UNIVERSITY OF CALGARY
FACULTY OF VETERINARY MEDICINE

UCVM SURE Research Day 2024

August 22nd, 2024

8:25 am – 4:00 pm

Health Sciences Centre Theatre 3 and HRIC Atrium

PROGRAM and ABSTRACT BOOKLET

Message from Prof. David C. Hall, Assoc. Dean, Emerging Scholars

Welcome to UCVM SURE (Summer Undergraduate Research Experience) Research Day, 2024 from the Office of the Associate Dean, Emerging Scholars. This year we have 43 students registered in the SURE program, funded by various sources including CIHR, NSERC, Alberta Innovates, Parks Canada, the UCVM Office of Emerging Scholars, and various supervisor grants. 13 of our SURE students are in the DVM program; others joined us from a wide range of programs including Biomedical Engineering, various Health Sciences, Chemistry, and Kinesiology.

The Faculty of Veterinary Medicine prioritizes research as a key element of our many activities. Today our SURE students will be sharing research results from their summer activities, as well as learning about the discoveries of their peers and research leaders. We have lined up 20 oral presentations and 21 poster presentations, with topics that include canine distemper virus, bovine sub-clinical mastitis, animal welfare at the Calgary Stampede, and the greater sage grouse. We are also delighted to present a keynote lecture from Dr. Ning Cheng, a leading researcher of neurodevelopment conditions including Fragile X Syndrome and autism. We encourage you to attend the presentations, ask questions, provide feedback, and learn.

From all the supervisors and myself, thank you and well done to all the SURE students for your engagement with research this summer. We hope you enjoyed learning about research design, experienced some success, and accepted the lessons that failure can teach. Most of all, we hope that the summer inspired you to include research in your future careers.

I want to thank the graduate students, postdoctoral fellows, staff, and faculty members who contributed to organizing and participating in today's activities including abstract adjudication, session chairing, and judging. I particularly wish to thank Rebecca Shippley (UCVM Office of Emerging Scholars) for exceptional support in communication and coordination of the day, as well as Barbara Banman (OES), and Jehangir Asghar (VMGSA) for their additional assistance.

Enjoy SURE 2024!

Sincerely,

David C. Hall, DVM, PhD

Associate Dean, Emerging Scholars, UCVM

Message from Dr John Gilleard and Hermann Schaetzl, Associate Deans, Research

On behalf of the UCVM research community, welcome to the 2024 UCVM SURE Research Day and thanks to all our undergraduate students, supervisors and research teams for your contributions this summer. The presentations and posters today really showcase the quality, breadth and depth of research undertaken at UCVM. It is great to see the SURE program attract a total of 43 students this year, many of whom secured scholarship awards amounting to a total of > $ 175,000!

The SURE program is an important part of the UCVM academic year providing a unique opportunity for students to develop research proposals, learn and apply scientific knowledge, develop critical analysis skills, work in teams, and communicate results. Equally, the presence of summer undergraduate students always energizes our research teams and stimulates innovation within our research programs. Hopefully you have been enthused to consider research as part of your future career options and we encourage you to build on the connections you have made this summer well into the future.

Organizing today's events is a major team effort and so many thanks to all the graduate students, postdoctoral researchers, faculty members, and staff involved. Particular thanks go to Rebecca Shippley and Barb Banman from the Emerging Scholars Office for all their hard work in preparing and supporting today's event.

Have a great day!

John Gilleard and Hermann Schaetzl

2024 SURE Research Day

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Health Sciences Centre Theatre 3 and HRIC Atrium

8:25	**Welcome and Introductions – Theatre 3:** David Hall
Oral Presentation Session #1 – Theatre 3 Chairs: Amish Dua, Corienne Gammariello Judges: Jehangir Asghar, Jieting Lin	
8:30	**Ethan Willms** (Dobrinski) *Effects of GDNF and GFRα1 on Germ Cell Proliferation in Porcine Testicular Organoids*
	Kismet Dhaliwal (Nobrega) *Prevalence of subclinical mastitis-causing pathogens on 15 Alberta dairy farms*
	Louise Caplan (Sparks) *Characterizing common blood-derived therapeutics from horses with Pituitary pars*
	Tausha Prisnee (Leguillette) *Repeated racing does not increase high sensitivity cardiac Troponin-T levels in chuckwagon*
9:30	**Mini-Break**
Oral Presentation Session #2 – Theatre 3 Chairs: Jehangir Asghar, Jieting Lin Judges: Eva Mutua, Eleanor Dickinson	
9:35	**Jennifer Black** (Davies) *Transplacental transmission of canine distemper virus in a Linnaeus's 2-toed sloth (Choloepus didactylus)*
	Lindsey Hampton (Rosa) *AMR profiling of commensal fecal E. coli in domestic and feral horses in Alberta.*
	Talia Turner (Soghigian) *Molecular detection of a novel species of Rickettsia endosymbiont in Aedes aegypti*
	Shayne McArthur (De Buck) *The Bacteriocin, Corynacin, as a Novel Antimicrobial Agent Against Methicillin-Resistant Staphylococcus aureus*
	Maria Greco (De Buck) *Investigating the presence of Mycoplasma and Bovine Herpesvirus 4 in digital dermatitis*
10:35	**Coffee Break - HRIC Atrium**
Oral Presentation Session #3 – Theatre 3 Chairs: Jehangir Asghar, Oshin Ley Garcia Judges: Corienne Gammariello, Eleanor Dickinson	
11:00	**Irene Dinh** (Canton) *Characterization of the Putative Pore-Forming Protein Apolipoprotein L 9A (APOL9A) in Macrophages*
	Kylie Tiedje (Cobo) *The involvement of inflammasome-activated macrophages in swine dysentery colitis.*
	MoonYoung Bae (Cheng) *Exploring Social Interactions in a Mouse Model of Fragile X Syndrome*
	Orchee Haque (Cobo) *Endogenous cathelicidins influence mast cell responses in the colon in a microbiota-independent manner*
	Yvonne Chen (Canton) *APOL7C and the great antigen escape of DNGR-ous materials*

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12:00	**Lunch and Poster Session - HRIC Atrium**
Oral Presentation Session #4 – Theatre 3 Chairs: Angelica Dias, Amish Dua Judges: Emma Roux, Jieting Lin	
14:00	**Annika Maj** (Trang) *Pannexin-1 dependent mechanisms in T-cells underlie neuropathic pain in females*
	Haley Young (Biernaskie) *Impact of Inbreeding on Breeding Success in a Herd of Captive Reindeer*
	Julia Gaume (Whiteside) *Determination of Ophthalmic Parameters in the Endangered Greater Sage Grouse (Centrocercus urophasianus)*
	Ryan Rahimi (Careem) *Nucleotide and Phenotypic Analyses of Quasispecies Detected in the Spike 1 Gene and its Encoded Protein following IBV Infection in Laying Hens*
	Emma Piercey (Sparks) *The rise and fall of tendon health: exploring cellular dynamics across the lifespan of equine tendon*
15:00	**Keynote Speaker – Theatre 3**
	Dr. Ning Cheng *Animal models in health research – can we better understand neurodevelopmental conditions by studying mice?*
15:45	**Prizes and Closing Remarks:** David Hall

ABSTRACTS

Listed alphabetically by first name of presenting author

Predicting the impact of somatic cell count on milk production in Thailand

Amber Cliffe, Ravisa Warin, David Hall

1 Faculty of Veterinary Medicine, University of Calgary
2 Faculty of Veterinary Medicine, Chaing Mai University

Keywords: Predictive models, milk production, Thailand

Introduction: The dairy industry in Thailand has seen immense growth since its infancy in the 1970's; further development within the industry routinely focuses on increasing production potential. Therefore, understanding the factors that influence milk production is vital. Somatic cell count (SCC) is one of the factors that can be used as a predictor for herd health and thus production.

Objective: This research aimed to build a model using regression techniques in order to predict milk production per cow using predictor variables including SCC, location, and milk composition factors (e.g., urea, fat%, and protein%). We hypothesized that increasing SCC is negatively associated with milk production per cow.

Methods: Data were obtained from the Government of Thailand from 2021-2024 totalling 335 125 observations from 25 cities. Four linear models (OLS estimator) were built using STATA v15; we assessed best fit by evaluating the F score, adjR-squared, and AIC values.

Results: Linear regression analysis revealed a negative association (b= -0.79, $p<0.001$) between lnSCC and milk volume. A best-fit model with independent variables lnSCC, city, urea (mg/ml) fat%, and protein% was selected with lowest AIC value (AIC= 2194348, F=2708.99, Adj R-squared= 0.0391).

Conclusions: The linear regression models in this study agreed with previous studies on Canadian dairy cattle (Durr, et al. 2008) that demonstrated increasing SCC was associated with decreased milk production. Our results support Thai policy and interventions that aim to decrease SCC among dairy cattle to improve production and, thus, profits for Thai dairy farmers.

Ecology and Host Preferences of the Invasive *Culex pipiens* in Alberta

Andrei Vasile, Michaela Seal, John Soghigian

Faculty of Veterinary Medicine, University of Calgary

Keywords: Invasive, Disease, Ecology

In 2018, an invasive mosquito species known as *Culex pipiens* was first detected in Alberta. On top of being more commonly associated with urban environments than native mosquito species, this insect is also known as one of North America's most significant vectors of West Nile virus and avian malaria. As a result, its arrival in Alberta poses potential epidemiological and wildlife conservation risks. Since *Culex pipiens* has become common in many Albertan municipalities, an investigation on this mosquito's ecology was carried out to understand what threats it may pose to veterinary and public health, and how we might mitigate its impacts. To gain insight on the ecology of this species and other mosquitoes in Calgary, we conducted extensive fieldwork throughout the city. This included a range of trapping methods to determine the best means of collecting the invasive species. We also used molecular analysis to evaluate the vertebrate blood-host of mosquitoes that were blood-fed. Here, we report our preliminary results from trapping mosquitoes throughout the summer, including the diversity of mosquitoes, the most effective methods for trapping mosquitoes, and what vertebrate hosts were most common among blood-fed mosquitoes. Finally, we discuss our results in a veterinary and public health context. Currently, *Culex pipiens* have been detected in all sample sites except for the rural Wildlife Conservation Center location. These mosquitoes first appeared approximately halfway through summer on July 11th and seem to prefer urban localities, represented by the Saddleridge Park Depot and Pumphouse Park depot sample sites.

