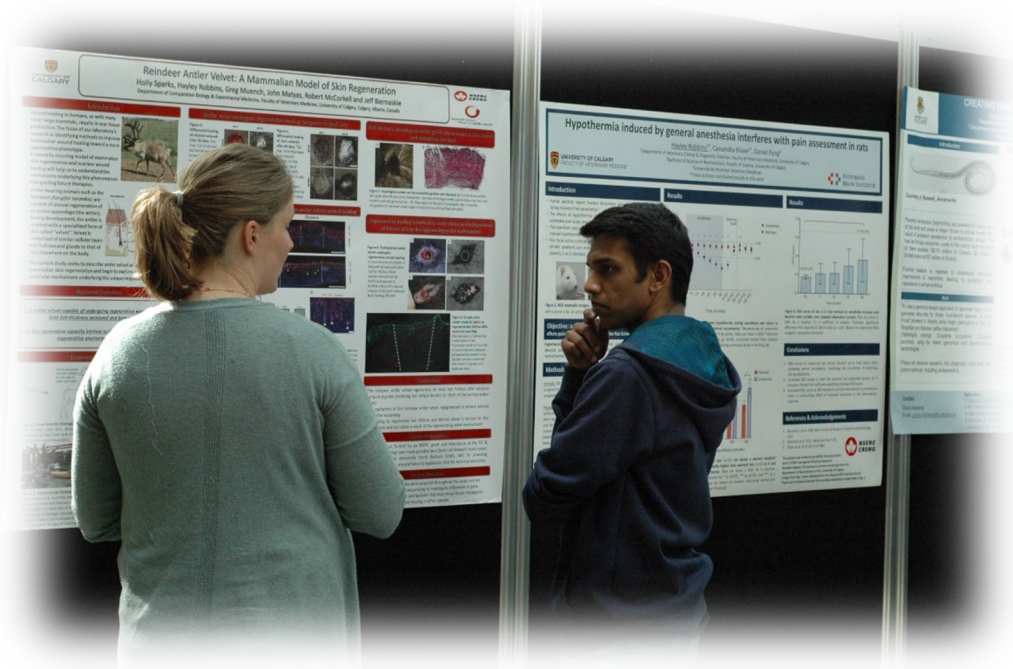




UNIVERSITY OF CALGARY
FACULTY OF VETERINARY MEDICINE



UCVM SURE Research Days 2021

August 25th and 26th, 2021

8:30 am – 1:00 pm

ABSTRACT BOOKLET

UCVM SURE Research Days: 2021

Message from Dr. Hermann Schaetzel, Associate Dean, Research



Dear summer students, Dear colleagues,

A warm welcome from the Associate Dean, Research. The purpose of this meeting is to showcase the wide range of research activities our 2021 summer students performed. This year over 50 SURE (Summer Undergraduate Research Experience) students registered, with 74% of them receiving competitive and UCVM-external stipend support (worth >\$220,000). This includes four prestigious fellowships from Merck for UCVM DVM students. The range of research activities showcased here is very broad, as is typical for our faculty, of high quality and exemplifies the UCVM research excellence. This is even more impressive as almost all our SURE students could not perform research activities within the first five weeks due to COVID restrictions.

Over the next two days, we will have 20 featured oral presentations and 31 short oral presentations in parallel breakout rooms, together with two keynote lectures and prizes for best long and short oral presentations. As for the Trainee Research Days, the organizing committee comprises students, postdoctoral fellows, staff and faculty members. We are confident that this meeting brings together the UCVM community and shows the high quality of research and training activities our faculty is known for. Most importantly, congratulations to all SURE students for their excellent work. They obtained real-life and real-time insight into the fascinating but complex world of research, an experience that hopefully stimulated their appetite for more in the future.

I would like to thank my co-organizer Brenda Moore from the UCVM Research Office, the members of the organization committee, and the prize judging committee for their outstanding help and efforts, and everybody else helping to make this meeting a success.

Sincerely,

Hermann M. Schaetzel

Associate Dean, Research

Message from Dr. Jacob Thundathil, Associate Dean, Graduate Education and Internationalization



Dear students,

In UCVM, summer studentship is a high priority, as this is an opportunity for us to showcase our rigorous laboratory and field research to a wide variety of undergraduate students and contribute to your academic journey. I sincerely hope all of you had a great time with our team (graduate students, staff, postdoctoral trainees, and professors). I expect some of you had a memorable rare moment of insight or discovery; those can be very rewarding! Regardless of what you discovered, I remind you that your happiness is largely a matter of your attitude, and that you will draw much more satisfaction and motivation from asking “what can I learn from this result” rather than asking “what went wrong”? I wish you all the best in your future endeavors and hope to see many of you back during summer 2022.

UCVM SURE Research Days: 2021

SURE Research Days Program 2021

Program August 25 th , 2021			
08:30	Welcome		Dr. Hermann Schaetzl (ADR-UCVM)
08:35	Session 1 (Long Oral Presentations)	Presenters	Session Chairs
		Arzina Jaffer (J. Biernaskie) <i>Fibroblasts exacerbate local inflammation and promote myeloid maturation during fibrotic skin wound healing</i>	Dr. Daniel Pang
		Mallory Goodmanson (M-F. Roy) <i>Clinical investigation of neutrophils oxidative burst, LPS response and endotoxin activity in healthy and sick horses</i>	
		Seth Colby (H. Schaetzl) <i>Novel cell culture model to analyze newly emerged camel prions</i>	
		Zhanika Gimeno (H. Barkema) <i>Teat sealant use on Canadian dairy farms</i>	
Katrine Gillett (S. Kutz) <i>Development of a protocol for recovering peripheral blood mononuclear cells from blood of muskoxen (<i>Ovibos moschatus</i>)</i>			
09:40	Break		
09:50	Session 2 (Long Oral Presentations)	Daniel Hung (D. Hall) <i>A retrospective study on the use of the health belief model in predicting rabies mitigation in Bhutan</i>	Dr. Tahir Ali
		Lauren Stoffregen (J. Pearson) <i>Assessing the accuracy of CowManager ear tags in beef bulls by comparison with direct observation</i>	
		Maggie Rusteika (J. Chu) <i>Investigating the role of HES1 gene expression in regulating porcine iPS cell self-renewal</i>	
		Theo Nelson (P. Whelan) <i>Identifying a connection between the A11 nucleus and MRF: an alternative descending dopamine pathway</i>	
		Brittany Munro (D. Pang) <i>Assessing the concentration at which loss of righting reflex occurs during carbon dioxide (CO₂) exposure</i>	
10:55	Break		
11:05	Short Oral Presentations (Three Breakout Rooms: Agenda Below)		
12:05	Break		
12:15	Keynote lecture: <i>The horse athlete and its amazing physiological adaptations to exercise</i>		Dr. Renaud Leguillette
12:55	Closing Remarks		

UCVM SURE Research Days: 2021

August 25th Breakout Room One

Moderator: Dr. Waqas Tahir

11:05	Leslie Cao (J. Biernaskie) <i>Epimorphic regeneration of reindeer antlers is enabled by an immune privileged microenvironment</i>
11:15	Lian Barkema (H. Barkema) <i>Examining factors used by Canadian dairy farmers to make treatment decisions of clinical mastitis</i>
11:25	Madina Shayne (M. Ungrin) <i>Hardware development for rodent home-cage monitoring</i>
11:35	Elise Romney (S. Cork) <i>Tick surveillance systems: A scoping review</i>
11:45	Julia Gee (D. Pang) <i>Building a 3D printed experimental apparatus for assessing loss of righting reflex in laboratory rodents</i>
11:55	Rita Hannawayya (D. Niu) <i>Genomic features and host range of Tequintavirus phages with infectivity against Shiga toxin-producing Escherichia coli</i>

August 25th Breakout Room Two

Moderator: Dr. Johnathan Canton

11:05	Tina He (I. Dobrinski) <i>Progression of Sertoli Cell Maturation</i>
11:15	Akaysha Envik (S. Cork) <i>Examining risk pathways for the entry of the Asian longhorned tick (<i>Haemaphysalis longicornis</i>) into Canada from the USA</i>
11:25	Anthony Do (J. Chu) <i>Investigating the role of NOTCH signaling pathway in regulating human segmentation clock model</i>
11:35	Caileah Ell (J. Wasmuth) <i>Computational analysis of hematophagous parasite anticoagulants for new antiparasitic drug development</i>
11:45	Stephen Moore (M. Ungrin) <i>Target identification to engineer an attenuated parasite with improved biosafety</i>

UCVM SURE Research Days: 2021

August 25th Breakout Room Three

Moderator: Dr. Ning Cheng

11:05	Sergio Sharif (H. Schaetzl) <i>Modulation of the heat shock response: a potential novel therapeutic target in prion disease</i>
11:15	Brittany Munro (D. Pang) <i>Determining the sequence of respiratory vs. cardiac arrest after magnesium sulfate euthanasia</i>
11:25	Anchita Shonak (P. Whelan) <i>The effects of sodium pump activation on spontaneous activity in the neonatal mouse spinal cord</i>
11:35	Vanessa Boone (H. Barkema) <i>Housing and outdoor access practices in the Canadian dairy industry</i>
11:45	Justin Ross (C. Windeyer) <i>Feasibility assessment on wearable technology for studying neonatal beef calves</i>

UCVM SURE Research Days: 2021

Program August 26 th , 2021		
08:30	Welcome	
08:35	Session 3 (Long Oral Presentations)	Presenters
		Akeel Faizal (D. Niu) <i>Interaction of Shiga toxin producing Escherichia coli O157:H7 and bacteriophages on human intestinal cells</i>
		Emma Foxcroft (C. Rolian) <i>Do bones that grow faster heal faster?</i>
		Geeta Kilari (E. Cobo) <i>Cathelicidin promotes secretion of mucus associated proteins in colonic goblet cells through increased reactive oxygen species (ROS)</i>
		Brandon Huynh (I. Dobrinski) <i>Testicular organoids derived from induced pluripotent stem cells as a bioassay for modelling testicular development and function in vitro</i>
		Kabita Baral
08:35		
09:40	Break	
09:50	Session 4 (Long Oral Presentations)	Nancy Ngo (J. Poissant) <i>Investigating parasite biodiversity and prevalence of Strongylus vulgaris in Alberta feral horse using an ITS2 DNA metabarcoding assay</i>
		Jaimie Warren (D. Whiteside) <i>Evaluation of genetic basis of degenerative heart conditions in Vancouver Island marmots</i>
		Mackenzie Campsall (C. Windeyer) <i>An experimental model of cryptosporidiosis in neonatal calves results in exaggerated systemic weakening and diarrheic enterocolitis</i>
		Derrick Zhang (M. Pruvot) <i>Does bat consumption of insect pests result in a mutualistic relationship between beef cattle and bats?</i>
		Madeleine Browne (R. Leguillette) <i>Effects of an innovative inhaled corticosteroid therapy on VO₂peak in horses with moderate asthma</i>
		Dr. Marie-France Roy
10:55	Break	
11:05	Short Oral Presentations (Three Breakout Rooms: Agenda Below)	
11:55	Break	
12:05	Keynote Lecture: Dendritic cells in Immunity and Homeostasis	Dr. Johnathan Canton
12:45	Prize distribution and closing	

UCVM SURE Research Days: 2021

August 26th Breakout Room One

Moderator: Kabita Baral

11:05	Nicole Wilson (S. Gilch) <i>The role of Rab7 in cholesterol metabolism upon prion infection</i>
11:15	Megan Sorenson (K. Orsel) <i>Learning from subsidized dog spay-neuter clinics: how can we better assess clinics impact in Indigenous communities?</i>
11:25	Danielle Korsrud (I. Dobrinski) <i>Feeder layers and exosomal exchange in porcine germ cell co-cultures</i>
11:35	Priyanka Mangat (K. Liljebjelke) <i>A scoping review: Identifying research gaps for the role of the environment in transmission of antimicrobial-resistant Escherichia coli in cow-calf operations in North America</i>
11:45	Melanie Jarbeau (H. Barkema) <i>Understanding Canadian dairy farmers' perspectives on outdoor access for dairy cows using an online questionnaire</i>

August 26th Breakout Room Two

Moderator: Dr. Anne-Marieke Smid

11:05	Naureen Othi (J. Poissant) <i>Evaluating the effectiveness of shallow shotgun metagenomics for characterising the gut microbiome of Ovis canadensis</i>
11:15	Stephanie Le (K. Liljebjelke) <i>Identifying research gaps for the role of the environment in transmission of antimicrobial-resistant Escherichia coli in cow calf operations in North America</i>
11:25	Sara Toner (A. Whitehead) <i>Seroprevalence investigation and isolation of endemic strain(s) of Neorickettsia species in the province of Alberta</i>
11:35	Louise Caplan (G. Lhermie) <i>Costs and benefits of domestic carnivore ownership in USA, Canada and Europe: a systematic review</i>
11:45	Sophia Lu (M. Ungrin) <i>Evaluation of pressure regulator performance for the construction of an emergency negative pressure ventilator</i>

UCVM SURE Research Days: 2021

August 26th Breakout Room Three

Moderator: Dr. Tahir Ali

11:05	Tahreem Asrar (D. Niu) <i>Muralytic and antibacterial activity of endolysins against Mannheimia haemolytica</i>
11:15	Hannah Horvath (J. Gilleard) <i>Sequencing complete isotype-1 and isotype-2 β-tubulin genes from BZ resistant isolates of Ancylostoma caninum</i>
11:25	Steffany Schluessel (E. Cobo) <i>Efficacy of treatment for diarrheic cryptosporidiosis in neonatal calves using bovine colostrum as therapeutic target</i>
11:35	Christina Nykyforuk (H. Barkema) <i>Selective dry cow therapy practices on Canadian dairy farms</i>
11:45	Rebecca John (P. Whelan) <i>A11 nucleus ablation and the effect on locomotor behaviours in mice</i>

