittum. Depts. Of Veterinary Preventive Medicine and Veterinary Clinical Sciences
Abstract	Uropathogenic <i>Escherichia coli</i> (UPEC) are the most common cause of canine urinary tract infections (UTI). Recent reports in both human and canine medicine suggest UPEC are acquiring antimicrobial resistance which may contribute to the growing incidence of recurrent and persistent UTI. One hypothesis for the increased frequency of antimicrobial resistance is increased selective pressure from the widespread use of antibiotics to treat UTI. Our objective was to evaluate antimicrobial use and other clinical and patient-based factors contributing to antimicrobial resistance phenotypes. Here we collected 101 UPEC isolates from 88 individual canine patients and generated isolate-specific minimum inhibitory concentration profiles to 26 antimicrobials. Utilizing medical record information, we collected additional demographic and clinical information including current antimicrobial use, antimicrobial use in the past 30 days, age, sex, breed, comorbidity status and other medication use. We constructed marginal regressions models using generalized estimating equations to identify significant risk factors that predicted antimicrobial resistance and multidrug resistance among UPEC isolates. Using the risk factors collected, we generated patient-based stratified antibiograms to identify empirical therapies that could be used in strata-specific UPEC UTI. The results and their implications of this study will be discussed.
Keywords for abstract	Antimicrobial Resistance Urinary tract infections Uropathogenic E. coli Patient-based stratified antibiograms

Title of abstract	PERCEIVED RISKS AND BENEFITS FOR PARTICIPATION IN POULTRY DISEASE MONITORING PROGRAMS IN THE UNITED STATES: A CLUSTER ANALYSIS
Authors	T. J. Beyene ^a , G. Lossie ^b , C-W Lee ^a , A. G. Arruda ^a ^a Department of Preventive Veterinary Medicine, The Ohio State University, Columbus, OH, 43210; ^b Department of Comparative Pathobiology, Purdue University College of Veterinary Medicine, West Lafayette, IN, 47907
Abstract	The development and implementation of disease monitoring systems is useful for rapid and efficient communication during outbreaks of infectious diseases affecting the poultry industry. The objective of this study was to describe perceived benefits and risks for participation in disease mapping and monitoring projects specific to the poultry industry; and to identify groups of poultry professionals with similar perceptions and attitudes towards monitoring/mapping projects as well as demographic features. An anonymous online survey was developed using Qualtrics and distributed to poultry professionals through industry associations. Factorial analysis and hierarchical clustering on principal components were applied to survey respondents. The analysis was based on specific features of perceived risks and benefits of participation, their roles, commodity and area of production in the United States. A total of 65 participants (54%) and breeders (49%) were the most represented commodities; (54%) and breeders (49%), turkeys (29%) and "other" flock type (7%). Using cluster analysis, two distinct groups of respondents were identified: 1) Optimistic group that perceived major benefits of sharing disease information while having major concerns of potential accidental data release and 2) Less optimistic group that perceived a lesser degree of benefits of sharing disease information with a high number of participants highly ranking competitive advantages to rival companies as a major concern. The first group was mostly composed of animal health professionals while the second group was mostly composed of executives and production managers. Results showed that there are identifiable groups of poultry professionals in regards to perceived benefits and risks of sharing disease information. For successful development of disease monitoring platforms in the future, poultry professions will likely need to be approached in different manners in order to achieve maximum participation.
Keywords for abstract	Benefit Cluster analysis Disease mapping Poultry Risk

Title of abstract	PIGS, PATHOGENS AND PEOPLE: A NOVEL APPROACH TO MONITORING INTERNAL BIOSECURITY IN SWINE PRODUCTION
Authors	N.J. Black, L.E. Moraes, A.G. Arruda. Depts of Veterinary Preventive Medicine and Animal Sciences
Abstract	Many infectious diseases that impact the swine industry have high economic consequences. Formite transmission facilitates the spread and persistence of pathogens within a herd, thus a strong internal biosecurity protocol is integral. While there are general internal biosecurity guidelines commonly implemented on farms, detailed quantification and characterization of within-farm employee movements is currently unavailable in the literature. The objective of this study was to utilize beacon-sensing technology to investigate the association between specific within-farm movements (growing pig rooms to farrowing rooms, loadout areas to farrowing rooms and between farrowing rooms) and a key production parameter: number of pigs weaned per sow (PWS). Three US commercial swine farms were enrolled in this project and an internal biosecurity system was installed. Sensors were placed in each room throughout each farm, and Bluetooth-based beacon devices were individually distributed to farm employees. Within-farm movement data was collected for approximately one year, sent to a central database and collapsed weekly. Weekly production records were obtained from each farm. A linear mixed-effects model was fit in STATA 15 with farm as a random effect. An increase in the frequency of movements between farrowing rooms over the two weeks prior to the week in which the outcome was captured was associated with a decrease in PWS (p = 0.025), after controlling for farm, season, pre-weaning mortality, and PWS the prior week. This finding supports the notion that excess movements between farrowing rooms facilitate pathogen transmission. Additionally, an increase in the frequency of movements from growing pig rooms to farrowing rooms tended to decrease PWS (p = 0.12), after controlling for farm, season, pre-weaning mortality, and PWS the prior week. In conclusion, sensor technology appears to be a useful tool in identifying gaps in internal biosecurity protocol and facilitate directed disease mitigation efforts.
Keywords for abstract	Swine production Biosecurity Technology Disease control

Title of abstract	STOCKING DENSITY IMPACTS GROUP-HOUSED COWS' ABILITY TO SEEK SECLUSION BEFORE CALVING
Authors	K. Creutzinger ¹ , H. Dann ² , P. Krawczel ³ , G. Habing ¹ , and K. Proudfoot ⁴ . ¹ Veterinary Preventive Medicine, ² William H. Miner Agricultural Research Institute, ³ University of Helsinki, ⁴ University of Prince Edward Island
Abstract	Dairy cattle in natural environments separate from conspecifics at calving to find a desirable calving site, but it is unclear if indoor-housed cows have retained the motivation to seclude at calving in group pens. Our objective was to determine if indoor group-housed cows changed their distance to penmates before calving. We hypothesized separation behavior would be impacted by stocking density and providing a physical space to seclude in the pen ('blind'). Holstein cows (n=374; mean parity±SD=1.4±1.4) were enrolled once weekly 21±3d before their expected calving date. Effects of stocking density and a blind were tested using a 2×2 factorial arrangement of treatments: 1) high stocking density (7.9×9.8 m; 9.7-12.9 m²/cow) without blind, 2) high stocking density with blind, 3) low stocking density (7.9×19.5 m; 19.4-25.8 m²/cow) without blind, and 4) low stocking density with blind. Blinds included plastic road barriers and plywood (3.6×0.6×1.5m). A subset of 62 cows with unassisted calvings were selected randomly for analysis. For analysis, high and low stocking density pens were divided into 9 and 18 grid-areas of equal size (3.3×2.6m). Instantaneous scan sampling (10-min) was used to count the number of cows within 1, 2, and ≥3 grid-areas relative to each focal cow 24h before calving. During the 24h before calving, cows in low stocking density pens had a lower number of penmates within 1 grid-area compared with those in high stocking density pens (P<0.001). Cows in low stocking density pens had fewer cows within 1 grid-area starting 4h before calving (P=0.002). Cows in high stocking density pens did not differ in the number of cows in each grid-area as calving approached. This suggests indoorhoused cows have retained the motivation to separate from penmates before calving but stocking density impacts this behavior. Restricting parturient cows' ability to perform natural calving behaviors may negatively affect welfare.
Keywords for abstract	Dairy Cattle Animal Welfare Stocking Density

Title of abstract	DRIVERS AND BENEFITS OF CANINE LYME BORRELIOSIS PREVENTION METHODS IN A LYME-ENDEMIC AREA
Authors	L. Giralico, T. Wittum, A. Smith, J. Stull Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio
Abstract	Human Lyme disease and its canine counterpart Lyme borreliosis are common tick-borne illnesses in the US. Transmitted via the bite of infected <i>Ixodes</i> spp. ticks, disease incidence mirrors the tick's home range, and control emphasizes tick and pathogen (<i>Borrelia burgdorferi</i>) prevention. The aim of this study was to explore drivers of Lyme borreliosis prevention strategies in a Lyme-endemic area and to determine if these strategies were significantly associated with <i>B. burgdorferi</i> serostatus. From 2017-2018, dog-owning clients at a Maine veterinary clinic were invited to complete an online survey assessing owner knowledge, attitudes, and tick prevention practices. <i>B. burgdorferi</i> serostatus (4Dx® Plus Test) was determined at enrollment. Several drivers were associated with reported use of prevention strategies. Respondents who were "extremely concerned" they or a member of their household could get Lyme disease were more likely to perform daily tick checks on their dog than less concerned owners (OR=1.7 <i>P</i> =0.02), and those with household children were more likely to modify their property than those without (OR=1.9 <i>P</i> =0.02). Dogs encountering fields (OR=2.4) and forests (OR=3.4) in the past year and those spending at least half of their time outside (OR=2.4) had higher odds of being vaccinated against <i>Borrelia</i> (all <i>P</i> <0.004). Owners of dogs that encountered fields and forests in the past year were more likely to use tick prevention medications (all <i>P</i> <0.011). Dogs vaccinated against <i>Borrelia</i> had lower odds of being seropositive (OR=0.26 <i>P</i> =0.001). Property modification was associated with lower odds of owners finding ticks on their dog at least weekly (OR=0.41 <i>P</i> =0.011) but was not associated with <i>Borrelia</i> serostatus.
Keywords for abstract	Tick-borne illnesses canine

Title of abstract	PREGNANCY DIAGNOSIS IN SOUTHERN WHITE RHINOCEROS (CERATOTHERIUM SIMUM SIMUM) BY NASAL SECRETION AND SERUM
Authors	<u>D. Guzman</u> , P. Joyner, M. Stoops, M. Flint. The Ohio State University College of Veterinary Medicine, The Wilds, Omaha Henry Dooly Zoo
Abstract	Successful reproduction of the threatened southern white rhinoceros (<i>Ceratotherium simum simum</i>) (SWR) in captive populations has been a challenge for conservation facilities. Feces, serum and ultrasound have been used to diagnose pregnancy in SWR. While feces is a plentiful and non-invasive means of pregnancy detection, rhinoceros use communal dung piles, making it challenging to identify and collect from specific individuals managed in herds on pastures. At The Wilds, SWR are managed on large pastures in large social groups for 6 months of the year. Given this husbandry practice, which is similar to many other facilities, the validation of a commercial test for pregnancy using serum and non-invasive biomarkers would be ideal for individual pregnancy diagnosis. We hypothesize that pregnancy tests used in other species can be used and validated in SWR. Commercial equine pregnancy tests, OVUCHECK PREMATE10 and BioPRYN, will be used to measure progesterone levels using commercial Salimetrics Human Salivary Progesterone test to determine if nasal secretions can be used as a noninvasive means of pregnancy detection. Each test will be validated by the gold standard of testing serum in a reproductive hormone lab for progesterone levels. Sample collection will occur on a monthly basis from July 2019-March 2020. Samples will be stored at -20°C and tested once all collection has been completed. Blood and nasal secretions will be collected from 2 confirmed pregnant and 7 non-pregnant SWR to determine which tests are accurate and effective for pregnancy diagnosis.
Keywords for abstract	Ceratotherium simum simum Southern White Rhinoceros Progesterone detection Pregnancy

Title of abstract	A SURVEY STUDY OF PROPHYLACTIC RABIES VACCINATION REGULATIONS FOR COMPANION ANIMALS IN OHIO
Authors	A. Jokerst, and J. O'Quin. Dept. of Veterinary Preventive Medicine
Abstract	Risk of rabies to humans and companion animals is quite preventable through the administration of regular rabies vaccinations in pets (CDC, 2019). This, in turn, additionally helps with prevention of rabies from wildlife (CDC, 2019). There are 38 U.S. states that have statewide rabies regulations, yet the state of Ohio is not among them (ODH, 2008a; ODH, 2008b). This cross-sectional survey study focuses on prevention at the local and state levels by surveying 113 local health jurisdictions within Ohio. The objectives of the study were to evaluate the status of rabies vaccination legislation requirements for companion animals (dogs, cats, ferrets, and horses) by jurisdiction, as well as to examine the availability of low-cost rabies vaccination options and the perception of risk of raccoon-variant rabies from wildlife. This study was reviewed by the Institutional Review Board of the Ohio State University and was approved with the status of "exempt". The survey was open for approximately one month between November 2019 and December 2019. 150 surveys were completed total, including 30 of those being repeat responses from jurisdictions that had already completed the survey. 103 out of 113 jurisdictions had responded, with a 91.2% response rate. A vast majority of responding jurisdictions had participants who supported enacting statewide rabies legislation for dogs, cats, and ferrets. 72% of responding jurisdictions indicated that they believed that there were low-cost rabies vaccine options within or nearby their jurisdiction. The results of this study support public health efforts surrounding education and legislation to improve rabies prevention and control methods. References CDC. (2019). How Can You Prevent Rabies in People? Retrieved from https://www.cdc.gov/rabies/prevention/people.html ODH. (2008a). 2008 Ohio Local Health Districts Prophylactic Rabies Vaccine Requirements for Dogs, Cats, Ferrets. Ohio Department of Health.
Keywords for abstract	Rabies, Companion animals, Wildlife, Statewide, Regulation, Racoon-variant, Low-cost, Cross-sectional survey, Legislation Jurisdiction, Vaccination, Ohio, Public health