Evolutionary Origins of Higher Taxa

Andrew Zhu, Jason Anderson, Jia Jia

University of Calgary Faculty of Veterinary Medicine; Institute of Vertebrate Paleontology and Paleoanthropology at the Chinese Academy of Sciences

Keywords: Salamander, musculoskeletal, development

The project aims to discover the evolutionary processes through which originally aquatic vertebrates developed feeding systems suited for on the different environment on land. We are unable to study directly these changes in fossils due to the absence of soft tissue, which is crucial to understanding how the vertebrates' mouths and limbs may have functioned. Because salamanders live in the intermediate area between purely aquatic and purely terrestrial and are one of the most primitive living tetrapods, they will be used as a model for this transition. I will be compiling a data set of current day salamander jaws and hind limbs, pre and post metamorphosis using contrast enhanced CT scanning to visualize both bone and soft tissues. Different salamanders also demonstrate various methods of feeding, such as suction, chewing, and tongue use, which encompasses the feeding methods of many other species, so a diversity will be scanned. After scanning, I will use software to digitally reconstruct the limbs, jaws, hyoid apparatus, and muscles related to feeding into a 3-D model to help us understand the mechanisms behind the evolution of vertebrate jaws and legs.

Pannexin-1 dependent mechanisms in T-cells underlie neuropathic pain in females

Annika Maj[1], Brendan McAllister[1], Churmy Fan[1], Tuan Trang[1].

[1]Faculty of Veterinary Medicine, University of Calgary

Keywords: Neuropathic pain, sex differences, leptin

Chronic pain is a leading cause of disability. Despite its higher prevalence among women, studies have focused on male subjects, contributing to inadequate pain treatment options for women. This disparity is evident in neuropathic pain which manifests in many conditions, including diabetes, cancer, back pain, and autoimmune disorders. Although the causes of neuropathic pain are greatly influenced by sex, the underlying causes are not well defined. Spared nerve injury causes allodynia in male and female rodents. We showed that in females, nerve injury increased spinal CD8+ T-cells and leptin levels. This leptin release from female derived CD8+ T-cells was pannexin (panx)-1 dependent, and intrathecal injection of leptin neutralizing antibody was able to sex-specifically reverse allodynia. Furthermore, the adoptive transfer of female derived CD8+ T-cells caused robust allodynia in uninjured rodents and was reversed by injection of leptin neutralizing antibody or leptin siRNA knockdown. This discovery is novel, and, in the future, we will continue to further elucidate the mechanisms by which panx-1 is sex specifically activated in CD8+ T cells to lead to the release of leptin and onset of allodynia.

Together in Paraphyly: A review on the taxonomic status of the tribe Aedini

Carmen Chan, John Soghigian, Huiqing Yeo

Faculty of Veterinary Medicine, University of Calgary

***Keywords*:** Taxonomy, Culicidae**,** Paraphyly

The tribe Aedini within the family Culicidae contains approximately a fourth of known mosquito species. Specifically, the tribe accounts for most mosquitos who serve as vectors for various vector-borne diseases. However, within the 20th century, there has been much debate on the taxonomy of mosquitoes with changes constantly being made regarding the genus *Aedes* and the discussion on whether it is monophyletic or paraphyletic. With a large veterinary and public health importance, a call for stable classification is needed to better understand the family and its competence as a vector. As such, we have conducted a review to determine whether the genus *Aedes* is monophyletic which has been previously concluded or paraphyletic. We analyzed and compared phylogenetic trees using molecular and morphological markers gathered from 15 papers published within the last 20 years. Through comparison of molecular and morphological markers results showed that the genus *Aedes* is paraphyletic. Furthermore, the genus *Aedes* is divided into two separate clades A and B within the tribe Aedini. Clade A containing largely known subgenus *Ochlerotatus* and *Finlaya*, were found to be sister to genera *Opifex* and *Haemagogus*. Clade B contains subgenus *Stegomyia* and *Aedimorphus*, sister to the remaining genera in the tribe Aedini. We have shown that morphological and molecular data both support the paraphyly of the genus *Aedes*, however careful consideration must be taken with reclassification due to the medical importance of the genus.

Quantifying c-FOS Expression to Explore Neuronal Excitation in Fragile X Syndrome Mice Models: Insights into Auditory Hypersensitivity

Demi Ma[1,2,3], Ning Cheng[1,2,3], Dorit Moehrle[1,2,3]

[1]Faculty of Veterinary Medicine, University of Calgary; [2]Alberta Children's Hospital Research Institute, Cumming School of Medicine, University of Calgary; [3]Hotchkiss Brain Institute, Cumming School of Medicine, University of Calgary

***Keywords*:** Fragile X Syndrome, c-FOS, Auditory hypersensitivity

Fragile X Syndrome (FXS) is the leading monogenic cause of autism, resulting from a CGG repeat expansion in the Fragile X Messenger Ribonucleoprotein 1 (FMR1) gene. Individuals with FXS often exhibit atypical social interactions, seizures, heightened anxiety, and sensory hypersensitivity. Studies have suggested that increased neuronal excitation in FXS may be linked to auditory hypersensitivity where every day sounds are perceived as unbearably loud. The implications for quality of life due to auditory hypersensitivity include social impairments, emotional distress, atypical behavioural responses, and limited participation in activities. This research investigates variations in the expression of immediate early gene, c-FOS, as a marker for neuronal activity after exposure to loud sounds in a mouse model of *Fmr1* KO using immunohistochemistry. Immunohistochemistry is a method that requires antibodies to detect and emit fluorescence when tagged to certain antigens in tissue. By employing microscopy and image analysis, we aim to quantify c-FOS expression, which is hypothesized to be upregulated in certain brain regions underlying auditory hypersensitivity. This study focuses on the inferior colliculus (IC), which relays auditory information from the inner ear to the auditory cortex and coordinates acoustic-motor functions. Preliminary findings indicate an increase in c-FOS signaling in postnatal day 20 *Fmr*1 KO mice compared to controls, suggesting that neuronal over-responsiveness in the IC during early development might contribute to auditory hypersensitivity in FXS. This study requires further investigation with a larger sample size to validate these results and better understand the underlying neuronal mechanisms resulting in auditory hypersensitivity in FXS.

Single cell transcriptomics reveals sex-specific alterations in neuronal signaling and gene expression in an ALS mouse model

Dominic Gerding[1], Isabel Rea[1], Minh Dang Nguyen[1,2,3,4], Jeff. A Biernaskie[1,2,3,4]

[1]Department of Comparative Medicine and Experimental Biology, Faculty of Veterinary Medicine, University of Calgary, [2]Alberta Children's Hospital Research Institute, [3]Hotchkiss Brain Institute, [4]Cumming School of Medicine, University of Calgary,

Keywords: TDP43, ALS, Metabolism

Amyotrophic Lateral Sclerosis (ALS) is a progressive neurodegenerative disorder characterized by rapid degeneration of motor neurons, leading to paralysis, and eventual death. The disease exhibits a pronounced sexual dimorphism in humans, with males displaying increased susceptibility and accelerated disease progression compared to females. To investigate this sexual dimorphism, a mouse model expressing the aggregate protein TDP43 (A315T variant of TAR DNA Binding Protein 43) was examined. Single-cell RNA sequencing was performed on the motor cortex at the age of 12-14 weeks, when males exhibit extensive motor dysfunction while females remained asymptomatic. Analyzing the differential gene expression across all clusters revealed inhibitory neurons to be the most perturbed within males. Furthermore, a heterogeneous response was observed among different inhibitory neuronal clusters, suggesting specific vulnerabilities within distinct inhibitory neurons in males, but not in females. Notably, the expression of transthyretin (Ttr), a transport protein involved in the clearance of TDP aggregates in neurons, was significantly lower in male inhibitory neurons. Additionally, male TDP43 mice showed reduced pathways related to neurodevelopment and differentiation, particularly in one subtype of inhibitory neurons, compared to both male wild-type (WT) and female TDP43 mice. Conversely, pathways regulating post-synaptic potentials, such as Glut-SLC17A7-GLS, were upregulated within excitatory neurons in male TDP43 mice relative to the other groups. In summary, these findings indicate that both excitatory and inhibitory neurons in the primary motor cortex of TDP43 mice display sex-specific alterations, alongside disrupted expression of genes associated with cellular transport and post-synaptic potentials.

The association between body conformation and percentage of normal spermatozoa in Angus beef bulls

Dusty Bennett, Vinicius Camargo, Ed Pajor, Jennifer Pearson

Faculty of Veterinary Medicine, University of Calgary

Keywords: Beef Bull Fertility, Sperm Analysis, Conformation Scoring

The fertility of bulls is estimated through a Breeding Soundness Evaluation (BSE), which includes assessing the overall health, reproductive organs, scrotal circumference (SC), percentage of sperm motility, and percentage of normal spermatozoa (NS) in individuals. Body conformation factors that affect a bull's ability to sire calves includes age, weight, claw score (CS), foot score (FS), leg score (LES), locomotion score (LOS), and body condition score (BCS). The objective is to investigate the association of body conformation scores with the percentage of normal spermatozoa and scrotal circumference. Thirty-one Angus bulls from the WA Ranches at the University of Calgary were enrolled during the BSE and age, body weight, leg, foot, and claw conformation, scrotal circumference, percent of normal spermatozoa, and locomotion score when the bull exited the chute were collected. Age ranged from 2 to 6.5 years old, body weights ranged from 1770-2450 lbs and BCS ranged from 3-3.5/5. Scrotal circumference ranged from 37-46 cm, and the NS ranged from 71% to 99%. Scores for CS, FS, and LES ranged from 3 to 8 (normal is 5), and no bulls were lame upon inspection. There was no statistical significance of age, weight, CS, FS, LES, LOS, and BCS on NS ($P > 0.05$). Age and body weight were associated with SC ($P < 0.05$). Body conformation did not predict semen quality but may still be important factors to investigate in overall bull fertility and siring capacity.

