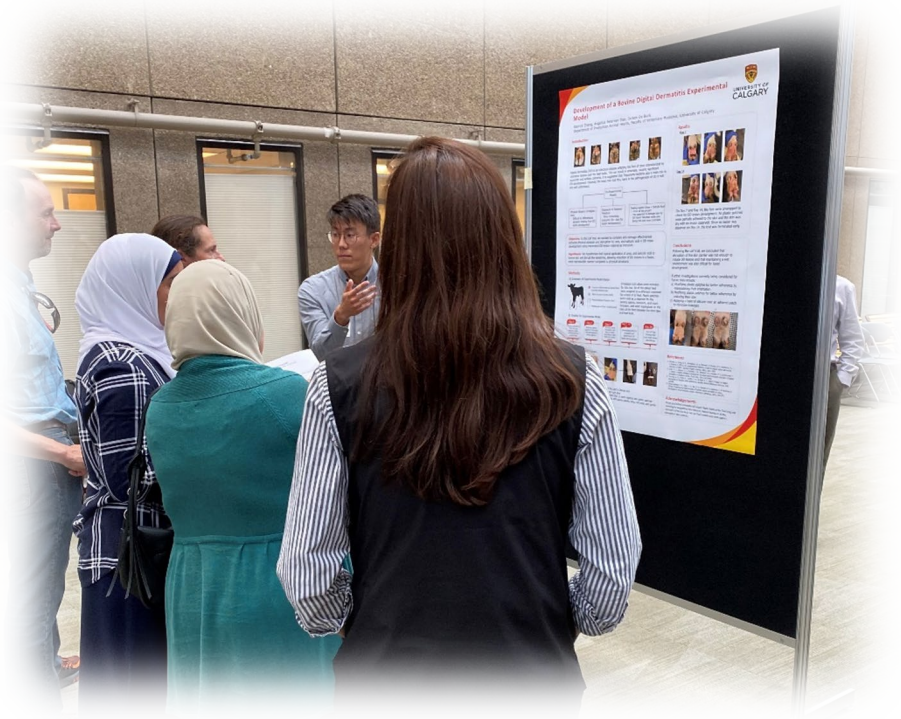
UNIVERSITY OF CALGARY
FACULTY OF VETERINARY MEDICINE



UCVM SURE Research Day 2025

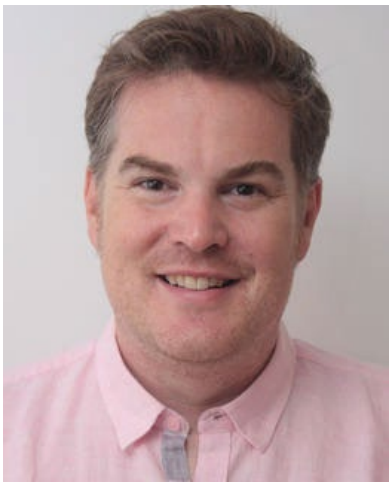
August 21st, 2025

8:25 am – 4:00 pm

Health Sciences Centre Theatre 3 and HRIC Atrium

PROGRAM and ABSTRACT BOOKLET

Message from Dr. James Wasmuth, Associate Dean, Emerging Scholars



Welcome to the 2025 UCVM SURE Research Day! This year 43 students registered in the SURE (Summer Undergraduate Research Experience) program. Funding to support students and the program has come from PURE, NSERC, Alberta Innovates, The McCaig Institute, O'Brien studentship awards, RDAR, the UCVM Office for Emerging Scholars, and supervisors' grants. Nine of our SURE students are in the DVM program; others joined us from Biomedical Engineering, Health Sciences and Medicine, Commerce, Kinesiology, and Arts. We also welcomed five students from other universities: Dalhousie, McMaster, USaskatchewan, UAlberta and UBC).

Education, training and research are central to the mission of the Faculty of Veterinary Medicine. Today's program features 16 oral presentations and 16 poster presentations spanning a diverse range of veterinary medical research. We are also delighted to have Dr. Ed Pajor deliver the keynote lecture. Dr. Pajor is recognized internationally for his research in food animal behavior and welfare, and for his leadership in animal welfare standards and legislation. We invite you to engage fully with all presentations: ask questions, offer feedback.

Above all, today celebrates what our students have achieved this summer. You planned and executed experiments, learned new methods, built datasets and tools, analysed results, and, as we will soon see, translated findings into engaging presentations. Many of you contributed to ongoing lab projects, improved protocols, and strengthened collaborations. Your work advances the research mission of the Faculty of Veterinary Medicine, while building your own skills in inquiry, communication, and teamwork. I hope that this experience fuels your curiosity and confidence to carry an interest in research into the next stages of your education and careers. I hope many of you consider coming back to VetMed. Thank you to our postdoctoral fellows and graduate students for contributing to the success of the SURE program. This includes for today: abstract adjudication, session chairing, and judging presentations.

Finally, thank you to Erin Fraser (Office of Emerging Scholars) for exceptional coordination and communication support for today's event.

Enjoy SURE 2025!

Sincerely,

James Wasmuth

Associate Dean, Emerging Scholars, UCVM

8:25	**Welcome and Introductions – Theatre 3:** James Wasmuth
Oral Presentation Session #1 – Theatre 3 Chair: James Wasmuth	
8:30	**Labib Chowdhury** (Anderson Lab) *Identifying fossil jawless fish from the Devonian-age Yahatinda Formation of Alberta*
	Reillee Duperron (Remnant Lab) *Exploring Cattle Producers Perspectives on Accessibility of Veterinary Services in Alberta: Using Thematic Analysis*
	Bryna Turk (Pruvot Lab) *Surveillance of Intestinal Parasites and Rotavirus Infection in Invasive Wild Boar Populations in Alberta, Canada*
	Ryan Karch (Whelan) *Electrical Stimulation of the A13 Nucleus as a Novel Therapeutic Approach in a 6-OHDA Rat Model of Parkinsons disease*
9:30	**Mini-Break**
Oral Presentation Session #2 – Theatre 3 Chair: Kaylee Rich	
9:35	**Curtis Huyghe** (Soghigian Lab) *Bloodsuckers & Bacteria: Testing Insecticide Resistance in the Invasive Culex pipiens Mosquito*
	Courtney Smith (Whiteside Lab) *Assessing bone strength and mineral composition of barren-ground caribou (*Rangifer tarandus groenlandicus*)*
	Sraddha Uppili (Cobo Lab) *A Multi-Omics Approach to Understanding the Host-Immune Response in Swine Dysentery*
	Jensen MacLean (Deardon Lab) *Behavioural Change in Canadian Disease Outbreaks*
10:35	**Coffee Break - Azrieli Atrium (nee HRIC)**
Oral Presentation Session #3 – Theatre 3 Chair: Chimone Dalton	
11:00	**Michael (Song Heo) Li** (Knight Lab) *Investigating the role of black flies (Simulium sp.) In the transmission of* Equus caballus *papillomavirus type 2*
	Marco Antonio Alarcon Aguilera (Nobrega Lab) *Restricted use of antimicrobials in the Canadian poultry industry: Impacts on antimicrobial resistance of* Enterococcus *spp. isolated from poultry farms*
	Talia Zhang (Chu Lab) *Generation of Canine HES1 Reporter in Induced Pluripotent Stem Cell Reporter Line to Study Developmental Timing*
	Sarah Stroh (Barkema Lab) *Prevalence of* Neospora caninum *in Alberta Dairy Herds*
12:00	**Lunch and Poster Session - HRIC Atrium**

Oral Presentation Session #4 – Theatre 3 Chair: Rachael Coon	
14:00	**Paige Robertson** (Niu Lab) *Evaluating Phage Cocktail Efficacy and Determining the Genetic Basis of Resistance in Multidrug-Resistant* Escherichia coli *ST131*
	Jordan Chen (Biernaskie Lab) *Optimizing Skin Tissue Clearance Across Species for 3D Reconstructions of Wound Healing*
	Mya Rose (Rothenburger Lab) *Parasites of wild white-tailed jackrabbits (*Lepus townsendii*) in Calgary, Alberta*
	Luke Xiu (Careem Lab) *Involvement of the Indoleamine 2,3 dioxygenase - Aryl Hydrocarbon Receptor Axis in Influenza A Virus Replication in Chicken Macrophages*
15:00	**Keynote Speaker – Theatre 3**
	Dr. Ed Pajor
15:45	**Prizes and Closing Remarks:** Chimone Dalton