Title of abstract	IDENTIFYING MEMBRANE-ACTIVE NEXT GENERATION ANTIMICROBIALS EFFECTIVE AGAINST AVIAN PATHOGENIC ESCHERICHIA COLI (APEC)
Authors	D. Kathayat, G. Closs Jr, Y. A. Helmy, L. Deblais, and G. Rajashekara. Food Animal Health Research Program, Department of Veterinary Preventive Medicine
Abstract	Avian pathogenic <i>E. coli</i> (APEC), an extra-intestinal pathogenic <i>E. coli</i> (ExPEC), causes high morbidity and mortality in poultry. A recent report has suggested APEC as foodborne human uropathogen and is also considered as source of antibiotic resistant genes (ARGs) to human pathogens. Currently, antibiotics are commonly used to control APEC infections; however, APEC strains resistant to multiple antibiotics have been reported worldwide. Therefore, new and potent anti-APEC therapeutics are critically needed. Our recent study has identified probiotic <i>Lactobacillus rhamnosus</i> GG (LGG) effective in reducing APEC burden in chickens. Further investigation revealed multiple small peptides (~40) prevalent in the LGG culture supernatant. The subsequent synthesis and testing of selected peptides identified three peptides (P-1, P-2, and P-3) exhibiting bactericidal activity (minimum bactericidal concentration: 12-18 mM) against APEC, including antibiotic-resistant APEC strains and APEC in biofilm. Confocal fluorescence and transmission electron microscopy studies revealed peptides affecting the APEC membrane integrity either by causing membrane shedding, rupturing or flaccidity. These peptides, at MBC, reduced the intracellular survival of APEC (>3 logs) in chicken macrophage HD11 cells. Further, the pre-treatment of wax moth larvae with these peptides at 25.5 mM, protected the larvae from APEC infection (>60% reduction in mortality) and decreased the APEC burden (>7 logs) inside the larvae. Structure-activity analysis of these peptides by alanine scanning identified amino acid residues crucial (N, E, R and P in P-1, D and E in P-2, and T, P and K in P-3) for their activity. Further, arginine and lysine substitutions identified peptide derivatives with enhanced anti-APEC activity. Our future studies will test the efficacy of these peptides against APEC infection in chickens and identify their antibacterial targets by expression and pull-down based methods. These studies will help to develop new generation antimicrobia
Keywords for abstract	APEC LGG peptides antimicrobial membrane integrity

Title of abstract	YEAR-ROUND INFLUENZA A VIRUS SURVEILLANCE IN ANAS PLATYRHYNCHOS REVEALS GENETIC PERSISTENCE DURING THE UNDER-SAMPLED SPRING SEASON
Authors	S.E. Lauterbach ¹ , D.S. McBride ¹ , J.M. Schmit ² , M.A. Piccutio ² , B.T. Shirkey ² , J.M. Nolting ¹ , A.S. Bowman ¹ ¹ The Ohio State University Department of Veterinary Preventive Medicine ² Winous Point Marsh Conservancy
Abstract	Active influenza A virus (IAV) surveillance efforts in wild waterfowl in the United States have largely been conducted during the summer breeding and autumn migratory periods due to convenience-based sampling methods. This sampling has resulted in a gap in surveillance during late winter and spring migration. Consequently, surveillance has not shown the complete picture of how IAV circulates through the population on a continuous timeline. We conducted active IAV surveillance in wild mallards (<i>Anas platyrhynchos</i>) continually, July 2017-July 2019, in order to understand the ecological and evolutionary dynamics of IAV across multiple seasons, including spring migration. Surveillance was conducted in the southwest Lake Erie marshes near Port Clinton, Ohio, USA, a popular migratory waterfowl stopover site. We collected 2096 cloacal swabs from mallards and estimated an overall prevalence of 6.1% (95% CI [0.051, 0.072]) by virus isolation. Prevalence was lowest during the spring months when it was estimated at 1.0% (95% CI [0.005, 0.016]). The current study detected genetic persistence of IAVs across multiple seasons, including spring migration. Time-scaled phylogenetic analyses revealed local persistence and evolution of genetic lineages of internal and antigenic gene segments. The highly conserved PA gene segment consists of a genetic lineage detected in summer 2017, spring, summer and fall of 2018, and spring of 2019 with a TMRCA of 2.48 years (95% HPD [2.16, 2.74]). Analysis of the H3 and H6 gene segments revealed close relation between viruses detected in the spring and following autumn migration. Though mechanisms behind viral persistence in a single location are not well understood, we provide evidence that viruses can persist within a single location across multiple seasons. In order to capture the breadth of genetic diversity of IAV in waterfowl to prepare for HPAI outbreaks and human pandemics, current longitudinal IAV surveillance methods must be adjusted accordingly.
Keywords for abstract	influenza A virus mallards surveillance spring season phylogeny

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

Title of abstract	MINDING THE GAP: INFLUENZA A VIRUS IN UNIQUE SEA
	DUCK HOST SPECIES
Authors	D.S. McBride, S.E. Lauterbach, J.M. Nolting, A.S. Bowman.
	Department of Veterinary Preventive Medicine
Abstract	Wild birds are considered the natural reservoir of influenza A viruses (IAVs) making them critical for IAV surveillance efforts. Previous evidence suggested possibly unique IAVs circulating in sea duck hosts. However, prior to 2014, only 42 out of 10,916 complete genome IAV strains in the Influenza Research Database (IRD) were isolated from sea duck hosts. From 2014-2017 we conducted focused surveillance at locations where sea ducks were commonly sampled. Our attempt to increase sea duck origin IAV data yielded 1135 samples from sea ducks of which 43 were positive by virus isolation and sequenced, accounting for 16 different HA-NA subtype combinations. To investigate phylogenetic patterns of sea duck IAVs, all gene sequences recovered from avian hosts were downloaded from IRD as of October 2018 (over 16,000 taxa for each internal gene). Phylogenetic analyses of IAV sequences from sea ducks revealed that in 2011, we recovered an IAV containing an H4 gene highly divergent from the majority of North American H4. Interestingly, the IAV that contained that divergent H4 gene, also contained an M gene with high relatedness to the H14 IAVs that reemerged in North American sea ducks after being sequestered in unsampled hosts for four decades. The time to most recent common ancestor (TMRCA) was 74.39 years. A Eurasian origin IAV lineage was detected in North American sea ducks in 2010, including several of the North American H14s. The NS gene from that lineage has since been detected in a sea duck in 2016. That 2016 NS has long branch length suggesting parallel evolution and persistence of that Eurasian origin clade in North American sea ducks (TMRCA 24.57 years). Sea duck host species seem to harbor unique diversity and may play an important role in antigenic shift and the long-term movement and persistence of IAVs.
Keywords for	Ducks
abstract	Surveillance
	Wild Birds
	Phylogeny
	i ilylogetty

Title of abstract:	CO-OCCURRENCE OF <i>CAMPYLOBACTER</i> SPECIES IN CHILDREN FROM EASTERN ETHIOPIA, AND THEIR ASSOCIATION WITH ENVIRONMENTAL ENTERIC DYSFUNCTION, DIARRHEA AND HOST MICROBIOME
Authors (see example above for format)	Y Terefe ^{1,2,3} , L Deblais ^{1,3} , M Ghanem ^{1,3} , Y A. Helmy ¹ , B Mummed ² , D Chen ⁴ , N Singh ⁴ , V Ahyong ⁵ , K Kalantar ⁶ , G Yimer ^{1,3} , J Y Hassen ² , A Mohammed ² , SL. McKune ³ , MJ. Manary ⁷ , M I Ordiz ⁷ , W Gebreyes ^{1,3} , A H. Havelaar ⁴ , G Rajashekara ^{1,3} ¹The Ohio State University, Columbus, OH, USA ²Haramaya University Dire Dawa, Ethiopia ³Global One Health initiative, The Ohio State University, Addis Ababa, Ethiopia ⁴University of Florida, Gainesville, FL, USA ⁵Chan Zuckerberg Biohub, San Francisco, CA, USA ⁶ Chan Zuckerberg Initiative, Redwood City, CA, USA ⁷ Washington University, St. Louis, USA
Abstract (300 word limit)	Campylobacter infection in early childhood has been associated with stunting and environmental enteric dysfunction (EED). Here, we assessed the prevalence, diversity, abundance of Campylobacter spp. in stools from children in eastern Ethiopia and their association with microbiome, diarrhea, and EED. Stool samples (n=100) were collected from randomly selected children (12 to 16 months) from five rural kebeles in Haramaya District, Ethiopia. Campylobacter prevalence and species diversity were assessed using PCR and meta-total RNA sequencing (MeTRS). Diarrhea, compromised gut permeability, and gut inflammation were observed in 48%, 45%, and 57% of children, respectively. The prevalence of Campylobacter spp. in children's stools was 50% (41-60%) by PCR and 88% (80-93.6%) by MeTRS. Seven Campylobacter species (C. jejuni, C. upsaliensis, C. hyointestinalis, C. coli, Campylobacter sp. RM12175) were detected by MeTRS in at least 40% of children stools in high abundance (at least 1.7-log rpm in positive children). Four clusters of Campylobacter species co-occurred in stool samples, suggesting that Campylobacter species co-occurred in stool samples, suggesting that Campylobacter species may co-inhabit in one reservoir. No associations between Campylobacter spp., EED and diarrhea were detected; however, characteristic microbiome profiles were identified based on prevalence of Campylobacter spp., EED, and diarrhea. Forty-seven bacterial species were correlated with Campylobacter, and thirteen of them also correlated with gut permeability, gut inflammation and/or EED severity. Forty-nine species not correlated with Campylobacter were correlated with gut permeability, gut inflammation, EED severity and/or diarrhea. This study demonstrated frequent detection of multiple non-thermophilic Campylobacter spp. and the association of Campylobacter, gut permeability, gut inflammation, EED severity, and diarrhea with characteristic microbiome composition. Further studies are needed to identify environmental reservoirs and the sources
Keywords for abstract	Campylobacter, Non-thermotolerant Campylobacter, EED, Diarrhea, Malnutrition, Stunting, Livestock reservoirs, MeTRS

	CONSISTENCY OF LYING TIME IS ASSOCIATED WITH
Title of abstract	REDUCED SERUM NON-ESTERIFIED FATTY ACIDS OF PREPARTUM DAIRY HEIFERS AND COWS
Authors	B.T. Menichetti, J.M. Piñeiro, A. Garcia-Guerra, A.E. Relling, W.P. Weiss, and G.M. Schuenemann Depts. Of Veterinary Preventive Medicine and Animal Sciences,
Abstract	The objective was to assess the association of pre-partum lying time (LT) with serum nonesterified fatty acids (NEFA) in prepartum dairy heifers and cows. Pregnant diary heifers (n=229) and multiparous cows (n=494) from 3 dairy herds were enrolled at 14±3d prior to parturition (dpp). At enrollment, electronic data loggers (IceQube, IceRobotics, Edinburgh, UK) were fitted to the hind leg of individual heifers and cows to assess their LT. To assess consistency of LT, the coefficient of variation (CV) of LT was computed for each individual animal by dividing the SD by mean LT within 7 d prior to blood NEFA collection and reported as an absolute ratio. Blood samples were collected at 7±3 dpp for serum NEFA concentration. Herd 1 regrouped animals three times per week while herds 2 and 3 regrouped animals once per week. PROC CORR procedure of SAS was used to assess the relationship between CV of LT and prepartum serum NEFA. Correlations were adjusted by parity, body condition score (BCS) at enrollment, season, and herd. Season, herd, parity, and BCS were associated with CV of LT (P<0.05). Pregnant heifers had an overall mild (r = 0.28, P<0.0001; herd 1: r=0.13, herd 2: r=0.52, and herd 3: r=0.19) significant positive correlation between mean CV of LT and serum NEFA. Multiparous cows had an overall weak (r = 0.11, P = 0.01; herd 1: r=0.07, herd 2: r=0.13, and herd 3: r=0.14) significant positive correlation between mean CV of LT and serum NEFA. The greater the CV of LT (<0.10 vs >0.30) within 7 d prior to blood collection, the greater the concentration of serum NEFA (302 μEq/L vs 450 μEqL; P=0.005). These findings provide evidence that consistency of LT of prepartum heifers and cows should be considered when troubleshooting metabolic problems at the herd level.
Keywords for abstract	Prepartum Lying time NEFA

Title of abstract	THE PRACTICAL APPLICATION OF ENVIRONMENTAL SURVEILLANCE AS A COMPONENT OF A COMPREHENSIVE VETERINARY ASP
Authors	E.E. Feyes, ¹ <u>D.F. Mollenkopf</u> , ¹ G.A. Ballash, ¹ J.C. Van Balen, ² A.E. Hoet, ¹ D.V. Diaz-Campos, ² T.E. Wittum ¹ ¹ Dept. of Veterinary Preventive Medicine and ² Dept. of Veterinary Clinical Science
Abstract	The OSU-CVM Antimicrobial Stewardship Working Group (ASWG) uses monthly environmental surveillance to understand the effectiveness of our VMC infection control and biosecurity protocols in reducing environmental contamination with multidrug resistant bacteria. Monthly surveillance allows us to monitor recovery trends of these resistant organisms and address issues that could negatively impact our patients, clients, staff, and students.
	The ASWG collects monthly samples from over 80 surfaces within the companion animal, farm animal and equine sections. Samples are collected from both human/animal contact and human-only contact surfaces using Swiffer® electrostatic cloths. These samples are cultured for <i>Salmonella</i> , extended-spectrum cephalosporin resistant Enterobacterales, carbapenem resistant Enterobacterales (CRE), and methicillin-resistant <i>Staphylococcus</i> .
	We commonly recover Enterobacterales resistant to extended-spectrum cephalosporins (977/2551, 38.3%) from the VMC environment. These antibiotic-resistant indicator bacteria are expected in a veterinary hospital setting where beta-lactam drug use is common. Recovery of both <i>Salmonella</i> and CRE has remained very low in our hospital environment (38/2551, 1.5% for Salmonella and 24/2551, 0.9% for CRE) over the past 24 months. Recovery of resistant bacteria from human-only contact surfaces (21.3%) is very similar to that from human/animal contact surfaces (28.8%).
	The active environmental surveillance component of our antimicrobial stewardship program allows us to reduce the threat of nosocomial infections within our hospital and address environmental contamination issues before they become a problem. Our consistent low recovery of bacterial pathogens is a good reflection of our existing cleaning and disinfection protocols and biosecurity measures. Due to the nature of our patient population, we expect to find resistant organisms in patient-contact areas. However, our frequent recovery of resistant bacteria from human-only surfaces such as keyboards, door handles, and Cubex machines, may indicate a need for better hand hygiene practices. This data is now supporting the implementation of a new Hand Hygiene Campaign in our hospital.
Keywords for abstract	Antimicrobial resistance Antimicrobial Stewardship Program Environmental surveillance

