March 23 and 24, 2019
at The University of Western Ontario

ABSTRACTS and TALK SCHEDULE

Saturday March 23rd 2019

CONCURRENT SESSION I *2:30 – 3:30*

Cell and Molecular Biology A
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 0153

2:30 – 2:45, Saturday, March 23rd, B&GS 0153

THE BIOCHEMICAL RESPONSE OF TYPE II PROTEIN SECRETION SYSTEM AND THE BEHAVIOURAL RESPONSE OF ESCHERICHIA. COLI WHEN EXPOSED TO EXTREMELY LOW FREQUENCY ELECTROMAGNETIC FIELD

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Electromagnetic field have been shown to have either inhibition or stimulation effects on the cell's molecular and behavioural functions. Applying the right combination of intensity, frequency, duration, and type of magnetic field results in different cellular behaviours. The purpose of this research is to investigate the effect of extremely low frequency electromagnetic field on type II protein secretion system and morphology in Escherichia coli (E. coli). Enterotoxigenic E. coli (ETEC) is a harmful strain of E. coli that contains two different enterotoxins proteins called heat-stable toxin (ST) and heat-labile toxin (LT), which are responsible for the cause of severe form of diarrhea. Two types of strains are used normal strain and mutant strain. An overnight sample was divided into five different treatments. The morphological results showed that bacterial samples that were exposed to the electromagnetic field had an increase in colony number and diameter over ten days of measurements after the exposure.The future work will involve examining the protein concentration inside the cell, and applying the same technique with different types of cells.

2:45 – 3:00, Saturday, March 23rd, B&GS 0153

SUBSTRATE SPECIFICITY OF OMPTIN PROTEASES OF ENTEROBACTERIACEAE

Bashal, J.B.[1]
1. Ryerson University

Enterobacteriaceae are a family of gram-negative, facultatively anaerobic, rod-shaped bacteria, and they can be associated with significant disease burden, including gastrointestinal infection and sepsis. The ability to colonize the host and cause disease requires the ability to resist host-mediated killing. In *E. coli*, omptin proteases are a family of outer membrane proteases that can cleave antimicrobial host defence peptides. In *E. coli* (and the closely related species *Citrobacter rodentium*) there are four different omptins alleles but differences among these proteins has not been investigated. This study characterizes the ability of four omptins (OmpT, OmpP, ArlC and CroP) to cleave the host defence peptide LL-37. We investigated the activity by cloning each omptin under the control of a conserved promoter. Using Forster resonance energy transfer (FRET) assays and an antimicrobial killing assay we show that different omptin alleles provide differential resistance to LL-37 mediate killing. This study provides molecular insights into the role of different omptin family proteases in resistance to host defense peptide mediated killing.

3:00 – 3:15, Saturday, March 23rd, B&GS 0153

GENOMIC SIGNATURES PROVIDE A UNIQUE PERSPECTIVE IN CLASSIFYING THE HETEROGENEITY IN SPECIES OF BACILLUS USING ALIGNMENT-FREE METHODS.

Pislaru, A.[1], Soltysiak, M. [1], Randhawa, G.S. [1], de Souza, C.M. [2], Kari, L. [3], Stueckmann, D. [4], Hill, K.A. [1]
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2. Department of Statistical and Actuarial Science, University of Western Ontario
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Bacillus is the largest genus of aerobic endospore-forming bacteria with great genotypic and phenotypic diversity due to broad species inclusion criteria. A key challenge with this taxonomic group is classification due to its heterogeneity, causing it to be as diverse as some bacterial families, thus its phylogenetic tree has potential to be split into further taxa. The alignment-free method ML-DSP, combining Chaos Game Representation (CGR) of DNA sequences with supervised machine learning, provides helpful insight into the taxonomic classification of species within this diverse genus. A genomic signature is the organization of a sequence specific to a species and can analyzed using alignment-free methods to aid in taxonomic classifications. Genomic sequence patterns can be visualized and classified into a genomic signature via CGR. Variation in CGR patterns of 199 *Bacillus* species was not surprising given the genomic diversity. Distinctions in CGR patterns included a pattern with CG, CC, GC, and GG underrepresentation accounting for 42% of the species studied and others with increased heterogeneity. These results were used to generate a 3D Molecular Distance Map of the *Bacillus* species using a distance matrix generated by ML-DSP, representing relationships among all genomes. The 3D map displayed distinct clusters of sequence similarity, having one dense cluster and several others spread further apart. These clusters are helpful in describing the subdivisions within Bacillus.

3:15 – 3:30, Saturday, March 23rd, B&GS 0153

INVESTIGATING THE QUEE STRUCTURE AND BACTERIAL VIABILITY ASSOCIATED WITH QUEE MEDIATED FILAMENTATION IN ESCHERICHIA COLI

Abuzar Zainul, Raymond Hyunh, Joseph B. McPhee
Ryerson University

In *Escherichia coli*, the PhoP/PhoQ two-component regulatory system regulates a complex response leading to antimicrobial peptide resistance. It has recently been shown that the PhoPQ system up-regulates the QueE protein, a protein normally associated with the biosynthesis of queuosine, however expression of QueE also leads to pronounced bacterial filamentation. Filamentation is a process in which normal bacterial cell division is altered, promoting the formation of long, thin filaments of connected bacterial cells. In spite of this, little is known about the interaction between QueE and the bacterial divisome complex. The PhoPQ system and downstream genes typically lead to enhanced survival during exposure to host-defense peptides and by implication we hypothesize that filamentation may result in increased survival. Here, we report that mutants of *E. coli* lacking queE have increased sensitivity to LL-37. Furthermore, we show that the ability of QueE to induce bacterial filamentation is not conserved amongst QueE orthologues from members of the Enterobacteriaceae family suggesting that the induction of filamentation may represent an adaptive response for antimicrobial peptide resistance. Here, we describe a project to show that QueE-induced filaments remain viable and exhibit increased resistance to antimicrobial peptides using a novel inducible GFP plasmid system in combination with flow cytometry to assess bacterial viability following an antimicrobial peptide exposure.

Cell and Molecular Biology B
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 0165

2:30 – 2:45, Saturday, March 23rd, B&GS 0165
ROLES OF SKP2 AND SAC IN PRESERVING GENOMIC INTEGRITY
Aryal, S., Swan, A.
University of Windsor Biology Department

Skp2 is an F-box protein of the SCF complex whose overexpression has been documented in a variety of human cancers. It is an oncogene known for its role in targeting the tumor suppressor p27 for proteasomal degradation at the end of G1 to promote entry of the cell into S phase. However, in-vivo studies in mice and Drosophila have shown a novel role of Skp2 as a potential tumor suppressor. The loss of Skp2 results in reduced ability to enter mitosis and subsequent polyploidy. However, when Skp2 mutant cells do enter mitosis, cells are delayed in prometaphase/metaphase due to activation of the Spindle Assembly Checkpoint (SAC), and mitosis is aberrant. Previous studies in the Swan lab have shown that knocking out Mad2, a critical component of the SAC, in Skp2 mutant cells is able to rescue the mitotic delay but it also results in failed chromosome segregation, chromosome breakage, increased polyploidy, and increased apoptosis, indicating that the SAC may be important for preventing further genome instability of Skp2 mutant cells. This project aims to first, confirm those results, and second, assess whether those results are indeed due to a SAC-specific role of Mad2, as opposed to a novel function of Mad2, by testing two other SAC components – BubR1 and Bub3. RNAi will be expressed in the wings to knock down Skp2 and the SAC components, and wing discs of larvae will be examined for the degree of polyploidy, potential mitotic defects, the mitotic index and the level of apoptosis.

2:45 – 3:00, Saturday, March 23rd, B&GS 0165
THE ROLE OF SPY1 IN THE CELL CYCLE AND THE DEVELOPMENT OF HEPATOCELLULAR CARCINOMA
Curtis, M.B., Fifield, B., Porter, L.A.
University of Windsor

Hepatocellular carcinoma (HCC) is the cause of approximately 1 million deaths worldwide per year, and accounts for 85-90% of all primary liver cancers. Effective therapies are limited leading to poor 5-year survival. The primary cell type of the liver, hepatocytes, display unique cell growth and proliferation properties. Hepatocytes become polyploid through development, which increases the DNA content in each cell, and they retain the potential to regenerate and proliferate. Increased polyploidy has been shown to be a protective factor in HCC. Misregulation of the cell cycle plays a critical role in the onset of HCC. Spy1, an atypical cyclin-like protein, can induce progression through the cell cycle by binding to cyclin-dependent kinases (CDKs). This binding allows for unique progression through various cell cycle checkpoints, and Spy1 is known to be elevated in HCC. A transgenic mouse model, MMTV-Spy1, that has decreased hepatocyte ploidy and increased susceptibility to liver tumour formation, will be utilized to study the effects of increased expression of Spy1 on hepatocyte regeneration, susceptibility to tumour formation and response to treatment. Expression of a mediator of cell cycle progression, differentiation and metabolism in hepatocytes, CCAAT/enhancer binding protein (C/EBP) will be examined. The results will provide insight into the effects that Spy1 has on cell cycle progression in hepatocytes, and may reveal a novel therapeutic target in the treatment of HCC.

3:00 – 3:!5, Saturday, March 23rd, B&GS 0165
DISSECTING HETEROGENEOUS NATURE OF BRAIN TUMOURS
Rodzinka, A.P., Lubanska,D.A., Porter, L.A.
University of Windsor

Glioblastoma multiforme (GBM) is the most aggressive form of brain tumour with 5-year survival rates of less than 10%. Past literature contends that select cell populations exist within the tumour mass that drive GBM growth. These populations are referred to as Brain Tumour Initiating Cells (BTICs). While the true origin of these cells is debatable, physiologically these cells possess immature properties of normal neural stem cells. They are highly resistant to drug treatment, radiation and form tumours at a high rate when transplanted into mice. The complexity of GBM is elevated due to the fact that not all tumour masses are the same. Historically, most patient tumours can be categorized into three specific subtypes based on their genetics.

Additionally, Spy1 is a unique cell cycle regulator that is found in normal neural stem cells during brain development; however, during rapid cancerous growth Spy1 is present in high levels and allows progress through the cell cycle without halting at the traditional checkpoints. Pinpointing which specific populations in a brain tumour mass drive tumour expansion would be of utmost value and Spy1 may be a pivotal target.

Patient-derived brain tumour populations may be sorted and isolated via fluorescence-activated cell sorting of well-characterized BTIC cell surface markers. I have established a BTIC reservoir which provides innumerable opportunities to study the populations in vivo and in vitro.

3:15 – 3:30, Saturday, March 23rd, B&GS 0165

THE EFFECTS OF METFORMIN AND BERBERINE ON MEDULLOBLASTOMA CELL VIABILITY IN VITRO

Wilsdon, D.W., Kelly, G.K.
University of Western Ontario

Medulloblastoma (MB) is the most common brain malignancy in children and has lifelong negative impacts on health and development, but its various genetic subtypes pose a challenge to treatment. Metformin (MET) and berberine (BER) have been shown to prevent tumorigenesis and promote cancer cell death by inhibiting oxidative phosphorylation and activating the AMPK signaling pathway. The aim of this study was to determine if MET and BER will affect the viability of MB cells and if so, the mechanism of action. MB cells were treated with a range of MET and BER and evaluated using a cell viability assay to determine the concentration at which a significant change in MB cell viability is seen 24 hours post-treatment and to determine if co-treatment of MET and BER had a synergistic effect on viability. The mechanism by which cell viability changed following treatment was elucidated through immunoblot analysis of PCNA and caspase-3 levels which serve as measures of cellular proliferation and apoptosis, respectively. A time-course experiment using immunoblot analysis to measure caspase-3 activation at 0, 12, and 24 hours post-treatment was also performed. The results demonstrate that MET and BER are capable of reducing the viability of MB cells, particularly in combination, and that the cause of decline is due to the activation of the apoptotic signaling pathway. This provides a basis for future studies on these compounds' beneficial effects on MB and other cancer cell types.

Cell and Molecular Biology C
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 1056

2:30 – 2:45, Saturday, March 23rd, B&GS 1056

EXAMINING THE DIVERSITY OF METABOLIC CAPABILITIES IN BACTERIA ISOLATED FROM WASTEWATER TREATMENT PLANTS

Ahmed, S., Gilbride, K.
Ryerson University

The secondary treatment process in municipal wastewater treatment plants (WWTPs) utilizes large microbial populations to degrade organic matter and reduce the overall biochemical oxygen demand (BOD) of the effluent. Bacteria isolated from WWTPs, particularly from the genus *Variovorax* and family Enterobacteriaceae, have strong, intrinsic metabolic abilities. *Variovorax* have been associated with the degradation of a wide array of xenobiotic organic compounds. This suggests that *Variovorax* may play an important role in the biodegradation of organic pollutants in contaminated environments. Therefore, the goal of this study was to characterize several of the *Variovorax paradoxus* strains that our lab has isolated from WWTPs. Their antibiotic resistance patterns were determined using the Kirby Bauer Disc susceptibility testing and correlated with the metabolite capabilities which were examined with Biolog Ecoplates and GenIII microplates. The strains were also tested for their ability to remove total organic carbon (TOC) from synthetic wastewater to determine their potential ability to enhance degradation within the wastewater system. Overall, *Variovorax* isolates carried multiple resistances to antibiotics and have been found to metabolize a wide variety of compounds (polymers, amino acids, and carboxylic acids). Understanding the intrinsic properties of Variovorax can be used in applications to improve wastewater treatment and biodegradation in contaminated environments.

2:45 – 3:00, Saturday, March 23rd, B&GS 1056

INVESTIGATING THE SOURCE OF LIPIDS DURING TUBULAR LYSOSOME FORMATION IN BONE-MARROW DERIVED MACROPHAGES FOLLOWING ACUTE LPS STIMULATION

Diaz, J., Hipolito, V.E.B., Botelho, R.J.
Ryerson University

Macrophages elicit a repertoire of defense mechanisms when exposed to threatening agents such as lipopolysaccharide (LPS) of gram-negative bacteria. Of these defense mechanisms, macrophages engulf the invading microbe and transport it to the lysosome for degradation. Lysosomes are tiny membranous sacs containing hydrolytic enzymes that serve to destroy foreign materials and cellular debris. Interestingly, when macrophages are exposed to LPS, their lysosomes convert from punctate structures into tubular networks. We have previously shown that this tubular phenotype is accompanied by increased volume and lysosomal protein synthesis, even after acute stimulation (2 hours). Therefore, we are interested in elucidating the source of lipids responsible for this lysosomal membrane expansion and accommodation of increased protein and volume. To test this, we investigated the activation of amp-activated protein kinase (AMPK) and acetyl-coA carboxylase (ACC) following acute LPS stimulation in bone-marrow derived macrophages. Preliminary data however suggests that their activation is not significantly altered under such conditions. Furthermore, we are currently investigating whether the nuclear migration of sterol regulatory element-binding protein (SREBP), a transcription factor involved in lipid biosynthesis, is increased following acute LPS exposure. Taken together, this work may exclude and/or uncover possible sources of lipids contributing to this fascinating tubular phenotype.

3:00 – 3:15, Saturday, March 23rd, B&GS 1056

DECIPHERING THE ROLES OF LDH AND PDK IN XEN DIFFERENTIATION

Guiot, L.D., Kelly, G.
Department of Biology, University of Western Ontario

In recent years, there has been increasing evidence showing the importance of metabolism in cell differentiation. Different states of pluripotency versus specified cell types are characterized by changes in the balance between glycolysis and oxidative phosphorylation (OXPHOS); both pathways being regulated by lactate dehydrogenases (LDHs) and Pyruvate Dehydrogenase Kinases (PDKs). The objective was to investigate the role of metabolism in the differentiation of extraembryonic endoderm (XEN), a cell type that generates supporting structures for the embryo prior to implantation. In this study, mESC were used to compare the metabolic profiles of pluripotent E14 cells and XEN derived E4 cells. RT-qPCR analysis confirmed the differentiation of the E4 cell line and showed a significant increase in Gata6 and significant decrease in Nanog. Immunoblot analysis of LDHA, LDHB, PKD1, PDK4, PDH and p-PDH showed an increase in LDHA and a decrease in PDK1 and PDK4 in XEN cells, suggesting there is a bivalent potential of glycolysis and OXPHOS. We sought to induce E14 cells towards a XEN lineage using retinoic acid and Activin. XEN population has proven difficult to isolate; however preliminary results show an increase in Gata6 as a differentiation marker. Metabolism is a vital cell process that is known to play a role in cell fate specification, understanding its role in XEN differentiation will add additional layer of regulation of the differentiation of this cell type in the early embryo.

3:15 – 3:30, Saturday, March 23rd, B&GS 1056

LYCAT REGULATES PIP2 SIGNALLING THROUGH MEDIATING FATTY ACYL CHAIN PROFILES

Khuffash, S.K., Bone, L.B., Antonescu, C.A., Botelho, R.B.
Ryerson University

Phosphoinositides (PIPs) are known to control numerous cellular processes through interactions on their inositol ring head group, such as cell migration. PIPs possess unique 38:4 fatty-acyl chain profiles that play a significant role in their function. LYCAT, an acyltransferase, regulates the acyl chain profiles on PIPs, potentially influencing many signalling pathways. Rac, downstream of phosphatidylinositol-3,4,5-trisphosphate (PIP3) governs the formation of lamellipodia, which is essential for cell migration. The link between altering the acyl species of PIPs and its effect on the actin formation remains unknown. Thus, we investigated the role of silencing LYCAT and its impact on actin formation. LYCAT silenced conditions demonstrated a decrease in levels of actin polymerization, compared to control conditions. Furthermore, LYCAT silenced conditions demonstrated perturbed cell migration compared to controls. Overall, our research proposes that the structure of fatty-acyl chains in PIPs alters cell signalling, specifically through actin formation.

Physiology and Biochemistry A
PHYSICS & ASTRONOMY BUILDING, RM 34

2:30 – 2:45, Saturday, March 23rd, P&A 34

EFFECTS OF SILVER NANOPARTICLES ON GROWTH OF SOYBEANS (GLYCINE MAX) AND BRADYRHIZOBIUM JAPONICUM USDA 110

Boersma, P. J., Macfie, S.M.
Biology Department, University of Western Ontario

Silver nanoparticles (AgNPs) are an antimicrobial material found in various household items. Use, production and destruction of these items releases AgNPs into the environment. Many plant species can take up AgNPs, which could have negative effects on plant growth and mutualistic relationships, especially bacterial interactions. We studied soybean (*Glycine max*) and its nitrogen-fixing bacterium, *Bradyrhizobium japonicum*. Our hypothesis was that AgNPs would inhibit both bacterial and plant growth. We also aimed to measure the amounts of Ag taken up and translocated within soybean. Inoculated seedlings and axenic *B. japonicum* cultures were grown in nutrient solution with up to 1 µg/mL of mixed (10, 40 and 100 nm) AgNP suspensions. We found no evidence of direct AgNP toxicity to either the bacterium or soybeans. Instead, 0.1 µg/mL AgNPs seemed to stimulate plant growth; in this treatment, leaf area was 30% larger than control. Using TEM imaging of root cross sections, we located AgNPs from each size class within cells and organelles of root tissue. Using ICP-MS, we determined that more than 97% of the Ag that was taken up by the plants stayed in the roots; only 1.3 to 3% of the Ag was in shoots, showing minimal translocation. While the amounts of AgNPs in this experiment did not inhibit soybean or bacteria growth, the possibility that AgNPs interfere with root bacterium communication during nodule formation remains to be tested.

2:45 – 3:00, Saturday, March 23rd, P&A 34

ASSESSING THE QUALITY OF DISSOLVED ORGANIC MATTER IN NORTHERN FRESHWATER ENVIRONMENTS

Mindorff, L.M. [1]; McGeer, J. [1]; Smith D.S. [2]
1. Biology Department Wilfred Laurier University
2. Chemistry and Biochemistry Wilfrid Laurier University

Dissolved organic matter (DOM) is capable of binding toxic free metal ions, such as copper (Cu), thereby reducing their bioavailability. While binding is known to occur in a concentration-dependant manner, the importance of DOM source quality is poorly understood. Most research on the subject is focused on DOM sourced from temperate regions. In this study, the quality of DOMs from subarctic sources were collected and assessed. DOM quality was

assessed by identifying aromatic content (SAC340), free Cu2+ binding capacity, and Cu toxicity mitigating ability. The SAC340 was used as an index for aromaticity; measured values ranged from 2 to 33. Free Cu2+ binding capacity of DOMs were measured using an ion-selective electrode. Acute 96-h toxicity tests for Cu using *Hyalella azteca* were conducted following Environment Canada Biological Test Methods (EPS1/RM/33). The *Hyalella* were exposed to a range of Cu concentrations (0-480 µg Cu/L) in the presence of DOM (10 mgC/L) to determine LC50 values. All DOMs were protective as LC50 values increased from 15.0 µgCu/L (95% CI 10.9-21.9 µgCu/L) with no DOM present, to as high as 315.0 µgCu/L (95% CI 245-433 µgCu/L) with DOM. LC50 values increased with SAC340 values suggesting that source differences did influence the Cu toxicity mitigating abilities of the DOM. However, the correlation between LC50 and SAC340 was not statistically significant (Pearson correlation, r = 0.79, P = 0.059, d.f. = 4).

3:00 – 3:15, Saturday, March 23rd, P&A 34

EXPOSURE TO Δ9-TETRAHYDROOCANNABINOL DURING GESTATION LEADS TO MITOCHONDRIAL DYSFUNCTION IN POSTNATAL LIFE

Moryousef-Abitbol, J. [1], Lee, K. [1], Laviolette, S. [2], Hardy, D.B. [3]
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3. Department of Physiology and Pharmacology, University of Western Ontario, London, Ontario, Canada & Departments of Obstetrics and Gynecology, Children's Health Research Institute, Lawson, Health Research Institute, University of Western Ontario, London, Ontario, Canada

Cannabis is the most common drug used by pregnant mothers and reports indicate 20% of pregnant mothers between the ages 18-24 screened positive for cannabis usage. While the concentrations of the main psychoactive ingredient, Δ9-tetrahydroocannabinol (Δ9-THC), have tripled in less than 20 years, little is known about its long-term effects on fetal and postnatal development. Given (i) Δ9-THC during gestation leads to placental insufficiency and reduced birth weight and (ii) impaired fetal development is associated with long-term hepatic disease, we hypothesize Δ9-THC leads to adverse liver development. The endocannabinoid system has been shown to negatively impact mitochondrial integrity and function. Our laboratory has shown that mitochondrial dysfunction underlies some of the programming effects of intrauterine growth restriction in postnatal life. Therefore, using a rat model of gestational Δ9-THC exposure, we examined the metabolic outcomes on the liver by measured well-established markers of mitochondrial impairment. Hepatic tissue from postnatal day 1 and 21 were isolated from offspring who were exposed to vehicle or Δ9-THC during pregnancy. At PND1, Δ9-THC offspring exhibited decreases in liver:body weight ratio concomitant with reduced expression of respiratory complexes I, V, and OPA1 while levels of SOD1/2 were augmented. Collectively, this suggests Δ9-THC has direct effects on hepatic mitochondrial dysfunction in the postpartum period.

3:15 – 3:30, Saturday, March 23rd, P&A 34

WOUND HEALING AND SUBERIZATION IN SOLANUM TUBEROSUM IS NOT EFFECTED BY APPLICATION OF REVUS FUNGICIDE

Sinka, J.L., Dokis, E
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In Canada, the seed potato (*Solanum tuberosum*) industry faces wound-associated challenges. High rates of injury occur during handling or when the seed potato is sectioned for crop initiation. Formation of the wound periderm of potato tubers is critical in protecting against dehydration and infections; this ensures longevity of the seed potato. Revus, a fungicide registered by Syngenta, is a translaminar agent containing 2-(4-chloro-phenyl)-N-[2-(3-methoxy-4-prop-2-ynyloxy-phenyl)-ethyl]-2-prop-2-ynyloxy-acetamide (mandipropamid) which protects against seed-borne late blight (Phytopthora infestans). To evaluate the effect of Revus on the sprouting and tissue suberization of potato tubers, five varieties of seed potato were treated with Revus. Healing an was assessed over 7 days through visualization of deposition of two major suberin components, suberin polyphenolics and suberin polyaliphatics, as identified by autofluorescence and staining with Toluidine Blue O, respectively. Analysis of ratings suggests that treatment with Revus fungicide has no effect on the rate of suberin polyphenolic deposition in all investigated potato varieties when compared to controls. In seed potatoes treated with Revus prior to sprouting length of sprouts and number of eyes sprouted were observed and the results will be presented. In conclusion, Revus could be recommended for use on potato seed tubers as a treatment against infection without any notable effects on sprouting or wound suberization.

Physiology and Biochemistry B
PHYSICS & ASTRONOMY BUILDING, RM 36

2:30 – 2:45, Saturday, March 23rd, P&A 36

THE BIOLOGICAL AND BIOPHYSICAL EFFECTS OF LAUGHTER ON SALIVARY CORTISOL

Banerjee, P. & Blake Dotta
Laurentian University

The purpose of the study is to test the effects of laughter on cortisol levels in saliva of 40 undergraduate students. In this between groups study there are four groups of ten for four different conditions. Each condition is identified by audio tracks where the first condition will contain humor content, the second audio will have non humor content, and lastly the third audio will be non humor content, (same as the second audio) with a superimposed laughter track, and lastly the fourth audio will be a laughter track or laughter yoga audio. Pre and post measures of cortisol will be obtained from the saliva test, and photon measures of the subject will be conducted through the photomultiplier tube before and after the exposure to the audio tracks. We hypothesize that cortisol has a proportional relationship with photons as cortisol is secreted with activation of the sympathetic nervous system. It can be hypothesized, due to the increased rate of metabolism; levels of photons are predicted to be elevated pre audio and decreased post audio. The less levels of cortisol will be detected in the saliva test and is independent of the laughter track itself. This study can further help us understand the therapeutic benefits of humor in stress prevention.

2:45 – 3:00, Saturday, March 23rd, P&A 36

ELECTROMAGNETIC FIELDS CAUSE HOMOGENIZATION OF PH VARIABILITY IN ARTIFICIAL CEREBROSPINAL FLUID

Hayhurst, O.E. [1], Carniello, T.N. [2], Dotta, B.T. [1,2]
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2. Neuroscience Research Group, and Biomolecular Sciences PhD Candidate, Laurentian University, Sudbury, ON, Canada

Throughout our entire lives we are continually exposed to electromagnetic waves. These magnetic waves can originate from natural sources such as our own brain's electrical impulses, to artificial sources like our cell phones and computers. It has been repeatedly shown that certain patterns of electromagnetic fields alter the pH of water. With cerebrospinal fluid (CSF) being 99% water, is it possible that the pH of CSF can be influenced by the application of magnetic fields? With this in mind, 6 electromagnetic fields of varying patterns were tested in this study: Burst Firing, FM-Thomas, LTP, Simulated Geomagnetic Storm, Sine 7 Hz, and a sham field. Artificial cerebrospinal fluid (aCSF) was synthesized to simulate the same chemical composition of human cerebrospinal fluid for testing purposes. We measured changes in pH continuously for 30 minutes: 5 minutes before exposure to the magnetic field, during the 20-minute exposure, and for 5 minutes after exposure. Measuring after exposure to the field is done to determine if any lasting effects were specifically caused by the electromagnetic field in the artificial cerebrospinal fluid. We have found that exposure to electromagnetic fields results in a homogenization of the variability associated with aCSF pH over the 20-minute exposure period when compared to no field conditions ($p<0.001$). Further studies would allow us to examine the effects of electromagnetic fields on CSF and the different ions and proteins within the solution.

3:00 – 3:15, Saturday, March 23rd, P&A 36

SYNERGISTIC EFFECTS OF ELECTROMAGNETIC FIELDS PAIRED WITH LIDOCAINE AND NATURAL REMEDIES AS AN INTERVENTION FOR NICOTINE ADDICTION AND WITHDRAWAL: A PLANARIAN MODEL

Lachapelle, H.M, Carniello, T.N, Dotta, B.T.
Laurentian University

Nicotine addiction is pervasive among humans and can be identified largely by the presence of withdrawal symptoms related directly to psychological distress: irritability, anxiety, and depression. The neuropharmacological effects of nicotine and concomitant withdrawal behaviours can be investigated using planarian flatworms. Comprised of all the main neurotransmitters as humans, their simplistic CNS anatomy allows for a closer look at the neurobiological behavioural correlates of drug effects and responses to environmental stimuli. The purpose of this study is to investigate potential synergistic effects of electromagnetic fields paired with pharmaceutical agents as a possible intervention for planarian withdrawal behaviours following acute exposure to nicotine. Planaria were exposed to 10μM nicotine and immediately observed for atypical behaviours before being individually housed for 24 hours. After 24 hours, planaria were exposed to 1 of 4 conditions: spring water, Stop Smoking Help (GABA), Smokers Cleanse (Tyrosine), and 10μM Lidocaine for 1 hour while simultaneously being exposed to one of two field conditions: Frequency modulated (FM) or Sham. Following this, an additional behavioural assay was performed, and all behaviours were recorded. Results demonstrated a significant time by field effect for planarian whipping behaviours: specimens which received a frequency modulated field for 1 hour had significantly fewer whips as compared to specimens receiving sham treatments.