Modulation of Inflammatory Cell Death in Infectious Bronchitis Virus-Infected Macrophages via the COX-2/PGE2 Pathway

Motamed Elsayed Mahmoud[1,2], Dylan Tingley[1], Ryan Rahimi[1], Akeel Faizal[1], Muhammed Azhar [1], Ishara M. Isham[1], Mohamed Faizal Abdul-Careem[1]

[1] Faculty of Veterinary Medicine, University of Calgary, 3330 Hospital Drive NW, Calgary, AB, T2N 4N1, Canada
[2] Department of Animal Husbandry, Faculty of Veterinary Medicine, Sohag University, Sohag 84524, Egypt.

Keywords: IBV, COX-2/PGE2, Apoptosis

Infectious bronchitis virus (IBV) was the first identified member of the Coronaviridae family in the 1930s, predating the discovery of human coronaviruses by approximately 30 years. IBV is a highly contagious virus that causes lesions in the respiratory, renal, gastrointestinal, and reproductive systems of infected birds creating a significant economic burden for the poultry industry. With the goal of discovering novel therapeutic targets for mitigating IBV pathogenesis, this study investigated the role of the cyclooxygenase-2 (COX-2)/prostaglandin E2 (PGE2) pathway in programmed cell death (PCD) during IBV infection in chicken macrophages. Cells were treated with a selective COX-2 inhibitor, caspase inhibitor, or PGE2 following infection with either the Delmarva (DMV/1639) or Connecticut (Conn A5968) variants of IBV. RNA extraction and cDNA synthesis was performed, followed by q-PCR for determination of Intracellular and extracellular viral genome loads. Cell viability, apoptosis, and necroptosis were assessed using flow cytometry. Our findings demonstrated that COX-2 inhibition results in a significant decrease in intracellular viral genome load for both strains, with no effect on cell viability. Caspase inhibition resulted in a significant decrease in extracellular genome load while maintaining cell viability. Furthermore, inhibition of apoptotic pathways with the pan-caspase inhibitor z-VAD-FMK mitigated virus-induced necroptosis. This study helped unveil the critical influence of targeted COX-2/PGE2 pathway modulation in IBV pathogenesis, offering insight into potential therapeutic interventions for combatting IBV infections in poultry.

The rise and fall of tendon health: exploring cellular dynamics across the lifespan of equine tendon

Emma Piercey, Ross Fitzsimmons, Dragana Ponjevic, Cameron Knight, John Matyas, Holly Sparks

Faculty of Veterinary Medicine, University of Calgary

Keywords: Tendinopathy, Horses, Cells

Tendon injuries, particularly those of the Superficial Digital Flexor Tendon (SDFT), are an unfortunately common and often devastating condition in equine athletes. Once injured, the equine tendon heals through the production of fibrotic scar tissue with reduced function and a propensity for reinjury. Although these injuries are common, little is known about 1) the underlying cellular changes preceding the age-related decline in tendon health, predisposing the tendon to injury and 2) the cellular and molecular mechanisms responsible for the production of functional tendon tissue. To begin to explore this, we will examine cadaveric SDFT samples from young and aged adult equine subjects, to characterize degenerative changes observed with aging, as well as fetal subjects at different stages of development to identify the biological mechanisms capable of tendon regeneration. Using immunohistochemistry, we will evaluate the differences in the density and proliferation of resident cells, tendon vascularity and innervation, as well as parallel changes observed of the extracellular matrix. While characterization is underway, one key histological finding is the observation of chondrogenic changes in resident tenocyte populations with age and injury, suggesting that aberrant changes in cellular phenotype may be occurring. Ongoing work seeks to better characterize the specific cellular dynamics of both tendon morphogenesis and gradual degeneration, as well as why endogenous tendon healing favours the production of fibrotic scar tissue over the regeneration of new tissue. This foundational work will provide vital information around tendon cell biology, uncovering potential targets for methods of better preventing and treating tendon injury in horses.

Effects of GDNF and GFRα1 on Germ Cell Proliferation in Porcine Testicular Organoids

Ethan Willms, Anja Elsenhans, Ina Dobrinski

Department of Biochemistry and Molecular Biology, Cumming School of Medicine, and Faculty of Veterinary Medicine, University of Calgary

***Keywords*:** Testis, Organoids, Germ Cell Proliferation

Cryopreservation of sperm before cancer treatment is a routine fertility-preservation measure that is not possible for prepubertal boys. Their fertility could be protected by preserving testicular cells for in vitro spermatogenesis. As findings from higher mammals may be more translatable to humans, our lab has shown that porcine testicular cells self-organize into testis-like three-dimensional testicular organoids (TOs), which could aid in developing in vitro spermatogenesis protocols. However, the germ cells (GC), located on the exterior of the TOs, are easily lost during media changes. Glial cell-derived neurotrophic factor (GDNF), produced by Sertoli cells, and its receptor GFRα1 , stimulate GC proliferation in vivo. Here, we explored if medium supplementation with GDNF (40 ng/mL) and GFRα1 (25 ng/mL) affects GC proliferation within TOs. TOs were cultured with or without supplementation for 1 and 2 weeks. To quantify GC proliferation, we assessed germ cell proliferation based on EdU incorporation and immunocytochemistry for GC-specific markers and counted at least 60 GCs per group (n=3). Proliferation was similar at 1 week (3.7±0.8% in controls vs. 3.7±3% in supplemented; p=>0.9999) but tended to increase at 2 weeks (8.4±1.3% in controls vs. 13.7±2.4% in supplemented; p=0.0549). Within the supplemented group, GC proliferation significantly increased from 3.7±3% (1 week) to 13.7±2.4% (2 weeks, p=0.0017), showing an additional positive effect of longer culture duration. Therefore, GDNF and GFRα1 stimulate GC proliferation within porcine TOs, potentially improving organoid functionality and comparability to in vivo. Furthermore, increasing GC proliferation may be a measure to counterbalance GC loss during testicular organoid culture.

Developmental milestones of a mouse model of Fragile X syndrome treated with an inhibitor of the extracellular signal-regulated kinase pathway

Evan Tigley[1,2,3], Moon Young Bae[1,2,3,4], Ning Cheng[1,2,3],

[1]Faculty of Veterinary Medicine, University of Calgary; [2]Alberta Children's Hospital Research Institute, Cumming School of Medicine, University of Calgary; [3]Hotchkiss Brain Institute, Cumming School of Medicine, University of Calgary; [4]Cumming School of Medicine, University of Calgary

Keywords: ERK-pathway, Fragile X Syndrome, Developmental

Fragile X syndrome (FXS) is the most prevalent inherited cause of autism spectrum disorder and developmental disability. It is attributed to the absence of the Fragile X Mental Retardation Protein (FMRP), a critical mRNA-binding protein required for neural protein translation. Characteristic symptoms of FXS in both humans and mice include cognitive and intellectual impairments and atypical motor activity. These differences may result from the upregulation of the extracellular signal-regulating kinase (ERK) pathway in individuals with FXS. The ERK-pathway has a key regulatory role in neural development and plasticity. This project utilizes the ERK-pathway inhibitor PD325901 (PD), to determine if remediation of behavioural differences associated with ERK-pathway upregulation could be observed in FXS-modeled mice from postnatal days (P)2 to (P)18. Two cohorts of wild-type (FVB) mice and two cohorts of FXS-modeled (FMRP_KO) mice were used. One litter from each genotype was treated with vehicle (DMSO) as a negative control, and the other was treated with PD administered through water treatment on P7. Developmental milestones were conducted every other day from P2 to P14 and consisted of multiple *somatic growth* measurements and various *somatosensory* tests. The Homing Test at P9 and Open Field Test at P18 were also employed. These methods provide a semi-quantitative procedure to observe the growth, motor, and cognitive abilities of developing pups. Comparing the results between these cohorts can provide insight into the mechanisms underlying Fragile X Syndrome and the ERK-pathway. Currently, we are still testing the hypothesis that PD can reverse differences associated with FXS.

Impact of Inbreeding on Breeding Success in a Herd of Captive Reindeer

Haley Young[1], Gregory Muench[1], Amy Martell[1], Robert McCorkell[1], Jeff Biernaskie[1,2,3]

[1]Faculty of Veterinary Medicine, University of Calgary; [2]Hotchkiss Brain Institute, University of Calgary; [3]Alberta Children's Hospital Research Institute,

Keywords: reindeer, inbreeding, reproduction

Introduction

The UCVM reindeer herd was founded in 2008 with eight breeding animals to support scientific research on *Cervidae* species. Since then, the herd has remained closed with no external reindeer introduced while breeding has taken place annually. Due to the small, closed breeding pool, the reindeer have become progressively inbred over time. Recent observations of higher rates of breeding failure have raised concerns about the potential impact of inbreeding on breeding success. Inbreeding depression, characterized by reduced fitness due to breeding between closely related individuals, can decrease survival and reproductive success through increased homozygosity and the accumulation of deleterious alleles. This project investigated the impact of inbreeding on breeding success in the UCVM reindeer herd.

Methods & Results

Breeding records were used to reconstruct pedigrees for all attempted breedings since the herd founding, and a coefficient of inbreeding (COI, %) was calculated for each potential offspring. Pregnancy was confirmed using rectal ultrasound and/or serum progesterone while other breeding outcomes were classified using health records and necropsy results. Out of 89 attempted breedings, 42% resulted in breeding failure (failure to conceive, abortion, stillbirth, or neonatal death ≤1-month old) while 58% resulted in live, viable calves that lived >1-month. Live-viable calves (median [IQR]: COI=15.2 [0.0–25.0]) were significantly less inbred than breeding failures (COI=25.6 [14.6–30.5], p=0.002).

Conclusions

These findings suggest that inbreeding is contributing to the herd's decreased breeding success. To mitigate this issue, future efforts will focus on expanding the genetic pool of the herd by introducing new reindeer.

