General Information
The Organizing Committee is pleased to present the OVC’s annual Graduate Student Research Symposium. Research achievements of current graduate students will be showcased at this annual symposium through oral and poster presentations. The goal of this symposium is threefold: 1) to share students’ research findings, 2) to practice presentation skills and 3) to celebrate research in the OVC community.

Additionally, we are honoured to have Dr. Mina Bissell PhD, Distinguished Scientist, Biological Systems and Engineering Division Lawrence Berkeley National Laboratory, Berkeley, CA, present the Chappel Memorial Lecture this year. The Chappel Memorial Lecture was established in 1988 through an endowment by Dr. Clifford Chappel. Since that time, internationally renowned researchers have been invited to the University of Guelph to summarize their research and career progression to inspire those engaged in, or considering, graduate studies in biomedical research. Dr. Bissell will be presenting on the topic “Why don’t we get more cancer: the critical role of extracellular matrix and microenvironment in malignancy or dormancy?”

Schedule
Poster sessions take place in OVC Room 1707 B & C from 9:30 a.m. to 11:45 a.m.

The Chappel Memorial Lecture will also be presented from 12:00 to 1:00 p.m. in Room 1714 LLC

There will be a reception from 1:00 to 1:30 p.m. in LLC 1707 B&C following the lecture

Oral presentations take place in Rooms 1810, 1812 in Pathobiology, and 1713, 1715 in the Lifetime Learning Centre from 1:30 p.m. to 4 p.m.

Award presentations will be at 4:15 p.m. in Room 1707 LLC.

The Graduate Student Research Symposium Organizing Committee:
Dr. Gordon Kirby, Associate Dean, Research and Innovation
Elizabeth Lowenger, Manager, Student Affairs
Barb Gaudette, Graduate Studies and Research Assistant
Allyssa Hooper, Biomedical Sciences
Emily Craig, Biomedical Sciences
Bianca Di Sabatino, Clinical Studies
Alexandra Camara, Clinical Studies
Daniel Gibson, Pathobiology
Alex Leacy, Pathobiology
Katherine Bishop, Population Medicine
Alisha Matte, Population Medicine
Contents
Poster Abstracts (Session I: 9:30 – 10:30) ..................................................................................................... 3
Poster Abstracts (Session II: 10:45-11:45) .................................................................................................. 17
Oral abstracts (Session I: 1:30-2:10) ........................................................................................................... 31
    Room: PAHL 1812 ................................................................................................................................... 31
    Room: PAHL 1810 ................................................................................................................................... 33
    Room: LLC 1713 ...................................................................................................................................... 34
    Room: LLC 1715 ...................................................................................................................................... 37
Oral Abstracts (Session II 2:20-3:00) ........................................................................................................... 39
    Room: PAHL 1812 ................................................................................................................................... 39
    Room: PAHL 1810 ................................................................................................................................... 40
    Room: LLC 1713 ...................................................................................................................................... 42
    Room: LLC 1715 ...................................................................................................................................... 44
Oral Abstracts (Session III: 3:10-4:00) ......................................................................................................... 47
    Room: PAHL 1812 ................................................................................................................................... 47
    Room: PAHL 1810 ................................................................................................................................... 49
    Room: LLC 1713 ...................................................................................................................................... 52
    Room: LLC 1715 ...................................................................................................................................... 54
Acknowledgements..................................................................................................................................... 57
1. **Expression of Follicular and Angiogenic Proteins in Bovine Cystic Ovarian Disease**

Stacey Del Castillo, Allyssa Hooper, Jim Petrik

*Department of Biomedical Sciences, University of Guelph*

Cystic ovarian disease (COD) is a common cause of infertility in cattle due to the development of cystic follicles resulting in ovulation failure during estrus. Throughout the ovarian cycle, angiogenesis is essential for follicle and luteal development. Vascular endothelial growth factor A (VEGF-A) is a protein known to stimulate angiogenesis while thrombospondin-1 (TSP-1) is an inhibitor of vessel formation. Furthermore, insulin-like growth factor-1 (IGF-1) and insulin-like growth factor-2 (IGF2) have been found to play a role in folliculogenesis. The purpose of this research project is to determine if the expression of these proteins is altered as a result of COD. Bovine ovaries were obtained from a local abattoir and follicles were selected based on diameter with large follicles measuring between 10-15mm and cystic follicles measuring > 20mm in diameter. Immunohistochemistry was performed to determine the expression of VEGF, TSP-1, IGF1, IGF2, VEGFR2 and IGF1R in both thecal and granulosa cells. ImageScope was used to quantify the proportion of immunopositive tissue from each sample and statistical analyses were conducted using an unpaired t-test with a Welch’s correction on GraphPad Prism6. Results showed a significant increase in the expression of TSP-1 in cystic follicles compared to large follicles (p<0.01). In addition, VEGFR2 had a significant increase in expression within cystic follicles (p<0.05). However, no significant differences in IGF1, IGF2 and VEGF expression were observed. Future analyses include Western Blots to quantify protein expression in granulosa cells and follicular fluid, as well as assessment of additional samples in order to increase sample size.

2. **Building a better ICU: Monitoring veterinary care settings to benefit animal health and welfare**

Jessica Joshua¹, Priya Mistry¹, Lee Niel², Tami Martino¹

¹*Department of Biomedical Sciences, University of Guelph*
²*Department of Population Medicine, University of Guelph*

Introduction: Circadian rhythms are crucial for healthy physiology in humans and animals. In human hospitals, constant light and noise in the intensive care unit (ICU) disrupts patient recovery. However, light and sound levels in veterinary ICUs and the benefits for animal health remain unknown.

Hypothesis: Monitoring veterinary ICUs can help to better maintain the diurnal environment to improve animal healing.

Methods and Results: First, to measure light intensity, a data logger was placed in the ICU at the Ontario Veterinary College (OVC) animal hospital. We show that average light intensity is 156.1±5.38 lux in the day however remains high at 69.0±2.43 lux at night, compared to a minimum of 11.8 lux measured at night-time. Second, to measure sound levels, a sound meter was placed in the OVC and we show hourly averaged sound levels range from 59.00±1.28 dB at 6pm to 51.56±0.41 dB at 4am, which is high compared to the World Health Organization recommendation of >40 dB at night time. Third, as proof-of-concept of how circadian disruption can be measured non-invasively, we collected murine cecal samples and profiled the microbiome by Mi-Seq and Mothur bioinformatics. We show significant increases in the families *Lactobacillaceae, Sutterellaceae, Porphyromondaceae* and *Clostridiaceae* 1 in mice living in constant light vs. a normal light-dark cycle. Finally, we will collect data from the animal ICUs, wards and shelters, leading to consultations on how to better the diurnal environment to improve animal healing.

Conclusion: Maintaining circadian rhythms in veterinary settings is a novel and important non-pharmaceutical approach that can benefit animal health and welfare.
3. The use of polyacrylamide hydrogels to evaluate the impact of extracellular matrix stiffness on tumorigenic properties of canine osteosarcoma
Rachel MacDonald, Anita Luu, Alicia Viloria-Petit
Department of Biomedical Sciences, University of Guelph

Osteosarcoma (OSA) is the most common primary bone tumor in canines with a poor prognosis due to metastasis. The physical and mechanical properties of the extracellular matrix (ECM) are altered during tumor progression, and may facilitate metastasis. Transcriptional co-activators TAZ/YAP transduce mechanical cues into cellular responses which involve cytoskeletal modifications. The protein ezrin links the cytoskeleton to the plasma membrane, and therefore may transduce external signals to alter cytoskeletal dynamics, and thus TAZ/YAP activity. TAZ, YAP, and ezrin have been independently implicated in human and canine OSA progression, but their connection as part of the same signalling cascade has not been previously demonstrated. This research aims to determine the potential link between ezrin and TAZ/YAP signaling and their role in OSA progression. To do this, collagen type I-coated polyacrylamide hydrogels with stiffnesses of 0.5, 5, 50, and 100 kPa were prepared and verified using atomic force microscopy. Canine OSA cell lines were seeded onto the hydrogels and phase contrast microscopy assessed cell morphology, while immunofluorescence evaluated ezrin activation, TAZ/YAP localization, and cytoskeletal changes. Cells on low stiffness hydrogels demonstrated a round morphology compared to those on stiffer hydrogels, which displayed elongation. Changes in ezrin activation and TAZ/YAP localization were also observed across stiffnesses. In the future, we aim to determine the functional consequences of this ezrin-TAZ/YAP signaling axis at different stages of progression by comparing primary and metastatic OSA cell lines.

4. Targeting the PI3K/mTOR pathway in combination with chemotherapy in a naturally-occurring model of osteosarcoma
Roxanne Hummel¹, Chesney Baldwin¹, Razvan Bojinca¹, Andrew Poon¹, Anthony Mutsaers¹²
¹Department of Biomedical Sciences, University of Guelph
²Department of Clinical Studies, University of Guelph

Osteosarcoma is the most common primary bone tumour in both humans and dogs and is in need of novel treatments for metastatic disease. The PI3K/mTOR pathway is a promising therapeutic target for osteosarcoma that, when suppressed, may improve response to chemotherapy. Furthermore, dual inhibition of this pathway may lead to greater anti-tumour effects. In this study, three canine osteosarcoma cell lines were treated with inhibitors of PI3K (LY294002), mTOR (rapamycin, everolimus) or dual PI3K/mTOR (GSK2126458) alone, and in combination with chemotherapy (doxorubicin, carboplatin). Viability was assessed using a resazurin assay and results were categorized using the combination index. Western blotting was performed to determine drug effects on PI3K/mTOR pathway activation. Most drug combinations showed synergism and decreased cell viability compared to either inhibitor or chemotherapy alone, and everolimus (mTORC1 inhibitor) showed the greatest synergism with doxorubicin. In contrast to previous literature, the dual PI3K/mTOR inhibitor GSK2126458 showed the least synergism in the doxorubicin group. However, when tested with carboplatin, dual PI3K/mTOR inhibition with GSK2126458 showed the greatest reduction in viability. Western blots revealed decreased phosphorylation of mTOR and downstream molecules such as P70S6K with combination treatment. These results in canine osteosarcoma cells show that mTOR inhibition had a greater synergistic effect with doxorubicin, but dual PI3K/mTOR inhibition was most effective when combined with carboplatin. Chemotherapy-related differences in response to PI3K/mTOR targeting may be relevant to the design of future clinical trials.
5. Preliminary characterization of canine Meningoencephalitis of Unknown Etiology by histopathologic examination and compilation of clinical data
Siobhan O’Sullivan¹, Robert Foster¹, Karen Vernau², Fiona James³, Stefan Keller¹
¹Department of Pathobiology, University of Guelph
²Department of Clinical Studies, University of California Davis
³Department of Clinical Studies, University of Guelph

Meningoencephalitis of Unknown Etiology (MUE) is an idiopathic category of inflammatory canine neurologic diseases. It includes the recognized subtypes Granulomatous Meningoencephalitis (GME), Necrotizing Meningoencephalitis (NME) and Necrotizing Leukoencephalitis (NLE). Despite immunosuppressive treatment, prognosis for clinical cases is guarded. Currently, antemortem diagnostics are insufficient to subtype clinical MUE. Post-mortem histopathology of the brain to visualize the distribution and extent of the lesions provides the most reliable specific diagnosis. Given different histologic presentations and acknowledged breed dispositions, subtypes of MUE appear to represent different diseases with different causes. However, individual cases can exhibit overlap in histologic features suggesting that subtypes of MUE may represent a spectrum of disease, rather than corresponding to well-defined categories. The objectives of this ongoing study are twofold; to determine whether MUE cases can be classified into subtypes based on established histologic criteria, and to identify correlations between histologic diagnosis and clinical data. Archived postmortem tissues from MUE cases at the University of Guelph and University of California Davis were collected and re-evaluated. The associated patient signalment, therapy and survival time were reviewed for simple prognostic trends related to MUE subtype. Of 105 MUE cases, 90 cases were easily subtyped, while 15 demonstrated mixed or atypical distributions. This histologic and historical source material will contribute to an ongoing study to differentiate subtypes of MUE using a novel antemortem diagnostic tool.

6. Towards a structural characterization of the leopard gecko cerebellum: purkinje cells and cells of the external granular layer
Stefanie Bradley, Craig DC Bailey, Matthew Vickaryous
Department of Biomedical Sciences, University of Guelph

The cerebellum is a major component of the hindbrain, and plays important roles in motor coordination, posture, and cognitive functions. Although the gross anatomy and histological organization of the cerebellum has been documented across many species, less is known about the contributing cell types, especially among non-mammals. Here we focus on Purkinje cells (PC) and cells of the External Granular Layer (EGL) in a representative lizard, the leopard gecko (Eublepharis macularius). Similar to other vertebrates, gecko PC are large, calbindin-immunopositive neurons located at the junction between the molecular layer and the granular layer. Golgi-cox impregnation reveals a dendritic arborization broadly comparable with that of alligators (and distinct from that of mammals). There is typically a single, lengthy primary dendrite that divides into a complex dendritic arbour. Adult geckos also retain an EGL, a progenitor cell population that characteristically disappears prior to adulthood in mammals. Cells of the gecko EGL are immunopositive for the transcription factor SOX2, a hallmark protein of neural stem/progenitor cells, and the radial glia marker glial fibrillary acid protein, but are immunonegative for NeuN, a marker of mature neurons. Using a bromodeoxyuridine pulse-chase strategy, we determined that a subset of gecko EGL cells were label retaining after a 140-day chase period. Combined, these data provide important new information about the evolutionary variability of the cerebellum, with implications for functional adaptations in a species capable of tail loss.
7. Synchronized Ovulation and Gedis® Semen Catheter Design to Increase Sow Productivity and Reduce Breeding Costs
Matthew McBride, Robert Friendship, Terri O’Sullivan, Maria D Rocio Amezcua, Glen Cassar
Department of Population Medicine, University of Guelph
Optimal timing of semen delivery is one of the most influential elements affecting swine reproductive performance. Sows exhibit a great deal of variation in the duration of estrus, wean-to-estrus interval and estrus-to-ovulation interval. Hormones can be used to induce ovulation and allow a single fixed-time insemination protocol to be used. This, combined with using a superior semen catheter design may aid in decreasing the number of inseminations and the number of sperm per insemination. The objective of this study is to determine if the use of single fixed-time insemination and improved insemination catheter design will result in optimal reproductive performance while using substantially smaller dosages of semen.

8. Impact of Dietary Management of Obesity on the Feline Fecal Microbiota’s Metabolic Function
Bianca DiSabatino1, Scott Weese2, Moran Tal1, Myriam Hesta3, Adronie Verbrugghe1
1Department of Clinical Studies, University of Guelph
2Department of Pathobiology, University of Guelph
3Laboratory of Animal Nutrition, University of Ghent
The functional potential of the obese feline intestinal microbiota is not well elucidated. The objective of this study was to compare the fecal microbiota’s metabolic function between lean and obese cats, and obese cats before and after weight loss. Fourteen lean and 17 obese client-owned adult cats participated in the study. Cats were fed a veterinary therapeutic weight loss food at maintenance energy requirement for 4 weeks. Lean cats subsequently completed the study, whereas obese cats continued for another 10 weeks, yet energy was restricted to promote weight loss. Fecal samples were collected following each period, and DNA was extracted, high-throughput sequenced, and metabolically profiled. Functional categories of lean cats, obese cats before weight loss (OBWL), and obese cats after weight loss (OAWL) had no significant difference in means. However, variation observed in six of 28 functional categories, i.e. carbohydrate metabolism, protein metabolism, membrane transport, stress response, sulphur metabolism, and metabolism of aromatic compounds were of significant interest. Comparison of these function categories showed OBWL were more variable than lean cats (P<0.05). Following weight loss, all but membrane transport showed no difference in variability between lean and OAWL. OBWL vs OAWL showed a significant difference between variability of groups (P<0.05). Therefore, weight loss in cats influences a wide variability in metabolic categories of obese felines towards that of a narrower more stable lean variability. Future research should aim at creating nutritional strategies to increase stability and decrease variability of the gut microbiotas metabolic functions.

9. MicroRNA expression in pre- and post-amputation plasma samples from canine osteosarcoma patients
Michael Edson1, Darren Wood1, Alicia Viloria-Petit2, Anthony Mutsaers2, Geoffrey Wood1
1Department of Pathobiology, University of Guelph
2Department of Biomedical Sciences, University of Guelph
Osteosarcoma is the most common primary bone tumor in both humans and canines. The median survival time of canine appendicular osteosarcoma is less than a year but clinical outcome is hard to predict between patients. The standard of care for appendicular canine osteosarcoma involves amputation of the afflicted limb and adjuvant chemotherapy. This treatment is aggressive and currently there is no decisive method to determine which dogs will benefit the most from this treatment. Therefore, it is necessary to discover and validate biomarkers that can predict clinical outcome after standard of care treatment for
canine osteosarcoma. MicroRNAs are small non-coding RNAs that are involved in numerous cell processes and have potential as biomarkers of various diseases including cancer. MicroRNAs are found in various tissues and fluids, including plasma, providing easy collection by routine blood sampling. This study aims to profile the plasma microRNA expression in dogs with osteosarcoma, both before and after amputation as well as healthy dogs. By examining both pre- and post-amputation samples from the same dogs we hope to determine which circulating microRNAs are associated with the primary tumor. Pooled plasma samples of five dogs for each group were collected and the RNA was extracted, followed by a reverse transcription PCR of the RNA. Quantitative real-time PCR was conducted to determine miRNA expression using a QIAGEN canine miRNome array featuring 277 canine microRNAs. The microRNAs of interest from these findings will be included in a custom microRNA array and examined with individual dog plasma samples.

10. The effects of nidogen-1 on proliferation and migration in claudin-low mammary tumor cells
Rebecca Jagroop, Roger Moorehead
Department of Biomedical Sciences, University of Guelph
Breast cancer is the most common type of cancer among women, with one subset of the triple-negative subtype, claudin-low, known to be highly metastatic. For invasion and metastasis to occur, cancer cells must cross basement membranes, which contain structural proteins such as laminin and collagen IV and linking proteins such as perlecan and nidogen, and colonize on distant basement membranes. Nidogen is a glycoprotein that makes up 2-3% of basement membranes and has two types: nidogen-1 (NID1) and nidogen-2 (NID2). There have been limited studies on NID1 and cancer, with results demonstrating decreased invasiveness and metastatic capabilities in Nid1 silenced cells of various cancer types. Through previous work, a murine cell line representative of the claudin-low subtype, known as RJ423, was developed; it demonstrated a 5000-fold increase in Nid1 expression compared to the luminal subtypes. To test whether high Nid1 expression contributes to the aggressive, metastatic nature of claudin-low tumors, Nid1 levels were knocked down in RJ423 cells and proliferation and migratory capabilities were assessed. Immunofluorescence using a phospho-histone H3 antibody demonstrated that suppressing NID1 reduced RJ423 cell proliferation. Additionally, apoptosis was assessed using a cleaved caspase-3 antibody; however, cell death was not detected. Currently, migration is being evaluated using scratch wound and invasion assays. So far, a reduction in migration of the NID1 suppressed cells has been observed; however, further trials will be conducted to confirm results. Thus, this may provide a new area of NID1 targeted therapies to lessen the metastatic nature of claudin-low breast cancer.

11. Exploring the geographical distribution of cryptosporidiosis in the human population of Southern Ontario from 2011-2014
Andrea Nwosu¹, Olaf Berke¹, David Pearl¹, Lise Trotz-Williams²
¹Department of Population Medicine, University of Guelph
²Wellington-Dufferin Guelph Public Health
Cryptosporidium is a protozoan parasite of increasing global public health concern because of its ability to cause lethal diarrheal disease in both humans and animals. Since 2005, incidence rates of Cryptosporidium in Ontario have been consistently higher than the national average; however, the reasons are unknown, suggesting an incomplete understanding of the pathogens ecology, epidemiology and transmission pathways. The goal of this study was to explore the spatial distribution of human cryptosporidiosis across the 29 Public Health Unit (PHU) areas of Southern Ontario from 2011-2014. Surveillance data on human cryptosporidiosis were obtained from Public Health Ontario. Choropleth and isopleth maps were used to display the distribution of human cryptosporidiosis. High rate clusters of human cryptosporidiosis were
identified using the flexible spatial scan test. Poisson and spatial Poisson regression models were used to determine the relationships between the incidence of human cryptosporidiosis and cattle density, dairy density, calf density and the smoothed farm-level prevalence of bovine cryptosporidiosis at the PHU level. The overall crude cumulative incidence rate was 6.91 [95%CI: 6.47-7.39] cases per 100,000 for the four-year study period. High-risk clusters of human cryptosporidiosis were identified in each year. The relative risk for the clusters ranged from 2.03 [95%CI: 1.63-2.55] to 6.87 [95% CI: 5.07-9.30]. A Spatial Poisson regression showed that the incidence rate ratio of cryptosporidiosis in humans increases with increasing dairy. Further studies on the transmission of cryptosporidiosis in Southern Ontario and the specific role of dairy cattle are warranted.

12. Branched chain amino acid transaminase 1 in claudin-low breast cancer
Lisa Reynen, Roger Moorehead, Robert Jones
Department of Biomedical Sciences, University of Guelph
Breast cancer, the most commonly diagnosed cancer in women, can be classified into five distinct subtypes. One subtype, claudin-low breast cancer, accounts for approximately 7% of the breast cancer cases and these tumors are aggressive and highly metastatic. RNA sequencing of human claudin-low breast cancers by other groups and RNA sequencing of a murine claudin-low mammary tumor cell line by our group has revealed that Bcat1 is significantly up-regulated in this breast cancer subtype. Bcat1 regulates the metabolism of branched chain amino acids and has been linked to numerous pathologies including heart disease, diabetes, and cancer. Based on this data we hypothesized that the expression of Bcat1 in claudin-low mammary tumors is driving the aggressive and metastatic nature of this cancer subtype and disrupting Bcat1 will deter these features. Elevated expression of Bcat1 in the murine claudin-low cell line RJ423, compared to the murine luminal mammary tumor cell line RJ345, has been confirmed at the mRNA and protein level. Bcat1 has been transiently down-regulated ~70% in RJ423 cells using siRNA and this suppression of Bcat1, contrary to the anticipated result, showed no effect on proliferation based on phospho-histone H3 immunofluorescence. RJ423 stably expressing Bcat1 shRNA and RJ345 stably expressing a Bcat1 expression vector are currently being selected. Further in vitro and in vivo studies will utilize these stably transfected cell lines. This study will determine whether further investigation into the effects of Bcat1 on claudin-low human breast cancer is prudent and if Bcat1 may be used as a therapeutic target.