Title of abstract	INFLUENCE OF SOCIODEMOGRAPHIC FACTORS ON INFECTIOUS AND ZOONOTIC PATHOGEN RISK IN A RESOURCE-LIMITED COMMUNITY AT THE LIVESTOCK-WILDLIFE INTERFACE, MPUMALANGA, SOUTH AFRICA
Authors	P. Oruganti ¹ , A. Berrian ¹ , E. Root ² , and I. van Wyk ³ . ¹ The Ohio State University College of Veterinary Medicine, Department of Veterinary Preventive Medicine, ² The Ohio State University College of Public Health, ³ University of Pretoria, Pretoria, South Africa.
Abstract	In the Mnisi community, a livestock-dependent community neighboring the Great Limpopo Transfrontier Conservation Area in South Africa, zoonotic pathogens contribute to as many as 77% of acute febrile illness cases. Gender-disaggregated analysis has shown a risk differential for men and women, suggesting exposure routes for zoonotic infections should be further explored to inform gender sensitive risk mitigation strategies. Using a One Health approach focused on interactions between community residents, domestic animals, and the built and natural environment, this study investigated potential exposure pathways for zoonotic infections from a gendered perspective. This study used an ethnographic approach, combining household observations and focus group discussions, to examine behaviors. Participating households were randomly selected from three villages under the leadership of the Mnisi Traditional Authority in Mpumalanga, South Africa. Four household observations were conducted in each village followed by two focus group discussions (one male/one male). Observations and discussions focused on daily productive tasks such as domestic animal care, water collection, food preparation, and the division of labor. Data was triangulated across methods, and analysis includes translation, transcription, and thematic coding using fundamental grounded theory. Common themes coded from the observations and focus group discussions highlighted gendered roles in terms of household tasks and animal care duties. Other common themes included water collection and availability in the community, household income and time spent in the bush, overgrazing bush areas by cattle, and wild animal interactions within the community. This study contributes to the understanding of risk behaviors and critical control points for zoonotic disease, a significant contributor to acute febrile illness in this rural, resource-limited setting. It advances ongoing One Health surveillance and education efforts in this transboundary conservation area and expa
Keywords for abstract	One Health Zoonotic Diseases Global Health Qualitative Research

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

Title of abstract	HOUSING, HUSBANDRY AND CLINICAL TECHNIQUES IN THE LABORATORY CRAYFISH (PROCAMBARUS CLARKII)
Authors	M. Palillo, J. Palillo, M. Glon, L. Pintor, W. Bidot, M. White, and R. Malbrue
Abstract	Crayfish of the <i>Procambarus spp</i> , are one of the few animals that have stem cells within hemolymph with the capacity to continuously produce differentiated neuronal structures throughout life. As crayfish and other invertebrates continue to become common models in research to study human disease, it is vital that we develop universal laboratory standards and guidelines on housing and husbandry practices. To the authors' knowledge, this is the first study to evaluate clinical pathology, housing, husbandry, and anesthetic techniques in crayfish (<i>Procambarus clarkii</i>).
	Wright Giemsa stained slide preparations of the crayfish hemolymph were minimally cellular and had a moderately eosinophilic, proteinaceous background. Three different types of hemocytes were identified: hyaline, semigranular and granular, with hyaline being the predominant hemocyte.
	The housing and husbandry experiments were performed over a duration of 37 days. Mortality rates, molting percentages, physical health and behavioral assessments were performed. Water quality parameters were concurrently evaluated: temperature, light cycle, pH, KH, GH, conductivity, total dissolved solids, salinity, ammonia, nitrate, and nitrite.
	Anesthetic techniques were evaluated in four experimental groups: (A-B) immersion in MS-222 (50mg/L & 150mg/L respectively), (C) immersion in Propofol (65mg/L) and (D) Propofol injection (100mg/kg) into tail hemolymph. Housing and husbandry techniques were validated with 0% mortality after initial shipping losses and normal observed environmental behaviors. MS-222 had no observable effect on crayfish. Propofol injection (100mg/kg) into tail hemolymph successfully created a plane of sedation without adverse effects after recovery.
	Crayfish Procambarus sp Anesthesia
Keywords for abstract	Phlebotomy Laboratory Animal Husbandry Housing Cytology Water Quality

Title of abstract	HIERARCHICAL SURVEY OF VETERINARIAN AND DAIRY FARM WORKER ANTIMICROBIAL USE PRACTICES
Authors	R. Portillo-Gonzalez ¹ , J. Pempek ¹ , S. Locke ¹ , G. Habing ¹
Abstract	Antimicrobial use in food-producing animals may contribute to the development of drug-resistant bacterial infections in humans. Veterinarians prescribe and dispense antimicrobials, but farmworkers are responsible for judging disease severity and initiating on-farm treatments. The objective of this study was to estimate the differences in antimicrobial selectivity between veterinarians and farm-workers at different levels of cattle disease severity. We hypothesized that the frequency with which veterinarians and farmworkers select antimicrobials is significantly different at varying levels of disease severity. This was a cross-sectional study that used hierarchical surveys and clinical case vignettes to collect information from veterinarians and workers on their dairy farm clients. The survey included vignettes of mild, moderate, and severe cases of lameness, metritis, and mastitis. In 2019, we received responses from 35 veterinarians and 66 farm-workers in Ohio. Fisher's exact tests were applied to evaluate the frequency in antimicrobial selectivity between veterinarians and farm-workers. The percentage of individuals that selected antimicrobials (PISA) was 31.4%, 34.3% (veterinarians) and 10.6%, 6.1% (farm-workers) for local (p=0.013) and systemic (p<0.001) mild interdigital pododermatitis (IP) respectively. Also, PISA was 74.3%, 85.7% (veterinarians) and 33.3%, 36.4% (farm-workers) for local moderate digital dermatitis (p<0.001) and systemic moderate IP (p<0.001) respectively. Likewise, PISA was 62.9%, 94.3% (veterinarians) and 37.9%, 59.1% (farm-workers) for intramammary (p<0.001) and systemic (p<0.001) severe mastitis respectively. However, No PISA differences between the groups were found in any of the different severity levels of metritis (mild p=0.542, moderate p=1.000, and severe p=0.079). This study demonstrates that farm-workers were less likely than veterinarians to select local and systemic antimicrobials for descriptions of routine cases of disease. Therefore, attention should be paid to implement
Keywords for abstract	Antimicrobial hierarchical survey dairy cattle antimicrobial use.

Title of abstract	THE EFFECT OF STOCKING DENSITY AND A BLIND ON THE SOCIAL BEHAVIOR OF PREPARTURIENT DAIRY CATTLE
Authors	J. Rose ¹ , K.C. Creutzinger ¹ , and K.L. Proudfoot ² . ¹ Veterinary Preventive Medicine, College of Veterinary Medicine, Ohio State University, Columbus, Ohio. ² Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, Canada.
Abstract	There is limited information on the appropriate housing for preparturient dairy cows. Our objective was to determine the impact of stocking density and the provision of a blind on social behaviors of pre-parturient dairy cows. We hypothesized that cows with low stocking density and a blind would have the most affiliative and fewest agonistic behaviors. A total of 374 cows (mean parity ± SD = 1.4 ± 1.4) were enrolled in one of 4 treatments using a 2×2 factorial arrangement with two factors: stocking density (high vs. low; 9.3 m²/cow vs. 18.6 m²/cow) and a blind in the pen (yes vs. no). Cows were loose-housed on deep-bedded sawdust. Pens were replicated 4 times. A sub-sample (n=64; nulliparous=32, parous=32) of cows were selected randomly for video analysis. The frequency of allogrooming and agonistic behaviors (head-butt, chase, threat, displacement, and pushing) were recorded continuously for 3 d during the 2 wk before calving for each cow. To date, the video analysis for 46 cows has been completed (high vs. low=18 vs. 28; blind vs. no blind=17 vs. 29). All data were analyzed using a generalized linear mixed model with negative binomial distribution. Fixed effects included stocking density, blind, and their interaction. We found no effect of stocking density (P=0.11), blind (P=0.26), nor an interaction (P=0.98) on the frequency of affiliative behaviors. There was a significant interaction between stocking density and blind for agonistic behaviors (P=0.05) which was greatest in low stocking density pens with blinds had more agonistic behaviors than the other treatments. We believe this could be the result of the cows having more room to perform behaviors and the competition for the use of the blind.
Keywords for abstract	Animal welfare Stocking density Social behavior Transition cows

Title of abstract	TONSIL SCRAPINGS FOR PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS DETECTION
Authors	H.L. Walker ¹ ; A.S. Bowman ¹ ; J.B. Ferreira ² ; S.W. Nelson ¹ ; A.G. Arruda ¹ Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, OH; ² Department of Population Health and Pathobiology, College of Veterinary Medicine, North Carolina State University, Raleigh, NC.
Abstract	Porcine reproductive and respiratory syndrome (PRRS) is the most costly disease currently affective the North American swine industry. Even though this virus has a predilection for respiratory and lymphoid tissues, research on the use of tonsil scrapings (TS) for PRRS virus (PRRSV) detection under field conditions is limited. The objectives of this study were to describe the use of TS, oral fluids (OF), nasal swabs (NS), and environmental swabs (ES) to detect PRRS virus (PRRSV) in pig herds; and investigate whether farm PRRS vaccination status was associated with PRRSV detection in TS. Two PRRS positive farms were enrolled; a wean-to-finish facility with unvaccinated pigs weaned from a newly positive sow farm and a finisher farm with pigs vaccinated at processing. Eight individual TS and NS samples and 8 pen-level OF and ES samples were collected for a period of 5 months from each farm as previously described ^{1,2,3} . Testing was done via RT-PCR, and a Ct value < 37 was used to declare PRRSV positivity ⁴ . The association between farm vaccination status and TS PRRSV detection was tested using Pearson's chi-squared test. A total of 256 samples were collected: 64 TS, 64 OF, 64 NS, and 64 ES. The majority of tonsil scraping samples (n=37, 59.4%) tested positive for PRRSV, while two (3.1%) OF samples, 6 (9.4%) NS samples, and 1 (1.6%) ES sample tested positive. Overall prevalence of PRRSV in the unvaccinated and vaccinated herds was 50.0% and 75.0% respectively, and there was no association between farm vaccination status and a positive TS PCR (P = 0.10). There are currently no established protocols for PRRSV sampling in growing pig populations, and our results show TS may be a promising sampling method. 1 Prickett et al. 2008; 2 Hess et al. 2018; 3 Rotolo et al. 2017; 4 Gerber et al. 2013.
Keywords for abstract	PRRS Oral fluids Tonsil scraping Growing pigs

Title of abstract	ORGANIC DAIRY FARMER HERD HEALTH DECISIONS ON TREATMENT AND PREVENTION OF DISEASE
Authors	K. Weaver, J. Pempek, C. Brock, D. Jackson-Smith, L. da Costa, G. Habing; Depts of Veterinary Preventive Medicine and School of Environmental and Natural Resources
Abstract	Little is known about the organic dairy farmer's approach to herd health management. Therefore, the goal of this study was to use semi-structured interviews to characterize organic dairy farmers' perspectives on disease prevention and treatment strategies. Twenty-three organic dairy producers in Ohio were interviewed to explore the decision-making processes on herd health challenges, as well as a focus on vaccine and antimicrobial use. Qualitative answers were analyzed to assess key concepts using NVivo TM software. The top reported herd health challenges were mastitis (74%), lameness (48%), and flies (48%). The top reported prevention strategies were dietary supplements (74%), cleanliness (61%), high forage diet or balanced rations (57%), and vaccinations (40%). The majority (57%) of producers reported using vaccines and the primary concerns of inconvenience and safety were cited by 80% (8/10) and 60% (6/10) of non-vaccinating producers, respectively. Any use of antimicrobials was reported by 45% of producers, most of whom reported isolated treatment events and grappled with a case definition to initiate therapy. Beyond removal from the organic herd, barriers to antimicrobial use included the inconvenience and financial disincentive of managing the majority vaccinated, not all producers viewed vaccination as a top prevention strategy, and findings highlight opportunity to address negative perceptions about vaccine safety. Further, protocols that clarify case definitions that warrant antimicrobial therapy are needed to guide farmers with this decision when treatment is necessary.
Keywords for abstract	Organic Dairy Producers Herd Health Vaccines Antibodies

CLINICAL RESEARCH

Title of abstract	SURVEY OF OWNER AWARENESS OF LITTER BOX HABITS IN HEALTHY CATS
Authors	S. Adams, J. Quimby, A. Rudinsky, S. Caney, S. Jones
Abstract	An online questionnaire was completed by cat owners around the world in order to survey cat litter box behaviors and learn more about owner awareness of defecation frequency in normal cats. Owners were asked to complete an initial survey, and then clean the box daily for 7 days and report results daily using Purina Fecal Score (1-7) to assess feces. Surveys from 389 owners were collected from 19 countries and came mainly from the United States, the United Kingdom, Australia, and Canada. On the initial survey, the most common defecation frequency was daily (59.3%), followed by twice a day (23.4%). Less than 5% reported defecations less than every other day. The average number of daily defecations was 1.2 +/- 0.7, and the average fecal score was 2.3 +/- 0.8. there was no significant difference between the average fecal scores between age groups (under 1, 1-6 years, 7-10 years, 11-14 years, and 15+ years). The average number of urinations reported was 2.8+/- 1.1. Similar results were found on day 2 after scooping the box (171 responders), with the average number of daily defecations being 1.3 +/- 0.6, an average fecal score of 2.3 +/- 0.9, and the average number of urinations being 2.4 +/- 0.9. All 7 days of the survey were completed by 88 responders and after scooping the box daily for a week, it was reported that the average number of daily urinations was 2.7 +/- 1. 61.4% of responders stated they were more aware of their cat's toileting behavior after completing all 7 days of the survey. In conclusion, the daily number of defecations for normal cats was typically 1-2, and the daily number of urinations was 2-3.
Keywords for abstract	Feline Urine Feces Defecation