ABSTRACTS

Listed alphabetically by first name of presenting author

Creating sustainable community-led preventive veterinary care programs: maximizing benefits while minimizing costs in underserved areas

Ahanaf Lazim[1], Tessa Baker[2]

[1]Haskayne School of Business, University of Calgary; [2]Faculty of Veterinary Medicine, University of Calgary

Keywords: Cost-Benefit Analysis, contraceptive implant, access to veterinary care

Access to veterinary care in many Indigenous communities across Canada is limited for many reasons (e.g. geographic isolation, financial barriers, mistrust, and cultural differences with Western veterinary medicine). Dog overpopulation, however, can be a recurring problem in some Indigenous communities is often managed through surgical sterilization (spaying/neutering), which is costly and resource-intensive, especially in remote areas. This study evaluates the feasibility of deslorelin acetate, a non-surgical contraceptive implant, as an alternative solution or supplement to traditional surgery to increase access to sterilization. A cost-benefit analysis was conducted for two types of communities: remote fly-in communities and a drivable community. Within each context, two scenarios, 4.7mg implants lasting 6 months and 9.4mg implants lasting 12 months, were compared to surgical sterilization. The findings of the analysis show benefits through reduced costs and the ability to prevent litters. In remote communities, implants reduced total costs of clinics by up to 54% compared to surgery. Cost per dog treated with the implant was half that of surgery for the 6-month scenario, and cost per litter prevented significantly decreased with the 12-month implant scenario compared to 6-month scenario. In drivable communities, implant costs were also lower, due to reduced personnel time and logistics. Overall, the main cost savings came from reduced staffing needs and shorter trip durations. Although the implant method is only temporary and prevented fewer litters in the 6-month window, it provided a useful and promising option to increase sterilization in underserved communities due to financial and time savings.

Isolation and characterization of lytic phages against enterotoxigenic *Escherichia Coli* K88, DSU-22, and DSU-23

Anna Zhu, Jenny Hyun, Mawra Gohar, Sidra Moqaddes, Dongyan Niu

Faculty of Veterinary Medicine, University of Calgary

Keywords: Bacteiophages, Phage therapy, Enterotoxigenic *Escherichia Coli*

Introduction Enterotoxigenic Escherichia coli (ETEC), which causes post-wean diarrhea in piglets, is now resistant to previously used antibiotics, creating a need for an alternative treatment. This project aims to isolate lytic bacteriophages against the K88, DSU-22, and DSU-23 ETEC strains and investigate whether phages with differing hosts can fulfill this role. **Materials and Methods** 13 pig, 39 dog feces, and 9 sewage influent samples were screened for phages by adding aliquots to early-log cultures and assessing growth inhibition. 10 phages with ETEC F4-20462 and F4-22774, and ST131 77, 611 and 630 hosts were tested for activity through microplate virulence assays, quantifying the multiplicity of infection (MOI). pH tolerance was characterized by comparing titers after incubation in varying pH environments. **Results** None of the samples contained phages capable of lysing the target strains. Of the phages with different hosts, K88 was highly susceptible to 5, DSU-23 was moderately to highly susceptible to 5, and DSU-22 was resistant to all. One-way ANOVA then Tukey's HSD confirmed after 1 hour incubation, phages 9P_Jan and 9P_Sep titer decreased below pH=4.5 and 7.0 respectively, and both titers decreased below pH=5.5 at 4 hours; characterization of remaining phages is ongoing. **Discussion and Significance** These findings suggest ETEC phages may be host-specific and less effective at low pH. Whole genome sequencing will be performed to identify genetic elements in the phages and hosts influencing interactions. Obtained and upcoming results of this project will contribute to further research into phage-based ETEC treatment and broader understandings of phage therapy.

Targeting ERK Pathway Dysregulation in Fragile X Syndrome Mouse Models Using MEK Inhibition

Assad Popal[1], Demi M [1 2 3 4 5], Ning Cheng[3 4 5]

[1]Department of Biological Sciences, Faculty of Science, University of Calgary; [2]Cumming School of Medicine, University of Calgary; [3] Faculty of Veterinary Medicine, University of Calgary; [4]Hotchkiss Brain Institute, Cumming School of Medicine, University of Calgary; [5]Alberta Children's Hospital Research Institute, Cumming School of Medicine, University of Calgary

Keywords: Fragile X Syndrome, ERK signaling, MEK inhibition

Introduction: Fragile X syndrome (FXS) is the most common monogenic cause of intellectual disability and autism spectrum disorder. It is caused by transcriptional silencing of the *Fmr1* gene, resulting in the loss of its protein, FMRP. FMRP modulates synaptic protein synthesis, and its loss leads to dysregulated signaling, including overactivation of the ERK (extracellular signal-regulated kinase) pathway. ERK is activated by upstream kinases MEK1/2 and regulates synaptic plasticity and cognition; its dysregulation contributes to the cognitive and behavioral symptoms seen in FXS. This study focuses on the prefrontal cortex (PFC), a brain region critical for cognitive processes like decision making, attention, and behavioral regulation, which shows synaptic abnormalities in FXS. We hypothesize that pharmacological inhibition of MEK1/2 will reduce ERK phosphorylation in *Fmr1* knockout (KO) mice.
Methods: Male and female *Fmr1* KO mice (n = 14 per group) were treated with PD0325901 (Mirdametinib), a selective MEK1/2 inhibitor. PFC tissue was collected at postnatal days 47 to 51 and analyzed by Western blot to measure phosphorylated ERK1/2 (pERK) and total ERK1/2. Actin served as a loading control, and protein level intensities were quantified for comparison. Group differences will be analyzed using unpaired two-tailed t-tests and two-way ANOVA, followed by a Tukey post-hoc test.
Results: We anticipate that PD0325901 will reduce pERK levels in the PFC of *Fmr1* KO mice, indicating a potential role for MEK inhibition in restoring ERK signaling to wild-type expression.
Discussion and Significance: This study investigates MEK inhibition as a targeted intervention for ERK signaling abnormalities in FXS. If effective, these findings may aid in the development of targeted biochemical therapies for FXS and related neurodevelopmental disorders.

The Role of the Thalamus in Innate Fear Responses to Predator Odor in Mice.

Brenda Wan, Demi Ma; Evan Tingley; Ning Cheng

Faculty of Veterinary Medicine, University of Calgary; Cumming School of Medicine, University of Calgary; Hotchkiss Brain Institute, Cumming School of Medicine, University of Calgary; Alberta Children's Hospital Research Institute, Cumming School of Medicine, University of Calgary

Keywords: Thalamus, Innate Fear

Introduction: Innate fear is an evolutionarily conserved response to threatening stimuli critical for predator avoidance and survival. Unlike conditioned fear, it arises independently of prior experience. In rodents, innate fear responses can be triggered by olfactory cues, such as predatory odours, leading to characteristic behaviors such as avoidance and freezing. While the neural basis of conditioned fear is well studied, the circuitry underlying innate fear remains less defined. The thalamus, a key relay for sensory information, has been implicated in conditioned fear, but its involvement in innate responses is unclear. This study aims to investigate the thalamus's role in innate fear processing. We hypothesize that, due to its role in sensory integration, the thalamus will show increased neuronal activation following exposure to innate fear stimuli.
Methods: Four postnatal day 40 female wildtype mice were used, with two exposed to fox urine and two serving as controls. Brain sections were stained with DAPI and c-Fos to visualize nuclei and recent neuronal activity, respectively. c-Fos expression in thalamic regions was quantified and compared using unpaired t-tests.
Results: Preliminary analysis of the mediodorsal thalamic nucleus revealed no statistically significant difference in c-Fos expression between groups. Initial findings suggest that the mediodorsal thalamus may not be significantly activated by innate fear stimuli. Ongoing analysis will clarify whether neuronal activity in thalamic regions or the thalamus overall contribute to innate fear responses.
Discussion/Conclusion: These findings could contribute to a deeper understanding of innate fear circuitry in mice models and the functional specialization of the thalamus.