Characterization of the Putative Pore-Forming Protein Apolipoprotein L 9A (APOL9A) in Macrophages

Irene Dinh[1], Liam Wilkinson[2], and Johnathan Canton[3,4]

[1]Cellular Molecular Microbial Biology, Faculty of Science, University of Calgary. [2] Biochemistry and Molecular Biology, Cumming School of Medicine, University of Calgary, Immunology, Cumming School of Medicine, University of Calgary, [3] Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Science, University of Calgary. [4] Calvin, Joan and Phoebe Snyder Institute for Chronic Diseases, University of Calgary.

Keywords: Macrophages, Apolipoprotein L 9A, *Escherichia coli*

Macrophages are immune cells crucial in identifying potential threats by internalizing and retaining extracellular material in membrane-bound organelles called phagosomes. This material typically undergoes digestion and recycling after phagosomal fusion with lysosomes. However, the internalized materials can remain undigested and are released directly into the cytosol. This process is critical during a bacterial infection, as the ingested material may contain pathogen-associated molecular patterns (PAMPs), which trigger an inflammatory response when transferred to the cytosol. It was found that Apolipoprotein L 9A (APOL9A), a putative pore-forming protein, is uniquely expressed in Kupffer cells, which are the tissue-resident macrophages of the liver. This protein could be recruited to the phagosomal membrane, creating pores that enable PAMPs to leak into the cytosol. Although this transfer is essential for a robust immune response, the underlying mechanisms remain poorly understood. Therefore, we hypothesize that APOL9A is recruited to the phagosome membrane of macrophages to initiate their rupture and activate cytosolic danger sensors. To investigate this, the study uses immunofluorescent assays to characterize APOL9A. The assays are conducted under varying conditions, including time courses, using different experimental particles such as *Escherichia coli,* fluorescent ROS-sensitive and insensitive OVA beads and various markers. Significance was assessed using a student's T-test, and confocal microscopy revealed that APOL9A is associated with phagosomal damage and accumulates on late phagosomes and *E. coli*. However, it still needs to be made clear if APOL9A is dependent on NADPH oxidase. These findings provide insights into the workings of macrophages and their potential immunotherapeutic roles.

Transplacental transmission of canine distemper virus in a Linnaeus's 2-toed sloth (Choloepus didactylus)

Jennifer E. Black[1], Erin Zachar[1], and Jennifer L. Davies[1]

[1]Diagnostic Services Unit, University of Calgary Faculty of Veterinary Medicine, Calgary, AB, Canada

Keywords: Canine distemper virus, veterinary anatomic pathology, sloths

Canine Distemper Virus (CDV) causes a highly contagious and often fatal disease in a broad range of mammals. The virus is regarded to have pronounced tropism for epithelial, lymphoid, and neurological cells. After aborting a fetus mid-gestation, a 4-year-old female Linnaeus's 2-toed sloth (*Choloepus diadactylus*) succumbed to respiratory and gastrointestinal disease. Routine necropsies were performed on both the adult sloth and the fetus. On histology, endothelial cells in maternal and fetal tissues contained amphophilic intranuclear and intracytoplasmic viral inclusion bodies. Endothelial syncytia were also noted. Microscopic evidence suggests that the abortion was the result of CDV infection inducing acute, necrosuppurative placentitis with vasculitis. Immunohistochemistry and real time PCR support a transplacental CDV infection. Sequencing identified the causative CDV strain as one that was first isolated from a raccoon in Iowa. Along with a novel viral tropism and reproductive disease presentation, this case represents the first reported vertical transmission of CDV in this host species.

Determination of Ophthalmic Parameters in the Endangered Greater Sage Grouse (Centrocercus urophasianus)

Julia M. Gaume[1], Douglas P. Whiteside[1,2]

1Faculty of Veterinary Medicine, University of Calgary, Calgary, AB T3R 1J3, Canada; 2Wilder Institute/ Calgary Zoo, Calgary, AB T2E7V6, Canada

Keywords: ophthalmology, avian, conservation

The greater sage-grouse (*Centrocercus urophasianus*) is an endangered avian species native to the sagebrush shrubland in North America. The goal of this study was to determine reference intervals for intraocular pressure (IOP) and tear production in healthy, greater sage grouse from a zoo-based conservation breeding for reintroduction program. Complete ophthalmic examinations were performed on 42 birds (33 adults and 9 juveniles). IOP was determined using a TonoVet rebound tonometer and tear production was evaluated using iTear meniscometry test strips. Iris colour and pectin structure were evaluated using a Panoptic ophthalmoscope with an iExaminer attachment. Mean IOP of adults and juveniles combined was 16.7 ± 2.5 mmHg (range: 10-25 mmHg). Mean tear production of adults and juveniles combined was 3.7 ± 2.3 mm/ 5 seconds (range: 1.1- 17.2 mm/5 seconds). Mean IOP between adults (17.8± 2.2mmHg) and juveniles (14.5 ± 1.6mmHg) was significantly different (P <0.001) as was mean tear production (adults- 3.1 ± 1.5mm/5 seconds; juveniles- 4.8± 3.2mm/5 seconds; p= 0.007). There was no significant difference found between the right and left eye for mean adult IOP (p= 0.147), mean adult tear production (p= 0.086), mean juvenile IOP (p= 0.667) or mean juvenile tear production (p= 0.826), nor for adult female and male mean IOPs or mean tear production (p= 0.919, p= 0.077 respectfully). In conclusion, this study provides key ophthalmic parameters in greater sage grouse, which will allow veterinarians and biologists to identify and treat ocular problems more accurately and efficiently in this species.

Association between strongyle parasite infections and overwinter survival in Sable Island feral horses

Katie Moyes[1], Micky Ahn[1], Philip D. McLoughlin[2], Jocelyn Poissant[1]

1Faculty of Veterinary Medicine, University of Calgary; 2Department of Biology, University of Saskatchewan

Keywords: Wildlife, Parasites, Host Survival

Wild animals are typically infected by numerous gastrointestinal parasites that significantly impact their health and fitness. Among these parasites, some are more pathogenic and thus pose a greater threat to host survival. For example, feral horses can be infected by over 40 different species of strongyle nematodes, but those in the genus *Strongylus*, known as large migratory strongyles, are believed to be particularly harmful due to their extensive migration through host tissues, which can cause severe internal damage. However, identifying gastrointestinal parasites non-invasively using traditional coprological techniques is challenging due to morphological similarities between the eggs of different species. In this study, we combined parasite fecal egg counts (FEC), a proxy for parasite load, with DNA metabarcoding to characterize mixed-species parasite infections in the feral horse population of Sable Island, Nova Scotia. Using infection data derived from approximately 3,000 samples collected from around 950 horses over nine years, as well as intrinsic and extrinsic variables including location, sex, and age, we applied linear models to test for associations between strongyle FECs and overwinter survival. We also investigated whether these associations differed between migratory and non-migratory strongyles. Our findings indicate that while large migratory strongyles have a strong negative association with overwinter survival in Sable Island horses, other types of strongyles do not. This study underscores the importance of applying molecular techniques to characterize mixed parasitic infections and understanding their associations with health and fitness traits in wildlife populations.

Beyond Dissection: Enhancing Veterinary Anatomy Education Through Cross-Sectional Learning

Kaitlin Paul BSc DVM Student, Robert McCorkell DVM PhD, Brandie Martin AHT BSc

Faculty of Veterinary Medicine, University of Calgary

Keywords: Veterinary Education, Anatomy, Cross-Sections

Our hypothesis is that cross-sectional anatomy specimens enhance students' spatial understanding of anatomical relationships and improves their ability to integrate knowledge of different body systems, thereby leading to better diagnostic skills and clinical application. This project used an embalmed male dog cadaver (Animal Care Control Protocol AC21-0149). The cadaver was sectioned transversely into thirty-two sections from the fourth cervical vertebra to the tail base. The sections were treated with acetone dehydration and Silicone 10 plastination according to UCVM protocols, displaying anatomical details of the musculoskeletal, abdominal, thoracic, pelvic, and urogenital systems which were then carefully identified in each section. A labled key was produced for study and reference. The educational objective is to use the cross-sectional teaching specimen to improve students' spatial reasoning. Spatial knowledge and an understanding of anatomical relationships are crucial for interpreting diagnostic imaging, performing physical examinations, doing treatment protocols, diagnosing diseases, and understanding disease processes. Unlike traditional body system-based anatomy teaching, cross-sectional specimens allow students to view the integration of different systems within the whole animal. Developing cross-sectional specimens for teaching anatomy acknowledges that spatial reasoning is a trainable skill essential for veterinary practice. The project aligns with the learning outcomes of the VETM Anatomy 320 course, where labeling cross-sections reinforces students ability to visualize the animals organization in three dimensions. The project investigates the educational value of cross-sectional anatomy towards bridging the gap between theoretical knowledge and practical clinical application in veterinary education.

Prevalence of subclinical mastitis-causing pathogens on 15 Alberta dairy farms

Kismet Dhaliwal, Breno Luis Garcia, Diego Nobrega

Faculty of Veterinary Medicine

Keywords: Mastitis, Sub-clinical, Pathogen

Bovine sub-clinical mastitis is an inflammation of the mammary gland characterized by decreased milk production and increase in somatic cell count (SCC) (>200,000 cell/mL) without visible clinical signs (Cheng & Han, 2020). Intramammary infection is the main cause of sub-clinical mastitis (McDougall, et al., 2022). Identifying mastitis-causing pathogens is crucial for targeted control and preventative measures, minimizing economic losses, and effective herd health management (Panchal et al., 2024). This study aimed to evaluate the prevalence of sub-clinical mastitis-causing agents in cows with high SCC (>200,000 cell/mL) in 15 dairy herds in Alberta. SCC assessments were obtained from Dairy Herd Improvement (DHI) systems or automated milking systems; farms without such assessments underwent full herd screening. Farms provided a list of cows with high SCC, and we aseptically collected milk samples for microbiological identification. Samples were processed in lab by inoculating them onto Blood Agar (BA), incubating them for 24 and 48 hours for bacterial growth and morphology identification. Isolates were placed on new BA and sent for Matrix-Assisted Laser Desorption/Ionization Time of Flight (MALDI-TOF) analysis, which identifies bacteria by measuring molecular masses. From 323 milk samples, 53.4% had microbiological isolation. The most prevalent pathogens were *Staphylococcus chromogenes* in 28.6% (92/323), *Corynebacterium amycolatum* in 6.5% (21/323), and *Staphylococcus aureus* in 6.1% (20/323). The finding indicates that *Staphylococcus chromogenes*, is the most prevalent pathogen in sub-clinical mastitis. Sub-clinical mastitis is not commonly treated therefore, the need for improved control measures rather than treatment of all affected cows is crucial.

