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Ontario Biology Day 2014
March 22-23
University of Toronto Mississauga

Conference Organizing Committee
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Published by:
University of Toronto Mississauga
Department of Biology
3359 Mississauga Road
Mississauga, ON L5L 1C6
http://www.utm.utoronto.ca/biology
Twitter: @UTMBiology
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Logo Design by Scott Winrow
Welcome to Ontario Biology Day 2014 at the University of Toronto Mississauga!

We are thrilled to welcome you to the 27th annual Ontario Biology Day (OBD) undergraduate student research conference. On behalf of the Department of Biology at the University of Toronto Mississauga, we wish you the best of success in presenting your research to your peers this weekend, and congratulate you on your achievement in undergraduate biology research.

OBD is an annual event that showcases and celebrates biology research conducted by undergraduate students across Ontario. This year, we welcome more than 220 participants to the conference at the University of Toronto Mississauga. We are also delighted to welcome several distinguished guest speakers. The conference will be opened by the neurologist and astronaut Dr. Roberta Bondar (via Skype), and will have a banquet with a keynote session given by David Evans, the palaeontology curator form the ROM. Dr. Patrick Gunning, a cancer researcher from UTM, and Dr. Dan Riskin from the Discovery Channel, will be giving invited lectures, and Dr. Deep Saini, Principal of UTM, will be giving the closing remarks.

We would like to thank and acknowledge the support of all the people that have contributed to the success of this event. Many UTM Biology faculty, staff, graduate students and undergraduate students have dedicated their time over the past year to prepare for this conference. Also, OBD is only possible due to the generous support of UTM-based as well as corporate sponsors. Please take a moment to send a message to these sponsors by signing the “Thank you to our sponsors” card at the registration desk. And importantly, we would like to extend a thank you to all of the supervisors and students that have travelled to the conference this weekend to present their work and share in this conference experience. This conference is a celebration of your research, and we congratulate you on your hard work and research achievements.

Sincerely,

The 2014 Ontario Biology Day Organizing Committee

Fiona Rawle, Associate Chair and Lecturer
Sanja Hinic-Frlog, Lecturer
Christoph Richter, Lecturer
Yen Du, UTM Biology Undergraduate Advisor,
Lisa Cheung, Teaching Technician
Audrey Reid, Graduate Student
Aaron LeBlanc, Graduate Student
Daniel Almeida, Undergraduate Student and Erindale Biology Society Executive Events Coordinator
Saturday March 22

Session 1 - IB 245

Cell Biology & Biotechnology

Studies on the Encapsulation of Salivary Anti-microbial Peptides

Towards DNA-PDA: Handheld DNA sequencer to enable on-site species identification

Transgenic expression of microbial and fungal carbohydrate-active enzymes in plants

Large Scale Study of Biomarker Impact on Clinical Trial Risk on Oncology: Colorectal, Melanoma, Breast and Non-small Lung Cancer

Regulation of Akt Activation by Phospholipase C

Lysosomal Structure Quantification During PIKfyve Inhibition

Session 2 - IB 235

Ecology

Inside Yogi's Picnic Basket: Getting Elk (Cervus canadensis) Off the Menu

Aggressive behaviour and combat in sexually mature male snapping turtles (Chelydra serpentina)

Murder mystery in Misery Bay: the demise of turtle species at risk

Session 3 - IB 250

Cell & Molecular Biology

CCN1 and fibrosis: does CCN1 recruit progenitor cells?

Assessment of ERG immunohistochemical staining patterns in prostatic evasive anterior tumours (PEATS)

Expression and Function of Tuberin in Early Embryonic Brain Development

AMPK signaling and autophagy in ovarian cancer cell survival

Purification and Characterization of the β-Barrel Domain of BcsC to Investigate its Role in Cellulose Export from E. coli

Metals in Sudbury Particulate Matter upregulate hypoxia-inducible factor (HIF)-1α and may be associated with airway remodelling

Session 4 - IB 260

Neurobiology

Neural versus peripheral contributions to the masculinization of male sexual preference in olfaction

The Effects of Sodium Salicylate on the Expression of GABAB Receptors in the Rat Hippocampus

How I got frozen out of my soil seed bank study and landed in a field of germinating invading plant species

Effects of defoliation frequency and saliva application on endophyte hyphal loading in Festuca rubra and Schedonorus pratensis
Organization of Glomerular Chains in the Olfactory Bulb of Chinook Salmon Fry .............................................................29

Neuroefficiency in Elite Curlers Related to Shot Performance ..................29

The Localization of Axons Projecting from the Accessory Olfactory Organ in the Sea Lamprey ..........................................................30

The spatial distribution of the serotonergic fibers in the olfactory bulb of the sea lamprey .................................................................30

Session 5 - IB 270
Health

Stress Hormones and their Effects on Reproduction in Captive Bactrian Camels ..................................................................................32

Identifying pathogenic mutations in patients with atypical progeria .........32

The Influence of chronic Cu exposure on the uptake and effect of Ag in Rainbow trout (Oncorhynchus mykiss) ........................................33

What is the evidence for post-operative prophylactic antibiotics after primary hip and knee arthroplasty? A systematic review .............33

Role of Spy1 in CKI-Treated Multiple Myeloma .....................................34

Session 6 - IB 280
Animal Behaviour

Influences of anthropogenic noise pollution on the calling patterns of the round goby, Neogobius melanostomus ...........................................36

Ecologically matching swim performance for the reintroduction of Atlantic Salmon into Lake Ontario ......................................................36

An investigation of grouping behaviour in a social fish in the presence of olfactory and visual cues of predation ........................................37

Social or solitary: Grouping preferences in invasive round goby (Neogobius melanostomus) ..............................................................37

Stability in the dominance hierarchy of a cooperatively breeding cichlid fish .......................................................................................38

Partner Preference in Naked Mole Rats with Consideration of Pregnancy Dynamics .................................................................38

Session 7 - IB 245
Cell & Molecular Biology

Stress Response of Starved Tetrahymena thermophilia ...........................40

In Vivo Functional Characterization of Human Mdm2 and MdmX RING Domains .................................................................................40

Determining the Role of Src Family Kinases on EGF-Stimulated Akt Phosphorylation ........................................................................41

Common Requirement for Clathrin in Signalling by distinct Receptor Tyrosine Kinases ........................................................................41

Structural and Functional Characterization of the Interaction between Ubiquitin Binding Domains of Arf-BP1 and Ubiquitin ..................42

RBM5 and RBM10 mRNA and Protein Expression in a Small Cell Lung Cancer Cell Line ..............................................................42
Session 8 - IB 235

Ecology

Does Garlic Mustard density have an impact on native species’ richness? A review of the literature and a long term dataset .................................................................44

Health Survey of Street Trees in London Ontario, with Special Focus on Fungal Infections ..................................................................................................................44

Litter position effects on the decomposition of Bromus inermis and Poa pratensis litter during the winter .........................................................................................45

Long-term Avian Migratory Data Reveal Differential Responsiveness to Climate Variation ...........................................................................................................45

Developing a standardized field-based approach to monitoring the effects of water quality on wetland plants ................................................................................45

The role of plant communities and plant quality on Dicyphus hesperus population growth .................................................................................................................46

Session 9 - IB 250

Cell & Molecular Biology

Shroom3 is required for nephron development ...........................................................................................................48

Determining the requirement for Shroom3 in epidermal morphogenesis in the mouse .........................................................................................................48

A piece of the CCN puzzle: the role of CCN1 in dermal fibroblast adhesion to the extracellular matrix ........................................................................................49

Evidence for the presence of the alternative oxidase (AOX) pathway in the copepod Tigriopus californicus ..................................................................................49

Pokeweed Antiviral Protein is Regulated by a Small RNA .........................................................................................50

Role of Spy1 in Functional Differentiation ...........................................................................................................50

Session 10 - IB 260

Evolution

Hemiclonal analysis of direct and indirect fitness and its associations with female choosiness .................................................................................................................52

The evolution of low-complexity regions in protein sequences .............................................................................................52

Cross-generational effects of male attractiveness on offspring immunocompetence ....................................................................................................................53

A population genetics study of Boletus edulis isolates from the Czech Republic ..................................................................................................................53

Using flow cytometry to assess the genetic and environmental factors influencing unreduced gamete production in Brassicaceae spp ................................................................54

Evolutionary History of the Class A Scavenger Receptors .........................................................................................54

Session 11 - IB 270

Genetics

The role of retrotransposable sequences on the evolution and individuality of the human genome ........................................................................................................56
Nmt: a candidate gene for behavioural isolation between Drosophila melanogaster and D. simulans

Investigation on de novo Structural Variant (SV) mutations using complete genome sequences in families with monozygotic twins

Examination of obesogenic related methylation changes of the POMC promoter in female CD1 mice neonatally exposed to bisphenol-A

Analyzing Gene Expression to Aid in the Quantification of Development Within the Pupal Stage of Lucilia sericata

Investigating the Conservation of Metabolic Function within Prokaryotic Species

Session 12 - IB 280
Genetics, Cell & Molecular Biology

Quality Control Removing Quality During Copy Number Variant Detection

Molecular analysis of ATRX-deficient mice

Ammonia toxicity may be an early trigger of neurodegeneration in the harlequin mouse, a model of premature neurodegeneration