3:15 – 3:30, Saturday, March 23rd, P&A 36

INVESTIGATING THE INDUCTION EFFECTS OF ELECTROMAGNETIC FIELDS ON NON LIVING BRAINS

Morris, F.A
Laurentian University

Human exposure to electromagnetic fields (EMFs) from man-made sources such as cellular devices has been increasing within the last decade. EMFs are known to have some effect on biological systems but the mechanisms by which this occurs is unknown as most of the data remains inconclusive and better yet the nature by which this affects brain activity and function is yet to be fully understood. In this experiment the aim is to investigate the inductive effects of EMFs on a post-mortem sheep brain. The sheep brain is an ideal model for this experiment because it contains almost identical structures to that of a human brain. The post-mortem sheep brain was cut into coronal sections and the rostral portion exposed to various EMFs at different frequencies. The electrical activity of the post-mortem sheep brain was recorded using electroencephalography. A discriminant analysis of the spectral frequencies was carried out and the results revealed a significant classification accuracy ($p<0.05$) between EMF and sham conditions (accuracy >85%).

Ecology and Evolution A
PHYSICS & ASTRONOMY BUILDING, RM 148

2:30 – 2:45, Saturday, March 23rd, P&A 148

INTERACTIVE EFFECTS OF MATERNAL PRENATAL GLUCOCORTICOIDS AND ELEVATED REARING TEMPERATURES ON COPING STYLES IN CHINOOK SALMON FRY

Cervini, M., Semeniuk, C.
University of Windsor

In teleost fish, cortisol, the main glucocorticoid hormone, can be transferred from a spawning mother to her eggs as a signal of stressful environmental conditions, thus priming offspring to cope with harsh environments. My research tests whether this pre-natal hormone signal could influence behavioural coping styles in Chinook salmon fry

(*Oncorhynchus tsawytshacha*) in response to environmental stimuli at emergence. After dosing with a cortisol or control solution, fertilized eggs were reared under two different temperature regimes, one representing native conditions and the other elevated (+3oC) to simulate a stressful environment. At 288 degree days, fry behaviour was recorded to analyzed degree of mobility, spatial distribution, and responses to multiple stimuli. Under elevated temperatures, I predicted prenatal stress-exposed fry will demonstrate bold behaviour, increased foraging, and take greater risks in comparison to non-exposed fry. Under current temperatures, I predicted non-exposed fry will not demonstrate these behaviours. I found cortisol-treated fry raised in elevated temperatures were significantly more likely to approach a novel object ($p = 0.044$), and food ($p = 0.041$). I found no significant difference in shelter use ($p = 0.15$) and durations of mobility ($P = 0.33$) between temperature and cortisol treatments. This research gives insight into the adaptive behaviours of Chinook salmon due to maternal prenatal hormones in an increased temperature environment.

2:45 – 3:00, Saturday, March 23rd, P&A 148

EFFECTS OF ACUTE ALARM CUE EXPOSURE ON EMBRYONICALLY PRIMED JUVENILE ATLANTIC SALMON

Elshikh, M. T. [1], Mokdad, A. [2], & Pitcher, T. [1,2]
1. University of Windsor Department of Biological Sciences.
2. Great Lakes Institute for Environmental Research (GLIER).

Alarm cues, chemical compounds released following physical damage to skin, are involved in most antipredator behaviours in fish that possess them. In hatchery-reared fish, a lack of early developmental experiences with predation can lead to lowered survival upon release into the wild. Previous studies have also found that embryonic exposure to alarm cues (i.e. priming) engenders plastic behavioural responses in salmonids. However, it is unknown whether priming affects the response of fish to acute alarm cue exposure. The purpose of this study is to test hypothesis that it does. Atlantic salmon (*Salmo salar*) gametes, collected from hatchery-reared adults, were fertilized using a split-clutch design to create two treatment groups (primed and non-primed), containing full-siblings in each group. During the alevin stage, the primed group was exposed to conspecific alarm cue once a day, three days a week, for four weeks. The non-primed group was likewise treated with distilled water. At the yearling stage, primed and unprimed fish were behaviourally tested either with acute exposure to alarm cue or distilled water (control). Behavioural tests included novel tank, novel object and foraging tests. Behavioural measures included time spent moving, time spent frozen, number of foraging attempts, as well as the number of aggressive acts. The results of this study will be explored in the context of improving the behavioural performance and survival of reintroduced hatchery-reared fish.

3:00 – 3:15, Saturday, March 23rd, P&A 148

SEA LICE, SOCKEYE SALMON, AND PARASITE HOST PREFERENCE: THE INDECISIVE CALIGUS

Xiong, Y., Yang, H.
University of Toronto

Recent field studies have observed a potential preference of *C. clemensi* (*Caligus clemensi*) towards sockeye salmon (*Oncorhynchus nerka*) hosts. This preference may be mediated by chemical cues. Parasite load on wild juvenile salmon affect fish fitness significantly, thus understanding host-parasite dynamics, whether farms act as a potential lice reservoir and parasitic management strategies adapted by fish farms will be crucial to the growth rate and fitness of the declining Frazer River sockeye population. We conducted a host-parasite choice experiment using Caligus sea lice (*Caligus clemensi*) and Fraser River juvenile sockeye salmon (*Oncorhynchus nerka*) to determine whether *Caligus* sea lice has a preference towards juvenile sockeye salmon over juvenile chum salmon hosts. Our experimental apparatus, the “u-tube”, aims to test live louse’s fish species preference, involving no live fish mortality nor infection. Power analysis was done for determining treatment and trial numbers, and histogram analysis were done for comparing control to all treatment groups. Our results supported lice preference towards juvenile sockeye salmon cues over juvenile chum salmon cues. Our exploration of the less studied *C. clemensi* infestation in Fraser River sockeye salmon may shed light to the conservation of this declining population.

3:15 – 3:30, Saturday, March 23rd, P&A 148

PERSONALITY AND SOCIAL LEARNING OF PREDATOR CUES IN ATLANTIC SALMON

Smith, I.S.
University of Windsor

While fish hatcheries produce fish for reintroduction to artificially supplement wild populations, the success of these initiatives can be poor. Compared to their wild counterparts, hatchery-raised fish have higher rates of mortality soon after being introduced to their environment. This is thought to be due to predation since released fish are never exposed to native predators in a hatchery setting and thus do not learn predator avoidance behaviours. By pairing a conspecific alarm chemical with a novel predator odor, naïve fish can be trained to display antipredator behaviors without being exposed to predation. However, the optimization of this training for large-scale hatchery practices has been little studied. My study attempts to address the possibility to train large groups of fish via social learning in Atlantic salmon (*Salmo salar*) fry, where an individual reacts to a predator stimulus by observing an experienced individual's reaction. A subset of fry (n=15) were trained with a paired predator and alarm cue, and individually retested with the predator cue only 24 hours later in the presence of five naïve conspecifics. Each individual was retested one week later to the predator cue, and their responses recorded. Testing in isolation had a greater impact on behaviours, and fish became more sensitized with repeated exposure. By investigating the success of various training practices, training of fish could be achieved cost-effectively, efficiently, and in large groups.

Ecology and Evolution B
PHYSICS & ASTRONOMY BUILDING, RM 106

2:30 – 2:45, Saturday, March 23rd, P&A 106

SENSORY HAIR CELL REGENERATION IN BLACK BULLHEAD (AMEIURUS MELAS) AFTER NOISE EXPOSURE

Aoun, J.A.
University of Windsor

Aquatic environments are often exposed to anthropogenic (man-made) noise that disrupt natural sounds in these environments, which has been shown to hinder fish's survival. High intensity sounds can damage sensory hair cells of fish leading to temporary threshold shifts, though fish are able to regenerate these hair cells. The current study was performed on black bullhead (*Ameiurus melas*) to investigate if anthropogenic noise at increasing intensities can permanently damage sensory hair cells. Black bullhead were exposed to boat noise at 165 dB re 1 Pa, 170 dB re 1 Pa and 175 re 1 Pa and a regeneration period was given to allow for sensory hair cell regrowth. Sensory hair cells were then counted along three positions of the saccule. Overall, hair cell counts were lowest at the beginning of this period, and continued to increase with each day. The trial conducted at 165 dB re 1 Pa had the highest hair cell count, while the trial at 175 dB re 1 Pa had the lowest hair cell count. Therefore, black bullhead are prone to sensory hair cell damage due to anthropogenic boat noise and this damage increases with higher sound intensities. However, permanent hair cell loss was not observed with the sound levels used in this study. The study contributes to the understanding of how humans are affecting hearing of fish, specifically fish species in the Great Lakes, an environment where black bullhead are often found.

2:45 – 3:00, Saturday, March 23rd, P&A 106

THE INFLUENCE OF SOUND ON ROUND GOBY (NEOGOBIUS MELANOSTOMUS) FORAGING BEHAVIOUR

El-Cheikh Mohamad, A.
University of Windsor

Anthropogenic noise serves as a stressor to many species, causing various negative consequences on their physiology and behaviour. In fish, anthropogenic noise can influence changes in behaviours such as communication, and foraging ability. The purpose of the current study was to examine the effect of anthropogenic noise, specifically boat noise, on the foraging behaviours of the round goby (*Neogobius melanostomus*). The foraging behaviour of round gobies on earthworms was video recorded while gobies were subjected to various sound files containing boat noise, white noise, no noise with speaker on, and no noise with speaker off. Videos were analyzed for behaviours such as foraging errors, foraging successes, and swimming duration. The analysis of these results is currently being conducted. If round goby foraging is affected by the presence of noise, then it is possible that fish species with the ability to hear larger frequency ranges than the round goby are also negatively impacted. Studies, like this one, are useful for assisting in the creation of guidelines to protect environments from stressors like anthropogenic noise.

3:00 – 3:15, Saturday, March 23rd, P&A 106

AUDITORY EVOKED POTENTIALS (AEP) TO QUANTITATIVELY ASSESS HEARING ABILITIES IN BLACK BULLHEAD (AMEIURUS MELAS)

Kotrri, E.
University of Windsor

Sound detection serves a survival function in fishes as it aids them with communication, prey detection and predator evasion, therefore many species have evolved specialized structures to hear a wide range of sound frequencies. A common technique used to assess the hearing abilities of fishes is that of the auditory evoked potentials (AEP), which records whole-brain potentials that are elicited during the presentation of sound stimuli. The current study sought to measure the hearing abilities of black bullhead (*Ameiurus melas*) using the AEP methodology. Bullhead were exposed to varying frequencies of sound at different sound levels to ascertain the sound level threshold of each frequency. Factors such as body size and length of residence in a noisy laboratory setting were also considered to determine how such factors may impact hearing. Sound detection occurred over the entire range of frequencies tested, with 400 Hz found to be the most sensitive. Hearing sensitivity also increased with body size, consistent with the development of specialized hearing structures as fish grow. Overall, these findings provide insights into the physiological capabilities of black bullhead in sound detection and how development may play a role in this ability. The current study also provides a better understanding of how hearing abilities of bullhead may be affected with greater exposure to a loud environmental setting, which can be applied in conservation efforts to reduce anthropogenic noise.

3:15 – 3:30, Saturday, March 23rd, P&A 106

EFFECT OF AGE AND SOUND ON HAIR CELL DISTRIBUTION IN MEMBRANOUS LABYRINTH OF THE SEA LAMPREY (PETROMYZON MARINUS)

Oozeer, D.N
University of Windsor

Fish live in a complex auditory environment filled with biotic and abiotic sounds, important for tasks such as orientation in their environment and communication. A common component to the interpretation of sound in many is the basic functional unit of the ear, the hair cell. The basic mechanism of sound interpretation is similar in most fish, but what differs is the location and number of hair cells within the ear. It is unclear what the distribution of hair cells is in the extant agnathan the sea lamprey (*Petromyzon marinus*), a basal vertebrate species. The purpose of the current study is to determine the density and regional distribution of hair cells within the sensory epithelium sea lamprey ears and if this changes in sound-treated adults and juveniles. Hair cell counts were used to determine regional densities to compare between the sound exposed adults, non-sound exposed adults, and juveniles. It is hypothesized that there will be a difference in regional densities between the sound exposed and non-sound-exposed adults, and the non-sound-exposed adults and juveniles, with juveniles and sound-exposed adults having lower regional densities. This would indicate that sea lamprey ears undergo developmental changes and can be impacted by sound. Results from this study will provide insight into sea lamprey ear development with respect to changes in hearing capabilities and into the evolution of fish hearing itself by quantifying the primitive hearing system of sea lampreys.

Ecology and Evolution C
PHYSICS & ASTRONOMY BUILDING, RM 150

2:30 – 2:45, Saturday, March 23rd, P&A 150

SEEDLING SURVIVAL AND SEED SIZE IN CUSCUTA

Dilliott, M.E., Costea, M.
Wilfrid Laurier University

Seedlings of the obligate parasite *Cuscuta* can only survive for a brief period of time, during which they must find and attach to a suitable host. Seedlings rely completely on the reserves stored in their endosperm for nutrients and if they cannot attach to a compatible host they will die. The purpose of the present study was to determine if seed size has an effect on seedling survival and growth across *Cuscuta* species. We examined 3 species with different seed sizes: *C. campestris*, a North American invasive species which succeeds in disturbed habitats, *C. costaricensis*, a Mexican species and *C. epithymum* a species native to Euroasia. Five hundred seeds per species were germinated and of those, 150 seedlings were grown in Petri dishes on moist filter paper. Seedling survival was monitored and once mortality was reached, seedlings were harvested and dry weighted. Results showed that seedlings of *C. campestris* (1.26 mm) survived significantly longer than those of *C. costaricensis* (1.08 mm) and *C. epithymum* (0.89 mm), respectively. This confirmed the hypothesis that seedlings from larger seeds survive longer than seedlings from smaller seeds. Seedling growth, indicated by dry weight, was weakly or negatively correlated with seedling survival across all species suggesting that seed size does not influence seedling growth. Our results will help understanding the dynamics and persistence of the species populations and offer effective control and conservation practices of *Cuscuta*.

2:45 – 3:00, Saturday, March 23rd, P&A 150

WHITE VARIANTS OF EDIBLE GOLDEN CHANTERELLES

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Department of Biology, University of Western Ontario, 1151 Richmond St., London, ON N6A 3K7, Canada.

Golden chanterelles (Cantharellus: Basidiomycota) are highly prized edible mushrooms that are found worldwide. Most chanterelles found in Newfoundland are golden-orange, but recently some rare all-white specimens have been found. In Europe, white chanterelles are rare white variants of normally golden species, whereas on the Pacific Coast of North America, *Cantharellus subalbidus* is a white chanterelle species with no known yellow complement and *C. cascadensis* varies in colour from golden to white. Phylogenetically informative DNA regions (ribosomal ITS and 5' LSU, and tef1) were sequenced from specimens of Newfoundland white chanterelles and compared with homologous sequences from various species of mushrooms in the genus *Cantharellus*. The objective was to determine if Newfoundland white chanterelles are variants of an already identified golden species in Newfoundland, an already identified white species in North America, or an unidentified white species with no golden counterpart. Multilocus phylogenetic analyses separated the specimens of Newfoundland white chanterelles from *C. cascadensis* and *C. subalbidus*, the other North American white chanterelles, and from *C. roseocanus* and *C. camphoratus*, other North American golden chanterelles, but clustered them with *C. enelensis*. This indicates that the Newfoundland specimens of white chanterelles represent a white variant of the Newfoundland golden chanterelle, *C. enelensis*. A

3:00 – 3:15, Saturday, March 23rd, P&A 150

COPPICE GROWTH OF RED OAK, RED MAPLE AND SUGAR MAPLE AFTER 14 YEARS UNDER UNIFORM SHELTERWOOD AND GROUP SELECTION TREATMENTS IN THE GREAT LAKES-ST. LAWRENCE FOREST REGION.

Johns, J.D., Nosko, P., and Dech, J.P.
Department of Biology and Chemistry, Nipissing University

Regeneration of red oak has proven difficult throughout its range as disturbance regimes of North American forests have been altered by fire suppression. Silvicultural approaches for red oak emphasize reducing canopy closure in partial harvests however, red oak seedlings are outcompeted in the understorey after harvest. Production of vegetative sprouts is an effective adaptation to persist after fire, which provides red oak with a mechanism of regeneration. The objectives of this study were to determine if sprout characteristics of red oak and its competitors differ among harvest treatments 14 years after harvest, and to examine the relationships between sprouting responses and the environmental and biological factors affecting the growth of sprouts. The study was initiated in a red oak-dominated forest near Redbridge, Ontario in August 2004. There were three treatments; 70% crown closure shelterwood, 50% crown closure shelterwood and group selection openings of 24 m or 36 m diameter. A total of 118 stumps were selected randomly across the treatments and species, and measured in 2005, 2006 and 2018. Sprout height, diameter and mortality were measured for each species, treatment and year. Preliminary results suggest that red oak sprouts had highest growth in the 50 % shelterwood. These results provide insight into the potential for stump sprouts to contribute to regeneration of red oak-dominated stands and the most effective harvest treatments to ensure sprouting success.

3:15 – 3:30, Saturday, March 23rd, P&A 150

DIFFERENCES IN THE FOLIAR CONCENTRATION OF ANTIHERBIVORE ALLELOCHEMICALS OF ADJACENT BALSAM FIR SAPLINGS GROWING IN DISTURBED FOREST GAPS IN WESTERN NEWFOUNDLAND

Talbot, K., Nosko, P.
Department of Biology & Chemistry, Nipissing University, North Bay, ON

Investment in antiherbivore defense by plants is influenced by genetic and environmental factors. Within plant populations, much variability occurs in the production of secondary metabolites which serve as allelochemicals to deter herbivores. Many studies report high variability in foliar levels of phenols and tannins; some indicate that certain individual plants can be defoliated while adjacent conspecific plants are untouched. Regarding susceptibility to herbivores, positive and negative associational effects of a palatable versus a non-palatable neighbor have been reported. In eastern Canada, intense browsing by overabundant ungulate populations is responsible for the inability of fir-dominated forests to regenerate after disturbance. It is unclear whether fir responds to severe browsing through compensatory growth or elevation of allelochemical levels. Foliar levels of phenols and tannins were compared in adjacent pairs of balsam fir saplings, affected by browsing intensity and proximity to the forest edge in western Newfoundland. Growth, browsing and chemical variables did not differ between adjacent saplings. As distance from the centre of the forest gap increased, percent of browsed fir branches per sapling and foliar level of tannins decreased, contradicting the notion that in winter, moose avoid open areas and prefer to browse along forest edges. This behaviour might be due to the lack of predators in the study area which otherwise influence moose browsing behaviour.

Ecology and Evolution D
PHYSICS & ASTRONOMY BUILDING, RM 117

2:30 – 2:45, Saturday, March 23rd, P&A 117

SEED STORY: ARE DRY, INDEHISCENT FRUITS AND SMALL SEEDS ADAPTED TO INTERNAL DISPERSAL BY WATERFOWLS?

ElMiari, H.A.
Wilfrid Laurier University

Endozoochory by birds requires diaspores to be accessible, nutritious, protected and visually attractive. Fleshy fruits or seeds with appendages satisfy these conditions; thus, they are considered adapted for endozoochory. Many small seeds and dry indehiscent fruits lack such adaptations, so they are considered non-adapted and their dispersal is thought to be unintentional. However, plants with such diaspores are widely distributed in wetlands making it

unlikely that their dispersal is only accidental. In fact, such diaspores have great nutritional value to nocturnal feeding mallards and are largely available in wetlands. Protection from gut passage is what remains to satisfy adaptation conditions. Thus, the aim of the study is to determine whether "non-adapted" diaspores can survive gut passage. The morphology and anatomy of diaspores, either seeds or dry fruits belonging to 11 angiosperm species, was examined with light and scanning electron microscopy, before and after passing through the digestive system of mallards. Overall, passed diaspores displayed a remarkable range of morphological modifications. Regardless of the degree of damage, variously structured seed coats or pericarps ensured seed survival which was determined through the observation of embryos and germination. No apparent relationship was detected between the degree of damage and different diaspore traits suggesting that various degrees of resistance to passing can be achieved in multiple ways.

2:45 – 3:00, Saturday, March 23rd, P&A 117

SYSTEMATICS OF THE GENUS HOHENBUEHELIA

Basu, A., Thorn R. G.
University of Western Ontario

The genus *Hohenbuehelia* includes mushroom fungi with complex biology involving both saprotrophy (decomposition of plant litter) and nematophagy (consumption of nematodes). Characteristics of this genus include gills on the underside of the cap; a gelatinous zone beneath the cap surface; and thick-walled, lanceolate cells (metuloids) on the gills. Because of similar morphology, species of *Hohenbuehelia* were misclassified as *Resupinatus* until their nematophagous anamorph and metuloids were observed. The genus *Pleurotus* is similarly characterized by nematophagy, and originally *Pleurotus* and *Hohenbuehelia* were both assigned to the genus Pleurotus before species with a gelatinous zone and metuloids were separated into Hohenbuehelia. Using morphology alone for fungal classification can be misleading because of the limited number of morphological characters available. Because the internal transcribed spacer (ITS) is the fastest evolving region of the ribosomal RNA cistron, it is the official DNA barcode marker for fungi and is used to differentiate between fungi at the species level.
The objectives of this project are to: (1) discover and describe diversity by studying specimens from understudied regions; (2) determine relationships within *Hohenbuehelia* based on molecular and morphological data; and (3) produce classifications for *Hohenbuehelia*. Through phylogenetic analyses of variable ITS sequences, resolution of evolutionary relations within *Hohenbuehelia* will be improved.

3:00 – 3:15, Saturday, March 23rd, P&A 117

DEFOLIATION OF BOREAL FOREST STANDS DURING SPRUCE BUDWORM OUTBREAKS IN RELATION TO SITE QUALITY

Craig, B., Nosko, P., and Dech, J.P.
Department of Biology and Chemistry, Nipissing University

Spruce Budworm is a significant agent of disturbance in the Boreal Forest, and outbreaks lead to reductions in timber volumes of host species balsam fir, white spruce, and black spruce. Across a landscape undergoing an outbreak, defoliation varies among stands. The objective of this study was to determine if differences in foliar nutrient concentrations on different site types affect the defoliation of boreal forest stands. The study was conducted during a recent outbreak in the Boreal Forest near Kapuskasing, Ontario in 2017. A stratified random sampling design was used to establish 26 plots (400 m2) that captured the full range of canopy structure, species composition and defoliation within the region. In each plot, three trees were selected and the shoot-count method was used to rate the defoliation of 25 shoots per foliage age class. An ocular defoliation was also measured from the ground. From each tree 3-5 representative branches were selected to collect 50 g of fresh foliage for analyses. Samples were analyzed for total nitrogen, phosphorus, potassium, calcium and magnesium. Preliminary statistical analyses suggest that there is a positive correlation between defoliation and levels of foliar N and Ca, and that site types with higher quality experienced greater defoliation than lower quality sites. These results are particularly useful given that the site types that were studied are available in inventory systems currently used for managing forest resources in Ontario.

3:15 – 3:30, Saturday, March 23rd, P&A 117

CHRONOSEQUENCE ANALYSIS OF CARBON SEQUESTRATION IN RECLAIMED FOREST SOILS IN SUDBURY, ONTARIO

Patterson, H., Brummel, M., Rantala-Sykes, B., Basiliko, N., Beckett, P.
Laurentian University

Sudbury Ontario was once the largest point-source of sulfur dioxide pollution globally due to mining and smelting activities; leading to vast deforestation. Long-term governmental regulation and technical improvements by industry led to >97% reduction in emissions over the past 50 years. Beginning in 1978, a world-renowned collaborative regreening program began reclamation of the Sudbury landscape. This program allowed us to identify re-established stands of known age and use a chronosequence approach to explore soil carbon storage over time. Quantification of carbon across 10 conifer stands ranging from 25 to 39 years of age, as well as re-assessment of the same sites from a 2002 study allowed for assessment of the accuracy of chronosequence approaches across heterogeneous sites. Carbon content of mineral and organic soil horizons were determined using loss on ignition analysis. We found statistically significant differences between stands of varying ages in the 2018 sampling, however patterns in stand age were not apparent. Organic soil horizons showed significant increases in carbon between 2002 and 2018 sampling in the majority of stands; however, no significant increases in mineral soil carbon were found. We conclude that afforestation of severely polluted landscapes can lead to carbon accumulation in organic soil horizons, and that spatially extensive sampling and a large range of stand ages is necessary to assess carbon storage using chronosequence sampling approaches.

Saturday March 23rd 2019

CONCURRENT SESSION II *4:00 – 5:00*

Cell & Molecular Biology D
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 0153

4:00 – 4:15, Saturday, March 23rd, B&GS 0153

THE ROLE OF DROSOPHILA HEAT SHOCK FACTOR IN THE REGULATION OF KEY DEVELOPMENTAL GENES

Filice, M.A., Westwood, T. J.
Department of Cell & Systems Biology, University of Toronto, Mississauga, Canada

Heat shock factor (HSF) acts as a master regulator of the heat shock response (HSR) during times of acute cellular stress, a mechanism that is conserved across all organisms. During heat shock, studies have shown HSF binds to developmentally regulated genes that are not involved in the HSR such as the early 20-hydroxyecdysone (20E) inducible genes (Eip74, Eip75, and Broad) that are responsible for metamorphic changes in arthropods.
Some of these HSF binding sites overlap with ecdysone receptor (EcR) binding sites, where EcRs are responsible for 20E activation. HSF binding to these sites during HS and/or non-shock conditions may alter EcR binding and/or affect early 20E inducible gene transcription. In this project, HSF binding sites within early 20E inducible genes were identified using in silico analysis. The most biologically significant sites were selected based upon their proximity to 20E enhancers and EcR binding sites. Electrophoretic Mobility Shift Assays are being done to detect whether HSF binds to the predicted sites within 20E inducible genes. To determine the role of HSF binding in the regulation of this class of genes in vivo, HSF's binding sites in the EiP74 gene will be mutated via CRISPR/Cas9 gene editing. The

transcription of the Eip74 gene in the mutated Drosophila will be studied under HS and non-shock using quantitative reverse transcriptase PCR.

4:15 – 4:30, Saturday, March 23rd, B&GS 0153

THE EFFECTS OF REDUCED PHOSPHATIDYLSERINE ON NERVE TERMINAL GROWTH AT DROSOPHILA LARVAL NEUROMUSCULAR JUNCTIONS

Nafal, S., Dason, J.S.
Biology Department University of Windsor

Phosphatidylserine (PS) is an anionic phospholipid that is enriched in the cytoplasmic leaflet of the plasma membrane in nerve terminals. PS is synthesized through a base-exchange reaction catalyzed by phosphatidylserine synthase 1 and phosphatidylserine synthase 2, both of which are located in the endoplasmic reticulum. PS is thought to play key roles in modulating synaptic growth, the release of neurotransmitters via exocytosis, recruiting synaptic proteins, and in assisting with membrane trafficking processes. Although normally confined to the inner leaflet of the plasma membrane, PS can be translocated to the cytosolic surface of the cell via interactions with PS flippases to induce or maintain an asymmetrical distribution of phospholipids. This lipid shuttling can contribute to the formation of new membrane structures, as well as induce membrane curvature, thereby supporting vesicle budding. The present study is aimed at evaluating the roles of PS flippase and PS synthase on nerve terminal growth at the Drosophila larval neuromuscular junction (nmj). We first used a genetically encoded fluorescent PS biosensor to show that PS is expressed in nerve terminals at the Drosophila larval nmj. We then used immunohistochemistry to examine PS flippase and PS synthase mutants and investigated how their absence influenced nerve terminal growth. We will present data on the effects of reduced PS levels on synaptic growth.