Surveillance of Intestinal Parasites and Rotavirus Infection in Invasive Wild Boar Populations in Alberta, Canada

Bryna Turk, Oshin Ley Garcia, Angela Schneider, Maria Bravo Araya, Sandra Damianos, Chloe Ingham, Mathieu Pruvot

Faculty of Veterinary Medicine, University of Calgary

Keywords: Wild Boar, Rotavirus, Intestinal Parasites

In the Canadian prairies, invasive wild boar (*Sus scrofa*) have expanded their range, threatening agricultural and natural ecosystems. As known hosts of various pathogens, they pose risks to livestock, wildlife, and human health. In Alberta, little is known about their health status and role in disease transmission. This study aimed to characterize the frequency of gastrointestinal parasites and rotavirus strains (RVA, RVB, RVC) in wild boars in Alberta. From 2018 to 2024, 191 fecal samples were collected from invasive wild boar across Alberta. Parasite eggs were identified using Wisconsin double centrifugation fecal flotation and light microscopy (Olympus BX53, 40X). RNA was extracted from 95 samples, and rotavirus detection was performed via RT-qPCR using established primers. Frequencies, 95% confidence intervals, and chi-square tests were calculated using R environment v4.4.0. Maps assessing the proximity of wild boar to free-ranging swine operations will be generated using QGIS v3.44.1. Gastrointestinal parasitic infection to *Ascaris suum* (0.06%; 11/191), *Trichuris suis* (0.05%; 10/191), *Eimeria spp.* (0.4%; 73/191), and *Metastrongylus spp*. (0.3%; 49/191) were detected. Rotavirus was detected in 26.3% (25/95) of samples: 79.3% RVA (23/29), 0% RVB (0/29), and 15.4% RVC (4/29). Infection was significantly associated with age for both parasites (p=0.05) and rotavirus (p=0.05). Spatial analysis is expected to reveal clusters of wild boar near free-ranging pig farms, indicating increased risk of pathogen spillover. These findings suggest that wild boar in Alberta may serve as reservoirs of intestinal parasites and rotaviruses relevant to domestic swine, underscoring the importance of surveillance and targeted management strategies.

Unraveling Evolutionary Relationships within the Genus Aedes Through Molecular Analysis

Carmen Chan, Huiqing Yeo, John Soghigian

Faculty of Veterinary Medicine, University of Calgary

Keywords: *Aedes*, Phylogenetics, Molecular Evolution

Mosquitoes are among the deadliest animals to humans due to their global distribution and their ability to serve as competent vectors for medically significant diseases. *Aedes* mosquitoes, for example, transmit pathogens responsible for chikungunya and yellow fever, causing millions of infections annually. Previous research has shown that mosquitoes that are evolutionarily close to one another are more likely to be capable of transmitting the same pathogens. However, despite extensive research on medically important mosquito species, the majority of evolutionary relationships between clades of mosquitoes remain unknown. This gap in knowledge limits further analyses aimed at understanding patterns behind disease transmission. *Aedes*, a genus estimated to be over 60 million years old, comprising more than 900 species, includes many species of medical importance, yet its evolutionary relationships are not well known. To reconstruct evolutionary relationships among *Aedes* mosquitoes, we used data from three sources: existing analyzed sequence data from the Soghigian lab, publicly available sequence data, and newly generated sequence data. Orthologous gene sequences were extracted from all three sources using established phylogenomic pipelines. Our phylogenetic tree will include 334 samples, representing 193 species across 9 aedine genera. Based on previous analyses, we expect to recover the genus *Aedes* in two distinct clades within the tribe Aedini. Our phylogenetic tree provides insight into reconciling evolutionary relationships within the genus *Aedes* and identifying shared vector capabilities among clades.

Assessing bone strength and mineral composition of barren-ground caribou (*Rangifer tarandus groenlandicus*)

Courtney G. M. Smith, Susan J. Kutz, Douglas P. Whiteside

Faculty of Veterinary Medicine, University of Calgary

Keywords: caribou, bone, mineral

Caribou (*Rangifer tarandus*) are a keystone species in northern Canadian ecosystems, serving as both a key food source for predators and people, and as important indicators of climate change. Barren-ground caribou populations have declined significantly over the past several decades, leading to their designation as “threatened” (COSEWIC report, 2016). Habitat loss, resource extraction, and climate change have all been linked to these declines. Indigenous peoples, biologists and veterinarians have anecdotally observed some animals may experience bone fractures more frequently than other individuals, especially female barren-ground caribou with calves, raising concerns about bone health. This research investigated variation in bone strength and mineral composition among six barren-ground caribou herds across northern Canada and Greenland. Using archived metatarsal bones previously collected by First Nations hunters we assessed bone density and composition using micro-computed tomography (micro-CT) and bone mineral analysis for Ca, Mg, K, Na, P, S, Fe, Cu, Mo, Mn and Zn. Mechanical properties such as bone stiffness were evaluated using CT data, which revealed statistically significant differences in cortical thickness and bone density across herds. Among these findings, the Bathurst herd showed significantly greater cortical thickness compared to the Ahiak, Bluenose West (BNW) and Greenland populations, whereas BNW exhibited significantly higher bone density compared to the Ahiak, Saskatchewan, and Greenland herds. By comparing samples from multiple regions, this study aimed to identify spatial patterns in bone health that may reflect geographical differences in habitat quality or nutrient availability.

Bloodsuckers & Bacteria: Testing Insecticide Resistance in the Invasive *Culex pipiens* Mosquito

Curtis Huyghe, Huiqing Yeo, Michaela Seal, Alex Coker, and John Soghigian

Faculty of Veterinary Medicine, University of Calgary

Keywords: Mosquitoes, Genome, Resistance

The invasive mosquito *Culex pipiens*, a prominent vector for diseases like West Nile virus (WNV), has recently been found in Alberta, where it has rapidly expanded into virtually all major municipalities in southern Alberta over the last 5 years. One of the many reasons this mosquito is problematic is due to knockdown-resistance (kdr) in these mosquitoes, where insecticides like pyrethroids, usually sprayed to target adults, are ineffective towards many populations of this species. It is currently unknown if Alberta populations are resistant to common insecticides or not. Over the Summer of 2025, resistance mutations in the *Cx*. *pipiens* genome have been identified in the voltage-gated sodium channel (vgsc) and ace-1 genes. Genomic data for this species was retrieved from public databases, and along with sequence data for Alberta *Culex pipiens* from the lab, was passed through a bioinformatics pipeline to detect potential resistance alleles previously described in the literature. To summarize, the pipeline trimmed reads, aligned them to a reference genome, and then extracted relevant genes associated with resistance, namely vgsc and ace-1. The results are expected to indicate genetic variants G119S in the ace-1 gene and among others, L1014F in the vgsc gene if kdr resistance is indeed present. After conclusive results, the next step of this research is conducting assays with insecticides to validate any presumed resistance alleles in Alberta *Culex pipiens*.