ABSTRACTS

Listed alphabetically by first name of presenting author

Examining risk pathways for the entry of the Asian longhorned tick (<i>Haemaphysalis longicornis</i>) into Canada from the USA	13
Interaction of Shiga toxin producing <i>Escherichia coli</i> O157:H7 and bacteriophages on human intestinal cells	14
The effects of sodium pump activation on spontaneous activity in the neonatal mouse spinal cord.....	15
Investigating the role of NOTCH signaling pathway in regulating human segmentation clock model.....	16
An Investigation into the Efficacy of Filter Paper to Identify and Measure Changes in Neopterin in <i>Rangifer tarandus</i>	17
Fibroblasts exacerbate local inflammation and promote myeloid maturation during fibrotic skin wound healing.....	18
Testicular organoids derived from induced pluripotent stem cells as a bioassay for modelling testicular development and function in vitro.....	19
Assessing the concentration at which loss of righting reflex occurs during carbon dioxide (CO ₂) exposure	20
Determining the sequence of respiratory vs. cardiac arrest after magnesium sulfate euthanasia	21
Computational analysis of hematophagous parasite anticoagulants for new antiparasitic drug development	22
Selective dry cow therapy practices on Canadian dairy farms.....	23
A Retrospective Study on the use of the Health Belief Model in Predicting Rabies Mitigation in Bhutan	24
Feeder Layers and Exosomal Exchange in Porcine Germ Cell Co-Cultures	25
Does bat consumption of insect pests result in a mutualistic relationship between beef cattle and bats?.....	26
Utilizing ITS-2 nemabiome metabarcoding to investigate the species composition of cyathostomin communities after ivermectin and moxidectin treatment	27
Tick Surveillance Systems: A Scoping Review.....	28
Do bones that grow faster heal faster?.....	29
Cathelicidin promotes secretion of mucus associated proteins in colonic goblet cells through increased reactive oxygen species (ROS).....	30
Sequencing complete isotype-1 and isotype-2 β -tubulin genes from BZ resistant isolates of <i>Ancylostoma caninum</i>	31
Evaluation of Genetic Basis of Degenerative Heart Conditions in Vancouver Island Marmots...32	

UCVM SURE Research Days: 2021

Building a 3D Printed Experimental Apparatus for Assessing Loss of Righting Reflex in Laboratory Rodents	33
Feasibility Assessment on Wearable Technology for Studying Neonatal Beef Calves.....	34
Development of a protocol for recovering peripheral blood mononuclear cells from blood of muskoxen (<i>Ovibos moschatus</i>)	35
Assessing the accuracy of CowManager ear tags in beef bulls by comparison with direct observation	36
Epimorphic regeneration of reindeer antlers is enabled by an immune privileged microenvironment	37
Examining factors used by Canadian dairy farmers to make treatment decisions of clinical mastitis	38
Costs and benefits of domestic carnivore ownership in USA, Canada and Europe: a systematic review	39
An experimental model of cryptosporidiosis in neonatal calves results in exaggerated systemic weakening and diarrheic enterocolitis	40
Effects of an innovative inhaled corticosteroid therapy on VO ₂ peak in horses with moderate asthma.....	41
Hardware development for rodent home-cage monitoring.....	42
Investigating the role of HES1 gene expression in regulating porcine iPS cell self-renewal	43
Clinical Investigation of Neutrophils Oxidative Burst, LPS response and Endotoxin Activity in healthy and sick horses.....	44
Learning from subsidized dog spay-neuter clinics: how can we better assess clinics impact in Indigenous communities?	45
Understanding Canadian dairy farmers' perspectives on outdoor access for dairy cows using an online questionnaire	46
Investigating parasite biodiversity and prevalence of <i>Strongylus vulgaris</i> in Alberta feral horse using an ITS2 DNA metabarcoding assay.....	47
Evaluating the effectiveness of shallow shotgun metagenomics for characterising the gut microbiome of <i>Ovis canadensis</i>	48
The role of Rab7 in cholesterol metabolism upon prion infection.....	49
A Scoping Review: Identifying Research Gaps for the Role of the Environment in Transmission of Antimicrobial-Resistant <i>Escherichia coli</i> in Cow-Calf Operations in North America	50
A11 Nucleus Ablation and the Effect on Locomotor Behaviours in Mice.....	51
Genomic features and host range of <i>Tequintavirus</i> phages with infectivity against Shiga toxin-producing <i>Escherichia coli</i>	52
Seroprevalence investigation and isolation of endemic strain(s) of <i>Neorickettsia</i> species in the province of Alberta	53
Modulation of the Heat Shock Response: A Potential Novel Therapeutic Target in Prion Disease	54

UCVM SURE Research Days: 2021

Novel cell culture model to analyze newly emerged camel prions	55
Evaluation of Pressure Regulator Performance for the Construction of an Emergency Negative Pressure Ventilator	56
Efficacy of treatment for diarrheic cryptosporidiosis in neonatal calves using bovine colostrum as therapeutic target	57
Identifying Research Gaps for the Role of the Environment in transmission of Antimicrobial-Resistant <i>Escherichia coli</i> in Cow Calf Operations in North America.....	58
Target identification to engineer an attenuated parasite with improved biosafety	59
Muralytic and Antibacterial Activity of Endolysins Against <i>Mannheimia haemolytica</i>	60
Identifying a connection between the A11 nucleus and MRF: an alternative descending dopamine pathway	61
Progression of Sertoli Cell Maturation	62
Vaccine evaluation against an emerging strain of avian coronavirus	63
Housing and outdoor access practices in the Canadian dairy industry	64
Teat sealant use on Canadian dairy farms	65

Examining risk pathways for the entry of the Asian longhorned tick (*Haemaphysalis longicornis*) into Canada from the USA

Akaysha Envik¹, Susan Cork¹, Sylvia Checkley¹, Isabelle Couloigner¹, Heather Ganshorn

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: Asian longhorned tick, *Haemaphysalis longicornis*, Risk Assessment

The emergence and spread of ticks and tick-borne diseases can impact human and animal health. One emerging concern is the discovery of *Haemaphysalis longicornis*, the Asian long-horned tick (ALHT) in Eastern USA with potential for it to enter into, and establish in, Canada. This tick is of concern as it has the potential to become a significant livestock pest and to transmit pathogens. In livestock, a pathogen of concern is *Theileria orientalis*, which can cause anemia, decrease in milk production and sudden death in cattle. The ALHT can transmit multiple pathogens to humans such as, severe fever with thrombocytopenia syndrome virus, which has a case-fatality rate of up to 30%. This study's objective was to examine how and where this tick could possibly enter and establish in Canada. We hypothesize that certain animal species such as migratory birds, imported dogs and cattle could bring the tick in to Canada. We predict that the tick has a probability of establishing in Canada should it enter from the Eastern USA into SE Canada. It could also establish in British Columbia if it was introduced. To evaluate the risk pathways, we contacted experts in entomology, risk assessment, import policy, and wildlife behaviour and reviewed 1542 peer reviewed articles. We also conducted a library search for habitat suitability for the ALHT in Canada, possible hosts, diseases and the biology of the tick. Our risk assessment concluded that the ALHT could pose significant human and animal health risks should it establish and spread in Canada.

Interaction of Shiga toxin producing Escherichia coli O157:H7 and bacteriophages on human intestinal cells

Akeel Faizal, Ruina Bao, Jane Fletcher, Dongyan Niu

Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: Human intestinal cell, Escherichia coli O157:H7, bacteriophages

Introduction: Enterohaemorrhagic Escherichia coli (E. coli) strains, particularly Shiga toxin (Stx) producing E. coli (STEC) (serotype O157:H7) are considered to be one of the major public health concerns since use of antibiotics as a treatment for STEC is controversial. In this context, one of the biological control methods of interests is the bacteriophage therapy. It is unknown if bacteriophage treatment could control STEC attached to human intestinal epithelial cells. We hypothesized that the STEC O157:H7 is able to attach to human enteric epithelial cells and this process can be prevented using selected bacteriophages given as individual and cocktail. The aim of the proposed work was to determine if bacteriophages as individual isolates or in cocktail are efficacious against STEC attached to human intestinal epithelial cells in-vitro. **Materials and methods:** The intestinal epithelial cell line, Caco2 was cultured and STEC O157:H7 attachment to these cells were assessed qualitatively and quantitatively. The effectiveness of phages, AKFV3, wV7, AHP24, AHS24 are being evaluated in various combinations against attachment of STEC O157:H7 on Caco2 cells. **Results:** 105 colony forming units (CFU)/ml of STEC O157:H7 of Caco2 cell attached bacteria were quantified and 107 CFU/ml of unattached bacteria were also recovered. Giemsa staining confirmed the attachment of bacteria onto the Caco2 cells. We are in the process of assessing the efficacy of bacteriophages against STEC O157:H7 attachment onto Caco2 cells. **Conclusions:** STEC O157:H7 is capable of attaching onto Caco2 cell and the work of bacteriophage efficacy is in progress.

The effects of sodium pump activation on spontaneous activity in the neonatal mouse spinal cord

Shonak, Anchita^{1,2}, Milla-Cruz, JJ.^{1,2}, Cheng, N.^{1,2,3}, Whelan, PJ^{1,2,3}

¹Hotchkiss Brain Institute, University of Calgary; ²Department of Neuroscience, University of Calgary;

³Department of Comparative Biology and Experimental Medicine, University of Calgary

Keywords: Electrophysiology, spontaneous activity, monensin

Na⁺/K⁺-ATPases, also known as “sodium pumps,” are one of the most abundant proteins in the nervous system and contribute to the resting membrane potential by using ATP to facilitate hyperpolarizing currents. Recently, it was discovered that sodium pump activation decreases the frequency of drug-induced locomotor activity in neonatal mice. Spontaneous activity in the developing spinal cord reinforces connections and ensures that spinal circuits develop in an appropriate way. However, the role of the sodium pump with regards to this activity is less well understood. Because spontaneous activity is related to locomotor activity in that both need an underlying spinal cord network to be generated, this study hypothesizes that sodium pump activation will also decrease the frequency of spontaneous activity. Using an in-vitro neonatal mouse spinal cord preparation, extracellular activity from nerve roots in response to bath application of monensin, a Na⁺/K⁺-ATPase activator will be measured. Results will then be analyzed using a spontaneous burst classification system, which quantifies changes in burst parameters with drug application. Preliminary data suggests that although burst amplitude does not change with monensin application, the peak frequency of large, non-rhythmic bursts does change. As such, Na⁺/K⁺-ATPase’s effects on spontaneous activity in the spinal cord may occur within interneurons; motor neurons may not be implicated since amplitude is not affected. Understanding how sodium pumps contribute to network regulation in this way is important with respect to potential drug targets in diseases of motor dysfunction such as amyotrophic lateral sclerosis and Parkinsonism.

Investigating the role of NOTCH signaling pathway in regulating human segmentation clock model

Anthony Do¹, Li-Fang (Jack) Chu^{2,3}

¹Department of Biological Sciences, Faculty of Science, University of Calgary; ²Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary; ³Precision Medicine & Disease Mechanisms Program, Alberta Children's Hospital Research Institute.

Keywords: NOTCH, Segmentation Clock, DLL1

Defects in somitogenesis is linked to a rare congenital spinal disorder, spondylocostal dysostosis-4 (SCDO-4), which is thought to be caused by mutations in the NOTCH signaling pathway. The NOTCH signaling pathway is important in regulating the segmentation clock, which is a molecular oscillator that controls somitogenesis. Delta-like ligand 1 (DLL1) is a ligand in the NOTCH signaling pathway that regulates various downstream segmentation genes. The Chu lab is currently using a human segmentation clock model to better understand the mechanisms of spinal development and SCDO-4. We hypothesize that DLL1 plays a central role in regulating the human segmentation clock. RNA-seq analysis showed that overexpression of DLL1 resulted in the significant downregulation of neurotensin (NTS) and galectin-1 (LGALS1), which are involved in neurotransmission and cell-cell interactions, respectively. In order to monitor the dynamic expression of DLL1 in segmentation clock model, we constructed a DLL1 reporter to enable the observation of its gene oscillation profiles. We designed suitable PCR primers to amplify the 5' and 3'-homology arms from human genomic DNA and cloned them into a reporter backbone vector using restriction enzymes and ligation reactions. Sanger-sequencing were performed to confirm that the correct constructs were obtained. The next step is to electroporate the DLL1 reporter construct with CRISPR-Cas9 and a designed guide-RNA into human embryonic stem cells. Future directions will be to understand the dynamics of DLL1 expression in the human segmentation clock model and its role in regulating NOTCH signaling pathway.

An Investigation into the Efficacy of Filter Paper to Identify and Measure Changes in Neopterin in Rangifer tarandus

Armaan Bhatia, K. Gillett, B. Malinge, A. Schneider, S. Kutz and M. Pruvot

Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: Caribou, Neopterin, Filter-Paper

Caribou (*Rangifer tarandus groenlandicus*) are ecologically and culturally important but are facing an increasing number of threats. This makes improving knowledge regarding caribou health critical. Neopterin is a marker of cellular immune function responding to both infectious and non-infectious stressors, making it useful in this respect. Filter paper (FP) is highly suited for sample collection in the Arctic, and this study aimed to validate its use to collect blood for neopterin analyses and to monitor reindeer neopterin response. We hypothesized that FP would be able to measure changes in neopterin concentrations as effectively as serum. In a cross-over study, two groups of three reindeer (*Rangifer tarandus tarandus*) were either challenged with lipopolysaccharide (LPS) or saline (control), injected into the jugular vein. Blood was collected at seven timepoints, on FP and in heparinized tubes. Samples were then assayed in duplicate, using a competitive enzyme linked immunosorbent assay that measured neopterin concentration. Results obtained from FP eluate were compared to those from serum. The Pearson correlation coefficient was calculated to be 0.674, showing a moderate, positive correlation. This test also saw $t(20)=4.081$ and $p=0.000583$. The LPS challenge resulted in a minor increase in serum neopterin levels, with this effect not detected in the eluate ($t(2.38)=-0.554$, $p=6.27$). This suggested FP has the potential to be used as a new tool to detect neopterin but is limited in measuring subtle changes. Additional validation, utilizing a larger range of neopterin concentrations, is needed to provide further insight on this particular use of FP.

Fibroblasts exacerbate local inflammation and promote myeloid maturation during fibrotic skin wound healing

Arzina Jaffer¹, S. Sinha¹, L. Cao¹, R. Arora¹, H. D. Sparks¹, H. Robbins¹, K. Gowing¹, N. Rosin¹, M. S. B. Raredon², L. Niklason², G. Muench¹, J. Matyas¹, R. McCorkell¹, J. Biernaskie¹

¹Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary; ²Department of Biomedical Engineering and Department of Anesthesia, Yale University

Keywords: Single-Cell Genomics, Inflammation, Immune Profiling

Introduction: Signals emanating from damaged tissues activate resident fibroblasts and circulating immune cells for repair. While inflammatory milieu within healing wounds vary widely across species and with age, its determinants remain poorly understood because of a paucity of animal models that exhibit divergent immune responses to identical injury. Our previous work in adult reindeer provides such a model in which wounds on antler velvet regenerate while those on back skin form scars. **Materials & Methods:** To understand how local microenvironments shape the inflammatory response, we performed temporal single-cell immune profiling of circulating and wound-recruited immune cells across velvet and back skin (n=3, pooled sequencing). **Results:** Our analysis revealed a striking enrichment of CD45+ immune cells in back skin compared to velvet (71% vs 31%, p<10⁻¹⁷) 3 days post-wound. Pro-inflammatory CD68+NOS+ macrophages were enriched in back skin (1.45FC, p<10⁻²) whereas immunosuppressive CD68+NCF1+myeloids were enriched in velvet (10FC, p<10⁻²). In addition to preferential immune cell recruitment, neutrophils and macrophages were rapidly matured within back skin wounds relative to velvet. Myeloid cell maturity was identical within distal vessels perfusing the two wounds, suggesting that local (tissue-specific) factors modulated immune cell homing and myeloid maturation acutely after wounding. Intriguingly, back skin fibroblasts exhibited preferential enrichment for immunomodulatory cytokines (e.g., CCL2, CXCL3, PTGDS) at baseline which were further intensified during reparative healing. **Conclusions:** These findings highlight that exuberant immune response during wound healing drives fibrotic repair whereas restrained inflammation promotes regeneration. Fibroblasts may function as cellular orchestrators shaping recruitment and maturation of immune cells, thereby driving divergent healing outcomes.