13. Streptococcus suis: Mathematical modelling of transmission dynamics and application of intervention strategies
Elissa Giang, Jan Sargeant, Zvonimir Poljak, Amy Greer
Department of Population Medicine, University of Guelph
Streptococcus suis infection is an emerging disease of pigs and a growing threat to the Canadian swine industry. Outbreaks of S. suis can result in significant morbidity and mortality among piglets during the post-weaning stage, whereby <1% to 20% of the herd can develop severe systemic infections. Gaining insight into the disease transmission dynamics for this pathogen is critical for helping to inform sustainable disease prevention and control programs for swine farmers. Mathematical models are valuable aids to a quantitative understanding of S. suis epidemiology and to the design of outbreak control programs. We have adapted a deterministic mathematical model to describe S. suis transmission among Ontario nursery swine, and to explore multi-level risk factors related to severity and clinical outcomes. Models will be parameterized using a combination of retrospective data available from swine producers and further informed by an ongoing longitudinal nested case-control field study of at-risk swine using all cases and
litter-matched controls. Model outcomes to be assessed include within herd attack rate, outbreak duration and the basic reproduction number, which will estimate the transmission degree of *S. suis* and examine the projected benefit of different control measures tested *in silico*.

14. **Effect of rapamycin on canine mast cell tumor cell survival following radiation therapy**

Morla Phan¹, Brenda Coomber¹, Valerie Poirier²

¹Department of Biomedical Sciences, University of Guelph
²Department of Clinical Studies, University of Guelph

Mast cell tumor (MCT) is the most common cutaneous cancer in dogs. Surgery is the primary method of local treatment, however it isn’t always possible to obtain adequate local control depending on the location of the tumour or the health of the dog. Radiation therapy is often used as a sole treatment or as an adjuvant for local control. Rapamycin is an inhibitor of mTOR, a pathway that is dysregulated in several cancers. This pathway mediates cell growth, proliferation and survival. mTOR inhibition may also interfere with repair of DNA damage caused by radiation therapy. Literature has shown that rapamycin reduces cancer cell survival following radiation therapy. We therefore evaluated the effect of rapamycin in combination with radiation therapy on a canine MCT cell line: MCT-1. Cells were treated with rapamycin at three clinically achievable doses: 5.5nM, 11nM and 16.5nM for 24h or 48h, and clonogenic survival assays were performed. The experiments were repeated, with the addition of a single exposure of radiation therapy: 0, 3, 6 or 10 Gy. Rapamycin alone did not impact survival of MCT-1 cells. Radiation therapy dose positively correlated with MCT-1 cell death but neither rapamycin dose nor pre-treatment incubation period had any statistically significant effect on cell survival following radiation. A synergistic or additive effect of rapamycin with radiation therapy was not found, perhaps because MCT-1 cells are very sensitive to radiation therapy alone. Therefore, rapamycin combined with radiation therapy could have a more pronounced effect on more radio-resistant cancer cells.

15. **Large-scale clustering of antigen receptor gene sequencing data using hyperdimensional point packing**

Haiyang Chang¹, Stefan Keller¹, Dan Ashlock²

¹Department of Pathobiology, University of Guelph
²Department of Mathematics and Statistics, University of Guelph

To recognize an almost infinite number of epitopes, lymphocytes generate antigen receptor (AR) gene sequences at random and the resulting repertoire is abundant. One challenge in studying the diversity and dynamics of immune repertoires is epitope-specific clustering, i.e. to group AR sequences based on the recognition of a common epitope. Traditional clustering methods are based on determining the genetic distance between pair of sequences after which the distances are used to group the sequences according to a selected linkage method. This comes at a significant computational cost, which makes the method unfeasible for very large datasets. The objectives of this project were two-fold: 1) To devise a more efficient clustering algorithm that avoids pairwise distance calculations across the entire dataset and 2) To determine a distance threshold for epitope-specific clustering. Point packing refers to arranging a given number of points into a specified set and guarantee any two points are well-spaced out by maximizing the minimum distance between pairs. This core algorithm was applied for picking anchor sequences from AR datasets in 2 new developed clustering pipelines. Both methods can be viewed as trees with anchor sequences as nodes and a descending anchor distance gradient for each layer. Large-scale sequences can incrementally be broken up into reasonably sized subsets, which limits the all vs. all comparison to the final cluster level and makes the determinant of distance thresholds easier. Meanwhile,
new sequences are allowed to add into a clustered dataset by comparison with existing anchor nodes to achieve quick positioning and relieve the computation burden.

16. Finasteride reduces the sex difference in amyloid beta deposition in 3xTG Alzheimer disease mice in a region-specific manner
Hayley Wilson¹, Ari Mendell², Samantha Creighton², Boyer Winters², Neil MacLusky¹
¹Department of Biomedical Sciences, University of Guelph
²Department of Psychology (Collaborative Neuroscience Program), University of Guelph

Gonadal steroid hormones are thought to be protective against Alzheimer’s disease (AD). In women, depletion of estrogen and progesterone levels after menopause are associated with an increased rate of AD diagnoses. Testosterone (T) in males is also protective against AD. In the brain, T can be converted via 5alpha-reductase (5a-R) to other neuroactive steroids. As females are more vulnerable to developing AD, T metabolites could contribute to the relative protection seen in AD males. In this study, we investigated whether 5a-reductase inhibition could increase amyloid beta (Ab) deposition in male triple transgenic AD mice (3xTg). Male wild type (WT) and 3xTg mice were given daily injections of finasteride (FIN; 5a-R inhibitor; 50mg/kg i.p) or vehicle (18% beta-cyclodextrin) for 20 days. Female WT and 3xTg mice received vehicle injections only. Immunohistochemistry was conducted to examine region-specific differences in Ab deposition. Female 3xTg mice had stronger Ab staining compared to all 3xTg males in dorsal cornu ammonis (CA) 1, the dorsal subiculum in the anterior ventral hippocampus (VHC), CA1 of the anterior VHC, and layer V of the primary somatosensory cortex, though no significant effects of FIN treatment were observed. However, female 3xTg mice had stronger Ab staining in CA3 of the posterior VHC compared to vehicle-treated, but not FIN-treated 3xTg males. These results suggest that 3xTg females in early stages of AD progression exhibit stronger Ab deposition compared to males, and that metabolites of testosterone may impact Ab levels in a region-specific manner.

17. Monitoring antimicrobial usage on Ontario swine nurseries
Chris McLaren-Almond

Department of Population Medicine, University of Guelph

Introduction: The nursery phase is the most challenging phase of pork production from a health standpoint. Pigs face changes in environment, feed, and social grouping at a time when they are losing passive immunity and becoming exposed to new disease challenges. The pressure to reduce antibiotic use may be difficult for pork producers to because of disease challenges. This study was intended to investigate the level of antibiotic use in Ontario swine nurseries.

Methods: Antibiotic usage data was collected from 33 Ontario swine nurseries from May 2016 to July 2017. Data collected included what antibiotics were used and route of administration. A survey was completed by the producer including questions about disease status, treatments and preventive steps such as sanitation and vaccination. A batch of pigs was followed with intentions of recording treatments.

Conclusions: The extreme variation in antibiotic use suggests that there are obvious opportunities to reduce use on certain farms. The largest quantity of antibiotics is delivered by medicating feed but the antibiotics of greatest concern for human medical use (cephalosporins and fluoroquinolones) are injectable products, and these appear to be used in a limited fashion on only a few farms.

Industry Implications: As concerns about antimicrobial usage and antimicrobial resistance continue to grow, it is important to better understand how antimicrobials are used and whether reducing antibiotic use can be accomplished without decreasing animal welfare. Antimicrobial monitoring programs at present are only mandatory for grower-finisher pigs but these should extend to the nursery phase because of disease challenges.
18. Expression of Hippo signaling pathway components during Bovine oocyte maturation
Diana Carvajal, Laura A. Favetta, Pavneesh Madan
Department of Biomedical Sciences, University of Guelph

Oocyte development is largely regulated by several ovarian signaling pathways. One of these pathways is the Hippo signaling pathway, known for its role in cellular growth and cell fate determination. In mammalian ovaries, this pathway can prevent follicular development and its disruption can stimulate follicular growth and oocyte maturation. However, no information exists about the role of this pathway during bovine oocyte maturation. Therefore, the purpose of this study is to test the hypothesis that Hippo signaling pathway is an important regulator of bovine oocyte maturation. Here, we characterize the expression of Hippo pathway components (Mst1, Mst2, Yap1 and Taz) for the first time during bovine oocyte maturation. Results show that the expression of pathway components Mst1 and Taz decreases, and the expression of Mst2 and Yap1 increases during oocyte maturation. Transcripts are also present in cumulus cells suggesting that this pathway may mediate its effects through cumulus cells to promote oocyte maturation. These results provide new knowledge about Hippo signaling pathway during oocyte maturation in the bovine species, suggesting that the pathway is active throughout maturation, and that the activity of the components may depend on specific stages of oocyte development. Further studies will involve localization of Hippo pathway constituents to determine how the location of these proteins changes with oocyte maturation. Collectively, these results will provide insight about the role of cumulus cells in modulating Hippo pathway components during oocyte maturation and highlight the importance of this pathway on the developmental capacity of oocytes.

19. Assessing the prevalence of Johne’s disease on Ontario Dairy farms after the implementation of a Johne’s management program
Jamie Imada, Dave Kelton
Department of Population Medicine, University of Guelph

Johne’s disease (Mycobacterium avium subspecies paratuberculosis) is a disease of ruminants resulting in wasting and death. On the farm this disease results in significant economic loss due to production losses and the voluntary and involuntary culling of animals. In Ontario between the years of 2010 and 2013 dairy producers had the opportunity to voluntarily participate in the Johne’s Education and Management Program. The program consisted of Johne’s herd tests, risk assessments performed by herd veterinarians, and culling of high titre cows. At the end of the program, approximately 50% of Ontario herds had participated, and of these herds, half had at least one positive cow. At completion of the program, bulk tank milk samples were taken from all herds in Ontario (n=3908) and a Johne’s hyper ELISA test was performed. The results showed that 46.8% of the samples tested positive for Johne’s. In 2017 and 2018 bulk tank milk samples from all Ontario herds were obtained to assess if there were changes in the prevalence of Johne’s disease 5 years after the completion of the Johne’s program. Interim results of these new samples (n=1600) have 61% testing positive for Johne’s. The objective moving forward is to use this data to compare prevalence’s between participants and non-participant herds as well as the changes over time.

20. Assessing the suitability of cerebrospinal fluid for next-generation sequencing studies in dogs
Tamara Morrill1, Fiona James2, Janet Beeler-Marfisi1, Olaf Berke2, Akash Jairaj1, Stefan Keller1
1Department of Pathobiology, University of Guelph
2Department of Population Medicine, University of Guelph
Central nervous system (CNS) disease diagnoses are complicated by overlapping clinical findings between diseases. This is a concern as CNS diseases can result in serious impairment and even death, yet, appropriate treatment can give patients a better prognosis. Next-generation sequencing (NGS) based methods are increasingly used as diagnostic adjuncts to characterize or diagnose CNS diseases in humans using cerebrospinal fluid (CSF). However, NGS-based tests are still infrequently used in veterinary medicine. The objectives of this pilot study were to determine: 1) if there was sufficient cell-free DNA (cfDNA) and cell-associated DNA (caDNA) in canine CSF for downstream NGS analyses, 2) if DNA levels were correlated with key CSF analytes, and 3) whether the practice of diluting CSF samples in fetal bovine serum (FBS) affects CSF DNA yields for downstream NGS. CSF from 48 dogs with neurologic disease were collected as part of a routine neurological assessment. FBS was added to 28 out of 48 (58%) samples and DNA was extracted from cell-associated and cell-free fractions of all samples. The average DNA yield concentration was 0.35 ng/μL (range: 0-1.93 ng/μL) and 0.54 ng/μL (range: 0-5.28 ng/μL) for caDNA and cfDNA, respectively, which is sufficient for downstream NGS analysis. The CSF analytes showed a moderately positive correlation between caDNA and hemocytometer cell count (r = 0.77). Initial data analysis does not show a difference between the mean DNA yield for samples diluted in FBS and non-diluted samples (t-test, p-values > 0.05). Future work will investigate the use of the harvested DNA in a NGS study aimed at expanding our diagnostic toolkit for canine CNS diseases.

21. Inhibition of the mevalonate pathway with simvastatin in transformed fallopian tube epithelial cells as a novel therapy in epithelial ovarian cancer
Madison Pereira1, Trevor Shepherd2, Gabriel DiMattia2, Jim Petrik1
1Department of Biomedical Sciences, University of Guelph
2Departments of Obstetrics and Gynecology, Oncology, Anatomy and Cell Biology, & Biochemistry, Western University (London Regional Cancer Program)

The 5-year survival rate for epithelial ovarian cancer (EOC) at < 30% indicates a need for new therapies. We have discovered that metastatic tumour cells from the abdominal ascites (28-2 cells) in a murine EOC model acquired a gain-of-function p53 mutation and upregulated the mevalonate pathway. This pathway is key to cancer cell viability as it is necessary for cholesterol biosynthesis, protein prenylation and activation of GTPases. Enhanced mevalonate signaling provided a survival advantage to 28-2 cells, resulting in sensitivity to simvastatin inhibition targeting the rate-limiting enzyme, HMG-CoA reductase. As high-grade EOC originates from the distal fallopian tube epithelium (FTE), and acquisition of p53 mutation is thought to be an initiating step, we hypothesize that transformed FTE cells will have upregulated mevalonate signaling and treatment with simvastatin will inhibit this pathway to induce disease regression. We have developed an orthotopic, syngeneic model of early-stage EOC, by injecting immortalized murine FTE cells into the distal fallopian tube. We will evaluate the role of p53 mutation and mevalonate signalling in reprogramming FTE cells to initiate EOC. Preliminary in vitro studies demonstrated that treatment with simvastatin significantly reduced cell viability in p53 mutant and p53 knockout FTE cell lines compared to wildtype p53 cell lines. Understanding the mechanistic relationship between p53 mutation and mevalonate signalling may provide novel therapeutic avenues, such as simvastatin, to target tumour initiating cells. Mevalonate pathway inhibition targets cancer cell metabolism which could potentially reduce the burden of metastatic disease.
22. Risk and protective factors for stress impacting academic performance in post-secondary students: Results from the 2016 National College Health Assessment survey
Konrad Lisnyj, Andrew Papadopoulos

*Department of Population Medicine, University of Guelph*

Stress is a significant contributor to developing poor mental health. Post-secondary students are particularly vulnerable to experiencing excess stress due to their overwhelming academic-, financial-, relational-, and career-related demands. Given the two-way relationship between health and education, post-secondary institutions are an ideal setting to promote optimal mental health and well-being. The American College Health Association collects information on post-secondary students’ habits, behaviours, and perceptions of various health topics, including stress, through the National College Health Assessment (NCHA). A multivariable logistic regression analysis will be performed using the 2016 NCHA data to measure the effect of various risk and protective factors associated with stress on academic performance at the University of Guelph in comparison with peer universities. Results will help institutions develop interventions that build resilience in students to alleviate the impact of stress on academic performance, as well as to proactively identify those individuals at risk.

23. A polymerase chain reaction-based assay for the determination of Eimeria spp. oocyst viability
Perryn Kruth, John R Barta

*Department of Pathobiology, University of Guelph*

Coccidiosis, caused by apicomplexan parasites of the genus Eimeria, is a parasitic disease of major impact to the commercial poultry industry. Oocysts shed in feces of infected birds sporulate in the environment to become infective. Infection is self-limiting and highly immunogenic but immunity conferred by one Eimeria species is protective against only that species; these factors make live vaccination an effective means of coccidiosis control. Vaccination requires establishment of infection with sufficient viable oocysts to stimulate development of protective immunity but few enough to avoid disease. Knowledge of actual viability of oocysts is therefore essential for calculating effective vaccine dosages. Unfortunately, no rapid and accurate method for determination of oocyst viability presently exists. Difficulty in assessing oocyst viability ultimately impedes successful implementation of vaccination programs. We have developed an initial in vitro assay that uses transcript abundance as a proxy for oocyst viability. Specific assay targets have been investigated using standard RT-qPCR; early data show a strong correlation between target abundance and oocyst viability. Ongoing work aims to identify optimal targets through transcriptomic analysis of sporulated oocysts. An optimized assay should allow for determination of individual species’ contribution to viability in mixed samples. Assay optimization of transcript quantification protocols, assessing one- and two-step RT-qPCR strategies and the use of digital droplet PCR (ddPCR) aim to increase assay sensitivity while decreasing any impacts of inhibitors.

24. Antimicrobial use in Ontario swine production
Angelina Bosman¹, Scott McEwen¹, Richard Reid-Smith², Anne Deckert², Carolee Carson², Zvonimir Poljak¹

¹*Department of Population Medicine, University of Guelph*
²*Center for Foodborne, Environmental & Zoonotic Infectious Diseases, Public Health Agency of Canada*

Introduction: Information on antimicrobial use (AMU) in animal production is needed to improve our understanding of its contribution to antimicrobial resistance (AMR) in humans. Data on AMU in the early stages of swine production in Canada are lacking. This research project will collect data on AMU from the early stages of swine production in Ontario during 2017, describe AMU in the early stages of production
and across the entire swine production cycle, and determine if associations between AMU, AMR, and other factors exist.

Methods: Swine veterinarians will enroll 25 farrowing and 25 nursery operations across Ontario and administer a questionnaire on AMU in feed, water, by injection and by oral bolus during the 2017 calendar year. A pooled fecal sample will be collected for AMR analysis (pending funding). Data from the early stages of production will be combined with Ontario grower-finisher data from the Canadian Integrated Program for Antimicrobial Resistance Surveillance, and a descriptive and comparative analysis of AMU in the early stages of production and across the entire production cycle will be performed. Associations between AMU, AMR, biosecurity, and herd health will be determined using modelling approaches. Estimates of AMU will be reported using several different metrics. Results/Conclusion: Ontario swine veterinarians have agreed to participate, and data collection is underway. It is anticipated that the collection of AMU data from the early stages of swine production will demonstrate the need for on-going surveillance and highlight the value of a more comprehensive understanding of AMU in swine production.

25. Two cases of equine mosaic X chromosome monosomy
Bahareh Ahmadi1, Tamas Revay1, Ruby Yoana Murcia Robayo2, Ignacio Raggio2, Daniel AF Villagomez2, Mouhamadou Diaw2, Keith Colquhoun4
1Department of Biomedical Sciences, University of Guelph
2Department of Clinical Sciences, University of Montréal
3Department de Producción Animal, Universidad de Guadalajara
4Colquhoun Equine Veterinary Services

Monosomy of the X chromosome, the most frequent sex chromosome abnormality associated with infertility and embryonic loss in mares, has been investigated since early 1970’s. Affected mares may show one or more of the clinical symptoms including short stature, undeveloped reproductive organs, and absent or irregular estrous cycle. It has been shown that some clinical features including fertility are correlated with the percentage of aneuploid cells present. In our study, the presence of chromosomal mosaicism (XO/XX) in two mares (Irish Cob maiden, Standardbred) with fertility problem was determined using three independent techniques. Case No. 1 was phenotypically normal with normal external genitalia appearance, normal ovaries, and two tubular structures compatible with cervices on the pelvic floor. Case No. 2 has flaccid uterus, small ovaries, and atonic cervix with normal size. Using chromosome-counting technique, fluorescent staining of interstitial C-band of X chromosome, and fluorescent in situ hybridization revealed 14.6% and 95% of X monosomy for each case, respectively. As the percentage of X monosomy in the first mare is low and the ovaries are functional, the fertility problem could be related to a different etiology rather than X monosomy. Therefore, there are some possibilities for the production of a foal in this case. The second horse with 95% of X monosomy and very small ovary is infertile, most probably associated to haplodeficiency of genes located at X chromosome. This report highlights the importance of molecular cytogenetic techniques in cases of equine infertility to decide whether to keep breeding from such individuals.

26. Modeling in-host dynamics of H9N2 avian influenza virus in poultry
Xiao Ting Xie1, Amy Greer1, Salah Uddin Khan1, Zvonimir Poljak1, Shayan Sharif2
1Department of Population Medicine, University of Guelph
2Department of Pathobiology, University of Guelph

Avian influenza (AI) outbreaks on poultry farms cause significant morbidity and mortality in birds, which is directly associated with economic losses for producers. AI remains a pandemic threat, and there is an
increasing urgency to better identify intervention strategies to reduce infections within poultry flocks. Few studies have examined the infection dynamics of AI virus in host cells. In-host modeling can be used to estimate parameters to improve our understanding of how the introduction of infectious AIV particles impacts a population of susceptible cells. Modeling outcomes can also be used to explain variations in cell-level infection severity, and how this relates to host disease outcomes. This study aims to use mathematical models to simulate the dynamics of low pathogenic H9N2 AI virus infection in a susceptible population of chicken epithelial cells. Stochastic in-host models parametrized using empirical data from laboratory transmission studies will be developed and analyzed using RStudioTM. Stochasticity will be implemented using Gillespie’s Direct Method. Model outcomes of interest include the basic reproductive number (R0: number of infected cells caused by a single infected cell), the life-span of an infected cell, and the total number of infected and lysed cells over the disease course. This model will also be used to compare the effectiveness of multiple vaccine interventions by assessing the level of hemagglutination inhibition (HI) antibody response. These findings can contribute to our knowledge of H9N2 infection kinetics, and provide support for optimal AIV disease prevention strategies in an effort to reduce animal morbidity and production losses.

27. Correlation of carbohydrate larval antigen (CarLA®) antibody response with parasitism in Ontario sheep

Emma Borkowski¹, Neil Karrow², Paula Menzies³, Jacob Avula¹, Brandon Lillie¹, Andre Peregrine¹

¹Department of Pathobiology, University of Guelph
²Department of Animal Biosciences, University of Guelph
³Department of Population Medicine, University of Guelph

Gastrointestinal nematodes (GINs) cause significant lost productivity on Ontario sheep farms. In light of the rising prevalence of anthelmintic resistance, selecting sheep with superior immune response to GINs has received considerable attention. In New Zealand, salivary antibody to a carbohydrate larval antigen (CarLA®, AgResearch Inc.) has been used to identify sheep with superior immunity. However, climate and GIN epidemiology in Ontario are different from New Zealand. The purpose of this study was to determine whether CarLA® correlates with GIN burden under temperate grazing conditions in Ontario. Replacement ewe lambs (n=107) were recruited from a commercial farm in Ontario and followed for two years (2016-2017), including their first lambing and lactation. GIN fecal egg count (FEC) was monitored every 6-8 weeks through both grazing seasons (May-Nov), and at mid-gestation in March 2017. Salivary CarLA® was measured at the beginning, middle, and end of each grazing season, and at mid-gestation. Mean CarLA® titre increased in 2016, declined over winter, and rapidly increased during the 2017 grazing season. CarLA® in October 2016 was significantly positively correlated with CarLA® in 2017. Two significant correlations were identified between CarLA® and FEC; a weak positive correlation between August CarLA® and October FEC in 2016, and a weak negative correlation between CarLA® and FEC in May 2017. These results indicate that CarLA® measured at the end of a lamb’s first grazing season are predictive of subsequent titres under Ontario grazing conditions, and selection of replacement ewes with elevated CarLA® may reduce pasture contamination in the periparturient period.