Identification of neutrophil hallmarks contributing to swine dysentery colitis

Delfina Cobo, Niloofar Mirzadzare, Rita Hannawayya, Senya Wickramasinghe, Sraddha Uppili, Yanshu Ye, Eduardo R. Cobo

Faculty of Veterinary Medicine, University of Calgary

Keywords: Neutrophil, Colitis, Swine

Background: Neutrophil's antimicrobial functions are a critical defense against microbial colonization, but uncontrolled inflammation leads to tissue damage. The role of neutrophils in swine dysentery, a diarrheic muco-hemorrhagic colitis produced by *Brachyspira hyodysenteriae (B. hyo)* in young pigs, was previously unidentified although it is hypothesized that aberrant neutrophil's secretion of antimicrobial substances,in turn contribute to damage in the colon. To determine whether the infiltration of a large number of neutrophils and the secretion of toxic substances predispose early colitis, I studied experimentally the role of neutrophils in swine dysentery.
Methodology: Weaned pigs were orally challenged with *B hyo* (n=18) or inert solution (n=7), colons collected at the peak of colitis (8-12 days post challenge) and infiltrating neutrophils studied by proteomics and imaging of myeloperoxidase (MPO).
Results: Our results show numerous MPO positive neutrophils (2-fold change) infiltrated in the lamina propria of colons infected with *B. hyo*, with upregulated specific neutrophil biomarkers, including a granule protein encoder (*azurocidin* , AZU1), a neutrophil surface marker (CD177), inhibitor of neutrophil serine proteases (SERPINB1), and a neutrophil chemokine (CXCL14).
Significance: Thus, neutrophils are relevant in the pathogenesis of *B. hyo -colitis* and likely contribute to the disease and symptoms, diarrhea with blood, in pigs with swine dysentery. Compounds that block neutrophil activity may be a target for therapies that rely less on antibiotics.

Improving the Study of Clinically Relevant Anatomical Limb Transections through Novel Study Materials

Emma Glover, Robert McCorkell, DVM, Phd

Faculty of Veterinary Medicine, University of Calgary

Keywords: Anatomy, Plastinated specimen, cross-sectional imaging

In veterinary medicine, ultrasound is an efficient and non-invasive diagnostic method that utilizes cross-sectional imaging of soft tissues. However, the anatomical knowledge required to properly interpret these images is complex and often challenging to learn, as the shape, size and location of limb musculature vary significantly from origin to insertion. It was hypothesized that the development of a specialized study tool for limb transections will aid future veterinary students in their pursuit of cross-sectional anatomical knowledge by enhancing retention and improving learning efficiency. To develop this specimen, multiple canine forelimbs were removed from cadavers, exposing the medial shoulder musculature. The limbs were then plastinated and transected in a plane directly distal to the shoulder joint. This location was chosen to represent the cross-sectional view one might see when diagnosing bicipital tendinopathy, a common affliction of the biceps brachii origin tendon in medium to large breed dogs. Magnets were then embedded into the bony area of the transection, allowing students to reattach the sections together and compare the cross-sectional view with externally palpable bony landmarks. Ultrasound imaging and a fresh tissue transection within the same plane were taken to serve as a comparable reference to the plastinated specimen. While plastinated specimens have been successfully used in the study of veterinary anatomy, their full benefits are difficult to effectively quantify during the summer break. Therefore, the effectiveness of this specimen will be tested through its use in upcoming veterinary anatomy courses.

Foot and mouth disease in wild animals: a scoping review of the risk in non-endemic regions

Erin N. Casper[1,2], Jamie L. Rothenburger[1,2], Emma Gardner[3]

[1]Faculty of Veterinary Medicine, University of Calgary; [2]Canadian Wildlife Health Cooperative – Alberta Region, [3]Canadian Animal Health Surveillance System

Keywords: Foot and mouth disease, wildlife, scoping review

Foot and mouth disease (FMD) is one of the most important livestock diseases globally, affecting all cloven-hooved animals. There is little known regarding the role wildlife populations play in the epidemiology of FMD, which has resulted in few prevention and control measures that target wild animals. To improve contingency plans for FMD in non-endemic regions, we conducted a scoping review following the PRISMA guidelines to: i) summarize the evidence across international jurisdictions of the susceptibility of wildlife to FMD and their role in the disease epidemiology; and ii) identify the strategies proposed in response to an outbreak of FMD in a wildlife population. Preliminary results indicate that out of the 203 publications that fit the inclusion criteria, 74 publications found evidence of susceptibility in various wildlife species, primarily through diagnostic testing (n=90) or experimental infection (n=14). Sampling strategies were largely risk-based (n=58) or convenience-based (n=35), and surveillance activities were predominately active (n=106) rather than passive (n=4). The most common control measures discussed were to erect large-scale fencing (n=49), manage wildlife populations through culling or other means (n=44), and to vaccinate livestock at the wildlife-livestock interface to prevent transmission to wildlife (n=41). The narrative synthesis for these variables is currently underway. The insights gathered here will improve contingency plans for FMD in non-endemic regions, including Canada, by addressing the current gaps in FMD preparedness regarding wild populations.

Behavioural Change in Canadian Disease Outbreaks

Jensen MacLean[1], Rob Deardon[1, 2]

[1]Faculty of Veterinary Medicine, University of Calgary; [2]Department of Mathematics and Statistics, University of Calgary

Keywords: Infectious diseases, epidemics, SIR model

During infectious disease outbreaks, populations react to outbreak severity, thereby shifting the transmission dynamics of the disease. Voluntary and government-mandated measures can slow the spread of disease, and the public's disease-avoiding behaviour tends to relax when case counts are low and increase when high. This work explores how behavioural change may evolve over time in response to outbreaks of a particular disease. Additionally, it investigates how behavioural change varies between diseases and outbreak intensities. Using incidence and population data from the Canadian Disease Incidence Dataset (CANDID), we analyze measles and influenza outbreaks in Ontario, Canada. To account for dynamic, time-varying transmission, we use a population-level Susceptible-Infectious-Removed behavioural change epidemic model with alarm functions, implemented in R Nimble within a data-augmented Bayesian framework to allow estimation on partially observed epidemic data. By comparing parameter estimates and alarm responses across years, we find evidence of a decline in outbreak-related behavioural change to influenza outbreaks over time, and a corresponding increase towards measles. Across both diseases, the model suggests greater alarm towards influenza outbreaks than to measles. These findings enhance our understanding of how public response to disease has shifted historically within varying societal contexts and differs between pathogens, while offering valuable insight for both behavioural scientists and epidemiologists. In doing so, this work also supports the development of more accurate early epidemic forecasting by identifying plausible alarm functions and informing prior distributions in Bayesian modelling frameworks.

Activities by veterinary medical colleges aimed at addressing the rural veterinary workforce shortage: A scoping review protocol

Jessica French[1], Angelica Galezowski[1], Heather Ganshorn[2], Robert McCorkell[1], Jenny Weston[3], Paul Wood[4], John Remnant[1]

[1]Faculty of Veterinary Medicine, University of Calgary; [2]Health Sciences Library, University of Calgary; [3]School of Veterinary Science, Massey University; [4]School of Veterinary Medicine, Scotland's Rural College (SRUC)

Keywords: Veterinary, rural, recruitment

A shortage of rural veterinarians – especially those with a food-animal focus – has been a source of concern within industry for decades. Numerous explanations for this issue have been reported including: changing population demographics, restructuring of agricultural business models, feminization of the veterinary workforce, and changes to veterinary programing. While larger scale, societal shifts are likely important driving forces behind rural veterinary shortages, actions taken by veterinary teaching institutions are instrumental in encouraging future recruitment and retention into large animal, mixed, or production animal practice. Thus, the objective of this scoping review is to present interventions applied by veterinary teaching institutions to increase recruitment and retention of veterinary students into rural practice. A search was completed in CAB abstracts, MEDLINE, and Scopus in July of 2025 for peer-reviewed articles pertaining to veterinary medicine rural recruitment and retention in the context of veterinary students. Studies were limited to the English language, and publication dates later than 1970. Data extraction was performed in Microsoft Excel and focused on key findings which were then categorized by theme. Data was extracted from 41 academic papers, which were predominantly cross-sectional survey studies. Four major themes identified, including: outreach, admissions, academic programing, and mentorship. Few, if any, scoping reviews are available to collect and summarize data regarding specific interventions that may be applied by veterinary teaching institutions. However, application of these findings may be useful guiding principles for veterinary institutions attempting to address the rural veterinary shortage.