Characterization of downstream elements of the miR156-SPL regulatory network in Arabidopsis thaliana root

Discovery of Protein Motifs in the Macrophage Scavenger Receptor Using MSA-PRP and APC

Investigating Nodal expression in mouse models of Duchenne muscular dystrophy

Sunday March 23
Session 13 - IB 245
Cell & Molecular Biology

The vacuolar pH in yeast phosphoinositide mutants

Orthology versus functional redundancy among selected genes in the Skp1-like gene family of Arabidopsis thaliana

ALS regulatory subunits, AIP1 and AIP3, play evolutionarily conserved albeit divergent roles in growth and development of Arabid

Defining the Mechanism of SCF-dependent SLBP Degradation: Finding the Magic F-box

Characterization of the Role of Cockayne Syndrome Group B (CSB) in Telomerase-Negative Cancer Cells

Repression of hypoxia-inducible factor-1 alpha gene expression by the transcription factor Kaiso

Session 14 - IB 235
Ecology

Estimation of bird mortality using comparative capture rates suggests decreased Juvenile survivorship during migration

Climate-growth relationship in snapping turtles (Chelydra serpentina): development of an innovative approach

Vegetative Analysis of Six Main Roadways in Greater Sudbury, Ontario, Canada
Effects of temperature and atmospheric carbon dioxide on microbe-mediated nitrogen and carbon dynamics of the boreal bryosphere ..........69

The production of canola and sunflower on thick verses thin compost layers over desulfized Ni-Cu Tailings .................................................................70

The effect of declining calcium concentration in freshwater biota on fitness of Daphnia and Bosmina species .................................................................70

Session 15 - IB 250
Ecology

Effect of Coxiella burnetti Infection on Body Mass of Rodent Hosts .......72

Geometric morphometric analysis of skulls of wolverine Gulo gulo and fisher Martes pennanti using digital calipers and a 3D Scan.........................72

Effects of Mining on the Physiological Ecology and Morphology of Herpetofauna in Sudbury, Ontario .................................................................73

Use of paraffin embedded larvae in studying feeding biology of two forest defoliating Lepidoptera .............................................................................73

Root structure and growth of wetland plants with contrasting root turnover strategies .................................................................74

The influence of physiological traits on climatic niche occupancy and competitive ability in the polyploid plant, Chamerion angu ..................74

Session 16 - IB 260
Microbiology

Tunable protein expression system in bacteria ........................................76

Characterization and Elucidation of Enterococcal and Clostridial Biofilms Under Environmental Stressors ..............................................................76

Structural and Functional Characterization of the Role of BcsG in Bacterial Cellulose Biosynthesis .................................................................77

Isolation and characterization of viruses infecting the freshwater algae Chrysochromulina parva .................................................................77

Investigating the effect of anaerobic shock on the antibiotic resistance profiles of environmentally isolated pathogens ........................................78

Evaluation of water quality indicators in amended and un-amended stormwater retention ponds .................................................................78

Session 17 - IB 270
Animal Physiology

Long-term stress of domestic and wild American mink (Neovison vison) ..80

Development of an artificial diet for gut loading in the fall field cricket (Gryllus pennsylvanicus) .................................................................80

Relevance of SNARE Protein Syntaxin-1A in Cardiac Function and ANP Release .............................................................................81

Modulation of the retinoic acid signalling pathway during the expansion of hematopoietic progenitor cells ..........................................................81

Implications of Consuming a Western Diet following an adverse in utero environment upon the fructose metabolic pathway in the Sk ................82

The Regulation of Ghrelin Secretion from Pancreatic Epsilon Cells ........82
Session 18 - IB 280

Physiology

Reproduction, Stress and Feather Quality in Tree Swallows ......................84

Effect of heavy metals and drought stresses on the stem conductive structure, leaf area and stomatal density of Dodonaea viscosa ..................84

Influence of sound direction on auditory midbrain response to novel sound ......................................................................................................................85

Integrin's Role in Maintaining Adhesions during Drosophila Heart Remodeling and Aging ...............................................................85

Physiological validation of infrared thermography (irt) for measuring the presence of brown adipocyte activity in health, male adults ..............86

Characterization of ion channel expression and function in pancreatic epsilon cells ................................................................................................................86

Session 19 - IB 245

Cell & Molecular Biology

Does HST3 have a role in double strand break repair? ..................................88

Roles of Cyclins A, B, and B3 in Drosophila Female Meiosis ........................88

Unraveling multiple oscillator mystery in Neurospora using Peroxiredoxins as biomarker of oxidation rhythm .................................................................89

Session 20 - IB 240

Cell & Molecular Biology

The Importance of the Disulphide Bond in the Carboxysomal Y-Carbonic Anhydrase, CcmM ........................................................................................................91

Role of 40 S ribosomal proteins in cell cycle control: characterization of Schizosaccharomyces pombe mutants .........................................................91

Role of Intracellular Calcium in Ghrelin Secretion from Mouse Pancreatic Epsilon Cells .......................................................................................................92

Exposure to Endocrine Disrupting Chemicals: Implications for Human Health ........................................................................................................92

Session 21 - IB 235

Ecology & Evolution

Comparison of Ectoparasites from North American Red Squirrels and Northern Flying Squirrels Using DNA Barcoding .........................................94

Fungal endophytes of Festuca rubra increase in frequency following experimental exclusion of herbivores .................................................................94

Multi-Level Selection in a Plant Capable of Kin Recognition ........................95

The Effect of Accessory Proteins on Sperm Survivability in Drosophila pseudoobscura .................................................................................................95

Session 22 - IB 250

Environment

Effect of Pesticides on Honey Bee Survivorship, Foraging and Immunocompetence .................................................................................................97
Survival and productivity of Daphnia mendotae in recovering acid and metal stressed lakes.................................................................97

The Effects of Benzo-a-pyrene on the Transcriptome of Brown Bullheads.98

The effects of toxicity modifying factors on the acute toxicity of samarium to Hyalella azteca ..........................................................98

Session 23 - IB 280
Ecology & Evolution

The effects of non-consumptive predation on encapsulation in dragonfly larvae (Libellulidae: Odonata) ..............................................100

Characterization of an acid mine drainage site sediment microbial community ..............................................................................100

The Effects of Salinity and Dissolved Organic Matter on Copper Toxicity in a Euryhaline Hydroid (Eudendrium carneum) .........................101

DNA Signatures: An Alternative for Metagenomic Investigation of Microorganisms ..........................................................101

Session 24 - IB 270
Plant Physiology

The chemoattractant potential of ginsenosides from American ginseng for Pythium irregularare ..................................................................103

Leaf anatomical acclimation of two boreal conifer species to growth in elevated atmospheric temperatures and [CO2] .........................................103

Phenotyping a 3-ketoacyl-CoA Synthase 16 over expression line in Arabidopsis thaliana .................................................................104

Diversity and Frequency of Fungal Species occurring in heavy metal polluted tailings in Sudbury, Ontario, Canada ........................................104

Session 25 - IB 280
Science Education

Using Animations Combined with Active Learning to Overcome Student Misconceptions .............................................................106

Revising Current Teaching Methods to Improve Student Learning in Introductory Science Courses ......................................................106

Developing Better Principles for Misconception Targeted Animations.....107

Poster Session A - IB Atrium

1 - Bile salts induced resistance to CAMPS: A comparative study of EHEC and EPEC .................................................................109

2 - The Impact of Short Chain Fatty Acids on Motility and Flagella synthesis in Enterohaemorrhagic E.coli O157: H7 ..................................109

3 - Tubular lysosomes appear to increase total lysosome volume in immune cells ..............................................................................110

4 - Characterization of the Cockayne Syndrome Group B piggyBac 3 Fusion Protein and piggyBac 3 Transposase .................................110

5 - The Development of Myc-Targeting Cancer Therapeutics: Utilizing the Bacterial One-Hybrid Assay for Screening a Library of Binder .....111
6 - Investigating cell viability when ERK pathway is inhibited during the ultrasound and microbubbles treatment .................................111

7 - Application of FISH to detect Adherent Invasive Eschericia coli in a vitamin D deficient murine model of IBD ...................................................112

8 - Bio-consolidated cellulosic ethanol production ................................................112

9 - The influence of egg size and hatching time on growth of juveniles of rainbow trout (Oncorhynchus mykiss) .................................113

10 - Delivery of RNAi against a gene of Tetranychus urticae via feeding on transgenic plants .................................................................113

11 - Treatment of dry eye disease in a dry-eye rabbit model using a novel sulfadiazine-hyaluronic acid formulation ..................................114

12 - Analysis of the ENU-3 family proteins in C. elegans .................................114

13 - Engineering a Vector to Knockdown Expression of ASF1 using RNAi Methods .................................................................115

14 - GluA2-lacking AMPA receptor expression in homeostatic synaptic plasticity .................................................................115

15 - Does Chronic Stress Exacerbate Noise-Induced Hearing Loss? ......116

16 - Effects of SK Inhibitor Apamin and Cognitive Diet on Acheta Domesticus Cognitive Abilities and Possible Mushroom Body Impacts ...116