Preliminary investigation of the interactions between equine immune cells and parasites: first steps to a better understanding of deworming agents

Kobe Belhumeur[1], Johnathan Canton[2], Brielle Rosa[2]

[1] Faculty of Chemistry, University of Calgary
[2] Faculty of Veterinary Medicine, University of Calgary

Keywords: equine, monocyte, strongyle

Ivermectin is an antiparasitic drug that causes paralysis in nematodes through actions on ligand-gated chloride channels. *In vitro*, at concentrations typically achieved in the plasma, this effect is reversible in equine strongyle larvae and results in temporary larval paralysis but not death. However, ivermectin is a larvicidal drug, which suggests that it may cause the death of nematode larvae in tissues through modulating interactions between the immune system and the parasite. The purpose of this study was to conduct a preliminary investigation of the interactions between equine nematode larvae and equine immune cells, specifically monocytes, to begin to better understand the parasite/monocyte interaction and with the aim of developing an assay suitable for investigating the effects of anthelmintic compounds on this relationship. Fresh feces from feral horses naïve to dewormers was collected in the Sundre Equine Management Zone and mixed populations of third-stage equine strongyle larvae (L3) were cultured and collected using the glass-over-petri-dish method. L3 were exsheathed to better simulate their *in vivo* parasitic state. Exsheathment technique was optimized in our laboratory. Equine peripheral blood mononuclear cells (PBMCs) were isolated from fresh whole EDTA-blood using the SepMate procedure. Larvae were added to PBMCs in each of 4 conditions: 1. Live L3, 2. Live exsheathed L3, 3. Dead (paraformaldehyde (PFA) fixed) L3, 4. Dead (PFA fixed) exsheathed L3. Preliminary results suggest differences between conditions in immune cell and L3 interactions.

The involvement of inflammasome-activated macrophages in swine dysentery colitis.

Kylie Tiedje[1], Rodrigo Puentes[2], Niloofar Mirzadzare[2], Rita Hannawayya[2] Eduardo R. Cobo[2]

[1]Department of Biological Sciences, Faculty of Science, University of Calgary
[2]Faculty of Veterinary Medicine, University of Calgary

Keywords: swine dysentery, macrophage, colitis

Introduction: Swine dysentery is a mucohemorrhagic diarrheal disease in weaned pigs caused by infections of the large intestine with *Brachyspira hyodysenteriae (B. hyo)*. Swine dysentery poses a significant challenge to the swine industry due to weight loss and death in pigs during the grower/finisher phase and the emergence of multi-drug-resistant *Brachyspira* species. In search of therapeutic alternatives, we aimed to determine the type of colitis present during swine dysentery to develop specific immunomodulators for this disease.

Methods: Inflammatory processes in the gut afflicted by swine dysentery were studied in colonic tissue samples collected from post-weaning pigs exposed to *B. hyo* or an inert solution for 2–3 weeks, histologically analyzed in hematoxylin-eosin-stained slides. The involvement of the inflammasome and release of pro-inflammatory cytokine IL-1β and reactive oxygen species (ROS) were studied in cultured murine macrophages exposed to *B. hyo*, measuring IL-1β by specific ELISA and ROS by fluorescence intensity (CM-H2DCFDA).

Results: Colons from *B. hyo*-infected pigs revealed epithelial erosion, hemorrhage, and increased leukocyte infiltration in the lamina propria, indicating acute hemorrhagic colitis. Macrophages primed by lipopolysaccharide (LPS) and then exposed to *B. hyo* showed elevated levels of secreted IL-1β and ROS, compatible with inflammasome activation.

Conclusion: Swine dysentery is driven by inflammasome-mediated colitis, in which *B. hyo* acts as an activator in primed macrophages. The roles of macrophages and the inflammasome in *B. hyo*-induced colitis are potential targets for anti-inflammatory therapies in post-weaning diarrhea in swine.

Preparation and identification of Permian-age fossils from the Briar Creek locality of the Nocona Formation in Texas

Chowdhury, L.[1], Cochran, N[1]. & Anderson, J.[2,1]

1 Department of Biological Sciences, Faculty of Science, University of Calgary;
2 Faculty of Veterinary Medicine, University of Calgary.

Keywords: Permian, fossils, palaeontology

The Red Beds of Texas comprises several early Permian formations recognized for their vertebrate fossil assemblages. We review material collected from the Briar Creek locality of the Nocona Formation, which has previously yielded remains of temnospondyls (*Eryops, Aspidosaurus, Zatrachys*, *Trimerorhachis*), embolomeres (*Archeria*), nectrideans (*Diplocaulus*), synapsids (*Dimetrodon, Edaphosaurus, Ophiacodon*) and reptiliomorphs (*Diadectes, Bolosaurus*). Such taxa are close to the origin of several tetrapod crown groups and are therefore of phylogenetic, morphological and ecological interest. We worked on excavated (designated BC-7) and surface-collected fossils recovered from scree (designated BCS), which were collected on field expeditions to Archer County, Texas in 2007 and 2009. We cleaned the fossils with toothbrushes and air scribes and consolidated with ultra-thin polyvinyl acetate (PVA) glue. We photographed the prepared material from multiple angles with a Nikon D200, including a scale for reference. Where possible, we established taxonomic identity by comparing osteological characters on the specimens to descriptions in the published literature, with the expectation that they would represent the prior identified taxa. We report remains of the basal synapsids *Dimetrodon sp.* and *Edaphosaurus boanerges*, as well as indeterminate temnospondyl fragments. None of the material represents new species but our fossils nevertheless add to the sample available for future palaeontological work.

AMR profiling of commensal fecal E. coli in domestic and feral horses in Alberta.

Lindsey Hampton, Beverly Morrison, Brielle Rosa, Marie-France Roy

Faculty of Veterinary Medicine, University of Calgary

Keywords: antimicrobial resistance, *Escherichia coli*, equine

Antimicrobial resistance (AMR) is a global problem that threatens human and animal health. While there has been much speculation regarding the role of animals and veterinary medicine in the spread of AMR, our current knowledge of AMR in Alberta horses or their role in the spread of AMR is very limited. The aim of our study was, therefore, to investigate current AMR patterns in domestic and feral horses in Alberta, while exploring the role that hospitalization, antimicrobial drug (AMD) administration or contact with other species might play in this complex problem. Fecal samples collected from various horse populations were used to isolate commensal fecal *E. coli* (a known AMR sentinel species) for AMD susceptibility testing. Fecal samples were collected from the following horse populations: 1) hospitalized horses on Day 0 and Day 2 or 3 of hospitalization, receiving or not receiving AMD; 2) feral horses before and after co-grazing with domestic cattle and 3) co-grazing cattle. Preliminary results suggest that feral horses usually harbor very little AMR *E. coli*, however, increased AMR in feral horses might be associated with grazing alongside domestic cattle or be inherent to specific small herds. Additionally, domestic horses appear to have, overall, a higher prevalence of AMR *E. coli* compared to feral horses and AMD administration seem to influence their AMR profiles. These results of this study will increase our understanding of prevalence and dynamics of AMR in Alberta horses and help us identify interventions that might limit the spread of AMR in the future.

Characterizing common blood-derived therapeutics from horses with Pituitary pars intermedia dysfunction

Caplan L., Toth K., Wilkinson L., Canton J., Caldwell T., Roy MF., Sparks H.

Faculty of Veterinary Medicine, University of Calgary

Keywords: Pituitary pars intermedia dysfunction, blood-derived therapeutics, peripheral blood mononuclear cells

Pituitary pars intermedia dysfunction (PPID) is an endocrine disorder affecting approximately 21% of horses over 15 years of age, leading to delayed shedding, immunocompromise, muscle wasting and often, the need to treat joint injury and osteoarthritis. Yet, traditional therapeutics such as corticosteroids carry an increased risk of causing laminitis. As an alternative, kits to process the patient's own blood in order to concentrate specific cells (platelets and leukocytes) as an "Orthobiologic" therapeutic (APS and ACS) are increasingly recommended in treating joint disease in horses. Yet, as PPID is known to affect the circulating immune cells, it is not known if orthobiologics produced from these patients are similar to that published in healthy horses. To explore this, we have collected blood from PPID-affected horses and age-matched healthy controls to produce APS and ACS and characterized the relative concentration of specific cell types as well as their cytokine and growth factor profile. A complete blood count on the peripheral blood and orthobiologic products occurred as well as an analysis of 23 cytokines from the orthobiologics and conditioned media of peripheral blood mononuclear cell (PBMC) samples. The PBMCs were treated with inflammatory products including silica, LPS and IL-1. Statistical analysis employing t-tests were conducted to compare cytokine, platelet, red and white blood cell concentrations between the PPID-affected and healthy horses. Findings indicate elevated inflammatory cytokines, including IL-1β and TNF-α, in the orthobiologics produced from PPID-affected horses. This research aims to enhance our understanding of the cellular differences in autologous products for PPID-affected horses, aiding clinical decision-making.