Testicular organoids derived from induced pluripotent stem cells as a bioassay for modelling testicular development and function in vitro

Brandon Huynh¹, N. L. M. Lara¹, I. Dobrinski¹

¹Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada

Keywords: Testes, organoids, iPSCs

Organoids are 3-dimensional structures that emulate the architecture and functionality of organs in vitro. Testicular organoid applications are limited by the low availability of primary cells. We hypothesized that induced pluripotent stem cell (iPSC)-derived germ cells (GCs) and Sertoli cells (SCs) could be used to form organoids and reduce its reliance on primary cells due to the iPSC's capacity for expansion. As a baseline, rat primary cells were used to generate organoids, which were characterized after 3 weeks of culture by transmission electron microscopy and fluorescence staining. The primary cell population expressed cell type specific markers in the following proportions (mean \pm SD): GATA4 (SC; $92.2 \pm 1.2\%$, $n=3$), SOX9 (SC; $74.1 \pm 8.0\%$, $n=3$), VASA (GC; $1.7 \pm 0.3\%$, $n=3$); 3β HSD (Leydig cells; $2.6 \pm 0.7\%$, $n=3$) and SMA (PMC; $19.9 \pm 2.8\%$, $n=3$). In parallel, porcine piPSCs were cultured and induced to differentiate along SC and GC fates following published protocols. In SC differentiation, the proportion of cells expressing GATA4 increased from 0% in piPSCs pre-differentiation to 31% at Day 10, while WT1-positive cells increased from 30% in piPSCs to 70% at Day 10 of differentiation. These results suggest that the protocol increased expression of SC markers, though additional experiments are necessary to confirm derivation of SCs from piPSCs. Ongoing work aims to improve the differentiation protocol used for piPSC-derived GCs, which did not yet yield any VASA-positive cells. Optimizing the iPSC differentiation protocols is the first step toward our goal of generating testicular organoids entirely from iPSCs, enhancing the accessibility and versatility of the testicular organoid model.

Assessing the concentration at which loss of righting reflex occurs during carbon dioxide (CO₂) exposure

Brittany A Munro¹, D Merenick¹, J Gee², DSJ Pang^{1,3}

¹Veterinary Clinical and Diagnostic Sciences, Faculty of Veterinary Medicine, University of Calgary, Alberta, Canada; ²College of Engineering and Physical Sciences, Faculty of Engineering, University of Guelph, Ontario, Canada; ³Department of Clinical Sciences, Faculty of Veterinary Medicine, Université de Montréal, Québec, Canada

Keywords: euthanasia, carbon dioxide, LORR (loss of righting reflex)

Overdose with CO₂ gas is a common euthanasia method in laboratory rodents. However, unanswered questions remain regarding the potential for pain before loss of consciousness occurs. CO₂ gas concentrations of approximately 37% and above activate nasal mucosa nociceptors in rats. Estimates of CO₂ concentrations causing unconsciousness range from 21-39%, with variable methods used to identify loss of consciousness (e.g. nose touching floor, loss of righting reflex). Loss of righting reflex (LORR) is an appealing proxy for unconsciousness as it is strongly positively correlated with methods used to identify unconsciousness in humans. However, LORR methodology varies substantially between studies. The aim of this study was to determine the concentration at which CO₂ results in LORR using a standardized method. To improve repeatability and reduce data variability, a motor-driven rotating cylinder was used for testing. CO₂ (carried in O₂) was flowed into the cylinder and measured using a calibrated CO₂ analyzer. Sample size estimation indicated 28 adult Sprague-Dawley rats (to allow comparison of sexes). Rats were habituated to handling and the rotating cylinder before experimentation. Order of animal use was randomized and researchers controlling the flow rate were blinded to animal order. The chamber was rotated at 3 rpm (0.024 m/s rotational velocity). CO₂ concentrations were increased in a stepwise manner and held for one minute once stabilized, with LORR testing performed once ataxia was exhibited. Preliminary data analysis (n = 12, probit regression) indicates an effective dose (ED₅₀) of 30.4% (95% CI = 29.6-31.2) for LORR.

Determining the sequence of respiratory vs. cardiac arrest after magnesium sulfate euthanasia

Brittany A Munro¹, D Merenick¹, DSJ Pang^{1,2}

¹Veterinary Clinical and Diagnostic Sciences, Faculty of Veterinary Medicine, University of Calgary, Alberta, Canada ; ²Department of Clinical Sciences, Faculty of Veterinary Medicine, Université de Montréal, Québec, Canada

Keywords: euthanasia, magnesium sulphate, cardiac arrest

Overdose of sodium pentobarbital (PB) is an accepted injectable euthanasia method for a variety of mammals (cats, dogs, cattle, laboratory rodents etc.) and birds. A current global shortage of PB has created a need to identify alternatives. Magnesium sulfate (MgSO₄) is conditionally acceptable, when preceded by anesthesia, for euthanasia in some species under the AVMA euthanasia guidelines. Intravenous injection of MgSO₄ induces hypermagnesemia, resulting in blockade of peripheral neuronal transmission at neuromuscular junctions and muscle paralysis. Reports suggest that this leads to death through respiratory muscle paralysis and hypoxia, followed by cardiac arrest. However, other studies indicate that respiratory and cardiac arrest may occur simultaneously following injection. The aim of this preliminary study is to identify the sequence of events (respiratory paralysis and cardiac arrest) leading to death. Twelve adult surplus Sprague-Dawley rats (males and females) will be maintained under general anesthesia with isoflurane (1.7% end-tidal), followed by an intravenous bolus of MgSO₄ (800 mg/kg). The following physiologic variables will be recorded: ventilation (capnography, thoracic excursion), heart rate and rhythm (ECG), invasive arterial blood pressure. This study is ongoing. It is anticipated that the results of this study will help clarify the primary means by which overdose of MgSO₄ causes death.

Computational analysis of hematophagous parasite anticoagulants for new antiparasitic drug development

Caileah Ell¹, Kaylee Rich¹, James Wasmuth¹

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: hematophagy, coagulation, computation

Blood-feeding, hematophagy, is a method by which many parasites obtain nutrients from their hosts. To ensure a constant supply of blood, hematophagous parasites commonly target their host's blood coagulation cascade. Coagulation consists of the stepwise activation of proteins, resulting in the formation of a clot. Different groups of hematophagous parasites have evolved different strategies to interfere with the coagulation cascade. Blood-feeding nematodes are one of the greatest production-limiting pathogens faced by Canadian and global livestock industries. An over-reliance on a small number of anti-parasitic drugs has led to the widespread emergence of drug resistant nematodes. There is an urgent need to discover targets for new drugs and vaccines. The anticoagulant proteins secreted by nematodes have attracted considerable interest. A few have been identified in hookworms and it is unknown if they are present in other species of blood-feeding nematodes.

We took a computational approach to compare known nematode anticoagulant proteins to proteins in other species of nematode. We used sequence similarity searches to identify potential orthologues. Our efforts were confounded by numerous inaccuracies in the published genome assemblies and annotations of important parasitic nematode species. These must be corrected. Nevertheless, we did find some potential anticoagulant orthologs with promising structural similarities. Our next step is to characterise nematode anticoagulants at a more detailed level. We will identify short linear motifs (SLiMs) that discriminate anticoagulants from other proteins. These motifs can be used to find other potential anticoagulants which may be promising targets for the next generation of antiparasitic drugs.

Selective dry cow therapy practices on Canadian dairy farms

Christina A. Nykyforuk, Zhanika J.D. Gimeno, Lian J.J. Barkema, Kayley D. McCubbin, Ellen de Jong, Herman W. Barkema

Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary. 3330 Hospital Dr NW, Calgary, AB, T2N 4N1

Keywords: Dry cow therapy, antimicrobial stewardship, dairy cow

Previously, on Canadian dairy farms, antimicrobial administration in all cows at drying off has been used to treat and prevent intramammary infections (IMI). Drying off is the beginning of the dry period, with cessation of milk production between one lactation cycle ending and giving birth to initiate a new cycle. However, blanket use of antimicrobials may no longer be necessary on all farms, as the incidence and prevalence of intramammary infection has decreased. Selective dry cow therapy (SDCT) aims to prevent and cure IMI by selecting cows for treatment based on several criteria, including a combination of milk culture results, somatic cell count, and clinical mastitis (CM) history. Therefore, SDCT can reduce on farm antimicrobial use (AMU), potentially contributing to antimicrobial resistance mitigation, and should be investigated further. To gain a deeper understanding regarding dry off AMU and selection methods, questionnaires answered by Canadian dairy producers during 2019 and 2020 were analyzed using R and R studio. Out of 140 participating Canadian dairy producers, 36% used SDCT. This highlights an increased adoption of SDCT, and higher numbers than previously reported (16%) in Canada. Median antimicrobial coverage on SDCT farms was 50% (ranging from 3-99%). The most important criterion considered when determining which cows to treat with antimicrobials at dry off was somatic cell count (70%), followed by CM history (64%), and milk culture (20%). SDCT can lead to AMU reductions and result in improved antimicrobial stewardship. The increase in SDCT shows progress in the Canadian dairy industry antimicrobial stewardship efforts.

A Retrospective Study on the use of the Health Belief Model in Predicting Rabies Mitigation in Bhutan

Daniel Hung, Louise Caplan, David Hall

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: Health Belief Model, Rabies, Mitigation

Introduction: Dog-mediated rabies challenges endemic regions of Bhutan with public health risks and economic losses. Mitigation efforts can be assessed with the Health Belief Model (HBM) which theorizes that an individual weighs the impact of an action's risks and benefits on their personal health; this in turn affects intention to engage in health mitigation. The aim of the study (hypothesis) was to identify whether the HBM could be used to predict intention to vaccinate dogs and visit a medical office if bitten by a rabid dog. Methods: To test our hypothesis, a retrospective cross-sectional study was conducted using secondary questionnaire data collected in Bhutan from 562 respondents by Rinchen, et al. (2020). Aggregated variables were used to capture perceptions of benefits and risks. Perception of risk of rabies was represented by a respondent's aggregated understanding of the outcome of rabies; perception of benefits was represented by aggregated acknowledgement that vaccination prevents rabies. Respondent's perceptions and intention to mitigate were compared between participants and non-participants of rabies control education programs (rabies awareness (RAP) and animal health training (AHT)). Results: Binary logistic regression identified association of high perceived benefit of rabies mitigation and vaccination of dogs or visiting a medical office after a rabid dog bite. Additionally, respondents who participated in AHT or RAP were more likely to express perceived benefits than those who did not participate. Conclusions: HBM was useful to identify benefits of health education programs and associated effects on rabies health mitigation, including intention to vaccinate dogs against rabies.

Feeder Layers and Exosomal Exchange in Porcine Germ Cell Co-Cultures

Danielle Korsrud¹, Shiama Thiageswaran², Dr. Ina Dobrinski^{2,3}

¹Cumming School of Medicine, University of Calgary, ²Department of Biochemistry & Molecular Biology, Faculty of Medicine, University of Calgary, ³Department of Comparative Biology & Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary.

Keywords: Testis, cell culture, exosomes

Background

Spermatogonial stem cells (SSCs) can be used to treat male infertility, but expansion is necessary. The overall objective of the study is to compare proliferation of germ cells co-cultured with different feeders and characterize exosomal cargo from feeders and co-cultures. We hypothesized that PMCs and/or TECs will be at least as supportive as feeders reported in the literature, and exosomal cargo will differ between feeders.

Methods

Sertoli cells (SCs), peritubular myoid cells (PMCs), and testicular endothelial cells (TECs) were passaged to 83-96% purity, assessed by immunofluorescence using cell-type specific markers. Pig fetal fibroblasts (PFFs) were obtained from 40- day old porcine fetuses. Feeders were mitotically arrested and seeded with prepubertal porcine germ cells. Proliferation was assessed at weekly intervals using Edu, and stem cell maintenance was assessed through qRT-PCR for stem cell specific transcripts. Exosomes were isolated from feeders and co-cultures via ultrafiltration and size-exclusion chromatography before being characterized by TEM.

Results

Proliferation of germ cells after 1 week and 2 weeks are significantly higher ($p < 0.05$) on PMCs, PFFs, and SCs compared with TECs and control conditions: $14.7 \pm 1.25\%$ and $13.7 \pm 1.53\%$ on PMCs, $15.8 \pm 1.8\%$ and $14.3 \pm 1.30\%$ on PFFs, and $14.6 \pm 2.71\%$ and $14.0 \pm 0.55\%$ on SCs, vs. $10.6 \pm 2.12\%$ and $9.3 \pm 0.93\%$ on TECs, and $7.5 \pm 1.31\%$ and $5.4 \pm 0.84\%$ in feeder-free controls, respectively ($n=3$; mean \pm SD). Exosome isolation and characterization experiments are ongoing.

Discussion

Proliferation data support the hypothesis. Identifying the most supportive feeder(s) can inform feeder- free expansion; as can exosomal characterization, which will serve to investigate the mechanisms underlying the benefits of using feeder layers in co-culture conditions.

Does bat consumption of insect pests result in a mutualistic relationship between beef cattle and bats?

Derrick Zhang¹, Mathieu Pruvot¹

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: Mutualism, foraging behavior, agroecosystems

Insectivorous bats provide important ecosystem services in agricultural systems, including the consumption of insect pests. Bat consumption of blood-feeding insects which parasitize cattle may mitigate production loss caused by these insects, resulting in a mutualistic relationship. We investigated whether bat foraging behaviour is associated with the occurrence of cattle and blood-feeding insects on pastures across WA Ranches at UofC. To assess co-occurrence of bats and cattle, sixteen pastures with or without cattle were sampled using four monitoring stations composed of two trail cameras and one autonomous recording unit (ARU), rotated every 3-4 days between locations from May to August. This resulted in 6 sampling periods for each location. Light insect traps were concurrently deployed for 24 hours to determine the composition and relative abundance of insect populations. Logistic and negative binomial regression models will be used to analyze bat presence/absence and call frequency against cattle occurrence and other covariates. Based on the observed temporal patterns of blood-feeding insect abundance, we expect a weak association between bat and cattle occurrence in May and June as biting insect abundance is still low, and an increase in bat foraging around cattle in July and August when biting insect abundance is greater. Understanding foraging behaviors of bats in relation to blood-feeding insects has the potential to inform the surveillance of biting insects and arthropod-borne pathogens, as well as to identify cattle production practices that support bat conservation and biting insect control.