Optimizing Skin Tissue Clearance Across Species for 3D Reconstructions of Wound Healing

Jordan Sandhu Chen, Edna Ayerim Mandujano-Tinoco, Jeff Biernaskie

Faculty of Veterinary Medicine, University of Calgary; Alberta Children's Hospital Research Institute

Keywords: Tissue Clearance, Wound Healing, Regeneration

Introduction: After deep skin injury, mammals typically form scar that is stiff, painful, and prone to re-injury. An exception is reindeer: while back skin scars normally, antler skin (velvet) heals without scarring. In mouse skin, centers of large wounds partially regenerate while peripheries scar. Mechanisms behind these regenerative responses are unknown. Restoring blood supply and innervation is critical in healing. To determine whether different spatial/temporal patterns of innervation/revascularization arise during skin regeneration, we optimized a whole tissue clearing method to create 3D reconstructions of regenerative/scarring models.
Materials and Methods: Skin-iDISCO+[1], a human skin clearance protocol, was tested and optimized. The protocol involves: 1) **decolorization** through depigmentation, delipidation, and dehydration; 2) **tissue clearance** through refractive index matching; and 3) **3D reconstruction** using immunofluorescence staining followed by light sheet microscopy. Samples from 20 mice under 3 pro-regenerative treatments were collected 3 months post-injury.
Results: Mouse and reindeer skin were successfully cleared. 3D reconstructions will be presented to illustrate differences in vascular density, complexity, and pattern across different skin types. Clearing of mouse wound samples is underway for future analysis of revascularization/reinnervation.
Discussion: The durations of decolorization, dehydration, and refractive index matching are important for tissue and 3D reconstruction quality. Notably, this protocol may cause structural alterations including mouse skin shrinkage and reindeer back skin softening, highlighting the need for tissue-specific optimization.
Significance: This work enables high-resolution 3D analysis of wound vascularization/innervation, laying groundwork to assess therapeutics and compare scarring/regenerative models. Understanding regenerative competence could lead to treatments improving wound healing outcomes.

Alterations in host range and virulence of genetically modified mutants of Shiga toxin-producing *Escherichia coli* -infecting *Tequintavirus*

Katie Bergen[1,2], Jenny Hyun[1], Yiran Ding[1], Dongyan Niu[1]

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

Keywords: Phage therapy, STEC, phage resistance

Introduction: Shiga toxin-producing *Escherichia coli* (STEC) is a major foodborne pathogen often introduced via fecal contamination of bovine-derived food products. Phage therapy has become an attractive STEC control measure due to its high specificity and pathogen targeted approach. Long tail fiber (Ltf) proteins are involved in host recognition and adsorption. Previously, using CRISPR/Cas 9 system, we successfully modified LtfB of AKFV33, a O157-infecting *Tequintavirus* (T5-like phage) to create mutants X-C17 (swapped LtfB from AXO103, an O103-infecting *Tequintavirus*), TIP-BX (swapped LtfB from AXO103, mutation C to T at 5'-17) and X-Bal (completely deleted LtfB). This study aims to screen host range and virulence changes of phage AKFV33 mutants.
Materials and Methods: Host range screening was conducted against STEC serotypes O157 (5), O103 (4) and O26 (3) using a 5-hour microplate virulence assay. Multiplicity of infection was determined by enumerating the highest dilution of phage that caused complete lysis. A growth curve was conducted to compare burst size between AKFV33/AXO103 and its mutants.
Results: Mutants X-C17 and TIP-BX gained lytic ability against O103 and O26 strains while retaining O157-infectivity. X-Bal remained capable of lysing O157 strains. Compared to AKFV33, with a burst size of 430 plaque-forming units (PFU) per lysed bacterial cell, burst sizes of TIP-BX, X-C17 and X-Bal against O157 R508 decreased to 187, 169 and 132 PFU/cell, respectively.
Discussion/Significance: These results indicate that LtfB contributes to the host specificity and lytic activity of *Tequintavirus* targeting STEC, warranting further investigation into its functional role.

Identifying fossil jawless fish from the Devonian-age Yahatinda Formation of Alberta

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Keywords: *Devonian, heterostracans, Yahatinda*

The Yahatinda Formation represents an ancient marine environment occupying what is now Southern Alberta and British Columbia. The formation has hitherto been dated to the middle Devonian period but a re-appraisal of fossil data pushes it back to the early Devonian. We describe and identify new fossil material from the CMC Valley locality in the Yahatinda Formation belonging to Heterostraci, a group of jawless armoured fish. We cleaned the fossils with air scribes and consolidated them with ultra-thin polyvinyl acetate (PVA) glue. We wrote systematic descriptions and photographed the specimens with a Nikon D200 camera for future publication. After consulting the published literature, we made a spreadsheet of known heterostracan taxa, their stratigraphy and their identifying features. The most important feature was the pattern of surficial ridges on the fossil armour. We report the presence of at least three distinct heterostracan morphotypes from CMC Valley. We specifically recognize *Clavulaspis finis* (Heterostraci: Protaspididae), and two different indeterminate cyathaspid heterostracans, representing higher heterostracan diversity in the Yahatinda Formation than previously known. We also note the similarities between our specimens and fishes found in the early Devonian. This supports the hypothesis that the Yahatinda Formation is older than previously thought.

Involvement of the Indoleamine 2,3 dioxygenase - Aryl Hydrocarbon Receptor Axis in Influenza A Virus Replication in Chicken Macrophages

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Keywords: Chicken macrophages, Influenza A virus, IDO-AhR Axis

Influenza viruses vary markedly in their ability to replicate. One determinant is viral conversion of tryptophan into kynurenine via the host indoleamine 2,3 dioxygenase aryl hydrocarbon receptor (IDO-AhR) axis, which suppresses innate immunity. However, whether the avian influenza H4N6 strain exploits this axis in macrophages remains unclear. We hypothesise that exploitation of this axis confers a replicative advantage in H4N6 and reduces the viability of macrophages.

Chicken macrophages were infected with H4N6 (LPS/PMA positive control). Extracellular/intracellular fractions collected at 3, 6, 12, 24, 48h past infection (hpi) were subjected to plaque assay, RT-qPCR (n = 3), IDO mRNA analysis (n = 3), and IDO enzymatic activity (n = 6). Supernatants will be assayed for the tryptophan/kynurenine ratio, while apoptosis-necrosis is profiled by double immunofluorescence staining (H4N6 vs necrosis). At 24h, cytotoxicity was measured by PE/Annexin flow cytometry after drug treatments (n = 3) with CH-223191 (5,10,20 μM), 1-methyl-tryptophan (0.25,0.5,1 mM), or kynurenine (0.1,0.2,0.4 mM). Infected cells will then receive these inhibitors at their determined effective doses for 24hpi, after which viral replication and apoptosis/necroptosis will be analyzed by two-way ANOVA with Tukey's HSD test.

We anticipate significantly higher IDO expression, elevated kynurenine/tryptophan ratio in infected cells, and a ≥1-log10 reduction in viral output when AHR or IDO are inhibited. Demonstrating that H4N6 leverages the IDO-AHR axis to impact viral replication and macrophage cell cycles would identify a druggable host pathway for broad-spectrum influenza control in the poultry industry.

Effects of Track and Curvature on Stride Parameters in Racing Thoroughbreds

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Keywords: Thoroughbred racehorse ; Stride parameter ; Injury Prediction

Introduction: Understanding how stride characteristics adapt to external factors during racing is critical for improving injury prediction. We analyzed in-race data collected at two racetracks with different track geometry (Century Mile, Century Downs). Specifically, we investigated how stride parameters change as a function of speed at various locations on the track, and whether these relationships differ between the two racetracks. **Methods:** GNSS recordings from 178 races (Downs: 38; Mile: 140) involving 38 Thoroughbred racehorses were segmented into 100-m sections and average speed, stride length, and stride frequency were computed. Track curvature was classified into straight (<5°) or curve (>30°) from cumulative heading change. Linear mixed-effects models (random factor: horse) assessed the effects of curvature and track on speed, and tested interactions between speed and stride parameters. **Results:** In straight sections, speed was 0.22 m/s higher at Century Mile than Century Downs ($p < 0.001$). Stride length and frequency showed no interaction with track, and both increased with speed ($p < 0.001$); stride length was 0.252 m longer and frequency increased by 0.06 Hz per 1 m/s increase. In curve sections, curvature had no significant effect at Century Mile ($p = 0.08$) but reduced speed by 0.014 m/s per degree at Century Downs ($p < 0.001$). Stride length increased by 0.257 m per 1 m/s ($p < 0.001$) and was 0.304 m longer at Century Mile ($p = 0.03$). Stride frequency increased with speed ($p < 0.001$) without significant track differences ($p = 0.07$). **Conclusion:** Stride parameters vary with speed, curvature, and track location. Given the reported link of reductions of stride parameters over time with musculoskeletal injury risk, understanding these relationships in-race allow better prediction models.