Longitudinal shifts in *Salmonella* Dublin positivity: Comparing herd status changes in hutterite and non-hutterite dairy farms in Alberta

Marco Alarcon Aguilera[1,2], Rebecca Roos[2,3], Marlinde de Pater[2,3], Jessie van Heumen[2,4], Waseem Shaukat[2], Herman Barkema[2]

[1]Depertmant of Biomedical Sciences, Cumming School of Medicine, University of Calgary
[2]Faculty of Veterinary Medicine, University of Calgary
[3]Faculty of Veterinary Medicine, University of Utrecht, Netherlands
[4]Faculty of Veterinary Medicine, Ghent University

Keywords: Salmonella; Cattle; Logistical

Salmonella enterica subspecies *enterica* serotype Dublin (*Salmonella* Dublin) is a zoonotic and multi-drug resistant pathogen adapted to cattle. Our objective was to evaluate longitudinal changes in herd-level *Salmonella* Dublin positivity by comparing current status with that from two years before, and to compare between Hutterite and non-Hutterite types of dairy farms in Alberta. Bulk tank milk samples were collected from all active Hutterite-colony herds (n=132) and non-Hutterite herds (n=322) in June 2024 in Alberta and tested for antibodies against *Salmonella* Dublin using an indirect ELISA. Herd infection status was classified according to manufacturer's recommended cut-off value. Prior *Salmonella* Dublin status for these herds was obtained from a previous study. Prevalence of *Salmonella* Dublin-positive herds was 4.5% and 12.7% in Hutterite herds and non-Hutterite herds, respectively. Association of current *Salmonella* Dublin status with prior status was assessed using logistic regression. When comparing summer 2022 with summer 2024 tests, 89.2% herds did not change their status. Interestingly, Hutterite farms had higher odds of maintaining their status (OR = 2.26) compared to non-Hutterite farms. The odds of testing positive in 2024 were significantly higher in farms that had tested positive once (OR = 5.44), twice (OR = 18.23), three times (OR = 23.24), or all four times (OR = 25.11) during the 2022 tests, compared to farms that were consistently negative in 2022. In conclusion, Hutterite farms had a lower prevalence of *Salmonella* Dublin positive herds. Furthermore, most farms maintained their original disease status, with Hutterite farms having higher odds to maintain status.

Investigating the presence of Mycoplasma and Bovine Herpesvirus 4 in digital dermatitis biopsy samples of beef and dairy cattle

Maria Greco, Corienne Gammariello, Jeroen De Buck

Faculty of Science, University of Calgary; 2Faculty of Veterinary Medicine, University of Calgary

Keywords: Digital dermatitis, Bovine Herpesvirus type 4, Skin Lesion microbiome

Digital dermatitis (DD) is a chronic and infectious disease of cattle that results in painful and ulcerative foot lesions. Multiple bacterial species such as *Treponema* and *Mycoplasma* spp. are associated with the DD lesion microbiota. A previous study (Vermeersch et al., 2024) determined *Treponema* spp., *Mycoplasma* spp., and BHV-4 to be a significant microbial network found within udder cleft dermatitis lesions of dairy cattle. It is unknown if this cluster of species would be significant in DD lesions. This study's objective was to investigate the presence of BHV-4 in DD lesion samples of Albertan beef and dairy cattle also positive for *Mycoplasma* species. A total of 32 DNA samples extracted from DD lesion biopsies of local Albertan beef and dairy cattle were used to assess the presence/absence of Mycoplasma spp. and BHV-4 via PCR. All samples were confirmed positive for the presence of *Mycoplasma* spp. via PCR beforehand. The BHV-4 PCR targeted a 180 bp fragment of the BHV-4 glycoprotein B gene. The PCR method was optimized for sensitivity using serial dilutions of BHV-4 gBlock DNA which served as the positive control. Additionally, the PCR annealing temperature was optimized to 58°C. Negative controls include purified water, *Mycoplasma bovis* DNA, *Treponema* spp. plasmid, and BHV-1 DNA. PCR product amplicons were visualized by gel electrophoresis. BHV-4 was not detected by PCR in any DD lesion biopsy samples of beef and dairy cattle. In conclusion, BHV-4 is not associated with the microbiota of DD lesions of local Albertan beef and dairy cattle.

Understanding the use of deslorelin acetate implants for fertility control in canids: A literature review

Lavoie, Mary[1], Kutz, Susan[2], Baker, Tessa[2]

[1]Department of Biological Sciences, Faculty of Science, University of Calgary; [2]Faculty of Veterinary Medicine, University of Calgary

Keywords: Canid, Deslorelin Acetate and Reproductive Control

Many underserved communities in Canada face challenges in accessing veterinary services, particularly for sterilization. Recently, deslorelin acetate implants, in a 4.7 mg dosage, became available for use in dogs in Canada. To explore how these implants could enhance access to fertility control, we conducted a systematic literature review of their use in domestic and wild canids. A set of keywords was used to search four databases: Google Scholar, PubMed, Scopus, and CAB Abstracts. The inclusion criteria were broad, with no restrictions other than needing to be in English. Initially, 448 articles were identified based on their titles, focusing on relevancy to canids, deslorelin, and reproduction control. This was reduced to 67 after removing duplicates and excluding articles not relevant to the review's scope. The final selection included 34 primary articles, 24 reviews, 4 case reports, and 5 grey articles, published between 2001-2023. The studies confirmed the advertised duration of effect of the 4.7mg and 9.4mg dosages. Articles demonstrated effective use in male dogs with minimal side effects. In some young female dogs, side effects of the implant included delayed epiphyseal closure and juvenile vaginitis. Its use in older females led to other side effects in some dogs, including heat induction, prolonged estrus, uterine diseases, and pyometra. Side effects were infrequent in both sexes, suggesting a high level of safety. Overall, considering its duration of efficacy and safety, the 4.7 mg deslorelin acetate implant could be an effective tool in improving access to fertility control for dogs in underserved Canadian communities.

Investigating Mucin Binding Properties of MAP-Lysing Bacteriophages

Meera Sylvain, Natali Shafer, Jeroen De Buck

Faculty of Veterinary Medicine, University of Calgary

Keywords: Johne's Disease, Bacteriophages, Mucin Binding

Introduction: Johne's Disease (JD), caused by Mycobacterium avium subsp. paratuberculosis (MAP), is a chronic infection of the small intestine affecting cattle and other ruminants. JD control and prevention is an ongoing challenge for the cattle industries of Alberta. The De Buck lab conducted a successful 18-week calf trial utilizing daily oral administrations of eight novel bacteriophages (phages), bacterial viruses, till weaning at 2 months, to prevent a MAP infection. We're investigating the properties of phages found from swabbing the intestinal tract of calves at the end of the MAP prevention trial. We hypothesize that the phages found in the intestinal mucosa were persistent throughout the trial due to their mucin binding capabilities.

Materials & Methods: A mucin binding assay was conducted using a Nunc-Maxisorp 96-well plate coated with porcine mucin. Blocking was done with BSA, a protein reagent. Three phages used in the trial were incubated in the plate, unbound phages were washed off and elution was attempted with 100 mM Galactose, Fructose, Mannose and a water control. The resulting eluant was pipetted out and plated using a standard plaque agar overlay assay to determine phage titers.

Results: More plaques were observed on plates containing phages eluted with Galactose in comparison to plates eluted with water. Phage D29 demonstrated the most significant difference. This indicates that phages may be binding to Galactose residues in mucin, which is supported by their genomic Galactose-binding domains.

Conclusion: Bacteriophages may bind to sugars present on mucin proteins, which possibly enabled them to prevent MAP infection in the calf trial.

The use of cognitive task analysis for the development of an equine nasogastric intubation simulator.

Melanie Jarbeau [1], Dr. Chantal McMillan, Dr. Cameron Knight and Dr. Ashley Whitehead

[1] Faculty of Veterinary Medicine, University of Calgary

Keywords: Equine, Education, Clinical Skill

Learning to perform nasogastric intubation is an important skill for future equine practitioners. The development of accurate models allows for the reduction of animal use and protects the safety of students, instructors and animals. There are several equine nasogastric intubation simulators used in veterinary programs. However, many have not been appropriately researched to ensure they are effectively replicating live practice. As a result, students may practice missteps that could result in severe complications or injuries when transitioned to live animals. This cognitive task analysis aims to determine all critical steps of the nasogastric intubation skill and the necessary features required to create a training model. Five experienced veterinarians intubated a live horse and simulators while verbalizing as if they were training students. Three non-experts, composed of faculty and students, watched the videos to produce a list of all the described and visualized steps. An additional non-expert compiled the steps for each instructor's live and simulated scenarios. The compiled data was reviewed by the non-experts and clinical instructors and then finalized by a new expert to ensure the list included all necessary skill steps. The comprehensive list of required steps for nasogastric intubation can be used to guide production of a new model that accurately simulates the experience of intubating a live horse. Clinical skills instructors may also use the list to highlight critical steps in the form of learning objectives and assessments so that students and new veterinarians are appropriately trained to execute the procedure safely on live animals.

Exploring Social Interactions in a Mouse Model of Fragile X Syndrome

Moon Young Bae [1,2,3,4], Bosong Wang [2,3,4], Abdullah Abdullah [2,3,4], Asim Ahmed [2,3,4], Raffay Ilyas [1,2,3,4], Veronica Rasheva [1,2,3,4], Kartikeya Murari [2,5,6], Ning Cheng

1. Cumming School of Medicine, University of Calgary, Calgary, Alberta, Canada
2. Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada.
3. Hotchkiss Brain Institute, Cumming School of Medicine, University of Calgary, Calgary, AB, Canada.
4. Alberta Children's Hospital Research Institute, Cumming School of Medicine, University of Calgary, Calgary, AB, Canada.
5. Department of Biomedical Engineering, Schulich School of Engineering, University of Calgary, Canada.
6. Department of Electrical and Software Engineering, University of Calgary, Calgary, AB, Canada

Keywords: Fragile x syndrome, neurodevelopment, social interactions

Fragile X Syndrome (FXS), caused by mutations in the *Fmr1* gene, is a neurodevelopmental condition linked to cognitive and behavioral differences, including atypical interactions and heightened anxiety-like responses in social settings. Most studies have been conducted in males, and the mechanisms of these differences are unclear. In this project, *Fmr1* knockout (KO) mice, a model of FXS, and wild-type (WT) mice of the C57BL/6J strain were compared on social behavior. We conducted tests on both sexes of mice, including adolescents and adults at postnatal day 40 (P40) and 70 (P70), respectively. We observed free interactions between a pair of mice, which were of the same age, sex, and genotype, but were strangers to each other. Key social interaction variables including head, body, and anogenital sniffing, as well as physical touch, were analyzed using a novel marker-less algorithm based on computer vision and deep learning. Our results revealed pronounced differences between sexes in general, with females displaying increased duration of a single social event but decreased total counts of events when compared to males. When comparing different genotypes, the KO mice displayed increased counts of social events compared to WT mice, especially when comparing the female juvenile KO versus WT mice. Interestingly, these results suggest potential enhancements in social exploration in the KO mice relative to the WT mice. Future studies are warranted to investigate the mechanisms of the differences we observed here between both sexes and genotypes.