Utilizing ITS-2 nemabiome metabarcoding to investigate the species composition of cyathostomin communities after ivermectin and moxidectin treatment

Drue Nooyen¹, Libby Redman¹, Ashley Steuer², Alyssa Carpenter⁴, Haley Anderson⁴, Holli Gravatte⁴, Craig Reinemeyer³, Stefan Gavriiuc⁵, Jocelyn Poissant⁵, Martin Nielsen⁴, John S. Gilleard¹

¹Department of Comparative Biology and Experimental Medicine, University of Calgary, 3330 Hospital Drive, Calgary, AB, Canada. ²Texas Tech University, Amarillo, USA. ³East Tennessee Clinical Research, Rockwood, USA. ⁴University of Kentucky, Lexington, USA. ⁵Department of Ecosystem and Public Health, University of Calgary, 3280 Hospital Drive, Calgary, AB, Canada.

Keywords: Cyathostomin, ITS-2 rDNA, Nemabiome

Gastrointestinal parasitic nematodes are ubiquitous to equine populations worldwide. Cyathostomins, small parasitic worms of the family Strongylidae, are extremely common and can cause equine disease and even fatalities. Management of cyathostomin infection via routine treatment with anthelmintic drugs has resulted in the emergence of widespread resistance to these drugs. There is little current information on the species of cyathostomin that are developing resistance to macrocyclic lactone drugs. The aim of this study was to use ITS-2 rDNA metabarcoding to investigate the species composition of cyathostomin populations at several time points after ivermectin and moxidectin treatment to investigate which species are developing macrocyclic lactone resistance. Thirty-six horses, aged 2-5 years, and naturally infected with equine cyathostomins in Kentucky USA, were randomly assigned to three treatment groups: Ivermectin (200 µg/kg), moxidectin (400 µg/kg), and untreated control. Pools of adult worms extracted from the cecum, ventral colon, and dorsal colon from each group at 2 weeks and 5 weeks post treatment underwent genomic DNA preparation and nemabiome metabarcoding on the internal transcribed spacer 2 region (ITS-2). A total of fifteen different species were identified in the study across all animals with the majority of the species diversity found in the drug-free animals (mean number of species: control group = 10.8, ivermectin group = 7.8, moxidectin = 5.5). In particular, *Coronocyclus coronatus*, *Cylicocyclus nassatus*, *Cyathostomum catinatum* and *Cylicocyclus insigne* predominate in both control and drug-treated animals and the proportions of *C. insigne* were significantly higher in the ivermectin and moxidectin treated animals.

Tick Surveillance Systems: A Scoping Review

Elise Romney¹, Akaysha Envik¹, Susan Cork¹, Isabelle Couloigner¹, Heather Ganshorn², Sylvia Checkley¹

¹University of Calgary, Faculty of Veterinary Medicine ²University of Calgary, Libraries and Cultural Resources

Keywords: Tick surveillance, *Ixodes scapularis*, One Health

Tick surveillance is important to detect new ticks or changes to tick occurrence and distribution within a region. Tick surveillance systems also provide a framework from which to assess tick-borne pathogens. This information can be used to launch further investigation and inform risk assessments for tick-borne disease in people and animals. For example, many tick surveillance systems focus on blacklegged ticks, like *Ixodes scapularis*, that can carry *Borrelia burgdorferi*, the causative agent of Lyme Disease. Lyme Disease is a prominent One Health problem, impacting the health of humans, animals, and the environment. The purpose of this scoping review is to describe the characteristics of tick surveillance systems globally from the 1960s onwards. The scoping protocol follows PRISMA guidelines. After a preliminary search of MEDLINE, BIOSIS Previews, CAB Abstracts, ProQuest Dissertations, and the Web of Science Core Collection databases, 2333 articles were selected for title and abstract screening, with 554 moving on to full-text screening using Covidence systematic review software, Veritas Health Innovation, Melbourne, Australia. Articles published prior to 1960 were excluded, and only articles written in English that described surveillance systems were included. A series of descriptive statistics were compiled upon completion of article selection. Information regarding the type of surveillance, method of sample collection, key findings, methods of reporting collected data, and the primary purpose of the surveillance system. The extracted data was summarized by geographical location for clarity. This information will be used to help direct changes in tick surveillance in Western Canada.

Do bones that grow faster heal faster?

Emma Foxcroft¹, C.M. Unger², C. Rolian²

¹Doctor of Veterinary Medicine Program, Faculty of Veterinary Medicine, University of Calgary;

²Department of Comparative Biology and Experimental Medicine, University of Calgary

Keywords: Longshanks mouse, Fracture healing, Bone strength

Fracture repair involves the reactivation of endochondral ossification, the mechanism responsible for longitudinal bone growth during development. The Longshanks mouse was selectively bred for longer tibiae and have tibiae that are 13-15% longer than random-bred Control mice. These bones achieve this remarkable increase in length through 15-20% faster growth. Since fracture repair involves the activation of the same processes that drive bone development, the rapid bone growth in Longshanks could have a significant impact on their bone repair rate. This ongoing study aims to answer the question of whether bones that grow faster also heal faster. To study bone healing in Longshanks, three-point bending will be used to generate closed mid-diaphyseal transverse fractures in Longshanks (n=10 in each of two independent lines) and Controls (n=10). *In vivo* microCT scans will be obtained at day 7, 10, 14, 21 and 42 post fracture, and will be used to calculate the fracture callus volume and bone mineral density at different time points throughout healing. By comparing longitudinal scans between the experimental groups, we will be able to determine the timing of healing events, including whether tissue mineralization is more advanced in Longshanks compared to Controls. At day 42 the healed bone will also undergo three-point bending to determine the strength of the repair site in both Controls and Longshanks. In the coming weeks this study will allow us to explore the potential link between the rates of bone growth and those of repair and clarify their relationship.

Cathelicidin promotes secretion of mucus associated proteins in colonic goblet cells through increased reactive oxygen species (ROS)

Geeta Kilari¹, Graham Blyth², Eduardo R Cobo²

¹ Department of Biological Sciences, Faculty of Science, University of Calgary

² Production Animal Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: cathelicidins, reactive oxygen species, goblet cells

The colonic mucus secreted by goblet cells forms a mechanical and immunological barrier that aids in detecting and eliminating pathogens in the gut. Cathelicidins, produced by the epithelium, are crucial microbicidal peptides in the gut, as previously evidenced by an increased enteropathogenic burden in cathelicidin knock-out mice (*Camp*^{-/-}); however, whether cathelicidin mediates the mucus layer is unknown. We hypothesize that exogenous cathelicidins (LL-37) have immunomodulatory roles that enhance the gut epithelial mucus layer from human goblet-like (LS174T) cells through Reactive Oxygen Species (ROS). To determine if cathelicidin modulates mucus secretion in colonic goblet cells, we evaluated the ability of synthetic human cathelicidin (LL-37) to stimulate the secretion of goblet cell-specific mucus associated trefoil factor 3 (TFF3) and resistin-like molecule beta (RELM β) in human goblet-like (LS174T) cells with ELISA. Non-cytotoxic doses of LL-37 (<20 μ M) increased the rapid (2 hour) secretion of TFF3 and RELM β , a response that was reduced in the presence of a ROS inhibitor (DPI). These findings reveal that the absence of ROS hinders LL-37's activity in upregulating secretion in goblet cells, implying that LL-37 increases goblet cell secretion via ROS. Additionally, *in vivo* effects of cathelicidins on ROS were observed with luminescent ROS dye (L-102), where *Camp*^{-/-} mice were challenged by *Citrobacter rodentium*, which revealed a deficiency in ROS production in the distal colon at the peak of infection (7 days) compared with wild-type littermates. These findings reveal a novel protective immunomodulatory function of cathelicidin in strengthening the colon mucin barrier by increasing goblet cell secretion via ROS.

Sequencing complete isotype-1 and isotype-2 β -tubulin genes from BZ resistant isolates of *Ancylostoma caninum*.

Hannah Horvath, Arianna Morosetti, John Gilleard, Abhinaya Venkatesan, Libby Redman

Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary

Keywords: *Ancylostoma caninum*, benzimidazole resistance, β -tubulin gene

Introduction: An increase in the drug resistance of *Ancylostoma caninum*, a canine hookworm, has recently been a growing concern. A common mutation at isotype-1 β -tubulin gene codon 167 is found to be responsible for benzimidazole resistance in most hookworm populations. However, several phenotypically drug resistant populations lacking this specific mutation, or other common mutations in strongylid nematode species at codons 198 and 200, have been identified. In order for these hookworm populations to be benzimidazole resistant, there are likely other mutations present in their genomes. The aim of this project is to investigate whether there are other non-synonymous mutations present in the open reading frame of the isotype-1 β -tubulin gene that could be responsible for the benzimidazole resistant phenotype of these strains. **Materials & Methods:** The near full-length isotype-1 β -tubulin gene from several resistant and susceptible *A. caninum* populations was PCR amplified. The samples being investigated were obtained from the USA and had an absence or very low frequency of the isotype-1 β -tubulin gene codon 167, 198, and 200 mutations. Cloning of the isotype-1 β -tubulin gene was performed, as well as sanger sequencing from multiple clones from each population. **Results:** From sanger sequencing, six sequences from three different populations were obtained. The sequences showed at least three different haplotypes present. **Conclusion:** The results suggest potential mutations causing drug resistance may be present in the β -tubulin gene of the samples, however, only a small number of sequences were analyzed, therefore, additional sequencing will need to be performed to confirm this.

Evaluation of Genetic Basis of Degenerative Heart Conditions in Vancouver Island Marmots

Jaimie Warren¹, Jocelyn Poissant², Malcolm McAdie³, Stephen Raverty⁴, Douglas Whiteside^{2,5}

¹Faculty of Veterinary Medicine, University of Calgary; ²Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary; ³Marmot Recovery Foundation; ⁴Animal Health Center, B.C. Ministry of Agriculture and Food; ⁵The Calgary Zoo

Keywords: Quantitative genetics, Conservation, Cardiomyopathy

Vancouver Island marmots (*Marmota vancouverensis*) are Canada's most endangered mammal and are classified as critically endangered. As a result, a multi-institutional conservation breeding program was established in 1997. Within this program, degenerative heart disease has been diagnosed in over 45% of adult deaths. These cardiac changes include dilative cardiomyopathy (DCM) and fibrosis, which are rarely noted in deaths in wild individuals. Due to this high prevalence, several genetically valuable individuals are lost annually from the program. We hypothesized that there is a genetic basis for heart disease and its expression may be precipitated in combination with environmental factors. To determine the potential heritability of these diseases, three pedigree-based animal models were run using the package MCMCglmm in R: one for DCM, one for fibrosis, and one combined model. Each model was composed of 10^6 iterations with a thinning interval of 100 and a burn-in period of 200,000 iterations with an inverse-scaled chi square prior. The posterior modes and their 95% credible intervals for the heritability of DCM, fibrosis and both traits combined were 0.0016 [3.87×10^{-9} , 0.42], 0.0032 [2.64×10^{-8} , 0.64] and 0.0015 [2.95×10^{-9} , 0.51], respectively. This indicates that the heritability values for these diseases are likely very close to zero and rather than having a heritable basis, could be due to environmental factors, fixed deleterious alleles, or cryptic inbreeding. Determining these diseases are not heritable not only provides important insight into their basis but will also guide future research on Vancouver Island Marmots.

Building a 3D Printed Experimental Apparatus for Assessing Loss of Righting Reflex in Laboratory Rodents

Julia Gee¹, B. Munro², D. Merenick², & D. Pang^{2,3}

¹College of Engineering and Physical Sciences, Faculty of Engineering, University of Guelph, Ontario, Canada; ²Veterinary Clinical and Diagnostic Sciences, Faculty of Veterinary Medicine, University of Calgary, Alberta, Canada; ³Department of Clinical Sciences, Faculty of Veterinary Medicine, Université de Montréal, Québec, Canada

Keywords: 3D printer, LORR, CO₂

There is an ongoing debate regarding the humaneness of using carbon dioxide (CO₂) gas to euthanize rodents¹. The goal of this study was to identify the concentration at which CO₂ gas induces loss of righting reflex, a proxy for loss of consciousness, in both laboratory rats and mice². Humans and rats both have nociceptors in their nasal and ocular epithelia that are activated by CO₂ at similar concentrations³. In humans, CO₂ is reported as painful at approximately 50% concentration.⁴ Identifying if the concentration at which rats lose their righting reflex is above or below this threshold has important welfare implications for CO₂ euthanasia. Through a trial- and-error building process, a motor-driven apparatus allowing tube rotation, gas inflow, outflow, and CO₂ sampling was designed and manufactured.

In creating the experimental apparatus for rats and mice, a 3D printer with plastic filaments (PLA) and SOLIDWORKS 2020 software were used to design and print the components. These included two endcaps to stabilize a Plexiglas tube, two circular stoppers to control the diffusion of both oxygen and carbon dioxide into the apparatus and connect to an axle for tube rotation, laboratory gas valves for gas flow into and out of the endcaps, and motor stands to support the motor. Testing consisted of placing weights (approximating mouse and rat masses) into the species-specific tube sizes and ensuring rotation was smooth at 3 rpm and above⁵. After encountering smoke with a worm-gear DC Motor and battery pack, we transitioned to using a wall outlet and a stepper DC motor to achieve consistent power and rpm.

By altering the design of parts, a reliable and efficient motor-driven cylinder was created for both laboratory rats and mice.

¹Hawkins P. 2016 A Good Death? Report of the Second Newcastle Meeting on Laboratory Animal Euthanasia. *Animals (Basel)* 6(9):50

²Franks NP. 2008 General anaesthesia: from molecular targets to neuronal pathways of sleep and arousal. *Nat Rev Neurosci* 9:370-386.

³Peppel, P. 1993 Responses of rat medullary dorsal horn neurons following intranasal noxious chemical stimulation—Effects of stimulus intensity, duration and interstimulus interval. *J. Neurophysiol* 70: 2260–2275.

⁴Danneman, P.J. 1997 S.O. Humane and practical implications of using carbon dioxide mixed with oxygen for anesthesia or euthanasia of rats. *Lab. Anim. Sci* 47:376–385.