4:30 – 4:45, Saturday, March 23rd, B&GS 0153

EFFECT ON NEURAL DEVELOPMENT BY SPECIFIC TYPE IS MOTOR NEURON EXPRESSION PATTERNS IN DROSOPHILA MELANOGASTER

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The *Drosophila melanogaster* neuromuscular junction (NMJ) is an important structure for studying neurobiology and synaptic function. Drosophila contains two glumatergic motor neurons (MN), type Ib and Is that innervate at an NMJ. Using UAS-GAL4 techniques, we have utilized GMR27E09-GAL4, which expresses GAL4 under the control of FMR1 regulatory regions, to selectively drive in type Is MN, altering expression in one of the MNs but not the other. This novel approach allows us to examine the response of Ib MNs when Is MNs are manipulated through gene expression. In the presence of apoptotic expression, via UAS-hid, NMJs show Ib boutons/synapses without Is bouton presence in Is specific expression, while observed lethal in all neuron expression, via positive control elav-GAL4/C155 line. Using an overgrowth reporter line, via UAS-NSF2 E/Q, type 1s specific expression does express overgrowth phenotype, characterized by long abnormal axons, showing no suppression of overgrowth phenotype. In overexpression in potassium channels, via UAS-KCN2, NMJs showed reduced branching, NMJ length, and significantly lower levels of Is and Ib boutons, with no significant change in Ib bouton morphology and count. Overall this research project explores how neuron development is affected by manipulating in one of two motor neurons that innervate a common target muscle.

4:45 – 5:00, Saturday, March 23rd, B&GS 0153

UNDERSTANDING THE ROLE OF CONSERVONS IN STREPTOMYCES VENEZUELAE DEVELOPMENT

Stoyanov, Y.R., Elliot M.A.
McMaster University, Institute of Infectious Disease Research at McMaster University

Streptomyces are soil-dwelling, Gram-positive bacteria, that have been renowned as prolific producers of secondary metabolites. In addition to their antibiotic potential, research has largely been centred around studying their incredibly complex life cycle, which resembles filamentous fungal growth. A new mode of growth termed

‘exploration’ was identified in the model organism *Streptomyces venezuelae*. Colonies undergoing exploration can rapidly spread on abiotic surfaces by extending their network of non-branching vegetative mycelium. This exploratory phenotype challenges the preconception that *Streptomyces* stay rooted in place. Based on a chemical mutagenesis screen, this work aims to identify the role of conservons in exploratory growth. Typically, these specific conserved operons are composed of a histidine kinase, a protein containing a GTPase domain, and two other proteins whose functions have yet to be identified. Notably, this study reveals that there is a conservon important for keeping explorer colonies in a vegetative state in *S. venezuelae*. That is, when this conservon is deleted, the colonies can produce aerial hyphae. To discover the mechanism by which the conservon holds an explorer colony in a vegetative state, a bacterial two hybrid screen was employed to track protein interaction. This screen demonstrated that the conservon products assemble into a membrane bound heterocomplex, which may implicate involvement in a signal transduction cascade.

Cell and Molecular Biology E
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 0165

4:00 – 4:15, Saturday, March 23rd, B&GS 0165

MALE WALLEYE REPRODUCTIVE FITNESS FROM WASSI FALLS, NIPISSING LAKE

Abikou, N., MARTÍNEZ, M. L.
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Organisms must balance energy investment between body growth and reproduction. Yet, the ability to produce viable offspring, or reproductive fitness, can greatly depend on the quality of the gametes produced by the organisms. Fish sperm quality varies amongst individuals, and can often depend on the fish physiological condition (Fulton’s condition, hepatosomatic index, and lipid content). In this study, we investigate whether intraspecific variation exist in male sperm quality in walleye fish, *Stizostedion vitreum* from Wassi Falls, Lake Nipissing, Ontario. A total of 36 mature walleye were sampled at the pick of their reproduction season and individual samples of sperm were collected for sperm quality traits (sperm morphology, sperm motility, sperm quantity). Furthermore, morphological and physiological traits were also collected such as Fulton index (K), hepatosomatic index (HIS), gonadosomatic index (GSI), and lipid content. A significant interindividual variation was observed based on age for fish fork length (P=0.0001), fish somatic mass (P<0.0001), lipid content (P=0.024), GSI (P=0.006). Interestingly, GSI significantly explain the variation on sperm head ratio (P=0.021). A total of 66% of the total variance in sperm morphology was explained by the first component (PC1) from the Principal component analysis. However, no significant variation on any of the sperm morphology existed among individuals based on fish age.

4:15 – 4:30, Saturday, March 23rd, B&GS 0165

CHARACTERIZATION OF THE MOLECULAR MECHANISMS REGULATING EPITHELIAL MORPHOGENESIS DURING ZEBRAFISH EMBRYONIC DEVELOPMENT

Chen, T., Willoughby, P. M. and Bruce, A. E. E.
Cell & Systems Biology, University of Toronto

A major question in developmental biology is how morphogenesis, or the coordination of cell movements, gives rise to the correct structure of tissues and organs in all animals. Epiboly, a conserved morphogenetic process, describes the thinning and spreading of cell layers during embryogenesis. Aberrant epiboly results in profound patterning defects to the developing embryo. Despite this, little is known about the molecular basis of epiboly. We use zebrafish to study epiboly, where an epithelial cell layer (EVL) thins and spreads over the embryo. Our lab uses both forward and reverse genetics to identify the molecular mechanisms of EVL morphogenesis. We previously found that Rab25, a small GTPase implicated in apical vesicle recycling, is upregulated at the onset of epiboly and is epithelial specific, making it a good candidate for epithelial morphogenesis. CRISPR/Cas9 mutants of both Rab25 paralogs, Rab25a and Rab25b, display defects in epithelial spreading which are associated with cell morphology

abnormalities and uneven tension within the EVL. Second to our approach targeting candidate genes, we took a pharmacological approach in forward genetic screens. Embryos treated with the molecule pimpinellin showed slowed epiboly and abnormal EVL actin distribution, consistent with a role in regulating EVL integrity, which is essential for normal morphogenesis. This study contributes to our understanding of embryonic development and coordination of cell movements in all animals.

4:30 – 4:45, Saturday, March 23rd, B&GS 0165

DETERMINATION OF GENE FLOW AND CONNECTIVITY AMONG TOURIST-FED AND UNFED *HYPANUS AMERICANUS* POPULATIONS AT GRAND CAYMAN

Najm, S. Patel, K. Heath, D. Semeniuk, C.
University of Windsor

Stingray City Sandbar (SCS) is a world-famous marine wildlife attraction located in Grand Cayman where over a million tourists per year gather to feed a congregation of *Hypanus americanus*, a charismatic stingray species. The high levels of supplemental feeding of an unnatural diet and the atypically high density of rays at SCS have decreased the overall viability of the population, with rays showing suboptimal physiological health, increased incidence of injuries and parasites, reversed diel patterns, and abnormal spatial and mating behaviour compared to unfed populations. This study aims to measure population structure among groups of rays around Grand Cayman, as well as to determine effective population size, gene flow, isolation and overall connectivity between the tourist aggregation and unfed control populations. DNA extracted from 192 individual stingrays from the SCS aggregation and three unfed control sites was used to determine genotypes at 10 microsatellite loci using PCR and Next-Generation Sequencing. Genotypes for each ray were used to determine population structure on Grand Cayman. The results of this study will determine whether the SCS aggregation is genetically isolated from other Grand Cayman populations and will thus inform the need for greater conservation efforts and stricter policies to prevent loss of genetic diversity that may be important for the survival of this economically-important population.

Cell and Molecular Biology F
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 1056

4:00 – 4:15, Saturday, March 23rd, B&GS 1056

ROLE OF PMRD PROMOTER ALTERATIONS IN HDP RESISTANCE

Huynh, R and McPhee, J.B
Department of Chemistry and Biology, Faculty of Science, Ryerson University, Toronto, Ontario

Bacteria have evolved a mechanism to resist host defense peptides (HDP) and other antibiotics. The PhoPQ and PmrAB two component regulatory systems are involved in bacterial resistance to HDPs and antibiotics, such as polymyxin B. Both PhoQ and PmrB are sensor kinases that phosphorylate PhoP and PmrA respectively. Downstream signaling and protein production of PmrA results in lipid A modification that allows for the bacteria to be resistant to HDPs. The PmrD connector protein connects the PhoPQ and PmrAB systems. In Escherichia coli and Shigella flexneri the pmrD gene contains three start codons in close proximity of the Shine Dalgarno Sequence. Here we demonstrate that only one of these three start sites result in the expression and production of functional PmrD restoring resistance in pmrD knockout mutants. We also demonstrate evidence of PmrD production under non-PhoP conditions, in which we see that pmrD transcription occurs sometimes under high and low magnesium conditions.

4:15 – 4:30, Saturday, March 23rd, B&GS 1056

AMP-ACTIVATED PROTEIN KINASE CONTROLS Β1-INTEGRIN VIA A NOVEL ARF6-DEPENDENT SIGNALING PATHWAY.

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Department of Chemistry and Biology, Ryerson University, 350 Victoria Street, Toronto, Ontario, M5B 2K3, Canada

Cancer cells rely on their diverse set of cell surface proteins for migration to control their spread to novel metastatic sites. To date, these mechanisms have primarily been studied in cultured cells with excess nutrients and growth factors; however, regulation of these processes under metabolic stress in typical physiological conditions is poorly understood. How metabolic stress controls the physiology of both normal and cancer cells is thus an important unanswered question. AMPK is activated upon energy insufficiency to regulate the cell surface proteome to conserve ATP. A target of AMPK-induced signaling is β1-integrin–a protein involved in signal transduction and migration. We previously showed that AMPK activation controls membrane traffic to reduce cell surface abundance of β1-integrin, impairing migration. This research aims to elucidate the mechanism by which AMPK regulates β1-integrin membrane traffic. We hypothesize that metabolic stress and AMPK regulate β1-integrin through control of ArfGAP3 and Arf6. To test this, we used knockdowns of ArfGAP3 and Arf6 to perturb the function of these signals, and fluorescence microscopy to quantify β1-integrin surface abundance. Our results suggest a new connection between regulation of membrane traffic by AMPK through control of ArfGAP3, Arf6, leading to control of β1-integrin localization. This work suggests a novel aspect of metabolic regulation on cell migration, which may provide further insight into cancer metastasis.

4:30 – 4:45, Saturday, March 23rd, B&GS 1056

NKG2D AND DNAM-1: THE KEY TO REVERSING POSTOPERATIVE NK CELL DYSFUNCTION?

Tennakoon, G.G. [1], Market, M.R. [2], Ng, J. [2], Tanese De Souza, C. [2], Kennedy, M. [2], Auer. R. [2]
1. University of Ottawa
2. Ottawa Hospital Research Institute

Cancer is the leading cause of death in Canada and a significant proportion of these deaths are due to solid malignancies. Surgery is a necessary treatment of localized solid cancers, however, evidence suggests that surgery increases rates of disease recurrence, metastasis, and death. There are numerous potential mechanisms behind this phenomenon, most notably, cellular immune suppression. This suppression is observed in Natural Killer (NK) cells which are innate immune cells critical for the anti-tumour immune response. Our lab and others have demonstrated impaired NK cell effector functions postoperatively, specifically a profound reduction in NK-derived IFNγ. NK cell activity is controlled by the integration of activating and inhibitory signals through cell surface receptors. However, little is known about the changes in expression of these receptors in postoperative NK cells. Using flow cytometry, we investigated receptor expression in the CD56+CD3- population of peripheral blood samples collected from patients pre- and postoperatively. We observed a significant reduction in critical NK cell activating receptors NKG2D and DNAM-1 on postoperative day (POD) 1. Given that a reduction in activating receptor expression is associated with impaired NK cell effector functions, these findings highlight a potential mechanism and possible therapeutic target for preventing postoperative NK cell dysfunction and metastatic recurrence.

4:45 – 5:00, Saturday, March 23rd, B&GS 1056

REGULATION OF EPIDERMAL GROWTH FACTOR RECEPTOR SIGNALING BY ACK1

Vural, D., Lucarelli, S., and Antonescu C.N.
Department of Chemistry and Biology Ryerson University

The Epidermal Growth Factor (EGF) Receptor (EGFR) controls many key components of cell physiology including proliferation, survival, and metabolism. EGF stimulation elicits EGFR phosphorylation and subsequent activation of Akt. EGF-stimulated Akt activation is dependent on the residence of EGFR within clathrin coated pits (CCPs) at the plasma membrane, but not receptor endocytosis. CCPs are well-known endocytic portals however, we have uncovered that these structures also play a role in spatially organizing certain receptor-proximal signals of EGFR, required for Akt activation. One of the many proteins that are known to bind to clathrin directly is Activated Cdc42 Kinase 1 (Ack1), a kinase implicated in oncogenic signaling and tumor cell survival. Ack1 also interacts with EGFR and other signaling intermediates of this pathway like Akt. In this study, cells overexpressing WT-Ack1 exhibited an increase in Akt phosphorylation. Notably, Akt phosphorylation was significantly lower in cells expressing an Ack1 clathrin-binding mutant (4A-Ack1) compared to those expressing WT-Ack1. This data suggests that clathrin binding by Ack1 is important for the activation of Akt. This project may be broadly important for cancer research because of the major role that the EGFR plays in driving cell growth and survival in many different types of cancer. As such, understanding the regulation and outcome of EGFR signals can lead to the development of novel cancer treatments.

Ecology and Evolution F
PHYSICS & ASTRONOMY BUILDING, RM 34

4:00 – 4:15, Saturday, March 23rd, P&A 34

POLAR BEARS' (URSUS MARTIMUS) TERRESTRIAL BEHAVIOURS DURING THE ICE-FREE SEASON ON EAST BAY ISLAND, NUNAVUT

Frank, C., Jagielski, P., Semeniuk, C.
University of Windsor

Climate change is globally altering abiotic and biotic factors resulting in a rapid decline in sea ice persistence and extent. One affected species is the polar bear (*Ursus martimus*), that relies on sea ice to hunt seal cubs in the late spring period. As a result of declining sea ice, polar bears are required to consume terrestrial food sources to supplement necessary fat reserves during summer months. It is unknown if their terrestrial behaviours are beneficial or maladaptive due to high costs of locomotion, a potential for overheating, and the energetic gain of their alternative food source (eider duck eggs). This lack of information is because polar bear on-island behaviours have not yet been systematically assessed. The goal of my study is to develop an ethogram of polar bears' terrestrial behaviours, using ground-based videography, on East Bay Island, Nunavut, Canada. Using trail cameras (n=48) situated around the 0.24km2 island, polar bears' proportion walking, eating and resting, were recorded and analyzed over 3 weeks, and conditions and age-classes noted. I predict fewer bears will be observed foraging during the day at relatively higher temperatures and as the season progresses; additionally, young bears and those in poorer body condition will spend more time foraging, and the majority of time spent on land will be allocated towards walking. Results will aid bioenergetic quantification studies to achieve more precise estimates of the energy spent and gained on land.

4:15 – 4:30, Saturday, March 23rd, P&A 34

A DIVISION OF LABOUR IS CAUSING SEXUAL SIZE DIMORPHISM IN THE CANIDAE FAMILY

Pyott, M.L., Mallory, F.F
Laurentian University Department of Biology

Class Mammalia show a predominance of male-biased sexual size dimorphism, where the males are larger than the females because of male-male competition. Monogamous species however. display little to no sexual size dimorphism due this lack of competition. The monogamous Canidae family are an exception. It was hypothesized that the sexual size dimorphism in this family is attributed to a division of labour between the sexes. If males are the ones predominantly hunting the prey, natural selection would likely favour larger males. Using the red fox (*Vulpes vulpes*), coyote (*Canis latrans*), and grey wolf (*Canis lupus*) to represent the Canidae family, I tested this hypothesis by comparing male and female skull parameters with the primary prey weight of the species. The mean degree of sexual dimorphism was largest between the male and female wolves, who had the largest prey weight, and smallest between the male and female foxes, with the smallest prey weight. There were no significant differences in the degree of sexual dimorphism between any of the species in regards to their skull width or mandible length. But, there was a significant difference in the degree of sexual dimorphism in skull length. There was also a significant association between the prey weight and the degree of sexual dimorphism shown in the skull length and width. These findings support the hypothesis that a division of labour in hunting creates a selective pressure towards larger males in the Canidae family.

4:30 – 4:45, Saturday, March 23rd, P&A 34

IMPACT OF SPATIAL CONSTRAINT ON THE SKELETAL GROWTH OF STRONGYLOCENTROTUS PURPURATUS, PURPLE SEA URCHINS.

Rushiraj Vansiya, Jonathon Stone
McMaster University

This study aims to identify whether a relationship exists between the skeletal growth of Echinoid tests at under spatial constraint, in *Strongylocentrotus purpuratus*. Each sea urchin test is a hard, radially symmetrical outer body composed of fused plates made from calcium carbonate. This is to be shown through detailed modelling of the ocular, which is a calcified element, when new elements are added at the terminus of the ray, defining growth. Specimens obtained were grown as a control with no spatial constraints and with the ability to grow in as much as required in the dorsal, aboral, and ventral directions. Experimental specimens were grown with spatial restraint restricting growth in the aboral direction. Purple sea urchins should exhibit an unnatural amount of lateral test growth in the treatment when vertical spatial constraint is applied, compared to control organisms. Test growth of the obtained samples will be recorded through the use of the MicroScribe G2™ Immersion (digitiser) software, and modelled using Rhinoceros (Rhino) 4.0 Non-Uniform Rational B-Splines (NURBS). The visual model formed allows for statistical analysis to determine whether there is a significant increase in the lateral growth in experimental conditions due to environmental constraints.

4:45 – 5:00, Saturday, March 23rd, P&A 34

ECOLOGICAL FACTORS INFLUENCE PRIMATE VOCAL BEHAVIOUR IN A NEOTRPOICAL DRY FOREST: HABITAT AND BEHAVIOUR IN THREE SPECIES OF MONKEY.

Wilder A.S., Switzer K.M., Owen K., Mennill D.J.
Department of Biology, University of Windsor, Windsor, Ontario ,Canada

Auditory signals are used across taxa to convey information over long distances. Animals can alter their vocal behaviour in response to environmental differences such as variation in habitat age or habitat complexity. The seasonal dry forests of the Guanacaste Conservation Area offer a unique situation to study the behaviour of primates in varying habitats as it is a large protected area of one of Earth's most endangered ecosystems. Our research uses a bioacoustic approach to explore the relationship between vocal behaviour and the environment in three tropical primate species: Golden-Mantled Howler Monkeys (*Alouatta palliata*), Geoffroy's Spider Monkeys (*Ateles geoffroyi*), and White-faced Capuchin Monkeys (*Cebus capucinus*). We hypothesize that habitat maturity and seasonal changes in habitat structure influence the presence of primates and their vocal behaviour. We collected recordings at 44 sites within the Guanacaste Conservation Area in both wet and dry seasons. Presently we are compiling and comparing vocal recordings to data of habitat maturity and time of year. We show that the vocal behaviour of all three monkey species varies with vegetation features and with time of year. Our results illustrate the impacts of restoration programs and provide support for further restoration efforts in at-risk tropical environments.

Physiology and Biochemistry C
PHYSICS & ASTRONOMY BUILDING, RM 36

4:00 – 4:15, Saturday, March 23rd, P&A 36

THE EFFECTS OF PH AND CHLORPROMAZINE ON DIFFERENTIATION AND VIABILITY OF PC12 CELLS.

Muhammad, F., Dotta, B., Hossack,V.
Laurentian University

The goal of this study was to analyze the cytotoxicity of the conventional phenothiazine neuroleptic (choi and kim) drug chlorpromazine (CPZ) and the effects of pH in relation to the viability and differentiation of PC12 cells, which are a model system well–established for neuronal differentiation and neurochemical investigations. The cultures were trialled through 3 rounds where the suboptimal concentration was found to be .Three trials were also conducted of separate cultures which were then manipulated to pH levels 6.5, 7.0, 7.5 and 8.0 using a bicarbonate buffer medium system with 25mM of HEPES before incubation. Cultures' pH were manipulated using 16N HCl and 15N NaOH. Cells differentiated were measured using microscopic images and the numbers counted manually. Viability of cells were measured using the Trypan blue dye exclusion method. Certain concentrations of chlorpromazine had variable effects on the two systems investigated, leading to possible further experimentation. Our hypothesis suggests the optimal pH for viability and differentiation be 7.4 while chlorpromazine concentration be 5μM. Furthermore combined effects of both optimal concentration of CPZ and pH were investigated with the same variables being measured.

4:15 – 4:30, Saturday, March 23rd, P&A 36

A QUANTITATIVE ELECTROENCEPHALOGRAPHIC ASSESSMENT OF MYALGIC ENCEPHALOMYELITIS / CHRONIC FATIGUE SYNDROME IN 46 ADULTS

Pellegrini, A.E., Saroka, K.S.
Laurentian University Behavioural Neuroscience

Myalgic Encephalomyelitis - also known as Chronic Fatigue Syndrome (ME/CFS) - represents a long-standing medical mystery entailing substantial difficulty for physicians who have been unable to identify an objective means of measuring ME/CFS, and for patients who insist they are objectively ill. Lack of evidence has disposed this area of inquiry to psychiatric interpretations that fail to provide material understanding or effective treatment. Recently, the Nightingale Research Foundation (NRF) has shown evidence that ME/CFS represents decreased arterial blood supply of the cerebral cortex measured with SPECT (Single Positron Emission Tomography) in combination with a persisting enteroviral presence in the gut measured by gastric biopsy and protein staining. With the intention of confirming these exciting findings we obtained 46 adult volunteers with a medical diagnosis of ME/CFS and measured their brain activity using qEEG (Quantitative Electroencephalography). We then compared the data both to a normative database and to SPECT maps of NRF defined ME/CFS. It is our goal to demonstrate the utility of qEEG as a tool to diagnose or support a diagnosis of ME/CFS; there exists a potential to highlight and better understand this misunderstood illness in the form of relatively inexpensive and non-invasive qEEG technology.

4:30 – 4:45, Saturday, March 23rd, P&A 36

BIOMARKERS FOR DISEASE

Ravindran, R., Lafrenie, R., Dotta, B.
Laurentian University

In the case of a degenerative disease, it is known that degradation of the cell is evident. Breakdown of a cell alters function, and these alterations are capable of producing deficits in individuals. A biomarker for early detection of cellular breakdown would help in ameliorating or treating any deficits produced via cell alteration. We postulated that biophotons emitted by the cell could reflect intracellular activity and potentially indicate future cellular breakdown. Using the measurement of biophoton emission as a model for cellular degradation, trials were taken to test the hypothesis. Each trial began with the plating of cancerous cells (B16-BL6 cells) and later poisoning these cells to induce cellular breakdown. Before and after poisoning biophoton readings were taken to determine the change in emission intensity and periodicity. After readings, harvesting of the cells took place to determine cell colony survival. Analysis revealed correlations between photon emission data and cell survival. Increases in photon emission from poisoned cells was evident when compared to non-poisoned cells ($p<0.001$). Along with differences in photon emission intensity, percent survival was correlated with variability in photon emission measurements (r value of .751). Where cells with higher variability scores reliably produced poor survivability measures. Data demonstrates photon emissions have the potential to be used as biomarkers of cellular degradation.

4:45 – 5:00, Saturday, March 23rd, P&A 36

THE EFFECTS OF EXAM INDUCED STRESS OF MEMORY SCORES AND EEG PROFILES

Roy, T. & Dotta, B.
Laurentian University

Stress is the response to a threatening situation and causes the body to secrete the adrenal corticosteroid hormones, known as stress hormones (Ranabir & Reetu, 2011). Generally, every individual has written some form of exam during his or her life whether it is school-related or not. These situations are often correlated with higher than normal stress levels. The purpose of this study is to determine how the stress that comes with examinations affect EEG profiles and memory scores. Nineteen Laurentian University students participated in the study. A cortisol saliva test was conducted in order to determine how stressed each participant is. The hypothesis is that the cortisol levels will be greater during the second trial (near exams), which will then poorly affect the memory scores and the EEG results will show a suppression of alpha waves and an increase in theta waves. Results are still pending.

Ecology and Evolution G
PHYSICS & ASTRONOMY BUILDING, RM 148

4:00 – 4:15, Saturday, March 23rd, P&A 148

DISPERSAL ABILITY & FLIGHT MORPHOLOGY IN THE ROCKY MOUNTAIN APOLLO BUTTERFLY, PARNASSIUS SMINTHEUS

Frizzelle, N., Chaulk, A., Keyghobadi, N.
Biology Department, University of Western Ontario

Dispersal can be defined as the movement of an individual from one habitat patch to another that is separated by an uninhabitable environment. This process plays a vital role in the function and survival of a species. Dispersal is driven by both internal and external factors; however, these internal factors are currently understudied. I expand the knowledge of which internal factors influence dispersal behaviour in insects by studying various morphological traits related to flight in the Rocky Mountain Apollo butterfly, *Parnassius smintheus*. In July 2018, I collected butterflies from a metapopulation in Kananaskis, Alberta, consisting of individuals that have completed a dispersal event (dispersers) and those that have not (non-dispersers). Individuals were then frozen, dissected, and weighed, while their wings were photographed to create high resolution images for digital analyses. I contrasted body mass, thorax mass, abdomen mass, wing area, and wing shape between dispersers and non-dispersers to investigate if flight morphology influences the ability of this species to cross forest matrices. Additionally, I contrasted these traits between the sexes to determine whether flight morphology is influenced by the species' sex-specific mating behaviours. By investigating how flight morphology influences dispersal, I am furthering our understanding of how dispersal operates, which is essential to understanding the ecology of a population.

4:15 – 4:30, Saturday, March 23rd, P&A 148

USING STABLE ISOTOPES TO DETERMINE NATAL ORIGIN AND LARVAL HOST PLANT USE BY THE WESTERN BEAN CUTWORM, STRIACOSTA ALBICOSTA (LEPIDOPTERA: NOCTUIDAE)

Gootgarts, J. [1], Hobson, K. A. [2], Longstaffe, F. [3], & McNeil, J. N. [1]
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3. Department of Earth Sciences, Director, Laboratory for Stable Isotope Science, University of Western Ontario, London, Ontario, Canada

Many animals migrate seasonally in response to habitat deterioration. One technique used to track migration is the use of naturally occurring stable isotope ratios in insect tissues. In North America, the levels of deuterium (δ2H) found in plants vary along a north-south axis. Thus, δ2H values in moth wings, reflecting the location of the host plant consumed during larval development can be used to assign natal origins of immigrants in Ontario. Similarly, the δ13C values in moth wings provides information on whether the larval diet was C3/C4 plants. In the last decade the Western Bean Cutworm, *Striacosta albicosta*, has significantly expanded its geographic range eastward. The use of transgenic corn has been proposed as a reason for the expansion, as WBC is hardly affected by Bt proteins. Furthermore, studies conducted at Western suggest that local survival is quite low which suggests that most individuals captured each year are immigrants. We analyzed the δ2H and δ13C profiles of moths captured near London in 2015, 2016 and 2018 to test the hypothesis that the majority of the moths captured would have higher δ2H values (originating from further south) and δ13C (originating from C4 corn). The data obtained to date shows that the moths fed on corn as larvae. Natal assignment origins are currently being carried out. HY-SPLIT was used to examine wind patterns 24h and 48h prior to days of peak trap catch, to determine a possible match between natal origin and prevailing winds.

4:30 – 4:45, Saturday, March 23rd, P&A 148

LONG TERM TRENDS IN ABUNDANCES OF AERIAL INSECTIVORES ACROSS STOPOVER SITES IN ONTARIO

Iyer, A., Chow-Fraser, P.
Department of Biology, McMaster University.

The decline of aerial avian insectivores in N. America has been attributed to this guild's dependency on declining insect taxa. Here, we hypothesize that the underlying decline may be due to degradation of habitat quality in nine stopover sites across Ontario. To test this, we used data from bird-banding stations (Canadian Migration Monitoring Network) at these locations to determine how abundance of thirteen aerial insectivores changed over 22 years (1995 to 2017). We classified land use and land cover (water, natural vegetation, urban, agriculture and barren) within 10-km circular buffers of the banding stations in Landsat images acquired between 1995 and 2018. Increases in insectivore abundances were associated with stations that had relatively stable or increasing proportion of naturally vegetated habitats, whereas steep declines in abundances were associated with stations that had an increase in urban and agricultural land uses. Species-level changes often correlated with site-level changes, an example being an increase in abundance of Purple martin (*Progne subis*) coincident with installation of artificial nest boxes. We found that birds in the northeastern areas appeared to have a steeper decline compared with those centered around the Laurentian Great Lakes. We suggest that while quality of habitat is an important driver for guild-level changes, species-level changes are often a result of many population-level drivers affecting reproductive success and fitness.