Endogenous cathelicidins influence mast cell responses in the colon in a microbiota-independent manner

Orchee Haque[1], Niloofar Mirzadzare[2], Rita Hannawayya[2], Eduardo R. Cobo[2]

[1]McGill University; [2]Faculty of Veterinary Medicine, University of Calgary

Keywords: Mast cells, cathelicidin, germ free

Introduction: Mast cells are crucial during colonic inflammation, releasing pro-inflammatory mediators and proteases. In mice, there are two primary mast cell populations: connective tissue mast cells (CTMCs) and mucosal mast cells (MMCs), with MMCs primarily involved in colitis. It has been reported that the gut microbiota regulates mast cells' immune response. Additionally, cathelicidin, an antimicrobial peptide secreted by neutrophils and epithelial cells, is suggested to mediate mast cell migration and activation, though its role in colitis is unclear. Therefore, this project aims to elucidate how the gut microbiota and cathelicidin influence mast cell responses during colitis.

Methods: Colitis was induced in mice by challenging them with *Citrobacter rodentium*, a Gram-negative attaching/effacing enteropathogen. Wild-type (WT) and cathelicidin-deficient (*Camp*$^{-/-}$) mice housed in germ-free (GF) conditions were infected with *C. rodentium*, and distal colon samples were collected at the end of the peak of infection (15 days post-infection). Mast cells were visualized using Toluidine blue staining, and MMCs were specifically identified via immunofluorescence for mast cell protease 1 (Mcpt1).

Results: Both *C. rodentium*-infected and control GF *Camp*$^{-/-}$ mice exhibited fewer mast cells in the colonic lamina propria than their WT counterparts. Similarly, the number of Mcpt1^{+} MMCs in the colonic mucosa was decreased in GF *Camp*$^{-/-}$ mice.

Conclusion: Endogenous cathelicidins promote mast cell presence in the colon during *C. rodentium*-induced colitis and homeostasis, and this does not require the gut microbiota. This study suggests a role for cathelicidin in regulating mast cells' immune response in the colon.

Prevalence of Salmonella Dublin in dairy herds in Alberta, Canada

Rebecca Roos[1,2], Marlinde de Pater[1,2], Marco Alarcon Aguilera[1,3], Jessie van Heumen[1,4], Waseem Shaukat[1], Herman Barkema[1]

[1]Faculty of Veterinary Medicine, University of Calgary
[2]Faculty of Veterinary Medicine, University of Utrecht, Netherlands
[3]Depertmant of Biomedical Engineering, Schulich School of Engineering, University of Calgary
[4]Faculty of Veterinary Medicine, Ghent University

Keywords: Salmonellosis; prevalence; dairy

Salmonella enterica subspecies *enterica* serotype Dublin (*Salmonella* Dublin) is a zoonotic pathogen host adapted to cattle. The objective of this study was to provide updated herd-level prevalence estimate of *Salmonella* Dublin in Alberta dairy herds. A 40 mL bulk tank milk sample was collected from all active dairy herds (n=468) in Alberta in June 2024 and tested for *Salmonella* Dublin antibodies using indirect ELISA. Two different percent positive (PP%) cut-off values were used (≥ 35 and ≥ 15) to classify samples into positive and negative. Apparent prevalence was calculated as proportion of positive herds out of total herds and a true prevalence was estimated using Rogan-Gladen method for both cut-off values separately. Using PP% ≥ 35 cut-off, apparent prevalence and true prevalence were estimated to be 10.3%, and 56.2%, respectively, with a positive and negative predictive value of 0.54 and 0.86 , respectively. Using PP% ≥ 15 apparent and true prevalence were 20.5% and 38.2%, respectively, with a positive and negative predictive value of 0.67 and 0.79, respectively. Medium and large herds had higher odds (odds ratio (OR) = 4.55; p-value = 0.03, and OR = 4.48; p-value 0.04, respectively) of testing positive using PP% ≥ 35 cut-off than small herds in central region. The small herds in south region were more frequent (OR = 4.96; p-value 0.02) positive than central region. These results provide latest updates on prevalence of herds positive for antibodies against *Salmonella* Dublin in Alberta and contribute to the ongoing surveillance efforts.

Nucleotide and Phenotypic Analyses of Quasispecies Detected in the Spike 1 Gene and its Encoded Protein following IBV Infection in Laying Hens

Ahmed Ali1, Ryan Rahimi1,2, Motamed Ali1, Rodrigo A Gallardo3, Faizal Adbul-Careem1

1Faculty of Veterinary Medicine, University of Calgary. 2 Department of Health Sciences, Cummings School of Medicine, University of Calgary. 3School of Veterinary Medicine, University of California Davis.

Keywords**:** IBV, Poultry, Quasispecies

Infectious bronchitis virus (IBV) is a pathogenic virus with an array of clinical manifestations in the respiratory, reproductive, and renal systems. The California 1737-04 (CA1737-04) serotype of this virus has been noted to cause permanent alternations in the female reproductive tract when infection occurs in the pullet stage, causing economic consequences on egg-laying chickens farms infected with IBV. An additional concern regarding IBV is the Coronaviridae nature of the virus, making it prone to constant mutation. A recent theory of interest is the quasispecies theory, which states a single parent genome of a virus will differentiate into a tissue-specific, heterogenous library of viral strains during infection. Studies have highlighted evidence of quasispecies generation in IBV, however, have yet to utilize next-generation sequencing (NGS) to analyze mutation within this virus. In this study, 30-week-olds hens were infected with CA1737/04 with tissue collection 9 days post-infection from respiratory, reproductive, digestive, and renal organs. RNA extraction and cDNA synthesis was completed for these samples, followed by targeting of the Spike 1 gene (S1) of IBV, due to its highly mutagenic capability, using conventional PCR. Sample purity and concentration was then confirmed using gel electrophoresis and were then submitted for next-generation sequencing. Following homology alignment of the S1 gene, mutations were assessed compared to the parental IBV strain, and confirmed the presence of mutations in organs tested. Significant mutation was observed in the cecal tonsil, large intestine, and trachea of birds. These results confirm the presence of quasispecies generation following infection with IBV.

A comparison of protocols for isolating and extracting host DNA from caribou (Rangifer tarandus) fecal pellets.

Samantha Barrette[1], Samuel Deakin[1,2], Agnes Pelletier[3], Pauline Priadka[3], Helen Schwantje[4], Caeley Thacker[4], Lalenia Neufeld[5], Sean Rogers[2], Marco Musiani[2,6], and Jocelyn Poissant[1]

[1]Faculty of Veterinary Medicine, University of Calgary; [2]Department of Biological Sciences, University of Calgary; [3]Ministry of Land, Water and Resource Stewardship, Government of British Colombia; [4]Ministry of Forests, Lands, Natural Resource Operations and Rural Development, Government of British Columbia; [5]Jasper National Park of Canada, Parks Canada; [6]Dipartimento Scienze Biologiche Geologiche Ambientali, Università Di Bologna

Keywords: Caribou, conservation genetics, methods

Non-invasive genetic sampling (NGS) is a useful technique for studying vulnerable or endangered animal populations, especially when capturing animals for collection of traditional samples is difficult or expensive. Canada's endangered caribou (*Rangifer tarandus*) populations provide an excellent model for the use of NGS. The use of fecal samples minimizes disturbance and harm to ecologically and culturally valuable herds while allowing for the collection of important data for use in conservation genomics and population management. However, fecal DNA can be difficult to work with due to high amounts of exogenous (non-host) DNA, and often contains PCR inhibitors which can make amplification of samples for downstream analyses problematic. Different methods for caribou fecal DNA extraction have never been comprehensively compared. I tested different lab protocols for isolating and extracting host DNA from caribou fecal pellets. The degree of efficacy of each protocol was compared based on amounts of total and target host DNA obtained, and success of PCR amplification. A novel method developed for this experiment involving pellet incubation in lysis buffer and the Qiagen QIAamp DNA Mini extraction kit were shown to yield the highest quantities of caribou DNA, suitable for a variety of downstream analyses. All lab protocols tested resulted in over 10ng of caribou DNA per pellet on average, and some methods resulted in over 200ng. These results could help inform and improve laboratory practices of researchers and wildlife managers non-invasively monitoring caribou across Canada and could potentially be extended for use in other species.

The Bacteriocin, Corynacin, as a Novel Antimicrobial Agent Against Methicillin-Resistant Staphylococcus aureus

Shayne McArthur[1], Jenna Buragina[1], Caden Albright[2], James La[3], Dr. Jeella Acedo[2], Dr. Jeroen De Buck[4]

1Department of Microbiology, Immunology and Infectious Diseases, Cumming School of Medicine, University of Calgary; 2Department of Chemistry, Faculty of Science, Mount Royal University; 3Department of Biology, Faculty of Science, Mount Royal University; 4Department of Animal Production, Faculty of Veterinary Medicine, University of Calgary

***Keywords*:** Bacteriocin, Methicillin-Resistant *Staphylococcus aureus*, Antimicrobial Resistance

Introduction: Antibiotic resistance is a major public health issue where bacteria evolve resistance to overcome antibiotics used against them. Methicillin-resistant *Staphylococcus aureus* (MRSA) is a highly pathogenic bacterium that causes infections worldwide and has acquired resistance to multiple antibiotics. With therapeutics diminishing, new MRSA antimicrobials are urgently needed. Bacteriocins, which are antimicrobial proteins produced by bacteria, make promising antibiotic alternatives. In this study, we investigated the antimicrobial capacity of a newly discovered bacteriocin, corynacin, against MRSA which was identified in a parallel study to be highly temperature and pH stable.