Title of abstract	EVALUATION OF FACTORS ASSOCIATED WITH SKIN DISEASE AND MORTALITY IN EASTERN HELLBENDERS (CRYPTOBRANCHUS ALLEGANIENSIS ALLEGANIENSIS)
Authors	A.C. Aplasca ¹³ , M.E. Martinez ² , R.E. Junge ³ , and M. Flint ¹ . Depts. Of ¹ Veterinary Preventive Medicine, ² Veterinary Biosciences, and the ³ Columbus Zoo and Aquarium
Abstract	Amphibian population declines have occurred across a diverse range of geographic regions, and of approximately 7900 described amphibian species, an estimated 40% are threatened. Various factors including overharvesting, disease, habitat loss, and environmental contamination have been linked to amphibian population declines. The Eastern hellbender (<i>Cryptobranchus alleganiensis alleganiensis</i>) is classified as endangered in the state of Ohio. To increase Ohio populations, collaborative programs 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, however, mortality rates are highly variable and causes of mortality are poorly understood. Our research aims to investigate major factors that impact morbidity and mortality in captive-reared hellbenders. Gross necropsies were performed on juvenile hellbenders that died over a three-month period in a captive-rearing setting (n=17). Fourteen individuals (14/17, 82%) had external cutaneous lesions in the form of abnormally thick mucus layers, ulcerations, papules, or white cottony aggregates. Preliminary histopathologic examination revealed cutaneous erosion, ulceration, and necrosis in all individuals (17/17, 100%). Bacteria was seen in 94% (16/17) and fungal hyphae were seen in 71% (12/17) of individuals examined. Mild interstitial nephritis was seen in 35% (6/17) of individuals examined and other lesions (e.g. myositis, neuritis, and enteritis) were seen in single individuals. Skin disease can significantly impact normal respiration and ion transport in amphibians and can lead to severe metabolic disturbance and death. Based on our preliminary findings, additional research is planned to further characterize cutaneous lesions in hellbenders. Future research will compare grossly normal and abnormal skin tissues histopathologically. In addition, molecular methods will be used to further characterize the bacterial and fungal composition in normal and a
Keywords for abstract	Amphibians Eastern hellbender Captive-rearing Pathology Head-start programs

Title of abstract	DIETARY CARBOHYDRATE CONTENT ALTERS HEPATIC GLUCOSE AND LIPID METABOLISM IN LEAN AND OBESE MIXED BREED PONIES
Authors	Bercz. A, Watts. M, Burns. T.
Abstract	Laminitis is a debilitating condition of the equine foot and a common complication of endocrine disease in equids. Insulin dysregulation (ID), associated with hyperinsulinemia and tissue insulin resistance, is the most important risk factor for laminitis in horses with endocrine disease and is associated with high carbohydrate diets and obesity. The liver is a central regulator of systemic insulin and glucose dynamics in other species, but its role in the pathophysiology of equine ID is not well characterized. Twenty-two mixed breed ponies were divided into lean and obese groups and fed a control, low-NSC diet or high-NSC diet for one week, after which samples of liver were collected and analyzed with real-time quantitative PCR for genes associated with carbohydrate and lipid metabolism and qualitative histopathology. Liver from lean and obese ponies fed high-carbohydrate diets expressed lower levels of insulin-dependent glucose transporter (GLUT)-4, higher levels of acetyl-coA carboxylase, and had subjectively greater hepatic lipid accumulation apparent on histologic examination than ponies fed the control diet. Obese ponies, regardless of diet, expressed nearly 2-fold greater levels of plasminogen-activator inhibitor and decreased transcripts of insulin-independent GLUT1 compared to lean ponies. Peroxisome proliferator-activated receptor γ (PPARγ) transcripts were lower in high-NSC fed ponies and generally lower in obese ponies. Alterations in hepatic expression of genes associated with carbohydrate, lipid and insulin metabolism in response to diet and obesity may be important in the pathogenesis of equine ID.
Keywords for abstract	Laminitis, metabolism, pony, insulin

Title of abstract	EFFICACY OF DISTAL LIMB CRYOTHERAPY IN A MODEL OF
าแอ บา สมอแสนเ	EQUINE ENDOCRINOPATHIC LAMINITIS
Authors	<u>Chia-Ming Chen</u> , Mauria R Watts, James K Belknap, Teresa A Burns. Veterinary Clinical Sciences, College of Veterinary Medicine
Abstract	Equine metabolic syndrome (EMS)-associated laminitis (EMSAL) is the most common form of laminitis in horses, and insulin dysregulation (ID) is the most important risk factor for its development. Ribosomal protein S6 (RPS6) has been shown to be consistently phosphorylated in lamellar tissue of horses with experimental EMSAL and is correlated with lamellar integrity. Distal limb cryotherapy is known to be effective in preventing sepsis-related laminitis (SRL), but its efficacy in EMSAL is unknown. Eight Standardbred horses were subjected to a euglycemic-hyperinsulinemic clamp (EHC) to induce laminitis with one forelimb submerged in ice-water slurry and the other maintained at ambient temperature for 48 hours, after which they were humanely euthanized. Immediately after euthanasia, digital lamellar samples were collected for Western blot, real-time quantitative PCR, and immunofluorescence. Activation of RPS6 (based on lamellar concentrations of P-RPS6) was significantly lower in the lamellae of the iced limbs compared to those at ambient temperature (p = 0.008). Lamellar immunofluorescence revealed that RPS6 activation was primarily localized to lamellar keratinocytes and was also markedly decreased in the iced tissue compared to ambient temperature. Lamellar expression of pro-inflammatory genes, such as IL-6, COX-2, and MMP-9, was also significantly mitigated by cryotherapy (p < 0.05). Cryotherapy appears to be similarly effective in attenuating the pathophysiologic events of EMSAL as it is in the setting of SRL, suggesting it may be clinically useful in treating EMSAL patients.
Keywords for abstract	insulin dysregulation (ID) Equine metabolic syndrome associated laminitis (EMSAL) Laminitis Ribosomal protein S6 (RPS6) Cryotherapy euglycemic-hyperinsulinemic clamp (EHC)

Title of abstract	SERUM IL-6 & MCP CONCENTRATIONS IN DOGS WITH LYMPHOMA BEFORE AND AFTER DOXORUBICIN TREATMENT AS A MARKER FOR OF CELLULAR SENESCENCE
Authors	B. Evans, M. Brown, J. Fenger, G. Ballash. Depts. Of Veterinary Clinical Sciences and Veterinary Preventative Medicine
Abstract	Cellular senescence (CS) is terminal cell-cycle arrest. During senescence, cells develop distinctive signaling features referred to as the senescence-associated secretory phenotype (SASP). CS is both tumor suppressing to prevent proliferation of cells exposed to genetic stress and cancer promoting as cancer cells can undergo CS in response to therapeutics, leading to chemotherapeutic resistance. Prior studies have documented increased IL-6 and MCP-1 in lymphoma (LSA) dogs; however, the impact of chemotherapy on cytokines has not been evaluated. The goal of this study was to evaluate IL-6 and MCP-1 in dogs before and after doxorubicin administration with a secondary aim of cytokine correlation with response and/or chemotherapeutic toxicity. We hypothesized that IL-6 and MCP-1 would increase following doxorubicin. A prospective cohort study was conducted in LSA dogs (N=16) undergoing doxorubicin-based chemotherapy. Serum IL-6 and MCP-1 was evaluated by ELISA at diagnosis, prior to doxorubicin, and 3hr, 6hr, 24hr and 1wk post-doxorubicin. We observed a significant decrease in IL-6 1wk post-doxorubicin compared to 0-6hr (p=0.001) and 24hr (p=0.045). MCP-1 significantly decreased prior to doxorubicin when compared to diagnosis (p=0.003), likely reflecting decreased tumor burden and reduced cytokines from chemotherapy. We observed an increase in MCP-1 24hr post-doxorubicin (p=0.001), consistent with an acute inflammatory reaction from chemotherapy. However, this increase was transient and MCP-1 levels decreased 1wk post-doxorubicin compared to 0-6hr (p=0.014) or 24hr (p<0.001). IL-6 or MCP-1 levels did not correlate with response, protocol, or doxorubicin dose. The lack of chemotherapy-associated toxicities precluded cytokine correlation. This study documents longitudinal variation in IL-6 and MCP-1 in LSA dogs undergoing chemotherapy. Cytokines implicated in SASP development did not show a significant increase following chemotherapy, suggesting that IL-6 and MCP-1 are not useful biomarkers for CS induction in dogs.
Keywords for abstract	Adriamycin Cytokine Cancer Canine Chemotherapy Terminal growth arrest Toxicity

Title of abstract	ASSESSING OPTICAL COHERENCE TOMOGRAPHY FOR SURGICAL MARGIN ASSESSMENT FOR CANINE MAMMARY TUMORS
Authors	C. Fabelo, MS, L. E. Selmic, BVetMed (Hons), MPH, DACVS, DECVS, P-C Huang, BS, MS, J. Samuelson, DVM, DACVP, J. K. Reagan, DVM, MS, DACVS, A. Kalamaras, DVM, V. Wavreille, DVM, MS, DACVS, M. Marjanovic, PhD, S. A. Boppart, MD, PhD
Abstract	Optical Coherence Tomography (OCT) uses near-infrared light waves to generate real-time, high resolution images on the microscopic scale similar to low power histopathology. Previous studies have demonstrated the use of OCT for real-time surgical margin assessment for human breast cancer. The use of OCT for canine mammary tumors (CMT) could allow intra-operatively visualization of residual tumor at surgical margins. The purpose of this study was to assess OCT imaging for detection of incomplete tumor resection following CMT surgery. We hypothesized that OCT images would have comparable features to histopathological images of tissues at the surgical margins of CMT resections along with a high sensitivity of OCT detection of incomplete surgical excision of CMT. Thirty surgical specimens were obtained from nineteen client-owned dogs undergoing surgical resection of CMT. Optical coherence tomographic appearance and characteristics of adipose tissue, skin, mammary tissue, and mammary tumor at surgical margins were distinct and different. The OCT images of normal and abnormal tissues at surgical margins were utilized to develop a dataset of OCT images for observer evaluation. The sensitivity and specificity for <i>ex vivo</i> images were 83.3% and 82.0% (observer 1), and 70.0% and 67.9% (observer 2). The sensitivity and specificity for <i>in vivo</i> images were 70.0% and 89.3% (observer 1), and 76.7% and 67.9% (observer 2). These results indicate a potential use of OCT for surgical margin assessment for CMT to optimize surgical intervention and clinical outcome. Improved training, experience of observers, and assessment of observers with different expertise may improve sensitivity and specificity.
Keywords for abstract	Optical Coherence Tomography OCT Canine mammary tumors Margins of excision Surgical oncology

Title of abstract	EVALUATION OF ESCHERICHIA COLI CONTAMINATION AND PATHOTYPE PRESENCE IN CONVENTIONAL AND RAW CANINE DIETS
Authors	J. F. Gibson, D. Diaz-Campos, C. Snell, J. Howard, J. Winston, C. Zumpetta, V. J. Parker, A. J. Rudinsky.
Abstract	Raw meat-based diets (RMBDs) are becoming increasingly popular amongst pet owners despite risks associated with enteropathogenic bacterial contamination. The most common enteropathogens cultured from RMBDs include <i>E. coli</i> , <i>Salmonella</i> spp., and <i>Clostridium</i> spp. The present study examined the frequency of <i>E. coli</i> contamination in commercial kibble diets and commercial RMBDs that included chicken or beef as the primary protein source. Nine cooked kibble diets (four beef, five chicken) and twenty-one RMBDs (eleven beef, one pork and beef, and nine chicken) were commercially purchased and analyzed. All diets were cultured for <i>E. coli</i> ; positive samples were analyzed using single-plex PCR for <i>E. coli</i> pathotype identification. No kibble diets cultured positive for <i>E. coli</i> , while fifteen (71%) RMBDs cultured positive. PCR testing identified a variety of <i>E. coli</i> pathotypes. This study highlights the potential enteropathogen risks associated with feeding diets containing raw meat, and should encourage closer inspection and control for bacterial contaminants in commercial RMBDs.
Keywords for abstract	Raw meat-based diets RMBDs Nutrition E. coli Bacteria Contamination food feeding

Title of abstract	PILOT STUDY: SERUM VITAMIN C LEVELS IN DOGS WITH NON-SEPTIC AND SEPTIC CRITICAL ILLNESS
Authors	D. Gordon, A. Rudinsky. Dept. of Veterinary Clinical Sciences
Abstract	Objective: To determine whether vitamin C levels in dogs decrease with critical illness
	Design: Prospective, observational, pilot study
	Methods: Blood samples were collected at presentation (D0), 24 hours (D1), and 48 hours (D2) of hospitalization and compared to healthy controls (n=10). Patients had evidence of septic or non-septic critical illness and clinical data was recorded for each patient. Serum vitamin C concentrations were measured via mass spectrometry.
	Results: Vitamin C levels at presentation (D0) were not statistically different between controls (n=10) and critical illness (n=16; p=0.86). Within the critically ill group, there was a trend toward a significant decrease in vitamin C level at admission and 24 hours of hospitalization (n=8; p=0.05). Critically ill dogs hospitalized for 48 hours (n=5), there was no difference in vitamin C levels between D0 vs. D1 (p=0.17), D0 vs. D2 (p=0.17), and D1 vs. D2 (p=>0.99).
	Conclusion: Vitamin C levels are not significantly different in patients with critical illness compared to healthy controls. Within the critically ill population, there may be a trend toward a significant decrease between vitamin C level at presentation and 24 hours of hospitalization. Further studies are needed with a more robust patient population to fully determine vitamin C levels in the critically ill patients.
Keywords for abstract	Vitamin C Critical illness Sepsis