28. A comparative exposure assessment of antimicrobial resistance from food-producing animals in Canada

Courtney Primeau¹, Carolee Carson², Brennan Chapman¹, Ed Topp³

¹Department of Population Medicine, University of Guelph
²Centre for Food-borne, Environmental, and Zoonotic Infectious Diseases, Public Health Agency of Canada
Antimicrobial resistance (AMR) is a global public health issue that poses a threat to the treatment of infectious diseases worldwide. AMR transmission routes are very complex, and the impact of AMR arising through the food chain on negative human health impacts is often debated. However, policy makers are interested in prioritizing the food animal species and understanding which species may contribute most significantly to AMR in humans. The objective of this project was to generate a semi-quantitative assessment comparing human exposure to resistant Salmonella spp., E. coli, and Campylobacter spp. from several domestically produced commodities in Canada using existing data. Food animal species were selected based on the quantity consumed by the Canadian population, per capita consumption rates, and the quantity produced domestically, according to data provided by FoodBook and Statistics Canada. Both scientific and social criteria were developed, weighted, and examined in order to rank the animal species. Scientific criteria included antimicrobial use, recovery and resistance rates of different bacterial species, human consumption rates, and projections for AMR and consumption trends. The social criteria examined included public perception and tolerance, and stakeholder perception and will. The results of this assessment provide a summary of these weighted criteria for each of the selected commodities, and also highlight the data gaps that exist in the literature. The goal of this research is to provide evidence-based recommendations to the policy and funding communities to prioritize areas for future surveillance, research and mitigation efforts in Canada.
1. Comparison of an active and passive surveillance system for determining the distribution and influence of host and environmental factors on canine distemper virus in Ontario Raccoons

Jolene Giacinti¹, David Pearl², Davor Ojkic³, Claire Jardine¹
¹Department of Pathobiology, University of Guelph
²Department of Population Medicine, University of Guelph
³Animal Health Laboratory, University of Guelph

In Ontario, Canine Distemper Virus (CDV) is frequently encountered in wild carnivores and is the most common infectious cause of death for raccoons. The recent isolation of CDV strains genetically distinct from vaccine strains in North America highlights the importance of studying epidemiological patterns of this virus in raccoons. However, wildlife surveillance is challenging and often requires a combination of active and passive surveillance methods with aggregation of data from multiple sources. Our objective was to compare CDV data obtained through passive and active surveillance of Ontario raccoons using a retrospective evaluation of 1079 raccoons submitted to the Canadian Wildlife Health Cooperative between 2007 and 2017. For each dataset, univariable logistic regression was used to identify associations between the occurrence of CDV infection and the following independent variables: age, sex, season, and year. Additionally, coordinates from each raccoon submission were mapped in QGIS to compare the areas represented by each surveillance method. Spatial data demonstrated that CDV infection was present throughout Southern Ontario and the areas captured by active and passive surveillance were overlapping and concentrated in similar regions. The risk factor analyses produced statistically significant associations between the presence of CDV and age, season and year of collection which were discordant between the two datasets and at times indicated opposite relationships. This study illustrates the impact that a surveillance strategy can have on the types of data that are obtained and our interpretation of the epidemiology of disease.

2. "I don't want to get anyone sick": A review of factors affecting safe food handling at retail and food service

Abhinand Thaivalappil¹, Lisa Waddell², Judy Greig², Richard Meldrum³, Ian Young³
¹Department of Population Medicine, University of Guelph
²Public Health Agency of Canada
³School of Occupational and Public Health, Ryerson University

Introduction: Many foodborne disease outbreaks originate in retail and food service locations, indicating poor food handling practices among food handlers.

Purpose: The aim of this systematic review was to synthesize the main across-study themes of determinants related to food handlers’ safe food handling, and to develop recommendations for interventions and future research on food handlers.

Methods: A comprehensive search strategy; relevance screening of abstracts; relevance confirmation of articles; study quality assessment; thematic synthesis of results; and quality-of-evidence assessment were completed. A minimum of two reviewers were involved during every stage of the review process.

Results: We analyzed 27 relevant articles reporting on 25 unique studies. Determinants were grouped according to constructs from the Theoretical Domain Framework, and further mapped onto larger themes using the COM-B model. A total of 13 categories of determinants of safe food handling were identified. Overall confidence ratings for identified theoretical constructs were rated as high (n=9) and moderate (n=4). The analysis revealed that: 1) food handlers were generally knowledgeable and viewed training favourably; 2) environmental factors (e.g. policies, constraints), and social influences played a significant
role in food handlers' intentions and practices); 3) food handlers were confident in their skills; 4) they experienced positive (e.g. pride) and negative emotions (e.g. anxiety) on the job; 5) workers demonstrated poor motivation to perform safe practices and were forgetful; and 6) culturally diverse food handlers had unique barriers (e.g. language).

3. Validating the mHippoE-14 and mHippE-18 cell lines as models for stress responsiveness
Emily Craig, Kate Nicholson, Carolyn Creighton, Neil MacLusky
Department of Biomedical Sciences, University of Guelph

Immortalized cell lines overcome many of the limitations associated with primary cell culture, and support mechanistic investigations in to physiological processes. The immortalized murine neuronal cell lines mHippoE-14 and mHippoE-18 are attractive models to study hippocampal responses in vitro. Commercially supplied by CELLutions Biosystems Inc., the mHippoE series promises to “enable accurate in vitro assays for use in the discovery, development and validation of new therapeutics targeted to central nervous system diseases and disorders”. Our lab seeks to validate these cell lines as an appropriate in vitro model for studying the stress response. We have shown that mHippoE-18, but not mHippoE-14, possess the \textit{SRY} gene, suggesting that mHippoE-18 is of male origin and mHippoE-14 is of female origin. Furthermore, we have shown that both mHippoE-14 and mHippoE-18 express the glucocorticoid receptor (GR). In order to determine the functionality of GR, we treated both cell lines with a synthetic glucocorticoid, Dexamethasone, and collected RNA 24 hours post treatment to assess genomic effects. Using quantitative polymerase chain reaction (qPCR), we show that the GR responsive gene FKBP5 increases in the presence of Dexamethasone, indicating both cell lines express a functional GR with glucocorticoid binding ability. The presence of two Dexamethasone responsive cell lines, one of male origin and the other of female origin, is a useful model. Establishing the mHippoE series as a useful in vitro model for basic investigations in to the hippocampal cellular stress responses will provide a framework for future investigations in our lab.

4. Assessing the repeatability of tick dragging as a method for \textit{Ixodes scapularis} surveillance
Katie Clow, Genevieve Lumsden, Rachel Finer, Claire Jardine
Department of Pathobiology, University of Guelph

Tick dragging is an important tool used by public health for \textit{Ixodes scapularis} surveillance to identify Lyme disease risk areas in Ontario, Canada. Concerns have been raised regarding the repeatability of tick dragging due to fluctuations that occur in the tick population in response to micro- and macroclimatic variations. Our objective was to assess the repeatability of tick dragging over a short timescale by examining three outcome measures: presence/absence of ticks, tick abundance, and likelihood of tick establishment. Likelihood of tick establishment was assessed by integrating data collected on tick life stage, overall abundance, and past surveillance findings and was assessed as non-zero, low, medium or high risk. We conducted tick dragging twice per site within a one month period at a total of 10 sites in eastern and southern Ontario. \textit{Ixodes scapularis} were detected at seven sites. The outcome of presence/absence was consistent at 9 out 10 sites. Abundance was highly variable, changing between each visit at sites where ticks were detected. The measure of likelihood of tick establishment was consistent at 8 of 10 sites. Based on the kappa statistic, there was substantial agreement between measurements for the presence/absence and the likelihood of tick establishment. Our results indicate that both presence/absence and the measure of likelihood of tick establishment provide more consistent outcomes for tick dragging than tick abundance alone; however, applying the dragging data to the
likelihood indicator provides additional information about the potential risk associated with I. scapularis establishment in the area.

5. Gonadectomy rapidly alters the morphology of pyramidal neurons in the hippocampus and medial prefrontal cortex of male rats
Eric Lawton, Lauren Isaacs, Ari Mendell, Craig Bailey, Neil MacLusky
Department of Biomedical Sciences, University of Guelph
Circulating testosterone (T) levels gradually decline in ageing males, which may be associated with impairments in cognition and memory. The effects of androgen loss may in part be explained by changes to the hippocampus and medial prefrontal cortex (mPFC), two brain areas critical for cognition and memory. Previous work in our lab has shown that after gonadectomy (GDX), the apical dendrites of pyramidal neurons in the CA3 region of the hippocampus undergo dramatic expansion compared to sham-operated controls. However, it remains unknown how rapidly these changes occur, if T replacement reverses the effects of GDX, or whether similar effects are observed in other regions of the brain, such as the mPFC. Whether the stress of surgery influences this response also remains to be determined. We hypothesized that the effects of GDX may include contributions from both loss of T and surgically-induced stress. To test this hypothesis, pyramidal neuron morphology was analyzed in hippocampal subfields CA1 and CA3 and layer 2/3 of the mPFC in animals that were surgically naive, sham operated, or GDX with or without T replacement. At 10 days post-surgery, dendritic branching in CA1 was relatively unaffected by either surgical stress or loss of T. Apical dendritic branching of both CA3 and mPFC neurons, however, was significantly greater in GDX rats than in either GDX/T replaced and unoperated male controls. The lowest level of branching was observed in the sham operated male animals. These results suggest a complex interaction between surgical stress and T in the regulation of pyramidal cell morphology in areas of the brain critical for cognition and memory.

6. Canine electroencephalography (EEG): proposed analogous electrode placement grid for dogs based on the human 10-20 system
Samantha McCarthy1, John Phillips2, Robert Dony3, Alex zur Linden1, Luis Gaitero1, Fiona James1
1Department of Clinical Studies, University of Guelph
2Centre for Advanced Manufacturing and Design Technologies, Sheridan College
3School of Engineering, University of Guelph
Electroencephalography (EEG) definitively diagnoses epileptic seizures. For humans, the 10-20 EEG electrode placement grid is an internationally accepted standard. Each named 10-20 electrode location indicates a specific cortical site. Seizures are the most common medical issue in veterinary neurology. A lack of protocol standardization hinders using canine EEG. This study proposes sufficient neuroanatomical similarities between humans and dogs to design an analogous grid for dogs. An extensive literature review identified comparative correlations between the cortical lobes based on location and function of the sulci and gyri. The occipital lobe/visual areas appear to be the most complementary between species. Temporal lobe association areas of the human brain appear similarly located in ventral-caudal regions of the temporal lobe in dogs. Stimulated voice areas involve anterior temporal regions in both humans and dogs for auditory cortex. The role of the parietal lobe in somatosensory information reception includes the primary somatosensory area in both humans and dogs. Frontal lobe motor regions in humans extend to areas of the gyrus sigmoideus in dogs. Next steps: establish skull landmarks to anchor grid, consider maxillary electrodes, use advanced imaging to validate grid, and design easy to use head cap. In addition to optimizing diagnosis of canine epilepsy, future research could use the standardized grid to explore areas of higher cognitive function in the dog brain. Establishing functional similarities between human
and dog EEG potentiates meaningful advancements in canine epilepsy and EEG with translational implications.

7. Melting syndrome in *Ricordea yuma*

Zachary Millar, Paul Huber, John Lumsden

*Department of Pathobiology, University of Guelph*

Corals face numerous anthropogenic threats, but also experience mortality due to infectious disease. Diseases of corals appear to be increasing in frequency and combined with environmental changes place a great deal of stress on coral reefs. Corallimorpharians are a subset of corals that, morphologically, fall between hard-corals and soft-corals. They are popular aquarium subjects and while noted to be relatively easy to maintain, experience ‘melting’ events with no known cause. A melting episode was recently observed in the Hagen Aqualab that was isolated to corallimorpharian *Ricordea yuma*. There is no scientific description of this occurrence either from coral in captivity or in nature. My hypothesis is that the melting episode is caused by an unknown pathogen. Samples were collected from morphologically normal and affected corals for bacteriology, electron microscopy (TEM), histology and virome analysis to be conducted. Detailed water quality logs were also maintained. To date, bacteriology, histology and TEM have all been completed. Twelve different types of bacteria were obtained using marine agar and 16S rDNA sequencing resulted in 7 different identifiable species. No inclusion bodies or virus were noted using TEM. Histology revealed a large amount of diffuse necrosis affecting multiple cell types in diseased corals compared to healthy specimens. There was also a noticeable decrease in zooxanthellae present in the gastrodermis. Water quality analysis revealed nothing unusual during the melting event as all results were within their accepted ranges. The virome analysis has not been performed yet.

8. Investigation into the molecular characteristics of *Streptococcus suis* isolates in Ontario nursery pigs

Leann Denich, Emily Arndt, Zvonimir Poljak, Vahab Farzan, Robert Friendship

*Department of Population Medicine, University of Guelph*

*Streptococcus suis* (*S. suis*) is a bacterium that naturally inhabits the nasal cavity and tonsils of many pigs. Factors related to host, farm management and bacteria likely contribute to systemic infections. The objective of this case-control study is to determine the serotypes and molecular characteristics of *S. suis* isolates, in 4-8 week old nursery pigs from Ontario farms, with clinical signs of disease and healthy controls. Cases showing clinical signs of *S. suis* are selected and matched with healthy controls. Nasal, tonsil and rectal swabs along with blood samples are collected from each case and control. Cases are also euthanized to collect meningeal swabs and tissue from spleen and ileum. Samples are cultured and tested for *S. suis* by presence of glutamate dehydrogenase and recombination protein N genes using a PCR method, along with 16S rRNA. A two step-multiplex PCR is used to serotype isolates, and a subset are subjected to whole genome sequencing to determine their molecular characteristics. To date, 363 isolates from 112 pigs have been serotyped. In cases, a wide range of serotypes were recovered from each location sampled such as 1/2,1,2,7,8,9,14,18,28,29 in the meninges and 1/2,2,3,7,9 in blood. In controls, a wide range of serotypes were recovered in the tonsil, nasal cavity and rectum. Untypable isolates were also found in all samples in cases and controls. Interestingly, multi-locus sequence typing indicated that one strain of serotype 9 appeared to be circulating through one farm over time. The results obtained from this study will give a better understanding of the serotypes and associated virulence genes involved in outbreaks in Ontario nurseries.
9. Circadian rhythms, sex, exercise and their role in the pathophysiology of myocardial infarction (heart attack)

Khizer Khurram-Hafeez

*Department of Biomedical Sciences, University of Guelph*

Introduction: Circadian rhythms play a crucial role in cardiovascular physiology and healing post-myocardial infarction (MI; heart attack). It is known that biological sex influences outcomes post-MI, however differences in infarct healing are unknown.

Methods and Results: To investigate the role of biological sex on healing post-MI, male and female mice were subjected to MI surgery. To evaluate whether biological sex influences early outcomes post-MI, we assessed survivorship in males and females, and found worse survivorship in males compared to females (22.22% vs. 77.77%), suggesting impaired matrix remodelling due to increased left ventricular (LV) rupture rates. Furthermore, to assess cardiac function post-MI, mice were followed by echocardiography. We show that females have increased LV dimensions at diastole (5.06 ± 0.08mm vs. 4.71 ± 0.05mm) and systole (3.77 ± 0.11mm vs. 3.42 ± 0.07mm), however similar % ejection fraction (56.67 ± 1.97% vs. 57.29 ± 1.46%) and % fractional shortening (25.66 ± 1.15% vs. 26.44 ± 0.82%) post-MI, compared to males. Next, to evaluate infarct healing, we will assess inflammatory recruitment to the heart, using flow cytometry. Finally, to investigate time-of-day benefits of exercise post-MI in males and females, we will use exercise protocols by Wu et al. (2009) at sleep time [zeitgeber time (ZT) 6] and wake time (ZT18).

Conclusion: Females are under-represented in heart disease research and understanding the mechanisms underlying female differences and circadian biology in post-MI outcome will lead to improved outcomes for patients.

10. Differences and similarities between variant frequencies in matched primary and metastatic canine appendicular osteosarcoma samples

David Szhachtayćź¹, Geoffrey Wood¹, Lewis Lukens², Alicia Viloria-Petit³, David Adams⁴

¹Department of Pathobiology, University of Guelph
²Department of Plant Agriculture, University of Guelph
³Department of Biomedical Sciences, University of Guelph
⁴Wellcome Trust Sanger Institute

Introduction: Osteosarcoma (OSA) is the most common primary bone tumor in both humans and dogs. OSA of long bones is a very aggressive cancer with the main cause of mortality being metastasis, which occurs mostly in the lungs in both species. Canine appendicular OSA is similar to human conventional OSA, but is more frequent and aggressive, making dogs a good model for the human disease.

Methods: Matched normal tissue, amputated primary OSA tumor, and metastatic OSA tumor in lung was collected from 16 dogs. Each sample had 4 sequencing runs, comprised of targeted sequencing of 586 specific genes using Illumina Hi-Seq. Their reads were aligned to the dog reference genome canfam3 using bowtie2. Variant calling was performed, using samtools and bcftools. Variants were compared between the different groups.

Results: Overall, all the samples shared ~1-8% of their variants within each dog, suggesting that most of the discovered variants were either undocumented SNPs or artefacts. Further inspection of the samples showed that only ~15% of detected variants were present in all 4 sequencing runs, suggesting that most of the variants are artefacts. Most of the dogs shared ~12-15% of their variants between primary and metastatic as well as between normal and primary samples. Taken individually the samples had very few variants in common within samples of the same tissue origin: normal: 0.0347075%, primary: 0.04545712%, metastatic: 1.992276e-04%.
Discussion: These results show that there is more similarity, within samples taken from the same dog, than within samples from the same group/stage of cancer. It’s also interesting that the similarity decreases as cancer progresses.

11. Presence of porcine reproductive and respiratory syndrome virus in nursery pigs
Emily Hanna, Robert Friendship, Zvonimir Poljak, Terri O’Sullivan
Department of Population Medicine, University of Guelph
Porcine reproductive and respiratory syndrome (PRRS) is considered the most economically important disease in swine production and outbreaks are associated with high mortality in young pigs due to respiratory disease. The nursery can become a reservoir, with the virus spreading from older pigs to newly weaned pigs, often with few apparent clinical signs. The objective of this study was to investigate the impact of PRRS status on growth performance in Ontario swine nurseries. Data were collected from 30 swine nurseries. A management and biosecurity questionnaire was collected. A subset of 20 'average' pigs were weighed on entry and exit from each nursery. Individual blood samples were collected and tested for PRRS using PCR. Descriptive statistics were generated for growth performance. Mixed effect regression analysis will be used to determine the impact of PRRS positivity on growth performance on a herd-basis. None of the farms reported PRRS as a clinical problem but 10 farms tested positive for PRRS virus. Descriptive analysis showed that mean ADG was 453 g/day (95% CI: 426.8, 479.5). The top 10 farms based on ADG were PRRS negative throughout the nursery phase with a mean ADG of 527 g/day (95% CI: 506.7, 546.5). Based on univariable analysis of the effect of PRRS +/- on the coefficient of variation: farms positive for PRRS had 4.3% more variation in ADG than negative farms (p < 0.05). Based on preliminary results, presence of PRRS virus in nurseries reduces growth and increases variation in growth. Further analysis needs to be done to better elucidate this relationship. This study demonstrates the value of disease monitoring whether or not clinical disease is observed.

12. The effects of testosterone and surgical stress on hippocampal dendritic morphology in adult male rats one month following orchidectomy
Lauren Isaacs, Eric Lawton, Ari Mendell, Neil MacLusky
Department of Biomedical Sciences, University of Guelph
Gonadal steroid and stress hormones induce profound changes in hippocampal dendritic morphology that may contribute to cognitive impairments and the development of neurological disorders. Previous work in our lab has shown that orchidectomy (ORCH) increases apical dendritic branching of pyramidal neurons in the CA3 hippocampal subfield compared to sham-operated control 2-months post-surgery. Current work from our lab shows that ORCH males display similar changes at 10-days post-surgery, while testosterone (T) replacement partially restores CA3 dendritic branching back to levels of intact controls. This is consistent with previous studies showing that short- and long-term recovery of dendritic morphology following ORCH or sham surgery in mice is mediated by circulating T levels. However, the long-term effects of T replacement in male rats remain unknown. We hypothesized that T replacement would aid in the long-term recovery of dendritic morphology in male rats following surgical stress. To test this hypothesis, dendritic morphology of pyramidal neurons in the CA1 and CA3 hippocampal subfields were analyzed in adult male rats sacrificed 1-month following ORCH, ORCH with T replacement (ORCH+T) or sham surgery. Consistent with previous findings, ORCH rats displayed increased CA3 branching compared to the sham controls, with a similar pattern observed in ORCH+T rats. No differences were seen in CA1 dendritic branching or CA1 or CA3 dendritic spine density. These results suggest that there are
important interactions between stress and T that contribute to the regulation of hippocampal dendritic
morphology.

13. Risk-based sample size estimation for scrapie surveillance towards demonstrating freedom from
disease
Jordan Pelkmans¹, Olaf Berke¹, Lorna Deeth², Paula Menzies¹
¹Department of Population Medicine, University of Guelph
²Department of Mathematics and Statistics, University of Guelph
Scrapie is a fatal, neurodegenerative disease of sheep and goats that is part of a family of diseases known
as transmissible spongiform encephalopathies (TSEs). TSEs are contagious and transmitted via infectious
misfolded proteins called prions. Scrapie’s presence in Canada gives Canada’s trading partners legal
grounds to restrict the import of Canadian sheep and goats. In order for these restrictions to be lifted
Canada must demonstrate that it is a country that is free from disease as is defined by the World
Organization of Animal Health (OIE). The OIE sets output-based disease surveillance standards that must
be met to demonstrate freedom from scrapie disease. Risk-based sampling for disease surveillance has
been proposed as a more efficient sampling method than traditional stratified sampling methods.
Efficiency is particularly important in the surveillance of scrapie because there is no reliable live animal
diagnostic test. Risk-based sampling involves dividing the population into risk strata and selecting a larger
sample from higher risk strata to increase the probability of finding a case of scrapie if the disease is
present in the population. This sampling method reduces the sample size required to demonstrate
freedom from disease compared to traditional stratified sampling without sacrificing confidence. This
presentation will outline how risk-based sampling can be used to design an efficient surveillance system
for scrapie in Canada towards demonstrating freedom from disease.