⁵Baker R. 2014 Altered activity in the central medial thalamus precedes changes in the neocortex during transitions into both sleep and propofol anesthesia. *J Neurosci* 34(40):13326-35.

Feasibility Assessment on Wearable Technology for Studying Neonatal Beef Calves

Justin Ross^{1, 2}, Christy Goldhawk², Rachael Coon³, Ed Pajor², Claire Windeyer²

¹Faculty of Engineering, University of Calgary; ²Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary; ³Davis, University of California

Keywords: Wearable Technology, Feasibility, Calf Health

This research project investigates device feasibility for studying neonatal beef calves in a range environment. The feasibility evaluation investigated data validity, data reliability, effects of device on cattle, and effects of animal/environment on devices. There were 10 Lotek calf collar and cow ear tag pairs used on 10 cow-calf pairs for a period of 21 days in a small pasture. Collars were designed to collect and store GPS, tri-axle accelerometer, and proximity data, and ear tags designed to function as proximity beacons only. Live observations of animal location, proximity, and behaviour were collected during the 21 days to evaluate device accuracy and validity for behavioural classification models. After completion of the trial, evaluation of device condition and animal health resulted in 1 collar requiring repair due to torn collar material, and no animals required treatment. Eight calves, however, had hair loss around their necks and five cows had ear tag holes that were not fully healed. These results indicate Lotek collar/tag devices may be physically durable and are not associated with severe health issues for cattle. Anticipated future results include further evaluation of device feasibility through analysis of data integrity. Additionally, if collar data is determined to be valid and reliable, it will be used for evaluating validity of behavioural classification models. Validity of these models will be assessed by comparison with live animal observations. Such models would allow for future automation of continuous behavioural observation of neonatal beef calves in range environments.

Development of a protocol for recovering peripheral blood mononuclear cells from blood of muskoxen (*Ovibos moschatus*)

Katrine Gillett^{1,2}, Susan Kutz¹, Craig Jenne^{1,3,4}, Douglas Whiteside^{1,5}

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary; ²Alberta Innovates; ³Department of Microbiology, Immunology and Infectious Disease, Faculty of Medicine, University of Calgary; ⁴Snyder Institute for Chronic Diseases, ⁵Calgary Zoo.

Keywords: Peripheral Blood Mononuclear Cells (PBMC), Density Gradient Centrifugation, Muskoxen (*Ovibos moschatus*)

Muskoxen are an indispensable part of the Arctic ecosystem that provide food security and socio-cultural enrichment to numerous Indigenous communities. As the Arctic climate changes, information on disease prevalence and susceptibility to disease becomes increasingly important to maintaining healthy muskox populations. Emergence of new pathogens such as *Erysipelothrix rhusiopathiae* and *Brucella suis*-biovar-4 observed in combination with large-scale mortality raises questions to how effectively their immune system is responding. This project aims to identify the density gradient medium required for species-dependent separation of peripheral blood mononuclear cells (PBMCs) in muskoxen, to attain cells for future immune stimulation studies. Fresh blood collected from a captive muskox was separated within 2hrs of drawing to maintain PBMC viability. Density gradient centrifugation was carried out on a range of Ficoll-Paque density gradient medias, including 1.084g/mL, 1.082g/mL, 1.080g/mL, and 1.077g/mL. A standard density gradient for isolating human PBMC is 1.077g/mL, and 1.084g/mL for bovine and other domestic species. It is expected the optimal density gradient required for muskox will be higher than 1.077g/mL, comparable to bovine, which are both in the Bovidae family. Parameters of blood volume and centrifuge tube diameter were selected first to maximize reproducibility of isolation. Viability was assessed using Trypan blue exclusion. Functionality was assessed measuring IL-6 protein production through western blotting, from PBMCs at baseline and PBMCs stimulated with lipopolysaccharide. Cell viability was 100% for all isolates prior to cryopreservation. A density of 1.082g/mL yielded the greatest separation of PBMCs at 1×10^6 cells/mL blood. Functionality of cells isolated is to be determined.

Assessing the accuracy of CowManager ear tags in beef bulls by comparison with direct observation

Lauren Stoffregen, E. Pajor, K. Orsel, and J. Pearson

Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada

Keywords: bull, behaviour, validation

The eating, rumination, and activity measurements of CowManager ear tags have been validated in dairy and feedlot cattle, but not beef bulls. The objective was to validate CowManager ear tags by comparison with the more time consuming direct behavioural observations. Twelve bulls had a CowManager ear tag placed on Day 1 and were housed together for 14 days in a large pen. Four, 1-hr videos were collected each day, giving three hours of video per bull. Scan data was collected for each bull every 5 minutes during 1-hr periods. One bull was excluded because of sensor malfunction. Behaviours were recorded for scan and continuous video data and grouped into the following mutually exclusive categories: ruminating, eating, no activity, and general activity. Concordance correlation, sensitivity, specificity, and predictive values were calculated by comparing CowManager with direct observations. Concordance correlation for video data and CowManager was 0.93 (CI: 0.86-1.00; $P < 0.001$), 0.90 (CI: 0.80-1.00; $P < 0.001$), 0.81 (CI: 0.64-0.99; $P < 0.001$), and 0.46 (CI: 0.16-0.77; $P = 0.003$) for eating, ruminating, no activity, and general activity respectively. As expected, the scan data was less correlated with the technology in all categories because of the instantaneous nature of the sampling method. Measurement of eating, ruminating, and inactivity is promisingly accurate. Although significantly correlated, the accuracy of activity measurement could be improved. Sensor malfunction, behaviours associated with ear infections, and tag location on the ear may disrupt activity measurement and contribute to variability. CowManager shows promise as an effective tool in beef bull behaviour research.

Epimorphic regeneration of reindeer antlers is enabled by an immune privileged microenvironment

Leslie Cao¹, S. Sinha¹, A. Jaffer¹, R. Arora¹, H.D. Sparks¹, N. Rosin¹, G. Muench¹, J. Matyas¹, R. McCorkell¹, J. Biernaskie¹

¹Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary

Keywords: Single-Cell Genomics, Tissue Regeneration, Mesenchymal Cells

Introduction: Seasonal regeneration of reindeer antlers is a unique mammalian epimorphic process in which new tissue is generated from permanent skull protuberances ('pedicles'), and fuelled by rapid proliferation within the pedicle periosteum. To understand the cellular composition and molecular programs underlying this remarkable multilineage tissue morphogenesis, we performed a comparative transcriptomic analysis of reindeer antler pedicle. *Materials/Methods:* Single-cell RNA-Seq was performed on biopsies of adult reindeer pedicle during initiation of antler growth and compared to skin profiles from resting reindeer back and antler ('velvet') as these sites are differentially primed to elicit fibrotic or regenerative healing following injury, respectively. *Results:* Relative to back skin and velvet, pedicle exhibited unique stromal and immune landscapes. Unbiased classification of pedicle fibroblasts using machine-learning algorithms trained on 'regenerative' or 'pro-inflammatory' fibroblast states predicted a complete dominance of regeneration-competent fibroblasts. We also observed a relative paucity of immune cells, including the absence of pro-inflammatory IL1 β + macrophages that comprised 4% and 17% of total back skin and velvet cells, respectively. While back skin stromal-immune interactions were dominated by inflammatory fibroblast signalling, pedicle was repatterned to favour stromal-epithelial crosstalk through ligands involved in induction of appendage formation (e.g., IBSP, INHBA, TNC, PTN). *Conclusions:* Our previous work highlights enrichment of pro-inflammatory fibroblasts as a key impediment to skin regeneration within the immune milieu. Here, we extend this concept to epimorphic regeneration, and suggest their absence in pedicle may be critical for establishing an immune-depleted environment that escapes immune surveillance to allow extensive tissue growth, reminiscent of neoplasia.

Examining factors used by Canadian dairy farmers to make treatment decisions of clinical mastitis

Lian J.J. Barkema, Ellen de Jong, Christina Nykyforuk, Zhanika Gimeno, Kayley D. McCubbin, Karin Orsel, Herman W. Barkema

Dept. of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada

Keywords: antimicrobial use, dairy cattle, clinical mastitis

Clinical mastitis (CM) is an inflammation of the udder, which can be painful and affect milk quality. CM is the most prevalent disease in dairy cattle and therefore a highly costly disease to the Canadian dairy industry. It is frequently treated with antimicrobials and is the most important reason for antimicrobial use on dairy farms worldwide. Considering the link between antimicrobial use and antimicrobial resistance, it is important to reduce antimicrobial use in livestock. Therefore, selective, rather than blanket treatment with antimicrobials is encouraged. It is not known how dairy farms in Canada selectively treat cows with CM. Questionnaires were administered in 2019 and 2020 to 140 farms in 5 provinces (Alberta, British Columbia, Nova Scotia, Quebec, and Ontario) to characterize factors influencing CM treatment decisions. Adoption of selective treatment of CM varied across provinces, most notably between Quebec (78%) and Alberta (45%) ($X^2 = 4.57$, $df = 1$, $P = 0.03$). Of the farms using a selective treatment protocol, farmers indicated that suspected bacteria (63%), high somatic cell count (52%), and mastitis history (40%) were important or very important decision factors. These results show there is an interprovincial gap in selective CM protocol uptake and indicate room for improved antimicrobial stewardship. Culture of CM cases should be encouraged as well as the use of other decision factors such as somatic cell count and mastitis history.

Costs and benefits of domestic carnivore ownership in USA, Canada and Europe: a systematic review

Louise Caplan¹, Sepideh Souril², Heather Ganshorn³, Guillaume Lhermie^{2,4}

¹Department of Biological Sciences, University of Calgary; ²The School of Public Policy, The Simpson Centre, University of Calgary; ³Libraries and cultural resources, University of Calgary; ⁴Department Faculty of Production Animal health, Veterinary Medicine, University of Calgary.

Keywords: Domestic carnivores, health benefits, OECD countries

Domestic carnivores (dogs and cats) are an important part of millions of households in a large number of OECD countries due to their positive outcomes on the health of individuals. However, the diet of carnivores contains an abundance of animal protein, the production of which can have a high environmental impact, especially in terms of water consumption and greenhouse gas emissions. The objective of this project was to evaluate the environmental costs compared to the health and societal benefits of carnivores. Part 1 of this review included conducting a systematic review to identify the physical and mental health benefits for individuals thanks to carnivores on 5 databases (PubMed (MEDLINE), CAB Abstracts, Scopus, Psycinfo and Environment complete). To be included, it was required that the study was original research conducted in an OECD country in English and published between 2005-2021. The screening was performed by two reviewers and the conflicts were resolved by a third reviewer. Of the 4767 studies imported for screening, 1535 were removed as duplicates. From the preliminary title and abstract screening, 341 studies continued to the full text review. Although the findings were not exclusively in favour of health benefits, the majority of studies indicated a certain benefit associated with carnivores. These benefits included increased physical health, mainly due to walking, and improved mental health, with a reduction in depression and anxiety. Part 2 of this search is an ongoing review on the environmental impact of carnivores in order to later perform a cost benefit analysis.

An experimental model of cryptosporidiosis in neonatal calves results in exaggerated systemic weakening and diarrheic enterocolitis

Mackenzie Campsall, Steffany Schluessel, Lisa Gamsjaeger, Claire Windeyer, Eduardo R Cobo

Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: cryptosporidium, enterocolitis, neonates

Animal models used to study cryptosporidiosis, a zoonotic diarrheic disease caused by *Cryptosporidium parvum*, have largely focused on the challenge of calves 7-14 days old. To evaluate if younger populations lacking mature immune defenses are particularly susceptible to the disease, individually housed neonatal (2-5 days old) calves (n=7) were exposed to orally administered *C. parvum* oocysts (5×10^7). Five age-matched calves remained as uninfected controls. All calves were monitored daily for clinical signs of cryptosporidiosis (i.e., diarrhea, mentation changes) and humanely euthanized six days post-inoculation (DPI) for post-mortem enterocolitis examination. Calves challenged by *C. parvum* exhibited a tendency for tachypnea and higher temperatures compared to uninfected calves, with marked fever observed by the study conclusion (DPI6). Diarrhea was present in *C. parvum* challenged calves for the duration of the study which gradually increased in severity until euthanasia. Both groups exhibited a similar ability to stand, but challenged calves became weaker, lethargic, depressed, anorexic, and dehydrated by DPI5-6. Microscopic analysis of the gastrointestinal tract in *C. parvum* challenged calves revealed epithelial erosion at the apex of the colonic crypts and ileum villi with hemorrhage and increased leukocyte infiltration in the lamina propria. This study demonstrated an experimental infection with *C. parvum* in neonatal calves that anticipates a higher mortality rate than observed in older calves because of broader systemic symptoms. This reproducible model of cryptosporidiosis in highly susceptible neonatal populations contributes to the further understanding of this parasitic disease and will aid in the development of future vaccines and therapeutics.

Effects of an innovative inhaled corticosteroid therapy on VO₂peak in horses with moderate asthma

Dr. Renaud Leguillette, Dr. Julia Israel, Madeline Browne, Annie Kelly.

Department of Veterinary Clinical & Diagnostic Sciences, Faculty of Veterinary Medicine, University of Calgary

Keywords: Equine, Asthma, VO₂peak

Introduction: A novel inhaled corticosteroid (InhC) is being used to treat severe asthma in horses by nasal administration. We aim to assess the effects of InhC on lung inflammation, airway mucous accumulation, and aerobic capacity in horse athletes with moderate asthma. The research gap on treatment for moderate asthma, and the potential for the InhC to avoid classical side effects of corticosteroids highlights the importance of this study. **Materials & Methods:** Randomized, controlled, parallel design using 11 Thoroughbred horses diagnosed with moderate asthma (lung inflammation quantified by cytology of a bronchoalveolar lavage, tracheal mucous visualized by endoscopy, cough and nasal discharge). Horses were blindly split into control and treatment groups, each which received 10 days of administration. Nasal discharge, coughing, and respiratory rate were recorded in conjunction. All horses performed a baseline and post-treatment 400m maximal VO₂peak test at High River Rodeo Grounds. During exercise, respiration and gas metabolism were measured using a unique equine mask developed by Dr. Leguillette. ECG data was recorded using Televet, and race speed and distance recorded using a Polaris timing lights system. Blood lactate and ammonia was also quantified post-exercise. **Results:** Results have not been compiled at this time. We hypothesize that the InhC will decrease lung inflammation and tracheal mucous and improve the peak aerobic capacity of the horses. **Conclusion:** Analysis has not been completed. A significant difference between groups will have positive implications on the use of this product in treating a widespread health issue in performance horses in Alberta.