Title of abstract	THE EFFECT OF CENTRAL CORNEAL THICKNESS ON INTRAOCULAR PRESSURE VALUES USING VARIOUS TONOMETERS IN THE DOG
Authors	A.Guresh, S. Horvath, A. Gemensky-Metzler, E. Miller, G. Newbold
Abstract	Objective: To compare intraocular pressure readings from three different tonometers, the Tono-Pen AVIA (TP), TonoVet (TV), and TonoVet Plus (TV+), and to determine how each is affected by central corneal thickness (CCT). Animals: 90 dogs of various genders, age, breed and ocular health statuses. Procedures: Dogs were evaluated for overall ophthalmic health and placed into three groups: normal, primary corneal disease, and primary intraocular disease. CCT measurements were gathered from each dog using the Pachette 4 ultrasonic pachymeter. Intraocular pressure (IOP) measurements were gathered with each of the three tonometers in random order. Results: Across all groups, tonometer readings were significantly different from each other in each dog. The TP generally produced the lowest readings and the TV+ consistently produced the highest readings. When comparing tonometers to each other, the TV+ was significantly different compared to the TV and TP; however, there was no significant difference between the TV and the TP. Across all groups and individuals, increase in CCT did not have any significant effect on IOP readings for any of the tonometers. Discussion: This study concluded that an increase in CCT did not have a significant effect on the difference in IOP readings produced by each of the tonometers. The TV+ produced consistently higher readings but did not exceed the expected IOP range in normal dogs. It is recommended that when measuring IOP on the same patient over time that the same tonometer be used for consistency.
Keywords for abstract	intraocular pressure central corneal thickness tonometry pachymetry ophthalmology dogs

Title of abstract	EVALUATION OF METAL LEVELS IN BLOOD AND LIVER OF WETLAND SPECIES ON AND OFF OF STRIP-MINED LAND IN SOUTHEASTERN OHIO
Authors	<u>J. Heinz</u> and M. Flint. Dept of Veterinary Preventive Medicine.
Abstract	Heavy metal toxicity has significant effects on the health of animals and can be found as a pollutant after human disturbance of the land. Strip-mining is an invasive mining technique that results in disturbance to the landscape, acid mine drainage and contamination of soils, plants and animals with heavy metals. Wetlands are concentrators of these heavy metals and also serve to help sequester and clean the environment, though increases the exposure to natural inhabitants. The aim of this study is to evaluate the heavy metal levels of several wetland fauna on and away from strip-mining locations in southeast Ohio. Additionally, samples of whole blood and liver will be analyzed and compared to evaluate whether antemortem sampling is a viable alternative in heavy metal testing of wildlife species. The species targeted are the North American beaver (<i>Castor canadensis</i>), common muskrat (<i>Ondatra zibethicus</i>), red-eared slider turtle (<i>Trachemys scripta elegans</i>), channel catfish (<i>Ictalurus punctatus</i>) and bluegill fish (<i>Lepomis macrochirus</i>). These species represent multiple niches within the wetland habitat, giving a more complete representation of exposure within the environment.
Keywords for abstract	Heavy metal Toxicity Wetland Beaver Turtle Liver

Title of abstract	MALDI SEPSITYPER™ TECHNOLOGY PROVIDES A MORE RAPID BUT LESS SENSITIVE METHOD FOR DIAGNOSIS OF BACTEREMIA
Title of abstract	IN VETERINARY PATIENTS
Authors	M. H. Hengy ^{1,2} , J. D. Garcia ² , J. A. Pempek ² , C. A. Hinds ³ , F. Hartmann ⁴ , R. Franklin-Guild ⁵ , J. Daniels ⁶ , G. G. Habing ² , D. Diaz-Campos ¹ Department of Veterinary Clinical Sciences ¹ and Department of Veterinary Preventive Medicine ² , The Ohio State University College of Veterinary Medicine, Columbus, OH Department of Food Animal Medicine and Surgery ³ , University of Missouri Veterinary Health Center, Columbia, MO Department of Microbiology and Clinical Pathology ⁴ , University of Wisconsin-Madison Veterinary Care, Madison, WI Department of Bacteriology and Mycology ⁵ , Cornell University College of Veterinary Medicine, Ithaca, NY Department of Bacteriology ⁶ , Colorado State University Veterinary Diagnostic Laboratory, Fort Collins, CO
Abstract	Culture-based diagnosis of bacteremia 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 time of flight (MALDI-TOF) mass spectrometry. Because it does not rely on culture to media, this method 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-TOF to detect bacteremia in a variety of veterinary patients with suspected septicemia. We hypothesized that Sepsityper would be more rapid and sensitive for detecting bacteremia relative to culture-based methods. Aseptic blood samples were collected from veterinary patients with clinical concern for sepsis according to individual protocol of the four participating diagnostic labs. Blood samples were used to innoculate a blood culture bottle (BCB), which was monitored at least daily for bacterial growth. At Ohio State, a positive BCB was defined as demonstrating turbidity and fluid translocation into the indicator top. Blood culture fluid from positive BCBs was analyzed by Sepsityper with MALDI-TOF and traditional culture to media-based isolation and identification methods. The Sepsityper method identified bacteria in 93.3% (n=98/105). Despite a lower sensitivity, results from the Sepsityper method were available at least 24 h sooner than culture-based methods. Therefore, the use of Sepsityper in conjunction with culture may maximize diagnostic potential, allowing for more rapid and appropriate treatment decisions in these critical cases.
Keywords for abstract	Septicemia Bacteremia Blood culture MALDI-TOF Sepsityper

	FEMOROTIBIAL KINEMATICS IN 4 DOGS TREATED WITH
Title of abstract:	CORA-BASED LEVELING OSTEOTOMY FOR CRANIAL CRUCIATE LIGAMENT RUPTURE
Authors (see example above for format)	N. Hughesa; S. Tingaa; S. Jonesa; S. MacArthurb; D. Lewisb; D. Hulseca The Ohio State University College of Veterinary Medicine, Columbus, Ohiob University of Florida College of Veterinary Medicine, Gainesville, Florida Callege of Veterinary Medicine, Gainesville, Florida Callege of Veterinary Medicine, Gainesville, Florida Callege of Veterinary Emergency & Specialty, Austin, Texas
Abstract (300 word limit)	The purpose of this study was to quantify 3D femorotibial kinematics during walking in dogs treated with CORA-based leveling osteotomy (CBLO) for cranial cruciate ligament (CCL) insufficiency. Four client-owned dogs with unilateral complete CCL rupture were prospectively enrolled. Custom 3D digital models of the femora and tibiae, with 3D coordinate systems, were created from pre- and postoperative computed tomographic scans. Lateral view fluoroscopy was collected during treadmill walking and craniocaudal translation was compared between the preoperative CCL-deficient, 6-month postoperative CBLO-treated, and unaffected contralateral (control) stifles during all phases of the gait cycle. The craniocaudal distance between the femoral and tibial CCL attachment sites was measured by overlaying the 3D models onto each fluoroscopic image, throughout the gait cycle. Craniocaudal femorotibial motion (CCFTM) was calculated by subtracting the minimum from the maximum measured craniocaudal distance between CCL attachment points over the entire gait cycle. The contralateral stifle of each dog was used as an internal control; control data was collected 6-months postoperatively. Force plate analysis was performed as an objective measure of lameness at all time points and symmetry indices (SI) between affected and control limbs were calculated for peak vertical force (PVF) and vertical impulse (VI). Preoperatively, CCFTM ranged from 7.6-11.7 mm, and 6-months postoperatively, CCFTM decreased in all dogs and ranged from 4.7-8.2 mm of motion. In the control stifles, CCFTM ranged from 0.26-0.56 preoperatively and 0.86-1.00 6-months postoperatively, and VI SI ranged from 0.20-0.48 preoperatively and 0.82-0.99 6-months postoperatively. Lameness improved by 78-99%, while craniocaudal stifle instability was mitigated by CBLO by 17-64%. This study documents marked improvement in limb function despite decreased but persistent craniocaudal instability after CBLO, suggesting that further studies investigating the kinematic effects of CBL
Keywords for abstract:	Cranial Cruciate Ligament CCL CORA-based Leveling Osteotomy Femorotibial Kinematics

Title of abstract	SURVEY OF DEFECATION FREQUENCY IN APPARENTLY HEALTHY AND CHRONIC KIDNEY DISEASE CATS
Authors	S. Jones, J. Quimby, S. Caney, S. Adams, S. Summers, A. Rudinsky. Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State; University, Columbus, Ohio (Jones, Quimby, Rudinsky, Adams), Vet Professionals Ltd, Midlothian; Innovation Centre, Edinburgh, United Kingdom (Caney), Colorado State University, Fort Collins, Colorado (Summers)
Abstract	Changes in bowel movements (BM) are an important clinical sign in many diseases, including chronic kidney disease (CKD), and the purpose of this study was to collect information on BM and fecal score (FS) in both apparently healthy and CKD cats. A secondary aim was to assess owner awareness of BM frequency.
	Owners were asked to complete an initial online questionnaire about their cat's health (to corroborate health status) and litter box habits. Owners were then asked to clean the box daily for 7 days and report results (observed frequency of BM and FS) daily using Purina Fecal Score (1-7) to assess feces. Differences in BM frequency and FS between apparently normal and CKD cats were compared using Mann-Whitney test. Difference in percentage of cats defecating less than once daily was assessed with Fishers exact test.
	Survey data from 124 owners of apparently healthy cats and 43 owners of CKD cats who submitted two or more days of daily observations (in addition to the initial questionnaire) were analyzed. Median serum creatinine (reported in n=26 CKD cats) was 2.5 mg/dL (range 1.6 mg/dL to 3.3 mg/dL). Eighty-five percent of apparently healthy cats were observed to defecate one or more times per day and 15% defecated less than once per day. Fifty-eight percent of CKD cats defecated one or more times per day and 42% defecated less than once per day. A significantly higher percentage of CKD cats defecated less than once per day in comparison to apparently healthy cats (p<0.0001). Observed BM frequency was significantly less in CKD cats compared to healthy cats (p=0.02). Observed FS was not significantly different between healthy and CKD cats.
	In conclusion, the observed BM frequency of cats with CKD was less than apparently healthy cats and represents a clinically important variation from normal.
Keywords for abstract	Chronic Kidney Disease (CKD) Fecal score cats

Title of abstract	COMPARISON OF PERIOPERATIVE ANALGESIC PROTOCOLS AND EVALUATION OF THE DEVELOPMENT OF A CHRONIC NEUROPATHIC PAIN STATE IN DOGS UNDERGOING TPLO FOR NATURALLY OCCURRING CRANIAL CRUCIATE LIGAMENT RUPTURE.
Authors	A. Kalamaras, N.R. Kieves, S.C. Jones, S.A. Moore, T.K. Aarnes, C. Ricco Pereira, J. Howard, J. Peng, (1) Department of Veterinary Clinical Science, The Ohio State University, (2) Center for Biostatistics, The Ohio State University
Abstract	INTRODUCTION: Neuropathic pain is a complex, chronic pain state caused by malfunction of the somatosensory nervous system and is manifested as reduced sensory threshold (ST). Our aim was to assess the effect of three perioperative analgesic protocols on ST in dogs with cranial cruciate ligament rupture (CCLR): perioperative opioid administration alone, epidural analgesia, and direct femoral and sciatic nerve blockade. We hypothesized that while perioperative opioids alone would provide equivalent immediate postoperative analgesia when compared to the two other treatments, that ST at later time points would be lower in dogs receiving only opioid administration.
	MATERIALS & METHODS: Client owned dogs with CCLR were enrolled. Dogs were randomly assigned to receive one of three different treatments: Treatment 1 - perioperative intravenous morphine, lidocaine, and ketamine; Treatment 2 - epidural; or Treatment 3 - a femoral and sciatic nerve blockade. Routine stifle arthroscopy followed by TPLO surgery was performed. Temporospatial gait analysis and ST data were collected before surgery, 1 day, 2 and 8 weeks postoperatively. Sedation and pain scores were assessed at 0, 2, 4, 8, and 24 hours following extubation.
	RESULTS: No significant differences were seen in ST or gait analysis among treatment groups at any time point. No dogs required rescue analgesia within the first 24 hours after surgery (as prescribed as Glasgow Composite Pain Score – Short Form > 5). Sedation scores for Treatment 1 were higher than other treatments. Pain scores for Treatment 3 were lower compared with other treatments.
	DISCUSSION/CONCLUSION: Perioperative analgesic protocol does not appear to significantly impact ST in dogs with CCLR when evaluated up to 8 weeks after TPLO surgery. Although all treatments appeared to provide adequate analgesia, femoral-sciatic blockade presented the best combination of analgesia without increased sedation.
Keywords for abstract	Cranial cruciate ligament rupture; CCLR; Tibial plateal leveling osteotomy; TPLO; Neuropathic pain; Sensory threshold; Analgesia Gait analysis

Title of abstract	OSSEOUS MORPHOMETRIC STUDIES OF THE SKULL OF THE RED PANDA (AILURUS FULGENS) AND FUTURE USE IN VETERINARY CARE
Authors	Caitlin Kiefer, Eric T. Hostnik, Caitlin Burrell, Copper Aitken-Palmer.College of Veterinary Medicine, The Ohio State University, Columbus, Ohio (Kiefer, Hostnik), Chicago Zoological Society, Brookfield Zoo, Brookfield, Illinois (Burrell, Aitken-Palmer).
Abstract	The red panda (Ailurus fulgens) is a small mammal native to the high altitude forests around China and been listed as endangered by the IUCN Red List since 2015. Red pandas are seen as a global conservation icon and are part of the Global Species Management Plan (GSMP) in zoos around the world. Computed tomography (CT) has increased in availability and use in zoos and has become an important diagnostic tool in veterinary medicine. The aim of this study was to develop a detailed description of the osseous anatomy of the skull of the red panda. Sixteen red pandas from the Smithsonian National Zoo underwent post-mortem CT, allowing for multi-planar reconstructions of the skulls in both CT and 3D formats. Digital calipers were used to determine baseline morphometric measurements of the osseous structures of the red panda skull, including mandible and dental arcade. Morphometric data was compared between the two visualization modalities to determine if they were interchangeable. Significant statistical differences were found between visualization modalities most in the orbital and facial parameter categories and indices. The red panda was determined to have the dental formula of I 3/3 C 1/1 PM 3/3(4) M 2/2 for a total of 32 or 34 teeth, with variation shown in number of mandibular premolars. Median measurement, interquartile ranges and overall ranges were determined for various skull morphometric parameters to give a baseline description of the normal osseous measurements for the red panda. This data can then be used as an essential reference in clinical zoological medicine for the diagnosis of osseous pathology like dental disease for red pandas under human management.
Keywords for abstract	Morphometric Red panda Computer Tomography Radiology