17 - The effects of KATP channels on skeletal muscle fatigue and recovery are dependent on muscle stimulus frequency and fibre type ..........117

18 - Radiation tolerance and the bystander effect in the hydrated tardigrade species H. dujardini .................................................................117

19 - Influence of Royal Jelly and Methoprene on the Life History and Longevity of the Cricket, Acheta domesticus ..................................118

20 - Intestinal Urea Handling in the Freshwater Rainbow Trout (Oncorhynchus mykiss) .................................................................118

21 - Changes in physical health following an adapted physical exercise program for adults with autism and an intellectual disability ..........119

22 - Growth Responses of Tamarack to Recent Climate Warming: A Dendrochronological Study from Canada’s Northern Boreal Peatlands ...119

23 - Effects of octopamine on forewing first basalar (M97) muscle activation in locusts, Locusta migratoria (L.) ........................................120

Poster Session B - IB Atrium

1 - Previous aggressive encounters and winning experience can predict aggression in subsequent fights in male Zebrafish ..................122

2 - Effects of Early Social Isolation on Zebrafish Behaviour in Response to Social Stimuli .................................................................122

3 - The genetic study of genes that regulate the larval foraging behaviour in Drosophila melanogaster .................................................................123

4 - Quantification and Analysis of Complex Behaviors in Zebrafish Using Argus ..................................................................................123

5 - Observing “boldness” behaviour in Sea Lamprey (Petromyzon marinus) in relation to susceptibility to capture in a trap .........................124

6 - The Tube Test: A Systematic Paradigm for Tracking the Social Hierarchy within a Naked Mole Rat Colony ........................................124
<table>
<thead>
<tr>
<th>Chapter</th>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>7</td>
<td>Effects of Habitat Fragmentation on the Spatial Ecology of Two Endangered Turtle Species</td>
<td>125</td>
</tr>
<tr>
<td>8</td>
<td>Effects of Scale in Observations of Spatial and Temporal Variation in Natural and Disturbed Landscapes</td>
<td>125</td>
</tr>
<tr>
<td>9</td>
<td>Monitoring bat populations on the University of Toronto Mississauga campus</td>
<td>126</td>
</tr>
<tr>
<td>10</td>
<td>Phylogenetic host-parasite-specificity in aphids of Churchill, MN</td>
<td>126</td>
</tr>
<tr>
<td>11</td>
<td>The influence of vegetation structure on avian habitat selection at Welgevonden Game Reserve, South Africa</td>
<td>127</td>
</tr>
<tr>
<td>12</td>
<td>Adaptive potential of populations: quantifying genetic variation at the MHC-1 locus in the guppy (Poecilia reticulata)</td>
<td>127</td>
</tr>
<tr>
<td>13</td>
<td>Phenotypic plasticity in the shells of apple snails (Pomacea flagellata) under geometric constraint</td>
<td>128</td>
</tr>
<tr>
<td>14</td>
<td>Phenotypic response to inhibition of meridional growth in adult Arbacia punctulata</td>
<td>128</td>
</tr>
<tr>
<td>15</td>
<td>Skull Morphology of Captorhinus aguti</td>
<td>129</td>
</tr>
<tr>
<td>16</td>
<td>Fossil Taphonomy in the Early Permian Richards Spur Locality, Oklahoma, USA</td>
<td>129</td>
</tr>
<tr>
<td>17</td>
<td>Morphology of the left humerus of a diadectid</td>
<td>130</td>
</tr>
<tr>
<td>18</td>
<td>Curriculum Map of the University of Ottawa Biomedical Science Program</td>
<td>130</td>
</tr>
<tr>
<td>19</td>
<td>University of Ottawa Biopharmaceutical Science Program Assessment Using Curriculum Mapping</td>
<td>131</td>
</tr>
<tr>
<td>20</td>
<td>Professor Perspectives on Barriers to Academic Success in the Sciences</td>
<td>131</td>
</tr>
<tr>
<td>21</td>
<td>Effect of first year biology courses on the students' understanding, and acceptance of evolution</td>
<td>132</td>
</tr>
</tbody>
</table>
Saturday March 22
Session 1 - IB 245
Cell Biology & Biotechnology
1:15 - 2:45 pm
Studies on the Encapsulation of Salivary Anti-microbial Peptides

Emily Chao, Rajesh Gupta, and Walter Siqueira
Western University

Keywords: oral health, antimicrobial, chitosan, drug encapsulation, drug delivery

Maintaining proper oral health is imperative to the quality and overall well being of an individual. Any interruptions in the beginning stages of digestion can compromise the function of other bodily systems. Unfortunately, oral diseases remain prevalent around the world and the practice of good oral hygiene is a challenge for many developing countries. Therefore, cost-effective and convenient means to control and promote good oral health are highly desirable. Recently, chitosan, a cationic polymer derived from the exoskeleton of crustaceans, insects, and fungi, has gained significant attraction in the biomedical field for its biocompatible, biodegradable, and non-toxic properties. Various methods have been employed in the past to prepare chitosan polymer particles for the encapsulation and delivery of desired active components to target tissues. In this study, chitosan nanoparticles have been constructed through ionic gelation methods to be used as a drug encapsulation and delivery system for anti-microbial therapeutic agents to the oral cavity for prevention and combat against various periodontal diseases. The nanoparticles were analyzed for their particle size, size distribution, drug encapsulation efficiency and in vitro release of the model protein Bovine Serum Albumin (BSA). The generation of protein-loaded chitosan nanoparticles is novel in concept and represents a new translational avenue for the modulation of oral biofilms and consequently, the prevention of dental caries, dental erosion, and/or periodontal disease.

Towards DNA-PDA: Handheld DNA sequencer to enable on-site species identification

Norsyuhada Mohktar, Huma Inayat, Mark Levy, Paul Piunno, Sasa Stefanovic, Ulli Krull, and Josh Milstein
University of Toronto Mississauga

Keywords: DNA, sequencing, PCR, bioluminescence, amplification

Significant demand exists for the development of field portable devices for species identification particularly in the areas of food authenticity testing, border inspections and forensics. This has served as the impetus for the development of a handheld DNA sequencer to enable rapid, specific and on-site species identification. The overarching goal of our research project was to investigate and assemble functional elements that are suitable for DNA-based species identification, including DNA extraction, amplification, and sequencing on a microfluidics platform. The two main components that were investigated are: 1) isothermal amplification to produce single-stranded DNA (ssDNA) by combining thermophilic helicase dependant amplification (tHDA) and LATE (asymmetric) PCR to establish new DNA amplification method – LATE tHDA; and 2) Analysis of ssDNA amplicons by on-chip pyrosequencing. The 120 bp mini-barcode region of Gromphadorhina portentosa (hissing cockroach) mitochondrial CO1 gene has been investigated, making use of LATE tHDA, and pyrosequencing that was based on bioluminescence signal production from 10 µL reaction volumes.
Transgenic expression of microbial and fungal carbohydrate-active enzymes in plants

Mary Yang, Katharina Braeutigam, Armand Séguin, Malcolm M Campbell, and Emma R Master

University of Toronto Scarborough

Keywords: Arabidopsis, Poplar, CAZyme, transgene, biorefinery

Plant cell walls have been receiving increasing interest as renewable and abundant starting material for a variety of biorefinery processes. They are comprised of three major fractions, lignin, hemicellulose and cellulose, and can be converted into products such as pulp or biofuels. Plant cell walls are recalcitrant, and the separation of the major fractions is associated with high costs and energy requirements. A modification of cells walls in the plants themselves and prior to pretreatments might provide a strategy to make downstream processes less energy and reagent intensive. In this study, microbial and fungal carbohydrate-active enzymes (CAZymes) were expressed in plants to investigate such an approach. First, the effect of the transgenes was studied in the model organism Arabidopsis thaliana and interesting patterns in plant and cell wall architecture and carbohydrate extractability were detected. Subsequently, Populus plants carrying CAZyme transgenes were investigated to study the effect of the transgenes in an economically important tree species. The described strategy has the potential to improve feedstock quality for biorefinery processes.

Large Scale Study of Biomarker Impact on Clinical Trial Risk on Oncology: Colorectal, Melanoma, Breast and Non-small Lung Cancer

Jayson Parker, Zain Shah, Ashini Weerasinghe, Andy Willan, Adam Falconi, Gilberto Lopes

University of Toronto Mississauga

Keywords: clinical trial, phase, risk, biomarkers, drug approval

Background. The high failure rates of new cancer drugs during clinical testing continue to be a problem. We conducted the largest study to date on biomarker use, by examining four cancers.

Methods. We conducted a retrospective screening of clinical trials sponsored by industry registered with clinicaltrial.gov from 1998 to 2013 for advanced or metastatic breast cancer, colorectal cancer, advanced stage IIIb-IV non-small cell lung cancer and metastatic melanoma cancer. Data was parsed by disease and biomarker status in a log rank analysis. Drugs were excluded if they commenced phase I testing prior to 1998.

Results. The study yielded a total of 36 approved drugs and 1043 drugs under development for all 4 cancers combined. An overall log rank model looking at the effect of biomarker in reducing clinical trial failure rates was statistically significant (p < 0.031) and was statistically powered to 68%. Correcting for data censoring did not find a statistically significant effect within any individual disease.