14. Effect of BPA and BPS on AMH expression during in vitro bovine oocyte maturation
Angela Saleh, Laura Favetta
Department of Biomedical Sciences, University of Guelph
Bisphenol A (BPA) and Bisphenol S (BPS), ubiquitous chemicals with endocrine-like functions, have
disrupting effects on oocyte development and, ultimately, on fertility. BPA is a world-wide used plasticizer
detected within blood, urine, tissue samples and follicular fluid. Previous experiments in our laboratory
showed that exposure of in vitro produced bovine oocytes to physiologically relevant doses of BPA
resulted in spindle abnormalities, reduced meiosis progression, increased number of male vs female,
decreased blastocyst rate and gene expression changes. Because of its detrimental effects, BPA has been
recently substituted with its analog BPS. Anti-Müllerian Hormone (AMH) has been shown in our laboratory
to be a good marker of ovarian reserve and oocyte developmental capability. There is evidence that
women undergoing IVF with higher BPA levels have lower AMH levels and pregnancy success. The aim of
this study is to assess the impact of BPA and BPS on AMH and its receptor as a measure of oocyte
developmental capability. Bovine oocytes were in vitro matured in four groups: i) control, ii) vehicle
(0.1%ethanol), iii) BPA (0.05mg/ml), iv) BPS (0.05mg/ml) and collected with (oocyte-cumulus complexes -
COCs) or without cumulus cells. Preliminary results show a decrease in AMH mRNA expression in COCs
and in oocytes without cumulus cells, while there are no changes in cumulus cells on their own following
BPA treatment. In addition, no significant changes in AMH receptor (AMHR) mRNA are detected in COCs
or oocytes, while AMHR is elevated in cumulus cells. Additional experiments will further investigate BPA
and BPS effects on AMH during oocyte maturation and embryonic development.
15. Mosaic reciprocal chromosome translocations in pigs
Samira Rezaei, Daniel Villagomez, Tamas Revay, Brendan Donaldson, Allan King
Department of Biomedical Sciences, University of Guelph
Mosaic chromosome rearrangements may result from post-zygotic events due to mistakes during mitotic division. This type of chromosome rearrangement may be found in one or more cell lineages, depending on the ontogenetic period where this abnormality arises during embryo development. The phenotypic and biological effects of mosaic abnormalities in pigs are unknown and have never been investigated in detail. Alternatively, constitutional chromosome translocations are of germline origin, present throughout the body and well known to cause low fertility. Here we present the first study of mosaic chromosomal translocations in pigs. To identify carriers of mosaic abnormalities, peripheral blood samples were obtained from young boars. Through routine karyotype analysis of 4000 young boars, the King lab at the University of Guelph has found 17 carriers of mosaic reciprocal chromosome translocations. All the 17 carriers were detected with low-level chromosomal mosaicism since less than 9% of cells carry a reciprocal translocation. Interestingly, 12 of the carriers were identified with the same translocation, m(7;9). Additionally, we identified that the dam of a mosaic m(7;9) carrier to have a different translocation, m(9;13), from its offspring. Heritable chromosome abnormalities are major contributors of low fertility, however, there are no reports of mosaic translocations in pigs. This type of chromosome abnormality is hard to detect through routine cytogenetic practices, thus, detection of 17 mosaic translocations within the screened Canadian population is an unexplained phenomenon. Therefore, the biological impacts of mosaic chromosome rearrangements needs to be elucidated in pigs.

16. Antibody responses to porcine reproductive and respiratory syndrome and influenza A viruses from weaning up to the finisher stage in commercial pigs
Elana Raaphorst1, Vahab Farzan2, Pauldeep Virk3, Robert Friendship2, Brandon Lillie1
1Department of Pathobiology, University of Guelph
2Department of Population Medicine, University of Guelph
3Department of Biomedical Sciences, University of Guelph
The present study aims to investigate antibody responses to porcine reproductive and respiratory syndrome virus (PRRSV) and influenza A virus (IAV) in commercial pigs at different stages of production, as well as assess the impact of diet complexity on antibody responses to those viruses. Fourteen groups of 50-60 pigs from eight farrowing farms were followed from birth to the end of the finisher stage. During the nursery stage, piglets were assigned to either a conventional high complexity (HC) or low complexity (LC) diet, in which animal protein was substituted with plant-based protein. Blood samples were collected and analyzed by ELISA. In total, 44.3% and 6.6% of sera (55.6% and 7.5% in the winter cohort and 35.4% and 5.2% in the summer cohort) tested positive for IAV and PRRSV, respectively. Overall, 61% and 7.9% of pigs at weaning, 30.6% and 1.1% of pigs at the end of the nursery stage, 37.7% and 8.2% of pigs at the end of the grower stage, and 47.9% and 10.7% of pigs at the end of the finisher stage tested positive for IAV and PRRSV, respectively. Additionally, 18.6% and 18.9% of sera tested positive for IAV in the HC and LC groups, respectively, while 2.0% (HC) and 4.0% (LC) tested positive for PRRSV. The preliminary findings indicate that diet complexity may not have an effect on antibody responses to PRRSV or IAV while there may be a seasonal variation in antibody responses to IAV. In addition, the maternal antibodies to IAV at weaning appeared to be relatively high, indicating circulation of the virus in the sow population. However, further statistical analyses are required in order to determine the significance of these findings.
17. Neuronal regeneration following injury to the medial cortex of the leopard gecko (*Eublepharis macularius*)

Laura Austin, Matt Vickaryous, Rebecca McDonald  
*Department of Biomedical Sciences, University of Guelph*

Radial glia (RG) are neural stem/progenitor cells capable of spontaneously generating new neurons in the central nervous system. Our lab has identified RG in the leopard gecko (*Eublepharis macularius*), lining the ventricular system of the brain. Under normal physiological conditions gecko RG routinely generate new neurons. However, less is known about their ability to contribute to neuron restoration following injury, a process known as reactive neurogenesis. My research seeks to study reactive neurogenesis in the forebrain of the leopard gecko, and for the first time, correlate structural with behavioural changes after injury. I hypothesize that RG will proliferate and differentiate in response to injury, leading to structural and behavioural recovery. I will use the neurotoxin 3-acetylpyridine (3AP) which has been shown to induce degenerative lesions within the lizard forebrain, especially in the medial cortex (MC). Interestingly these lesions appear to resolve within weeks of 3AP treatment, suggesting that reactive neurogenesis is occurring. My first objective is to characterize the structure of the MC before and at various timepoints following 3AP treatment using protein markers for RG, apoptosis and proliferation, as well as the thymidine analog BrdU to track newly generated cells. My second objective is to quantify the behavioural outcomes of injury and regeneration. Using an open-field monitoring system and a touchscreen chamber, I will evaluate general locomotor activity and extinction of a conditioned response before and at several timepoints after injury. These results will help provide a better understanding of the biology of reactive neurogenesis in vertebrates.

18. Glucocorticoid regulated expression of the G-protein coupled estrogen receptor in immortalized hippocampal neurons

Kate Nicholson, Carolyn Creighton, Ari Mendell, Neil MacLusky  
*Department of Biomedical Sciences, University of Guelph*

Estrogens are well-established to exert neurotrophic and neuroprotective effects within the hippocampus, a vital component of the brain’s learning and memory circuitry. The recently identified G-protein coupled estrogen receptor (GPER) has been shown to bind estradiol with high affinity and mediate many of these neuroprotective effects. Activation of GPER has been shown to exhibit sexually dimorphic effects on both anxiety and cognitive behaviours in rodents. However, the regulation of GPER expression and activation remains poorly understood. Two novel lines of immortalized murine hippocampal neurons, mHippoE-14 and mHippoE-18, have been generated by retroviral infection with a T-antigen. These lines have been characterized for their rapid proliferation and expression of important neurotransmitter and neurosteroid receptor mRNAs. These phenotypically distinct cell lines have been shown to exhibit high levels of GPER and glucocorticoid receptor (GR) expression, while the androgen receptor (AR) appears to be differentially expressed within the mHippoE-14 cells only. As stress exerts profound effects on anxiety and cognitive behaviours, we tested the hypothesis that glucocorticoid exposure might regulate the expression of GPER in the mHippoE-14 and mHippoE-18 cell lines. Cells were treated with 10 nm of dexamethasone, a potent synthetic agonist of GR. Changes in GPER protein expression levels were examined at 10 minutes, 1 hour, 10 hours, 24 hours, and 48 hours time points after treatment. Preliminary findings indicate that GPER expression is downregulated in the mHippoE-14 cell line and upregulated in the mHippoE-18 cell line following 10 nm glucocorticoid treatment.
19. Characterization of microRNA, gene, and protein expression in large and cystic bovine ovarian follicles
Allyssa Hooper, Stacey Del Castillo, Jim Petrik
*Department of Biomedical Sciences, University of Guelph*

Cystic ovarian disease (COD) is a major contributor to infertility in cattle, with 30% of cows developing ovarian cysts and becoming anovulatory. The cause of COD is multifactorial, with both angiogenic and genetic contributions proposed. We aim to characterize the miRNA, gene, and protein expression levels in large and cystic bovine follicles in order to better understand the pathophysiology of COD. Bovine follicles were selected based on diameter and fixed for histology or aspirated to collect follicular fluid (FF) and granulosa cells (GC). Total RNA was extracted from GCs and cDNA was generated. RT-qPCR analyses showed VEGF expression in cystic follicles to be significantly greater than large follicles \((p<0.05)\), however no significant difference in TSP-1 expression was observed \((N=14)\). Western blot analysis showed a significant increase in VEGF protein expression in the FF of cystic follicles \((p<0.05)\) \((N=3)\). Eight different miRNAs which have been shown to target either VEGF or TSP-1 were analyzed including miR-15a, -18a, -20a, -21, -29a, -126, -132, and Let7a. A significant increase in miR-29a \((p<0.05)\) and a significant decrease in miR-132 \((p<0.05)\) was observed in cystic follicles. Immunohistochemistry was performed on GC and theca cell layers of fixed bovine follicles. Protein expression of VEGF, TSP-1, IGF1, IGF2, and VEGFR2 was quantified. A significant increase in VEGFR2 \((p<0.05)\) and TSP-1 \((p<0.01)\) protein expression was observed in cystic follicles. In conclusion, expression of miRNAs and their angiogenic targets were altered in cystic follicles, therefore suggesting that this expression imbalance may be contributing to the development and progression of COD.

20. Veterinarians’ communication of diagnostic test results and data trends during companion animal appointments
Natasha Janke¹, Jason Coe¹, Theresa Bernardo¹, Cate Dewey¹, Elizabeth Stone²
¹*Department of Population Medicine, University of Guelph*
²*Department of Clinical Studies, University of Guelph*

Veterinarians play an important role in the decision-making process of their clients. The clarity and content of veterinary communication can assist clients in making informed decisions, particularly about complex subjects such as diagnostic testing. The American Animal Hospital Association (2015) found that the likelihood of compliance of pet owners with recommendations would increase if diagnostic testing enabled both the veterinarian and the owner to track their pet’s health overtime. Additionally, clients were interested in diagnostic testing for disease prevention and confirming that their pet was healthy. This research examines the extent to which veterinarians engage their clients in the decision-making process and the type of discussion that occurs about diagnostic test results and individual pet’s data trends (i.e. tracking diagnostic test results over time). Veterinarian-client-patient interactions will be captured through audio-video recordings of approximately 1000 companion animal veterinary appointments. Analysis of the videos will provide a description of the current communication practices used to discuss clinical data with clients, and a scoring method will determine the extent to which veterinarians involve clients in the decision-making process. Results will be used to develop evidence-based best practices to benefit veterinarians, clients and veterinary patients.

21. Identifying Eimeria species causing coccidiosis in sheep and goats using molecular and morphological methods
Evelin Rejman¹, Paula Menzies², Cathy Bauman², John Barta¹
¹*Department of Pathobiology, University of Guelph*
²*Department of Population Medicine, University of Guelph*
Protozoan parasites in the genus Eimeria cause coccidiosis in small ruminants with its associated high morbidity and mortality. Several Eimeria species are highly pathogenic and cause an economical burden. Less pathogenic species can be excreted at large numbers with minimal clinical impact and pathogenic species can cause damage with little oocyst shedding; consequently, conventional enumeration methods maybe unreliable for assessing the severity of infections. Further, morphological identification of Eimeria species oocysts is unreliable due to overlapping characteristics. Sequence-based genotyping of specific mitochondrial and nuclear loci is a robust means of identifying Eimeria species. This project will differentiate Eimeria species infecting small ruminants using mitochondrial and nuclear genetic loci and link these molecular data to conventional oocyst morphometrics. Eimeria oocysts were isolated from sheep and goat fecal samples from Canada and abroad. Morphometric data (oocyst/sporocyst dimensions [length, width, shape index] supplemented with oocyst/sporocyst features) were collected (50 oocysts per sample); DNA isolated from samples provided sequence data from genetic loci in the nuclear and mitochondrial genomes (using PCR and NGS amplicon sequencing). Molecular phylogenetics was used to establish relationships among identified species; morphometric data were mapped onto the molecular tree to assist in selecting morphological characteristics that reflect the evolutionary relationships among these genotyped Eimeria species. At least 5 distinct Eimeria species have been detected in sheep fecal samples and at least 4 distinct species in goat fecal samples.

22. Disruption of hippo signaling pathway during bovine preimplantation embryo development
Jyoti Sharma, Diana Carvajal, Pavneesh Madan
Department of Biomedical Sciences, University of Guelph
Blastocyst formation is an important milestone during preimplantation embryo development. Two distinct cell lineages namely trophectoderm and inner cell mass develop during blastocyst formation. Recent studies have shown Hippo signaling pathway to be responsible for lineage segregation during blastocyst formation in murine model. For the first time our lab has established the presence of mRNA transcripts and protein localization of Hippo signaling pathway components (MST2, YAP1 and TAZ) during all the stages of bovine preimplantation embryogenesis. Nevertheless, the role of this cell signaling pathway components in early bovine embryos requires further investigation. Thus, in this study we hypothesize that inhibition of Hippo signaling pathway components disrupt lineage segregation and henceforth the formation of bovine blastocyst. In addition to the components mentioned above, recently mRNA transcripts of Mst1 were detected during all the stages of bovine embryogenesis. To elucidate the role of YAP1/TAZ in bovine embryogenesis, presumptive zygotes were treated with different concentrations (0.5, 1 and 5 µM) of Atorvastatin, a known inhibitor of Hippo signaling pathway. A significant decrease was observed in the cleavage rate of bovine embryos. Further studies comprising GapmeR knockdown (Cdh1) and mass spectrometric analysis will be performed to establish the function of Hippo signaling pathway in the development of preimplantation bovine embryos. The present study will shed more light on the molecular mechanisms involved in cell fate determination, leading to the formation of blastocyst during bovine preimplantation embryonic development.

Steven Lam1, Warren Wood2, Chloe Zivot1, Kelly Skinner2, Andrew Papadopoulos1, IHACC Research Team3, Sherilee Harper1
1Department of Population Medicine, University of Guelph
2School of Public Health and Health Systems, University of Waterloo
3Indigenous Health Adaptations to Climate Change
Many Indigenous communities worldwide face food security challenges, which climate change is expected to exacerbate. Community-based monitoring is increasingly recognized as a crucial strategy for tracking and responding to changes in food security; yet, this approach remains poorly understood, particularly for Indigenous peoples’ food security. Understanding and learning from experiences documented in the literature can help improve food security monitoring efforts. As such, we systematically identified and synthesized the peer-reviewed literature on Indigenous community-based food security and climate change monitoring. We searched AGRICOLA, PRISMA, MEDLINE, CabDirect, and Web of Science databases. We identified 3986 articles, of which 86 met a priori inclusion criteria. We observed a large year-over-year increase in the publication of articles since the first identified publication in 2001. Most research was conducted in North America and South America. Monitoring approaches were mainly categorized as either collaborative local monitoring or externally-driven monitoring. Initiatives focused primarily on wildlife (29%), followed by natural resources (16%), environmental change (15%), fisheries (13%), climate change (9%), and a combination of these topics (18%). Based on our review of these initiatives, we argue that more discussion on the challenges and opportunities of Indigenous community-based monitoring, along with thoughtful consideration of food security, climate change, and gender metrics are necessary to guide monitoring and support adaptive capacity to climate change with these communities.

24. Influence of host factors and seasonality on Baylisascaris procyonis infections in raccoons in Ontario
Shannon French1, David Pearl2, Douglas Campbell1, Andrew Peregrine1, Claire Jardine1
1Department of Pathobiology, University of Guelph
2Department of Population Medicine, University of Guelph
Raccoons (Procyon lotor) are definitive hosts for Baylisascaris procyonis, the raccoon roundworm. This parasite has the ability to infect and cause severe neurological disease in a large range of aberrant hosts, including humans. There is conflicting information regarding the influence of demographic and environmental risk factors on the prevalence of the parasite in raccoons. Our objective was to assess the impact of host factors and seasonality on the occurrence and intensity of infection in raccoons. From 2013-2016, we recorded the number of B. procyonis worms present in the intestinal tracts of 1551 Ontario raccoons submitted to the Canadian Wildlife Health Cooperative for necropsy. Univariable hurdle models were fitted to simultaneously estimate associations between the presence and intensity of infection with the following independent variables: age, sex, body condition, season and year of collection. The odds of having a non-zero count were significantly greater for juveniles vs adults, being in excellent body condition vs poor condition, and being collected during the dispersal season (late summer and fall) vs all other collection seasons. For non-zero counts, the worm count was significantly higher for juveniles. No statistical differences were found between collection years. This improved understanding of the risk factors influencing parasite carriage in Ontario raccoons has the potential to guide public education efforts aimed at reducing the potential for transmission of this parasite to humans.

25. How network analysis can help us understand the 2014 Canadian porcine epidemic diarrhea outbreak
Amanda Perri1, Zvonimir Poljak1, Cate Dewey1, John Harding2, Terri O’Sullivan1
1Department of Population Medicine, University of Guelph
2Large Animal Clinical Sciences, University of Saskatchewan
Porcine epidemic diarrhea virus (PEDV) emerged into Canada in January 2014 and it was suspected that a single feed company (FC) was the likely origin of the virus for the early cases in Ontario. The spray-dried
porcine plasma (SDPP) from FC reproduced the infection under experimental conditions, however the complete feed did not. The objective of this study was to describe the contact structure of feed suppliers and porcine epidemic diarrhea (PED) case and control herds during early months of the 2014 Canadian outbreak. Separate case and control networks were generated to represent contact patterns with feed suppliers. The case network consisted of 21 network nodes (n= 9 case herds; n= 12 feed suppliers) and 161 connections. This network contained 2 weak components. The mean number of direct connections from feed suppliers to herds was 1.8 (range: 1-8). The maximum number of direct and indirect connections among feed suppliers and herds in a sequence was 9 (outgoing contact chain). The control herd network included 27 network nodes (n= 13 control herds; n= 14 feed suppliers) with 105 connections. This network consisted of 5 weak components. The mean number of direct connections from feed suppliers to control herds was 1.4 (range: 1-3). The maximal number of direct and indirect connections among feed suppliers and herds in a sequence was 4. In conclusion, the case network had several network measures which suggested a higher degree of connectivity between feed companies and herds than the control network. This study indicated that FC played an important role in the network as it had the highest number of direct and indirect connections to case herds in the network.

26. Risk assessment for the incursion and establishment of orbiviruses in Ontario, Canada
Samantha Allen¹, Claire Jardine¹, Tara Furukawa-Stoffer², Aruna Ambagala³, Kathleen Hooper-McGrevy³, Mark Ruder⁴, Nicole Nemeth⁴
¹Department of Pathobiology, University of Guelph
²National Centres for Animal Disease, Canadian Food Inspection Agency
³National Centre for Foreign Animal Diseases, Canadian Food Inspection Agency
⁴Southeastern Cooperative Wildlife Disease Study, University of Georgia
Epizootic hemorrhagic disease (EHDV) and bluetongue viruses (BTV) are midge-borne orbiviruses that are imminent threats to Ontario wildlife and livestock populations. They are spreading northward in North America, which may be facilitated by climate change. Recent detection of BTV-seropositive cattle and Culicoides sonorensis midges in the province suggest that Ontario is at risk for EHDV and BTV incursion and establishment. Ontario ruminants are immunologically naïve to these viruses; thus, their introduction may lead to negative impacts on wild cervid populations and livestock (farmed cattle, sheep and deer) through morbidity, mortality and production loss. We sought to characterize Culicoides vector biology and assess for recent and/or ongoing transmission of EHDV and BTV in wild cervids and livestock in Ontario for two field seasons (2017-2018). From May-Oct. 2017, LED light traps were placed on farms and natural areas in southwestern Ontario, and Culicoides spp. were taxonomically and molecularly identified. Blood from wild cervids and livestock were screened for antibodies by ELISA and confirmed by virus neutralization assay. Thus far, we have collected 1460 Culicoides spp., including individuals of the following species: C. variipennis, C. crepuscularis, C. stellifer, with C. stellifer as the most commonly identified species. Data will be analyzed for regional and temporal patterns in vector distribution and disease associations with age, sex, seasonality, and weather. Furthermore, in Sept. 2017, we identified two white-tailed deer that died of EHDV and 15 seropositive cattle (both serotype 2); these represent the first EHDV cases reported in Ontario.