4:45 – 5:00, Saturday, March 23rd, P&A 148

THE EFFECT OF THERMAL STRESS ON MYTHIMNA UNIPUNCTA

Jalilian.N and McNeil.J.N.
University of Western Ontario

Increased frequency and duration of extreme temperatures associated with climate change are expected to significantly affect poikilotherms. The true armyworm, *Mythimna unipuncta* (Lepidoptera, Noctuidae) has been studied as a model system for insect migration in North America. *M.unipuncta* undertakes north-south migration in the spring and fall. In 2017, for the first time in over 100 years there was an outbreak in British Columbia. Given, the winter conditions are less rigorous than eastern Canada, a permanent population might establish. A colony of B.C. *M.unipuncta* was used to determine the tolerance of 1 or 3-day-old eggs and pupae exposed to cold (0 ℃) or heat (30 ℃) for 24H, 48H and 72H. The emergence patterns for larvae and adult moths were recorded. It was hypothesized that survival would decline with greater exposure time to either temperature extremes. Exposed one day old eggs showed approximately 60% mortality regardless of length of exposure compared to 30% in the control. Mortality was significantly less when 3 day old eggs were exposed to 0 ℃ and slightly different from controls. There was little mortality when eggs were exposed to 30 ℃ regardless of age or exposure time. It was evident that pupae exposure to 30°C resulted in low emergence after 72H compared to control and a significantly higher proportion of deformed wings. These findings suggest that *M.unipuncta* would have difficulty establishing a resident population in the current climate.

Ecology and Evolution H
PHYSICS & ASTRONOMY BUILDING, RM 106

4:00 – 4:15, Saturday, March 23rd, P&A 106

THE FISH PERSPECTIVE OF ARTIFICIAL LIGHT AT NIGHT

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2. Carlton University.

Almost all organisms rely on natural cycles of light and dark to provide reliable cues for diverse aspects of their ecology such as foraging, growth, reproduction, and migration. As a result, artificial light sources can have a variety of negative consequences for both plants and animals. The potentially negative effects of artificial light are predicted to become more widespread as the geographic extent of artificial light at night (ALAN) increases by 6% per year. In particular, with one quarter of the human population living with 100 kilometres of a coastline, there is great potential for ALAN to influence the physiology, behaviour, and fitness of fish. Through meta-analysis we quantitatively illustrate that fish have been under-represented in the scientific literature that documents and interprets the effects of ALAN in comparison to birds, mammals, reptiles, and invertebrates. To understand where research has been focused, we partition studies on ALAN in fish by physiology, behaviour, fitness, and other aspects of general ecology and summarize the major research findings in each of these categories. Finally, we provide recommendations for future research that can aim to understand how changing intensity, coverage, and spectral compositions of artificial light could have downstream consequences for fish health and persistence.

4:15 – 4:30, Saturday, March 23rd, P&A 106

BIOLOGY OF THE ROUGHHEAD GRENADIER (*MACROURUS BERGLAX*) IN THE EASTERN CANADIAN ARCTIC

Beach R., Barkley, A., Edwards, J., Christie, L., Hussey, N.E.
University of Windsor

The roughhead grenadier, *Macrourus berglax*, is a common by-catch species in North Atlantic fisheries. Limited information about this species suggests that slow growth rate, late sexual maturity and low annual fecundity may increase overfishing vulnerability. Given that COSEWIC lists grenadier as “special concern”, a better understanding of the species and their ecological role is needed. Size-based diet and condition index profiles of two roughhead grenadier groups, sampled from a northern and southern site, were examined. By using gonado- and hepatosomatic indices, stomach content analysis and stable isotopes we can draw conclusions on fitness, energy storage, diet and trophic ecology. It is anticipated that there will be a difference in both the gonado- and hepatosomatic indices across the two sampling sites due to different reproductive stages. Latitudinal differences between locations may show a more restricted diet in the northern group due to lower prey availability in the North. Since stable isotope values are influenced heavily by diet ($\delta 15N$) and location of foraging ($\delta 13C$), it is predicted that grenadier body size, prey diversity, and $\delta 15N$ will be positively correlated in both sampled sites, whereas $\delta 13C$ will differ between sites. The results from this study will aid in creating an ecological baseline for roughhead grenadier, assist in the development of ecosystem management approaches, and enhance vulnerability assessments of this understudied species.

4:30 – 4:45, Saturday, March 23rd, P&A 106

SEASONAL PLASTICITY IN THE GUT OF *SALVELINUS NAMAYCUSH* AND *MICROPTERUS DOLOMIEU*

Dao, A.T., McMeans, B.C.
University of Toronto

The digestive tract is one of the body's more expensive systems to maintain, due to its high energy requirements. In order to compensate, many organisms have shown plasticity in their digestive tract in response to changing environments. In particular, the literature has suggested that many fish will downregulate their digestive tract during fasting, which results in lower intestinal length, intestine wet mass and an overall lower maintenance cost. In natural lakes, fish are subjected to varying levels of resources and environmental conditions during each season. In particular, very few studies have observed fish's activity levels and foraging behaviour during the winter. During the winter, there is a decrease in sunlight and productivity, which limits food availability. Therefore, we predicted a decrease in the size of the digestive tract during the winter. If the variation in food abundance is predictable throughout the seasons, then the fish should show plasticity in their gut size to converse the energy that's associated with maintaining a large digestive tract. In this study we will be observing a cold water species, *Salvelinus namaycush* and a warm water species, *Micropterus dolomieu* over four seasons between the years of 2017-2018. Samples were dissected, and their intestine length and weight were measured. Based on the findings of this study, it will help furthermore our understanding of fish behaviour in the winter and how they respond to their changing environment.

4:45 – 5:00, Saturday, March 23rd, P&A 106

EFFECTS OF HABITAT COMPLEXITY ON PERFORMANCE AND SURVIVAL OF DIFFERENT BEHAVIOURAL PHENOTYPES IN FISH USING AGENT-BASED MODELLING

Kuindersma, E., Semeniuk, C.
University of Windsor

Animals exhibit behavioural phenotypes, a consistent set of behaviours that contribute to fitness in varying and contrasting ways. These phenotypes allow for some animals to be better equipped for particular environments over others. Populations that contain a diversity of behavioural traits may be more likely to persist as conditions change. The application of behavioural phenotypes is relevant for reintroduction efforts, which often lead to failure. A specific reintroduction effort is found in hatcheries where fishery managers select fish that perform best under hatchery conditions. A problem associated with this practice is oftentimes the juvenile fish selected are overly aggressive and are not representative of the wild population as a whole. As a result, these individuals suffer reduced fitness when reintroduced. A goal of my study is to examine how hatchery selection processes, coupled with restoration actions interact to influence overall juvenile survivability. I predict survivability in the wild will be influenced by behavioural phenotypes (bold versus shy). Using Agent-Based Modelling, I aim to show bold fish, typically selected for reintroduction efforts, are better equipped for less complex habitats. Conversely, I predict shy fish will have a higher survival rate in more complex environments. I will furthermore model the type of habitat that can optimize co-existence of both behavioural phenotypes, providing guidance to fishery managers tasked with reintroduction.

Ecology and Evolution I
PHYSICS & ASTRONOMY BUILDING, RM 150

4:00 – 4:15, Saturday, March 23rd, P&A 150

MATERNAL INFLUENCES ON LAKE WHITEFISH (*COREGONOUS CLUPEAFORMIS*) EMBRYONIC FITNESS FROM AN EXPLOITED STOCK WITH A RECENT FOOD WEB CHANGE IN LAKE HURON

LaRochelle, L.
Laurentian University

Recent changes in the food web of Lake Huron have occurred since the invasion of *Dreissenisdae* sp. which has reduced the quantity of an essential native food source (*Diporeia* sp.) for Lake Whitefish (*Coregonous clupeaformis*), a species that receive a larger amount of commercial fishing pressure. The changes in the food web have reduced the lipid content of their diet that has an impact on body maintenance, reproduction and growth. Lake Whitefish is

an iteroparous species that employs an intermediate life history strategy. Fitness of offspring can be determined by the maternal effects and how females are able to allocate nutrients from a sub-par diet towards reproduction in order to maximize fecundity and fitness of her eggs. Female's with large bodies produce larger livers and eggs, while larger livers also produced significantly larger eggs. Larger eggs have greater survival rate post-hatch giving the offspring a greater resistance abilities towards food deprivation and predation levels. Liver, an important energy reserve for reproduction, is an essential organ in egg production. When females increase in size, they have the ability to allocate greater amounts of nutrients towards the production of eggs. No significant relationship was able to explain the survival of the eggs. Age of the female shows a slight trend when considering survival of the eggs, but should be lightly interpreted. Future focus should be on how nutrient content of female body's affects embryo fitness.

4:15 – 4:30, Saturday, March 23rd, P&A 150

GETTING DEEP INTO SKATES: BIOLOGY OF *AMBLYRAJA HYPERBOREA* (ARCTIC SKATE) IN THE EASTERN CANADIAN ARCTIC

Sokolowski, M. A., Christie, L., Edwards, J., Barkley, A., & Hussey, N. E.
University of Windsor

The Arctic skate (*Amblyraja hyperborea*) is a deep-water species that has been identified as one of the most common bycatch species in commercial Arctic fisheries. Although categorized as 'Least Concern' on the IUCN Red list, global skate populations have declined by 90% since 1970, raising concern of over exploitation of *A. hyperborea* in expanding northern fisheries. To better understand the ecological role of this species, this project examined the diet, niche, trophic level, movement, and biological metrics of Arctic skates sampled across 6 study sites in the Eastern Canadian Arctic region, through stomach content analysis, stable isotope (δ13 C and δ15 N of liver and muscle) analysis, and biometric profiles. From previous data, it is expected that Arctic skate has a mainly fish-based diet and falls within the estimated trophic levels for all Rajiformes. We predict that biometric profiles of gonadosomatic index, hepatosomatic index, and δ15 N ratios will increase with increasing body size, while δ13 C ratios are predicted to show variation among study sites. This study is of importance due to the continued growth of demersal fisheries that may lead to an increase in Arctic skate bycatch. Through comparison with previous data, this study will allow a revaluation of the status of this species and bycatch management in Arctic fisheries.

4:30 – 4:45, Saturday, March 23rd, P&A 150

AN INTEGRATIVE APPROACH TO QUANTIFYING SENESCENCE IN SPAWNING FEMALE CHINOOK SALMON DURING FRESHWATER RESIDENCY

Sturba, M.A., Currier, S.L., Harris, C.M & Love, O.P
University of Windsor

Age-related declines in physiological functioning and overall health with the passage of time can be described as senescence. Senescent phenotypes can be manifested differently across taxa, with species varying in their rate of senescence. Semelparous Chinook salmon (*Oncorhynchus tshawytscha*) display rapid and irreversible senescence during their single reproductive attempt. Although variation in the onset of senescence has been observed within natural populations, the underlying mechanisms driving the process are not well understood. I will examine potential contributing factors of individual variation observed in senescing female Chinook salmon, focusing particularly on the impacts of freshwater residency, reproductive readiness, and markers of energetic physiology. To do this, females were moved into freshwater at different times. Blood samples, digital photographs, and body mass metrics were taken upon removal of fish from freshwater and used to provide a quantitative analysis of senescence. Females are expected to be more senesced with longer freshwater residency due to changes in behaviour and physiology. To protect egg quality and maximize reproductive success, females with lower reproductive readiness for the same time spent in freshwater should be less senesced and have more unripe eggs. This study aims to examine how and why individual variation in senescence occurs in Chinook salmon to better understand the fitness consequences of reproductive strategies.

4:45 – 5:00, Saturday, March 23rd, P&A 150

EFFECTS OF ALARM CUE PRIMING ON ANTI-PREDATOR BEHAVIOUR AND PHENOTYPIC VARIATION IN ATLANTIC SALMON (*SALMO SALAR*)

Wright, S. L.
University of Windsor

Alarm cue are naturally produced by fish following mechanical damage to the skin and elicit an innate anti-predator response in conspecifics. They are often used in short-term conditioning experiments to prepare hatchery-reared individuals for reintroductions into the wild; however, the effects of long-term priming with alarm cue during fish development are not well understood. This study primed hatchery-raised Atlantic salmon (*Salmo salar*) fry with conspecific alarm cue and examined the effects on their behavioural responses to novel environments, novel objects, and predation risk stimuli in comparison to an untreated control group. I predicted priming with alarm cue will increase fry sensitivities causing them to take longer to acclimate to a new environment and explore new objects, exhibit a greater response to predators, and produce less variation in responses than the untreated fry. A behavioural assay analyzed the degree of mobility, spatial distribution, latency to resume normal activity post disturbance, and overall inter-individual variation of behavioural phenotypes. Results demonstrated that primed individuals exhibited decreased overall mobility, increased latency to approach novel objects and to resume normal activity, and decreased inter-individual variation. Therefore, priming with alarm cue significantly impacts fry behaviour and requires further studies to determine whether the resulting trade-offs are adaptive under reintroduced conditions.

Ecology and Evolution J
PHYSICS & ASTRONOMY BUILDING, RM 117

4:00 – 4:15, Saturday, March 23rd, P&A 117

TERRESTRIAL MAMMALIAN PREDATOR/PREY RATIOS IN SOUTH AMERICA

Burgess, N. N., Mallory, F. F
Laurentian University

Terrestrial mammalian predator/prey ratios were examined in South America and ratios were determined between terrestrial mammalian predators and terrestrial mammalian prey within each biome. Six biomes were examined through meta-analysis to determine the number of terrestrial mammalian predators and prey in each biome, which was then organized into biome specific lists. Ratios for each biome were determined and compared. Fossorial mammals, aquatic mammals, and bats were excluded from this study, as data indicated that none of these were primary prey of terrestrial predators. Additionally, it was determined that large insectivorous species and arboreal primate species were not a significant part of any terrestrial mammalian predator prey items. While many of the species overlap in distribution among biomes, no biome had the same composition of species. In comparing these ratios to past research, the ratio for South America (approx. 0.50) was smaller than that of the Northern Hemisphere (approx. 0.75), and more akin to that of Africa (approx. 0.50). Biomes in warmer climates have a higher species richness, which may reduce predator specialization when compared to colder climates. Another possibility is that terrestrial mammalian predator/prey systems may have evolved differently in Gondwana versus Laurasia. This evolutionary link may explain why there is a ratio difference between the Northern and Southern Hemispheres.

4:15 – 4:30, Saturday, March 23rd, P&A 117

DATING *CUSCUTA* (CONVOLVULACEAE): EXPLORING A MOLECULAR CLOCK APPROACH IN THE DIFFICULT CASE OF PARASITIC PLANTS

Milne, S., Stefanovic, S.
University of Toronto

The molecular clock, a fixed rate of mutation of heritable biomolecules across lifeforms, is a useful tool for estimating the divergence times of clades where other evidence (such as a fossil record) is lacking. Unfortunately, it has been shown that a “global” molecular clock that would apply across broad and deep history is not always a sound assumption. This effect may be even more pronounced in parasitic organisms because such groups tend to have extreme levels of DNA substitution and consequently have diverged quite a lot from their non-parasitic ancestors. A promising alternative is the uncorrelated relaxed-clock, which is a model intermediate between a strict molecular clock and unrooted models of phylogenetic inference. In this research project, we attempted to determine the age of the parasitic plant genus *Cuscuta* as well as infer divergence times of major clades within *Cuscuta*. To achieve this, we are using an uncorrelated relaxed-clock model in order to explore the accuracy of this methodology when applied to parasites. We used an iterative approach, testing different tree topologies and the inclusion of different primary and secondary calibrations and noting their effects on the inferred dates. The analysis places the divergence of the *Cuscuta* lineage in the late Oligocene to mid Miocene epochs. The ages of major lineages within *Cuscuta* (subgenera/sections) will also be discussed.

4:30 – 4:45, Saturday, March 23rd, P&A 117

THE ROLE OF POPULATION DENSITY IN BIRTH SEX RATIOS OF DEER MICE (*PEROMYSCUS MANICULATUS*)

Sullivan, C., Veitch, J., Schulte-Hostedde, A.
Laurentian University

For decades, sex ratios have been an intriguing area of research as there is much evidence that they deviate from a once assumed 1:1 ratio for reasons such as mother’s condition around conception. Yet underlying mechanisms are still unknown. Considering mothers in good condition with rich resources tend to produce the more reproductively successful sex, we expected to find a greater proportion of males produced when population density was low. To determine birth sex ratios, we trapped deer mice (*Peromyscus maniculatus*) over five summers (2010, 2011, 2013, 2016, and 2018) and housed pregnant females in a laboratory mimicking natural conditions. Pups were sexed and weighed upon birth then released back to their home range with their mother seven days post-parturition. In order to determine how the number of males produced was altered, we used regression and correlation analyses to compare deer mouse birth sex ratios to population density from respective years. However, our results did not show a significant correlation between sex ratio and population density ($r = 0.086$, $p = 0.34$), nor between sex ratio and litter size ($r = -0.12$, $p = 0.20$). These results play an important role in evolution and may set groundwork when studying birth sex ratios of larger mammals that produce fewer young at a time.

4:45 – 5:00, Saturday, March 23rd, P&A 117

THE IMPACT OF WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) ON THE DIVERSITY, GROWTH, AND SPECIES ABUNDANCE OF URBAN PLANT COMMUNITIES

Balgobin, J., Havelka, M., Richter, C., Wu, T., Younen, T.
University of Toronto

The unique interactions between the white tailed deer (*Odocoileus virginianus*) and the diverse plant ecosystems co-existing amongst the urban setting is not very well known. In this study the impact of white-tailed deer presence in respect to the diversity, abundance, and plant growth of both the native and invasive plant species set within a secluded urban area will be done. During the time of study, results have suggested the presence of white-tailed deer

correlating to a greater diversity among the plant community, higher abundance the growth of invasive species, and reduction of general plant height. This research has highlighted the importance of altercation of the urban plant community ecosystem in the presence of white-tailed deer activity, while lays the fundamental steps for developing and implementation suitable environmental management actions.

Sunday March 24th 2019

Concurrent Session III *9:00 – 10:30*

Cell and Molecular Biology G
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 0153

9:00 – 9:15, Sunday, March 24th, B&GS 0153
REGULATION OF STAT5 ACTIVATION BY CLATHRIN-MEDIATED ENDOCYTOSIS
Borges, J., Rahmani, S., Antonescu, C.
Ryerson University

Triple negative breast cancers (TNBC) comprise 10-20% of breast cancer cases with limited treatments, poor prognoses and low survival rates. The epidermal growth factor receptor (EGFR) is expressed in many cases of TNBC; aberrant EGFR signaling is known to drive a variety of cancers. Upon ligand binding, EGFR activates numerous signaling pathways, such as that involving the phosphorylation and nuclear translocation of STAT5, which has intriguing and possibly conflicting roles in breast cancer depending on its regulation. Concomitantly to activation of intracellular signaling upon ligand binding, EGFR undergoes clathrin-mediated endocytosis from the cell surface to endosomes. The mechanism by which receptors phosphorylate and activate STATs is not well understood. We hypothesize that endocytosis is required for STAT5 activation to occur at endosomes. We used pharmacological inhibitors and siRNA gene silencing to perturb stages of endocytosis and intracellular trafficking to determine which are required for STAT5 activation in epithelial and TNBC cell lines. We also used immunofluorescence microscopy to observe the localization of phosphorylated STAT5 upon EGF stimulation. We find that EGF-stimulated STAT5 phosphorylation requires clathrin-mediated endocytosis, providing a new understanding of the molecular mechanisms leading to STAT5 activation. Understanding the mechanisms by which STAT5 is regulated has numerous implications in impacting current and future cancer treatments.

9:15 – 9:30, Sunday, March 24th, B&GS 0153
INVESTIGATING THE REGULATION OF R-LOOPS BY THE CHROMATIN REMODELER ATRX
Langlois, L. [1], Shafiq, S. [2], Bérubé, N. G. [3]
1. University of Western Ontario
2. Children's Health Research Institute
3. Lawson Health Research Institute

R-loops are three-stranded nucleic acid structures comprised of a DNA:RNA hybrid and a displaced single strand of DNA. In vivo, Rloops can influence DNA replication, gene regulation, epigenetic modifications, and transcription initiation and termination. Given their involvement in so many molecular processes, Rloop abundance is tightly regulated in the cell. When loss of regulation ensues, these structures accumulate, which poses great threats to genome stability. The mechanisms of Rloop regulation are not fully elucidated, but recent evidence suggests that the ATRX (α-thalassemia/mental retardation, Xlinked) protein can suppress the formation of these nucleic acid structures. ATRX encodes a chromatin remodeling protein and hypomorphic mutations cause a rare syndrome known as α-thalassemia retardation syndrome, X-linked (ATR-X syndrome). Our lab has shown that ATRX aids in transcriptional elongation by promoting a chromatin state that limits the accumulation of secondary structures in DNA. Taken together, current evidence suggests that ATRX is recruited by R-loops to promote a normal chromatin landscape during transcription and replication, thus preventing DNA damage. It is predicted that deletion of ATRX will result in increased R-loop levels. In this study, we seek to characterize the molecular mechanism by which ATRX interacts with R-loops by generating a CRISPR-mediated Atrx knockout (KO) neuroblastoma cell line and assessing levels of R-loops in the KO clones.

9:30 – 9:45, Sunday, March 24th, B&GS 0153

PROTEINS ASSOCIATED WITH NEURODEGENERATIVE DISEASE REGULATE RNA POLYMERASE II TRANSCRIPTION AT RIBOSOMAL DNA REPEATS

Liu, Y., Abraham, K., Mekhail, K.
University of Toronto, Department of Laboratory Medicine and Pathobiology

Cellular lifespan and aging are linked to processes that maintain a healthy balance between growth-fueling ribosome biogenesis and growth-stalling senescence. Synthesis of ribosomes, the machinery for translation, depends on the stability and function of the rDNA genes. In humans, the highly repetitive rDNA harbours coding genes, which are read by RNA polymerase I (Pol I) to synthesize ribosomes, and flanking intergenic spacers (IGS), which are less intensively studied. Unexpectedly, we uncovered novel RNA polymerase II (Pol II)-dependent processes at rDNA IGS. We sought to identify factors that maintain Pol II function at rDNA and why they function there. We show that inhibition of Pol II function and genetic ablation of Pol II-associated RNA-DNA hybrid suppressors elevate Pol I IGS transcription in human embryonic kidney cells. Our data suggests that these RNA-DNA hybrid suppressors likely maintain Pol II function by limiting the excessive buildup of co-transcriptional RNA-DNA hybrids along the IGS, which cause Pol II to stall during transcription. In our current model, maintenance of Pol II function at rDNA IGS is required for preventing aberrant IGS transcription by Pol I, and possibly defects in ribosome biogenesis. Interestingly, mutations in many RNA-DNA hybrid suppressors leads to fatal neurodegenerative diseases. Our results indicate that defects in rDNA function and stability might underlie the neuronal aging phenotype in these disorders.

9:45 – 10:00, Sunday, March 24th, B&GS 0153

IDENTIFYING THE REGULATION OF OMPT OMPTIN PROTEASE ACTIVITY BY THE EXPRESSION OF RNA POLYMERASE SIGMA FACTOR 54 IN ESCHERICHIA COLI

Mapili, A. M., McPhee, J. B.
Ryerson University Department of Chemistry and Biology

Omptins are outer membrane proteases that contribute to the bacterial virulence of gram-negative pathogens in the Enterobacteriaceae family. OmpT is a member of the omptin family in Escherichia coli. Omptins cleave proteins such as antimicrobial peptides to increase the overall pathogenicity of that particular bacteria. A prime example of targeted proteins are small cationic proteins called “host defense peptides”, which are an integral part of the human innate system. These peptides are primarily known for their protection against bacterial threat. They achieve this through targeting the negatively-charged bacterial membrane, where they form disruptive pores in the lipid bilayer, ultimately leading to bacterial cell death. Recent findings in the McPhee lab show that the deletion of rpoN, the gene that codes for RNA polymerase sigma factor 54, results to higher omptin protease activity of ompT. RNA polymerase sigma factors aid in the recognition of specific promoter sites during transcription, and in the early stages of RNA synthesis. In this study, different assays including Fluorescent Resonance Energy Transfer assay, Green Fluorescent Protein assay, and Western blots were performed to further investigate how rpoN regulates ompT expression and the peptide cleavage of cathelicidin LL-37 by ompT. The results suggest that ompT omptin protease activity is not regulated by rpoN and that the deletion of the gene may be inhibiting bacterial growth.

10:00 – 10:15, Sunday, March 24th, B&GS 0153

THE SPECIFIC ROLES OF DNAJ CHAPERONES IN CELLULAR PROTEIN QUALITY CONTROL

Sandhu, A.S. [1], Bour D.Y.N. [2], Ngo, V. [2], Duennwald, M. [2]
1. Department of Biology, University of Western Ontario.
2. Department of Pathology and Laboratory Medicine at Schulich School of Medicine & Dentistry, University of Western Ontario.

Cellular stress, such as heat shock or oxidative stress results in protein misfolding and aggregation. Protein aggregation is prevented or reversed by cellular protein quality control pathways. DNAJ proteins are central in many protein quality control pathways and work along with Hsp70 to regulate de novo protein folding, refolding of misfolded proteins, and protein degradation. I will determine which DnaJs specifically interact with other components of cellular protein quality control pathways and thus determine their distinct function under normal and stress conditions. I hypothesize that specific DnaJs act as a co-chaperone to Hsp90 in cellular protein quality control to reverse protein misfolding. To this end, I employ a mating-based variant of the split-ubiquitin assay in yeast (Saccharomyces cerevisiae) since this method detects even transient protein-protein interactions, such as those between different molecular chaperones.

10:15 – 10:30, Sunday, March 24th, B&GS 0153

VALIDATING DROSOPHILA MELANOGASTER AS A TOOL TO STUDY TUBERIN CELL CYCLE REGULATION

Semaan, A., Pillon, A., Fidalgo da Silva, E., Porter, L.
University of Windsor

To preserve cellular integrity, checkpoints must be fulfilled in order to pass through each cell cycle phase. The G2/M checkpoint is regulated by a Cyclin B1-CDK1 complex. In late G2 phase, Cyclin B1 (CycB1) accumulates in the nucleus from the cytoplasm. The overexpression of CycB1 has been associated with tumor aggressiveness and, therefore, CycB1 may have the potential to be a new therapeutic target in many aggressive cancers. Tuberin is a tumor suppressor protein that can bind CycB1 in the cytoplasm to regulate entry of CycB1 into the nucleus during the G2/M transition. Research into the Tuberin and CycB1 interaction may be promising for the field of cancer research. The Porter lab has studied the Tuberin-CycB1 interaction in vitro using established cell lines, but no one to date has studied this using an in vivo model which would provide us with more in-depth information about disease models. Drosophila melanogaster offers the unique advantage of having short generation times to permit high-throughput data to be collected. Moreover, the imaginal discs in the eye and wing of Drosophila contain regions of cells that are synchronized in the various phases of the cell cycle, providing the advantage that results can be seen at every phase of the cell cycle using this system. Our goal for this project is to first develop a Drosophila disease model for Tuberin-CycB1 interactions and use it to gain more insight on possible targeted treatments for cancer using Cyclin B1.

Cell and Molecular Biology H
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 0165

9:00 – 9:15, Sunday, March 24th, B&GS 0165

EXAMINATION OF BACTERIAL SURVIVAL FOLLOWING PRIMARY AND SECONDARY INFECTION IN MAMMALIAN MACROPHAGE CELLS

Acharya, D. , McPhee, J.
Ryerson University

Adherent-invasive Escherichia coli (AIEC) are a leading candidate for causing inflammatory bowel disease (IBD). AIEC, a pathovar of E. coli, are defined by their ability to adhere and invade epithelial cells in vitro. AIEC also exhibits resistance to killing by macrophages. Currently, we do not know why AIEC are able to survive better inside host intestinal macrophages than other commensal E. coli strains. The aim of the experiment is to study intracellular bacterial growth in mammalian macrophages after infection with AIEC and non-AIEC bacteria. We planned to infect

macrophages with bacterial strains in primary infection. These macrophages were infected with secondary non-pathogenic bacteria that are highly susceptible to macrophage phagocytosis. All AIEC strains showed survival at 24 hours of primary and secondary infection. On the other hand, non-AIEC strain, K-12, showed no survival at 24 hours of primary and secondary infection. In conclusion, all AIEC strains have higher bacterial counts and survival rates in macrophages at 24 hours of infection, compared to non-pathogenic strain, K-12, at 24-hr. Creation of mutants can strengthen our understanding of the pathogenesis mechanism of experimental strain, HM605. The mutants will contain a deletion in one protein that is thought to play a role in autotransporters and type VI bacterial secretion system. Each gene is thought to play a role in virulence which could affect a macrophages' ability to kill bacteria.