Conclusion: This is the largest study on biomarker use and provides the first strong evidence that such practices reduce clinical trial failure rates for new drugs developed in oncology. Physicians should prioritize their participation in oncology clinical trials that use a biomarker.
Regulation of Akt Activation by Phospholipase C

Stephen Bautista and Costin Antonescu
Ryerson University

Keywords: EGFR, Akt, PLC, Cell Survival, Cancer

Epidermal Growth Factor (EGF) controls many aspects of cell physiology by binding to its receptor (EGFR). By this mechanism, EGF stimulation leads to the phosphorylation and activation of the kinase Akt, which controls cell survival, metabolism, and proliferation. The secondary signals activated by ligand-bound EGFR leading to Akt activation include the phosphorylation of Gab1, activation of phosphatidylinositol-3-kinase and generation of phosphatidylinositol-(3,4,5)-trisphosphate (PIP3). By a separate pathway, EGF stimulation also activates phospholipase C (PLC), which catalyzes the hydrolysis and consumption of phosphatidylinositol-(4,5)-bisphosphate (PIP2) to generate diacylglycerol (DAG) and inositol triphosphate (IP3). PIP2 is required to generate PIP3. Moreover, PIP2 is required for formation of clathrin-coated pits, protein scaffolds which our laboratory has recently shown to be required for EGF-stimulated Akt activation. Hence, the consumption of PIP2 by PLC may regulate EGF-stimulated Akt activation; however, how this regulation occurs is not known. Using several pharmacological or molecular methods to perturb PLC function including the small molecule PLC inhibitor U73122 and siRNA gene silencing, we have examined the role of PLC in EGF-stimulated Akt activation. RPE cells treated with U73122 showed significant inhibition of EGF-stimulated Gab1 and Akt phosphorylation, but not that of EGFR. Preliminary data suggests that siRNA knockdown of PLCγ1 of inhibited EGF-stimulated Akt phosphorylation. These initial results suggest that PLC may play a significant role in EGF-stimulated Akt activation. Using a Dynamin inhibitor, Dyngo4a, simultaneously with the PLC inhibitor, U73122, resulted in partial rescue of EGF-stimulated Akt activation. Together, these results suggest that PLCγ1 regulates EGF-stimulated Akt activation via control of clathrin-coated pits. Since EGFR, Akt and PLC are often upregulated in human tumors and can each drive tumor progression, this work may allow development of new therapies to treat cancer.

Lysosomal Structure Quantification During PIKfyve Inhibition

Philip Garwood, Christopher Choy, and Roberto J. Botelho
Ryerson University

Keywords: Lysosome, Phosphoinositides, PIKfyve, Vacuolation, Voxels

Cells are composed of organelles, each marked with specific functions and locale. Lysosomes are the end products of the endocytic pathway, maturing into acidified organelles functioning to degrade extracellular material and providing nutrients for cell maintenance and growth. Proteins and lipids associated with endocytic compartment membranes are altered during the course of the maturation process and phospholipids play an integral part of forming organelle identity. Phosphoinositides are a specific species of phospholipid involved in this identification. In particular, phosphatidylinositol 3,5-bisphosphate (PI[3,5]P2), is found to be enriched on lysosomal membranes. The protein kinase responsible for generating PI(3,5)P2 is known to be PIKfyve within mammalian cells and Fab1 in yeast. During inhibition of this protein kinase, it has been shown within yeast to cause severe vacuolation resulting in a 2.5 fold increase in surface membrane of the vacuole. Similar morphological effects can be seen in mammalian cells resulting in the vacuolation of lysosomes, yet the extent of vacuolation has not yet been quantified or examined in great detail. The objective of my research is to quantify lysosomal protein labeled structures during PIKfyve inhibition. Structures can be quantified by attaining three-dimensional images utilizing confocal microscopy, and examining voxel data. My current research involving the inhibition of PIKfyve has shown lysosomal protein voxel increases, raising further questions in determining whether PI(3,5)P2 is an essential phospholipid for lysosomal protein synthesis.
Session 2 - IB 235

Ecology

Saturday March 22
1:15 - 2:45 pm
Inside Yogi's Picnic Basket: Getting Elk (Cervus canadensis) Off the Menu

Sabrina Desjardins, Frank Mallory, and Dave McGeachy
Laurentian University

Keywords: elk calf, Cervus canadensis, diversionary feeding, predation, calf:cow ratios

Information on fluctuations between mortality and natality is essential for understanding population dynamics and to improve management practices. In this study, we examined the impact of diversionary feeding of black bears (Ursus americanus) on elk calf (Cervus elaphus) recruitment in the Burwash area of Ontario, Canada. Black bears (Ursus americanus) are found to predate on calves during a limited time frame, primarily during the first two weeks of life. We used a before after, control impact study design to assess the effectiveness of diversionary feeding during the critical neonate period for elk. Black bears were baited in the Burwash area, whereas no baiting occurred in the Raft Lake area. These two areas are similar in terms predatory species and were used to compare calf/cow ratios in elk. We hypothesize that the use of diversionary feeding would decrease calf mortality, resulting in an increase in recruitment. We visually spotted collared cows from August to December and observed whether there was a calf at heel using a variety of methods including spot and stalk, trail cameras, drives and aerial surveys. Of the 14 female elk in Burwash and 9 in Raft Lake that were collared, 64% in the Burwash herd successfully recruited a calf, while only 33% of collared females in the Raft Lake herd had successfully recruited a calf. We found that female elk in the Burwash herd had a 3.6 times greater chance at successfully recruiting a calf than females in the Raft Lake herd. Further research relating to diversionary feeding should be continued, as this method may be effective for mitigating black bear specific predation on neonate ungulates.

Aggressive behaviour and combat in sexually mature male snapping turtles (Chelydra serpentina)

Brittainy Hewitt, Matt Keevil, Ron Brooks, and Jacqueline Litzgus
Laurentian University

Keywords: snapping turtle, combat, aggression, sexual dimorphism, injury

Aggression between males is observed in many sexually dimorphic animals and male combat often occurs in response to limiting resources such as shelter, food, or females. If females or mating opportunities are limiting factors, then males may compete with one another for access to females. Sexually mature male snapping turtles (Chelydra serpentina), which are larger than females, engage in combat during the mating season and often sustain injuries to the face and tail. I hypothesized that larger males would sustain more injuries compared to smaller males because larger individuals engage in combat more frequently. I also predicted that females would not display combat injuries. Data regarding injuries were extracted from Microsoft Access ® database records spanning 2009 to 2013 from a long-term study (started in 1972 by R.J. Brooks, University of Guelph) in Algonquin Provincial Park, and only records with individual physical descriptions were included in the statistical analyses. I found that larger males sustained more injuries than smaller males indicating that larger males were more aggressive and were more likely to engage in combat. Males had significantly higher than expected rates of injury, and females and juveniles had lower than expected rates of injury. Furthermore, there was a positive relationship between rate of injury and carapace length, supporting the idea that larger body size is advantageous in species that engage in male-male combat. No juveniles had combat-related injuries, suggesting that male-male combat comes with sexual maturity and increased levels of testosterone. In future studies, head measurements of males of different body sizes should be taken to test for allometry, and blood samples should be collected to examine testosterone levels of males involved in combat. Understanding combat between males in snapping turtles has important implications for better understanding the evolution of mating strategies.
Murder mystery in Misery Bay: the demise of turtle species at risk

Andrea Mendler, David Lesbarreres, Anna Sheppard, Matthew Allender, and Jacqueline Litzgus
Laurentian University
Keywords: turtles, mass mortality, ranavirus, molecular, predation

Turtle populations are declining worldwide. Habitat loss, climate change, and disease are some of the major causes associated to these declines. In Misery Bay Provincial Park on Manitoulin Island, 49 Blanding’s Turtles (Emydoidea blandingii; BLTU), a threatened species, were discovered dead last summer. I tested two hypotheses to explain this mass mortality: (1) The mortality was caused by predation; (2) The mortality was a result of an outbreak of ranavirus. Deceased BLTU were photographed and examined for signs of predation. Bone (spine and small bones) and dried skin were collected from deceased animals. Blood, tail tips, cloacal and oral swabs were collected from 4 live BLTU. Toe tips were collected from 13 frogs (n=5 Lithobates clamitans; n=8 Lithobates pipiens) and DNA was extracted from all tissues (n=98) using standard protocols and tested for ranavirus using TaqMan quantitative PCR. Similar inner carapace markings were found in 31 specimens and broken limbs were associated with 14 BLTU; however, no obvious pathologies resulting from predation or scavenging were observed. It is inconclusive whether or not a predator caused the mass mortality. Further studies of the park and its turtle population must be conducted to understand and test the predation hypothesis. Of all 98 DNA samples, only 1 green frog toe clip had low levels of FV3-like virus. Despite these negative results, we cannot confidently exclude ranavirus as the cause of the mortality because the virus is short-lived, therefore it is possible too much time had elapsed for it to be detected. Also, the bone samples may not have had enough marrow, which is where the virus would likely be present. Future studies include collecting different sample types from deceased BLTU for molecular analysis and monitoring of the turtle population for any signs of disease.