27. 25-hydroxyvitamin D concentrations in dogs with lymphoma during chemotherapy treatment
Nicole Weidner¹, J Paul Woods², Anthony J Mutsaers¹,², Julie Bayle³, Adronie Verbrugghe²
¹Department of Biomedical Sciences, University of Guelph
²Department of Clinical Studies, University of Guelph
³Royal Canin Research Centre
Lower blood vitamin D concentrations (25-hydroxyvitamin D (25(OH)D)) have been reported in dogs with lymphoma, but no studies have followed 25(OH)D concentrations in these dogs over chemotherapy. This study determined 25(OH)D concentrations of healthy dogs and dogs with lymphoma at baseline, and investigated if 25(OH)D increased when lymphoma dogs were in remission. Client-owned dogs with lymphoma (n=24) and healthy dogs (n=25) were enrolled. Initial blood samples were collected from both groups. At week 6 of chemotherapy, another blood sample was drawn from lymphoma dogs, and remission status was recorded. Plasma 25(OH)D was analyzed with radioimmunoassays. Healthy dogs had higher 25(OH)D than lymphoma dogs (means±SD=128±40nmol/L, 96±33nmol/L, p=0.004). Most lymphoma dogs had 25(OH)D concentrations within the laboratory reference range at baseline (20/24, 83%) and at week 6 (21/24, 87%). 20/24 dogs were in remission at week 6. 25(OH)D concentrations were similar before treatment and after remission (means±SD=94±34nmol/L, 87±31nmol/L, p=0.695). 25(OH)D were also similar before treatment and at week 6 for 4 dogs not in remission (means±SD=109±28nmol/L, 110±21nmol/L, p=1.000). The clinical relevance of decreased 25(OH)D with lymphoma is unclear, as most dogs fell within the lab reference range. More work is needed to define optimal 25(OH)D concentrations, as many reference ranges consider bone health only. Since 25(OH)D concentrations did not change after remission, 25(OH)D may already be sufficient and unresponsive to remission state. Dogs may have needed to be in remission for &gt;6 weeks before 25(OH)D improved. More work is needed to understand why 25(OH)D did not change.

28. Chromosomal landmarks of porcine reciprocal translocations
Brendan Donaldson1, Tamas Revay1, Daniel Villagomez2, Samira Rezaei1, Allan King1
1Department of Biomedical Sciences, University of Guelph
2Department of Animal Production, University of Guadalajara
During meiotic cell divisions chromosomes may break and subsequently mis-repair, creating a rearrangement between two nonhomologous chromosomes. Chromosome rearrangement (CR) carriers present without phenotypical effects, however experience predictable reproductive declines of approximately 50%. CR are prevalent in pigs, occurring in 1/200 live births, however the genetic factors behind CR formation remain unknown. Thus, it is important to study their nature thoroughly to elucidate the mechanisms behind chromosomal rearrangement formation. To study the structural nature of CR we reviewed the literature, as well as rearrangements found in our own laboratory, and conducted a comprehensive analysis of all known CR. This included examining the positions of the rearrangement breakpoints in relation to whole chromosome organization: length and large structural features, as well as trends in rearrangement positions. Our study analysed 188 reciprocal translocations, with 340 defined chromosome breakpoints. We demonstrate that proximity to large structural features has no relationship to the number of rearrangement events, while length is positively associated with CR. In contrast we show that breakpoints preferentially occur in light cytogenetic bands (84%), a relationship strengthened by the presence of a fragile site. Additionally, 16 cytogenetic bands which constitute 5.5% of bands, but 27% of breakpoint locations are highlighted as potential genomic hotspots for rearrangement. From our research we show that CR occur non-randomly, and demonstrate molecular logic, preferentially locating themselves within light GTG-cytogenetic bands.
Oral abstracts (Session I: 1:30-2:10)

Room: PAHL 1812

1. Educating dairy producers to systematically evaluate the cows they cull
   Allison Moorman¹, Todd Duffield³, Ann Godkin², David Kelton¹, Derek Haley¹
   ¹Department of Population Medicine, University of Guelph
   ²Veterinary Science, Ontario Ministry of Agriculture, Food, and Rural Affairs
   According to section XII of the Canadian Health of Animals Regulations, dairy cattle must meet certain health and welfare standards to be eligible to be transported. Recent research has documented that dairy cattle have been transported to auction markets, despite being physically unfit for transport. To help prevent this from occurring, a cow evaluation form was designed to guide dairy producers in assessing whether cows being culled were suitable for transport. A total of 16 veterinarians and 54 dairy producers participated in this study. All participants received a pre-study survey to assess their knowledge and attitudes regarding culling cows, and a post-study survey to determine whether their knowledge and attitudes had changed as a result of using the form. Producers completed an evaluation form for every cow they culled from the milking herd between January and August, 2017. Results indicated that use of the form encouraged producers to record more information on the cows they were assessing, spend more time deciding whether a cow was fit for transport, and use the form as a documented SOP for transporting cattle. Results also showed that participants’ confidence increased after using the evaluation form. The form, however, was not effective in educating producers and veterinarians about Canadian transport requirements. Lastly, there was no increase in the amount of veterinarian involvement in the decision to cull and transport after implementation of the form. The potential implications of this project include providing producers with an effective tool to help assess their cattle prior to transport, and prevent the transport of unfit cattle.

2. Understanding the relationship between tonsil microbiota and clinical Streptococcus suis infection in nursery pigs
   Sarah Hill¹, Sarah MacInnes¹, Vahab Farzan²
   ¹Department of Pathobiology, University of Guelph
   ²Department of Population Medicine, University of Guelph
   The gram-positive bacterium Streptococcus suis is part of the normal commensal microflora (microbiota) of the upper respiratory tract (URT) of pigs of all ages. However, in response to unknown factors, S. suis can cause disease leading major economic losses in the swine industry. The tonsils of the soft palate are an important site of bacterial colonization in the URT. Although these tonsils are secondary lymphoid organs that survey, detect and initiate the immune system they have a large number of small indentations (crypts) that may be the portal of entry for S. suis and other pathogens. Currently, it is not known why some pigs remain healthy while others develop clinical S. suis disease. The aim of the current research is to compare the microbiota of healthy and S. suis affected piglets, in the hopes of being able to identify bacterial species that might promote or inhibit S. suis disease. The tonsils of the soft palate were removed from “healthy” culled animals and from weanling pigs with signs of S. suis disease, and subjected to DNA extraction. Illumina MiSeq sequencing of the 16S V3-V4 hypervariable region was done to assess the composition of the microbiota. Phylogenetic classification of the bacteria making up the microbiota was assigned using the 16S Metagenomics app available as part of the Illumina BaseSpace Sequencing hub. Based on preliminary data, it appears that there are spatial differences in the microbiota of the tonsil of the soft palate of swine, but the 5 core phyla are Firmicutes, Bacteroidetes, Fusobacteria, Proteobacteria and Actinobacteria.
3. *In vitro host restriction of aquatic bird bornavirus-1 in different avian fibroblasts*
Alex Leacy¹, Li Deng², Eva Nagy¹, Nicole Nemeth³, Csaba Varga⁴, Leonardo Susta¹

¹Department of Pathobiology, University of Guelph  
²Department of Pathology and Molecular Medicine, McMaster University  
³Department of Pathology, University of Georgia  
⁴Ontario Ministry of Agriculture, Food, and Rural Affairs

Viruses of the family *Bornaviridae* are the causative agents of neurological disease in a variety of vertebrate hosts. Avian bornaviruses, first identified in 2008, were determined to be the cause of proventricular dilatation disease (due to ganglioneuritis) in captive psittacine birds. More recently, it was revealed that a divergent virus, aquatic bird bornavirus (ABBV), is highly prevalent among migratory waterfowl (swans, geese) and is associated with ganglioneuritis and encephalitis. Additionally, ABBV strains have been sporadically isolated from other birds, including gulls, bald eagles, and emus, suggesting a broad host range. Given the ability to infect multiple species, strains of ABBV may have the potential to infect commercial poultry (i.e., chickens and turkeys). In this study, we aimed to evaluate the host restriction of ABBV through *in vitro* replication kinetics in primary embryonic fibroblast cell lines of geese, ducks, chickens, and turkeys using single step and multi-step growth curves. Virus replication was assessed by immunofluorescence, as the percentage of cells positive for viral nucleoprotein (infected) in the total cell population over time. Results showed that ABBV replicated well in goose and duck embryo fibroblasts but that infection and spread of virus was limited or non-existent in chicken or turkey fibroblasts. This research is the first to characterize ABBV in *vitro*.

4. *Feather damage in Canadian laying hens and its associations with furnished cage housing and management factors – a cross-sectional study*
Caitlin Decina¹, Olaf Berke¹, Nienke van Staaveren², Christine Baes², Tina Widowski², Alexandra Harlander²

¹Department of Population Medicine, University of Guelph  
²Department of Animal Biosciences, University of Guelph

Feather pecking is a continuous welfare challenge in the housing of egg-laying hens. Canada is currently making the transition from conventional cages to alternative housing systems. However, feather damage (FD) due to feather pecking remains a welfare concern despite increased space allowance and better opportunity to perform natural behaviours. With the goal of improving hen welfare in practice, an explorative approach was taken to assess bird, housing, and management associations with FD in Canadian laying hens housed in alternative systems. A questionnaire, focused on housing and management practices, was designed and administered to 122 laying farms nation-wide in autumn of 2017 (response rate of 52.5%), providing information on a subset of 26 flocks kept in furnished cages. Additionally, a three-point feather cover scoring system was developed for farmers to estimate the prevalence of FD present on-farm. Farmers assessed a sample of 50 birds per flock. Flock prevalence of FD was determined. Linear regression modeling was applied to explain FD prevalence as a function of 6 (out of 54 available) variables. Of the 6 modeled variables, age, brown feather colour, midnight feeding, and no access to a scratch area were found to be associated with higher levels of FD. The model explains 77% of variation in the FD prevalence at farm level (R²=0.77). The results indicate that FD, as a result of feather pecking, is a multifactorial problem and support existing evidence that FD increases as birds age. These results also suggest that genetics, feeding patterns/management, and access to (or lack of) a scratch area of any type play a role in FD prevalence in furnished cages.
1. Growth factors expression by cardiac tissues in the leopard gecko (*Eublepharis macularius*)
Kathy Jacyniak, Matthew Vickaryous
*Department of Biomedical Sciences, University of Guelph*

Tissue homeostasis is a dynamic process involved in the maintenance of tissue structure and function in response to physiological fluctuations in biochemistry, metabolism, and physical conditions. Despite the profound role that growth factors play in homeostasis of organs such as the heart, constitutive patterns of expression are only known for a handful of species. Here, we investigated growth factor expression in the heart of a representative reptile, the leopard gecko (*Eublepharis macularius*; hereafter, ‘gecko’). We focused our investigation on three major classes known to be expressed by mammalian cardiac tissues: transforming growth factor β (TGFβ); vascular endothelial growth factor A (VEGF); and basic fibroblast growth factor (FGF-2). Similar to other squamates (snakes and lizards), geckos have a three-chambered heart with two atria and one ventricle. The ventricular myocardium includes a trabeculated or spongy-like inner compartment, and a thin, compact cortical layer. We determined that cardiac cells in both compartments of the gecko myocardium (trabeculated and compact) constitutively express a diverse panel of growth factor ligands and receptors commonly associated with wound healing and repair, including: TGFβ1, activin-βA, and phosphorylated SMAD2; FGF-2; and VEGF, VEGF receptor 1 (VEFGR1), VEGFR2, and phosphorylated VEGFR2. Using double immunofluorescence, we observed co-localization of VEGF/VEGFR2 and VEGFR1/VEGFR2, indicating that – similar to mammals – reptilian cardiomyocytes may use paracrine and autocrine signalling. Taken together, these findings indicate a homeostatic role for these growth factors in the heart that is conserved across vertebrates.

2. Reducing dog fear during veterinary visits
Anastasia Stellato1, Tina Widowski2, Cate Dewey1, Lee Niel1
1*Department of Population Medicine, University of Guelph*
2*Department of Animal Biosciences, University of Guelph*

Companion dogs are can be fearful during veterinary visits and dogs are often separated from their owners for certain aspects of their visit. The effect of this separation has not yet been examined during these visits and thus our objective was to evaluate the influence of owner presence on behavioral and physiological indicators of fear during a routine physical exam in a veterinary clinic. Dogs received a standardized physical examination with (n=16) or without (n=16) their owner present. For behavioral measures, mixed poisson and logistic regression models assessed the effects of owner presence, exam phase, sex, and age, with dog as a random effect or repeated measure. For physiological measures, linear regression models and t-tests were used. When the owner was present versus absent, dog had a reduced rate [95% CI] of vocalizations (present, 0.11 vocalizations/min [0.03-0.39] vs absent, 1.84 vocalizations/min [1.2-2.8]; F(1,29)=19.84, p<0.0001), reduced mean temperature (present, 37.2˚C [36.7-37.7] vs absent, 38˚C [37.5-38.5]); F(1,27)=6.13, p<0.02), increased rate of yawning (present, 0.24 yawns/min [0.08-0.69] vs absent (0.05 yawns/min [0.01-0.21]; F(1,30)=4.25, p<0.048). When the owner was present, female dogs had a reduced heart rate (F(1,27)=4.4, p<0.046) and older dogs had a lower lip licking rate (F(1,28)=6.39, p<0.0174). Results suggest that owners are able to reduce fear levels in dogs when present during an examination and should be encouraged to remain with their dog whenever possible during veterinary visits.

3. Infection of stimulated leukocytes by oncolytic viruses: Implications for single- versus multi-dosing protocols
Ashley Ross1, Amanda AuYeung1, Robert Mould1, Thomas McAusland1, Jim Petrik2, Sarah Wootton1, Byram Bridle1
The field of oncolytic virotherapy was founded on the premise that the dominant mechanism of action was direct virus-mediated killing of cancer cells. This resulted in a paradigm of rapid, repeated delivery of oncolytic viruses (OVs) to maximize infection of tumours before the immune system cleared the virus. However, recent research argues that induction of tumour-specific immune responses is an equally important mechanism. If OVs are to be used as in situ or conventional transgene-encoding vaccines, the ideal dosing regimen may need to be reconsidered. From an immunological perspective, rapid, multi-dosing protocols for vaccines are usually avoided. Further, studies have shown that activation of leukocytes can promote their infection with viruses. Therefore, we hypothesized that activated leukocytes might become susceptible to killing by OVs, making single-dosing regimens superior in some contexts. In vitro flow cytometry studies demonstrated that activation of spleen- and bone marrow-derived leukocytes with PMA and ionomycin rendered CD4+ and CD8+ T-cells and natural killer cells susceptible to infection with vesicular stomatitis virus (VSV) expressing green fluorescent protein (GFP). Flow-sorted GFP-positive cells died due to infection. Intravenous administration of VSV to mice followed two days later by VSV-GFP showed that multi-dosing potentiates infection of leukocytes in vivo. Moreover, multi-dosing with a VSV-vectored booster vaccine at a two-day interval abrogated survival of mice with intracranial melanomas, as compared to a single-dose protocol. These results suggest that optimal dosing frequencies should be carefully evaluated before OVs enter clinical trial.

4. Whole genome analyses of *Escherichia coli* positive for the blaCTX-M gene family collected from chicken, swine, beef cattle, and dogs in Canada
Ashley Cormier, Pauline Zhang, Gabhan Chalmers, Patrick Boerlin
Department of Pathobiology, University of Guelph

The increase in extended-spectrum cephalosporins (ESCs) resistance in *Escherichia coli* recovered from animals and people in Canada is of particular concern since this class of antibiotics is widely used for the clinical treatment of infections. Domestic animals have been suggested as a vehicle for the transfer of resistant bacteria to humans through the food chain and/or direct contact. Historically, ESC resistance in Canada has been mostly attributed to variants of the TEM, SHV and CMY β-lactamase families. This is beginning to change as we are now seeing the emergence and spread of the CTX-M family among bacterial isolates recovered from various animal species. Here we use whole genome sequencing to compare CTX-M-positive *E. coli* isolates from chicken (n=33), swine (n=23), beef cattle (n=67), and dogs (n=42) collected in Canada between 2014 and 2016. Genome sequences were obtained and whole genome multi-locus sequence typing was used to compare these isolates. The CTX-M-1, -14, and -15 variants were found among *E. coli* from all animal species, at various levels of frequency; the CTX-M-27, and -55 variants were found among 4/5 species. Isolates from different species do not appear to be closely related, however some clustering within some species is apparent. The presence of the same variants across animal species demonstrates the critical role of mobile genetic elements in the spread of CTX-M in Canada. Most noteworthy of these are the CTX-M-14-15, -27 and -55 variants that have been associated with the global spread of CTX-M in humans and whose presence, could be indicative of transfer between human and animals.

Room: LLC 1713

1. Changes in pet feeding practices over the past decade
Sarah Dodd1, Nick Cave2, Jennifer Adolphe, Anna-Kate Shoveller3, Adronie Verbrugghe1
1Department of Clinical Studies, University of Guelph
2Institute of Veterinary, Animal, and Biomedical Sciences, Massey University
Trends in companion animal nutrition often shadow trends in human nutrition, and a perception exists among veterinarians that many pet owners now prefer ‘natural’ and ‘holistic’ diets over processed foods. The purpose of the study was to determine what and how dog and cat owners feed their pets and to compare to a study published ten years ago (Laflamme et al. 2008). A survey was promoted to general pet owning and pet appreciation groups. Approval by the research ethics boards of participating institutions was granted (REB #17-08-029). Descriptive data were reported as percentages, while significant differences between the two studies were determined using Chi Square analysis, with significance set at p < 0.05. Information from Australia and the United States only were included for analysis. Where data were comparable, significant differences in feeding practices over time included: increase in feeding homemade and raw diets, decrease in daily feeding of treats, and decrease in feeding a commercial diet as the main food source in both dogs and cats. Additionally, an increase in exclusive feeding of homemade diets was also detected in cats only. In essence, the trend appears to be a shift in pet nutrition away from complete and balanced diets, in favour of home-prepared ‘human’ foods and raw meat diets. These changing practices may predispose pets to dietary imbalances, nutritionally-responsive diseases, and infectious diseases. Given this information, clinicians must be aware of the risks associated with homemade and raw diets, obtain comprehensive dietary histories from their clients, and be prepared to diagnose and treat nutritionally associated diseases.

2. Epidemiology of canine heartworm (*Dirofilaria immitis*) infection in domestic dogs in Ontario: geographic distribution, risk factors and effects of climate
   Erin McGill¹, Olaf Berke¹, Andrew Peregrine², Scott Weese²
   ¹Department of Population Medicine, University of Guelph
   ²Department of Pathobiology, University of Guelph

*Dirofilaria immitis* is the causal agent of heartworm infection, a mosquito-borne parasite that primarily infects domestic and wild canines. In Canada, the recommendation for preventive treatment is to treat dogs in risk areas seasonally (June to November) with anthelmintic drugs. The current status of heartworm infection among domestic dogs in Canada requires re-evaluation due to climate change, as countries in Europe and the US have observed a change in distribution of heartworm that has been associated with climate change. Serological test results submitted by veterinary clinics for the years 2007-2016 were used to conduct a spatial risk analysis of heartworm in domestic dogs in Ontario. Ontario has previously been identified as a hot spot for heartworm infection in Canada. The geographic extent of the apparent heartworm prevalence in Ontario was examined through smoothed choropleth maps for all 49 census division regions. The regions were assessed for local hot-spots in apparent prevalence using a flexible spatial scan test. Three hot spots were found: western Ontario (Rainy River), southern Ontario (Chatham-Kent, Lambton, Elgin, Oxford, Haldimand-Norfolk) and eastern Ontario (Renfrew and Lanark). A spatial Poisson regression model was used to assess the impact of dog age, human population density, heartworm development units (HDUs), precipitation, and moisture index on heartworm infection risk among domestic dogs in Ontario; spatial distribution of HDUs and human population density were identified as important predictors of heartworm infection among domestic dogs in Ontario.

3. Growth performance in antibiotic-free and conventional swine nursery herds in Ontario
   Karen de Bruyn¹, Robert Friendship¹, Vahab Farzan¹, Terri O'Sullivan¹, Paisley Canning²
   ¹Department of Population Medicine, University of Guelph
   ²Southwest Veterinary Services

Introduction: In the nursery barn, piglets that are newly weaned and are losing passive immunity are mixed together in an environment where endemic diseases seem to linger. This stressful transition may result in reduced growth rate and increase susceptibility to disease. Feeding low levels of antibiotics in
feed is a common practice that is used to improve growth rates in the nursery barn. However, due to public concern about antibiotic usage, pigs being raised without antibiotics is a growing niche market in Ontario. The objective of this study is to compare growth rates of antibiotic-free nursery pigs to those of conventionally raised nursery pigs.

Methods: A preexisting data set containing 21 conventional nursery barns was used. Samples were collected from antibiotic-free nursery barns. Each barn was visited shortly after pigs entered the nursery and again shortly before they left. At the first barn visit, producers answered a survey describing their management practices. Twenty pigs at each farm were selected and tagged. The selected pigs were weighed at both visits. Weight gain and average daily gain (ADG) were calculated for each pig and used to determine the average production parameters for each farm.

Results: Preliminary results comparing 6 antibiotic-free nurseries to the 21 conventional farms show that the mean growth rate of antibiotic-free farms is lower, at 380.5 g/day, than that of conventional farms at 469.2 g/day.

Conclusions: Antibiotic-free nursery pigs may have lower growth rates than conventionally raised nursery pigs. However, the variation that may exist between management practices of the two production types need to be investigated.