Title of abstract:	EFFECTS OF PIMOBENDAN ON LEFT ATRIAL TRANSPORT
Authors	FUNCTION IN CATS S. Kochie, K. Schober, R. Winter, J. Bonagura, A. Showers, V.
7 (011010	Yildiz, J. Rhinehart. Department Of Veterinary Clinical Sciences
Abstract	Background - Arterial thromboembolism (ATE) is a sequelae of
	hypertrophic cardiomyopathy (HCM) in cats related to left atrial
	(LA) enlargement and dysfunction.
	<u>Hypothesis/Objectives</u> - Pimobendan, an inodilator, improves LA transport function in healthy cats and cats with HCM.
	Animals - Twenty-two client-owned cats with primary HCM and
	eleven healthy control cats.
	Methods - Prospective, double-blind, randomized, placebo-
	controlled clinical cohort study. Cats underwent two examinations
	4-7 days apart. Cats were randomized to receive either
	pimobendan (0.25 mg/kg body weight q12h) or placebo. Two-
	dimensional and Doppler echocardiographic variables of LA
	function (LA shortening fraction, fractional area change, ejection
	fraction, and stroke volume; velocities of A and AR waves; LA
	ejection force; LA kinetic energy; and peak left auricular flow
	velocity) were evaluated. Data were statistically compared using
	standard test procedures for before-after comparisons and
	multivariable analysis.
	Results - Several echocardiographic variables characterizing LA
	size and function were increased after pimobendan: Left auricular
	flow velocity (0.85±0.20 m/s vs. 0.71±0.22 m/s, p=0.009),
	estimated total LA volume (p=0.030), LA emptying area (p=0.036)
	and LA emptying volume (p=0.032), and A velocity (0.77±0.12 vs.
	0.62±0.17, p=0.049). The effect of pimobendan was stronger in
	cats with HCM compared to healthy cats: LA fractional shortening
	$(\Delta 2.09 \pm 1.63 \text{ vs. } \Delta - 2.13 \pm 1.31, \text{ p=0.051}), \text{ velocity time integral A}$
	wave $(\Delta 0.58 \pm 0.14 \text{ vs. } \Delta 0.01 \pm 0.15, \text{ p=0.012})$, left auricular flow
	velocity ($\Delta 0.20 \pm 0.05$ vs. $\Delta 0.02 \pm 0.03$, p=0.015), LA kinetic energy
	$(\Delta 3.51 \pm 1.84 \text{ vs. } \Delta$ -0.10 \pm 0.64, p=0.05), and LA ejection force
	$(\Delta 1.93 \pm 0.63 \text{ vs. } \Delta -0.07 \pm 0.64, \text{ p=}0.005)$. The presence of LA
	enlargement was not identified as an independent predictor of drug
	effect in the multivariate model.
	Conclusions and Clinical Importance - This study identified positive,
	albeit minor, effects of pimobendan on LA function in cats with pre-
	clinical HCM. Whether or not chronic therapy with pimobendan can
	reduce the risk of cardiogenic embolism deserves further study.
	Arterial thromboembolism
Keywords for	Feline hypertrophic cardiomyopathy
abstract:	Calcium-sensing agent
	Inodilator
	Vetmedin
	Vounoun

Title of abstract:	A PILOT STUDY OF DIFFUSION TENSOR IMAGING CHARACTERISTICS OF MENINGOENCEPHALITIS OF UNKNOWN ETIOLOGY IN DOGS
Authors (see example above for format)	M. Ledesma, E. Hostnik
Abstract (300 word limit)	Meningoencephalitis of unknown etiology (MUE) is a clinical syndrome that encompasses several diseases characterized by inflammation of the brain and meninges. Diffusion tensor imaging (DTI) characterizes the organization and movement of protons within water molecules and can be characterized by the fractional anisotropy (FA) and apparent diffusion coefficient (ADC). We hypothesized that the FA would be significantly lower and the ADC would be significantly higher in the cases of MUE compared to controls. The MUE group was compared with a control group consisting of dogs diagnosed with idiopathic epilepsy. DTI tractography, FA, and ADC were recorded for multiple standardized regions of interest in both groups. Four subjects with MUE and 6 subjects without MUE met the inclusion criteria at the time of submission of this abstract. It was found that the median ranks for FA and ADC of all fiber tracks were not statistically different between the affected and unaffected groups (P-value > 0.05). However, the tractography of the more severely affected subjects with MUE showed subjective deviation of and fewer fiber tracks in the hyperintense regions seen on T2W sequences. FA and ADC do not objectively differentiate structurally normal, idiopathic epileptic dogs from those with MUE, though the subjective assessment of white matter fiber tractography corresponds with MRI findings and may be useful if conventional MRI findings are equivocal.
Keywords for abstract: Please list your keywords – one per line	DTI MUE Encephalitis Diffusion Weighted Imaging

Title of abstract	GLUCAGON, ADRENOCORTICOTROPIC HORMONE, AND CORTISOL CONCENTRATIONS IN RESPONSE TO CARBOHYDRATES AND FASTING IN HEALTHY NEONATAL FOALS.
Authors	H. Manning, L. Hostnik, L. Rings, J. Swink, R. Toribio. Department of Veterinary Clinical Sciences
Abstract	Maturation of the endocrine pancreas in the neonatal foal is delayed into the post-natal period, making them highly susceptible to energy dysregulation and hypoglycemia. Little information exists regarding the energy dynamics of enteral and parenteral carbohydrates in healthy neonatal foals. In order to further evaluate the endocrine disturbances that commonly affect neonates, we investigated glucagon, ACTH, and cortisol concentrations in response to fasting, enteral, and parenteral carbohydrates.
	Twenty-two healthy neonatal foals were assigned to treatment groups: fasted (n=6), intravenous dextrose (n=5), oral dextrose (n=5), and oral lactose (n=6). Blood samples were collected at frequent intervals for 210 minutes. Nursing was allowed from 180 to 210 minutes. Nonparametric methods were used for data analysis.
	No differences in glucagon concentrations were observed from baseline to 180 minutes in the fasted, oral dextrose, or intravenous dextrose treatment groups. Lactose resulted in decreased glucagon concentrations from baseline to 90 minutes (P=0.03). Nursing (180 to 210 minutes) stimulated marked increases in glucagon concentrations (P<0.0001). Fasting (P=0.03) and lactose administration (P=0.0076) stimulated a significant increase in ACTH concentrations from baseline to 180 minutes. No differences in ACTH concentrations were observed from baseline to 180 minutes in the oral dextrose or intravenous dextrose treatment groups. Nursing stimulated significant decreases in ACTH concentration (P=0.0001). No differences in cortisol concentration were observed from baseline to 180 minutes in all treatment groups. Nursing stimulated significant decreases in cortisol concentration (P<0.0001).
	While the administration of enteral and parenteral carbohydrates stimulated minor changes in these hormones, more significant changes in glucagon, ACTH, and cortisol were observed in response to nursing. The inverse relationship between glucagon and ACTH/cortisol concentrations stimulated from nursing indicates the increase in glucagon is likely not due to a stress response. We conclude that other factors in milk contribute to glucagon secretion, and further investigation is warranted.
Keywords for abstract	Glucagon, ACTH, Cortisol, Energy axis, Neonate

Title of abstract:	LONG-TERM CLINICAL AND MAGNETIC RESONANCE IMAGING FOLLOW-UP OF DOGS WITH OSSEOUS- ASSOCIATED CERVICAL SPONDYLOMYELOPATHY
Authors	Nye C, Hostnik E, Wittum T, Parker, Elizabeth, da Costa RC Depts.
	of Veterinary Biosciences and Veterinary Clinical Sciences
Abstract	Osseous associated cervical spondylomyelopathy (OA-CSM) is a common spinal disease of large and giant breed dogs. In order to understand its progression, we aimed to perform a long-term magnetic resonance imaging (MRI) follow-up study of dogs previously diagnosed with OA-CSM. Our goal was to describe changes on MRI over a two-year minimum period. We hypothesized that the spinal lesions would show progression in the majority of dogs.
	Eleven dogs previously diagnosed with OA-CSM were prospectively enrolled for follow-up MRI. Median time between MRI studies was 30 months (r24-54). Two dogs were treated surgically (dorsal laminectomy), while nine were treated medically with anti-inflammatories.
	Morphologic and morphometric assessments were performed. Morphologic assessment evaluated vertebral canal stenosis, spinal cord compression, foraminal stenosis, regularity of articular processes, and spinal cord signal changes. Morphometric assessment included vertebral canal area, spinal cord area, area of articular processes and foraminal height. Three reviewers evaluated the MRIs, grading sites as same (unchanged), better or worse when comparing MRIs for each parameter.
	On follow-up MRI, the most affected site progressed in two out of 11 dogs, improved in three, and was unchanged in six. Clinically, all dogs except two were unchanged to improved at follow-up. At the initial time point 50 out of 60 (83.3%) of intervertebral spaces showed vertebral canal stenosis. Follow-up time point showed 82.3%. Of the sites with stenosis, 45.7% were unchanged, 18.6% improved and 38.9% worsened. Morphometry demonstrated significant reduction in vertebral canal area and spinal cord areas at C4-C5 through C6-C7, and significant progression of articular process irregularities at C3-C4 and C6-C7.
	Our long-term MRI follow-up study documented progression of vertebral canal stenosis in two out of eleven dogs. The percentage of sites with vertebral canal stenosis was mostly unchanged. The majority of dogs did not show clinical or MRI progression.
Keywords for abstract	Articular process regularity and proliferation Morphologic assessment Morphometry Natural history Osseous-associated cervical spondylomyelopathy, Vertebral canal area

Title of abstract	ENDOGENOUS HEALING IN EQUINE NAVICULAR DISEASE: DEEP DIGITAL FLEXOR TENDON PROGENITOR CELLS EXHIBIT CHONDROGENIC PHENOTYPE
Authors	V. Quam, N. Altmann, M. Brokken, S. Durgam Department of Veterinary Clinical Sciences
Abstract	Paucicellular equine deep digital flexor tendon (DDFT) at the navicular region is intrasynovial and responds poorly to injury. Formation of adhesions and chondroid degeneration are common during healing and are sources of persistent lameness in navicular horses. As a first step to understand the cellular responses involved in healing, the objective of this study was to characterize resident progenitor cells that maintain the heterogenous structure of DDFT (Fig. 1A). We hypothesized that multipotent progenitor cells are present in both 'superficial dorsal' (SD-DDFT) and 'deep dorsal' (DD-DDFT) zones.
	Forelimb DDFTs from five QHs were dissected by zone (Fig. 1B) and digested in 0.15% collagenase II and I, respectively prior to monolayer expansion. Freshly isolated and third passage SD- and DD-DDFT cells were immunophenotyped for MSC surface markers. Standard trilineage (adipogenesis, osteogenesis and chondrogenesis) differentiation assays were conducted with third-passage progenitor cells. All data were analyzed with ANOVA ($p \le 0.05$).
	Monolayer expansion enriched for CD29+, CD73+, CD44-, and CD45- progenitor cells in both SD- and DD-DDFT zones. Although Oil-Red-O positive lipid droplets and Alizarin Red staining mineralized nodules were detected in end-point cultures, the intensity was minimal (Figure 2). Similarly, osteogenic gene expression (Runx2, ALP, OSN mRNAs) of day-21 SD- and DD-DDFT cells was not significantly upregulated from untreated controls. In contrast, day 20 chondrogenic gene expression (Sox9, ~10- fold; aggrecan, ~25-30-fold; and col II, ~350-fold), and proteoglycan content (dimethyl-methylene blue assay and toluidine blue staining) of both SD-DDFT and DD-DDFT cell pellets were significantly increased.
	Although the in-vivo cellular morphology within DDFT is zonally distinct, our data demonstrates that progenitor cells from both zones exhibit MSC characteristics and are restricted to a chondrogenic phenotype. This serves as a guideline for future work focused on delineating cellular processes mediating DDFT healing and identifying optimal therapeutic agent to enhance healing.
Keywords for abstract	Equine navicular disease Deep digital flexor tendon Progenitor cells Trilineage differentiation

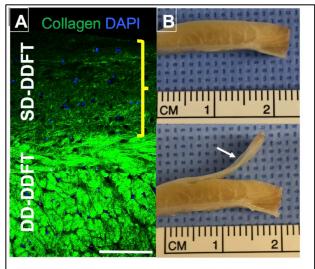


Figure 1A: Second harmonic generation (SHG) image of transverse section highlighting the heterogenous structure of DDFT; yellow bracket represents SD-DDFT; Scale = 100 microns

Figure 1B: Intact gross cross-section of DDFT (top) and with SD-DDFT dissected (arrow, bottom).

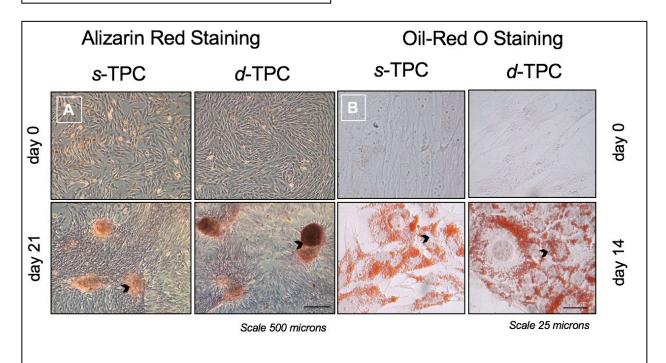


Figure 2A:Day 21 osteogenic cultures of S- and D-TPC showed minimal cell aggregation and mineralized matrix secretion on Alizarin Red staining.

Figure 2B: Day 14 adipogenic cultures of S- and D-TPC showed minimal stained intracellular lipid droplets on Oil-Red-O staining.