Restricted use of antimicrobials in the Canadian poultry industry: Impacts on antimicrobial resistance of *Enterococcus spp.* isolated from poultry farms

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Keywords: Antimicrobial, Resistance, Genome

Agricultural antimicrobial resistance (AMR) poses an economic burden and a public health risk through zoonotic infection. Initially linked to antimicrobial use in hospitals, AMR has been rising in prevalence outside clinical settings. To combat AMR, the Canadian poultry industry has instituted restrictions on the use of specific antimicrobials. *Enterococcus spp*. are commonly detected on poultry farms and known to be prone to develop AMR. We aimed to identify AMR genes in *Enterococcus spp.* from Canadian poultry farms and assess if their prevalence had changed following phased antimicrobial restrictions. In collaboration with the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS), *Enterococcus spp.* isolates were harvested from archived floor fecal samples and grown to sequence their genome through short-read sequencing using an Illumina platform (384 total samples). *Fastq-mcf* was used within the *ea-utils* suite to trim the sequenced reads, then the reads were combined into contigs with SPADES. ABRICATE was used to detect AMR genes within contigs. AMR gene presence was compared across different stages of Canada's antimicrobial phasing out policy for poultry farms using chi-square tests.

Genes encoding for resistance against aminoglycosides ($p = 0.008$), streptogramins ($p = 0.0001$), macrolides ($p = 0.019$) and tetracyclines ($p = 0.002$) were found to decrease in prevalence after their respective use was restricted by the Canadian poultry sector. These results indicate that the restricted use of antimicrobials is lowering the frequency of AMR genes detected in *Enterococcus spp.* on poultry farms.

Quaternary Structure of Prions in Chronic Wasting Disease: A Determinant in Brain-Region Specific Replication

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Keywords: Chronic Wasting Disease, Prion, Replication

Chronic Wasting Disease (CWD) is a highly contagious prion disease threatening cervids across North America. Prion diseases are fatal, neurodegenerative disorders caused by prions, which are unique, protein-only agents that lack nucleic acids and carry their infectious properties in their three-dimensional structure. This structure allows prions to replicate through misfolding of the host's normal cellular prion protein into the infectious disease isoform (PrPSc). Misfolding and replication occur differently and distinctly across brain regions depending on the PrPSc structure; the mechanisms behind this remain unknown.

In previous studies with elk model mice infected with CWD, we showed that different quaternary structures of PrPSc (High and Low molecular weight- LMW and HMW) lead to distinct clinical signs and brain region tropism. To investigate further, we used immunohistochemistry to assess prion associated pathology throughout disease progression, focusing on neuroinflammation (astrogliosis) across all brain regions. We also used protein misfolding cyclic amplification (PMCA) to examine how aggregates of differing quaternary structures replicate in distinct brain microenvironments. At 22 days post-infection (DPI), HMW and LMW aggregates induced similar astrogliosis. By 33 DPI, LMW showed a significant increase in neuroinflammation in several regions (e.g., occipital cortex, $p=0.01$). At 110 DPI, PMCA revealed that HMW seeds, especially from the cortex, replicated more readily in whole brain homogenate. These differences diminished by the terminal stage, suggesting late-stage convergence in replication behaviour. Together, we present novel findings that prion quaternary structure influences region specific neuropathology during the early pre-clinical stage of the disease, which determines the later clinical presentation.

Investigating the role of black flies (*Simulium sp.*) In the transmission of Equus caballus papillomavirus type 2

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Keywords: Equine, Papillomavirus, Mechanical Vector

Penile squamous cell carcinoma (PSCC) is a common genital cancer in horses linked to infection with Equus caballus papillomavirus type 2 (EcPV2). The mechanism of transmission of EcPV2 between horses is unknown, however. Unlike high-risk human papillomaviruses, which are spread via sexual contact and cause cervical, anogenital and throat cancer in people, EcPV2 infection and its associated penile cancer can occur in horses with no breeding history or close contact with other horses. We hypothesize that hematophagous insects, such as black flies (*Simulium sp.*), may serve as mechanical vectors for EcPV2. To test this, an excised equine PSCC tissue sample was confirmed by PCR and Sanger sequencing to contain EcPV2 and then used as an inoculum in controlled exposure trials. 324 pathogen-free laboratory-grown black flies were exposed for 2 hours to EcPV2-inoculated feeding stations and then allowed to move to spatially separated virus-free feeding stations for 12 hours. After this, flies were killed and tested for the presence of EcPV2 using semi-nested PCR. A proportion of flies was found to carry EcPV2 DNA still, suggesting that insects are capable of retaining viral particles on their bodies for at least 12 hours and that they are plausible mechanical vectors. This is the first experimental evidence of hematophagous insects having the potential to transmit EcPV2 mechanically, challenging the current assumption that direct contact between horses is the sole method of transmission

Investigating Sex Differences in Social Behaviour of P70-P80 C57Bl/6J Mice in the Three-Chamber Social Interaction Test

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Keywords: Three-chamber social interaction test, Sex differences, C57Bl/6J mice

Introduction: The three-chamber social interaction test is commonly used to assess sociability and preference for social-novelty in mouse models for neurodevelopmental disorders. While there is abundant literature regarding the behaviour of C57Bl/6J male mice for this test, there is limited research exploring social behaviour in females. Our lab is studying social behaviour in female mice with Fragile X Syndrome, the leading monogenic cause of autism, and observed an absence of preference during the social-novelty phase in the three-chamber test.
Methods: To establish baseline behaviour, we performed a three-chamber test using female wildtype C57Bl/6J mice with males as a positive control. In this study, seven males and seven females (postnatal days 70-80) were tested across three phases: habituation, sociability (novel object vs. stranger mouse 1), and social-novelty (stranger mouse 1 vs stranger mouse 2). Each phase spanned 10 minutes and time spent in each chamber was tracked using Ethovision software.
Results: We hypothesize that male mice will exhibit a strong preference for stranger 1 in the sociability phase and for stranger 2 in the social-novelty phase, consistent with current literature. Based on previous experiments, we expect female mice to exhibit a weaker preference than male mice for stranger 1 in the sociability phase and for stranger 2 in the social-novelty phase.
Discussion: This study will further our understanding of baseline sex differences in wild-type behaviour. We aim to not only interpret true differences in phenotypic behaviour of mice modeled for neurodevelopment disorders, but to also better understand sex differences, a perspective neglected historically.

Parasites of wild white-tailed jackrabbits (*Lepus townsendii*) in Calgary, Alberta

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Keywords: Urbanization, jackrabbits, parasites

As urbanization expands, understanding urban wildlife and their diseases is vital for public and animal health. White-tailed jackrabbits (*Lepus townsendii*) have adapted to urban ecosystems, but their health status remains poorly understood amid population declines. This study aimed to: i) identify parasite types and prevalences in urban jackrabbits; ii) assess infection risk factors and health impacts. We analyzed cross-sectional samples of jackrabbits found dead near roadways in Calgary, Alberta using fecal flotations and PCR on tissue cysts. We analyzed associations between parasitic infections and health/demographic factors using univariable logistic regression.