4. Tracking molecular disease in canine lymphoma

Akash Jairaj1, Stefan Keller1, Dorothee Bienzle1, Anthony Mutsaers2,3, Victoria Sabine2, Karolina Skowrons1, Olaf Berke4, Nikos Darzentas5,6

1Department of Pathobiology, University of Guelph
2Department of Clinical Studies, University of Guelph
3Department of Biomedical Sciences, University of Guelph
4Department of Population Medicine, University of Guelph
5Department of Internal Medicine II, University Hospital Schleswig-Holstein
6Central European Institute of Technology, Masaryk University

One quarter of all canine neoplasms are lymphomas. Multicentric B cell lymphoma (mBCL) is the most common type. Despite the standard of care treatment (CHOP), remission rates and duration vary. Minimal residual disease (MRD) assessment by next generation sequencing (NGS) is used to monitor treatment efficacy and to detect early relapse in human medicine. The aims of this ongoing study are: 1) to determine whether MRD assessments in canine lymphoma can predict time to relapse or overall survival, 2) to determine the best sampling time points, and 3) to assess whether cell-free DNA (cfDNA) or cell-associated DNA (caDNA) collected from peripheral blood is a more sensitive sample type. To date, clinical inclusion criteria were met and study consent was obtained for 45 patients. Of these, 31 were of B cell lineage, and in 26 the neoplastic clone was detected in lymph node aspirates. Blood samples were collected at 2-4 week intervals during 26 weeks of treatment and at 1-3 month intervals thereafter, and separated into cell-associated (PBMC) and cell-free (plasma) fractions. MRD assessment by NGS has been completed for one patient. This patient went into complete remission within 8 weeks, relapsed 8 months after initiation of therapy and was euthanized 2 months thereafter. The neoplastic clone could be identified by NGS 7 weeks before clinical relapse. The neoplastic clone could be detected more readily from cfDNA (plasma) than from caDNA (PBMCs). Our preliminary data suggests that relapse may be detected more sensitively by NGS than by clinical assessment. However, additional data is required to substantiate these results and assessment of additional patients is in progress.
1. Tissue specificity of ruminant respiratory oncogenic retroviruses JSRV and ENTV
Maria Rosales Gerpe¹, Scott Walsh², Laura van Lieshout¹, Jakob Domm¹, Sarah Wootton¹
¹Department of Pathobiology, University of Guelph
²Department of Pathology and Molecular Medicine, McMaster University
Studying the oncogenic and pathogenic properties of retroviruses has helped shed light on cellular mechanisms such as oncogenesis. Two small ruminant betaretroviruses which have contributed to our knowledge of oncogenesis are Jaagsiekte Sheep Retrovirus (JSRV) and Enzootic Nasal Tumour Virus (ENTV). JSRV and ENTV share high homology at the nucleotide and protein level, utilize the same cellular receptor, Hyal2, and drive oncogenesis through an envelope (Env) glycoprotein; yet, they target different areas of the respiratory tract, the lung and nasal tract, respectively. Interestingly, the morphology of JSRV Env-induced ovine lung adenocarcinoma is reminiscent of human bronchioloalveolar adenocarcinoma, a rare cancer largely affecting never-smoker females. This tissue selectivity and disease morphology make them great tools to study oncogenesis. To uncover the genetic determinant for tropism, we constructed JSRV-ENTV hybrids within a JSRV backbone and established different lentivirus pseudotypes. We also developed a tissue slice ex vivo model to circumvent JSRV and ENTV’s cell polarity problems. Through infection of lung and nasal turbinate slices, we observed that the viral envelope protein is crucial for entry, but that the promoters of these viruses are likely responsible for tissue-specificity. Interestingly, we also found that Hyal2 abundance seems to act as the limiting step for ENTV entry. Furthermore, we show positive staining for ENTV Env in ENTV-infected ovine nasal turbinate tissue’s extracellular matrix (naturally enriched with Hyal2). Finally, our work points to a tentative novel ENTV pathogenic mechanism, and promoter and envelope protein concerted effort.

2. Developing a comprehensive evaluation framework for the Nurturing Neighbourhoods Initiative of Guelph, Canada
Aarabhi Rajendiran
Department of Population Medicine, University of Guelph
The overall purpose is to develop a program evaluation framework that will measure the impact of the Nurturing Neighbourhoods Initiative (a community based population health intervention) and will provide a greater understanding of how a broad community initiative can address the needs of vulnerable populations (specifically through preventing and mitigating adverse childhood experiences and building resilience), thus advancing the current understanding of neighbourhood-based early interventions in the field of population health intervention research. To achieve the purpose, this research project aims to use research methods to: 1. Evaluate the NNI to gain an understanding of the evolving needs of children and families in priority neighbourhoods; 2. Identify important factors that will lead to the successful implementation and adaptation of NNI and; 3. Measure its impact on the health and well-being of vulnerable children and families. This project will build upon the initial evaluations of the Parent Outreach Worker program by collaborating with stakeholders to identify important measures of impact that are not currently being tracked. This research will address the need for early community-based interventions to prevent chronic disease by evaluating how neighbourhood-based initiatives can be implemented to successfully support vulnerable populations.

3. Investigation of transportation practices in an Ontario swine system using descriptive network analysis
Dylan Melmer, Terri O’Sullivan, Zvonimir Poljak
Department of Population Medicine, University of Guelph
The transportation of livestock, and in particular, the use of transportation vehicles to move them can play an important role in disease spread between locations. Therefore, knowledge regarding livestock movement patterns is essential for understanding the potential for disease spread and control. A dataset containing animal movements among 224 swine production facilities was obtained from an Ontario swine management company. The data contained 5,398 unique movements that occurred between January and December of 2015. These data were then used to construct networks of contacts between production facilities that occurred over a weekly period, after considering connections through transportation vehicles. From each of these series of contacts, features of networks that could be critical for understanding the potential for disease spread were extracted and examined over time. The maximum MWCw ranged from 3 to 123 facilities, and significantly increased during the year \( (p<0.01) \). The composition of MWCw was stable over time, with trucks accounting for an average of 24% of the MWCw, but only 11% of the trucks in the source population were present in the MWCw. Number of facilities with high betweenness and high in-out degree value (i.e. transfer points in animal movement) was higher during warmer period of the year \( (p<0.05) \). The number of trucks utilized per week was increasing as the year progressed \( (p<0.01) \), together with the number of trucks that had a high betweenness \( (p<0.01) \). The network analysis presented here makes it possible to conceptualize how disease could spread within a network, either through potential outbreak size (MWCw), or node measures (betweenness/degree).

4. Exploring the management of companion animal euthanasia and support of bereaved pet owners
Alisha Matte, Deep Khosa, Michael Meehan, Jason Coe, Lee Niel
*Department of Population Medicine, University of Guelph*

Previous research has shown that pet owner grief related to companion animal euthanasia may be affected by the actions of their veterinary professionals (VPs). Underexplored however, is how VPs are currently managing companion animal euthanasia and pet owner support. Following a two-phase mixed-method study design, phase one consisted of focus groups \( (n=10) \) with companion animal clinic staff. Thematic analysis of verbatim transcripts resulted in three main themes relating to the management of companion animal euthanasia; 1) VPs utilize technical protocols which they feel are most likely to result in a successful euthanasia and, 2) VPs integrate pet owner support into almost every aspect of euthanasia, such as preparing a private space to sending a condolence card and, 3) VPs desire better access to acceptable grief counselling services for pet owners. Phase one results informed the development of phase two, an online questionnaire surveying Ontario VPs \( (n=774) \) who assist with or perform companion animal euthanasia. Descriptive statistics provided insight into the most common practices currently used by VPs. Results support qualitative findings in so far that veterinarians technical protocols may differ from one another (e.g. sedation or intravenous catheter use), use a variety of methods to support pet owners, and few clinics are using grief counselling services or resources to support pet owners. Findings suggest that VPs are confident in performing euthanasia, assisting and supporting pet owners through euthanasia, but are not satisfied with current pet owner counselling services. These findings highlight areas which warrant further exploration and additionally, provide VPs with information that may enhance their owner management of companion animal euthanasia and client support.
1. Distance support for on-farm investigation of adult small ruminant mortalities
Jeanette Cooper¹, Andria Jones-Bitton¹, Paula Menzies¹, Jocelyn Jansen², Maria Spinato³
¹Department of Population Medicine, University of Guelph
²Ontario Ministry of Agriculture, Food, and Rural Affairs
³Animal Health Laboratory, University of Guelph
Improving the overall health of a sheep flock or goat herd can reduce mortalities and improve productivity on-farm, thereby improving profitability for small ruminant producers. Postmortems on adult small ruminants are rarely performed, likely due to low animal value, or poor understanding of the value in knowing why an animal died, which can prevent the improvement of flock or herd health. The “Distance support for on-farm investigation of adult small ruminant mortalities” project has therefore developed a tool to facilitate the performance of postmortems by veterinarians on farm and their submission to the Animal Health Laboratory. The project has thus far accepted over 70 sheep and goat postmortem cases. Preliminary results showed nasal adenocarcinoma, copper toxicosis, and dental disease were major causes of death in sheep. In goats, major causes of death included caprine arthritis encephalitis (CAE), clostridial enterotoxaemia and pneumonia. It is perceived that a health management approach to veterinary services for small ruminants has not been well adopted. Additional research will utilize focus groups to explore the attitudes of veterinarians and producers towards flock and herd health services and what motivations and barriers exist towards adoption of a more robust flock or herd health management program.

2. Stimulation of nasal innate immune responses to aid in prevention of bovine respiratory disease
Ksenia Vulikh¹, Laura Bassel¹, Shayan Sharif³, Janet MacInnes¹, Joanne Hewson², Lauren Sergejewich¹
¹Department of Pathobiology, University of Guelph
²Department of Clinical Studies, University of Guelph
It is well known that bacteria, such as Mannheimia haemolytica, under the influence of stress provoke bovine respiratory disease (BRD), an economically important disease for the Canadian beef industry. This research seeks to clarify if bovine tracheal antimicrobial peptide (TAP) plays any significant role in directly reducing amount of M. haemolytica in the nasal cavity of calves. In previous studies, bovine TAP reduced the population of M. haemolytica in vitro. The hypothesis of this research is that tracheal antimicrobial peptide, delivered to the nasal cavity of cattle, should reduce the population of intranasal M. haemolytica in vivo. We use partially colostrum-deprived calves challenged at 1-month-old by aerosolized M. haemolytica, then one group is treated with TAP, and the other group receives water. After 5 days calves are euthanized and nasal tissues, tonsils and lymph nodes are sampled to determine the effect of TAP on M. haemolytica infection status using histology, qPCR and bacterial culture. A set of in vitro experiments was also done, clarifying the relevance of salt levels, serum, and peptide types (oxidized vs. non-oxidized) in the bactericidal activity of this defensin. We found that salt levels are important to TAP activity, while peptide oxidization does not have any significant effect, and studies of the effect on innate immune responses are pending. Our in vivo experiments are still in progress but preliminary findings will be presented.

3. Extended-spectrum cephalosporin and gentamicin resistance in Escherichia coli from Canadian turkeys
Jonathan Moffat¹, Patrick Boerlin¹, Gabhan Chalmers¹, Agnes Agunos², Mike Mulvey³
¹Department of Pathobiology, University of Guelph
²Public Health Agency of Canada
The goal of this study is to determine the prevalence of resistance in Escherichia coli from turkeys to the critically important subclass of antibiotics, extended-spectrum cephalosporins (ESCs) as well as gentamicin and their associated resistance determinants. Susceptibility to these antibiotics was assessed using the disc diffusion method and genes responsible for ESC and gentamicin-resistance identified via PCR. E. coli isolated from turkey fecal samples with and without cephalosporin enrichment were compared to diagnostic submissions. Low prevalence of ESC resistance was found in isolates from both diagnostic submissions and fecal samples without enrichment, however, using enrichment 65% of samples were found to contain ESC-resistant E. coli. The majority of this resistance, 72%, was caused by the well-established CMY beta-lactamase, but 13% were caused by the emerging CTX-M beta-lactamases. Of the isolates that were enriched for cephalosporin resistance, 37% are resistant to gentamicin as well, compared to only 20% of isolates that were gentamicin resistance when there was no selection for ESC resistance. These data show that although few E. coli are resistant to ESCs, they can be found at low concentrations in a majority of fecal samples from turkey. As well, it appears that ESC-resistant isolates are also more likely to have gentamicin resistance than generic isolates. Our results also show that the genetic determinants for ESC resistance in E. coli from turkey may be evolving.

4. Evaluating the stringency and comprehensiveness of indoor tanning legislation across Canada
Sydney Gosselin, Jennifer McWhirter
Department of Population Medicine, University of Guelph
Skin cancer is the most common cancer in Canada. Ultraviolet radiation emitted by tanning equipment is known by the International Agency for Research on Cancer to cause skin cancer. Canadian provinces and territories have legislation to regulate access to and use of commercial indoor tanning services. This legislation has not been analyzed. To assess the components of these laws, we conducted a content analysis. Acts and regulations were collected from a Canadian legal database. Supplementary information was obtained from health ministry websites. A directed content analysis of legislative information was conducted using a 59-variable codebook developed based on previous research and evidence-based guidelines. All ten provinces and one of three territories had legislation to regulate indoor tanning. All prohibited youth from accessing indoor tanning services. Seven (64%) prohibited advertisement to youth, five (46%) restricted misleading advertisements toward youth, and two (18%) prohibited misleading advertisements toward the general public. Ten (91%) required the posting of health warning signs. Four (36%) required inspections of tanning facilities at a specific frequency. Four (36%) mandated the use of protective eyewear. No jurisdiction required clients to be screened based on personal risk factors. Most provincial and territorial jurisdictions in Canada regulate indoor tanning. Youth access, restrictions on advertisements to youth, and warning signs were covered in most jurisdictions. There was limited coverage of misleading advertisements, protective eyewear, screening, and inspection. These gaps have implications for compliance, risk communication, and safety.

Room: PAHL 1810

1. The use of electronic medical records to explore the relationship between weight and signalment in cats
Adam Campigotto1, Theresa Bernardo1, Zvonimir Poljak1, Elizabeth Stone2, Deborah Stacey3
1Department of Population Medicine, University of Guelph
2Department of Clinical Studies, University of Guelph
3Department of Computer Sciences, University of Guelph
The use of over 19 million felines patients' electronic medical records were used to determine the average body weight of different breeds of intact and neutered cats. The average weight development can provide
important health information for discussion between owners and veterinarians. The analysis of electronic medical records can help to fill in the gaps in missing fundamental knowledge. The objective of this study was to determine the impact of breed and reproductive status on the body weight in cats. A retrospective cohort study using data from records of domestic felines was performed. Data was collected from 3972 unique, anonymized veterinary clinics in the United States and Canada between the years of 1981 and 2016. The data was provided by a veterinary diagnostic company (IDEXX Laboratories, Inc), consisting of signalment and weight from 19,416,753 records. The association between body weight with age, breed, sex, reproductive status and decade of measurement was assessed using linear regression. The predictive ability of the models was also evaluated. This study shows the value in using historical electronic medical records to address questions that have not previously been explored.

2. Combining 3TSR-mediated vascular normalization with Newcastle Disease Virus enhances intratumoral immune cell trafficking in advanced stage ovarian cancer
Kathy Matuszewska1, Lisa Santry2, Jacob van Vloten2, Sarah Wootton2, Byram Bridle2, Jim Petrik1
1Department of Biomedical Sciences, University of Guelph
2Department of Pathobiology, University of Guelph
Epithelial Ovarian Cancer (EOC) is the most lethal gynecological malignancy, taking 1,750 Canadian lives per year. Due to a lack of specific symptomology and screening techniques, women are often diagnosed with Epithelial Ovarian Cancer (EOC) at stage III/IV when tumors have already metastasized. At this advanced stage, the 5-year survival rate is less than 27%, prompting the need for innovative therapies. Oncolytic virus (OV) therapy uses natural or engineered viruses that lyse tumor cells while leaving non-neoplastic tissues unharmed. These agents also have an immunostimulatory role, although intratumoral immune cell trafficking is compromised by OV-mediated vascular shutdown. Our lab has previously demonstrated that pre-treatment with a potent anti-angiogenic molecule called 3TSR has the ability to normalize tumor vasculature. Normalized vasculature proved to be more efficient in delivering chemotherapeutic agents to the primary tumor, thereby increasing survival of mice treated with 3TSR prior to Paclitaxel. We now investigate the efficacy of 3TSR in preventing the vascular shutdown caused by an oncolytic virus. Using an orthotopic, syngeneic mouse model of advanced EOC, we treated mice with NDV alone or following pre-treatment with 3TSR. Mice given combination therapy had significantly smaller primary tumors as well as less abdominal ascites and secondary lesions. Our current data suggests that the observed differences in disease regression are immune mediated rather than strictly a result of direct viral lysis. Together, we propose a novel use for 3TSR in improving immunotherapy when combined with an oncolytic virus.

3. Inhibition of neurosteroid synthesis impairs memory and dysregulates hippocampal dendritic morphology in male 3xTg-AD mice
Ari Mendell1, Samantha Creighton2, Hayley Wilson1, Lauren Isaacs1, Boyer Winters2, Neil Maclusky1
1Department of Biomedical Science, University of Guelph
2Department of Psychology, University of Guelph
Gonadal steroid hormones naturally decline with age, and this is associated with an increased risk for the development of Alzheimer’s disease (AD). Men are less likely to develop AD compared to women, which may be due to the gradual decline in testosterone levels in aging men, while the menopausal decline of ovarian steroids in women is more abrupt. Recent studies have shown that 5alpha-reduced metabolites of testosterone may contribute to neuroprotection conferred by their parent androgens, as well as to sex differences in the incidence of AD. In this study, we investigated the effects of inhibiting synthesis of testosterone-derived neurosteroids on object recognition memory (ORM) and hippocampal dendritic morphology in male triple transgenic AD mice (3xTg-AD). Male 6-month old wild-type (WT) or 3xTg-AD mice received daily injections of finasteride (5alpha-reductase inhibitor; 50mg/kg i.p) or vehicle (18%
beta-cyclodextrin) for 20 days. Female WT and 3xTg-AD mice only received vehicle injections. Finasteride treatment in males differentially impaired short-term (3xTg-AD only) or long-term (3xTg-AD and WT) ORM, while all 3xTg-AD mice had impaired long-term ORM. Dendritic spine density (DSD) and dendritic branching of pyramidal neurons in the CA3 hippocampal subfield were reduced in 3xTg-AD females, but not males. Both DSD and dendritic branching were significantly reduced by finasteride in 3xTg-AD males, abolishing the sex difference. These findings suggest that 5alpha-reduced neurosteroids contribute to the protection conferred by testosterone, and may play an important role in the observed sex differences in the development and severity of AD.

4. Understanding the association between hock injuries on lameness in dairy cattle
Amanda Armstrong, Todd Duffield, Derek Haley, David Kelton
Department of Population Medicine, University of Guelph

Injuries and lameness are both prevalent across the dairy industry, however, there is little research addressing the potential link between them, and whether one predisposes the other. The objective of this study is to determine the association between mild, moderate and severe hock and knee injuries with lameness in dairy cattle. This research is being conducted at the Livestock Research and Innovation Centre (LRIC), Elora, Canada from November 2017-2018. Working with the hoof trimmer at the LRIC, cows between 120 and 160 DIM, cows entering the lactating herd, and cows that are being examined as a follow-up to a previous lameness intervention, are being trimmed and scored for the presence of hoof lesions. As of January 2018, 136 cows have been enrolled in the study: 114 lactating cows, 5 dry cows, and 17 heifers. Hock injuries are being scored on a 4-point scale, 0-3; with 0 indicating no injury and 3 indicating severely injured. Of the sampled cows, hock injury scores of 2 or greater were distributed as follows: 44% on right lateral, 15% on right point, 32% on left lateral, and 8% on left point. Lameness is being scored on a 5-point scale, with 1 being sound and 5 being severely lame. Twenty-six percent of cows had a lameness score of 3, 4% a score of 4, and 22% of cows have been treated for lameness. Lesions included digital dermatitis (3%), white line disease (2%), sole ulcers (1%), the remaining 16% were listed as treated with unknown causes. Based on preliminary analysis (Fisher’s exact test), cows with hock injury scores of 2 or 3 were 3.82 (95% CI: 1.55-10.1) times more likely to be lame than cows with a hock injury score of 0 and 1. Further analysis is underway.

Room: LLC 1713

1. Steps towards standardized assessment and use of immunomodulatory equine mesenchymal stromal cells
Olivia Lee, Rames Salcedo, Sarah Lepage, Thomas Koch
Department of Biomedical Sciences, University of Guelph

BACKGROUND: Inflammation-associated disorders are significant causes of morbidity in horses. Equine mesenchymal stromal cells(MSC) holds promise as cell-therapy candidates due to their secretory non-progenitor functions. Using lymphocyte suppression assay(LSA), we have shown that MSCs are mononuclear cell(MNC) suppressive in vitro. Due to the inherent heterogeneity of MSCs and varied culture expansion protocols, the development of methods to circumvent donor heterogeneity, as well as robust and easily deployable methods of potency assessment may be beneficial for improving MSCs’ predictability in treating inflammatory diseases.

HYPOTHESIS: LSA using pooled MNC(pMNC) is a robust in vitro assay for the evaluation of MSCs' immunosuppressive potency. APPROACH: MSC cultures were assessed with pMNC LSA using Brdu ELISA and CFSE. MSCs were stimulated with inflammatory cytokines and electrohydraulic shock wave and their potencies were compared. pMNC and pMSC cultures were generated by pooling respective cells from multiple unrelated donors in equal ratios.
RESULTS: LSA using MNCs from single donors indicated MNC donor variability. pMNC LSA of stimulated MSCs demonstrated MSC donor heterogeneity. pMSCs are able to suppress MNC proliferation under all culturing conditions tested.

CONCLUSION: Using LSA based on pMNCs to minimize individual immune response variability, we have developed a consistent and reproducible equine MSC potency assay. Utilizing this assay, we have also demonstrated that pMSC have immune suppressive properties. This knowledge could be used in production monitoring of cellular potency and as release criteria prior to clinical use.

2. Cross-sectional study of the association between veterinarian mental wellness and veterinarian-client interaction outcomes

Jennifer Perret, Andria Jones-Bitton, Colleen Best, Jason Coe, Amy Greer, Deep Khosa
Department of Population Medicine, University of Guelph

Veterinarian mental wellness has been a topic of growing concern in the veterinary and research communities as increasing attention is being paid to poor mental health outcomes, including death by suicide, in this profession. In addition to the impact on the veterinarians themselves, research on caregivers in other professions suggests that the impact may also extend to veterinary patients and clients. In Canada, veterinarians provide a wide range of services, from food safety and agricultural support, to caring for the pets that over 60% of Canadians own. This cross-sectional field study explores the association between quantifiable aspects of veterinarian wellness (stress, anxiety, depression, compassion fatigue, burnout, and resilience, as measured via validated scales) and outcomes of veterinary care (including patient-centered communication and interaction-specific veterinarian and client satisfaction). Recruitment of companion animal veterinarians and their clients in southwestern Ontario began in 2017 and will continue throughout 2018. Participating veterinarians complete a questionnaire including the mental wellness scales, and both clients and veterinarians complete appointment-specific questionnaires on satisfaction and communication. Audio- and video-recordings of veterinarian-client interactions are used to score veterinarian behavior using a standardized measure of patient-centred communication. Associations between veterinarian wellness and client interaction outcomes will be assessed using multivariable regression analysis. These novel data will help inform wellness education and intervention efforts for the veterinary profession.

3. Optimization of an explant culture model to characterize cancer-associated exosomes in canine osteosarcoma

Anita Luu1, Rachel Macdonald1, Michelle Oblak2, Brigitte Brisson2, Alicia Viloria-Petit1
1Department of Biomedical Sciences, University of Guelph
2Department of Clinical Studies, University of Guelph

Osteosarcoma is the most common bone tumor in canines and humans. Previous studies have shown that both tumor and tumor-associated cells promote osteosarcoma progression through extracellular vesicle secretion, such as exosomes. Various factors within the environment can impact exosome release. The goal of this research was to develop an explant culture model to purify and characterize extracellular vesicles from canine osteosarcoma tissue, focusing on exosomes. We reasoned that explant cultures would allow for a more accurate representation of tumor exosomes in vivo, enhancing the potential for clinical translation. With owner consent, tumor and normal bone (control) samples were obtained using sterile tools following limb amputation. Tissue samples were washed with PBS, mechanically dissociated, and incubated in culture media under standard conditions overnight. The next day, conditioned media was recovered, and fresh media was added to the explants and incubated for another 48 hours. Media from both time points were centrifuged to remove cell debris, and the supernatant was collected. qEV size exclusion chromatography columns were used to isolate extracellular vesicles from the explant media. Vesicles were characterized via immunoblotting, electron microscopy, and particle tracking. Both
tumor and normal tissue media contained extracellular vesicles, expressed markers of exosomes, and displayed different elution profiles. Electron microscopy and particle tracking showed an enrichment of particles with morphology and size typical of exosomes. Further optimization steps are required to improve exosome yield and purity prior to mass spectrometry.