How I got frozen out of my soil seed bank study and landed in a field of germinating invading plant species

Aqeel Ahmad
York University
Keywords: soil seed banks, urban to rural gradient, germination rates, native species, non-native species

The structure of the soil seed bank analysis is a relevant though often under-researched aspect of the species composition of present-day forests. Knowledge of seed bank composition is crucial for understanding how future forest regeneration may proceed, because seed bank species are one source of the plants that will grow in the gaps that result from deforestation and forest fragmentation. My project was intended to examine germinable soil seed bank composition along an urban to rural gradient in the Greater Toronto Region. I hypothesized that soil seed banks collected from urban environments will contain a higher abundance of non-native species compared to those in rural environments. Due to unforeseen weather conditions this year, with one of the earliest freeze-ups and coldest winters in 15 years, I was unable to obtain soil samples from the frozen ground. Consequently I shifted my research to questions about the germination rates of native and non-native species sampled from the Greater Toronto Area (GTA). I asked whether the germination rates of non-native, invasive species are greater than those of indigenous species. One often cited life-history characteristic of invasive species is that of high germination of dispersed seeds. I studied four non-native species; Rhamnus cathartica, Cynanchum rossicum, Festuca glauca Elijah Blue, Spartina pectinata Aureomarginata and two native species; Solidago canadensis, and Andropogon scoparius. Preliminary results show moderate germination for 3 of 4 non-native species and moderate to no germination in the two native species.
Some fungal endophytes infect their host plants without producing external symptoms. A group of asymptomatic, systemic endophytes in grasses have been shown to provide their host plant with various benefits, including anti-herbivore resistance, via the production of toxic alkaloids. Previous work on the St. Kilda archipelago (Scotland), where feral sheep undergo periodic population crashes, showed that endophyte hyphal load in the host grass, red fescue, Festuca rubra, increased with increasing grazing pressure. In a separate study, herbivore (moose) saliva applied to artificially cut plants was shown to increase hyphal branching rates of the fungus. I investigated the effects of defoliation (proxy for grazing) and human saliva (proxy for sheep) application on: 1) the endophyte Neotyphodium uncinatum and its host grass meadow fescue, Schedonorus pratensis, and 2) the endophyte Epichloë festucae and its host red fescue. Replicates of five endophyte-infected genotypes of each grass species were assigned to control, low and high cutting treatments in combination with control, low, high saliva applications. Immunoblot (ELISA) assay was used to measure the response in hyphal loading. A bioassay with armyworm, Spodoptera frugiperda, larvae determined the impact of the treatment combinations on toxicity to herbivores. My preliminary results will be discussed.
Session 3 - IB 250

Cell & Molecular Biology

Saturday March 22
1:15 - 2:45 pm
**CCN1 and fibrosis: does CCN1 recruit progenitor cells?**

Megan Kumm and Andrew Leask

Western University

Keywords: fibrosis, CCN1, progenitor cells, migration, wound healing

Fibrosis is implicated in 45% of deaths in the developed world. As such, it is necessary to find an appropriate target for drug intervention. Previous targets have failed, and the attention has now been placed on the CCN family of matricellular proteins. Previous studies have shown that CCN2 is necessary for recruitment of progenitor cells in response to fibrogenic stimuli, but it is unknown if CCN1 acts in a similar manner. Additionally, it has been shown that deleting CCN1 and CCN2 in fibroblasts does not inhibit normal wound healing. Using migration assay and qPCR, we have further characterized the role of CCN1 in progenitor cell recruitment. CCN1-deficient cell culture-activated fibroblasts show impaired migration of fibroblasts. This was accompanied by a reduction in genes associated with migration. Currently, progenitor cells are not believed to be required for wound healing, but they are required for a fibrotic response to occur. These results suggest that a loss of CCN1 inhibits migration which may lead to an inability of progenitor cells to migrate to sites of injury and, therefore, may inhibit a fibrotic response.

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**Assessment of ERG immunohistochemical staining patterns in prostatic evasive anterior tumours (PEATS)**

Osman Mahamud

University of Toronto

Keywords: prostate cancer, TMPRSS2-ERG, immunohistochemical, FISH, anterior

Most prostate cancers arise in the posterior peripheral zone (PZ) of the gland as opposed to the transition zone (TZ) or fibromuscular zone (FMZ) located in the most anterior part of the prostate. Prostatic evasive anterior tumors (PEATS) are prostate cancers characterized by tumours in the anterior prostate, making them difficult to diagnose through conventional transrectal biopsies which target the posterior gland. TMPRSS2-ERG gene fusions are found in approximately 50% of all prostatic cancers and said to be present in 15% of TZ cancers. Positive immunohistochemical staining (IHC) of prostate cancer cells with ERG has been shown to correlate strongly with the presence of this gene rearrangement. The pattern of ERG staining with respect to zonal location of the cancer has not been studied. The aim of our study was to determine the frequency of ERG staining with respect to tumour location in prostatectomies from PEATS cases. Sixteen cases meeting the clinical definition of PEATS were identified in our database. In fifteen, all original H&E prostatectomy slides were available for review. The slides were reviewed to classify the cancer location as being PZ, TZ or FMZ and to select sections for ERG IHC. One or two sections from the anterior prostate with the largest cancer foci were chosen to represent PEATS areas and one section (where possible) with a separate cancer focus in the posterior PZ were chosen for analysis. The selected sections were stained with ERG and the cancer foci scored as being positive or negative. The anterior cancer foci were located predominantly in the TZ in 7/15 (48%) cases, FMZ in 4/15 (26%) or straddling the TZ and PZ in 4/15 (26%). No PEATS cases were found where the tumour was predominantly in the anterior PZ. Positive ERG IHC was found in 6/15 cases (40%) when posterior and anterior cancer foci were considered, with 4/6 (67%) positive foci being exclusively in the PZ. Only 1/6 (17%) ERG positive cases had positive IHC in the TZ-predominant focus. Similarly, only 1/6 (17%) ERG positive cases had positive IHC in the FMZ-predominant focus. The cancer in PEATS cases are predominantly located in the TZ and FMZ of the prostate and are 2-fold less likely to show positive ERG IHC than most prostate cancers which are found in the PZ. Our findings suggest PEATS may represent a distinct subset of prostate cancer in terms of molecular pathogenesis.
Expression and Function of Tuberin in Early Embryonic Brain Development

Rutu Patel
University of Windsor

Keywords: Tuberin, Tuberous Sclerosis, brain development, neurogenesis, hamartomas

Tumour suppressor genes TSC1 and TSC2, coding for proteins Hamartin and Tuberin respectively, are two key controllers of cell growth and proliferation. Mutations in either TSC1 or TSC2 lead to an autosomal dominant disorder, Tuberous Sclerosis (TS), which is characterized by the formation of tumours known as hamartomas, in several organs. Mutations in TSC2 present more severe phenotypes associated with pathologies in many tissues including the brain. TSC2 null mice are embryonic lethal with improper development of the brain. Collectively these data support the hypothesis that Tuberin plays an important role in neurogenesis. The focus of my research is to monitor changes in Tuberin expression levels from early embryonic time points to later periods of growth in various regions of the brain. Using immunohistochemistry techniques, I have early data to indicate that Tuberin protein levels are elevated in regions of the brain critical for development of the cerebellum and at stages of development that are critical for neurogenesis. The results from my study may provide insight into the developmental processes and pathways that are involved in TS.

AMPK signaling and autophagy in ovarian cancer cell survival

Aneesha Sood and Trevor Shepherd
Western University

Keywords: ovarian cancer, AMPK signalling, autophagy pathway, cell viability, cell morphology

Ovarian cancer is the most serious of all gynaecologic cancers in the Western world, and the sixth most prevalent cancer among women. Almost all ovarian cancer patients die from chemotherapy-resistant metastasis, a period of the disease during which ovarian cancer cells require altered metabolism for cell survival to combat conditions of nutrient deprivation. SKOV3, OVCA429, and HEYA8 ovarian cancer cells were used to determine whether the metabolic stress response pathway of AMP-activated protein kinase (AMPK) signaling promotes cell survival via activation of autophagy. Synergistic effects on reduced viability and morphology were apparent when cells were treated with the AMPK activator AICA riboside in combination with the autophagy inhibitor chloroquine. Activation of AMPK and inhibition of autophagy were verified by western blotting. These results identify that the AMPK-autophagy survival pathway could be an effective target with novel therapeutics to more effectively kill metastatic ovarian cancer cells that evade current chemotherapies.
Purification and Characterization of the β-Barrel Domain of BcsC to Investigate its Role in Cellulose Export from *E. coli*

Deanna MacNeil, Emily Wilson, and Joel Weadge

Wilfrid Laurier University

Keywords: Cellulose, *E. coli*, Biofilms

The ability of a bacterial colony to persist within its environment is influenced by the colony’s capacity for biofilm formation. This is of particular interest in enteric bacteria like *Escherichia coli*, which colonize the gut of living organisms and are frequently responsible for chronic infections leading to diarrhea, nausea, and severe stomach cramping. Biofilms are complex extracellular matrices which confer protection to a colony of bacteria functioning as a cohesive group. Exopolysaccharides are primary components in these matrices; a known major component in biofilms of *E. coli* is cellulose. Three proteins from the bacterial cellulose synthase family have already been described in some detail though BcsC, the protein necessary for cellulose export has not yet been characterized. Understanding more about the β-barrel functional domain of BcsC will provide insight into the export of bacterial cellulose, as well as knowledge of important features for other outer membrane porin proteins. The ultimate goal of this research is to purify and characterize the β-barrel functional domain of BcsC in *E. coli*.