Tissue cysts, attributable to *Taenia spp.* tapeworms, were preliminarily confirmed in 18/142 jackrabbits (13%). The prevalence of *Eimeria spp.* and *Strongyle spp. oocysts* in feces was 89% (117/131) and 45% (59/131), respectively. No risk factors were associated with the presence of *Strongyle oocytes*. The odds of an animal testing positive for *Eimeria* were significantly increased in mature vs. immature individuals (Odds Ratio [OR] =4.9; 95% CI=1.5-16.0; p=0.007) and in heavier vs. lighter weight individuals (OR=3.1; 95% CI=1.7-6.1; p=0.003). Female jackrabbits with low *Eimeria* eggs per gram had increased odds of pregnancy compared to those with high *Eimeria* (OR=5.0; 95% CI=1.2-22.9; p=0.03).

Eimeria spp., fecal-orally transmitted protozoan parasites that infect the liver and intestines of jackrabbits, were associated with maturity and increased body weight—likely age-related indicators of increased exposure. Heavy infection burden was associated with decreased pregnancy rates. Parasites, including the potentially zoonotic tapeworm, *Taenia spp*., commonly infect urban jackrabbits and may have important health impacts in urban ecosystems.

Validation and Optimization of the Opentrons OT-2 Robot for Semi-Automated Mammalian Cell Culture: A Combined Biological and Engineering Approach

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Keywords:

Manual maintenance and propagation of adherent mammalian cells in well plates is time-intensive, prone to variability, and can limit reproducibility in biological workflows. Automation can address these issues, but commercial liquid handling systems are costly and inflexible for small or medium throughput laboratories. In this study, we developed and validated a semi-automated protocol for subculturing, with the Opentrons OT-2, an affordable, open-source liquid handler. Sterility validation through various methods confirmed that the OT-2's open-deck design is suitable for short durations of testing cell culture workflows. Engineering validation included spectrophotometry assays for residual volume, which consistently measured residual amounts of 10-15uL per well, indicating a need for further pipetting optimization. Attempts at complete automation, specifically through room temperature trypsinization, resulted in significantly reduced detachment, highlighting a key limitation of the OT-2's default setup. Mixing performance tests also uncovered practical pipette flow rate limitations, with the Opentrons Python API's maximum allowed mixing speed producing lower detachment efficiency than traditional techniques in the biological safety cabinets (BSCs) using micropipettes. Despite these limitations, custom Python scripting with the API enabled significant flexibility and customization, including custom functions and hardware, highlighting the potential of cheaper, adaptable automation platforms for cell culture workflows. These tests revealed comparable cell viability and efficiency between automated and traditional techniques in BSCs. Future improvements should focus on overcoming environmental constraints and pipetting mechanics, to fully emphasize the platform's potential for cell culture automation.

Evaluating Phage Cocktail Efficacy and Determining the Genetic Basis of Resistance in Multidrug-Resistant *Escherichia coli* ST131

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Keywords: Bacteriophage, Phage Cocktail, Multidrug Resistance

Introduction *Escherichia coli* ST131 is a highly virulent and clinically significant pathogen known for its multidrug resistance, making it a public health threat. As antibiotic resistance becomes more widespread, phage therapy, which uses viruses to target bacteria, offers an alternative. However, phage resistance reduces its efficacy. Phage cocktails, which combine two or more phages, may enhance treatment efficacy and reduce the likelihood of resistance. This project evaluated the efficacy of single-phage vs six-phage cocktail treatment on *E. coli* ST131. **Materials & Methods** Six phages were chosen based on receptor diversity and prior characterization of efficacy against the selected universal host strain, EC16-425. Bacterial growth suppression and treatment efficacy was evaluated using 24-hour kinetic assays, with optical density (OD600) recorded hourly. Six single phages and a six-phage cocktail were tested at eight multiplicities of infection (MOIs), alongside a bacteria-only control. Analysis was performed using RStudio (v4.5.2) to determine which treatments was most effective. **Results** The phage cocktail, along with phage 186B, showed most growth reduction at an MOI of 10, while the other single phages reduced bacterial growth most effectively at MOIs ranging between 100-10,000. Additionally, the phage cocktail maintained greater efficacy across lower MOIs of 1 and 0.1 compared to the single phages. **Discussion & Significance** These findings demonstrate the efficacy of phage cocktail treatment compared to single phage treatments, especially at lower MOIs, which may lower treatment costs and potentially reduce the rate of resistance. Furthermore, this research can help guide future phage cocktail design and optimization.

Exploring Cattle Producers Perspectives on Accessibility of Veterinary Services in Alberta: Using Thematic Analysis

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Keywords: Accessibility, Veterinary, Cattle Producers

Veterinary shortages are a growing concern in many countries, Canada included. The issue of veterinary shortages spans many areas of veterinary medicine, especially food animal veterinarians in rural communities where many cattle producers are located. Limited research exists on Canadian cattle producers' use of veterinary services, particularly access to veterinary care. The purpose of this study is to understand the use of veterinary services and to evaluate their accessibility for cattle producers in Alberta.

This qualitative study used semi-structured interviews to gather first-hand accounts from producers. Purposive sampling via intermediaries was the primary method of participant recruitment, followed by snowball sampling. Interview questions were informed by the Access to Health Care theoretical framework. This framework was designed and has been used to evaluate access to healthcare in human medicine. To our knowledge, this is the first time it has been used in a veterinary context. Data for this study is comprised of transcripts from recorded interviews with producers from the cow-calf, feedlot and dairy sectors. Data analysis consisted of using a hybrid inductive and deductive approach to perform thematic analysis.

Data collection and analysis is ongoing, and the results are pending. We expect to identify which services are most impactful for producers and which specific barriers to access they experience.

This information will contribute to understanding underlying barriers contributing to difficulties accessing veterinary services. Findings from this study will help inform policy development to better support cattle producers and farm animal veterinarians.

Electrical Stimulation of the A13 Nucleus as a Novel Therapeutic Approach in a 6-OHDA Rat Model of Parkinsons disease

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Keywords: Parkinson's, A13, DBS

Parkinson's disease (PD) is neurodegenerative disorder characterized by progressive motor impairments, including slow movement, rigidity, and gait dysfunction such as freezing. Medications and current deep brain stimulation (DBS) targets offer limited efficacy for locomotor dysfunction. A recent paper from our lab suggests that optogenetic stimulation of the A13 nucleus, located below the thalamus, can elicit robust locomotor responses in rodents. This study aims to assess the efficacy of the A13 nucleus as a novel DBS target for rescuing locomotor function in a 6-hydroxydopamine (6-OHDA) rat model of PD. Ten rats underwent stereotaxic surgery to implant a custom-made, bipolar, stainless-steel electrode above the A13. Six of the rats received a unilateral 6-OHDA injection to lesion the substantia nigra pars compacta (SNc), and four rats received a vehicle injection. Healthy and lesioned rats underwent a battery of behavioural assays assessing locomotion, exploratory behaviour, and forelimb dexterity, with and without A13 stimulation. Post-hoc analysis, including c-Fos and tyrosine hydroxylase (TH) immunohistochemistry, will quantify the extent of neuronal activation and lesion development, respectively. The unilateral lesion significantly increased the proportion of ipsilateral turns in the open field test ($p<0.001$). Preliminary data suggests that A13 stimulation increases locomotion and exploratory behaviour in both healthy and lesioned rats. Data collection and analysis are ongoing, and more results will be presented on research day. The A13 is a novel DBS target that holds promise for treating PD-related gait dysfunction. A13 stimulation may also offer improved and additional benefits and overcome limitations of traditional DBS targets.

Prevalence of *Neospora caninum* in Alberta Dairy Herds

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Keywords: Alberta dairy herds*, Neospora caninum,* prevalence

Introduction: *Neospora caninum* is a protozoal parasite that causes abortion and mortality in dairy cattle. *Neospora* caninum spreads when a cow ingests faeces that is contaminated with the parasite's eggs from dogs or wild canids, or through vertical transmission. The objective was to estimate the herd-level prevalence of *N. caninum* infection in Alberta dairy herds.

Methods: Bulk tank milk samples were collected in April 2025 from all 460 active dairy herds in Alberta through Alberta Milk. A commercial ELISA antibody testing (IDEXX *Neospora* X2) was used to detect antibodies against *N. caninum* following manufacturer's recommendations. ELISA results were dichotomized using a cut-off value of ≥0.50 sample-to-positive ratio. The Chi-square test was used to determine differences in prevalence.