4. Investigating kid mortality on Ontario dairy goat farms
Julia Kim¹, Cathy Bauman¹, Jeff Wichtel¹, Paula Menzies¹, Charlotte Winder¹, Robert Foster², Jocelyn Jansen³
¹Department of Population Medicine, University of Guelph
²Department of Pathobiology, University of Guelph
³Ontario Ministry of Agriculture, Food, and Rural Affairs

The Ontario dairy goat industry has undergone tremendous growth in response to an increased demand for goat milk-based products. The main limiting factor to increasing production is the lack of available milking age does. Mortality in kids less than 4 months has been estimated to be approximately 20% in Ontario. Our proposed study is attempting to investigate kid mortality in Ontario dairy goat farms, and is being conducted in three phases. Phase I is characterized by a comprehensive questionnaire and on-farm assessment. Our phase I questionnaire was designed to capture various management aspects on farm to elucidate major risk factors for morbidity and mortality from birth to weaning. This questionnaire has been offered to a random sample of all licensed Ontario dairy goat producers with a goal of recruiting 75-100 responses stratified by herd size. Once each questionnaire is completed, an on-farm assessment is conducted that evaluates parameters such as stocking densities, ventilation and housing. In the second phase of the study a cohort of producers from phase I will be recruited and followed for a 12-month period. These producers are collecting the carcasses from all kids that die on-farm under the age of 4 months, which will then undergo post-mortem analysis at the University of Guelph. The third phase of our study will be focused on knowledge transfer, with our results being disseminated at producer meetings, industry and breeder organizational meetings, published in industry and peer-reviewed journals, and incorporated into a kid-rearing workshop currently in development.

Room: LLC 1715

1. Neuronal regeneration following injury to the medial cortex of the leopard gecko (*Eublepharis macularius*)
Laura Austin, Matt Vickaryous, Rebecca Macdonald
Department of Biomedical Sciences

Radial glia (RG) are neural stem/progenitor cells capable of spontaneously generating new neurons in the central nervous system. Our lab has identified RG in the leopard gecko (*Eublepharis macularius*), lining the ventricular system of the brain. Under normal physiological conditions gecko RG routinely generate new neurons. However, less is known about their ability to contribute to neuron restoration following injury, a process known as reactive neurogenesis. My research seeks to study reactive neurogenesis in the forebrain of the leopard gecko, and for the first time, correlate structural with behavioural changes after injury. I hypothesize that RG will proliferate and differentiate in response to injury, leading to structural and behavioural recovery. I will use the neurotoxin 3-acetylpyridine (3AP) which has been shown to induce degenerative lesions within the lizard forebrain, especially in the medial cortex (MC). Interestingly these lesions appear to resolve within weeks of 3AP treatment, suggesting that reactive neurogenesis is occurring. My first objective is to characterize the structure of the MC before and at various timepoints following 3AP treatment using protein markers for RG, apoptosis and proliferation, as well as the thymidine analog BrdU to track newly generated cells. My second objective is to quantify the behavioural outcomes of injury and regeneration. Using an open-field monitoring system and a touchscreen chamber,
I will evaluate general locomotor activity and extinction of a conditioned response before and at several timepoints after injury. These results will help provide a better understanding of the biology of reactive neurogenesis in vertebrates.

2. Reporting characteristics of disease maps evaluating zoonotic infectious diseases

Inthuja Selvaratnam, Olaf Berke, Jan Sargeant

*Department of Population Medicine, University of Guelph*

Disease mapping is a basic descriptive method employed by epidemiologists for centuries. With the advent of Geographic Information Systems, the practice of disease mapping has become an easy task and even more popular. And recent calls for “precision public health” demand spatially precise data, their analysis and visualization for improved decision making. Nonetheless map making is a complex process and when done carelessly can result in distorted visualizations and thus misleading conclusions. In this study, disease maps of zoonotic diseases are reviewed with respect to the following questions: 1) What purposes are disease maps used for? 2) What type of maps (e.g. point and choropleth maps) are used? 3) Which map characteristics (e.g. projection and scale) are reported? Population health studies with zoonotic disease maps will be searched in Web of Science and other appropriate databases. Key search terms will include: disease map, and zoonoses. Screening, and data extraction of studies will be conducted by two reviewers in duplicate. Any disagreements on study selection and data extraction will be cleared by discussion or by a third reviewer. Study characteristics will be quantitatively and qualitatively summarized as informed by research questions and data charting. Experts in the field (e.g. spatial epidemiologists, medical geographers, health service researchers) will also be consulted to inform data charting fields of interest. The findings from this investigation are expected to identify gaps in the reporting of basic map information in the literature. This will facilitate best practices for map making and guide future disease mapping and map assessments.

3. Estrogen receptor regulation of the heart in an animal model of menopause: is timing of hormone replacement therapy important?

Rosephine del Fernandes, Vishali Balasubramaniam, Ilka Lorenzen-Schmidt, Glen Pyle

*Department of Biomedical Sciences, University of Guelph*

Preclinical studies support the protective effects of estrogens against cardiovascular disease; however, hormone replacement therapy trials are inconsistent. One hypothesis for these discrepancies are the differences in therapy timing. Interestingly, no study has examined the chronological myocardial changes associated with menopause. This study is the first to identify changes in estrogen receptor (ER) regulation of the heart using a unique mouse model involving gradual ovarian failure to capture peri-menopause. 4-vinylcyclohexene diepoxide (VCD) injection of female mice caused accelerated ovarian follicular atresia over 120 d. Hearts were perfused for 15 min with ER-alpha (4,4',4"-(4-propyl-[1H]-pyrazole-1,3,5-triyl)trisphenol, PPT, 100 nM) or ER-beta (diarylpropionitrile, DPN, 1 nM) agonists. Contractility declined in both PPT and DPN treated hearts in intact mice. ER-alpha and ER-beta-dependent decreases in contractility were attenuated 60-days post-VCD, representing the peri-menopausal period. 120-days post-VCD (end of menopause) ER-alpha regulation was normalized, whereas ER-beta control remained attenuated. Myofilament function was significantly altered in a non-linear fashion during peri-menopause in conjunction with myofilament protein phosphorylation. ER-dependent regulation of myofilament function and protein phosphorylation was disrupted earlier in menopause. We are the first to show the rapid effects of ER activation on myocardial function and their mechanisms of action are altered early in menopause. The significant and non-linear changes in the heart during menopause may help explain the paradoxical findings of clinical trials.
Skin cancer is a significant, but preventable, global public health problem. Despite the cancer risks of indoor tanning (IT), over 1 million Canadians continue to engage in this behaviour. IT facilities use marketing to encourage the public to use their services. Little is known about the messages the IT industry uses in online contexts, and whether the content complies with advertising and marketing restrictions mandated by IT legislation. We conducted a content analysis of IT salon websites in Ontario, Canada. We developed a comprehensive catalogue of IT salons using InfoCanada’s directory, YellowPages.com, and Google. We then developed a codebook to assess the content of salon websites based on previous literature and a sample of websites. The 288 variable codebook covered 16 key categories, including the presence of health and aesthetic claims, benefits and risks of IT, and whether messages were directed towards youth. In 2017, there were 421 IT salons in Ontario. Of those, 265 had active websites that were included in the analysis. A 91.15% percent agreement was calculated for inter-coder reliability (n = 20). Qualitative findings demonstrated that the IT industry utilizes false health claims (e.g., tanning is safe, tanning prevents disease) and promotions to youth to sell their services (e.g., student discounts), suggesting non-compliance with provincial IT legislation. This research helps to illustrate how the Ontario IT industry markets artificial UV to the public. Policy makers and health communication specialists may find this information useful towards developing counter communication strategies and legislative amendments to deter misleading health claims.
1. Effect of different carbohydrate sources on glycemic index and satiety-related gut hormones in dogs

Alexandra Rankovic¹, Jennifer Adolphe², Anna Kate Shoveller³, Dan Ramdath⁴, Adronie Verbrugghe⁴

¹Department of Clinical Studies, University of Guelph
²Petcurean Pet Nutrition
³Department of Animal Biosciences, University of Guelph
⁴Guelph Research and Development Centre, Agriculture and Agri-Food Canada

Obesity and diabetes are major health concerns for pets. In humans, the glycemic index (GI) has significant impact on glucose control and weight management. This study compared GI, postprandial insulminemic response and gut hormones related to satiety, to commercial extruded dog foods containing different carbohydrate sources. Four commercial extruded diets were classified based on the type of carbohydrate sources they contained: traditional grains (corn, wheat), whole grains (oats, rye), grain-free (peas, lentils) or vegan (no animal ingredients). Each diet was tested once and the control (50% w/vol glucose solution) was tested twice in 11 adult Siberian Huskies in a randomized cross-over design. Each meal and control provided 25g of available carbohydrate. Pre- and postprandial (15, 30, 45, 60, 90, and 120 minutes) blood samples were collected to measure whole blood glucose concentrations using a handheld blood glucose monitor. Serum insulin, ghrelin, gastric inhibitory polypeptide (GIP), glucagon-like peptide 1 (GLP-1), leptin, total peptide tyrosine-tyrosine (PYY), and pancreatic polypeptide (PP) concentrations were analysed using a magnetic bead multiplex assay. No significant differences were detected in GI (p<0.05). The GI for traditional grains was 76.9±18.3 (mean±SEM), while the grain-free diet had the lowest GI of 50.5±13.1. The whole grain diet and vegan diet had GI values of 60.8±7.4 and 71.4±17.3. There was no effect of diet on insulinemic response or any satiety hormones (p<0.05). These results suggest that different carbohydrate sources in extruded diets may not have a significant effect on GI or satiety in dogs.

2. Causes of morbidity and mortality in captive psittacines submitted to the Ontario veterinary college teaching hospital

Daniel Gibson¹, Leonardo Susta¹, Nicole Nemeth², Hugues Beaufreire³, Csaba Varga⁴

¹Department of Pathobiology, University of Guelph
²Department of Pathology, University of Georgia
³Department of Clinical Studies, University of Guelph
⁴Ontario Ministry of Agriculture, Food, and Rural Affairs

Psittacines are beloved companion animals, and are also kept in a variety of zoos and private collections. The medical diagnostic literature of psittacine birds (e.g., parrots, macaws) is based largely on data derived from case reports with an overall lack of systematic approaches. The goal of this project is to better understand the prevalence and presentations of psittacine diseases in order to improve diagnostics. To this aim, we conducted a retrospective review of post-mortem diagnostic data from psittacine birds submitted to the Ontario Veterinary College teaching hospital and the Animal Health Laboratory from 1998 - 2017 (n = 1850). Through development of a comprehensive database of local psittacines, we summarized diseases and their presentations. We also conducted a risk factor analysis to determine associations between age and genus, and specific diseases. Overall, birds from 46 psittacine genera, in two different families were submitted for post-mortem diagnostic evaluation. The most common causes of death were non-infectious (42.5%) followed by infectious (39.9%). Cause of death could not be determined for 17.6% of cases. The most prevalent non-infectious causes of death were degenerative (24.8%) and metabolic (23%). The most prevalent infectious causes of death had viral etiology (52.8%) and bacterial (29.8%). The risk factor analysis revealed significant associations between specific diseases, and psittacine genera or age groups. This study is one of few large summaries of overall pathological findings...
in psittacine birds, and will contribute to improving diagnostics modalities for regional and larger-scale applications toward improving psittacine health.

3. Circadian microbiome benefits outcome post-myocardial infarction (heart attack)

Priya Mistry¹, Cristine Reitz¹, Tarak Khatua¹, Kaitlyn Oliphant², Sameer Al-Abdul-Wahid³, Emma Allen-Vercoe², Tami Martino¹

¹Department of Biomedical Sciences, University of Guelph
²Department of Molecular and Cellular Biology, University of Guelph
³Department of Physics, University of Guelph

Introduction: Circadian rhythms are critical for healthy cardiovascular physiology and healing post-myocardial infarction (MI; heart attack). The microbiome is implicated in healing post-MI, however the role of the circadian-microbiome axis in benefiting outcome is unknown.

Hypothesis: The microbiome is critical for healing post-MI and this is regulated by the circadian mechanism.

Methods and Results: First, to create a model of gut dysbiosis, mice were given antibiotics and microbiome disruption was confirmed using bacterial culture and 16S rRNA sequencing. Second, to implicate the microbiome in post-MI outcome, mice were given antibiotics pre-MI surgery and followed by echocardiography, in vivo hemodynamics, and histopathology. Antibiotic-MI mice show worsened cardiac structure and function by reduced % ejection fraction (46.04±0.70% vs. 53.27±1.62%) and reduced % fractional shortening (19.68±0.36% vs. 23.64±0.89%), compared to MI. Third, to evaluate the role of the microbiome in regulating immune responses contributing to infarct healing, we quantified inflammatory cell recruitment and show reduced immune cell infiltration in antibiotic-MI mice. Mechanistically, we show that dysbiosis alters the functional metabolite profile of the microbiome, reducing short-chain fatty acids butyrate, propionate, and acetate, using 1H NMR spectroscopy. Finally, we show that the microbiome is governed by circadian rhythms and this regulates the microbiome to affect healing post-MI, using ClockΔ19/Δ19 mice.

Conclusions: These findings show for the first time that the circadian-microbiome axis is crucial for heart disease outcomes and will lead to new approaches to benefit patients post-MI.

4. Chemosensitization effects of the potassium-sparing diuretic amiloride in canine osteosarcoma

Andrew Poon, Jordon Inkol, Anita Luu, Anthony Mutsaers

Department of Biomedical Sciences, University of Guelph

Canine osteosarcoma (OSA) is an aggressive malignancy that typically presents within the appendicular skeleton. While chemotherapy delays metastasis, most dogs succumb to this disease within one year of diagnosis. Comparable to the evolution of multidrug resistance transporters, many chemotherapeutics become sequestered within acidic lysosomes. Furthermore, the high metabolic demand of cancer cells contributes to microenvironmental acidosis, fostering immune evasion and chemoresistance. A pilot study in companion animals suggested that proton pump inhibitors are potential anti-cancer agents in OSA. Among this class of inhibitors is amiloride, a potassium-sparing diuretic for heart failure treatment in dogs. Assessments of cell viability, apoptosis and metabolism were performed in three canine OSA cell lines after amiloride treatment, and pharmacological synergism with doxorubicin and carboplatin was calculated using the combination index (CI). Amiloride strongly synergized with doxorubicin (CI < 1) to reduce viability in canine OSA cells. Significant increases in early apoptosis (p < 0.0001) were observed with combination treatment, compared to treatment with amiloride or doxorubicin alone. Amiloride treatment also upregulated p53-dependent apoptosis and downregulated Akt-specific activation. Finally, Seahorse metabolic profiling of OSA cells treated with amiloride revealed significant decreases in extracellular acidification rates (p < 0.01) and maximal respiration rates (p < 0.05). Taken together, the
well-known safety profile of amiloride and its potential for synergism with doxorubicin may justify drug repurposing for clinical trial evaluation in canine OSA.

5. Evaluation of risk factors associated with seropositivity for Borrelia burgdorferi in Ontario horses.
Megan Neely1, Scott Weese2, Luis Arroyo2, Alison Moore3, Claire Jardine1
1Department of Pathobiology, University of Guelph
2Department of Clinical Studies, University of Guelph
3Ontario Ministry of Agriculture, Food, and Rural Affairs
The blacklegged tick, Ixodes scapularis has undergone rapid range expansion within Ontario. This tick transmits the Lyme disease bacterium Borrelia burgdorferi as well Anaplasma phagocytophilum, the cause of equine Granulocytic Anaplasmosis. Currently, there is a lack of basic data on the equine population and therefore we have limited understanding of the risk these pathogens may pose. The objective of our study was to establish baseline seroprevalence of B. burgdorferi and A. phagocytophilum in Ontario horses and assess potential risk factors associated with exposure to B. burgdorferi. Serum samples were obtained from 551 clinically healthy horses across Ontario. Horse owners filled out a questionnaire that evaluated demographics, clinical history and farm management. Sera were examined with an in-clinic ELISA (IDEXX SNAP® 4Dx®) and an equine Lyme Multiplex ELISA. The odds of being seropositive on any test were significantly higher if deer were seen ‘occasionally’ on the property when compared to the referent of ‘never’. Horses that had insect repellent applied also were more likely to be seropositive. The odds of being seropositive were significantly lower for horses that spent 6-12 hours outside in the winter and may be a protective factor for B. burgdorferi exposure. Additional risk factors that significantly increased the odds of being seropositive varied depending on the serological test in use. Our findings illustrate that certain ecological factors may increase the risk of pathogen exposure, but further investigation is needed. This information may be used to propose changes in farm management to decrease the risk of exposure to blacklegged ticks.

Room: PAHL 1810
1. Short-term drug targeting of the circadian factor REV-ERB limits infarct expansion and remodeling after myocardial ischemia/reperfusion injury in mice
Cristine Reitz1, Faisal Alibhai1, Elena Tsimakouridze1, Thomas Burris2, Tami Martino1
1Department of Biomedical Sciences, University of Guelph
2Department of Pharmacology and Physiology, Saint Louis University School of Medicine
Rationale: Myocardial ischemia/reperfusion (mI/R; heart attack) triggers adverse cardiac inflammation and remodeling. The circadian mechanism is a key regulator of cardiac immune responses, yet whether this can be targeted pharmacologically to improve outcomes is unknown.
Hypothesis: Short-term administration of the REV-ERB agonist SR9009 will benefit long-term outcomes post-mI/R.
Methods and Results: To evaluate the effects of REV-ERB agonism on cardiac remodeling post-mI/R, we used echocardiography, and found less adverse remodeling in mice treated for 5 days with SR9009 vs. vehicle (e.g. %EF, 66.4±1.67% vs. 53.3±1.46%). To investigate whether SR9009 reduced reperfusion injury, we assessed cardiac inflammation by flow cytometry, and found reduced immune cell recruitment in SR9009 vs. control hearts (e.g. CD11b+F4/80+ macrophages, 40x103±5x103 vs. 180x103±41x103). Next, we examined whether adverse activation of the NLRP3 inflammasome was also reduced, by RT-PCR, and found less cardiac expression with treatment (5.06±0.64 vs. 8.72±0.8, fold change from sham). Finally, to demonstrate how activating the circadian repressor REV-ERB benefits post-mI/R outcomes, we show 1) better outcomes in ClockΔ19/Δ19 mice with a suspended circadian mechanism (e.g. %EF, 67.16±2.17% vs. 59.04±2.12%) consistent with that observed with REV-ERB agonism, and 2) the effects of SR9009 are
prevented in Nr1d1/- (Rev-erbα null) mice (%EF, 62.46±0.96% vs. 63.47±0.74%), demonstrating REV-ERBα as the key molecular mediator.

Conclusion: This is the first study using circadian medicine to limit adverse cardiac reperfusion injury and reduce remodeling post-mI/R, through direct targeting of REV-ERB.

2. Morphological and molecular characterization of Klossiella equi (Adeleorina; Apicomplexa) infecting the kidneys of Ontario horses
Alex Leveille, Karlyn Bland, Karen Carlton, Cedric Larouche, Emily Brouwer, Brandon Lillie, John Barta
Department of Pathobiology, University of Guelph
Klossiella species are unique among the Adeleorina as monoxenous parasites of mammals unlike other Adeleorina that utilize invertebrate definitive hosts. Adeleorina undergo syzygy (microgamonts and macrogamonts associate before maturation and syngamy). Phylogenetic placement of Klossiella has been questioned based on its unique host affinity. Two cases of Klossiella equi are reported from kidneys of Ontario horses examined post mortem. Stages of the life history were documented in histological preparations of infected kidneys. Multiple stages of Klossiella equi were identified including meronts, microgamonts and macrogamonts (associating in syzygy) as well as thin walled oocysts in various stages of sporogonic development. PCR and Sanger sequencing were used to generate a partial nuclear 18S ribosomal DNA sequence (1,443 bp) and typical circular mapping mitochondrial genome (6,569 bp). The 18S rDNA sequence was aligned with publicly available apicomplexan sequences to generate a Bayesian Inference phylogenetic tree in which Klossiella equi was found within the monophyletic Adeleorina clade. Details of the life cycle supplemented with the nuclear 18S rDNA sequence provided both morphological and molecular evidence supporting the phylogenetic placement of Klossiella within the Adeleorina (Apicomplexa).

3. Assessing the transmission dynamics of antimicrobial resistant Salmonella Heidelberg in Canadian poultry production using draft genome sequence data
Benjamin Hetman1, David Pearl1, Richard Reid-Smith2, Eduardo Taboada3
1Department of Population Medicine, University of Guelph
2Centre for Foodborne, Environmental, and Zoonotic Infectious Disease, Public Health Agency of Canada
3National Microbiology Laboratory, Public Health Agency of Canada
Objective: We aim to identify key elements in the transmission of antimicrobial resistant Salmonella Heidelberg (SH), and genetic determinants of antimicrobial resistance throughout the farm-to-fork continuum in Canadian poultry production.
Methods: For the present study, we selected SH isolates from federal surveillance programs at poultry farm, abattoir and retail levels in Ontario, Canada in 2013, and characterized them by whole genome sequencing (WGS). Using a novel SH core-genome multi-locus sequence typing assay, we examined the genetic diversity present in the bacterial core genome to assess the underlying population structure of SH circulating in the Canadian food chain.
Results: Intra-genomic diversity measured by single nucleotide variant differences in the core genomes of SH clustered in the same establishment was found to be greater than the inter-genomic diversity at this level. This effect was more pronounced at the farm and abattoir levels than at the retail level, where the trend was reversed. Analysis of the WGS data uncovered several genetic determinants of AMR, providing a molecular basis for results of phenotypic testing, and identifying 38% of isolates as multidrug-resistant. We identified a total of 15 chromosomal and mobile AMR determinants that included CMY-2, an ampC gene that encodes resistance to clinically important broad and extended-spectrum cephalosporin antibiotics. Finally, we identified a several plasmid replicon elements in our dataset, including the IncI1 plasmid, a mobile element known to be associated with the carriage of CMY-2.
Conclusion: Results from our analysis demonstrate the ability to extract meaningful information from draft

4. Inuit childbirth in Canada: An exploration of place, culture, and health in Baffin Island, Nunavut
Laura Jane Brubacher¹, Naomi Tatty, Gwen K. Healy², Cate E. Dewey³, Ashlee Cunsolo⁴, Sally Humphries⁴, Sherilee L. Harper¹
¹Department of Population Medicine, University of Guelph
²Qaujigiartiit Health Research Centre
³Labrador Institute, Memorial University
⁴Department of Sociology and Anthropology, University of Guelph

INTRODUCTION: Inuit in Canada experience the highest infant mortality rate in the country and significantly higher rates of preterm births, stillbirths, and maternal health issues, as compared to non-Inuit. These differences result from a complex interaction of determinants, including smoking, food security, housing quality, and the availability and type of obstetrical care women receive. Baffin Island women often fly out of their communities for birth, and remain in southern hospitals for weeks (obstetric evacuation, OE). A qualitative study was conducted in Iqaluit, Nunavut to characterize the connections between Inuit health, culture, and place, by hearing Inuit perspectives on (i) what childbirth was like historically, and presently, in communities; and (ii) how the healthcare system and obstetric policies in Canada may more fully reflect Inuit culture, knowledge, and conceptions of well-being.