Metals in Sudbury Particulate Matter upregulate hypoxia-inducible factor (HIF)-1α and may be associated with airway remodelling

Chanelle Frappier-Doyon, Sandhya Khurana, Sarah White, Stacey A. Ritz

Laurentian University

Keywords: HIF-1α, airway remodelling, SPaM, nickel, air pollution

Air pollution is a heterogeneous mixture of suspended liquid droplets and particulate matter (PM), which is known to have many adverse health effects. The chemical composition of PM varies with the local environment, and is known to contain a variety of metals. PM in Sudbury, ON (SPaM) is relatively high in nickel (Ni) and cobalt (Co) due to the mining, smelting and refining activity in this region. Previous preliminary data had suggested that airway remodeling and angiogenesis may occur in mice exposed to SPaM. In this study our objective was to quantify airway remodeling in SPaM-exposed mice, and to elucidate the molecular pathways involved.

Lung tissues from Balb/c mice exposed to an aerosol containing SPaM 5x/week were evaluated histologically in a semi-quantitative fashion. Mice exposed to SPaM for 8 weeks had higher numbers of blood vessels and elastin in the walls of the vessels than control mice or those exposed to other types of particulates, though this did not reach statistical significance. We hypothesized that these changes could be caused by upregulation of hypoxia inducible factor 1α (HIF-1α) by Ni or Co, which is known to promote angiogenesis and tissue remodeling by upregulating expression of vascular endothelial growth factor (VEGF-1) and transforming growth factor β (TGFβ). To investigate these pathways further, A549 airway epithelial cells were exposed to Ni, Co, or SPaM in vitro. Immunofluorescence analysis demonstrated an upregulation of HIF-1α in cells stimulated with Ni, Co, and SPaM compared to controls. VEGF-1 levels were increased in cell culture supernatants in response to SPaM, however no increase in TGFβ was observed. Further studies will use real-time quantitative PCR to examine gene expression of VEGF-1 and TGFβ from lung tissues. These findings suggest that inhalation of particulate air pollution could affect lung architecture due to metal-induced upregulation of HIF-1α.
Session 4 - IB 260

Neurobiology

Saturday March 22
1:15 - 2:45 pm
Neural versus peripheral contributions to the masculinization of male sexual preference in olfaction

Daniel Almeida, Ashlyn Swift-Gallant, Barrington Kretschmer, and Ashley Monks
University of Toronto Mississauga

Keywords: androgen receptors, hormones, sexual differentiation, sexual behaviour, olfactory preference, transgenic mice

It is well known that sexual dimorphisms in the CNS are the result of complex interactions between an organism's genetic sex, and their hormonal profile. These neuroanatomical dimorphisms translate into differences in sociosexual behavior, including sexual preferences observed in olfaction. The role that androgens receptors (AR) play in the masculinization of this preference has been widely studied in models of androgen insensitivity, namely testicular feminization mutation (Tfm). Based off of the current Tfm literature, AR acts to organize the masculinization of neural circuitry responsible for the execution of male specific sexual behavior. However, it is unclear as to whether AR's exert their masculinizing effects on sexual preference via neural or non-neural (peripheral) tissue. Unlike much of the AR literature, we have employed the use of transgenic mice lines that overexpress AR globally (CMV\textsuperscript{Cre}) and selectively in neural tissue (CMV\textsuperscript{Cre}). Our data suggests that global, but not neural overexpression of AR impairs male sexual olfactory preference.

The Effects of Sodium Salicylate on the Expression of GABAB Receptors in the Rat Hippocampus

Nam Vo, Sehrish Butt and Huiming Zhang
University of Windsor

Keywords: GABA receptor, sodium salicylate, hippocampus, immunohistochemistry, albino rats

Sodium salicylate (SS) is an anti-inflammatory drug and it is an active ingredient of Aspirin. SS can produce side effects including a phantom auditory sensation, i.e., tinnitus. Research in our laboratory has shown that systemic application of SS causes a decrease in the expression of GABAB receptors in certain auditory structures. Such a change might affect the function of the auditory system and result in tinnitus. The GABAB receptor is a metabotropic receptor essential for the function of the nervous system. A functional GABAB receptor consists of two subunits, i.e., GABABR1 and GABABR2. High levels of GABAB receptors are found in the hippocampus. Existing results indicate that this receptor is important for neurobiological processes in the hippocampus including those related to learning and memory. In light of the fact that SS can reduce the expression of the GABAB receptor in auditory neural structures, we hypothesized that SS could also reduce the expression of the GABAB receptor in the hippocampus. In the present study, SS was given to male Wistar rats using intraperitoneal injections. Immunohistochemical techniques were used to probe drug-induced change in the regional as well as cellular distribution of both subunits of the GABAB receptor in the hippocampus of these rats. Preliminary results show that the expression of the GABABR1 subunit in dorsal regions of the hippocampus can be reduced 3 hours after the injection of a single dose of SS. The present study of the effect of SS on the expression of the GABAB receptor in the hippocampus will help us understand side effects of the drug including those on spatial learning.
Organization of Glomerular Chains in the Olfactory Bulb of Chinook Salmon Fry

Tina Suntres  
University of Windsor  

Keywords: olfactory bulb, Chinook salmon, glomeruli, immunohistochemistry, calretinin

Vital to a Chinook salmon’s success in life is its olfactory system. Olfactory sensory neurons (OSNs) project from the nasal epithelium, where odour molecules are detected, to the olfactory bulb (OB), where odour information is processed, OSNs stimulated by amino acid odours project to the lateral OB region where axon endings cluster forming glomerular chains. Chinook salmon use amino acids for feeding and possibly for imprinting and homing to natal waters to spawn. To develop an understanding of the organization of OSN axon endings in the OB of Chinook salmon fry, we applied immunohistochemistry to label serial OB sections. An antibody against keyhole limpet hemocyanin non-selectively labelled OSN axons and a calretinin antibody which labelled microvillous OSNs that extend to lateral OB glomeruli. An extended protocol was adapted to optimize the labelling and sections collected in three different planes created a multidimensional perspective of glomerular chain organization within the OB. We found large glomerular chains located dorsally, as well as a clustering of small chains ventrally. A large calretinin immunoreactive chain was located in the lateral portion of the OB. Our results showed consistent organization of glomerular chains in Chinook salmon fry. These techniques are now being used to test the effects of olfactory enrichment of the organization of OSN axons in these same glomerular chains.

Neuroefficiency in Elite Curlers Related to Shot Performance

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Laurentian University  

Keywords: EEG, curling, neuroefficiency, experts, novice

Past studies have demonstrated that elite athletes possess a neuroefficiency that corresponds to better performance. The purpose of this study was to observe differences in cortical activation between novice and expert curlers during the pre-shot routine period, as well as discovering the electrophysiological activity that represents a peak performance state. Seven experienced curlers (four novices and three experts) took part in this study in which electroencephalographic data were recorded for four seconds prior to each shot for a total of eight shots to the button (target), the performance of which were measured by the distance from the target in cm. We found that experts had significantly lower activation in the left hemisphere than novices; the most consistent differences being in the occipital lobe where experts had significantly more power in the right occipital, whereas novices were more active in the left (P<0.05). When viewing individual trials between participants we observed considerable differences in hemispheric alpha power between experts and novices. There were no significant differences between groups in the first trial of the experiment; however, by the final trial, experts demonstrated significantly different inter-hemispheric alpha power (increased right and decreased left) compared to novices (P<0.05). These differences in cortical activation suggest a neuroefficiency in experts during performance of a task which they have practiced on numerous occasions, further supported by significantly better performance by experts (P<0.05). We also found that better performance was indicated by increased activation in the right parietal lobe due to increased beta, and decreased alpha power (P<0.01); however, individual EEG profiles differed between participants. These findings lay the groundwork for future studies into personalized neurofeedback training strategies for the development of superior curling athletes.
The Localization of Axons Projecting from the Accessory Olfactory Organ in the Sea Lamprey

Akhil Sharma, Warren Green, and Barbara Zielinski

University of Windsor

Keywords: retrograde labeling, anterograde labeling, accessory olfactory epithelium, main olfactory epithelium, medial glomerulus

Abstract: Olfaction plays an important role in the social and reproductive behaviours of many animals in the vertebrate subphylum. The olfactory system of the sea lamprey (Petromyzon marinus) contains two spatially distinct olfactory subsystems that respond to pheromones and amino acids. Olfactory sensory neurons in the main olfactory epithelium (MOE) project to non-medial olfactory bulb regions, that stimulate the lateral pallium. Previous retrograde labeling has shown that short ciliated sensory neurons in the accessory olfactory epithelium (AOE) project to the medial glomerulus of the olfactory bulb, which activates the posterior tuberculum, a dopaminergic midbrain structure that stimulates movement control by activating reticulospinal cells. AOE projections also reach the dorsal telencephalic neuropil. While these retrograde labeling studies are informative, anterograde labeling will directly demonstrate the location of axons projecting from the AOE. We applied neuroanatomical tracers to AOE and observed the labeling of axonal projections in the brain. Although these studies are ongoing, initial observations confirm that the AOE neurons extend to the medial region of the olfactory bulb. This observation confirms the pathway of AOE olfactory sensory neurons terminating to medial glomerulus. These projections from the AOE to the medial glomerulus are spatially distinct from fibers extending from the MOE. This study supports previous studies of the lamprey's two subsystems that control movement through two different brain relays.