Hardware development for rodent home-cage monitoring

Madina Shayne¹, L. Molina², K. Murari³, P. Whelan¹, M. Ungrin¹

¹Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary; ²Department of Clinical Neurosciences, Cumming School of Medicine, University of Calgary; ³Department of Electrical and Software Engineering, Schulich School of Engineering, University of Calgary

Keywords: scalable, home-cage, monitoring

Home-cage monitoring is a useful tool for collecting research data while animals are in familiar environments and for monitoring animal welfare. While there exist cage-side monitoring systems, many are expensive or require invasive animal procedures, cage modifications, or specialized enclosures. This project developed hardware for three camera options: Raspberry Pi camera module, Lucid Vision Labs Phoenix PHX016S camera, and ESP32-CAM module. The hardware for the three systems allows the cameras to be placed inside the home-cage, secured to the lid, and expose their power cables without modifications to the plastic cage. These camera systems provide inexpensive and scalable methods of continuous home-cage monitoring. Models were developed using SolidWorks and 3D printed with PLA filament. The hardware for the Raspberry Pi camera system involves a holder for the Raspberry Pi 4 Model B placed on top of the lid, a cover, and a camera module holder that attaches to the lid from inside the cage. The Phoenix camera system hardware involves a camera holder that attaches to the inner side of the lid and a cover placed over the holder on the outer side of the lid. The ESP32-CAM system consists of the ESP32 microcontroller with camera module, a lithium-ion battery, and a battery shield. The three options are designed for rapid mounting and removal on Tecniplast Green Line cages. The next steps are to assess manufacturing costs, data quality, and usability of the systems and to deploy them in multiple cages in the long-term room of the CSM Optogenetics facility.

Investigating the role of HES1 gene expression in regulating porcine iPS cell self-renewal

Margaret Rusteika^{1,2,3}, Li-Fang (Jack) Chu^{2,3}

¹O'Brien Centre for the Bachelor of Health Sciences, Cumming School of Medicine, University of Calgary; ²Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary, ³Precision Medicine & Disease Mechanisms Program at Alberta Children's Hospital Research Institute

Keywords: Induced pluripotent stem cells, HES1, Gene oscillation

Induced pluripotent stem cells (iPS) can proliferate indefinitely *in vitro* while retaining the capacity to differentiate into all cell types present in an adult body, creating an unlimited source of material for cell-based therapies. The similarity to humans in organ size, physiology, and anatomy, makes pigs the prime model organism to test the safety and efficacy of cell therapies before human use. The Chu lab is currently working on understanding the role of the HES1 gene in maintaining pig iPS cells (PiPSCs), as HES1 oscillation has been shown to affect the switch between the pluripotent state and differentiation. We performed RNAseq analysis of PiPSC lines and pig fibroblasts and found that the HES1 gene was significantly upregulated in PiPSC. We hypothesize that HES1 expression dynamics are critical to maintain pluripotency. To further analyze HES1 we began generating a gene reporter to allow the investigation of gene oscillation. To generate the reporter, we used PCR amplification and molecular biology methods to clone homology arms into a vector backbone containing fluorescence reporters. These homology arms are expected to allow the homologous recombination of the gene targeting vector to knockin the reporter into the pig genome. In addition to the homology arms, we generated reporter-specific guide RNA to be used for CRISPR Cas-9 gene editing. Future work on this experiment will focus on the use of CRISPR Cas-9 to knockin the reporter into PiPSCs to monitor endogenous HES1 expression and its response to perturbations using signaling chemical inhibitors, siRNA gene-knockdown, and gene-editing approaches.

Clinical Investigation of Neutrophils Oxidative Burst, LPS response and Endotoxin Activity in healthy and sick horses

Mallory Goodmanson and Marie-France Roy

Department of Veterinary Clinical and Diagnostic Science, Faculty of Veterinary Medicine, University of Calgary

Keywords: Neutrophils, oxidative burst, endotoxins

Introduction: Reliable assessment of the clinical status of sick horses is important for accurate diagnosis, monitoring, prognostication and cost of care discussion with owners. Various clinical and clinicopathological parameters are used by clinicians to assess their patient on a daily basis, however, many biomarkers used can lag behind the horse's clinical status or require shipping to a referral laboratory, implying several days delay prior to availability of results. *Objective:* Using the Endotoxin Activity Assay (EAA), optimized in our laboratory for use in horses, we investigated whether measurement of neutrophil oxidative burst, LPS response and endotoxin activity might help in clinical assessment of horses presenting with various naturally occurring diseases. *Method:* Blood was collected on healthy and sick horses and an EAA was performed within 90 minutes. The same blood sample was submitted for a CBC and fibrinogen, and blood smears were prepared and saved for future analysis. Clinical and clinicopathological data pertaining to the horse were collected. *Results:* Baseline neutrophil oxidative burst seems to be a sensitive and reactive measurement of the acute phase response in horses. The relation between the magnitude of the baseline neutrophil oxidative burst and response to exogenous LPS seems to correlate with appropriate or undermining response to acute illness. Finally, the measurement of neutrophil endotoxin activity might be useful in rapid detection of gram-negative infection in horses. *Conclusion:* The EAA provides reactive and sensitive information that can help in the assessment and monitoring of sick horses.

Learning from subsidized dog spay-neuter clinics: how can we better assess clinics impact in Indigenous communities?

Megan Sorenson¹, Susan Kutz², Alanna Collicutt³, R.J Bailot³, Karin Orsel¹

¹Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary

²Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

³Canadian Animal Task Force

Keywords: Spay-Neuter, Dogs, Population Management

The purpose of this SURE position was to use the dog registration data from Canadian Animal Task Force (CATF) spay-neuter clinics to describe temporal trends and provide suggestions for future monitoring. Dog participation numbers, age, sex, breed, and weight were compared within six First Nations communities between 2008-2019 using Mood's Median Tests, two-way ANOVAs, and two-proportion z-tests. In addition, community socioeconomic factors were normalized, descriptively compared, and used to explain community differences in participation and sex ratios. Dog participation was high in low-density communities and significantly increased over time with some exceptions. As expected, two-proportion z-tests showed that females were more likely to participate in earlier years, however small population communities differed. Due to insignificant community differences, age, breed, and weight were temporally compared by combining all community data. Mood's median tests showed that dog age significantly decreased over time. In addition, temporal breed structure significantly varied, however always by less than 8%. Finally, age, weight, and reference growth curves were used to calculate weighted residuals that were used as a weight status indicator. Weight status increased over time within large and medium breeds by an equivalent of almost one BCS. Weight status was also validated using limited body condition score (BCS) data and Mood's Medians Tests which showed significant differences between BCS values except for BCS=5 due to power related issues. Suggestions for future data collection focus on incorporating consistent indicator variables to assess objectives of the CATF programs and collecting dog information at a population level.

Understanding Canadian dairy farmers' perspectives on outdoor access for dairy cows using an online questionnaire

Melanie Jarbeau*, Anne-Marieke C. Smid^{*1}, Vanessa Boone*, Marina A.G. von Keyserlingk[†], Daniel M. Weary[†], Shane Sinclair[‡] and Herman W. Barkema^{*}

^{*}Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB T2N 4N1, Canada [†]Animal Welfare Program, Faculty of Land and Food Systems, University of British Columbia, 2357 Main Mall, Vancouver, BC. V6T 1Z6, Canada [‡]Faculty of Nursing and Department of Oncology, University of Calgary, 2500 University Drive NW, Calgary, AB T2N 1N4

Keywords: dairy farming, dairy farmer view, thematic analysis

The provision of outdoor access to dairy cattle differs around the world, from the use of primarily pasture-based systems in Australia, New Zealand and parts of Europe, to primarily indoor housing systems in the US and Canada. Dairy cattle have a partial preference for outdoor access, especially at night. Additionally, the public values the provision of outdoor access to dairy cows. As only 18% of the lactating dairy cows in Canada have access to pasture, it is important to better understand Canadian dairy farmers' perspectives on outdoor access. Therefore, the aim of our study was to understand the perspectives of Canadian dairy farmers on providing outdoor access to the different cow classes in their herd. An online survey on outdoor access was distributed by all provincial milk boards (9% response rate with 896 fully completed surveys). Data were analyzed using template analysis. Perspectives of farmers who did or did not provide outdoor access fell into 8 themes: climate, cow welfare, economics, infrastructure, management, farmer beliefs around outdoor access, role of the public, and effects of outdoor access on the environment. Many participants indicated that on-farm practices depended on farm-specific circumstances and some mentioned that the perspectives of the public played a role in their decision to provide outdoor access. We conclude that Canadian dairy farmers' perspectives on the decision to provide outdoor access differ due to a multitude of on- and off-farm factors.

Investigating parasite biodiversity and prevalence of *Strongylus vulgaris* in Alberta feral horse using an ITS2 DNA metabarcoding assay

Nancy Ngo¹, Stefan Gavriiuc¹, Micky Ahn¹, Mason Stothart¹, David Robinson², Libby Redman², John Gilleard², Jocelyn Poissant¹

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary;

²Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary

Keywords: Epidemiology, Parasitology, Molecular diagnostic

Horses are widely infected by a vast diversity of gastrointestinal strongyle nematodes. Highly pathogenic species such as *Strongylus vulgaris* pose great concern for domestic horse owners because they can cause colic and mortality when present in large quantities. Though extensive research has been developed to combat nematode transmission and infection in horses, few studies have investigated the composition and structure of complex infections, termed the “nemabiome”. This is, in part, due to the inefficient nature of non-invasive methods relying on morphological identification of parasite eggs from feces. The nemabiome composition of feral horses in Alberta is of interest since untreated feral populations can act as parasite reservoirs and therefore present a biosecurity risk to domestic horses. To gain greater insight into the prevalence of parasite nematodes species and especially *S. vulgaris* in Alberta feral horses, we applied a recently developed DNA metabarcoding nemabiome assay to 110 fecal samples collected across Southern Alberta. Results showed that Alberta feral horses are infected by >30 parasitic strongyle species and that most are infected by *S. vulgaris*. Spatial analyses suggested little variation in parasite community composition across the province. This lack of variation may be due to insufficient isolation time between individuals or weak environmental impacts on nematode larvae development. Given the high prevalence of *S. vulgaris* in Alberta’s feral horse population, we recommend diligent anthelmintic treatment of adopted feral horses and domestic horses used for backcountry riding.

Evaluating the effectiveness of shallow shotgun metagenomics for characterising the gut microbiome of *Ovis canadensis*

Naureen Othi¹, Mason Stothart¹, Marco Festa-Bianchet², Jocelyn Poissant¹

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta; ²Department of Biology, University de Sherbrooke, Sherbrooke, Quebec

Keywords: Microbiome, shotgun sequencing, wildlife

Microbes, particularly those inhabiting the gut microbiome, are critical in shaping individual health and fitness. Since the laboratory or human biomedical context has framed much of our understanding of the host-microbiome relationship, the causes and consequences of microbiome variation in free-living and captive wildlife populations remain unclear. The primary objective of this study was to evaluate protocols for characterizing gut microbiome composition and function in wild bighorn sheep (*Ovis canadensis*), with a secondary objective of exploring taxonomic diversity and functional variation within and among individuals. The effectiveness of shallow shotgun sequencing, which consists of sequencing random DNA fragments isolated from a sample, was evaluated for bighorn sheep feces. Millions of reads were generated for a total of 96 samples collected from individually monitored sheep at Ram Mountain, Alberta, and processed bioinformatically. KneadData was used to perform quality control, taxonomic classification was done through Kaiju, and microbiome profiles were explored using phyloseq. In investigating the depth of shallow shotgun sequencing needed for this technique to be successful, it was determined that the percentage of host DNA, as opposed to other organisms and bacteria was <1%. Further analysis demonstrated varying relationships between age and sex, and alpha and beta diversity of microbial communities. These results indicate that shallow shotgun sequencing is a promising approach for microbiome research in bighorn sheep and set the stage for further research on host-microbiome associations in this species.

The role of Rab7 in cholesterol metabolism upon prion infection

Nicole Wilson, Pearl Cherry, Sabine Gilch

¹Calgary Prion Research Unit, Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary; ²Hotchkiss Brain Institute, University of Calgary

Keywords: prion, cholesterol, rab7

Background

Prions are infectious protein particles formed upon misfolding of the cellular prion protein PrP^C into its infectious isoform PrP^{Sc}. They cause fatal and transmissible neurodegenerative disorders affecting both humans and animals. With no treatment options available, insight into the cellular processes affected by prion infection is crucial to develop life-saving therapies. Rab7 is a small GTPase known for its role in endosome to lysosome maturation and its ability to shuttle low density lipoprotein to the lysosomes for degradation. Specifically, this shuttling process is critical for feedback regulation of cholesterol synthesis. Our previous studies determined that increased cholesterol synthesis but decreased membrane-bound Rab7 occurs upon prion infection. We hypothesize that prion-induced Rab7 reduction leads to increased cholesterol levels that aggravate PrP^{Sc} conversion. By rescuing Rab7 function, we anticipate seeing reduced levels of cholesterol.

Methods

We transiently overexpressed wild-type, constitutively active or transdominant-negative mutants of Rab7 in prion (22L)-infected neuroblastoma cell lines (N2a5). After 48 hours, cells were subjected to lysis and cholesterol extraction. Total cholesterol levels were quantified by Amplex cholesterol assay, and protein concentrations were determined by BCA assay. Cholesterol levels were normalized to the respective protein concentration.

Results/Conclusions

We were able to optimize cholesterol extraction and confirmed increased cholesterol levels in prion-infected cells. Transient over-expression of all Rab7 mutants was successful. However, preliminary data indicate that constitutively active Rab7 did not consistently reduce cholesterol. Neither were any consistent patterns of cholesterol regulation observed with the over-expression of the active and dominant-negative mutants of Rab7.

A Scoping Review: Identifying Research Gaps for the Role of the Environment in Transmission of Antimicrobial-Resistant *Escherichia coli* in Cow-Calf Operations in North America

Priyanka Mangat¹; Stephane Le¹; Heather Ganshorn²; Sylvia Checkley¹, Karen Liljebjelke¹

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary;

²Libraries and Cultural Resources, University of Calgary

Keywords: Antimicrobial resistance, Environment, Cow-calf

Antimicrobials are essential for treating and preventing disease in food animal production. Overuse of antimicrobials in animal production contributes to antimicrobial resistance (AMR). The WHO has declared that AMR is a significant global threat to human health. To implement successful mitigation strategies that target AMR, extensive knowledge about the mechanisms that result in AMR transmission is required. The purpose of this scoping review is to gain a better understanding of the quantity and nature of research that exists with regards to the environmental transmission of AMR in *E. coli* in cow-calf production in North America. The scoping review of the literature was conducted using Covidence: an online systemic literature review management platform. In developing a literature review strategy, the following databases were used in preliminary searches: CAB Abstracts, MEDLINE, Embase, BIOSIS Previews, and the Web of Science Core Collection. After development, the scoping review protocol was published in the online PRISMA collection of the University of Calgary library. Initial screening of fourteen thousand articles was conducted by three independent reviewers according to the inclusion and exclusion criteria. Conflicts were resolved by a fourth independent reviewer. Two hundred articles were selected for full-text review by two independent reviewers. Conflicts will be resolved by a third independent reviewer. Inclusion-exclusion and study tag data will be extracted and analyzed. The results of this scoping review will provide data for identifying research gaps in understanding the role of the environment in maintaining and disseminating AMR in *E. coli* within cow-calf operations in North America.