METHODS: Seven focus groups (conducted as two-day sewing groups), 24 semi-structured interviews, and 8 oral histories were conducted with pregnant Inuit women, community members, and Elders in Iqaluit.

RESULTS: Based on the literature and preliminary data analysis, women report feeling isolated, lacking prenatal support, and receiving obstetrical care from a Western model incongruous with Indigenous teachings on well-being. Importantly, place-attachment – one’s psychological, emotional, and spiritual connection to the land – is central to Indigenous peoples’ well-being. As such, OE may have especially serious impacts on the well-being of Inuit mothers.

CONCLUSION: This study reveals integral connections between place, culture, and health in relation to Inuit experiences of OE.

5. MicroRNAs as prognostic markers for chondrogenic differentiation potential of mesenchymal stromal cells derived from equine cord blood
Hamid Alizadeh, Thomas Koch
Department of Biomedical Sciences

Background: MSCs are a heterogeneous cell population and large inter-donor variation about the chondrogenic potential of these cells has been reported which may hamper development of reproducible therapies and influence the use of MSCs in research and regenerative medicine. Currently, there is a huge lack of biomarkers predicting the chondrogenic differentiation potential of culture expanded MSCs derived from multiple donors.

Objectives: The objective of this study is to identify such prognostic markers for equine MSCs. Methods: In this study ten equine cord blood-derived MSC (eCB-MSC) donors were initially evaluated for their ability to produce cartilage in a standard chondrogenic differentiation assay. The chondrogenic differentiation potential was scored based on histological matrix formation and quantitative glycosaminoglycan deposition. Subsequently, total RNAs were isolated for determination and comparison of a panel of microRNAs (miR-34a, miR-140, miR-148a, miR-199a, miR-410) between eCB-MSC cultures with high and low chondrogenic potential.

Results: Three donors were identified as low chondrogenic potential, whereas 3 showed high and 4 moderate chondrogenic. Expression analysis of candidate microRNAs, previously implemented in chondrogenesis, showed a very distinctive pattern between good and bad performing donors.
Conclusions: In conclusion, MicroRNA profiling of eCB-MSC cultures may have prognostic value to select MSC donors with regards to their chondrogenic differentiation potential and their capacity to restore cartilage homeostasis after intra-articular injection in the osteoarthritic joint.

Room: LLC 1713

1. Using a one health approach to examine acute environmental drivers of human verocytotoxigenic Escherichia coli infections in Ontario
Roksolana Hovdey1, Jan Sargeant1, David Fisman2, Amy Greer1
1Department of Population Medicine, University of Guelph
2Department of Epidemiology, Dalla Lana School of Public Health, University of Toronto

Environmental and hydrological conditions such as temperature, precipitation, and river levels are hypothesized to be drivers of human verocytotoxigenic Escherichia coli (VTEC) infections. The objective of this project is to evaluate the magnitude and direction of effects of environmental factors on human VTEC incidence using human case data and environmental and hydrological data from Ontario. Data for this study was obtained from Public Health Ontario, the Public Health Agency of Canada’s FoodNet Surveillance, and Environment Canada. We are using a case-crossover study design to examine the acute effects of environmental conditions (including temperature, levels of rainfall/snow, and water flow) on human case occurrence. There were 1,534 reported primary cases of VTEC infection in Ontario between January 1, 2005 and December 31, 2013. Cases that were travel related were excluded from the study. Our preliminary analyses demonstrate that there is a seasonal pattern of human cases, with most cases occurring between May-November. Improving our understanding of the acute environmental drivers of human VTEC can help develop strategies to prevent future cases from occurring.

2. Dietary intake of essential vitamins in obese cats energy restricted for weight loss on a veterinary therapeutic food
Caitlin Grant1, Anna-Kate Shoveller2, Shauna Blois1, Marica Bakovic3, Adronie Verbrugghe1
1Department of Clinical Studies, University of Guelph
2Department of Animal Biosciences, University of Guelph
3Department of Human Health and Nutritional Sciences, University of Guelph

Insufficient data exists regarding provision of adequate amounts of essential nutrients to obese cats during energy restriction. This study aimed to investigate predicted dietary intake of essential vitamins in obese cats undergoing energy restriction for weight loss and compare with National Research Council (NRC) 2006 recommendations. Sixteen obese cats, included in a non-randomized retrospective observational study, were fed a veterinary weight loss food during a 10-week period of energy restriction (0.6 x 130Kcal/kg^0.67). All procedures were approved by the University of Guelph Animal Care and Use Committee (AUP#2496). For each cat, minimum, maximum and average daily vitamin intakes were calculated from measured values of dietary vitamin and food logs and compared to NRC recommended allowance (RA), adequate intake and minimum requirement (MR) for adult cats. Cats lost 672 g ± 303 g over the 10-week period, representing a weight loss rate of 0.94 ± 0.28 % per week. Energy consumption was 138.2 ± 10.2 kcal per day. Intakes of all vitamins except choline were within NRC RA per (kg ideal body weight)^0.67. Average and maximum daily choline intakes were 11.1% (0-24.8%) and 9.6% (0-24.8%) below RA respectively. Minimum daily choline intakes were 12.3% (3.5-24.8%) below RA, and fell below MR for two cats. Despite lower calculated intakes of choline, cats remained clinically healthy. As choline is considered lipotropic, intake less than NRC recommendations in obese cats during energy restriction may impact hepatic lipid metabolism. Choline requirements and health risks associated with intakes below recommendations during energy restriction warrant further investigation.
3. Effect of warmed and humidified carbon dioxide for pneumoperitoneum on core body temperature, cardiorespiratory variables, thromboelastography, systemic inflammation, peritoneal response, and post-operative pain during laparoscopy in healthy mature dogs

Jacqueline Scott1, Ameet Singh1, Alexander Valverde1, Shauna Blois1, Robert Foster2

1Department of Clinical Studies, University of Guelph
2Department of Pathobiology, University of Guelph

Objective – To evaluate the effect of warmed, humidified carbon dioxide (WHCO2) pneumoperitoneum on core body temperature, cardiorespiratory variables, thromboelastography, systemic inflammation, peritoneal response, and post-operative pain in healthy, mature, dogs undergoing laparoscopy. Design – Randomized, crossover study. Animals – Mature, purpose-bred dogs (n=6). Procedures – Each dog, in two separate anesthetic episodes, had a pneumoperitoneum created using differing CO2 environments; standard CO2 (STCO2: 22°C, 0% relative humidity), and WHCO2 (37°C, 98% relative humidity). During each episode, data collected included core body temperature, cardiorespiratory parameters, thromboelastography, and inflammatory biomarkers. All dogs had peritoneal biopsies evaluated with scanning electron microscopy and were assessed for post-operative pain. Results – Mean core body temperature was significantly lower (35.2 °C, 95% CI 34.5 – 35.8 °C) with WHCO2 compared to STCO2 (35.9 °C, 95% CI 35.3 – 36.6 °C) across all time points. Cardiac Index increased over the duration of the procedure for both treatments and was not significantly different between treatments. No significant difference in thromboelastography was found between groups as indicated by the coagulation index. Subjective evaluation of peritoneal biopsies revealed mesothelial cell loss with STCO2. There was no significant difference in circulating C-reactive protein or IL-6. There was a significant increase in the number of post-operative pain scores above 0 in the WHCO2 treatment group. Conclusions and Clinical Relevance – These data suggest the use of WHCO2 for pneumoperitoneum in healthy, mature, dogs undergoing laparoscopy did not differ from the use of STCO2.

4. Eco-epidemiology of Babesia odocoilei in Ontario cervids

Ellie Milnes1, Grace Thornton1, Pauline Delnattet, Alexandre Leveille1, John Barta1, Dale Smith1, Nicole Nemeth1

1Department of Pathobiology, University of Guelph
2Wildlife Health Centre, Toronto Zoo

Babesia odocoilei, the protozoan hemoparasite of white-tailed deer (Odocoileus virginianus) transmitted by Ixodes scapularis ticks, is an increasingly recognized cause of disease in cervids in North America. Following an outbreak of babesiosis in reindeer (Rangifer tarandus tarandus) and wapiti (Cervus canadensis) at the Toronto Zoo in Ontario, Canada, we utilized a prospective postmortem survey to investigate the prevalence of Babesia odocoilei in wild, farmed, and zoo cervids in Ontario (n=270; 2016-2018) by polymerase chain reaction (PCR) and sequencing of DNA extracted from tissue samples. Babesia odocoilei was identified in 1.4% (2/142) of farmed red deer (Cervus elaphus), 4.4% (3/68) of wild white-tailed deer, and 3.4% (1/29) of captive wapiti. Wild white-tailed deer are the candidate wildlife reservoir for Babesia odocoilei in Ontario. This is the first record of Babesia odocoilei in red deer; the pathogenicity of Babesia odocoilei in this species is unknown, and the finding of Babesia odocoilei-infected, apparently healthy red deer on two farms on Ontario is concerning for the health of commercially farmed cervids. Additionally, we designed a study to investigate the hypothesis that birds can disperse Babesia odocoilei-infected ticks along migratory flyways. Birds (n = 1,102) were captured during spring migration; the prevalence of I. scapularis infestation was 3.7% in 2016 and 6.7% in 2017, and 0.2% of birds carried one or more I. scapularis ticks that tested PCR-positive for Babesia odocoilei. Blanket dragging for questing ticks in southern Ontario revealed a minimum infection prevalence for Babesia odocoilei of up to 4.1% in ticks found in environments used by wild cervids.
5. Flow cytometric identification and quantification of circulating tumor cells in dogs with naturally occurring osteosarcoma throughout the course of standard of care treatment and disease progression
Tanya F. Wright¹, Brigitte A. Brisson¹, Angela Tiessen¹, Catherine R. Belanger¹, Geoffrey Wood², Dorothee Bienzle²

¹Department of Clinical Studies, University of Guelph
²Department of Pathobiology, University of Guelph

Detection of early metastasis in dogs with osteosarcoma (OSA) is limited by the sensitivity and specificity of available imaging modalities. Enumeration of circulating tumor cells (CTCs) in people has shown that detection and quantification of CTCs throughout the course of disease correlates with cancer malignancy and stage. The objectives of this study were to devise a method for detecting OSA CTCs in dogs, and to prospectively and over time apply this assay to blood samples from clinical OSA patients. A flow cytometry protocol was developed for detection of OSA CTCs and used to analyze blood from clinical OSA patients prior to and following limb amputation, and at each time point of chemotherapy and thoracic radiography until the detection of metastasis or euthanasia. Results of this indicate that CTCs can be differentiated from other cells in blood using a novel flow cytometry protocol. Twenty-eight OSA patients with no evidence of pulmonary metastasis were enrolled, and CTC enumerated at multiple time points. Thus far, 17/28 dogs have developed metastasis and 16 have died. In dogs with high CTCs prior to amputation CTCs decreased following amputation and chemotherapy. A 5 to 50-fold spike in CTC number was present 0 to 58 days prior to radiographic evidence of pulmonary metastases in 14/17 dogs. The main limitation is that not all dogs have developed metastasis at this time, precluding complete statistical analysis. To our knowledge this is the first study to establish and assess clinical utility of such an assay in dogs with neoplasia.

Room: LLC 1715

1. Factors influencing the provision of an antibiotic for treating enteric infections
Brendan Dougherty¹, Rita Finley², Andrea Nesbitt¹, Danielle Dumoulin², Amy Pavletic³, Tara Hluchy⁴, Rod Asplin⁵, Andrew Papadopoulos¹

¹Department of Population Medicine, University of Guelph
²Public Health Agency of Canada
³Middlesex-London Health Unit
⁴Alberta Health Services
⁵Fraser Health Authority

Understanding antimicrobial prescribing practices is essential to developing successful antimicrobial stewardship programs. Many institutional based stewardship programs rely on methods such as chart reviews to analyze prescribing trends. At the community level, such methods are not practical. This study aims to use surveillance data to better understand trends in antimicrobial prescribing practices at the community level for enteric infections. Data was collected from three sentinel sites that participate in an enteric illness enhanced passive surveillance system in 2015. A standardized questionnaire was administered to all confirmed cases of enteric illness, which collected information on demographics, symptomology, hospitalization status, travel history, and antibiotic use. Logistic models were developed to determine which factors were associated with a case having received an antimicrobial prescription. A total of 1202 laboratory confirmed cases of enteric illness were analyzed. The majority of cases (n=633, 53%) received an antibiotic prescription. Several factors were identified as being significantly associated (p<0.05) with cases having a higher odds of receiving a prescription for antibiotics. These factors included age, international travel, hospitalization, being ill for < 7 days, nausea, weight loss, dizziness, and abdominal bloating. This analysis has identified several factors associated with the provision of an antimicrobial prescription for treating enteric infections, including several that are not in alignment with
clinical guidelines. These factors may highlight targets for future interventions aiming to reduce inappropriate antimicrobial use.

2. Developing the Collection of Epidemiologically Derived Associations with Resistance (CEDAR) database

Brennan Chapman

*Department of Population Medicine*

When performing data extraction in the context of an informal, or semi-formal literature search (i.e. not a systematic review), the acquisition and use of specialized software tools is often unwarranted, and financially unreasonable. Conversely, a simple (yet accessible) flat file approach rapidly becomes impractical as the volume of data increases, and screening/extraction is distributed amongst several persons. Using the example of the Collection of Epidemiologically Derived Associations with Resistance (CEDAR) database, created in Microsoft Access, I demonstrate the utility of a relational database approach versus a flat file approach, and highlight some challenges faced when migrating from one or more disparate and unstructured flat files to a database.

3. Meteorological parameters and hospital admission associations: Implications for climate change adaptation in the healthcare sector in Uganda

Katherine E. Bishop-Williams¹, Lea Berrang-Ford²,³, Jan M. Sargeant¹,⁴, David L. Pearl¹, Shuaib Lwasa²,⁵, Didacus Bambaiha Namanya²,⁶,⁷, Victoria L. Edge¹,²,⁸, Ashlee Cunsolo⁹, IHACC Research Team², Bwindi Community Hospital¹⁰, Sherilee L. Harper¹,²

¹*Department of Population Medicine, University of Guelph*

²*Indigenous Health Adaptation to Climate Change Research Team: James Ford, Alejandro Llanos, Cesar Carcamo*

³*Priestley International Centre for Climate, University of Leeds*

⁴*Centre for Public Health and Zoonoses, University of Guelph*

⁵*Department of Geography, Geo-Informatics and Climatic Sciences, School of Forestry, Environmental and Geographical Sciences, College of Agricultural and Environmental Sciences, Makerere University*

⁶*Ministry of Health, Kampala, Uganda*

⁷*Uganda Martyrs University, Kampala, Uganda*

⁸*Public Health Agency of Canada*

⁹*Labrador Institute, Memorial University, Happy Valley-Goose Bay, Newfoundland and Labrador, Canada*

¹⁰*Bwindi Community Hospital, Kanungu District, Uganda*

Seasonal and meteorological parameters may impact the incidence of many diseases. Examining potential associations between hospital admissions (all diagnoses), and meteorological factors in rural Uganda is likely to provide valuable insights for future hospital planning in regions that are vulnerable to climate change. Hospital admissions data (e.g. ward, date, diagnosis) were collected from Bwindi Community Hospital (2011-14). Meteorological data were collected from a satellite weather database (2011-14). Monthly rates and the proportion of admissions related to common infectious diseases were estimated. A mixed-effects Poisson regression model investigated associations of hospital admissions with seasonal and meteorological parameters (i.e. precipitation and temperature). Hospital admission counts were highest for acute respiratory infections (25%), malaria (16%), and acute gastrointestinal illness (10%). Accounting for season, year, and ward, the number of admissions to the hospital were 1.16 times (95%CI:1.04-1.31, p=0.008) higher during extreme high temperatures (i.e. >95th percentile) on the day of admission and a significant interaction between season and year indicated potential changes to seasonal patterns over time, where increasing temperature and changing timing of rainfall events lead to increases in hospital admissions. Our results suggest that the health of the study population may be affected by heat, which has implications more generally for health care systems in a warming climate throughout the
continent. Further, progression of climate change and its related local health impacts may present new challenges for regional hospitals with limited capacity.

4. *Echinococcus multilocularis*: an emerging zoonosis of public health and veterinary significance in southern Ontario

Jonathon Kotwa¹, Mats Isaksson², Claire Jardine¹, Olaf Berke³, David Pearl³

¹Department of Pathobiology, University of Guelph
²Department of Microbiology, National Veterinary Institute
³Department of Population Medicine, University of Guelph

Alveolar echinococcosis (AE), disease due to the intermediate stage of *Echinococcus multilocularis*, is potentially fatal in humans and dogs when left untreated. Transmission occurs when eggs of the tapeworm, shed by definitive hosts (i.e., foxes, coyotes, dogs), are ingested. Prior to 2012, Ontario was considered free of this parasite. Since then, AE has been reported in six dogs, two lemurs, and a chipmunk in southern Ontario. Due to public health concerns, the prevalence and distribution of infection was estimated in wild canids across the region. Between 2015-2017, rectal fecal samples were collected from 460 wild canids (416 coyotes, 44 foxes) during post-mortem examination and analyzed for the presence of *E. multilocularis* DNA. Overall, 23% (95% confidence interval: 19-27%) of wild canids tested positive. Using a spatial scan test, an infection cluster was identified (relative risk=2.26; p=0.002) among 10 contiguous public health units in the central-west region; the cluster encompasses areas of dense human population, suggesting zoonotic transmission is a serious public health issue. Based on these results and the aforementioned cases of AE, as of January 1 2018, Ontario became the first region in North America to designate *E. multilocularis* a reportable infection in animals. This may be important as the ability to anticipate *E. multilocularis* exposure, and detection of early-stage human AE, can reduce the need for long-term treatment and minimize the economic burden associated with the disease. Notably, as of May 1 2018, human AE has been designated a disease of public health significance in Ontario and must be reported to the local Medical Officer of Health.

5. A systematic review of compliance with indoor tanning legislation

Jessica Reimann, Jennifer McWhirter, Cate Dewey, Andrew Papadopoulos

Department of Population Medicine, University of Guelph

Many jurisdictions have enacted indoor tanning legislations in response to the health risks of artificial ultraviolet radiation exposure. Key components of these legislations include banning minor access, posting health warning signs, and providing protective eyewear, among others. However, legislation must be complied with to be impactful. Evidence around compliance with indoor tanning legislations has not been synthesized and is an important step toward determining changes in indoor tanning practice due to legislation. A systematic review was conducted to obtain peer-reviewed literature about compliance with indoor tanning legislations worldwide. Six databases were searched, resulting in 12,398 citations. Fifteen studies met the inclusion criteria. Compliance with most aspects of indoor tanning legislation varied. Compliance with age restrictions ranged from 20% to 89% (mean=55%; standard deviation=27), while compliance with posting warning labels as required within a tanning facility ranged from 8% to 72% (mean=44%; standard deviation=27). There was good compliance for provision of protective eyewear (84% to 100%; mean=92%; standard deviation=8). The reasons for such low and varied compliance with certain aspects of legislation, and high compliance with other aspects of legislation deserve further attention in future research. Variability in compliance with indoor tanning legislation suggests there may be problems with enforcement of the legislations, indicating they are not having their intended protective effects on the public’s health. Best practices around ensuring high and consistent compliance with indoor tanning legislations need to be determined.
Acknowledgements

We would like to thank our faculty and student judges for participating in this event and for making the time and effort to provide helpful feedback to our student researchers. We would also like to offer many thanks to the funding agencies for providing financial support for our students and their research projects.

- AAVN/Waltham
- ArticNet
- Bayer Animal Health
- Beef Cattle Research Council
- Canada Foundation for Innovation
- Canadian Agricultural Adaptation Program
- Canadian Cancer Society
- Canadian Institute of Health Research (CIHR)
- Canadian Poultry Research Council
- Canadian Research Chairs Program
- Dairy Farmers of Ontario
- Dairy Research Cluster
- Eastgen
- Egg Farmers of Canada
- ELISA Genetics Canada
- Equine Guelph
- Food From Thought
- Heart and Stroke Foundation of Canada (HSFC)
- Hill’s Pet Food
- Indigenous Health Adaptation to Climate Change (IHACC)
- KARYOTEKK Inc
- Merck Animal Health
- Mink Breeders Association
- Morris Animal Foundation
- National Centre of Excellence in Biotherapeutics for Cancer Treatment (BioCanRx)
- Natural Sciences and Engineering Research Council of Canada (NSERC)
- Ontario Graduate Scholarship (OGS)
- Ontario Ministry of Agriculture, Food and Rural Affairs (OMAFRA)
- Ontario Pork and National Pork
- Ontario Sheep Marketing Agency
- Ontario Veterinary College Pet Trust
- Ontario Veterinary Scholarship
- Ovarian Cancer Canada
- OVC Rapid Prototyping of Patient Specific Implants for Dogs (RaPPID)
- Polar Knowledge Canada
- Public Health Agency of Canada
- Queen Elizabeth II Graduate Scholarships in Science & Technology (QEII-GSST)
- Royal Canin
- SRC Seed Grant – Faculty of Community Services, Ryerson
- Swine Innovation Porc
- Terry Fox Research Institute
- University of Guelph Graduate Excellence Entrance Scholarship
- Virbac Animal Health
- Waltham Research Grant
- Zoetis