Materials & Methods: The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of corynacin was obtained by an agar-based-spot-on lawn and broth microdilution. In the agar-based-spot-on-lawn, concentrations of corynacin were spotted on agar inoculated with bacteria and were incubated. The MIC was defined as the lowest concentration where growth was visibly prevented. In the broth microdilution, serial dilutions of corynacin in broth were inoculated with bacteria and incubated. The content of the wells with no turbidity were then plated and incubated. The MBC was defined as the lowest concentration where 99% bacterial killing occurred.

Results & Conclusions: Corynacin was identified to be active against all four *S. aureus* strains and the MIC and MBC values were within range of other bacteriocins that have been published in literature. Further characterization of corynacin's mechanism of action, toxicity, *in vivo* activity, and synergistic effects with antibiotics should be investigated to further establish corynacin's potential as a novel antimicrobial for MRSA infections.

Examination of zinc and copper tolerance in Escherichia coli collected from cattle, poultry, and wastewater samples

Shelby Jennings[1], Keilan Williams[1], Alyssa Butters[1], Fernando Guardado[2], Sylvia Checkley[1], Karen Liljebjelke[1]

[1]Faculty of Veterinary Medicine, University of Calgary, [2]Ontario Veterinary College, University of Guelph

Keywords: Metal tolerance, AMR, E. coli

Metal tolerance assays were performed on 110 Escherichia coli samples to assess the relationship between metal tolerance and antimicrobial resistance (AMR). Antimicrobials are widely used in the veterinary industry and as a result, resistance poses a threat to public health, animal health, and food security. In 2019, AMR contributed to 4.95 million deaths globally. Previous studies have shown a statistical association between AMR and metal tolerance, suggesting that co-selection may exist. An excess of metals provided in supplements to livestock may select for increased antimicrobial resistance. The mechanisms relating to metal tolerance and its co-selection for AMR are not well understood. E. coli sample sources included well and wastewater, cattle, poultry, and retail meats. Metal tolerance was tested on microtiter plates, using various concentrations of Zinc (Zn) or Copper (Cu) dilutions. Plates were analyzed via spectrophotometer following a 24-hour incubation period. Preliminary findings indicate that the mean minimum inhibitory concentration (MIC) of the isolates for Zn was 300ug/ml and 600ug/ml for Cu. CU tolerance was more variable than Zn with a greater number of isolates exhibiting Cu tolerance. Isolates used in this assay have undergone whole genome sequencing and will be examined for genes associated with metal tolerance and AMR. Additional research is needed to further investigate the mechanism of co-selection between AMR and metal tolerance genes. This will contribute to animal health and welfare through its impacts on feedlot management and cow-calf production as well as to human and environmental health.

AMR prevalence in healthy dogs living in the Calgary area

Alvaro Guzman Daireaux, Diego Nobrega, Sukhman Cheema
1Faculty of Veterinary Medicine, University of Calgary

Keywords**:** antimicrobial resistance, interspecies transmission, staphylococcus prevalence

Staphylococcus aureus and *Staphylococcus pseudintermedius* are bacteria commonly found on the skin and mucous membranes of humans and animals, respectively, known for causing infections (Hanselman et al., 2009). The prevalence of *S. aureus* colonization is 28% in humans and 14% in dogs, while *S.pseudintermedius* is found in 46% of dogs (Hanselman et al., 2009; Šleiniūtė and Šiugždaitė, 2015). This can cause the potential for interspecies transmission between humans and their companion animals. This study aims to assess the prevalence of *S. aureus* and *S. pseudintermedius* in dogs and their owners, and identify resistant strains. Samples, including oral swabs from dogs and nasal swabs from their owners, were collected in Calgary, Alberta with epidemiological data through a questionnaire.

Laboratory analysis using selective *Staphylococcus* chromogenic media was conducted to recover and identify the pathogens. Methicillin-resistant *S. aureus* (MRSA)-selective chromogenic media, with an additive antibiotic, was then used to determine bacterial resistance. Growth on MRSA presumptively identifies the bacteria as methicillin-resistant *S. aureus* or *S. pseudintermedius*. There were 23 isolates obtained from oral dog swabs and 16 from human nasal swabs using *Staphylococcus* media. The prevalence of MRSA strains were 39% (9/23) in dogs and 6.3% (1/16) in humans. These findings indicate a higher prevalence of MRSA in dogs compared to humans, suggesting that dogs may serve as a reservoir for MRSA and highlights the need for continued monitoring of MRA transmission between dogs and their owners to inform public health strategies related to antimicrobial resistance.

Molecular detection of a novel species of *Rickettsia* endosymbiont in *Aedes aegypti*

Talia Turner, John Soghigian, Gen Morinaga

1Faculty of Veterinary Medicine, University of Calgary

Keywords: Rickettsia, Vector Control, Endosymbiosis

Pathogenic *Rickettsia* have been the subject of scientific inquiry for the better part of the 21st Century for their implication in human health as the causal agent of many known rickettsioses. However, not all *Rickettsia* are implicated in disease, and are found widespread in arthropods as endosymbiotic organisms. As endosymbionts, *Rickettsia* can alter host biology, influencing sex determination in offspring by both induction of parthenogenesis and male killing mechanisms. Using molecular methods, we extracted the full genome of an unknown species of *Rickettsia* from *Aedes aegypti* sampled from Burkina Faso. The analysis of the sample utilized both fastANI software and the Prokaryotic Genome Annotation Pipeline (PGAP) to determine the average nucleotide identity (ANI) in comparison to 165 *Rickettsia* genomes available on NCBI. The results indicated that in conjunction with other known ANI values used for the order of Rickettsiales (ANI=96), the genome extracted is that of a novel species of *Rickettsia*. The phylogenetic analysis inferred that the query genome was monophyletic with other identified species of *Rickettsia* endosymbionts of arthropods, such as *Culicoides* and *Odeothorax*. We propose a new species designation with submission of this genome to online databases for further analysis. More research on the consequences of *Rickettsia* endosymbionts on mosquito biology is required to fully understand their evolutionary relationship, as well as to comprehend the full scope of interactions present within arthropod microbial communities. While non-pathogenic, these endosymbionts may prove efficient in reducing the prevalence of harmful bacterial species and may be of veterinary and medical importance.

Repeated racing does not increase high sensitivity cardiac Troponin-T levels in chuckwagon horses

Tausha Prinsee [1], Annie Kelly[1], Elsa Vezinhet[2], Clara Hugonet[2], Renaud Leguillette[1]

[1]Faculty of Veterinary Medicine, University of Calgary; [2] National Veterinary School of Toulouse

Keywords: Troponin, Cardiac, Equine

The sudden death of chuckwagon horses during the Calgary Stampede (CS) poses considerable risks to both human and animal safety. Approximately 55% of sudden deaths in racehorses are attributed to myocardial damage, termed sudden cardiac death (SCD). Cardiac troponin-T is a blood marker for myocardial damage. We have previously validated a high-sensitivity cardiac Troponin-T (hscTnT) assay for horses and found that approximately 4.7% of horses exhibit abnormally high hscTnT levels after their first race, with an additional 13.6% showing moderately elevated hscTnT levels. However, the impact of subsequent cardiac stress from racing on hscTnT levels remains unclear. **Methods:** A total of n=420 chuckwagon racehorses had blood sampled via jugular venipuncture 12h after their first race at the 2024 CS. Horses with moderately elevated hscTnT levels were resampled 12h after subsequent races. **Results:** No horses experienced SCD during the 2024 CS. After race 1, 87.6% of horses had normal hscTnT levels, while 8.6% had had moderately elevated levels and 3.8% had abnormal levels. One additional race during the CS did not alter hscTnT levels (P=0.29), however mean hscTnT decreased by race 3 (P=0.01) and tended to stay lower than race 1 after race 4 (P=0.06) and 5 (P=0.07). However, there was individual variation in response to repeated races. Rest days between races increased hscTnT levels (P=0.003). **Conclusions:** Cardiac stress from racing does not appear to be cumulative and may not increase the risk of SCD. The hscTnT assay continues to be a useful screening tool for horses as risk of SCD.

APOL7C and the great antigen escape of DNGR-ous materials

Yvonne Chen[1], Gerone Gonzales[2], Johnathan Canton[3,4]

[1] Biological Sciences, Faculty of Science, University of Calgary.[2] Biochemistry and Molecular Biology, Cumming School of Medicine, University of Calgary.[3] Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Science, University of Calgary. [4] Calvin, Joan and Phobe Snyder institute for Chronic Diseases, University of Calgary

Keywords: Immunology, cross-presentation, cancer

Antigen cross-presentation is a process that is responsible for the generation of cytotoxic T cells that go on to defend the body against cancer, viruses, and other pathogens. Cross-presentation requires phagocytic dendritic cells to ingest antigens from cells that have “danger” signals and present these antigens to the T cells. Without cross-presentation, the body would have very limited means of detecting and combating infection and tumours. Recently, the Canton lab has gathered evidence that a putative pore-forming protein known as APOL7C is recruited to phagosomes of dendritic cells to initialize cross-presentation by rupturing the phagosomal membrane and allowing the antigens to escape to the cytosol, where they can be presented to T cells via the major histocompatibility complex (MHC) class I antigen processing pathway. Still, the exact mechanism of how APOL7C is selectively recruited to phagosomes remains largely unknown. Interestingly, a receptor uniquely expressed in dendritic cells known as DNGR-1 has been implicated in triggering phagosomal rupture in a NADPH-oxidase dependent manner. Using immunofluorescent assays and confocal microscopy to visualize APOL7C, my project investigates whether APOL7C pore formation on dendritic cells and DNGR-1 signaling are mechanistically linked. Our results show that DNGR-1 signalling does lead to APOL7C recruitment to phagosomes when the DNGR-1 receptor is engaged with an anti-DNGR-1 antibody (7H11) compared to our control of horse radish peroxide (HRP). These findings give us insight into the molecular mechanisms of cross-presentation and open new avenues for vaccine and cancer therapy development.

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