The spatial distribution of the serotonergic fibers in the olfactory bulb of the sea lamprey

Zeenat Aurangzeb, Barbara Zielinski, and Karl Boyes

University of Windsor

Keywords: immunocytochemistry, serotonergic (5-HT) fibers, neurons, microscopy, the olfactory bulb

Abstract: The basal vertebrate, the sea lamprey (Petromyzon marinus), senses odours such as pheromones and transmits this information to the olfactory bulb (OB) in a spatially organized manner. From the OB, projection neurons send this information to higher brain structures. In the OB, olfactory sensory neurons (OSN) terminate in the glomerular layer, which surrounds the granular cell layer. The OB also contains serotonergic (5-HT) fibers that have been demonstrated to attenuate odour responses. The distributions of 5-HT fibers have been observed to extend into the OB from the dorsal raphe in the midbrain. However, the distribution of 5-HT in the OB remains unclear. In this study, the 5-HT fibers were immune-labelled and the OSN's were labelled with GS1β4 lectin. Fine intertwined 5-HT fibers were located in the OB granule cell layer and did not enter the glomerular layer, but some 5-HT fibers were seen between individual glomerular groupings. Within the granular cell layer, 5-HT fibers were sparse in the rostral portion of the OB, compared to the dense network of fibers in the caudal region. The 5-HT-immune-reactive fibers were evenly distributed in the medial, lateral, ventral, and dorsal regions of the OB in which each region responds to different odours. Overall, this distribution may imply that 5-HT attenuation of olfactory sensory responses may be more prevalent at the caudal end of OB than in the rostral region.
Session 5 - IB 270

Health

Saturday March 22
1:15 - 2:45 pm
Stress Hormones and their Effects on Reproduction in Captive Bactrian Camels

Albrecht Schulte-Hostedde, Gabriela Mastromonaco, and James Howatt
Laurentian University

Keywords: camel, reproduction, captive breeding, cortisol, endangered

In this study the cortisol levels of captive bred Bactrian camels were studied to look at the relation between long term stress and reproduction. Hair samples were taken from 14 subjects in three different zoos and put through cortisol extraction techniques such as cortisol assay. Data on temperature and precipitation from the three study sites were collected. The correlation between cortisol levels and offspring produced was not significant. The correlation between average precipitation for each study site and the average cortisol level was found to be significant. It is theorized that the fluctuation in environmental parameters causes a direct fluctuation in the cortisol level of the camels. This fluctuation in cortisol is also theorized to cause health side effects that can potentially alter the animals’ ability to reproduce at a level seen in animals with a lesser cortisol levels. For future studies in this field a greater sample size would be needed in order to get an idea of the captive populations’ cortisol level. Long term studies can also include a look at the reduction in cortisol level over generations of captive animals and that effect on re-release and survival rate.

Identifying pathogenic mutations in patients with atypical progeria

Amanda Tong, Sali M. K. Farhan, Adam Mcintyre, Henian Cao and Robert A. Hegele
Western University

Keywords: metabolism, next generation sequencing (NGS), rare disease, Hutchinson-Gilford Progeria Syndrome, aging disease

Hutchinson-Gilford Progeria Syndrome (HGPS), commonly known as progeria, is an extremely rare genetic disease which dramatically shortens the lifespan of those afflicted the cellular growth rate is eight to ten times faster than healthy individuals. Typically, HGPS is due to a single base substitution within the LMNA gene, resulting in a truncated and toxic protein called progerin. There have been instances of genetic heterogeneity in which patients presenting HGPS have no LMNA mutations, but may have mutations in other metabolism-related genes. My thesis project aims to uncover the genetic basis of atypical forms of progeria, by screening four genetically idiopathic progeroid patient samples for mutations in other genes that are involved in similar metabolic pathways. Recently, our lab has developed a custom designed next-generation sequencing (NGS) gene panel that allows for rapid detection of genetic variants in a subset of 73 preselected metabolism-related genes. This targeted sequencing approach known as LipidSeq, is an economic and specific approach and has been successful in identifying the genetics of monogenic dyslipidemias, and related disorders, and is used instead of the current genome tools such as Sanger, whole-genome or whole-exome sequencing. Following sequencing, genome assembly was performed using CLC Bio Genomics Workbench, a genome analysis pipeline that aligns the patients' newly sequenced genome to the full NCBI human genome and allows for variant calling. Given the rarity and severity of the patients’ phenotype, a non-synonymous, rare variant (minor allelic frequency <1%) was employed and identified several potentially pathogenic genetic variants in each patient sample, which will be presented. All genetic variants identified will be validated using functional studies to determine the genetic cause of HGPS observed in these patients. Results of this study could help elucidate the genetic cause of progeria, implicate new biological pathways, and provide possible drug therapy targets for HGPS-like symptoms.
The Influence of chronic Cu exposure on the uptake and effect of Ag in Rainbow trout (Oncorhynchus mykiss)

Amy Clement and James McGeer
Wilfrid Laurier University

Keywords: rainbow trout, copper, silver, stress physiology, accumulation

Exposure to metals is known to have detrimental effects on aquatic life forms such as fish. Toxicity of metals depends on the exposure conditions that influence bioavailability and also on the mechanisms of toxic action. Copper and silver are known to have the same mechanism of acute toxicity, which involves disturbance of sodium homeostasis. Extensive research has been conducted on the toxicity of each of these metals individually but in reality, fish in contaminated environments experience exposure to a mixture of these and other metals. The research I worked on is helping to develop an understanding of how metals with similar mechanisms of toxicity interact to influence physiological outcomes of exposure. In my study I examined how acclimation to one metal (Cu) influences the accumulation and impact of Ag. Rainbow trout were exposed to Cu concentrations from 0 to 80 µg/L for 14 d. Following this, fish were exposed to Ag at a concentration of 2 µg/L for 4 days. My hypothesis is that exposure to Cu will alter Na uptake dynamics and this will exacerbate the impact of Ag exposure. Throughout the exposures samples of gill, liver, bladder, kidney and white muscle were collected and analyzed to determine concentrations of accumulated metal. Blood samples were also collected via caudal puncture and centrifuged in order to extract plasma which were then analyzed for Na. Comparisons were made between the accumulation of Ag and disruption of plasma sodium levels in fish that had previously been exposed to copper and those that have not by ANOVA.

What is the evidence for post-operative prophylactic antibiotics after primary hip and knee arthroplasty? A systematic review

Silvio Ndoja, Michael Riediger, Nathan Evaniew, and Michelle Ghert
McMaster University

Keywords: systematic review, prophylactic antibiotics, post-operative antibiotics, evidence based medicine, total joint replacement, orthopaedic surgery

The number of total joint arthroplasties (TJAs) is on the rise as it provides an effective treatment for osteoarthritis. While TJAs are effective at returning quality of life, the risk of infection is becoming more apparent. Prosthetic joint infections (PJIs) can be very difficult to treat and can result in devastating outcomes. Prophylactic antibiotics are administered as a precautionary measurement in order to minimize the incident rates of PJIs and there is considerable evidence for their efficacy in the literature for their pre-operative use. The literature is mixed for continuous use of prophylactic antibiotic use post-operatively, resulting in a large variability in what surgeons are prescribing in their practice. Guidelines recommend continued antibiotic administration to not extend past 24 hours, with some recommending to not extend past wound closure. However, the inappropriate use of antibiotics has led to an increase in antibiotic resistant strains, such as MRSA, and antibiotic related side effects. The purpose of this systematic review is to assess the available evidence for post-operative prophylactic antibiotic use in patients undergoing primary total knee, and, or hip replacement due to primary osteoarthritis. Our search strategy yielded 4863 articles to be reviewed. Upon titles and abstract screening, 416 were included for full review, 98 of which were included for analysis. Our results showed an absence of high level evidence for continued antibiotic administration after total knee and hip replacement surgery. RCTs in the literature are very heterogeneous comparing different agents or time courses, but overall there were no significant differences in infection rates in the comparator groups. Surgeons should proceed with caution in antibiotic administration in total joint replacement surgeries given the absence of strong evidence to support added benefit of the use of antibiotics post-operatively.
Role of Spy1 in CKI-Treated Multiple Myeloma

Jacob Pfaff
University of Windsor

Keywords: multiple myeloma, cancer, CKIs, Spy1, chemotherapy

Human multiple myeloma, the second most prevalent hematopoietic malignancy, is a cancer affecting the plasma cells of the bone marrow. Presently, myeloma is an incurable malignancy; thus, novel biologically based therapies are urgently needed.