A11 Nucleus Ablation and the Effect on Locomotor Behaviours in Mice

John, Rebecca K.¹; Thurston, EMS^{3,2}, Whelan, PJ^{1,2,3,4}

¹Department of Kinesiology, University of Calgary; ²Hotchkiss Brain Institute, University of Calgary; ³Department of Neuroscience, University of Calgary; ⁴Department of Comparative Biology and Experimental Medicine, University of Calgary

Keywords: locomotion, dopamine, hypothalamus

The A11 nucleus is a small dopaminergic nucleus found in the posterior hypothalamus that projects to the spinal cord and provides the primary source of spinal dopamine across several species. My work is expanding upon an observed locomotor role for the A11 nucleus. My project utilized a diphtheria neurotoxin virus combined with a transgenic mouse line, allowing for a precise ablation of the dopaminergic cells of the A11 nucleus. It was hypothesized that locomotor changes would be observed following A11 ablation, including in general locomotor patterns, anxiety-like and exploratory behaviours and in skilled locomotion. Experimental TH-IRES-Cre mice (n = 9, 7M, 2F) were injected with AAV-mCherry-FLEX-dtA, while control mice (n = 9, 7M, 2F) received AAV DJ-CaMKII-eYFP. Behavioural tests were completed prior to and at several time points following ablation. Interestingly, in male mice, divergent results were obtained. Preliminary work indicated a non-significant trend towards decreased locomotion following ablation. However, an additional cohort of both male and female mice displayed a non-significant trend towards increased locomotion. As well, females and males in the first cohort showed a trend towards decreased exploratory behaviours compared to controls, while additional work in male mice trended towards increased exploratory activity in ablated mice. Initial post hoc analysis indicates differences in the cells ablated throughout the A11 nucleus and surrounding areas which may be responsible for the differences observed. Future work will require matching of the ablated cells to the behaviours observed to more fully understand the locomotor behaviours associated with these regions.

Genomic features and host range of *Tequintavirus* phages with infectivity against Shiga toxin-producing *Escherichia coli*

Rita Hannawayya, Nghi Nguyen, Dongyan Niu

Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: *Tequintavirus*, Shiga toxin-producing *Escherichia coli* , host range

Introduction: Shiga toxin-producing *Escherichia coli* (STEC) continues to be responsible for many foodborne outbreaks worldwide. Phage therapy has been re-visited as a potential tool to treat bacterial infection and to control this pathogen. However, the molecular mechanism of phage infection and their host specificity remains unclear. The objectives of this study were to determine genomic contents and host range of STEC O103-infecting phages (AXO103A, AXO103B, AXO103C , *Tequintavirus* genus, *Siphoviridae*). **Methods:** The phage genomes were sequenced and annotated using in-house pipeline and online tools (molbiol-tools.ca). Phages' host range and lytic activity against 36 strains from STEC serogroups O26, O45, O103, O111, O121, O145, O91, O113, O128 and 5 strains from STEC O157 with clinical importance were assessed by microplate virulence assay. **Results:** Their genome size is 106 – 108 kb with 23-24 tRNA and encode for 150 – 156 coding regions. AXO103B and AXO103C genomes were nearly identical (108.6 kb and 108.1 kb). However, their host range differed. While AXO103C is highly susceptible to O103, O26 and O145 serogroups, AXO103B shows high susceptibility on only O103 serogroups. AXO103A can infect both O103 and O26 serogroups. Long tail fiber proteins (LTFs) and receptor binding proteins (RBP), which are known to be involved in phage infection process of AXO103A are different from those of AXO103B and AXO103C. However, those tail proteins of AXO103B and AXO103C are almost identical. **Conclusions:** Genetically similar *Tequintavirus* may exhibit distinct host range against STEC serogroups. Further investigations are required to identify mechanism underlying their phenotypic difference of host spectrum.

Seroprevalence investigation and isolation of endemic strain(s) of *Neorickettsia* species in the province of Alberta

Sara Toner², Marie-France Roy¹, Ashley Whitehead¹

¹Department of VCDS, Faculty of Veterinary Medicine, University of Calgary

²Class of 2023, Faculty of Veterinary Medicine, University of Calgary

Keywords: Potomac Horse Fever, *Neorickettsia* species, serology

Potomac Horse Fever (PHF) is a seasonal infectious disease, occurring in Alberta mainly during the summer months (July to September). It has traditionally been associated with the causative bacterium *Neorickettsia risticii*. In 2020 a new species, *Neorickettsia findlayensis*, was identified in association with PHF in horses in eastern Ontario. The objectives of this study were to investigate the seroprevalence of PHF in horses from Alberta, and to isolate the endemic specie(s) of *Neorickettsia* from horses with clinical disease in Alberta for molecular analysis. Seroprevalence sampling for PHF is being conducted by collecting serum samples from 210 horses represented in each of the 6 natural regions of Alberta and determining antibody titers via the indirect fluorescent antibody test. Isolation of endemic species is being determined by collecting whole blood, serum, and fecal material from suspected clinical cases of PHF. The blood and feces are being tested for the presence of *N. risticii* by real time PCR. Results from samples collected in the summer of 2020, have been analyzed and the first ever strains of *Neorickettsia* have been isolated in Alberta. Nested PCRs to confirm species are ongoing but not yet available at time of abstract submission. However, real time PCR on blood and feces from 3 of these cases were negative for *Neorickettsia risticii* likely indicating that the new *Neorickettsia* species is present in Alberta. Due to very dry hot weather systems in Alberta during this 2021 summer clinical cases of PHF have not been identified at time of abstract submission.

Modulation of the Heat Shock Response: A Potential Novel Therapeutic Target in Prion Disease

Sergio Fernandez Sharif^{1,2,3}, Cristóbal Marrero-Winkens^{2,3,4}, Hermann M. Schätzl^{2,3,4}

¹Department of Biological Sciences, Faculty of Science, University of Calgary; ²Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine; ³Calgary Prion Research Unit; ⁴Hotchkiss Brain Institute, University of Calgary, AB, Canada

Keywords: Prion, Heat shock, Chaperone

Prion diseases are fatal transmissible neurodegenerative disorders caused by the misfolding of the cellular prion protein (PrP^C) into PrP^{Sc}, a toxic and aggregate-prone form. In response to cellular stress (e.g., protein aggregation) there is an increased production of heat shock proteins (Hsps). Some Hsps serve as molecular chaperones, capable of disaggregating protein aggregates, which may contribute to increased prion misfolding. This project sought to elucidate the interplay between prion infection and the heat shock response (HSR) by both its abrogation and upregulation. Downregulation was achieved through CRISPR-Cas9-mediated gene editing in mouse neuroblastoma cells, which had various Hsps knocked out. Cells were subsequently infected with prions and passaged. Western blotting (WB) was performed for PrP^{Sc} every 2nd passage. Our results suggest that there was a lack of infection, which prevents us from drawing any conclusions. Upregulation of the HSR is currently being investigated in two ways. First, we exposed mouse cell lines (both infected and non-infected) to high temperatures (heat shock) and then analyzed via WB for the heat shock-inducible chaperone Hsp72. Initial results suggest an impaired HSR in infected MEF cells but a stronger response in infected CAD5 cells, both compared to non-infected groups. However, these experiments need to be replicated. Second, we plan to treat prion-infected cells with Celastrol, an HSR-inducing drug, to determine its impact on PrP^{Sc} levels. Understanding the role of the HSR in prion infection could reveal novel therapeutic targets in both prion and other neurodegenerative diseases with the common mechanism of protein aggregation.

Novel cell culture model to analyze newly emerged camel prions

Seth Colby^{1,2,3}, Waqas Tahir^{1,2,3}, Hermann M. Schätzl^{1,2,3}

¹Department of Comparative Biology & Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada, ²Calgary Prion Research Unit, University of Calgary, Calgary, Alberta, Canada, ³Hotchkiss Brain Institute, University of Calgary, Calgary, Alberta, Canada.

Keywords: Neurodegeneration, Prion diseases, Camel prions

Prion diseases are fatal neurodegenerative diseases affecting a broad range of species and caused by the misfolding of cellular prion protein (PrPC) into the infectious scrapie prion protein isoform (PrPSc). Recently, a novel camel prion disease has been reported in Northern Africa with a little known about its transmission potential both within and across species, or robust models to use for the analysis of camel prion transmission. To establish such models, I explored the propagation potential of camel prions using a gene-edited cell line expressing bank vole (BV) PrPC; for its “universal acceptor of prions” feature. CAD5, mouse neuronal cells, firstly knocked out for mouse PrPC followed by reconstitution to express BV-PrPC (CAD5-BV-PrPC), were challenged with either brain homogenate of a prion infected camel, or mock brain (negative control), or BV-adapted 22L or RML mouse prions (positive controls) followed by culturing of these cells for multiple passages. CAD5-BV-PrPC cells from passage 2, 4, and 6 were harvested for analysis of prion propagation with prion conversion assay (RT-QuIC) and immunoblotting for PrPSc. Interestingly, CAD5-BV-PrPC cells infected with camel prions at passage 2 appeared positive in RT-QuIC, indicating successful propagation, although negative in less sensitive immunoblotting. Non-reconstituted control cells were negative. Similarly, I will be analyzing the infected CAD5-BV-PrPC cells from P4 and P6 for prion propagation. Overall, this data indicates that CAD5-BV-PrPC cells can propagate new and old prions, and represent a novel cell culture model for analyzing prion infectivity, as well as underlying molecular mechanisms of various prions.

Evaluation of Pressure Regulator Performance for the Construction of an Emergency Negative Pressure Ventilator

Sophia Lu^{1,2}, V. Maslieieva¹, I. Ariza², M. Ungrin^{1,2,3}

¹Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary; ²Biomedical Engineering Calgary, University of Calgary; ³Alberta Children's Hospital Research Institute, University of Calgary

Keywords: negative pressure ventilation, hydraulic pressure regulator, COVID-19

The COVID-19 pandemic triggered a global demand for mechanical ventilators, but also highlighted the issue of chronic ventilator shortages, particularly in developing regions. While there has been a surge in conventional positive pressure ventilation (PPV) designs over the past year, few designs have explored negative pressure ventilation (NPV). As NPV systems avoid direct contact with air breathed by the patient, manufacturing and quality control requirements are greatly simplified, offering the potential for a low-cost and mass-manufacturable alternative. The objective of this study was to compare the performance of a hydraulic pressure regulator prototype with a previous weight-controlled pressure regulator prototype. Clinical guidelines suggest using $<30\text{cmH}_2\text{O}$ (standard unit in clinical applications, $1\text{cmH}_2\text{O} \approx 0.098\text{kPa}$) of plateau pressure during PPV to prevent lung injury. As such, a corresponding range of weights and water levels were used by the weight-controlled and hydraulic regulators respectively, to deliver chamber pressures between 0 and $-30\text{cmH}_2\text{O}$. To maintain chamber pressures between 0 and $-30\text{cmH}_2\text{O}$, 0.0 to 1.0kg of weight was required for the weight-controlled regulator—a consequence of the specific hardware used. In contrast, the hydraulic regulator employed a water column between 0 to 30cm in height—a more intuitive control variable that is independent of the materials available for construction. The hydraulic regulator demonstrated greater consistency in maintaining a set chamber pressure compared to the weight-controlled regulator. In the future, we seek to improve the current hydraulic regulator so that the chamber pressure can be safely/easily adjusted while the system is under operation.

Efficacy of treatment for diarrheic cryptosporidiosis in neonatal calves using bovine colostrum as therapeutic target

Steffany Schluessel, Mackenzie Campsall, Lisa Gamsjaeger, Claire Windeyer, Eduardo R Cobo

Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: cryptosporidium, colitis, colostrum

Cryptosporidiosis is a zoonotic disease caused by *Cryptosporidium parvum* parasite and is transferred by direct contact with infected feces or indirect contact with environmental contaminants. *C. parvum* causes watery diarrhea (scours) in calves, however, more life-threatening issues typically arise in neonates when co-morbidities are present. Therapeutic agents are limited to oral electrolyte solutions which alleviate symptoms of dehydration but do not target the clinical syndrome of diarrheic enterocolitis. This study aims to assess if bovine colostrum with abundant IgG mitigates clinical cryptosporidiosis in neonatal calves experimentally challenged with *C. parvum*. Individually housed (2-5 days of age) calves (n=25) fed with milk replacer were challenged with *C. parvum* oocysts (5×10^7) and either received colostrum (1 Lt) (n=7) or milk replacer (n=7) daily at breakfast feedings starting 48 hours post challenged for 4 days. Remaining calves (n=11) served as uninfected controls. Once infected, personnel collected health parameters such as fecal score, attitude, hydration, temperature, and heart rate four times daily until day 6 post-inoculation, when all calves were euthanized for gastrointestinal sampling. The hypothesis is that calves given colostrum will have milder symptoms of scours as shown in health check parameters, as well as less severe epithelial gastrointestinal damage and lower immunological responses seen in histological samples of the colon and ileum. With these anticipated outcomes, we hope to provide indication of bovine colostrum as a therapeutic agent for cryptosporidiosis-related scours.

Identifying Research Gaps for the Role of the Environment in transmission of Antimicrobial-Resistant *Escherichia coli* in Cow Calf Operations in North America

Stephanie Le¹, Priyanka Mangat¹, Heather Ganshorn², Sylvia Checkley¹, Karen Liljebjelke¹

¹Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary;

²Libraries and Cultural Resources, University of Calgary

Keywords: Antimicrobial Resistance; E. coli; Cow-calf

Introduction: Antimicrobial resistance (AMR) refers to mechanisms which microorganisms develop for protection against antimicrobial compounds. AMR has been declared by the World Health Organization as a substantial threat to animal, human and ecosystem health, making it a One-Health concern. Increasing antimicrobial use in animal production increases development of AMR. For these reasons, it is crucial to gain information and understand how the use of antimicrobials affects AMR in the production animal environment. The objective of this study is to perform a scoping review of the literature providing evidence on the role of the environment in the transmission and maintenance of antimicrobial-resistant *Escherichia coli* within cow-calf operations.