9:15 – 9:30, Sunday, March 24th, B&GS 0165

THE EFFECT OF ADHERENT-INVASIVE ESCHERICHIA COLI ON HOST MACROPHAGES

Miraglia, E., Campisi, D., Fountain, A., McPhee, J.B., Botelho, R.J.
Department of Chemistry and Biology, Ryerson University

Inflammatory bowel diseases (IBD), including Crohn's disease and ulcerative colitis, are becoming increasingly prevalent. These diseases are characterized by chronic inflammation of the gastrointestinal tract, caused by a combination of interacting factors including the host immune system and an altered gut microbiome. Pathogenic adherent-invasive Escherichia coli (AIEC) strains are associated with IBD symptoms and are more prevalent in the gut microbiome of IBD patients. Multiple AIEC strains contain genes that encode for the type VI secretion system (T6SS), a molecular machine that delivers protein effectors to prokaryotic and eukaryotic target cells. Bacterial secretion systems including the T6SS are critical to the pathogenicity of many disease-causing microbes. However, the role of T6SS expression in AIEC pathogenesis is not well understood. We set out to further characterize the host-pathogen interaction between AIEC and host immune cells using an in vitro RAW264.7 macrophage infection model. Macrophages were infected with Crohn's-associated clinical isolates of AIEC strains HM605 and NRG857c, as well as an NRG857c mutant strain bearing deletions in key T6SS genes clpV1 and clpV2. We observed a novel virulence phenotype in AIEC, finding that both wild type strains killed the macrophages. This phenotype was lost in the mutant, implicating the T6SS in this killing phenotype.

9:30 – 9:45, Sunday, March 24th, B&GS 0165

POTENTIAL FOR ANTIBIOTIC DISCOVERY AND PRODUCTION BY THE GENERATION OF A STREPTOMYCES VENEZUELAE-DERIVED CHASSIS STRAIN

Pepler, M. A., Hindra, H., Elliot, M. A.
McMaster University

The antibiotic resistance crisis is implicated in 700,000 deaths a year. Historically, new antibiotics were discovered by isolating compounds directly from cultures of microorganisms. Streptomyces bacteria are exemplary of this antibiotic potential, by producing two-thirds of all known naturally-derived antibiotics. Today, this mode of discovery is obsolete given the difficulties associated with detecting novel antibiotics, which are produced at low-yeild under laboratory conditions. A solution to this problem lies in the heterologous expression of predicted biosynthetic gene clusters in a surrogate host, or chassis strain. The development of a Streptomyces venezuelae-derived chassis strain was a principal goal of this work, which entails removing the endogenous biosynthetic gene clusters to reduce background antibiotic activity. Specifically, this was done in a strain of S. venezuelae in which the global repressor of secondary metabolism lsr2 was removed. This limits the potential for a heterologously introduced cluster to have its expression naturally repressed. In tandem, this research aimed to screen through a library of wild Streptomyces species, in which Lsr2 activity has been knocked-down, for new antibiotic activity. It follows that any of these wild Streptomyces species demonstrating significant production of antibiotics would be interesting candidates for further investigation and may encode biosynthetic gene clusters that would benefit from heterologous expression.

9:45 – 10:00, Sunday, March 24th, B&GS 0165

ROLE OF PHAGOLYSOSOME FRAGMENTATION IN THE REFORMATION OF LYSOSOMES WITHIN MURINE MACROPHAGES

Somerville, E.N., Fountain, A.
Molecular science at Ryerson University

Phagocytosis is the cellular process of internalizing large particles (>0.5 µm in size) by engulfment, for the purposes of degrading the target particles. In mammalian systems, phagocytosis is primarily carried out by specialized cells called phagocytes, which employ such processes to clear unwanted particles, such as bacteria, from the body. Lysosome fusion with the phagosome forms a phagolysosome, acidifying the organelle, and introducing hydrolytic enzymes to allow the phagocyte to break down internalized particles. While phagocytosis and phagosome maturation are well-studied, there is little known about the fate of phagolysosomes after particle breakdown in mammalian cells. To continue phagocytosis, a phagocyte must destroy the phagolysosome and return its components to their origins, a process called phagosome resolution, to make resources available for subsequent phagocytosis. Through the utilization of cell culturing, Immunofluorescence and Spinning Disk Microscopy, our lab has observed vesicular budding and fragmentation of phagolysosomes in RAW 264.7 murine macrophages, and that these fragments have been observed to possess lysosomal properties. These observations suggest that fragmentation generate vesicles that eventually form into functional lysosomes. We aim to characterize the properties of these fragments to reveal the mechanism in which lysosomes are reformed, and the ultimate fate of the phagolysosome in phagosome resolution.

10:00 – 10:15, Sunday, March 24th, B&GS 0165

EXPANDING THE VIRULENCE ONTOLOGY (VIRO) TO DETERMINE THE VARIABILITY OF SECRETION SYSTEM EFFECTORS

Tran, H.K.R., Ahmad, S., Whitney, J.C., McArthur, A.G.
McMaster University, Hamilton, ON, L8S 4K1, Canada

Antimicrobial resistance threatens modern medicine as multidrug-resistant pathogens emerge. An understanding of virulence offers another avenue for antimicrobial development. The Virulence Ontology (VIRO) within the Comprehensive Antibiotic Resistance Database (https://card.mcmaster.ca) is an ontology-centric knowledgebase of the bacterial virulence literature. The Virulence Gene Identifier (VGI) uses VIRO for in silico bacterial virulome prediction. Secretion systems are used by pathogenic bacteria to deliver virulence factors into host cells. Type six secretion systems can secrete a diverse set of species-specific type six exported (Tse) toxic effectors. These toxins have high variability at the C-terminus. As a proof of concept of VGI, we investigated and identified novel isoforms of Tse toxins among 326 Pseudomonas aeruginosa genomes, basing our search on the N-terminus of a P. aeruginosa representative strain. From phylogenetic analyses, we found that the genomes can be generally separated into two clades, between which horizontal gene transfer is present. We then experimentally validated that these novel isoforms mediate competition between P. aeruginosa PAO1 and PA14. Future directions include elucidating the functions of these isoforms. As Tse proteins are antibacterial, our work demonstrates the utility of virulome prediction in uncovering vulnerabilities of pathogenic bacteria that can be further explored in antimicrobial development.

10:15 – 10:30, Sunday, March 24th, B&GS 0165

INTRIGUING SEQUENCE SIMILARITIES BETWEEN VIRAL GENOMES AND THEIR HOSTS

Valente, B.S. [1], Soltysiak, M.P.M. [1], Randhawa, G.S. [2], Stueckmann, D. [1], de Souza, C.P.E. [3], Kari, L. [4], Hill, K.A. [1]
1. Department of Biology, University of Western Ontario
2. Department of Computer Science, University of Western Ontario
3. Department of Statistical and Actuarial Sciences, University of Western Ontario
4. Department of Computer Science, University of Waterloo

Viruses and their hosts have been reported to share genomic signatures, a sequence composition pattern that is species specific. Many integrating retroviruses and vertebrate hosts share CpG underrepresentation, consistent with

similar mutational mechanisms and selective pressures. Here, relationships between genomic signatures of hosts and viruses from many viral families were analyzed. Viruses were categorized into integrating, occasionally integrating, or non-integrating groups. It was hypothesized that nuclear selective pressures experienced by integrating viruses underlie the shared subsequence biases with their hosts. Using the alignment-free method, Chaos Game Representation, both integrating and non-integrating viruses showed similar genomic signatures in many host-virus pairings. Associations were identified between host-virus pairs in comparisons of proportional subsequence frequencies of varying lengths (k-mers). Significant positive correlations were found between k-mer frequencies of 10 integrating, 31 occasionally integrating, and 120 non-integrating viruses with human hosts at different subsequence lengths (k=2 to 7). Machine learning with digital signal processing (ML-DSP) was used to predict host-virus associations and the greatest variation was found for non-integrating viruses. Although currently unidentified, these findings are consistent with the existence of nuclear and cytoplasmic molecular mechanisms driving co-evolution of viruses and their hosts.

Cell and Molecular Biology I
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 1056

9:00 – 9:15, Sunday, March 24th, B&GS 1056

CHARACTERIZING EMBRYONIC OPTIC NEUROBLASTS IN THE DEVELOPING DROSOPHILA MELANOGASTER BRAIN

Akheralie, Z.
University of Toronto - Mississauga

The optic lobe is the visual processing center of the Drosophila melanogaster brain and is comprised of four compartments; the lamina, medulla, lobula, and lobula plate. These compartments are derived from a group of embryonic epithelial cells called the optic placode. During larval stages, these cells undergo expansive symmetrical divisions before converting into asymmetrically diving stem cells, termed neuroblasts, in the 3rd instar larval stage. While it has been widely accepted that optic lobe neuroblasts are first generated in the 3rd instar larva, recent research has identified an earlier window of neuroblast formation. Embryonic Optic Neuroblasts (EONs) have been shown to develop in the late embryo, two days earlier than previously anticipated. However, the neurons generated by EON's have not yet been characterized. I have used a combination of Drosophila genetics, immunohistochemistry, and confocal microscopy to identify the neural types generated by EONs. Preliminary data suggest that EONs contribute to two populations of neurons in the adult, one that arborizes in the lobula and another that arborizes in the lobula plate and medulla. I will further determine the developmental stage in which EONs generate these neurons. My findings suggest that an early wave of neurogenesis serves to increase neural diversity in the visual system by generating unique classes of neurons. These early born neurons may play a role in the initial assembly of the visual neural circuit.

9:15 – 9:30, Sunday, March 24th, B&GS 1056

TESTING CANCER CHEMOTHERAPY SENSITIVITY AND RESISTANCE RELATIONSHIPS FOR A PANCREATIC CANCER DRUG

Calcagno, G., Kianford, Z., and Sabatinos, S.A.
Dept. Chemistry and Biology, Ryerson University, Toronto, ON

Gemcitabine is a cancer chemotherapeutic, recognized for its safety and efficacy against many solid tumours. Gemcitabine has become one of the primary treatment options for pancreatic cancer therapy. However, the positive effects of Gemcitabine to eliminate pancreatic cancer are limited. This is due to rapidly acquired resistance against gemcitabine that occurs following initial gemcitabine treatment. Some factors of gemcitabine resistance are well documented, yet the mechanisms driving the acquisition of gemcitabine resistance remain relatively unknown. The yeast Schizosaccharomyces pombe is a powerful model organism that can be used to explore drug sensitivity and resistance. We have tested gemcitabine in specialized S. pombe mutants and modelled cell death resulting from gemcitabine exposure. Mutations in cell cycle checkpoints are commonly found in cancers, and promote both the development of cancer and the potential for drug sensitivity. We have found that DNA replication stress caused by

gemcitabine stimulates later resistance in specific checkpoint mutants. By knowing which cell-cycle checkpoint mutants are more susceptible to gemcitabine we hypothesize that specific patients will benefit more from gemcitabine without the added risks of drug resistance.

9:30 – 9:45, Sunday, March 24th, B&GS 1056

EXPLORATION OF EVOLUTION IN B-CELL LEUKEMIA: IDENTIFYING POTENTIAL GENES THAT ENABLE CLONAL EVOLUTION BY WHOLE EXOME SEQUENCING AND MOUSE MODELS

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University of Western Ontario
Cornell University

Leukemia is a highly common cancer in young patients. B-cell acute lymphoblastic leukemia (B-ALL) is theorized to develop through clonal evolution, a theory based on driver and passenger mutations. Drivers confer an advantage for cell growth and division, causing development of a cancerous phenotype. In B-ALL, prior work has identified primary drivers as SpiB and Spi1, but secondary drivers remain less understood. Using a double knockout mouse model for SpiB and Spi1, we performed whole exome sequencing (WES) to determine which genes had mutated during B-ALL development in eight specimens. Once the genes were identified using Strelka software, we calculated variant allele frequency (VAF) to identify mutated genes in the exomes. Utilizing the VAF metric with filters for missense, start, stop, and splice region SNVs, we identified genes that were commonly mutated in multiple exomes. The genes that overlapped most were Ikzf3 and Jak3. By utilizing filters according to base pair changes in the DNA sequence, we found that nucleotide changes shifted from predominantly C>A to C>T as VAF increased, with significant differences in the ratio between C>A/C>T mutants. Protein structure analysis also predicted that observed missense variants of these genes altered the protein structure for Ikzf3 and Jak3. Taken together, these results indicate that Ikf3 and Jak3 are likely secondary drivers facilitating clonal evolution of our B-ALL phenotype.

9:45 – 10:00, Sunday, March 24th, B&GS 1056

MEASURING THE EFFECTS OF BMAL1 ON TUMOR CHARACTERISTICS AND INCIDENCE RATES IN APC MIN/- MICE

Curran, C.
University of Windsor

The circadian rhythm is a highly conserved set of molecular processes which allow cells to coordinate activities in relation to internal and external cues over a twenty-four hour period. This coordination is governed by negative feedback mechanisms that result in regular oscillations in the abundance of circadian rhythm related proteins. Circadian rhythm disruption has been proposed to cause increased rates of tumorigenesis and tumor growth. Bmal1 is a protein critically involved in the formation of the circadian clock. My thesis aims to identify if and to what extent Bmal1 influences tumorigenesis and tumor characteristics. The APC gene codes for the APC protein, which is a tumor suppressor which has been shown to suppress colorectal tumors. Min is a mutant allele of APC which produces a truncated APC protein. APC Min/- mice are genetically predisposed to develop colorectal cancer. My thesis tests the role of Bmal1 in determining tumor attributes by staining distal, medial, and proximal colon sections from a population of APC Min/- Bmal1 -/- mice and comparing them to an APC Min/- Bmal1 +/+ population. I will then test for the abundance of cells expressing three cellular markers; Phosphohistone H3 (PHH3), Caspase 3, and Lysozyme. These stains test for actively dividing cells, apoptotic cells, and Paneth cells respectively. This will allow a comparison to be made between wild type and mutant Bmal1 tissues to determine its affects on tumorigenesis and tumor attributes.

10:00 – 10:15, Sunday, March 24th, B&GS 1056

INVESTIGATING AIOLOS MUTATIONS AS DRIVERS OF B CELL ACUTE LYMPHOBLASTIC LEUKEMIA IN MICE

Knight, D.D., Lim, M., Clemmer, K.S.F., and Dekoter, R.P.
University of Western Ontario

B cell acute lymphoblastic leukemia (B-ALL) is a blood cancer that occurs most frequently in children between ages 0-5. In the quest to identify safer treatments of B-ALL, using animal models of disease is paramount in evaluating

treatments. It has been shown that mice that are knockout for transcription factors: PU.1 and Spi-B, develop B-ALL. However, additional mutations may be driving B-ALL in these mice. Using whole exome sequencing of leukemias from PU.1/Spi-B knockout mice, we identified several mutations in the transcription factor, Aiolos. In this study, we asked if the Aiolos mutations are driving B-ALL in these mice. We found that sequence analysis located Aiolos mutants in DNA-binding and protein-binding domains. Interestingly, three-dimensional prediction software showed that Aiolos mutations may directly disrupt zinc from occupying zinc-finger domains involved in binding DNA. Further in-vitro analysis of ectopic expression of mutant Aiolos in healthy pro-B cells remains to be advanced. The findings thus far suggest that loss-of-function mutations in the transcription factor Aiolos in PU.1/Spi-B knockout mice may drive B-ALL. By elucidating the progression of B-ALL in these mice, researchers and oncologists will be one step closer to providing better patient care by utilizing a model to analyze new treatments.

10:15 – 10:30, Sunday, March 24th, B&GS 1056

THE ROLE OF THE MICROENVIRONMENTAL LANDSCAPE IN GBM PROGRESSION AND THERAPY RESISTANCE

Nadeem, F., Lubanska, D., & Porter, L. A.
University of Windsor

Glioblastoma multiforme (GBM) is a type of brain tumour that is categorized as having the highest degree of aggressiveness, accounting for 60% of adult brain tumours with poor prognosis. Despite extensive chemo- and radio-therapy treatments, patients' relapse. Therefore, better understanding of GBM biology is crucial to the advent of effective therapeutic interventions. The tumour niche, also known as the cancer stroma, is composed of the extracellular matrix and several types of recruited cells including fibroblasts. Fibroblasts secrete diverse molecules which were found, in other types of cancer, to contribute to the maintenance of the malignant characteristics of the tumour mass. Therefore, we hypothesize that fibroblast activation plays a crucial role in the aggressiveness and progression of GBM. We will first study the characteristics and content of the fibroblast populations in sections obtained from GL261 glioma cell line-derived brain tumours, in comparison to normal brain tissue. We will employ commercially available mouse embryonic fibroblasts to establish co-cultures with GL261 cells in-vitro. Both monolayer and 3D culture models will be utilized to study the activation and the role of the fibroblast component in the control of GBM progression and therapy resistance. In summary, my project will not only contribute to a better understanding of the mechanisms regulating the GBM microenvironment, but it will also identify potential novel treatment approaches.

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9:00 – 9:15, Sunday, March 24th, P&A 34

AN EXPLORATION OF EPIGENETIC EFFECTS IN DUTCH AND BANGLADESHI HISTORICAL FAMINE POPULATIONS: A LITERATURE REVIEW

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Famines are devastating events that are causes and consequences of social upheaval, inequity, and the suffering of the most vulnerable. Though famines have immediate dire effects on the population, their transgenerational consequences have been of emerging interest since the mid 1900s . Exposure to adverse environmental conditions, especially inadequate maternal diet, during gestation have been shown to cause differential DNA methylation in several prenatal exposure studies. Epidemiological data have shown the increased risk of obesity and type 2 diabetes in subsequent generations of populations exposed to famine. A limited number of studies based mainly on the Dutch Hunger Winter of 1944-45 have found DNA methylation changes, causing over- or under-expression, in several physiologically relevant gene loci, such as IGF2, LEP and VTRNA2-1. Historical famines like the Dutch famine have been described as quasi-experimental conditions, sources of data that can bridge the gap between experimental studies in animals and short-term prenatal exposure studies in humans. There remains a need for literature that adequately explores epigenetic changes in these populations and corresponding phenotypic expression. This paper groups imprinted genes, non-imprinted genes, and metastable epialleles found to be significantly differentially methylated in historical famine cohorts, to explore the link to phenotypic changes associated with metabolic syndromes, specifically obesity and T2DM.

9:15 – 9:30, Sunday, March 24th, P&A 34

FROM MOUSE TO HUMAN: AN IMPERATIVE KEY TO UNLOCKING THE INTERACTION BETWEEN THE STB TOXIN AND AN INTESTINAL CELL SURFACE RECEPTOR

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Since the 1800s, Escherichia coli (E.coli) has been studied extensively for the causation of diarrheal illness and other intestinal disorders. Non-pathogenic E. coli inhabit the normal flora of the intestines, symbiotically causing no illness. However, pathogenic strains have evolved past this relationship; developing disease-eliciting mechanisms, one such strain being the Enterotoxigenic E. coli (ETEC). Caused by different virulence factors produced by ETEC within the intestine, one significant factor produced is the heat-stable enterotoxin b, or STb. STb is a protein comprised of 48 amino acids with a molecular weight of 5.2 kDa. Studies on various animals such as mice, rats, pigs and rabbits have been thoroughly conducted, as these animals have been majorly affected by ETEC. An investigation was conducted on the characterization of a cell surface receptor which STb binds to upon an NCI-H716 human cell line, while comparing and contrasting results found from a previous thesis on an STC-1 mouse cell line using the same toxin. This way, not only will we be able to uncover the motif which the STb toxin follows for its toxigenic properties, but also be able to give some insight to the similarities and differences in the mechanisms of infection between the different species being studied. Our hypothesis states that there will be a positive binding of the toxin to the human cell receptor, showing similar cell signalling and binding mechanisms with that of the mouse cell line.

9:30 – 9:45, Sunday, March 24th, P&A 34

COMPARISON OF THE GENE EXPRESSION IN THP-1 CELLS INDUCED BY NORMAL, PRE-FIBROTIC AND DUPUYTREN'S DISEASE MYOFIBROBLASTS

Lau, C., Pena, A.M., Gan, B.S., Grewal, R., Suh, N., O'Gorman, D.B.
University of Western Ontario and St. Joseph's Hospital

Dupuytren's Disease (DD) is a fibrosis in the palmar fascia leading to the permanent contracture of fingers. The development of DD is due to abnormal palmar fascia repair, likely involving the interactions between immune cells and myofibroblasts. Although immune cells can activate myofibroblasts and vice versa, the interactions between fibrosis-derived myofibroblasts and immune cells are not well understood. In this research, we compare the effects of fibrosis-derived myofibroblasts and normal myofibroblasts on the cytokine gene expression of THP-1 cells (leukemia monocytes). The THP-1 cells are treated with 5 different conditions: collagen (negative control), collagen with LPS (lipopolysaccharide) as positive control, Dupuytren's Disease derived myofibroblasts (DD), visibly non-fibrotic palmar fascia tissue from a DD patient (PF) and normal tissue from patients without DD (CT).
DD, PF and CT myofibroblasts (3.6x105 cells) were cultured in the fibroblast populated collagen lattice (FPCL) (N=3, n=3) for 3 days. THP-1 cells (3x105 cells) were then cultured on top of the FPCL with 1% FBS (Fetal bovine serum) and 1:1 ratio of DMEM (Dulbecco's Modified Eagle Medium) and RPMI (Roswell Park Memorial Institute medium) for 6 days. For the positive and negative control, THP-1 cells were cultured with or without LPS respectively. RNA extraction, reverse transcription and qPCR were conducted to quantify the THP-1 gene expression of CCL2, IL6, TGFB1, TNF, IL1B, IL10 and FN1.

9:45 – 10:00, Sunday, March 24th, P&A 34

ANALYSES OF TLY GENE EXPRESSION IN CUTIBACTERIUM ACNES IN A TISSUE MIMETIC MODEL OF SHOULDER JOINT INFECTIONS

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2. Lawson Health Research Institute
3. Departments of Surgery and Biochemistry
4. Schulich School of Medicine and Dentistry

Cutibacterium acnes (C. acnes) is a human skin commensal and opportunistic pathogen of joint arthroplasty surgery. These bacilli are gram positive, anaerobic, and have been identified as the most common cause of periprosthetic joint infections (PJIs) of the shoulder, where it causes local tissue necrosis and implant loosening. These infections are the result of transferring C. acnes cells from pilosebaceous follicles in the skin to the implant site. Very little is known about this infection process, which is predicted to be the opportunistic colonization of an avascular foreign object embedded in vascular tissue. We hypothesize that the transfer of C. acnes to the implant site induces the expression of C. acnes virulence factors, establishing an infection. To model this process in 3D, we are inoculating fibroblast populated collagen lattices (FPCL) with C. acnes, in the presence or absence of primary human teno-fibroblasts under near-anaerobic conditions (0-5% O2). We have developed a RT-qPCR assay to measure the expression of the C. acnes tly gene, encoding a putative hemolysin. We will compare two commercial C. acnes strains to a C. acnes isolate from a PJI, in co-culture and in suspension culture, to determine how these various culture conditions affect C. acnes tly expression. We predict that 3D co-cultures of C. acnes with teno-fibroblasts will potently induce tly expression, mimicking the tissue necrosis caused by this pathogen during an infection.

10:00 – 10:15, Sunday, March 24th, P&A 34

INSIDE THE LUNGS OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE PATIENTS: A METAGENOMIC MICROBIAL RE-ANALYSIS

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Microbes have diverse effects on human health and disease. Metagenomics is a culture-free method of microbial study by environmental sample shotgun sequencing. Shotgun metagenomic sequencing is being used to collect data on many different human microbiota, including the lungs. Both clinical and scientific conclusions are being drawn based on analyses of such data, but non-standardized analysis methods lead to different results and conclusions. Here we present the re-analysis of a publicly available shotgun metagenomics, microbiome dataset from the lungs of patients with Chronic Obstructive Pulmonary Disease (COPD). Using recently developed analysis pipelines, we elucidate metagenomically-assembled genomes (MAG), a strain level taxonomic classification. Currently, COPD is diagnosed clinically by lung capacity, a low specificity method. MAGs from healthy controls and disease patients are compared and discussed in this presentation, as well as the limitations of assembling genomes with low-coverage sequencing. This approach may allow the determination of bacterial strains associated with disease or control patients, which can further be used to guide in-depth studies of bacterial effects on COPD or as a clinical biomarker.

10:15 – 10:30, Sunday, March 24th, P&A 34

CHANGES IN BRAIN MORPHOLOGY AND MICROGLIAL ACTIVATION FOLLOWING MATERNAL IMMUNE ACTIVATION

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Epidemiological studies have shown the link between maternal infection during pregnancy and increased incidence of psychiatric disorders such as schizophrenia (SZ) and autism spectrum disorder (ASD) in offspring. Evidence suggests maternal immune activation (MIA) to be the mechanism through which offspring brain phenotype and behavior is altered. In addition, studies have also shown progression of ASD and SZ related phenotypes and

subsequent related behavior in a translational rodent immune model system by administration of a viral mimetic. However, how exactly MIA impacts the brain and the implications of maternal infection are largely unknown. With the global increase in infections and pathogen exposure, this maternal-fetal-immune interaction should be investigated. This study aims to investigate the influence of MIA on brain development. If MIA impairs neurodevelopment, then I hypothesize there to be alterations in phenotypes reflective of psychiatric disorders such as increased microglia, lower Purkinje cell density and reduced cortical thickness in the fetus brain. I will examine and compare these phenotypes amongst 6 weeks and 4 months old Sprague Dawley offspring treated with a viral mimetic (poly I:C) on gestation day 9.5 or 14.5.

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9:00 – 9:15, Sunday, March 24th, P&A 36

ROLE OF O-GLCNACYLATION IN EXTRAEMBRYONIC ENDODERMAL DIFFERENTIATION OF THE F9 MOUSE CELL LINE

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University of Western Ontario

Mouse F9 cells differentiate into primitive endoderm (PE) under retinoic acid (RA) and parietal endoderm under RA and dibutyryl cAMP (DB) treatment. This differentiation may be influenced by O-GlcNAcylation, a type of post-translation modification where proteins are glycosylated by an addition of sugar molecule O-GlcNAc. O-GlcNAc is a glucose metabolite made in the hexosamine pathway, and relies on rate-limiting enzyme GFAT. Addition of sugar is done via O-GlcNAc transferase (OGT), and removed via O-GlcNAcylase (OGA). O-GlcNAcylation maintains pluripotency of mouse stem cells in ectodermal differentiation, but their role in endodermal differentiation is not known. We hypothesized that O-GlcNAcylation may prevent differentiation of F9 cells into its endodermal structures. Cells were treated with RA and RA+DB to induce differentiation; DMSO-treated cells were the control. We found there was a decrease in global levels of O-GlcNAcylated proteins in RA+DB treated cells. There was no difference between treatments for mRNA expression levels. Finally, studies suggest that galectins, which are -galactoside binding proteins, may be linked to O-GlcNAcylation. A galectin expression profile was created for all known galectins in mice. With exception of Galectin 3, all showed decreased mRNA expression levels in experimental treatments. Together, we demonstrate the role of O-GlcNAcylation in differentiation of F9 cells along with its potential link with galectin expression.

9:15 – 9:30, Sunday, March 24th, P&A 36

INVESTIGATING THE ROLE OF P66SHC IN OXIDATIVE STRESS SENSITIVITY IN AB-RESISTANT PC12 CELLS

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Alzheimer’s disease (AD) is the most common neurodegenerative disease leading to cognitive dysfunction. AD is thought to arise due to the production and extracellular deposition of plaques composed of amyloid beta (Aβ) peptide. Aβ promotes oxidative stress within the central nervous system (CNS) leading to extensive cell death and synaptic loss. Although amyloid plaques within the brain are a strong pathological indicator of AD, a large proportion of the elderly display significant levels of amyloid plaque deposits without cognitive dysfunction; suggesting that some CNS cells can acquire resistance to Aβ toxicity. Previous studies have found that Aβ-resistant CNS cells display a greater glycolytic metabolic phenotype when compared to Aβ sensitive cells. Additionally, the adaptor protein p66Shc, has been shown to promote mitochondrial metabolism. Thus, p66Shc might play a pivotal role by preventing Aβ resistance. Currently no connection between Aβ resistant PC12 cells and p66Shc has been studied. Our current research shows higher levels of endogenous p66Shc within wild type PC12 cells when compared to the Aβ resistant PC12 lines. Additionally, we see a greater shift towards a glycolytic metabolism in the resistant lines. Overexpression of p66Shc in Aβ resistant cells resulted in a greater shift towards mitochondrial metabolism; whereas the opposite effect was seen after p66Shc knockdown. Thus p66Shc may represent a pharmaceutical target to promote Aβ resistance in CNS cells.

9:30 – 9:45, Sunday, March 24th, P&A 36

INVESTIGATING THE INTERPLAY BETWEEN AMP-ACTIVATED PROTEIN KINASE, P38 MAPK AND O-LINKED Β- N-ACETYLGLUCOSAMINE IN RESPONSE TO CELL STRESS

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The cellular response to stress is a complex phenomenon in which various signals and pathways are involved to re-establish homeostasis. One of the main metabolic sensors is AMP-activated Protein Kinase (AMPK), which senses energy stress and regulates the activity of various substrates. AMPK may co-operate with or antagonize other key metabolic switches such as 1) the enzyme O-linked -N-Acetylglucosamine (O-GlcNAc) transferase (OGT) that modifies nucleocytoplasmic proteins and 2) Mitogen-activated signalling pathways such as p38 MAPK. Using retinal pigment epithelial (RPE) cells, our experimental model investigated the interplay between AMPK, p38 MAPK and OGT in stress states. We found that the cells stress response is unique to the nature of the stress, and that hydrogen peroxide (H2O2) was the most potent activator of all pathways. Upon short-term treatment with H2O2, results show that all pathways relied on AMPK or p38 activity to respond, but were not impacted by OGT inhibition. Alternatively, siRNA knockout of OGT greatly reduced AMPK protein levels, and the same trend was observed for OGT upon AMPK knockout. These results indicate that there is a degree of communication between each pathway during the stress response, and that the duration of exposure to stress may play a role in the level of cross-talk occurring. This study has important implications for the pathogenesis of diseases like Alzheimer’s and cancer, which are induced by persistent stress.