Title of abstract	EFFECTS OF SPERM CRYOPRESERVATION MEDIA IN SAUGER (Sander canadensis)
Authors	E. Ranney, B. Blawut, E. Runcan, M. Coutinho da Silva
Abstract	Fish sperm cryopreservation generally yields ow fertility, despite proficient post-thaw motility. Sub-lethal damage negatively affecting sperm physiology is likely responsible for this diminished fertilization capacity. Our lab has proposed new methodologies for evaluating fish sperm physiology in fresh and frozen/thawed sperm, but these criteria have not been compared among multiple freezing media. The objective of this study was to evaluate the effect of different cryopreservation media on post-thaw sperm quality. We hypothesized that cryopreservation would differentially influence physiological parameters relevant to fertilization depending on the media. Sauger sperm was collected during the 2019 breeding season and cryopreserved using three separate media: (M1) Rathbun extender + 10% DMSO, (M2) Modified Ringer's Lactate (MRL) + 7.5% methanol, or (M3) MRL + 7/5% ethylene glycol based a preliminary cryoprotectant toxicity trial. Sperm physiology in both fresh and frozen sperm was assessed and compared based on: motility, viability, intracellular calcium content, and surface WGA and ConA binding intensity and localization using computer assisted sperm analysis, flow cytometry, and fluorescent microscopy, respectively. Experimental endpoints were compared among groups using mixed linear models with an α-value of 0.05. Motility activation did not alter WGA and ConA binding in fresh or M1, whereas frozen sperm in M2 and M3 showed a decrease in binding upon activation. Intracellular calcium was unaffected by motility activation in sperm frozen using M1 and M3, but increased upon activation of fresh sperm and M2. The ~50% increase in apical WGA staining seen after activation in fresh sperm was absent in all cryopreservation treatments. Our results showed that cryopreservation-induced changes to sperm physiology were dependent on the choice of media, with methanol maintaining more similar parameters to fresh sperm. Future protocol development should utilize methanol to better maintain normal sperm physiology, and p
Keywords for abstract	Spermatozoa Cryopreservation Physiology Cryoprotectant Fish

Title of abstract	CLINICAL EVALUATION OF MICROWAVE ABLATION THERAPY IN DOGS WITH DISTAL RADIUS OSTEOSARCOMA.
Authors	S. A. Salyer ¹ , DVM, MS; V. A. Wavreille ¹ , DVM MS MRCVS DACVS ACVS Fellow Surgical Oncology, J. M. Fenger ¹ , DVM, PhD, ACVIM; R. N. Jennings ² , DVM, PhD, DACVP; L. E. Selmic ¹ BVetMed (Hons) MPH DACVS-SA, DECVS, ACVS Founding Fellow Surgical Oncology
Abstract	Objective: To evaluate the efficacy and safety of microwave ablation (MWA) therapy as a modality to induce cell death within distal radial osteosarcoma (OSA) tumors.
	Study Design: Prospective clinical study
	Animals: Six client-owned dogs diagnosed with distal radius OSA
	Methods: Subjects with cytologically confirmed distal radius osteosarcoma were included in this study. The patients underwent a computed tomography (CT) scan for surgical planning and were then placed under general anesthesia for fluoroscopic-guided ablation. The temperature was kept between 45-55°C at the bone/soft tissue interface. A second CT was performed 48 hours following MWA prior to amputation. Histopathology of the ablated tumor was then performed.
	Results: Six dogs underwent microwave ablation of distal radius osteosarcoma. Two subjects underwent lower power settings for the initial testing: the power was set at 30W and increased to 75 W for the last 4 dogs. Tumor necrosis of 30-90% was identified on histopathology. No dogs that underwent ablation had intra-operative or immediate post-operative complications.
	Conclusion: We were able to demonstrate that MWA is a safe and efficacious modality for local treatment of distal radial OSA.
	Clinical Significance: MWA may have implications as a modality for tumor destruction in patients with appendicular OSA that can be used in limb-sparing procedures.
Keywords for abstract	Osteosarcoma, Microwave ablation

Title of abstract	COMPARISON OF HEMORRHAGE COMPLICATIONS WITH DOUBLE-LIGATED VERSUS AUTO-LIGATED FELINE OVARIAN PEDICLES BY 4 TH YEAR VETERINARY STUDENTS
Authors	A. Showers, S. Horvath, D. Pontius, M. Forman, A. Hanthorn
Abstract	The objective of this study was to evaluate if the occurrence of hemorrhagic complications associated with feline ovarian pedicle ligation was significantly different between the traditional pedicle double ligation and the newer pedicle-tie technique when performed by students. 287 cats underwent an ovariohysterectomy performed by a fourth-year veterinary student surgeon. The students performed the pedicle-tie technique to ligate the ovarian pedicle in 146 cats, and the pedicle double ligation technique in 141 cats. Patient characteristics of each group, including mean and median age and weight, along with heat status, were recorded. 4 of 146 cats in the pedicle-tie group experienced pedicle ligation related intra-operative hemorrhagic complications (2.7%). 8 of 141 cats in the pedicle double ligation group experienced similar complications (5.7%). There was no statistically significant difference detected between the complication proportions of each pedicle ligation method (p-value = 0.21443). This study demonstrates that novice surgeons can perform the pedicle tie technique on feline ovarian pedicles without significantly increasing the occurrence of hemorrhagic complication. Veterinary institutions should consider including the pedicle tie method as a standard feline ovarian pedicle ligation technique in their curricula. This will facilitate the development of entry-level practitioners that are more proficient in an efficient feline spay technique that can be offered to clients and shelter facilities.
Keywords for abstract	Auto-ligation Pedicle-tie Student Surgery Teaching hospital Complication

Title of abstract	OSSEOUS MORPHOMETRY OF THE THE GIANT PANDA SKULL (AILUROPODA MELANOLEUCA) AND VETERINARY CARE IMPLICATIONS
Authors	L. A. Shusterman, E. T. Hostnik, C. Burrell, C. Aitken-Palmer. College of Veterinary Medicine (Shusterman, Hostnik), The Ohio State University, Columbus, Ohio; Chicago Zoological Society / Brookfield Zoo (Aitken-Palmer), Brookfield, Illinois; University of Illinois Zoological Pathology Program, Brookfield, Illinois (Burrell)
Abstract	The giant panda (<i>Ailuropoda melanoleuca</i>) is an example of a species whose population has increased with conservation efforts. No longer endangered, giant pandas are part of a global species breeding program, therefore many giant pandas are under direct care by professional management. These ex situ individuals are admired as not only a symbol of China, but also the representative for conservation of essential bamboo forests and its other inhabitants in the natural environment. To better understand these creatures and treat them in a veterinary setting, it is imperative that their full anatomy be understood and this information be readily available. Computed tomography (CT) allows caregivers a noninvasive approach to screening, characterizing, and treating pathology. The use of CT is becoming more common in a zoo setting. Fourteen post-mortem adult giant panda skulls associated with the Smithsonian National Museum of Natural History were imaged using CT. The dental formula was recorded as 40 teeth; Incisor (I) 3/3, Canines (C) 1/1, Premolars (Pm) 4/3, Molars (M) 2/3 x 2=40. In addition, tooth roots and anatomic comparisons of measurements using two visualization techniques, CT and reconstructed 3D images, were described. These comparisons were categorized into different parameters: skull, facial, orbital, mandibular, and cranial cavity. Based on statistical analysis, the measurements which were significantly different between CT and 3D reconstructions were foramen magnum width, orbital length, infraorbital canal to root of canine and root of first premolar, maximum mandibular height, condyloid process to ventral border of mandible, diastema length, and caudal cranial fossa maximum width.
Keywords for abstract	Giant panda Computed tomography

Title of abstract	EFFICACY OF HIGH-CONCENTRATION BUPRENORPHINE (SIMBADOL) AS AN ANALGESIC IN CD-1 MICE
Authors	B. Singh, A. L. Bailey, B. J. Smith, E. Houston, K. Patil, C. J. Doane, and L. V. Kendall
Abstract	Opioid analgesics are among the most commonly used agents in managing acute pain in laboratory animals. In recent years, a high-concentration formulation of the opioid buprenorphine, Simbadol, has received FDA approval as a single-dose, long-lasting analgesic in cats. Given that rodents are one of the most commonly utilized models in research, our study aimed to determine the efficacy of Simbadol (0.9 mg/kg) in mice. 40 CD-1 mice were divided evenly into 4 groups (ovariectomy or sham surgery with and without Simbadol treatment). Animal well-being was assessed 24 h prior to surgery, 3, 6, 12, 24, and 48 h after surgery using ANY-Maze video tracking software, Avisoft-SASlab Pro recording software, and behavioral assessments of grooming, rearing, wound licking, and orbital tightness. Our findings indicate that wound-licking was significantly increased in the saline-treated surgery group compared to those treated with Simbadol at 3 and 6 hours. Orbital tightness at 3 hours was significantly increased in the saline-treated surgery group compared to the Simbadol group at 3 hours. The number of activity bouts recorded in the Simbadol-treated surgery mice at 6 hours was significantly greater than those in the saline-treated surgery group and anesthesia-only group. Finally, total distance traveled was found to be significantly greater at 3 hours in Simbadol-treated surgical mice compared to saline-treated, and was less than the sham control groups. Based on these data, we posit that Simbadol is an adequate analgesic agent in mice.
Keywords for abstract	Analgesia Opioids Ovariectomy Pain Model Behavior Recognition Rodent

Title of abstract	CHARACTERIZATION AND <i>IN VITRO</i> SUSCEPTIBILITY OF FELINE UPEC ISOLATES TO A NOVEL <i>E. COLI</i> PROBIOTIC
Authors	C. Snell ¹ , J. Gibson ¹ , C. Zumpetta ¹ , J. Byron ¹ , J. Quimby ¹ , A. Harrison ¹ , S. Justice ² , A. Rudinsky ¹ ¹ College of Veterinary Medicine, The Ohio State University, USA ² Nationwide Children's Hospital, Columbus, Ohio USA
Abstract	The rise in antibiotic resistance amongst urinary tract infections (UTIs) in both cats and dogs underscores the need for non-antibiotic approaches to UTIs. The probiotic Escherichia coli Nissle-1917 (EcN) has many benefits including antimicrobial activity against many human pathogens including uropathogenic E. coli (UPEC). The aim of this study was to phylogenetically characterize UPEC in feline UTI cases and investigate the in vitro susceptibility of these isolates to EcN.
	Twenty-nine cats with thirty-five positive <i>E. coli</i> urine cultures were included in the study. Samples used in this study were obtained from surplus urine collected for routine evaluation of possible urinary tract infections. Characterization of UPEC isolates was performed by clade analysis, serotyping and virulence factor analysis by multiplex PCR testing. EcN effectiveness against UPEC isolates was tested in vitro using microcidin plate analysis.
	Serogroup and virulence factors correlated with clade analysis as reported in human UPEC studies, with the most isolates belonging to phylogroup A, B2, or D. Seventy eight percent of isolates were found to be multidrug resistant. However, seventy three percent of UPEC isolates were susceptible to the EcN probiotic in vitro with an average zone of growth inhibition of 4.33 mm (range 1.67 - 10.67 mm).
	UPEC isolates from feline patients were similar to isolates in human patients in pathogenicity, susceptibility, and genetic background. In vitro susceptibility of feline UPEC isolates were frequently susceptible to the EcN probiotic through growth rate characteristics and/or microcin production. These findings suggest the potential use of Nissle as a novel therapeutic to treat feline urinary tract infections.
Keywords for abstract	Urinary tract infection Probiotic Antimicrobial resistance Uropathogen Nissle E. coli

Title of abstract	SEX STEROIDS AND THE EFFECT OF IN-UTERO ALTRENOGEST EXPOSURE IN HEALTHY AND HOSPITALIZED
THE OF ADSTRACT	NEONATAL FOALS
	Swink JS ¹ , Rings LM ¹ , Snyder HA ¹ , McAuley RC ¹ , Dembek KA ² ,
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Authors	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 and neonatal maladjustment syndrome (NMS) are major causes of morbidity and mortality in neonatal foals. Dysfunction of the hypothalamic-pituitary-adrenal axis is frequent in critically ill newborn foals. Some information is available on glucocorticoids and mineralocorticoids in healthy and sick foals, but little is known about sex steroids. Administration of exogenous progestogens (altrenogest) is common practice in the equine industry. Elevated endogenous progesterone concentrations have been associated with illness in newborn foals. Therefore, the goal of this study was to evaluate sex steroids as well as determine the association between in-utero altrenogest exposure and the steroid profile in neonatal foals.
	Blood samples were collected on admission (0) and 24, 48, and 72 hours from 62 healthy, 56 septic, and 41 sick non-septic (SNS) foals of <3 days of age. Foals within groups were further divided into born to altrenogest-treated or -untreated mares. Serum steroids and plasma adrenocorticotropic hormone (ACTH) were measured using immunoassays.
	At admission, progestogen (pregnenolone, progesterone, 17α -hydroxyprogesterone), and estrogen (DHEA, testosterone, 5-dihydrotestosterone), and estrogen (estrone, estradiol) concentrations were higher in septic compared to healthy and SNS foals (P<0.05). Steroid concentrations were higher in NMS foals (P<0.05). Some steroids were higher in non-surviving foals (P<0.05). All hormones decreased over time in healthy but remained elevated in septic foals. Steroid concentrations at single time points and longitudinally predicted mortality. Altrenogest-exposed septic foals had altered ACTH, 17α -hydroxyprogesterone, and progesterone concentrations (P<0.05). Altrenogest-exposed non-surviving foals had higher pregnenolone and progesterone concentrations than unexposed foals (P<0.05).
	This study showed that sex steroid concentrations are altered in sick foals and could influence disease progression. Steroid dynamics during hospitalization are associated with disease severity and outcome. Increased sex steroid concentrations likely reflect delayed clearance and organ dysfunction. This study also demonstrates that exogenous progestogens could potentially influence the steroid profile of sick newborn foals.
Keywords for abstract	Foal Neonatal maladjustment syndrome Sepsis Altrenogest Steroids