Methods: A method for performing a comprehensive scoping review of the literature was developed using results from preliminary searches. The following databases were used for the scoping review: CAB Abstracts, MEDLINE, Embase, BIOSIS Previews, and Web of Science. The scoping review was conducted using COVIDENCE, an online literature review management platform. The study data will be extracted into Excel using COVIDENCE 2.0 for analysis.

Results: The scoping review protocol was published in the U of C libraries online PRISMA collection (<http://hdl.handle.net/1880/113568>). Title and abstract screening were performed on fourteen thousand articles by three independent reviewers, and full text screening was conducted on 200 articles by two independent reviewers. A fourth independent reviewer resolved conflicts.

Conclusion: The results obtained from this study will provide data for understanding the gaps in knowledge regarding the role of *E. coli* in transmitting AMR in the cow-calf production environment.

Target identification to engineer an attenuated parasite with improved biosafety

Stephen Moore^{1,2}, S. Lu^{1,2}, V. Maslieieva¹, E. O'Grady, C. Finney, J. Wasmuth, M. Ungrin^{1,2,3,4}

¹Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada; ²Biomedical Engineering Calgary, University of Calgary, Calgary, Alberta, Canada; ³Alberta Children's Hospital Research Institute, University of Calgary, Calgary, Alberta, Canada; ⁴McCaig Institute for Bone and Joint Health, University of Calgary, Calgary, Alberta, Canada

Keywords: *Toxoplasma gondii*, attenuated parasite, biosafety

Toxoplasma gondii is a widespread obligate intracellular parasite capable of infecting most warm-blooded animals worldwide. While *T. gondii* infections are generally asymptomatic in humans, infections during pregnancy or in the immunocompromised can cause serious illness or death. The clinical manifestations of these diseases, including encephalitis and chorioretinitis, are caused by the reactivation of the latent bradyzoite life stage into the rapidly dividing tachyzoite life stage. While drugs are available to manage these acute infections, they do not cure the infected individual, doing little to affect latent bradyzoites. Current research methods, particularly those examining the tachyzoite-bradyzoite interconversion, rely on cell culture methods to induce differentiation. We aim to engineer a defined attenuated strain of *T. gondii* with replication and differentiation under the control of the experimenter, which will provide more detailed access to *T. gondii* biology while enhancing biosafety. We use bioinformatics tools available on toxoDB.org in combination with the published literature to identify suitable targets. **Conclusion:** A review of the extensive information available both in toxoDB.org and in the literature resulted in a shortlist of approximately 100 target genes. An initial strategy is proposed around three parallel goals: ablate sexual reproduction completely; make asexual reproduction controllable; and allow for tachyzoite-bradyzoite interconversion regulation. Proposed methods include a combination of gene knockouts, gene substitution (with e.g., "suicide genes"), and the use of inducible promoters. Specific recommendations for technical approaches will also be discussed.

Muralytic and Antibacterial Activity of Endolysins Against *Mannheimia haemolytica*

Tahreem Asrar¹, Jenny Hyun¹, Dongyan Niu¹

¹Department of Ecosystems and Public Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: Endolysin, *Mannheimia haemolytica*, antimicrobial activity

Introduction: Bovine respiratory disease is primarily caused by *Mannheimia haemolytica* and is a common and costly disease in the Canadian beef and dairy industries. Extensive use of antibiotics has led to widespread multidrug resistant *M. haemolytica* among North American cattle. Endolysins, antimicrobial enzymes produced by bacteriophages at the end of their lytic cycle, degrade the peptidoglycan layer in the bacterial cell wall. Because of their nontoxicity, high specificity, and low propensity for resistance development, endolysins are considered an alternative treatment for many infectious agents. The objective of this study was to evaluate muralytic (peptidoglycan degrading ability) and antimicrobial activity of two engineered endolysins. **Materials and methods:** two endolysins derived from lysogenic phages infecting *M. haemolytica* 587 and USDA-ARS 185 were expressed alone or fused with polycationic peptide. The muralytic activity was determined on *M. haemolytica* cells treated with outer membrane permeabilizing chloroform-saturated 0.05M Tris-HCl buffer. Drop in turbidity of cells incubated with endolysins was measured at an optical density of 600 nm for 3 hours using a microplate reader. Enzymatic activity of the endolysins was then calculated. To assess antibacterial activity, serially diluted mid-exponential phase *M. haemolytica* cells, incubated with standard or peptide-fused endolysins, were plated on blood agar and colony forming units (CFU/ml) were compared before and after endolysin treatment. **Results and conclusions:** Preliminary data indicates that peptide-fused endolysin produces greater levels of antibacterial activity than the endolysin alone.

Identifying a connection between the A11 nucleus and MRF: an alternative descending dopamine pathway

Theodore L. Nelson¹, J.R. Grams^{2,3}, D.A.Elliott², P.J. Whelan^{2,4}.

¹Univ. of Calgary, Calgary, AB, Canada., ²Hotchkiss Brain Institute, Univ. of Calgary, Calgary, AB, Canada; ³Dept. of Neurosci., ⁴Dept. of Comparative Biol. and Exptl. Med.

Keywords: Dopamine, A11 nucleus, MRF

Dopamine (DA) is a key neurotransmitter involved in movement, exerting its effects primarily through the nigrostriatal pathway. Degradation of this pathway and subsequent loss of DA signalling can lead to Parkinson's Disease (PD). Alternative descending DAergic pathways may supplement DA loss and lead to effective PD treatment; however, these pathways have been understudied. The A11 nucleus is the spinal cord's primary source of DA and may also provide DA input to supraspinal brainstem regions responsible for integrating and producing locomotor output. We hypothesized that A11 fibers extend to and form putative synapses with key locomotor regions in the medullary reticular formation (MRF). A viral vector was injected into the A11 region in male mice (n=7), allowing for specific fluorescent labelling. Confocal images were obtained across the rostrocaudal extent of the MRF and analyzed in IMARIS 9.7.2. GFP labelled A11 fibres were reconstructed and traced using the surface rendering and filament tracer functions. Overall axon length was calculated and normalized according to volume. Since the presence of fibres alone does not indicate neural innervation, the spots function was used to quantify synaptophysin expression, a presynaptic glycoprotein and marker of putative synapses. Preliminary results show decreasing axon density in subregions distal from the A11 concomitant with increasing density of putative synapses. These findings confirm DAergic innervation throughout the MRF. It is anticipated that results from this study will contribute to our understanding of the complex neural networks that underlie the control of movement.

Progression of Sertoli Cell Maturation

Tina He¹, Anna Voigt¹, Nathalia de Lima e Martins Lara¹, Wendy Dean³, Ina Dobrinski^{1,2}

¹Department of Comparative Biology & Experimental Medicine, UCVM; ²Department of Biochemistry & Molecular Biology, CSM; ³Department of Cell Biology & Anatomy, CSM.

Keywords: Spermatogonial stem cell maturation, niche development, male reproduction

Spermatogonial stem cells (SSCs) are the foundation for continuous sperm production and male fertility. Isolation of SSCs and subsequent transplantation could serve as a powerful tool for the treatment of infertility. Gonocytes mature to functional SSCs while migrating into the stem cell niche, yet it is still unknown how this transition is defined or when it occurs. A primary niche component are Sertoli cells, which undergo highly complex maturation processes to facilitate SSC self-renewal and differentiation.

By investigating the changes Sertoli cells undergo with maturation, we can better define the microenvironmental benchmarks SSCs experience during development. We hypothesized that the assessment of Sertoli cell maturation can predict SSC maturation. In this study, we investigated maturation events by comparing 1-week and 8-week-old pigs. Histology showed that nuclear localization changes from $15.8 \pm 1.2\%$ luminal in earlier stages to $12.2 \pm 1.5\%$ in older stages ($p=0.11$, $n=7$). TEM displayed a nuclear shape transition from a round to a more matured irregular shape. Furthermore, more desmosome-like cell-cell interactions could be observed in maturing samples. In TEM, we detected a significant accumulation of vesicles in 8-week-olds, which were confirmed to be neutral lipid derivatives with BODIPY staining in IHC. Moreover, IHC with PCNA staining showed a decline in Sertoli cell proliferation from $29.40 \pm 1.6\%$ in 1 week-old to $12.85 \pm 1.2\%$ in 8-week-old ($p=0.0002$, $n=4$). This study defined hallmarks of Sertoli cell maturation concurring with early SSC development, which could be used to predict SSC maturation in humans, promoting the translation of SSC usage from laboratory studies to clinical use.

Vaccine evaluation against an emerging strain of avian coronavirus

Tithi Bhatt, Mohamad S. H. Hassan and Mohamed Faizal Abdul-Careem

Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary

Keywords: Vaccine, Infectious Bronchitis, Chickens

Infectious bronchitis virus (IBV) is a gammacoronavirus that causes a highly contagious disease in chickens, namely, infectious bronchitis (IB). IBV replicates in the respiratory, urinary, and reproductive tracts. The IBV DMV/1639 variant has been associated with egg production complications in layer flocks in Eastern Canada. Commercial IB vaccines are present in Canada, however, the protective ability of the current vaccinations against heterologous IBV strains is questioned. A group of 40 laying hens were divided equally into two groups: vaccinated and non-vaccinated. The vaccinated group received live attenuated IB vaccines followed by an inactivated vaccine before onset of laying. At 30 weeks of age, 10 birds from each group were infected with 1×10^6 EID₅₀ of the strain and all birds were observed for 14 days post infection (dpi). Oropharyngeal and cloacal swabs were collected at 5 and 12 dpi and tissues including lung, trachea, kidney, ovary, and oviduct were also collected. RNA was extracted from swabs and tissues and then converted into cDNA through the use of PCR. Quantification of the IBV genome loads within the four groups was performed by qPCR. The results were statistically analysed to reach a conclusion. No IBV genome loads were quantifiable in non-infected groups. In the infected groups, the IBV genome loads from the vaccinated group were lower than those of the non-vaccinated group with a statistical significance detected only in the ovary ($P > 0.05$). Concluding data has not been obtained yet, however, the preliminary results suggest of partial protection against the variant infection in layers.

Housing and outdoor access practices in the Canadian dairy industry

Vanessa Boone^{*}, Anne-Marieke C. Smid^{*}, Melanie Jarbeau^{*}, Marina A.G. von Keyserlingk[†], Daniel M. Weary[†], and Herman W. Barkema^{*}

^{*}Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB T2N 4N1, Canada

[†]Animal Welfare Program, Faculty of Land and Food Systems, University of British Columbia, 2357 Main Mall, Vancouver, BC. V6T 1Z6, Canada

Keywords: Welfare, Housing, Dairy cows

Dairy cows are highly motivated to access pasture and show a partial preference for alternative forms of outdoor access such as deep-bedded sand or wood-chip packs. The public in many parts of the world favours outdoor access for dairy cattle as they perceive this system as better for cow welfare than indoor housing. In contrast to Europe, Oceania, and the US, little data exist on the use of housing and outdoor access on Canadian dairy farms. Therefore, the aim of this study was to assess current housing and outdoor access practices for dairy cows in Canada. An online survey was used to perform a cross-sectional study of housing and outdoor access practices on Canadian dairy farms. The survey was distributed by the 10 provincial milk boards, resulting in a 9% response rate. Of the 893 farms surveyed, 28% and 43% provided pasture access to their lactating and dry cows, respectively. Alternative forms of outdoor access (e.g., dirt lot, straw pack, or concrete pen) were provided to lactating cows on 6% of farms, and to dry cows on 16% of farms. For all provinces, pasture was the primary form of outdoor access provided for both cow classes except for Alberta and Saskatchewan, where alternative forms of outdoor access were more prevalent than pasture for these cow classes. Our results are crucial in informing future decisions regarding outdoor access for dairy cows in the Canadian dairy industry.

Teat sealant use on Canadian dairy farms

Zhanika J.D. Gimeno, Christina Nykyforuk, Lian J.J. Barkema, Kayley D. McCubbin, Ellen de Jong, Herman W. Barkema

Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary. 3330 Hospital Dr NW, Calgary, AB, T2N 4N1

Keywords: Teat sealant, dairy cow, antimicrobial stewardship

On Canadian dairy farms, antimicrobials are used most often for treating or preventing intramammary infections. However, concern regarding antimicrobial resistance has led to consideration of limiting antimicrobial use, and non-antimicrobial preventative measures. Non-antimicrobial substances, such as teat sealants (TS), can be used to reduce preventative antimicrobial use during the dry period by forming a physical barrier, preventing bacterial entrance into the udder. In Canada, no previous research regarding teat sealant use decision making and uptake has been conducted. Therefore, structured questionnaires were conducted during 2019 and 2020 to determine TS uptake throughout the Canadian dairy industry, and how they select which cows to receive TS at dry off. Questionnaires were analyzed using the programs R and R Studio. Out of 140 participating farms, 98 (70%) farms used teat sealant at drying off. A blanket method, where all cows were given TS was preferred (83%), compared to selective TS use (17%), where only a portion of cows were given TS at dry off. Internal TS was the preferred application type (86%), followed by external TS (9%), with 4% of farms using a combination of the two. Criteria used for selective TS use included somatic cell count (53%), followed by clinical mastitis history (29%), and milk culture (6%). Study results indicate producers used the same criteria for TS selection as they did for antimicrobials. Overall, these results strengthen the need for better producer education regarding goals of TS use in their drying off practices to maintain udder health.

ACKNOWLEDGEMENTS

Special thanks to Rahil Tarique for his time and expertise in the website design and implementation and to members of the organizing committee for abstract adjudication, session chairs/moderators, and session judges.

2021 SURE Research Days Organizing Committee

Anne-Marieke Smid	John Soghigian
Brenda Moore	Julia Canet Pons
Charlie Kwok	Kabita Baral
Daniel Pang	Kayla Strong
Dongyan Niu	Marie-France Roy
Hermann Schaetzi	Ning Cheng
Holly Sparks	Tahir Ali
Johnathan Canton	Waqas Tahir

Session Chairs and Moderators:

Anne-Marieke Smid	Marie-France Roy
Daniel Pang	Ning Cheng
Johnathan Canton	Tahir Ali
Kabita Baral	Waqas Tahir

Session Judges:

Angelica Petersen Dias	Jack Chu
Brielle Rosa	Kyle Plotsky
Cameron Knight	Nilesh Sharma
Camila de Queiroz	Regina Krohn
Ellen de Jong	Sabine Gilch
Haley Silas	Stephanie Peacock
Hermann Schaetzi	Steven Hersch

We would also like to thank Merck Animal Health for providing \$20,000 towards the Merck Undergraduate Summer Research Awards (USRA) for our DVM summer students.

Merck USRA award holders:

Emma Foxcroft (CBEM, supervised by Campbell Rolian)
Jaimie Warren (EPH, supervised by Doug Whiteside)
Mallory Goodmanson (VCDS, supervised by Marie-France Roy)
Steffany Schluessel (PAH, supervised by Eduardo Cobo)