9:45 – 10:00, Sunday, March 24th, P&A 36

THE ROLE OF G9A AND PUMILIO ON THERMAL NOCICEPTION

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When animals experience painful stimuli, they elicit an escape response that is guided by nociceptive neuronal circuitry. Drosophila melanogaster larvae curl and roll in response to thermal nociception. The Drosophila foraging (for) gene encodes a cGMP-dependent protein kinase that regulates this response. for expression is regulated by the histone methyltransferase G9a and the RNA-binding protein Pumilio. Here, we test the effects of G9a and Pumilio on thermal nociception. We found that both G9a and Pumilio regulate this response. We will also present data on whether these effects are dependent on the for gene.

10:00 – 10:15, Sunday, March 24th, P&A 36

THE CYTOPLASMIC DOMAIN OF MT1-MMP ASSISTS IN THE REGULATION OF AEROBIC GLYCOLYSIS

Mishan, N., Damjanovski, S.
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Membrane-Type 1 Matrix Metalloproteinase (MT1-MMP) is a multifunctional, transmembrane protease implicated in the regulation of aerobic glycolysis, particularly through its cytoplasmic domain. This shift in metabolism is characterized by a reduction in oxidative phosphorylation and upregulation of lactic acid fermentation. Previous work suggests that MT1-MMP interacts with hypoxia inducible factor-1 alpha (HIF-1α), a transcription factor which alters the expression of relevant glycolytic proteins. My research uses MCF-7 breast cancer cell lines that overexpress MT1-MMP (C2) or express MT1-MMP lacking its cytoplasmic domain (ΔCD) to evaluate the role of MT1-MMP cytoplasmic domain in aerobic glycolysis. Cells were treated with metformin, a drug known to increase aerobic glycolysis, to assess any changes in growth or metabolism in response to stress. Aerobic glycolysis was highest in C2 cell line, followed by parental and ΔCD cell lines, results that were further amplified upon treatment with metformin. Interestingly, metformin treatment appears to have variable effects on cell growth in each cell line. These results suggest the cytoplasmic domain of MT1-MMP aids in the activation of aerobic glycolysis in MCF-7 cell lines.

10:15 – 10:30, Sunday, March 24th, P&A 36

IDENTIFYING THE CINNAMATE 4-HYDROXYLASE ENZYME FAMILY IN SOYBEAN AND DETERMINING THEIR SUBCELLULAR LOCALIZATION IN NICOTIANA BENTHAMIANA

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Soybean (Glycine max L. Merr.) is a legume that is commonly consumed in many parts of the world and is of great agricultural value. The phenylpropanoid pathway in plants leads to a variety of compounds including isoflavonoids, flavonoids, anthocyanins, proanthocyanidins and lignins. Isoflavonoids are produced in a legume-specific branch of this pathway and plays a key role in nitrogen fixation and plant defense. Human consumption of isoflavonoids is also associated with a variety of health benefits. Cinnamate 4-hydroxylase (C4H) is an enzyme that converts cinnamic acid to p-coumaric acid, one of the early steps in the phenylpropanoid pathway. The objective of this project was to identify the soybean C4H family members and discover their subcellular localization in Nicotiana benthamiana. Subcellular localization was studied by constructing a translational fusion of the candidates to a yellow fluorescent protein (GmC4H-YFP) and transiently expressing them in N. benthamiana leaves, followed by confocal microscopy imaging. Previous studies have shown that two GmC4Hs, GmC4H14 and GmC4H02, localize to the endoplasmic reticulum (ER). In the current study two more GmC4Hs, GmC4H10 and GmC4H20, were identified. GmC4H20 was found to be localized to the ER, whereas the subcellular localization of GmC4H10 is in progress. Understanding the genes involved in the regulation of this pathway will sharpen our knowledge of isoflavonoid biosynthesis in soybeans.

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9:00 – 9:15, Sunday, March 24th, P&A 148

DOES PARKIN REGULATE MITOCHONDRIAL DEGRADATION AND METABOLIC SUPPRESSION IN DIAPAUSING COLORADO POTATO BEETLES?

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Most temperate insects overwinter by entering diapause, a pre-programmed process that favours physiological changes over morphological development. Diapausing insects consistently suppress metabolism to conserve energy stores, but we have a limited understanding of the biochemical mechanisms driving this metabolic suppression. The Colorado potato beetle (CPB; Leptinotarsa decemlineata) suppresses its metabolism by 88% and degrades nearly all mitochondria in its flight muscle during diapause. In this study, we investigated the role of Parkin, a ubiquitin ligase that targets mitochondria for degradation, in regulating mitochondrial degradation and metabolic suppression in diapausing CPB. CPB increase parkin expression during diapause, so we knocked down parkin in diapausing CPB using RNA interference and measured how knockdown affects 1) whole animal metabolic rate using flow-through respirometry, 2) mitochondrial abundance in flight muscle using a citrate synthase enzyme assay, and 3) mitochondrial morphology in flight muscle using transmission electron microscopy. Knocking down parkin in diapausing CPB increases metabolic rate and citrate synthase activity, suggesting Parkin is a key regulator of mitochondrial degradation and metabolic suppression during diapause. This study will help contribute to our understanding of how insects suppress metabolism during diapause, and provide new insights into the mechanisms regulating the diapause phenotype.

9:15 – 9:30, Sunday, March 24th, P&A 148

THE EFFECTS OF TEMPERATURE ON ANOXIA-INDUCED BRAIN SWELLING IN GOLDFISH (CARASSIUS AURATUS)

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Wilfrid Laurier University

Exposure to anoxia can culminate in fatal brain swelling in mammals and lower temperatures seem to attenuate it, but the mechanism behind this anoxia-induced brain swelling is unknown. The present study used goldfish (Carassius auratus) to determine the effect temperature has on brain swelling upon exposure to and recovery from anoxia. To do this, goldfish were acclimated to either 6 °C or 13 °C in the summer of 2018 and were exposed to anoxia for 4, 8, 12 and 24 h, followed by 1 and 12 h recovery. There was an 80% mortality observed after 24 h of anoxia in the 13 °C group, while the 6 °C group had only 20% mortality. In addition, after 12 h of exposure to anoxia, cold-acclimated fish experienced less brain swelling (8.4%) than the warm-acclimated fish (12.8%). Plasma and muscle lactate and ethanol levels increased with exposure to anoxia and remained elevated during the recovery period in both temperature groups. The ethanol levels in the plasma and muscle of the warm-acclimated fish, however, were 1.5 to 2-fold higher than in the cold-acclimated individuals, despite the lactate levels being comparable, suggesting that lower temperatures reduce the ability of the fish to produce ethanol. Therefore, we propose that lower temperatures reduce mortality rates by reducing brain swelling, even though fish appear to be less efficient at producing ethanol under these conditions. We are currently investigating the mechanism behind this temperature-induced reduction in brain swelling.

9:30 – 9:45, Sunday, March 24th, P&A 148

BRAIN SIZE IN BRACHYHYPOPOMUS OCCIDENTALIS FROM PANAMA

MICHEL GROSSAUER[1], L. DE LEÓN[2], M. L. MARTÍNEZ[1]
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2. University of Massachusetts Boston

Allometry is the direct relationship between body size and specific body parts. A significant correlation has been noted between brain size and body size. This allometric relationship can be subjected to environmental pressures creating trade-offs between tissues when a metabolically expensive tissue such as the brain increases in size. In this study, we investigate brain allometry in the electric fish Brachyhypopomus occidentalis from four sites displaying divergent predation risk: Frijolito and Lapuente in the Chagres drainage, and Tumagantí and Tapagrilla in Bayano drainage. Significant differences exist between sites for: body length (TL), body mass (MT), body condition factor (K) and brain mass (BM) [$P< 0.0001$ for TL, BM; $P=0.003$ for MT, K]. Significant differences in brain size were only evident in Bayano sites ($P < 0.0001$), where high predation site (Tapagrilla) displayed lower brain mass than low predation risk (Tumagantí). The overall brain allometry shows a slope of 0.64 which is very close to slope for brain in most vertebrates (0.67). Static allometric slope among adults shows a slope of 0.5. Interestingly little variation was observed based on predation risk ($b= 0.55$ high predation; $b=0.48$ low predation) or sex ($b=0.49$ females; $b=0.55$ males). These results suggest little evolutionary constraints in brain size for this species. Furthermore, it seems that there might be environmental factors related to each drainage contributing to the variation in brain size.

9:45 – 10:00, Sunday, March 24th, P&A 148

CAPACITY FOR PLASTICITY OF CARDIAC PERFORMANCE IN ATLANTIC SALMON PARR, *SALMO SALAR*

Neufeld, S.B., Muir, C.A., Garner, S.R., Neff, B.D.
University of Western Ontario

Environmental temperature is one of the most important ecological factors that affects ectotherms. Ectotherms may respond to environmental temperature through phenotypic plasticity, in which they modify their physiological performance to match the environmental temperatures they experience. However, the timescale over which phenotypic plasticity operates in response to environmental temperature remains largely unexplored. Here, I used Atlantic salmon to test the effect of varying durations of exposure to an elevated temperature on cardiac performance, a key trait influencing aerobic performance. Atlantic salmon parr were exposed to an elevated temperature (+4°C) for 0 days (control), 2 days, 21 days, or 60 days. I then measured maximum heart rate as a function of temperature to generate a thermal performance curve for 10 fish from each treatment. I found a significant positive relationship between the duration of exposure and both the thermal optimum for cardiac performance and the arrythmia temperature at which cardiac function began to fail. However, even after 60 days, the thermal optimum and arrythmia temperatures did not show full compensation as the increase in each of these measures was only about 2°C, which was half of the change in exposure temperature (+4°C). My results suggest that phenotypic plasticity cannot provide full recovery of cardiac performance over the temperature range and duration that I tested.

10:00 – 10:15, Sunday, March 24th, P&A 148

METABOLIC COSTS OF FREEZING AND RECOVERY IN THE SPRING FIELD CRICKET, GRYLLUS VELETIS

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Freeze tolerant insects can survive a significant portion of their body water being converted to ice, presumably through a greater capacity to prevent or recover from freeze-induced damage. Previous studies suggest that the processes of freezing and thawing do not induce active metabolic responses from freeze-tolerant insects, but the physiological mechanisms underlying recovery from freezing and thawing are poorly understood. I used the spring field cricket (Gryllus veletis) as a model of freeze-tolerance to measure metabolic rate during freezing or thawing and the time course of energy expenditure during recovery. Using respirometry, I continuously measured carbon dioxide (CO2) production by G. veletis as a proxy for metabolic rate during cooling, freezing and thawing. I observed a steep, transient increase in CO2 production at the onset of freezing in all crickets, including crickets that had been killed by cyanide. I interpret these results as evidence that freezing and thawing are likely passive process, and that the expulsion of CO2 is the result of the expansion of water in the haemocoel upon freezing. By comparing the metabolic rates of crickets that had been frozen to those that had been chilled (but not frozen), I determined the metabolic costs associated with recovery from freezing and chilling. Understanding the metabolic costs associated with recovery from freezing can provide insight into the mechanisms underlying insect freeze tolerance.

10:15 – 10:30, Sunday, March 24th, P&A 148

THE EFFECT OF ELEVATED REARING TEMPERATURE ON GILL MORPHOLOGY IN JUVENILE ATLANTIC SALMON (SALMO SALAR)

Wise, R.A., Muir, C.A., and Damjanovski, S.
University of Western Ontario

Average global air temperatures are expected to increase by 4°C by the end of the century. With the decrease in oxygen solubility as temperatures rise in aquatic environments, aerobic activity of cold-tolerant ectotherms such as Atlantic salmon are constrained. Salmon populations experiencing peak summer temperatures close to their upper thermal limits may become threatened. In this study, we focused on elucidating the effect of increased rearing temperature on gill morphology in juvenile Atlantic salmon raised in present-day (+0°C) or future (+4°C) temperature conditions. Parr were euthanized with a lethal dose of MS-222, weighed for body mass, measured for fork length, and tail removed for blood collection for hematocrit measurements. The dissected specimen was placed in 10% formalin for approximately 5 days, then moved to 70% ethanol for storage. Dissected specimens were sectioned and stained with hematoxylin and eosin for gill morphometric analysis. The greatest effect of elevated rearing temperature was seen throughout the interlamellar cell mass (ILCM) with decreased mass in the +4°C treatment. Gill filament length, number of primary lamellae and mean primary lamellae length did not significantly differ between the two treatment groups. Hematocrit measurements did not reveal significant differences of oxygen carrying capacity. These results indicate the greatest plasticity to allow for increased oxygen uptake at the gills in elevated temperatures is seen at the ILCM.

Physiology and Biochemistry E
PHYSICS & ASTRONOMY BUILDING, RM 106

9:00 – 9:15, Sunday, March 24th, P&A 106
THE EFFECTS OF WESTERN DIET IN UTERO AND POSTNATALLY ON HEPATIC MITOCHONDRIAL FUNCTION IN GUINEA PIGS

Barbu, E. A. [1], Regnault, T. R. [2], Staples, J. F. [1], Mathers, K. E. [1]
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The supply and quality of nutrients provided to the fetus during gestation can dictate the later-life metabolic health of the offspring. The consumption of a high-fat, high-sugar diet, known as the Western diet (WD) is highly prevalent in North American humans and is linked to the development of metabolic disorders. A central organelle in metabolism is the mitochondrion and its activity can be impaired by consuming WD maternally and postnatally. The aim of this study was to determine how maternal and postnatal Western diet affect hepatic mitochondrial function in 8-month old male guinea pigs. I hypothesized that the consumption of Western diet during gestation or postnatally or both, will decrease the expression and activities of complexes I – IV. Eight sets of female guinea pig twins were weaned onto either an energy-dense Western diet or a control diet (CD) and then mated to control males. The resulting male offspring were then weaned onto either a control or Western diet which generated four experimental groups: CD-CD, CD-WD, WD-CD, WD-WD, where the first and last two letters denote the diet of the mother and the offspring respectively. I found that the activity of complex I significantly decreased in WD-WD guinea pigs. Interestingly, postnatal diet had a significant effect on complex I activity. It was also found that complex I protein expression increased in WD-CD guinea pigs. Finally, increased liver to body mass ratios were observed in CD-WD and WD-WD offspring.

9:15 – 9:30, Sunday, March 24th, P&A 106
CAN BIRDS CARB LOAD? USING STABLE ISOTOPES TO DETERMINE THE EFFECTS OF DIET ON PREFERENTIAL FUEL USE IN THE YELLOW-RUMPED WARBLER (SETOPHAGA CORONATA CORONATA)

Denomme, M. R., Guglielmo, C. G., Jessica, D. E.
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Human athletes have been eating a high carbohydrate diet before exercise, otherwise known as “carb loading”, to improve exercise endurance by increasing glycogen stores. However, when it comes to feats of exercise endurance, migratory birds are in a league of their own. Birds have maximal metabolic rates several times higher than comparable mammals, and may sustain it for days while migrating. They can put on 50% of their body weight as fat prior to departing, which may be partly accomplished by shifting to a more frugivorous diet. Indeed, it is well established that fat is the primary fuel source for migration, but migrating birds also lose protein during flight, and it is unknown how diet may alter fuel use. Using plasma metabolites, several studies found conflicting results on how diet effects preferential fuel use between and within species, but plasma metabolites may not be directly related to flux. In contrast, stable isotopes have been used to reliably study nutrient oxidation. Using technology that allows the analysis of stable isotopes in real time, this study employed artificial enrichment to examine nutrient oxidation in yellow-rumped warblers fed a high carbohydrate or high protein diet. When administered via gavage, a greater amount of tracer was oxidized, but peak oxidation was reached significantly later than administration via injection. In birds given enriched leucine, those on a high protein diet showed altered cumulative oxidation.

9:30 – 9:45, Sunday, March 24th, P&A 106

ALARM CUE STIMULATION OF GILL PORE PAPPILLAR CHEMOSENSORY RESPONSES IN THE ADULT SEA LAMPREY (PETROMYZON MARINUS)

Gatti, D.M.
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In the diffuse chemosensory system, there are spindle shaped epidermal cells, innervated by single nerve fibers. In the sea lamprey (Petromyzon marinus), innervated solitary chemosensory cells are located on the oral disc, nasal pore, gill pores and the dorsal fin papillae. The functionality of the chemosensory responses within this adult lamprey's diffuse chemosensory system is unknown. One hypothesis is that these chemosensory fibers are associated with detecting danger. Alarm substances can be utilized by the sea lamprey to navigate from harm. The alarm cueing molecules in this experiment were derived from dead sea lamprey skin and have been separated into isolates of recognizable compounds: creatine, inosine and hypoxanthine. This study investigates the activity of the gill pore chemosensory fibers after the application of alarm substances. Electrophysiological recordings detect and measure the frequency of action potentials taken from the chemosensory fibers. The results show, that action potential frequency increased during the application of each of these three alarm substances. This suggests that the chemosensory cell fibers on the gill papillae may serve a function in detecting danger. This adaptive, evolutionary mechanism is important for the fitness of adult sea lampreys. This research may be applied to population control within the Great Lakes fishing industry and help with behavioural studies.

9:45 – 10:00, Sunday, March 24th, P&A 106

UPTAKE AND TRANSLOCATION OF CADMIUM IN SOYBEAN (GLYCINE MAX) IN RESPONSE TO SULFUR ADDITION

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Cadmium (Cd) is a toxic metal that is increasing in concentration in agricultural soil due to anthropogenic activity (industrial waste, impure fertilizers, etc.). Contaminated crop plants could be ingested, resulting in possible health issues for humans and other consumers. Many studies have been done on the positive effects of sulfur (S) in reducing Cd uptake and translocation in rice (Oryza sativa). However, the extent to which this phenomenon applies to other crop species is unknown. This study examined the effects of exogenous S supply on Cd uptake and translocation in soybean (Glycine max). Plants were grown in nutrient solution with two concentrations of Cd (0 and 20 uM) and three concentrations of S (0, 2.5, and 5 mM). Total Cd in roots and shoots was measured, and the localization of Cd in root cross sections was examined using histochemistry. Sulfur addition decreased amounts of Cd taken up by roots from about 50 to 2 ug per plant, likely due to the formation of plaques on the root surface. Within S-treated root cross sections, more Cd was localized at the exodermis, less Cd was in the stele, and Casparian bands were thicker. These patterns suggest reduced opportunity for Cd to enter the xylem and to be translocated aboveground. However, although exogenous S resulted in less Cd uptake by soybean plants, proportionately more of the Cd was translocated to the shoots. Soybean is therefore an unsuitable crop for growth on Cd-contaminated soils, even with exogenous S.

10:00 – 10:15, Sunday, March 24th, P&A 106

EFFECT OF DIET MANIPULATION AND WING MORPHOLOGY ON BURST FLIGHT PERFORMANCE IN YELLOW-RUMPED WARBLERS (SETOPHAGA CORONATA CORONATA)

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Optimal burst flight performance is crucial for bird survival. Also called predator avoidance flight, it allows birds to swiftly take off when they are attacked. The ability to take off is affected by various factors, such as body composition and wing morphology. Previous studies have shown a decrease in take-off flight velocity with larger fat loads – however, during migration, birds need to accumulate extra fat in order to fuel their migratory flight. Diet

changes associated with migration could also alter take-off flight performance by changing muscle fuel metabolism. To test the effect of diet on burst flight performance, we conducted a repeated-measures experiment with yellow-rumped warblers. Birds were acclimated for 2 weeks to a high carbohydrate diet or high protein diet and then burst flight performance was measured using a motion-triggered vertical flight tower. Following this, the birds were acclimated to the opposite diet and burst flight performance was measured again. Quantitative magnetic resonance was used prior to each flight test to determine fat and lean mass. We found that birds had greater body mass, fat mass and lean mass on the high carbohydrate diet. However, despite being heavier, their take-off velocity was not significantly different than when on the high protein diet. Our findings suggest that birds may pay no cost to take-off flight performance from increased body mass during migration because they compensate by increasing flight muscle size.

10:15 – 10:30, Sunday, March 24th, P&A 106

STUDYING THE IMPACT OF PHOTOPERIOD AND FEEDING TIME ON CIRCADIAN RHYTHMS IN CHINOOK SALMON

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In animals, a molecular system known as the circadian clock is used to regulate physiological processes. These processes occur over a 24-hour period and can be synchronized by external cues such as photoperiod and food consumption. The circadian clock creates fluctuations in gene expression whose output results in daily processes such as waking/sleeping, eating and digestion, and metabolism and hormone secretion.
The purpose of this project is to determine the impact of photoperiod and feeding time on intestinal circadian rhythms in Chinook salmon, a wide-ranging Pacific fish species of ecological and economic importance. To test this, salmon were raised in two conditions: one group was raised in 16 hours of light and 8 hours of dark (16:8 LD), and another group was raised in all light (LL), with both groups being fed at 5 pm. Quantitative polymerase chain reaction was used to determine the gene expression of four circadian genes, and two control genes. Two other colleagues in my lab tested additional photoperiod and feeding schedules to establish an overview of how the circadian clock is regulated by these conditions.
We found that the circadian clock functions in an unexpected, synchronous fashion in the intestine. Findings from this study may provide insights on the role of the circadian clock in the intestine, as well as on how environmental cues affect the physiology of Chinook salmon to improve aquaculture and conservation.

Physiology and Biochemistry F

PHYSICS & ASTRONOMY BUILDING, RM 150

9:00 – 9:15, Sunday, March 24th, P&A 150

THE ROLE OF ENHANCER OF ZESTE HOMOLOG 2 (EZH2) IN REGENERATION OF ADULT ACINAR CELLS FOLLOWING CERULEIN-INDUCED PANCREATITIS IN MICE

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1. University of Western Ontario
2. Children’s Health Research Institute

Pancreatitis involves inflammation of the pancreatic tissue due to premature activation of digestive enzymes. If the inflammation is not resolved, damage progresses, causing destruction of the acinar cell and acinar to ductal metaplasia (ADM). Maintained ADM, seen in chronic pancreatitis and pancreatic cancer, potentially occurs through epigenetic silencing. Our laboratory studies Enhancer of Zeste Homolog 2 (EZH2), which methylates histones through its SET domain. EZH2 is expressed at high levels during pancreatic injury and upregulated in 70% of pancreatic cancers. Conversely, previous studies examining Ezh2 deletion in embryonic development show that EZH2 is required for pancreatic regeneration following injury. The goal of this project was to determine the requirement of EZH2 in regeneration from adult acinar cells. Recurrent pancreatic injury was induced in wild-type mice and mice allowing for inducible deletion of the SET domain within EZH2 (EZH2ΔSET). 7 days after cessation of injury, histological staining and gene expression analysis was performed. Wild-type and EZH2ΔSET mice showed equivalent acinar tissue, suggesting that EZH2 is not required for pancreatic regeneration. Immunofluorescence, immunohistochemistry, and protein analysis also suggested that factors that promote (SOX9) or prevent (MIST1 and amylase) ADM formation were not altered by EZH2 loss. Combined, these results suggest that EZH2 is dispensable for acinar cell regeneration in adult tissue.

9:15 – 9:30, Sunday, March 24th, P&A 150

UBISOL-Q10 (A NANOMICELLAR WATER-SOLUBLE FORMULATION OF COQ10) SUPPLEMENTATION REDUCES BEHAVIOURAL AND PATHOLOGICAL SYMPTOMS IN DOUBLE TRANSGENIC MOUSE MODELS OF ALZHEIMER'S DISEASE

Culmone, L., Vegh, C., Wear, D., Huggard, R., Okaj, I., Pandey, S., Cohen, J.
University of Windsor

Alzheimer's disease (AD) is the most common neurodegenerative disorder and is characterized by the progression of debilitating symptoms which affect the daily lives of those afflicted. Despite extensive research, an effective treatment for AD which halts its neurodegenerative progression has yet to be discovered. Due to the rapidly aging global population, the prevalence of AD is increasing dramatically and, therefore, the discovery of a treatment is imperative. Although the molecular mechanisms of AD are not fully understood, mitochondrial dysfunction, oxidative stress, and dysfunctional protein accumulation are known to be involved in its pathology. It has previously been demonstrated that a water-soluble formulation of Coenzyme Q10 (Ubisol-Q10), an integral part of the election transport chain, stabilizes mitochondria and prevents neuronal death by reducing free radical generation. In the present study, researchers report that providing Ubisol-Q10 (~6 mg/kg/day) to transgenic mouse models of AD (TgAPEswe, PSEN1E9) reduced circulating amyloid-β peptide and amyloid-β plaques, increased microglia activation, and upregulated Beclin-1, a regulator of autophagosome formation. The Ubisol-Q10 treated mice also showed improved long-term memory and working spatial memory. These results provide evidence that Ubisol-Q10 supplementation has the potential to reduce neurodegeneration in patients with AD, which could lead to a better quality of life for those living with this disease.

9:30 – 9:45, Sunday, March 24th, P&A 150

EVALUATING THE EFFICACY OF ETHANOLIC LEMONGRASS EXTRACT (CITRATUS CYMPBOPOGON) IN TREATMENT OF COLON CANCER AND DRUG-DRUG INTERACTIONS OF LEMONGRASS EXTRACT AND CHEMOTHERAPEUTICS FOR TREATMENT OF COLON CANCER

Scaria, B., Ruvinov, I., Nguyen, C., Baskaran, K., Zaitoon, O., Vegh, C, Pandey, S.
University of Windsor

Cancerous cells have certain vulnerabilities that can be targeted by therapeutic cancer treatments. Chemotherapeutics, which are conventional treatments for a wide range of cancers exhibit toxicity towards non-cancerous cells, which cause a plethora of side effects that reduce the patient’s quality of life. Natural extracts have been shown to selectively target cancerous cells. Specifically, we have shown that lemongrass extract (Cymbopogon citratus) can induce apoptosis in in-vitro and in-vivo leukemia and lymphoma models. Ethanolic lemongrass extract is investigated here for its efficacy and anti-cancerous properties in colon cancer models. Cell viability was reduced after treatment with varying concentrations of ethanolic lemongrass extract, without a negative effect on a non-cancerous colon cancer cell line. Drug-drug interactions between lemongrass extract and chemotherapy drugs, namely FOLFOX (5-fluorouracil, folinic acid and oxaliplatin) and Taxol, were not disruptive, showing that cell death either remained the same or was slightly increased in combination treatment groups compared to individual treatment groups. Further research is being conducted to elucidate the mechanism of apoptosis induction, specifically looking at reactive oxidative stress (ROS) production, activation of the caspase pathway, and mitochondrial membrane potential.

9:45 – 10:00, Sunday, March 24th, P&A 150

THE POTENTIAL FOR DNA DAMAGE EFFECTS IN HIV ANTIRETROVIRAL THERAPY

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1. Department of Chemistry and Biology, Ryerson University, Toronto, ON.
2. Toronto General Research Institute, Department of Immunology, University of Toronto, Toronto, ON.

Individuals infected with the Human Immunodeficiency Virus (HIV) rely on combination antiretroviral treatment (cART). cART is essential to manage HIV symptoms and delay disease progression into Acquired Human Immunodeficiency Syndrome (AIDS). Antiretrovirals in cART target at least 2 steps of the HIV replication process. The World Health Organization (WHO) recognizes several classes of antiretrovirals, including: virus fusion and entry inhibitors, viral transcriptase inhibitors, viral integrase inhibitors, and viral protease inhibitors. WHO guidelines recommend that at least 2 different classes of antiretroviral are given as cART following patient diagnosis. Although cART is lifesaving, it is not without side effects. Previous research in the Serghides lab has shown that protease inhibitors used during pregnancy increase the risk of adverse fetal outcomes.

Our current study uses a mouse model to examine the long-term effects of cART exposure in utero on male fertility. We are examining DNA damage effects on sperm nuclei using toluidine blue to test chromatin compaction. DNA breaks are detected using the terminal deoxynucleotidyl transferase-mediated deoxyuridine triphosphate nick end labeling (TUNEL) assay.