Results: The provincial herd-level prevalence of *N. caninum* was 25.6% (95% CI 21.9-29.8%). The prevalence was 45.0, 20.1, and 17.3% for herds in the North, Central, and South of Alberta, respectively ($p<0.001$). The prevalence was 25.9% and 26.0% for conventional milking and automated milking herds, respectively ($p=1.00$). Also, the prevalence was 25.9 and 26.0% for non-Hutterite and Hutterite colony farms, respectively ($p=1.00$). Furthermore, small, medium-size and large herds had a prevalence of 29.8, 25.0 and 17.3%, respectively ($p=0.10$).

Conclusion: These prevalence estimates provide up-to-date information of *N. caninum* frequency and distribution across Alberta. Prevalence tended to be higher in small and medium-size dairy herds and was particularly high in the North which suggests that wild canids and dogs may plan a larger role in the transmission of *N. caninum* infections in these herds.

A Multi-Omics Approach to Understanding the Host-Immune Response in Swine Dysentery

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Keywords: swine dysentery, host-pathogen interaction, transcriptional profiling

Brachyspira hyodysenteriae is a Gram-negative spirochete that colonizes the colon, causing swine dysentery, a diarrheic mucohemorrhagic colitis. Despite well-characterized symptoms, the host inflammatory-immune response producing tissue-damaging colitis remains elusive. We hypothesize that the colonization of *B. hyodysenteriae* triggers a damaging form of colitis. The pathogenesis of swine dysentery was studied in a controlled experiment in weaned pigs, which were orally challenged with *B. hyodysenteriae* or an inert solution (n = 10 per group). Disease progression was evaluated daily during the period of the disease (2 weeks). Fecal samples were collected periodically and analyzed for bacterial shedding (qPCR). At peak infection, colons were harvested for transcriptional profiling (bulk RNA-seq) and imaging of microscopic damage (H&E), neutrophil infiltration (MPO) and mucin barrier integrity (Alcian-PAS). Infection was confirmed by *B. hyodysenteriae* DNA in feces. Leukocyte infiltration (H&E) and neutrophil recruitment in the colonic lamina propria (MPO) were microscopically visible in the infected groups. There was a transcriptional upregulation of inflammatory cytokines (IL-1β, IL-17, IL-22) and matrix metalloproteinases (MMPs). Proteomics showed abundant MMP and decreased claudin (CLDN6). The mucin layer was visibly thinned (Alcian-PAS) while mucin producing genes (MUC2, MUC5AC) were upregulated in infection.
B. hyodysenteriae infection induces mucohemorrhagic colitis due to increased neutrophil infiltration and pro-inflammatory cytokines linked to increased proteases that disrupt the mucin layer and cause tissue damage. Simultaneously, mucin-producing proteins overcompensate to restore homeostasis. This colon destruction and compromised mucin barrier contribute to the presence of blood in the feces. Overall, these findings advance the understanding of swine dysentery pathogenesis.

Evaluating Zoonotic Potential of Chronic Wasting Disease in Transgenic Mice Using Prion Amplification Assays

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Keywords: prion; CWD; PMCA

Chronic wasting disease, a transmissible spongiform encephalopathy found in cervids, is spreading rapidly across North America, and concerns about its zoonotic potential are growing. We evaluated the zoonotic potential of chronic wasting disease using protein misfolding cyclic amplification (PMCA) and real-time quaking-induced conversion (RT-QuIC) to detect infectious prions. Initially, macaques were inoculated with tissues from cervids that were sick with chronic wasting disease. Tissues from macaques who became symptomatic with the disease were passaged into mice expressing human or cervid prion protein. Tissues from clinically sick mice were further passaged into new mice via intracerebral inoculation. Although no detectable infectious prion material was detected via PMCA or RT-QuIC in any of the clinically sick cervidized or humanized mice we tested, passaging of these tissues in live animals increases infectivity. Additionally, we found that passaging tissue from an infected cervid through bank vole prion via protein misfolding cyclic amplification successfully converted human prion protein providing evidence for zoonotic potential. Our inability to detect infectious prion material in clinically sick mice may indicate a detection threshold we have not solved for or a systemic issue with our understanding of the relationship between infectious prion levels in the brain and clinical symptoms rather than an absence of zoonotic potential. While prions are known to cause brain disease, there is evidence that other tissues may be sources of infectivity. In our work, we focused on brain tissue, so in the future, other tissues, like intestines or immune organs, should be tested for infectious prion.

Generation of Canine HES1 Reporter in Induced Pluripotent Stem Cell Reporter Line to Study Developmental Timing

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Keywords: HES1 Ocillatory gene expression, Canine Induced pluripotent stem cells (CiPSCs), Comparative animal biology

Precise control of event timing is critical for proper embryonic development; even subtle disruptions can cause severe developmental abnormalities. The gene Hairy and Enhancer of Split-1 (HES1) exhibits oscillatory expression patterns that regulate stem cell fate decisions. We hypothesize that while HES1 oscillations are conserved across mammals, their periodicity is species-specific. To test this, we developed a canine model for real-time tracking of HES1 expression, as part of a broader cross-species comparison project on developmental timing. Using CRISPR-Cas9 genome editing, we generated an endogenous HES1 knock-in reporter encoding tdTomato and Nanoluciferase in canine induced pluripotent stem cells (CiPSCs). The reporter plasmid was designed with canine-specific homology arms for targeted integration through homologous recombination (figure 1). Each step was validated by polymerase chain reaction (PCR), Sanger Sequencing, and restriction digests. CiPSCs were electroporated with the construct, Cas9 protein, and canine HES1-specific sgRNA to target the stop codon. Colonies were selected with geneticin and picked based on tdTomato fluorescence.
Assembly of the reporter construct was confirmed by PCR and sequencing, with 6/12 clones positive for the first homology arm and 1/10 for the second. After electroporating into CiPSCs, we applied geneticin selection (75-100 ng/uL) and manually picked 12 clones based on visually observed tdTomato fluorescence for further validation and characterization.
Once validated, this model may support comparative analysis with human, mouse, and pig HES1 reporter systems developed by our lab. Future experiments will validate the HES1 CiPSC reporter line and characterize HES1 oscillatory behaviour with high temporal resolution.

Characterization of Embryonic Development in a Novel Mouse Model for Spondylocostal Dysostosis Type 7

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Spondylocostal Dysostosis Type 7 (SCDO7) is a rare congenital vertebral malformation and autosomal recessive disorder associated with Glycine-to-Arginine missense mutation (Gly-512-Arg) in Delta-like 1 (DLL1). Our lab recently established a novel mouse model harboring the SCDO7 missense mutation, which displayed a congenital vertebral malformation phenotype and perinatal embryonic lethality. Because Dll1-null mutation results in early embryonic lethality around E11.5, we hypothesize that the SCDO7 mutation is a hypomorph of the wild-type Dll1 but not a complete loss-of-function. To investigate the effects of this mutation, embryos from two founder mouse lines (31 and 35) were genotyped, where those carrying the homozygous SCDO7 mutation were collected between embryonic day (E) 9.5 and E18.5 and compared to heterozygous or wildtype littermates of the same developmental stage. I performed morphological assessments, including histological analysis of paraffin-embedded sections and skeletal staining using Alcian Blue and Alizarin Red, and observed defects in vertebral morphology. Since a prior report suggested impaired osteogenic differentiation, I am currently using human pluripotent stem cell lines carrying the SCDO7 mutation to test whether osteogenic differentiation is compromised compared to isogenic controls, along with immunofluorescence staining for bone-related markers to assess differentiation capability. Preliminary results suggest that genotypic ratios follow Mendelian inheritance, with homozygous mutants consistently displaying vertebral segmentation defects and truncated tails. Additional histological differences and potential sex biases are currently a work in progress. This project aims to uncover the role of *Dll1*-mediated Notch signaling in embryonic development and to understand how broader developmental disruptions contribute to lethality in SCDO7.

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