Title of abstract	PLASMA CYTOKERATIN 18 AND FECAL ALPHA-1 ANTITRYPSIN CONCENTRATIONS IN DOGS WITH OSTEOSARCOMA RECEIVING CARBOPLATIN CHEMOTHERAPY
Authors	Kathryn Taikowski¹, Adam J. Rudinsky¹,², Darian S. Louke¹, Emma Warry³, Joelle M. Fenger¹ ¹ Department of Veterinary Clinical Sciences, College of Veterinary Medicine, The Ohio State University, Columbus, OH 43210 ² Comparative Hepatobiliary and Intestinal Research Program (CHIRP), College of Veterinary Medicine, The Ohio State University, Columbus, OH 43210 ³ Department of Small Animal Clinical Sciences, College of Veterinary Medicine, Texas A&M University, College Station, TX 77843
Abstract	Gastrointestinal (GI) toxicity is a common adverse effect in both humans and dogs receiving cytotoxic chemotherapy, and represents a major dose-limiting side effect of chemotherapy. Cytokeratin 18 (CK18) is an intracellular epithelial structural protein which is released during apoptosis, and in humans, has been found to correlate with severity of chemotherapy induced GI mucositis. Markers such as fecal alpha1-antitrypsin (A1-AT) that reflect increased intestinal permeability have been shown to correlate with the severity of lacteal dilation and GI protein loss in dogs. The goal of this study was to evaluate the clinical utility of plasma CK18 and fecal A1-AT levels as non-invasive biomarkers of GI toxicity induced by cytotoxic chemotherapy. We conducted a prospective cohort study in dogs (N=10) with appendicular osteosarcoma undergoing amputation followed by adjuvant carboplatin chemotherapy treatment. We hypothesized that plasma CK18 and fecal A1-AT levels would increase following carboplatin administration due to drug-induced GI epithelial cell damage/apoptosis, and that plasma CK18 and fecal A1-AT levels would correlate with the severity of GI toxicity. Mean baseline plasma CK18 concentration was variable amongst patients; however, mean plasma CK18 concentration prior to carboplatin chemotherapy treatment was not significantly different from CK18 levels measured after treatment. There was significant intra and inter-patient variability in mean fecal A1-AT levels at baseline. Mean fecal A1-AT concentration did not change significantly from day 0 to day 21. Gastrointestinal toxicity was minimal; therefore, we were unable to determine the association of plasma CK18 and fecal A1-AT concentrations with the development of signs of GI toxicosis. In this study population, plasma CK18 and fecal A1-AT concentration were not clinically useful biomarkers for the detection of GI toxicosis secondary to carboplatin administration. Further prospective evaluation of CK18 and A1-AT as biomarkers of drug-induced GI toxicity i
Keywords for abstract	Canine Chemotherapy-associated gastrointestinal toxicity Cytotoxic chemotherapy Cytokeratin 18 Alpha1-antitrypsin

Title of abstract	EFFECT OF AMPK AGONISTS ON INSULIN AND GLUCOSE DYNAMICS IN EXPERIMENTALLY-INDUCED INSULIN DYSREGULATION IN HORSES
Authors	K.J. Timko, L.D. Hostnik, M.R. Watts, C. Chen, A. Bercz, R.E. Toribio, T.A. Burns
Abstract	Departments of Veterinary Clinical Sciences Insulin dysregulation (ID), a hallmark component of equine metabolic syndrome, is linked to the development of laminitis, a condition for which there are few pharmacologic treatment options. 5'-Adenosine-monophosphate-activated protein kinase (AMPK) is a highly conserved heterotrimeric enzyme essential to cellular energy regulation and an important therapeutic target in humans with metabolic syndrome. The objective of this study was to assess the effects of AMPK agonist administration (metformin [MET], aspirin [ASP], and combination [MET/ASP]) on insulin and glucose dynamics in experimentally-induced ID in light breed horses. Insulin dysregulation was induced in 14 adult light breed horses with dexamethasone (0.08 mg/kg PO q24h); horses were assigned to groups and received either ASP (10 mg/kg PO q24h; n=7) or MET (30 mg/kg PO q12h; n=7) for 7 days. Seven horses then received MET/ASP for an additional 7 days. The oral sugar test (OST) and combined glucose and insulin test (CGIT) were used to assess ID at four time points: baseline, ID, ID + monotherapy, and ID + combination therapy. The OST area under the curve for glucose (AUCgluc0-240) after combination treatment was significantly lower than at the ID and ID + monotherapy timepoints (P = 0.0052). The CGIT AUCgluc0-150 was not significantly affected by AMPK agonist treatment (P = 0.0779). These findings suggest that MET/ASP combination therapy can synergistically improve insulin and glucose dynamics in horses and may have therapeutic value.
Keywords for abstract	Insulin dysregulation (ID) Equine metabolic syndrome (EMS) Laminitis 5'-Adenosine-monophosphate-activated protein kinase (AMPK)

Title of abstract	THE VERTEBRAL HEART SCALE ON CT IS CORRELATED TO RADIOGRAPHS
Authors	L. Timperman, E. Green. Dept. of Veterinary Clinical Sciences
Abstract	The vertebral heart scale (VHS) has long been used as an objective standard for evaluation of cardiac silhouette size on thoracic radiographs and plays a key role in the diagnosis as well as the assessment of the severity of canine and feline heart disease. No method for assessing overall size of the cardiac silhouette on CT has been defined either in human or veterinary patients. The goals of this study are to describe a repeatable method for objectively evaluating heart size on thoracic CT images, show that there is a correlation between the vertebral heart scales when applied to a right lateral thoracic radiograph and a sagittal slice of a thoracic CT scan, and determine the effect of cardiac phase on a VHS measured on CT. A method for measuring VHS on CT is defined. Data was collected on canine patients admitted to The OSU Veterinary Teaching Hospital receiving a thoracic CT. Each patient received an ECG-gated thoracic CT immediately followed by a right lateral thoracic radiograph. For these patients, the VHS was measured on nongated, gated systolic, and gated diastolic sagittal reformats. Our results show that there is little difference in the VHS measured on gated and non-gated CT, indicating that cardiac gating is likely unnecessary when assessing heart size on CT. Additionally, when comparing the VHS on gated and non-gated CT to the VHS on radiographs, there was a moderate to high degree of correlation. However, the VHS on CT does not fall within the previously defined radiographic reference range, and the high degree of variability between CT and radiography, as well as a small sample size, prohibits establishment of a CT-based reference range.
Keywords for abstract	Vertebral heart scale Computed tomography Heart size

Title of abstract	THE ROLE OF SULFONYLUREA RECEPTOR 1 (SUR1) IN CANINE FIBROCARTILAGINOUS EMBOLIC MYELOPATHY
Authors	S. Moore, G. Nuovo, and <u>A. Vasyliev</u> . Depts. Of Veterinary Biosciences and Veterinary Clinical Sciences
Abstract	Fibrocartilaginous embolic myelopathy (FCEM) is a blockage within the spinal cord vasculature that results in acute spinal cord infarction and transient or permanent paralysis. FCEM is frequently seen in dogs, but also occurs in people and other species. Prognosis depends on the severity of the ischemic injury, but recovery is often slow or incomplete and there are currently no available treatments. Sulfonylurea receptor 1 (Sur1) is expressed in the vascular endothelium of the central nervous system (CNS) post-injury and couples with Trpm4 to produce an ion channel that facilitates rapid endothelial cell death, hemorrhage, and necrosis. Blocking Sur1/Trpm4 has been shown to improve outcome in several types of CNS vascular injury including human stroke and experimental traumatic spinal cord injury. This study aims to evaluate the role of Sur1 in canine archival autopsy spinal cords from dogs diagnosed with FCEM using immunohistochemical (IHC) staining and digital quantification of Sur1 to gain additional insight regarding 1) the presence and timing of maximal expression of Sur1 in dogs with FCEM and 2) the relevance of Sur1 in FCEM compared to other spinal cord diseases. We hypothesize that Sur1 IHC signal will be higher in FCEM-affected dogs compared to control dogs, and that enhanced staining in FCEM will be associated with more severe and more acute lesions. The results from this study may provide rationale for future clinical trials evaluating the use of glibenclamide, an FDA approved potent Sur1 inhibitor, in dogs with FCEM.
Keywords for abstract	Fibrocartilaginous embolism Glibenclamide Ischemic infarction Spinal cord injury Sur1 Trpm4

Title of abstract	LIPONUCLEOTIDE THERAPEUTICS FOR CANINE ASPIRATION PNEUMONIA: A PILOT STUDY OF 17 DOGS
Authors	A. Young, DVM, I. Davis, DVM, PhD, E. Cooper, VMD, MS, DACVECC
Abstract	Objective – To examine the effect of intravenous treatment with the liponucleotide (lipoNT) CPD-choline on lung function in dogs with aspiration pneumonia. Design – Single institutional randomized, double-blind, placebocontrolled, prospective clinical trial conducted from 2017-2019. Setting – Single Institution Intensive Care Unit. Animals – 17 ICU hospitalized dogs with a diagnosis of aspiration pneumonia lacking significant co-morbidities. Interventions – Patients were randomized to administration of CPD-choline (5 mg/kg in 0.1 ml saline/kg) vs. saline placebo (0.1 ml/kg) IV every 12 hours for up to 96 hours or until dismissal or death. Arterial blood gases were measured every 12 hours for serial evaluation of pHa, PaO2, PaCO2, SaO2%, calculated A-aDO2 gradients and PaO2/FIO2 ratios. Hematologic analysis and clinical chemistry were measured at 0 and 48 hours. Adverse event monitoring was integral to the protocol. Dogs were provided with standard of care supportive care measures for the treatment of aspiration pneumonia at the discretion of the attending clinician. Measurements and Main Results – 9 dogs were randomized to receive lipoNT, 8 dogs were randomized to receive placebo. No significant differences were found between groups with regard to mortality rate, time on supplemental oxygen, SaO2%, PaCO2, or pHa at any time point. In lipoNT treated dogs, PaO2/FIO2 ratios progressively and significantly increased while A-aDO2 gradients progressively decreased over the first 48 hours. In placebo-treated patients, PaO2/FIO2 ratios and A-aDO2 gradients did not significantly change over the first 48 hours.
	At 48 hours, platelet counts decreased significantly in saline-treated patients (-23.5%). Significant reductions in platelet counts were not observed in lipoNT-treated dogs. At 48 hours, chemistry evaluation demonstrated a significantly increased alkaline phosphatase in saline-treated patients. Conclusions – CPD-choline is associated with a significant and progressive improvement in pulmonary gas exchange and appears safe for use as an adjunct to supportive care therapy in the treatment of aspiration pneumonia.
Keywords for abstract	canine, aspiration pneumonia, CPD-choline, liponucleotide

	EFFECT OF EJACULATION FREQUENCY, PROSTAGLANDIN
Title of abstract	F-2α, AND COLD STORAGE ON CANINE SEMEN YIELD AND POST-THAW QUALITY
Authors	K. Zelachowski, E. Runcan, B. Blawut and M. Coutinho da Silva. Department of Veterinary Clinical Sciences
Abstract	The objective of this study was to determine a more effective collection regimen to increase the total number of sperm available for cryopreservation without compromising post-thaw motility parameters. We hypothesized that multiple collections and prostaglandin F-2 α (PGF-2 α) administration would increase sperm yield without detriment to post-thaw semen quality. Five sexually mature male dogs (n=5) were submitted to all five collection regimens in random order: single collection (1, control), two collections 1h (2), 24h (3) or 48h (4) apart, and a single collection 20 minutes after PGF-2 α (5). Semen was either frozen immediately after collection (regimens 1 and 5) or stored at 4°C, pooled with a second ejaculate (regimens 2, 3, 4), and then frozen. Dogs were allowed seven days of sexual rest between regimens. Total motility (TM), progressive motility (PM), viability (VIA) and acrosome integrity (ACR) were determined using computer-assisted sperm analysis and flow cytometry. Data were analyzed using a general linear mixed model and Tukey's HSD Post Hoc with significance set at P < 0.05. All regimens resulted in a higher sperm yield compared to the control. All parameters were similar among regimens 1, 2 and 5 (TM: 50.4 \pm 5.1%, 49.4 \pm 5.1%, 53.8 \pm 5.1%, PM: 36.8 \pm 4.7%, 35.4 \pm 4.7%, 40.2 \pm 4.7%, VIA: 61.9 \pm 3.4%, 65.3 \pm 3.4%, 61.7 \pm 3.4%, ACR: 23.2 \pm 2.7%, 18.1 \pm 2.7%, 20.4 \pm 2.7%, respectively). Post-thaw parameters were lowest in regimen 4 and intermediate for regimen 3. In conclusion, two collections performed one hour apart or a dose of PGF-2 α dramatically increase sperm yield without impacting post-thaw quality. Cooled storage before cryopreservation was increasingly detrimental with increasing time between collections. These results provide practitioners with two alternative semen collection regimens to maximize the number of breeding doses cryopreserved in a single visit.
Keywords for abstract	Canine Spermatozoa Yield Cryopreservation, Prostaglandin

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Title of abstract	SPECTRAL FLOW CYTOMETRY FOR VETERINARY DIAGNOSTICS AND RESEARCH AT OSU CVM
Authors	S. Evans. Dept. of Veterinary Biosciences
Abstract	Spectral flow cytometry represents a shift in the paradigm of expected performance from a flow cytometer. With only three lasers, the Cytek Aurora flow cytometer can analyze up to 24 different fluorophores by distinguishing between their unique spectral signatures. This technology allows for concurrent use of highly similar dyes (ex: Alexa Fluor 647 and APC) that would be considered indistinguishable by conventional flow cytometer optical systems. This represents an enormous advantage for those working in the field of veterinary medicine and research, where reagent availability is often limited. Moreover, the Cytek Aurora is very stable and highly sensitive; it can analyze particle sizes down to several hundred nanometers (subcellular microvesicle range). Here at the OSU Veterinary Medical Center, we currently use the Cytek Aurora to diagnose and classify hematopoietic neoplasms (i.e., leukemia and lymphoma) in canine and feline patients. Our canine panel includes markers for CD3, CD4, CD5, CD8, CD14, CD18, CD21, CD34, CD45, MHC Class II, and a viability stain (11 colors in total), all in one tube. Our feline panel includes CD4, CD5, CD8, CD14, CD18, CD21, and a viability stain (7 colors in total), all in one tube. The massive multiplexing of these panels allows for comparison of each parameter against every other parameter in the panel, and greatly enhances the dataset gathered from each patient. A case of hepatosplenic T-cell lymphoma with aberrant immunophenotype (CD5+, CD4-/CD8-) is included as an example of the diagnostic utility of this instrument. Beyond hematopoietic neoplasia, development of additional flow cytometry-based assays for use in veterinary diagnostic medicine is ongoing. Moreover, the Cytek Aurora has strong potential to be useful in many other areas of research. This powerful, versatile instrument is now available for use by OSU CVM researchers and their collaborators.
Keywords for abstract	Flow cytometry Lymphoma Leukemia Hematopoietic neoplasia