Science Education A
PHYSICS & ASTRONOMY BUILDING, RM 117

9:00 – 9:15, Sunday, March 24th, P&A 117

HOW FEAR OF FAILURE AFFECTS STUDENTS' ATTITUDE TOWARDS LEARNING

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Fear of failure may be perceived positively or negatively, as it may drive some students to achieve success in the face of challenges whereas it may render others vulnerable to setbacks, preventing them from succeeding academically. The goal of this study was to provide first-year students with a chance to reflect on their attitudes towards fear of failure. The Quadripolar Model was used to frame these reflections, as it illustrates different attitudes towards fear of failure which can affect the academic performance of students. A pre-designed 13-item survey was used to gain insights into the students' understanding of the model and to compare the attitude they manifest. The first part of the survey questions students' perception of fear of failure, followed by an introduction of the model in a 4-minute video. The last part asks students to identify themselves with one of the four attitudes. The comparison of their answers from the first and last parts will be used to see whether the students' perception align with the attitude they possess. We expect to have an even distribution of students identifying among the four attitudes and a vast majority identifying themselves correctly. Introducing this model will allow students to understand how fear of failure affects their academic performance, as they will be able to apply this knowledge to many different courses. This model may help them develop strategies to cope with fear of failure and transform it into a positive factor.

9:15 – 9:30, Sunday, March 24th, P&A 117

DEVELOPING CAREER RESOURCES FOR BIOLOGY UNDERGRADUATE STUDENTS

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University of Toronto Mississauga Department of Biology

Undergraduate students in biology have a limited understanding of the breadth of careers available to them. Incoming students are often focused on Medicine as a career and this goal may narrow their focus and course choices during their biology degree. Additionally, students may not broaden their career goals or gainfully employ the resources available to them via the Career Centre until late in their undergraduate degree. As of 2016, 7.1% of Biology majors in Ontario remain unemployed while 21.8% have switched into different fields. Professors, having highly focussed careers and knowledge-bases are not best placed to comment on the breadth of the opportunities in the job market. In contrast our Alumni can be helpful in guiding students to make better career decisions by giving insights into their chosen careers, the skills required for them, and lessons learnt from their academic experience. For this purpose, we interviewed University of Toronto Biology Alumni. We divided alumni into two groups, academic and industry-professionals. We presented the same set of questions to all the alumni and recorded their responses in written and in video format. The content was edited together to create a stimulating and engaging video series to be presented to the target audience of biology undergraduate students.

9:30 – 9:45, Sunday, March 24th, P&A 117

EFFECTIVENESS OF VIDEOS USED AS A PEDAGOGICAL TOOL TO TEACH BASIC LABORATORY STATISTICS

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Textbook teaching, used by instructors globally, is an exclusive pedagogical method, yet is a very conventional approach to education. In a survey conducted with science students at Ryerson University, 24% of students agreed that they would prefer to read the textbook rather than use other external sources to supplement their learning. Instead, it was found that 79% of students use online formats to watch videos on topics they need extra information on. With such a high proportion of students already depending on videos as an additional knowledge source, the act of implementing videos in classroom has great potential to be an effective pedagogical tool for teachers. The objective of this project is to measure the effectiveness of a video as a pedagogical tool in lab, specifically to teach basic statistics. A 5-minute animated video was produced using VideoScribe that highlighted key statistical terms and applications. This video was played once for the first lab and only in half of the sections. Grades of the first lab reports were analyzed with a Kruskal-Wallis test to determine differences in grade. The results confirm the effectiveness of videos for the first lab report, which required to students to perform calculations and analyze data. Overall, the difference in final grades in the laboratory component was significant between the two sections as well, and our statistical analysis confirms that video implementation is a highly probable factor for this difference.

9:45 – 10:00, Sunday, March 24th, P&A 117

INCORPORATING VIDEOS AS A PEDAGAGICAL TOOL IN UNDERGRADUATE BIOLOGY LABORATORIES

Ridgeway G.R*, Puddephatt K.J, Laursen A.E, de Araujo C.
Ryerson University

Science students often learn and reinforce concepts in a variety of ways. As science students begin to do more laboratory based work, reinforcing key concepts is essential to develop practical skills. The current method of introducing students to many laboratory topics such as Good Laboratory Practice; How to use a microscope? and Preparing a wet mount slide, are predominantly based on reading manuals and watching a demonstration from their laboratory supervisor. However, we would like to provide additional resources to help students with these core concepts. For this reason, detailed videos were created for students demonstrating proper laboratory techniques. In order to evaluate the effectiveness, a Likert-type evaluation was given to students after they had both reviewed the manual and viewed the video resources. Student performance (based on grades) in the laboratory component in first and second year biology courses was higher with supplemental resources compared to previous offerings. Based on the observations and feedback, further videos may be produced to cover other topics of interest related to the laboratory component.

10:00 – 10:15, Sunday, March 24th, P&A 117

CAN FIRST YEAR NON-MAJOR BIOLOGY STUDENTS ACCURATELY PREDICT THEIR ABILITY TO APPLY THE SCIENTIFIC METHOD? EXPLORING THE CORRELATION BETWEEN METACOGNITION AND DISCIPLINE-BASED LEARNING.

Shaikh, S. [1], Jenne, A. [2], Sadeghi, Y. [1], Ashok, A. [1]
1. Department of Biological Sciences, University of Toronto Scarborough.
2. Department of Chemistry, University of Toronto Scarborough

Metacognition is defined as the ability to be aware of one's own cognitive processes. Metacognitive development is linked to students' ability to better monitor and regulate their learning, and is hence a strong predictor of academic success(1,2). The goal of our current study is to explore the correlation between students' self-reported abilities (indicative of metacognition) and a measurement of their abilities using a scored problem. Our study population are students enrolled in a non-biology majors, who represent a unique demographic compared to all other courses offered by the department of Biological Sciences at our institution. Consistent with previous studies, we found a positive correlation between students who self-reported higher confidence ratings with their ability to accurately apply the scientific method in the scored problem. We further explored other demographic factors that may influence students' self-reported abilities. The outcomes of this study allow us to understand the factors that influence metacognitive development of non-majors students, which could be used to create course environments and resources that promote student learning.

10:15 – 10:30, Sunday, March 24th, P&A 117

STUDENTS' PERCEPTIONS OF THE PEER REVIEW PROCESS IN ACADEMIC WRITING IN A SECOND-YEAR UNDERGRADUATE SCIENCE COURSE

Tu, J.K.
University of Western Ontario

Most research manuscripts undergo peer review prior to publication; however, the peer-review process remains an underused tool in undergraduate science education. This underuse may be because students are unwilling to participate in peer review. Students having a positive perception of the peer-review process—specifically, believing peer review is useful—is critical for successful integration of peer review in undergraduate courses. To explore current students' perceptions of the peer-review process for reviewing written work, I surveyed students in a second-year undergraduate scientific methods in biology course before and after they participated in an in-class peer-review session. This study aims to identify aspects of the peer-review process that require improvement to increase successful implementation of peer review in undergraduate education. Students' perceptions before and after completing the in-class peer review will be compared to identify aspects of the peer-review process that correlate with students' positive or negative perceptions of peer review. Preliminary data indicate an overall positive perception of the peer-review process. This study seeks to identify the degree to which reviewer identity (i.e. friend or non-friend), perceived qualification of peer reviewer, and number of reviewers influences students' perceptions of peer review usefulness.

Sunday March 24th 2019

Concurrent Session IV 11:00 – 12:00

Cell and Molecular Biology L
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 0153

11:00 – 11:15, Sunday, March 24th, B&GS 0153
CHASING THE NEUROLIGINS: QUANTIFICATION OF LOW COPY TRANSCRIPTS IN DROSOPHILA MELANOGASTER
Brown, L.P., Yost, R.T., Simon, A.F.
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The Neuroligin (NLG) family of postsynaptic cell adhesion molecules has a conserved role in the modulation of social behaviour in many species, including humans, mice, honey bees, and in the fruit fly, *Drosophila melanogaster*. In honey bees, *neuroligins* are responsive to changes in the social environment, though this effect has yet to be investigated in the fruit fly. To measure the expression of these gene homologs in *D. melanogaster*, primer sets for *nlg1–nlg3* were successfully designed for use in reverse transcriptase quantitative PCR (RT-qPCR). The variation between threshold cycle values of technical replicates was too great for accurate quantification of the *neuroligins* using RT-qPCR, likely due to low transcript abundance. To measure these low copy transcripts, a different technology was deployed: droplet digital PCR (ddPCR). Preliminary ddPCR data of adult *D. melanogaster* head cDNA reveal an approximately 1000-times lower transcript abundance of *nlg3* relative to the housekeeping gene *RpL32*. Methods used to troubleshoot RT-qPCR and the molecular mechanisms underlying ddPCR will be described. Future work will involve using ddPCR to quantify the expression of *nlg1–nlg3* in D. melanogaster in response to changes in the social environment.

11:15 – 11:30, Sunday, March 24th, B&GS 0153
DETERMINING GENETIC INTERACTIONS WITH NSF IN DROSOPHILA MELANOGASTER
Kaushal, A.
Department of Cell and Systems Biology, University Of Toronto Mississauga, Mississauga, ON, L5L 1C6

N-ethylmaleimide sensitive factor (NSF) is one of the most important molecules involved in molecular signaling. It allows for the reuse of SNARE proteins by disassembling the cis-SNARE complex that is formed after vesicle fusion. Understanding the genetic interactions between NSF and various other genes may provide a deeper understanding of some important signaling pathways, such as Wingless and Notch. In Drosophila melanogaster, disruption of the dNSF2 gene leads to a notched-wing phenotype. In this study, I conducted a screen to find suppressors of the wing phenotype. Through deletion interactions and gene mapping I found that mutants in the gene Lethal (2) giant larvae suppress the dNSF2 wing phenotype. This result reveals a novel genetic interaction and provides insights into dNSF2 function.

11:30 – 11:45, Sunday, March 24th, B&GS 0153
THE ROLE OF FRUITLESS P3 AND P4 TRANSCRIPTS IN DROSOPHILA MELANOGASTER
Kulinski, S.A., Moehring, A.J.
University of Western Ontario

The well-studied fruitless gene is highly conserved across many insect species. The role of fruitless in sex determination and sexual behaviour in males has been extensively explored, but little is known about the role of this gene in other traits. In Drosophila melanogaster, fruitless transcripts are composed of one of five alternative first exons (P1-P5), a central common set of exons, and one of three alternative final exons (A, B, C). This alternative splicing gives rise to 15 known alternative transcripts. Transcripts containing the P1 first exon have been the most heavily studied, as these transcripts are involved in courtship and sex determination. In contrast, very little is known about the role of transcripts starting with the P3 and P4 first exons other than their inviability when both transcripts are simultaneously disrupted. While the individual functions of transcripts P3 and P4 are unknown, it is hypothesized that they may play a role in the viability, development, locomotion, or mass of D. melanogaster. Through the use of RNA interference (RNAi), I generated flies with a knockdown of either P3 or P4 transcripts. I scored developmental time, climbing ability, and dry mass to determine whether the individual functions of P3 or P4 transcripts affect these general fitness traits. The results from the three aforementioned assays and conclusions will be presented.

11:45 – 12:00, Sunday, March 24th, B&GS 0153

DETERMINING THE ROLE OF DOPAMINERGIC FRUITLESS NEURONS ON THE SOCIAL SPACE OF DROSOPHILA MELANOGASTER

Stewart, M. P, Simon, A. F.
University of Western Ontario

Behaviour is an individual’s response to internal or external stimuli. It is dependent on the internal state of the individual and is influenced by the environment. Social space is a measurable characteristic of social behaviour that enables the identification of underlying genetic mechanisms responsible for behaviour. Responses to internal or external stimuli have been previously observed to be sexually dimorphic, however the genetic mechanisms and neural circuitry involved are currently unknown. Alterations of both neurons expressing the transcription factor Fruitless and those that are dopaminergic have elicited sexually dimorphic social behaviour. In addition, there is evidence that a subset of dopaminergic neurons express the gene fruitless. It is hypothesized that the manipulation of dopamine in fruitless-expressing neurons will affect the social space of Drosophila melanogaster. I have used the Gal4/UAS system to drive a tyrosine hydroxylase (TH) RNAi knockdown in fruitless-expressing neurons, in order to reduce dopamine synthesis where fruitless is being expressed. Social space assays of these transgenic flies have given insight into the likelihood of dopamine playing a role in the mechanisms behind sexually dimorphic social space.

Ecology and Evolution K

BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 0165

11:00 – 11:15, Sunday, March 24th, B&GS 0165

EXPLORING COMPETING THEORIES OF THE ORIGINS OF THE GENETIC CODE THROUGH STATISTICAL ANALYSIS

Sacka, N., Stone, J.
McMaster University

How did the standard genetic code evolve to its current form? Two prominent theories about its evolution exist; one, the four-column theory, suggests that the standard code gave was arranged so the physicochemical properties of the amino acids were least disturbed by mutations, while the other, co-evolution theory, proposes that as amino acids diversified, they took some of the codon domain from their precursor amino acids, eventually leading to the standard genetic code. This thesis takes a statistical approach to determine which theory, if any, is more likely to have resulted in the standard genetic code. 10,000 alternative genetic codes that could have arisen according to each theory were created, and the values for certain amino acids properties were calculated. It was found that for almost all of the examined properties, the standard genetic code’s values fell outside of one standard deviation from the values of the codes created by either theory. The only exception was polar requirement, for which the standard genetic code scored within one standard deviation of the mean for the four-column theory.

11:15 – 11:30, Sunday, March 24th, B&GS 0165

PROBLEM-SOLVING IN BLACK-CAPPED CHICKADEES, *POECILE ATRICAPILLUS*, ACROSS AN URBANIZATION GRADIENT ALONG THE CREDIT RIVER OF MISSISSAUGA, ONTARIO

Crozier, A.C., Hinić-Frlog, S.H.F.
University of Toronto

Birds exhibit various morphological, physiological, and behavioural responses to urbanization. To date, most work related to urbanization and avian problem-solving focused on laboratory trials of captive individuals. We instead conducted a field observational study where we assessed problem-solving of black-capped chickadees, *Poecile atricapillus*, across an urbanization gradient. If urbanization affects problem-solving in chickadees, we expected that individuals in urban areas will solve more problems and more quickly than individuals in non-urban areas. We conducted field observations in four different sites (n=15-35) along the Credit River of Mississauga, Ontario, while exposing chickadees to a novel foraging innovation task. This innovation task consisted of an inverted test-tube blocked by a cotton ball, filled with seeds, and clamped to a bird feeder pole. We observed individuals at each location for a 30-minute period during which we measured problem-solving latency and number of problem-solving attempts. Our preliminary data indicate that chickadee populations at urban sites showed both a greater average number of problem-solving attempts and the only single successful problem-solving event. This provides support for the hypothesis that urbanization affects problem-solving in chickadees.

11:30 – 11:45, Sunday, March 24th, B&GS 0165

SEX-SPECIFIC PERFORMANCE OF AN ALLOCENTRIC SPATIAL MEMORY TASK IN BROWN-HEADED COWBIRDS

Huang, N. [1], Brodbeck, M.I.R. [2,3], MacDougall-Shackleton, S.A. [2,3]
1. Department of Biology, University of Western Ontario
2. Department of Psychology, University of Western Ontario
3. Advanced Facility for Avian Research, University of Western Ontario

Spatial memory is the encoding, consolidation, and retrieval of information relating to space. Spatial information within an environment can be categorized into geometric and featural cues. Brown-headed cowbirds (*Molothrus ater*), an obligate generalist brood parasite, exhibits sex-specific differences in spatial memory performance. However, it is unclear whether female cowbirds outperform their male counterparts by using more geometric or featural cues. We examine sex-specific differences in brown-headed cowbirds' reliance on geometric and featural cues when relocating a food reward. We investigated the allocentric spatial memory performance of three male and four female brown-headed cowbirds within a rectangular arena, in which the presence of geometric and featural cues were manipulated. Preliminary analyses show no significant difference in spatial memory performance between male and female cowbirds in the two testing conditions, regardless of the presence of geometric and featural cues. The results from this study reinforce the notion that differences in spatial memory performance between male and female brown-headed cowbirds vary depending on the type of task.

11:45 – 12:00, Sunday, March 24th, B&GS 0165

IDENTIFYING SITES OF PRODUCTION OF WATERFOWL HUNTED IN THE GREAT LAKES REGION, USING STABLE HYDROGEN ISOTOPES.

Wojtaszek, D., Rubin, B.D., Hobson, K.A.
Department of Biology, University of Western Ontario

To develop efficient conservation and management plans for migratory waterfowl, linkages between sites of production and where individuals are harvested are required. Unfortunately, this is extremely difficult using conventional techniques such as mark-recapture via leg bands. The measurement of naturally occurring stable isotopes of hydrogen (2H/1H; δ2H) in bird feathers provides a means of inferring origins in North America. This approach was taken to describe the origins of 9 waterfowl species hunted throughout the Great Lakes region (Wood Duck, Green-winged Teal, American Wigeon, Gadwall, Lesser Scaup, Greater Scaup, Redhead, Northern Pintail, Common Goldeneye). Two species with a larger sample sizes, Wood Duck and Green-winged Teal, were separated

by age and sex to investigate differential migration. Only one species was produced in the Great Lakes region (Common Goldeneye) and one species was produced in Atlantic Canada (Greater Scaup). The rest of the study species hunted in the Great Lakes were produced elsewhere, especially the Canadian prairies and throughout the Canadian boreal forest region of the Yukon and Northwest Territories. There was no evidence of differential migration in Green-winged Teals. The δ2H of adult male Wood Duck samples was significantly higher from female and juvenile samples, showing evidence of a moult migration. There was no significant relationship between day that the individuals were harvested and their origin.

Ecology and Evolution L
BIOLOGICAL & GEOLOGICAL SCIENCES BUILDING, RM 1056

11:00 – 11:15, Sunday, March 24th, B&GS 1056

HABITAT, SEASON, AND VOCAL BEHAVIOUR OF NOCTURNAL BIRDS IN A NEOTROPICAL DRY FOREST

Begin-Dyck, H.R., Owen, C.K., Mennill D.J.
University of Windsor

Neotropical dry forest has experienced dramatic habitat fragmentation. This is due to many anthropogenic impacts, including cattle ranching and climate change. By defining relationships between the behaviour of species within tropical dry forests and habitat condition, we can better restore them following these impacts. Since they are cryptic, nocturnal species can be overlooked in such studies of animal communities. Bioacoustic approaches are an effective way to study vocalizations of nocturnal animals that are difficult to detect under cover of darkness, especially birds. The goal of our research is to assess if the vocal behaviour of nocturnal birds in dry forest is affected by seasonal conditions and forest complexity using bioacoustic methods. Our study site, Sector Santa Rosa of the Guanacaste Conservation Area, Costa Rica, is a mosaic of dry forest sites differing in age. We collected data using autonomous recording units during dry and wet seasons. We annotated recordings from 20 sites and identified all species that vocalized between dusk and dawn at each site and for each season. Our data suggest there is variation in the number of species that make nocturnal vocalizations, including some diurnal species. Future research should examine nocturnal vocalizations made by diurnal birds, and why different diurnal species might vocalize at night. Our findings will further our understanding of the vocal behaviour of nocturnal birds in tropical dry forest.

11:15 – 11:30, Sunday, March 24th, B&GS 1056

MODELLING SONG ASSIMILATION AND TRANSMISSION IN WHITE-THROATED SPARROWS (*ZONOTRICHIA ALBICOLLIS*)

Ching, B.J., Ramsay, S.M.
Department of Biology, Wilfrid Laurier University

Historically, the white-throated sparrow (*Zonotrichia albicollis*) has been known to sing a triplet-ending song, but recently, a novel song variant – the doublet-ending song - has emerged, resulting in clinal song variation originating west of the Canadian Rockies, migrating eastward at a rate of approximately 200 kilometers per year. White-throated sparrows are wide-spread and well-studied songbirds, however little is known about the song-learning process in this species. This study aims to explore the nature of song learning of the doublet-ending song at the local scale and investigate changes in representation of terminal strophe types using four different probability-based models based on different song sources: tutoring by neighbouring males, tutoring by fathers, tutoring on the wintering grounds and improvisation. Simulated data was then compared to field data collected from 2007-2017 in Algonquin Park, contrasting spatial patterns and song proportions over time. The four models have produced vastly different results, highlighting variables that may influence song learning such as mortality and long distant dispersal. Preliminary analysis suggests that tutoring on the wintering grounds provides is most consistent with findings in the field. In my presentation, I will expand further on these simulations and the implications they have for white-throat song learning and cultural change in animals.

11:30 – 11:45, Sunday, March 24th, B&GS 1056

THE EFFECTS OF PHOTOPERIOD AND TEMPERATURE ON REPRODUCTIVE READINESS IN BLACK-CAPPED CHICKADEES (*POECILE ATRICAPILLUS*)

Kruger, M.C.[1], Martin, R.J.[1], Sherry, D.F.[2]
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2. Department of Psychology, University of Western Ontario, London, ON, N6A 3K7

Photoperiod is the major environmental cue birds use to time reproduction. However, it is possible that other cues, such as temperature, could be used to fine tune this timing. Ambient temperature can affect birds both behaviourally and physiologically and thus can potentially influence reproductive success if unaccounted for. We investigated the effects of ambient temperature and photoperiod on reproductive readiness in a resident bird, the Black-capped chickadee (*Poecile atricapillus*). Birds were exposed to either natural winter day length (10L:14D) or photostimulatory long days (14L:10D), and to either a colder (6°C) or a warmer (14°C) ambient temperature in a 2x2 factorial design. Additionally, we recorded territorial vocalizations, obtained hormone profiles from blood samples, and determined the testes size by laparotomy and post-mortem observation. We hypothesized that elevated ambient temperature can affect reproductive readiness in photostimulated male birds. We predicted that photostimulated males held at the warmer temperature will show increases in territorial vocalizations, androgen levels, and gonadal growth compared to birds in other conditions.

11:45 – 12:00, Sunday, March 24th, B&GS 1056

CARRY-OVER EFFECTS OF CHRONIC STRESS AND ENVIRONMENTALLY RELEVANT MERCURY EXPOSURE ON MIGRATORY BEHAVIOUR IN SONG SPARROWS, *MELOSPIZA MELODIA*

Whiley, R.E., Bottini, C., MacDougall-Shackleton, S.A.
Department of Biology, University of Western Ontario; Advanced Facility for Avian Research, University of Western Ontario

Migration is a challenging life history stage that can leave birds more susceptible to the adverse effects of stressors, including environmental contaminants like methylmercury (MeHg). Determining whether the carry-over effects of chronic stress and MeHg impact migratory behaviour through the energetic cost of exposure (affecting energy exertion and activity), hormonal regulation (affecting thyroid and stress hormones linked to migration), alterations to energy storage (affecting body fat composition), or motivation to depart poor environments (affecting stress responses) is important for interpreting the interactive effects of stressors on migration. We evaluated the carry-over effects of summertime exposure to chronic stress and/or dietary MeHg on fall migratory behaviour in song sparrows, *Melospiza melodia*. To test a series of predictions to distinguish among competing hypotheses explaining the effects of both stressors on migration, we used migratory restlessness intensity as a proxy for fall migratory disposition, date of onset of migratory restlessness as a proxy for departure date, and quantitative magnetic resonance to measure changes in body composition (fat, lean, and water masses) with exposure. Although birds often experience stressors concurrently in the wild, no study to date has investigated how simultaneous exposure to chronic stress and MeHg could affect migratory ability.

Ecology and Evolution M
PHYSICS & ASTRONOMY BUILDING, RM 34

11:00 – 11:15, Sunday, March 24th, P&A 34

POTENTIAL EVIDENCE SUPPORTING *HALICTUS CONFUSUS* AS AN OBLIGATELY SOCIAL SPECIES FOUND AT ITS NORTHERNMOST RANGE IN ALBERTA

Gjevori, J., Hein, C., Wagner, H.
University of Toronto Mississauga

Halictus confusus is a sweat bee commonly found in North America and classified as eusocial; however, detailed social organization information is lacking at its northernmost ranges. Sweat bees show varying degrees of sociality; some species are obligates while others are able to use both social and solitary strategies in response to

environmental variation (socially polymorphic). Understanding sociality can reveal how sweat bees respond to climate change. We investigated the sociality of *Halictus confusus* in Alberta at a Southern and Northern habitat using physiological measurements and dissections from 2015 pan trap samples. If this species is socially polymorphic, we would expect to see a lack of a worker brood at the North site. If it is obligately social, these colonies are expected to show stronger sociality compared to the South. Both sites showed a bimodal bee capture distribution over time. 2-way ANOVAs revealed Northern queens were larger on average compared to the South (n=12). The same was true for the respective worker broods (n=11) with statistically significant interactive effects of caste and region. Ovarian development of Northern queens was comparable to that of her workers, potentially due to disease, and did not support a reproductive skew towards queens. Taken together, these results could suggest some evidence for Halictus confusus as obligately eusocial; however, further analysis of additional Northern sites are required to confirm.

11:15 – 11:30, Sunday, March 24th, P&A 34

DETERMINING SPECIES LEVEL COMPLIANCE IN COMPLETE GENOMES OF *E.COLI*

Irani, T., Moreno-Hagelsieb, G.
Wilfrid Laurier University

In recent decades, species delimitation methods have changed drastically, as new techniques are introduced. One of the best ways to define a species using bioinformatic techniques is to calculate the average nucleotide identity (ANI) of individuals. A new method for species delimitation is clustering using DNA signatures based on the distance at which strains condense. Recently, when using this method, it was found that strains of *E.coli* clustered into three groups. Based on these results two other methods were tested to see if strains *of E.coli* should be classified as different species. The two methods tested were ANI, and 16s rRNA identity. Results of ANI and 16s rRNA identities gave insight into whether DNA signatures is an effective method to use for species delimitation. The third objective of the study was to determine the most efficient method for determining ANI, in which three different programs were tested. Results showed that DNA signatures clustered strains of *E.coli* slightly differently than ANI and 16s rRNA identities. However, ANI and DNA signatures clustered out the same 24 strains, suggesting that they should not be classified as *E.coli*. This suggests that many species may not be defined correctly as there are many different methods of species delimitation, causing great variance. Going forward, research should focus on comparing different methods of species delimitation to determine the most accurate strategy of defining species.

11:30 – 11:45, Sunday, March 24th, P&A 34

DON'T BE A BUZZ KILL: AGRICULTURAL FIELD MARGINS AS BUMBLEBEE HABITAT

Purvis, E., Meehan, M.L., Lindo, Z
University of Western Ontario

Bumblebees are declining globally, largely due to habitat loss driven by agricultural intensification. Within agriculturally dominated landscapes, such as in Southwestern Ontario, natural habitat patches (e.g. meadows, wetland edges) are fragmented, increasing the value of uncropped agricultural field margins for providing a source of food and nesting resources to bumblebees. We compared bumblebee communities sampled in agricultural field margins and natural habitats across Southwestern Ontario in order to assess differences in habitat quality. We then examined the effect of floral resources, soil/nesting characteristics, and surrounding land use on the bumblebee communities present in each habitat patch. We found bumblebee abundance and diversity did not differ between habitat types. However, when examined independently of habitat type, bumblebee abundance and diversity increased with floral abundance and diversity, sandy soil texture, number of pre-existing rodent burrows, and the proportion of natural habitat patches in the surrounding landscape. This suggests that agricultural field margins are not inherently degraded bumblebee habitat, and can provide food and nesting resources comparable to natural habitats in Southwestern Ontario. Ensuring field margins contain the necessary resources for bumblebees has implications for mitigating habitat loss caused by the agricultural fields themselves.

11:45 – 12:00, Sunday, March 24th, P&A 106

HOW ARE CANADIAN ZOOS AND AQUARIUMS CONTRIBUTING TO PEER-REVIEWED LITERATURE?

Pyott, B.E.
Laurentian University

With the widespread loss of biodiversity, zoos and aquariums are striving to become leaders in biodiversity conservation and research. Canada's Accredited Zoos and Aquariums (CAZA) is a non-profit organization created to ensure Canadian zoos and aquariums are contributing to these efforts. However, nobody has quantified this contribution for all 31 CAZA members. Thus, I used research productivity to systematically quantify biodiversity conservation engagement by CAZA members. To do this, I extracted publications from the Web of Science database from 1993 to 2017. I determined that CAZA members published 492 times during this time period and that total publications increased over time. The most published in subject area was veterinary science, with 159 publications, while only 21 biodiversity conservation publications were produced. CAZA members also published significantly less than the Association of Zoos and Aquariums (AZA) members. I also sought to determine the organizational factors contributing to research productivity, and discovered that financial assets are the only significant predictor of research productivity at CAZA institutions. Zoos and aquariums are key resources that need to be utilized to mitigate the biodiversity crisis. Hence, CAZA members must seek to increase their participation in biodiversity conservation efforts and research. Zoos and aquariums can longer be idle entertainment centres, but must be fully engaged in science and conservation.

Cell and Molecular Biology M
PHYSICS & ASTRONOMY BUILDING, RM 36

11:00 – 11:15, Sunday, March 24th, P&A 36

CONSTRUCTING PLASMID MAPS USING DNA SEQUENCE DATA FROM WILD-TYPE CULTURES ISOLATED FROM WASTEWATER TREATMENT PLANTS.

Aradanas, M.E., Tehrani,A., Gilbride, K.
Ryerson University

Antibiotic resistance (AR) in environmental and pathogenic bacteria has risen in prominence since the inception of antibiotics. In this study, we are interested in plasmids, which are transferred through the process of horizontal gene transfer (HGT). Wastewater treatment plants (WWTP) have been considered in literature as a hotspot for antibiotic gene proliferation via plasmids. Culturable isolates were previously acquired from WWTP and some were chosen for sequencing. Assembly software SPAdes and PlaScope were used to assemble short-read sequences of the isolates into longer DNA sequences. The sequences were entered into NCBI's Basic Local Alignment Search Tool (BLAST) to find reference genomes to construct plasmids. Nine predicted plasmids (from Acinetobacter sp., E. coli, Aeromonas sp. and two other isolates) were constructed with BLAST and PCR. We annotated the predicted plasmids using Rapid Annotation using Subsystem Technology (RAST). We were able to find a conjugative plasmid carrying a β-lactamase gene in one of the plasmids from the E. coli isolate. Most of the predicted plasmids also contained other important genes encoding transposes, other ARs, toxin systems, secretion systems and more. The results suggest that plasmids provide a medium for rapid dissemination of a large variety of genes not limited to AR. With this work, we were able to look into some patterns in the distribution of genes within plasmids and contribute to the understanding of plasmid mechanisms.

11:15 – 11:30, Sunday, March 24th, P&A 36

CERTAIN GENE REGIONS OF THE HUMAN GENOME HAVE A DISTINCT SEQUENCE COMPOSITION

Crooks, A.M. [1], Soltysiak, M.P.M. [2], Randhawa, G.S. [1], Stueckmann, D. [1], de Souza, C.P.E. [3], Kari, L. [4], Hill, K.A. [1]
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2. Department of Statistical and Actuarial Science, University of Western Ontario
3. Department of Computer Science, University of Waterloo
4. Department of Biochemistry, University of Western Ontario

A specific pattern of underrepresentation at the dinucleotide level (CpG), and all subsequences that contain this dinucleotide (a fractal pattern) forms a significant part of the human genomic signature. A genomic signature describes the sequence organization unique to a species and is in general pervasive in a genome. Chaos Game Representations (CGR) of a DNA sequence, which is in essence a simultaneous visualization, plays the role of a quantitative genomic signature. Regional deviations in CGR patterns have been reported in the human genome, but how many regions and the potential mechanisms for those deviations are as yet unknown. Human mRNA (n=72) and intronic (n=78) sequences, share this CG underrepresentation and dinucleotide composition. However, the Rat Sarcoma oncogene family (RAS, n=158) and Human Leukocyte Antigen (HLA, n=209) gene families have members (n=24 and n=31, respectively) that have sequence compositions statistically different from the human CGR genomic signature. Purifying selection is hypothesized to limit mutational diversity in RAS genes given resultant oncogenic phenotypes. Positive selection is predicted to underlie the deviation in signature observed for HLA genes. Regional deviations from a global CGR genomic signature may reveal evidence of selection and as yet poorly defined determinants of sequence organization. Characterization of other regional variations in genomic signatures is informative of localized mutation and selection pressures.

11:30 – 11:45, Sunday, March 24th, P&A 36

NOVEL BIOINFORMATICS APPROACH TO EXAMINE THE RELATIONSHIP BETWEEN HETEROZYGOSITY AND NEW DELETIONS AND DUPLICATIONS.

McDonald, D.W.[1], Boehler, N.A. [1], de Souza, C.P.E. [2], Hill, K.A. [1]
1. Department of Biology, University of Western Ontario
2. Department of Actuarial and Statistical Sciences, University of Western Ontario

Heterozygosity caused by differences in parental genomes may lead to new mutations within the genome. The phenomenon of heterozygosity inducing mutations has been explored in yeast and Arabidopsis, but not in a mammalian species. Using a novel quantitative analysis, we examined the occurrence of this phenomenon in 617 Mus musculus of eight subgroups with differing levels of heterozygosity. These subgroups include inbred strains (heterozygosity of 0-4%), wild-derived (heterozygosity of 2-5%), and outbred strains (heterozygosity of 5-15%). Our analysis pipeline includes bar plots which portray the levels of heterozygosity surrounding a mutation of interest, followed by a statistical analysis indicating the presence of a proximal relationship between heterozygosity and the mutation of interest. We used single nucleotide polymorphism (SNP) heterozygosity as a proxy for the overall heterozygosity of each mouse. The mutations of interest studied were copy number variants (CNVs), mutations that are typically produced from non-allelic homologous recombination and gene conversions. We predict that if heterozygosity does induce mutations, there will be a proximal relationship between heterozygous SNPs and CNVs. The discovery of a phenomenon where differences in maternal and paternal genomes impose meiotic mutations has implications in germ cell biology.

11:45 – 12:00, Sunday, March 24th, P&A 36

CHARACTERIZATION OF SPECIES – DIAGNOSTIC ISSR AND SCAR DNA MARKERS DIFFERENTIATING RED MAPLE (*ACER RUBRUM*) AND SILVER MAPLE (*A. SACCHARINUM*)

Panoyan M.
Laurentian University

Plant species identification based on morphological characteristics can be hampered by environmental conditions. Development of molecular markers is the most reliable approach for accurate identification of taxa. Red maple (*Acer*

rubrum) and silver maple (*A. sacharinum*) are closely related species that readily hybridize in nature. The main objective of the present study is to develop and characterize molecular markers distinguishing *A. rubrum* and *A. sacharinum* and to validate the hybridity of A. freemanii derived from their crossings using ISSR markers.Thirteen *A. rubrum* and seven *A. sacharinum* populations were used for this study. Four ISSR primers including ISSR 5, ISSR 8, ISSR 10, and ISSR 825 were selected to amplify genomic DNA from the two species and their hybrids. Each primer generated at least one species diagnostic ISSR marker. Analysis of *A. fremanii* collected from North Dakota (USA) confirmed that the genotypes screened were true hybrids between *A. rubrum* and *A. sacharinum*. These markers were cloned and sequenced. Successful sequences were converted to SCAR markers using specifically designed primers flanking the marker sequences. One *A. sacharinum* specific SCAR marker was characterized and its sequence deposed in the National Center for Biotechnology Information (NCBI) Genbank.

Physiology and Biochemistry G
PHYSICS & ASTRONOMY BUILDING, RM 148

11:00 – 11:15, Sunday, March 24th, P&A 148

INVESTIGATING THE ROLE OF NAD SYNTHETASE 1 IN EARLY *XENOPUS LAEVIS* DEVELOPMENT

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2. Department of Paediatrics, University of Western Ontario
3. Department of Physiology and Pharmacology, University of Western Ontario

VACTERL association is a developmental disorder diagnosed when there are at least three of vertebral defects, anal atresia, heart defects, tracheo-esophageal fistula, kidney defects and limb abnormalities. Recently, two genes in the de novo NAD synthesis pathway have been shown to associate with VACTERL association. We have identified a third gene in the pathway, NAD Synthetase 1 (nadsyn1), strongly suggesting this pathway plays a role in the early development of several, primarily mesodermal, organ systems. Understanding the role of NAD synthesis is both clinically important and intriguing because this fundamental pathway is causing such specific developmental defects. We hypothesize that nadsyn1 is differentially regulated in early development with higher expression or activity in mesodermal derivatives. To test this, we examined the expression of nadsyn1 in early *Xenopus* embryos. Nadsyn1 transcripts were only detectable by in situ hybridization in the hatching gland and developing pronephric kidney. Given kidney defects are a key feature of VACTERL association, we used CRISPR/Cas9 to test whether mutations in nadsyn1 result in developmental defects in the kidney. Mutations in nadsyn1 in *Xenopus* embryos cause diminished kidney pronephros complexity and occasionally total loss of kidney organogenesis. These findings provide groundwork for future studies examining additional genes in this pathway for their potential effect on tissues implicated in VACTERL association.

11:15 – 11:30, Sunday, March 24th, P&A 148

ELECTROPORATION OF CELLS IN THE PERIPHERAL OLFACTORY ORGAN IN *PETROMYZON MARINUS*

Hamdoon, A. M., Aurangzeb, Z.
University of Windsor

In sea lampreys (*Petromyzon marinus*), the olfactory system is of importance because it is used to detect cues in the form of odorants to perform activities such as feeding and reproduction. Olfactory sensory neurons detect cues and transmit sensory information to higher brain structures. The peripheral olfactory organ contains a large olfactory epithelium, and small diverticula called the accessory olfactory organ (AOO) that are linked by narrow ducts to the main olfactory epithelium. The AOO contains sensory neurons that project to the medial region of the olfactory bulb, where post-synaptic neurons project to the posterior tuberculum. AOO sensory neurons have been labelled previously by retrograde dye loading from the medial region of the olfactory bulb. This project aims to label the AOO cells by using an anterograde strategy, where fluorescent dextran was loaded into the nasal cavity. Various dye loading techniques included electroporation to increase the permeability of the cell membrane. These experiments

encompassed several variables including the loading time, current intensity, continuous vs alternating current, and the use of surfactants. In all cases, the cells of the main olfactory epithelium labelled robustly, whereas there was a low success rate of loading AOO cells, as the dye was stopped at ducts connecting the AOO to the main olfactory epithelium. These findings suggest that ducts may regulate odorant access to the sensory neurons in the AOO.

11:30 – 11:45, Sunday, March 24th, P&A 148

SPECTROSCOPIC CHARACTERIZATION THE REGULATORY REGION OF YEAST CADMIUM FACTOR 1

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Department of Chemical and Physical Sciences, University of Toronto Mississauga

The yeast cadmium factor, Ycf1p, transports glutathione-conjugate toxic metal ions such as cadmium from the cytosol into the vacuole. Ycf1p is a member of the ABC (ATP-binding cassette) superfamily of transporters and, as such, contains the core ABC structure of two membrane-spanning domains (MSD1, MSD2) and two nucleotide binding domains (NBD1, NBD2). Ycf1p also contains an additional membrane-spanning domain (MSD0) that is connected to the core ABC structure by a cytoplasmic L0 linker. ATP binding and hydrolysis at the NBDs drives transports of solutes across biological membranes. In addition, ABC transporters are also regulated by phosphorylation. In the case of Ycf1p, phosphorylation of one site in the L0 linker inhibits transport. In contrast, phosphorylation of the intrinsically disordered regulatory region (RR), which connects NBD1 to MSD2, increases transport. This presentation shows the in vitro characterization of the RR by nuclear magnetic resonance (NMR) and circular dichroism (CD) spectroscopies. These tools were used to determine whether or not phosphorylation alters the conformation of RR and its interactions with NBD1. Future studies with involve RR/NBD2 binding studies and involve obtaining NMR resonance assignments for RR so that phosphorylation-dependent changes in structure and binding can be analyzed at residue-level resolution. These studies promise to address how intrinsically disordered regions in ABC transporters regulate transport.

11:45 – 12:00, Sunday, March 24th, P&A 148

THE ROLE OF ROOT SUBERIN IN *ARABIDOPSIS* DEFENSE AGAINST *PHYTOPHTHORA PARASITICA*

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Suberin is a biopolymer consisting of phenolic and aliphatic domains that form a protective barrier in specialized cells such as root epidermal and endodermal cells. Suberin is deposited in all plant roots and is involved in protection against abiotic and biotic stresses such as drought and microbes, respectively. Since the amount of root suberin varies across species, in this study I assess if the amount of root suberin deposition plays a part in plant protection against a plant-pathogen. To demonstrate this interaction, I selected Arabidopsis mutant strains of horst and StCYP86A33, and a wildtype strain – genotypes that show a gradient of varying levels of reported suberin deposition. Plants were inoculated with the pathogen Phytophthora parasitica and infection was monitored non-invasively using chlorophyll fluorescence imaging. The objective of this study was to establish whether genotypes that deposit more root suberin, show more resistance to P. parasitica as measured by a delay in response to infection. I hypothesize that higher amounts of root suberin will correlate with longer delays in symptom development across the different genotypes when inoculated with the plant-pathogen.

Physiology, Behaviour and Science Education O
PHYSICS & ASTRONOMY BUILDING, RM 106

11:00 – 11:15, Sunday, March 24th, P&A 106

IF YOU GIVE A RAT AN IPAD: OPTIMIZATION OF A MULTIMODAL TEMPORAL ORDER JUDGEMENT TASK USING TOUCHSCREENS

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Currently, there are limited tools for translational rodent research of multisensory perception disruption in Autism Spectrum Disorder. The temporal order judgment (TOJ) task is used to probe multisensory processing in both humans and rodents, but variability exists between the testing protocols across species. We addressed this variability by designing a multimodal TOJ task using the Bussey-Saksida Touchscreen Box. The goal of the present study was to train Sprague Dawley rats to accurately report the temporal order of acoustic and visual stimuli presented 400ms apart using the touchscreens. Rats progressed through several pre-training steps after reaching appropriate criteria of high accuracy and unbiased selection. Most rats successfully learned the task and performed with an accuracy of 75% or higher. To determine how perception of stimulus presentation varies when temporal order becomes less clear, we tested using ambiguous trials ranging in stimulus onset asynchronies (SOAs) of 200ms, 100ms, 50ms and 0ms (simultaneous presentation). Rats were generally more sensitive to the acoustic stimulus, with high accuracies up until the 50ms SOA and a higher perception of acoustic stimulus presented first at simultaneous presentation. Overall, this study is the first to demonstrate that Sprague Dawley rats can learn a TOJ task using touchscreens, with results to support this as a highly translational and standard protocol measuring audio-visual perception in the rat.

11:15– 11:30, Sunday, March 24th, P&A 106

BEEF FROM GRASS-FED CATTLE CONTAINS A HIGHER CONTENT OF ALPHA-LINOLENIC ACID (ALA), AND CONSEQUENTLY A HIGHER RATIO OF OMEGA-3: OMEGA-6 FATTY ACIDS, THAN BEEF FROM GRAIN-FED CATTLE

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There has been rising consumer interest, driven by health concerns, in traditional grass-fed over commercialized grain-fed cattle. However, the mechanism through which grass-fed cattle exerts its potential health benefits is not well appreciated by the public. Grass-fed cattle have been shown to have a higher content of omega-3 fatty acids than grain-fed cattle, especially with respect to alpha-linolenic acid (ALA; 18:3n-3), and which results in an overall higher omega-3 (n-3) to omega-6 (n-6) ratio. It has been proposed that ALA, and omega-3 fatty acids in general, confers multiple health benefits in neurodevelopment, anti-inflammatory processes, and cardiovascular health. Furthermore, the modern Western diet contains a very low n-3/n-6 ratio in general, which has been linked to various public health issues such as cardiovascular and neural diseases. We analyzed the fatty acid composition of rib-eye steaks from grass-fed and grain-fed cattle to determine if there was a difference in the ALA content and overall n-3/n-6 ratio resulting from the two different feeding approaches. Grass-fed steaks were found to have a significantly higher ALA content ($p < 0.01$) and a significantly higher n-3/n-6 ratio ($p < 0.01$) than grain-fed steaks. Considering the health benefits associated with omega-3 fatty acids and the health risks associated with a low n-3/n-6 ratio, it may be of interest to meat consumers to choose grass-fed cattle.

11:30 – 11:45, Sunday, March 24th, P&A 106

BEHAVIOURAL ANALYSIS OF SEA LAMPREY (*PETROMYZON MARINUS*) UPON EXPOSURE TO DEAD TROUT WATER

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Sea lampreys utilize chemosensation for spawning migration, reproduction, feeding, as well as alarm response. Ongoing research and electrophysiological recordings have recently determined that dead trout water (water that held a dead trout) stimulates chemosensory responses in the sea lamprey, however, behavioural experiments have not been conducted. This study explores behavioural effects of sea lamprey upon exposure to dead trout water. Each lamprey was subjected to a blank control of dechlorinated water, followed by an experimental stimulus of dead trout water, and a recovery period. Results show that the lamprey increased movement upon addition of dead trout in comparison to the blank control. Prior to application of dead trout water, behaviours observed include sucking to the side of the tank and swimming. While behavioural responses after the addition of dead trout water include increased swimming and breeching out of water. Observing behaviour of sea lamprey may give insight to predator and prey interactions, habitat selection, and understanding the effects of decaying material to the chemosensation in the sea lamprey. Additionally, behavioural experiments show significance as they can be applied to invasive species management for the future of the Great Lakes.

11:45 – 11:30, Sunday, March 24th, P&A 106

IS THERE A GENDER ACHIEVEMENT GAP IN INTRODUCTORY SCIENCE COURSES AT WESTERN?

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Women represent the majority of students at Canadian universities studying in science fields, yet they only make up 25% of STEM professions. Research has suggested many possible explanations like social attitudes, high stakes tests and undergraduate GPA. Statistical testing of male vs female marks from introductory science courses at Western University for the last five years found a gender gap in achievement. Female students do significantly worse in introductory biology and physics courses than male students. Scoring up to 3% lower than male students even with the same incoming averages. This gap was consistent and persistent in each year tested. The gap increased when courses used more high-stakes testing. Courses with a multiple components and assessments did not have a gap in achievement. A gender gap is present and may be addressed by reducing high stakes tests and increasing classroom engagement.

Physiology and Biochemistry H
PHYSICS & ASTRONOMY BUILDING, RM 150

11:00 – 11:15, Sunday, March 24th, P&A 150

ROLE OF FRAGILE X MENTAL RETARDATION PROTEIN IN DROSOPHILA COURTSHIP CONDITIONING

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Fragile X syndrome is a broad-spectrum neurological disorder resulting from a mutation in the fmr1 gene, which leads to altered protein expression of the Fragile X mental retardation protein (FMRP). The FMRP protein regulates the translation of numerous proteins, some of which contribute to synaptic plasticity and learning and memory. We used a Drosophila melanogaster courtship conditioning assay to examine the effects of Fragile X mental retardation protein (dFMRP) on learning and memory. The courtship conditioning assay examines behavioural changes in the courting behaviour of male flies. In a courtship conditioning assay, a naïve male fly learns to modify his courtship behaviour after experience with an unreceptive female. This experiment examines short-term memory and learning by placing a naïve male with an unreceptive female for one hour before placing him with a naïve female and examining courtship alterations following rejection. We predict that the absence of FMRP will result in impaired learning and memory. Future studies will examine putative targets of FMRP.

11:15 – 11:30, Sunday, March 24th, P&A 150

USING FEV1/FVC AS A PREDICTOR TO SKIP EARLY DOSES IN METHACHOLINE CHALLENGE

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The methacholine challenge test (MCT) is a useful tool to rule out a diagnosis of current asthma. However, MCT is time consuming and difficult in children, due to the effort dependent nature of spirometry. Previous studies proposed protocol modifications to shorten MCT while preserving safety and outcome resolution. This study aims to see if excellent baseline FEV1/FVC z-scores can be used as a predictor to skip early methacholine doses. Methods:MCT data from children of age 8 were obtained as part of the Canadian Healthy Infant Longitudinal Development study. Spirometry and MCT were performed per ATS/ERS criteria, with the provocative dose (PD20) obtained using a 1-minute tidal breathing protocol with the AeroEclipse II nebulizer. FEV1/FVC cutoffs were determined using an ROC curve. Results:Eighty-one MCTs were completed and 71 met acceptability and reproducibility criteria. Mean age was 8.93 years. 21 children tested positive (PD20<100µg) and 50 children tested negative for MCT. A baseline FEV1/FVC z-score < 0.394 had 95.2% sensitivity and a negative predictive value of 0.888, thus children with a baseline FEV1/FVC z-score > 0.394 are unlikely to react to methacholine doses <100µg. Conclusions:A baseline FEV1/FVC z-score > 0.394 can be used to skip early methacholine doses up to 100µg, given the low probability of a positive MCT result. Therefore, early methacholine doses can be safely skipped, improving data quality by reducing fatigue in pediatric patients.

11:30 – 11:45, Sunday, March 24th, P&A 150

LOSS OF ACTIVATING TRANSCRIPTION FACTOR 3 REDUCES THE SEVERITY OF INDUCED CHRONIC PANCREATITIS IN MICE

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3. Children's Health Research Institute

Chronic pancreatitis (CP) is a progressive inflammatory disease of the exocrine pancreas in which healthy tissue is damaged and replaced by fibrous tissue leading to pain and malnutrition. CP is a major risk factor for the development of pancreatic ductal adenocarcinoma (PDAC) but the molecular links are currently unknown. Activating transcription factor 3 (ATF3) is a mediator of the unfolded protein response pathway and is rapidly upregulated following pancreatic injury. Our previous work suggests ATF3 promotes acinar to duct cell metaplasia (ADM), a potential morphological link between CP and PDAC. The objective of this project was to determine if ATF3 promotes injury and fibrosis in response to pancreatic injury. We hypothesized that ATF3 promotes more extensive damage in response to experimentally-induced pancreatitis. Recurrent pancreatitis was induced with cerulein in wild type (WT) and Atf3 deficient mice (Atf3-/-) for 14 days and the extent of pancreatic injury was assessed one and seven days post-cessation of treatment. Histological analysis indicated Atf3-/- mice had reduced tissue damage and more rapid pancreatic regeneration than WT mice. Western blot analysis determined Atf3-/- mice returned to normal amylase levels, an enzyme produced exclusively by pancreatic exocrine cells, quicker than WT mice, indicating enhanced pancreatic regeneration. These results indicate loss of ATF3 reduced the severity of pancreatic injury and enhanced regeneration in response to CP.

11:45 – 12:00, Sunday, March 24th, P&A 150

USE OF IMAGE ANALYSIS TO QUANTIFY HYPOXIA AND PROLIFERATION RELATIVE TO VESSEL DISTANCE

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The formation of hypoxic microenvironments within solid tumours is known to contribute to radiation resistance, increased metastasis, and an overall poor prognosis. It is crucial to understand the spatial and molecular mechanisms that contribute to tumour hypoxia formation to improve the efficacy of radiation treatment, develop hypoxia-activated prodrugs, and increase patient survival. This study aims to develop an image analysis pipeline to quantify hypoxia and proliferation relative to the distance from the nearest perfused blood vessel. Immunofluorescent staining was done on xenograft models for DAPI (nucleus), EF5 (hypoxia), EdU (proliferation), CD31 (vessels), and Hoechst (perfusion). Image registration was done in MATLAB, and image analysis was performed in Definiens. Perfused blood vessels were detected based on CD31 and Hoechst staining. Each cell detected using DAPI was assigned a “distance to the nearest perfused vessel” value. Mean EF5 and EdU intensity was measured in each cell and plotted against their distance to the nearest perfused vessel. The results of this analysis show a positive correlation with hypoxia and a negative correlation with proliferation, relative to vessel distance. This pipeline shows promise for potential use in clinical scenarios by assessing patient tumour hypoxic status and can be used to evaluate the efficacy of hypoxia-activated prodrugs or radiation sensitization prior to radiation treatment to promote a positive patient prognosis.

Ecology and Evolution N
PHYSICS & ASTRONOMY BUILDING, RM 117

11:00 – 11:15, Sunday, March 24th, P&A 117

SECONDARY INVASION? INTERACTING EFFECTS OF THE EMERALD ASH BORER (*AGRILUS PLANIPENNIS*) AND ECOLOGICAL INTEGRITY ON INVASIVE SHRUB ESTABLISHMENT

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The emerald ash borer (*Agrilus planipennis*; EAB) is an invasive beetle that causes high levels of ash (*Fraxinus* spp.) mortality in eastern North American forests. While the immediate impacts of the EAB are well studied, the indirect consequences are less well understood. Secondary invasions occur when one invasive species facilitates the entry or establishment of another invasive species. Forest responses to insect invasions may be influenced by ecological integrity–the degree to which ecosystem composition, structure, and function deviate from their natural range of variation. Here we investigate the effect of the EAB on invasive shrub establishment and, for the first time, assess its interaction with an index of ecological integrity. We quantify these impacts by comparing understory vegetation communities in EAB-induced canopy gaps, other canopy gaps, and regions without a canopy gap at sites near London, ON. We hypothesize that the EAB facilitates invasive shrub establishment through the rapid and synchronous creation of canopy gaps, and that plots with lower ecological integrity are more susceptible to non-native plant invasions following EAB infestation. Preliminary results suggest that the EAB may facilitate the establishment of *Rhamnus cathartica*, an invasive shrub, at some sites. Continued research expands on these preliminary results and contributes to an understanding of the indirect impacts invasive insects have on forest structure and function.

11:15 – 11:30, Sunday, March 24th, P&A 117

TIMING AND FREQUENCY OF AVIAN PREDATION ON GOLDENROD GALL FLIES (*EUROSTA SOLIDAGINIS*)

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This study focuses on the timing and frequency of avian predation on goldenrod gall flies (*Eurosta solidaginis*). Gall fly larva induce the production of a tumor-like structure, a gall, to form in the goldenrod plant (*Solidago* spp.). Gallfly

larvae are energetically rich and used as a food source for the downy woodpecker (*Picoides pubescens*) and the black-capped chickadee (*Poecile atricapillus*), both preferentially selecting large galls. This system is a well-used example of stabilizing selection, but there have been few studies on the seasonal timing and intensity of avian predation. Four sites were used, one primary site and three secondary sites, within Southwestern Ontario to study frequency and timing of avian predation, and the effects of environmental conditions on avian predation. Seasonal trends of gall hardness, goldenrod plant fall rate, percent moisture of galls and density of galls were studied at the primary site. At all sites percentage of galls predated over time was measured to assess the similarity of trends. Most goldenrod plants were blown over and the goldenrod fall rate was almost continuous over time. This suggests that avian predation rates recorded in the spring may be inaccurate, as the sample will no longer reflect the true population. Onset of predation occurred at similar times across the sites, but predation after onset was variable between the sites and over time.

11:30 – 11:45, Sunday, March 24th, P&A 117

MODELLING INVASIVE *PHRAGMITES* BIOMASS AND LIVE:DEAD SHOOT RATIO USING WORLDVIEW-3.

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Originating from Eurasia, *Phragmites australis subsp australis* (common reed) has become ubiquitous across North American roadsides and wetlands since the mid 20th century, dramatically reducing biodiversity and destroying critical habitat. To track their expansion and monitor effectiveness of control programs, managers have used remote sensing to successfully map the extent of invasive *Phragmites*, with accuracies ranging from 80-90%; however, information regarding the biomass or ratio of living:dead shoots would allow contractors to customize the rate of herbicide application and improve efficiency of chemical control programs, which are costly and currently the most important component in *Phragmites* eradication programs. In this paper, we use Worldview-3 (WV3) image data to classify Phragmites stands in two heavily colonized wetlands in Southern Ontario. We developed 52 indices using different combinations of satellite bands based on strength of their correlation with known biomass and live dead ratios of common reed. Significant indices were then used in the random forest regression model, an ensemble learning technique in R, which has been used in other studies to quantify biomass of other vegetation forms. The random forest model yielded a RMSE of 0.62 kg for biomass determination and 0.129 for live dead ratio and exceed the performance of all 52 indices. We will show how this approach can be used along with current mapping practices to aid management efforts.

11:45 – 12:00, Sunday, March 24th, P&A 117

MATERNAL STRESS EXPOSURE AND CLIMATE CHANGE EFFECTS ON SOCIAL BEHAVIOURS IN CHINOOK SALMON FRY

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Cortisol, a glucocorticoid (GC) hormone involved in stress response in fish, is used as a maternal stressor signal to prepare offspring to its anticipated environment. Little is known, however, how elevated egg GC's levels in combination with raised rearing temperatures can affect social behaviours in offspring. My study tests how exogenous cortisol administration affects offspring social behaviour in Chinook salmon (*Oncorhynchus tsawytshacha*) under an environmental stressor. After dosing with a cortisol or control solution, fertilized eggs were reared under two temperature regimes: current ambient or elevated (+3oC). At 288 degree days, grouped individuals (n=3) were observed for aggregative and agonistic behaviours in acclimation, mobility, and responses to disturbance and food. Under elevated conditions, I predicted GC-exposed grouped fry will exhibit greatest aggression, boldness, exploratory behaviours and willingness to forage. Contrary to my predictions, neither cortisol dosage or temperature influenced conspecific behaviours, with the exception that GC-exposed fry were more likely to attempt escape under elevated temperatures. Under current temperatures, non-exposed grouped fry showed a more prevalent initial reaction to novel food entry. Understanding how prenatal signals in conjunction with temperature stress affect social behaviours of emerging Chinook salmon fry allows a better prediction of how these organisms will react to changes in their future environments.