An attractive therapeutic approach is the use of synthetic cyclin dependant kinase (Cdk) inhibitors (CKIs), which function analogous to endogenously expressed CKIs to inhibit Cyclin-Cdk complexes and halt the cell cycle. Despite some success in early clinical trials, the use of synthetic CKIs alone does not eradicate the cancer and some patients are unresponsive. Our lab studies a novel cell cycle regulator protein, Spy1, which is capable of uniquely activating Cdns. One important aspect of Spy1-mediated Cdk activity is the ability of Spy1 to activate the Cdk in the presence of CKIs. This suggests that Spy1 levels may play a role in the resistance of multiple myeloma to CKI treatment. Importantly, prior work in the lab has demonstrated that Spy1 protein is found at elevated levels in a variety of human myeloma tumours. Our work tests the hypothesis that the cell cycle regulator, Spy1, plays an important role in the relative sensitivity of multiple myeloma cells to synthetic CKIs treatment. Using western blot analysis to quantify relative amounts of Spy1 protein over a panel of cell lines, we have correlated levels with relative sensitivity to the CKI, purvalanol A. Early results suggest that cell lines with higher expression of Spy1 are less sensitive to the treatment of the CKI, purvalanol A. These results provide the exciting possibility that more effective treatments may be possible through the use of CKIs in conjunction with Spy1 inhibitors.
Session 6 - IB 280

Animal Behaviour

Saturday March 22
1:15 - 2:45 pm
Influences of anthropogenic noise pollution on the calling patterns of the round goby, *Neogobius melanostomus*

Bronson Goodfellow, Sarah Humphrey, and Dennis Higgs

University of Windsor

Keywords: acoustic signalling, anthropogenic noise, round goby, passive acoustics, masking

Anthropogenic noise pollution has been shown to have a variety of effects on acoustic communication and subsequent reproductive success may be decreased in many species of fish that use sound as their primary sensory modality. Biologically relevant sounds can be masked by anthropogenic noise such as passing vessels and pile driving. In the current study we used passive acoustics to monitor low frequency, pulsatile auditory signals produced by the round goby, *Neogobius melanostomus*. Stationary acoustic dataloggers were submerged the near the channel entrance to the Rondeau Harbor in Erieau, Ontario along the north western basin of Lake Erie between May and September of 2013. This location provided ample anthropogenic noise via commercial and recreational boat traffic through the channel. Dataloggers were deployed in shallow and deep waters where they recorded sound at a rate of one minute every ten minutes. Goby calls were identified visually through spectral analysis and organized by the presence or absence of background anthropogenic noise. Preliminary results indicate less acoustic signaling during periods of high anthropogenic background noise disturbance. This study aims to contribute to advances in the general understanding of the impact of anthropogenic noise pollution.

Ecologically matching swim performance for the reintroduction of Atlantic Salmon into Lake Ontario

Jessica Mayrand and Trevor Pitcher

University of Windsor

Keywords: Atlantic salmon, anthropogenic extirpation, swim performance, morphology, ecological matching

Extirpation of Atlantic Salmon (Salmo salar) from Lake Ontario occurred in the early 1900s due to anthropogenic pressures. Since the 1980’s when habitat quality in tributaries of Lake Ontario improved significantly, there has been an ongoing effort to reintroduce Atlantic salmon to Lake Ontario in the hopes of establishing a self-sustaining population. Recent efforts have focused on the use of two stains of salmon from the LaHave River and Sebago River. Because swim performance is directly related to juvenile survivorship in Atlantic salmon, this study examined the swimming performance and body shape morphometric data of the two populations. Critical swim speeds of juveniles from each population was examined using a swim flume. Morphometric analyses included seven phenotypic variables (important to swimming performance in juvenile salmon). These results will be discussed in the context of which strain of Atlantic salmon is hypothesized to be more ideal for reintroduction to Lake Ontario tributaries.
An investigation of grouping behaviour in a social fish in the presence of olfactory and visual cues of predation

A. Odetunde, C.M. O'Connor, A.R. Reddon, and S. Balshine

McMaster University

Keywords: anti-predator behaviour, visual predator, olfactory alarm cue, grouping behaviour, Neolamprologus pulcher

Group living is associated with both benefits, such as more efficient defence of a shared territory, as well as costs, such as increased competition for food and mates. Therefore, the degree to which individuals are expected to prefer to group and preferred group size will depend on the ecological conditions. For example, previous studies have shown that many fish species form larger groups when exposed to predators, but tend to disperse when exposed to food odours. In the current study, we investigated how group size preference changed in the presence of olfactory and visual cues of predation, using a full-factorial design, in a cooperatively breeding cichlid fish, Neolamprologus pulcher. We presented focal N. pulcher with the choice between joining a small or large group, when exposed to different combinations of cues of predation. We found that these social fish had a baseline preference for the larger group when not exposed to predation cues. However, this preference disappeared when the focal fish were exposed to cues of predation. This somewhat counter-intuitive result suggests that N. pulcher do not use a simple ‘safety in number’ grouping response as an anti-predator behaviour. Thus, more complex factors, such as the superior ability to maintain or defend a territory or offspring in a group, are likely important factors in driving the evolution of group living in this highly social fish.

Social or solitary: Grouping preferences in invasive round goby (Neogobius melanostomus)

Pauline Capelle, Erin McCallum, and Sigal Balshine

McMaster University

Keywords: Invasive species, Round goby, Social behaviour, Aggression, Hamilton Harbour

Invasion biology research has identified two juxtaposing behavioural traits, aggressiveness and sociality, that may both increase the success of invasion. Highly aggressive invaders can out-compete native species for resources, while gregarious invaders can live in high density groups. In order to tease apart the impacts of these seemingly conflicting behaviours on the success of invasive species, we studied round goby (Neogobius melanostomus), a highly successful invasive fish species in the Laurentian Great Lakes. While round goby are known for being aggressive, less is known about their social tendencies, despite the fact that they thrive in extremely high densities. We collected round goby from Hamilton Harbour, ON, Canada, and looked at group-forming behaviour by measuring preference for a single conspecific versus remaining alone, preference for small versus large groups, and preference for a conspecific versus a shelter. We found that round goby have a strong preference to associate with a conspecific, but this preference is not modulated by sex or group size. Females chose the safety of shelter over safety in numbers, while males did not show this preference. Our results provide new insight into the roles of aggressive and social behaviours in the rapid spread of invasive round goby.
Stability in the dominance hierarchy of a cooperatively breeding cichlid fish

Q. Y. Joanne Tan, Cody J. Dey, Adam R. Reddon, Constance M. O'Connor, Jonathan Dushoff, and Sigal Balshine

McMaster University

Keywords: Social network analysis (SNA), dominance behaviour, reproduction, cooperative breeding, Neolamprologus pulcher

Dominance relationships are an important part of the social lives of many animals. In the cooperatively breeding Neolamprologus pulcher cichlid, reproduction is highly skewed to a pair of dominant breeders, and subordinate helpers form a size-based queue for social rank and reproduction. In a previous study, dominance relationships within N. pulcher groups were found to be highly transitive, and dominance interactions were most intense among high-ranked individuals. However, we do not currently know how patterns of dominance interactions vary between ecological contexts. For example, reproductive periods can be intensely competitive and animals may adjust their aggressive and submissive behavior in order to influence their inclusive fitness or suppress the reproduction of other group members. Reproductive events therefore, represent an important life-history stage in which to study dominance interactions. Here, I use social network analyses (SNA) to examine changes in dominance interactions over different contexts. Using SNA, I compare dominance interactions in 13 N. pulcher groups during reproductive periods and non-reproductive periods. I found that patterns of dominance interactions did not show significant changes between reproductive and non-reproductive periods. Dominance networks did not become more skewed towards the top of the hierarchy, nor did they become more sex-specific during reproductive periods. This is the first study to use SNA to compare replicate N. pulcher groups under different contexts, and thus is able to draw general conclusions about the focal species. These findings suggest that dominance relationships within the N. pulcher groups are stable and unaffected by reproductive bouts.

Partner Preference in Naked Mole Rats with Consideration of Pregnancy Dynamics

Yamna Rizwan

University of Toronto Mississauga

Keywords: Naked mole rat, partner preference, eusociality, breeding male, subordinate male, queen, subordinate female, pregnant

Partner preference has been studied extensively in social animals such as the mouse, rat and prairie vole. However, partner preference in the eusocial naked mole rat (NMR), Heterocephalus glaber, has not been explored thus far. The present study examined partner preference in NMRs, with regards to the pregnancy status of the colony queen. The potential preferential behaviour of breeding males and subordinate males to queens (pregnant or non-pregnant) or subordinate females was analysed via Ethovision XT video-tracking of a 10 minute experimental period. Throughout this period, a colony’s (breeding or subordinate) male’s movements toward one or the other female was tracked as it moved around the centre of a 3-sectioned chamber with side-boxes holding the queen of the colony and a subordinate female - also from the same colony - on either side. Four non-pregnant colonies and four pregnant colonies were used, with four individuals selected from each colony: a breeding male, a subordinate male, a non-pregnant/pregnant queen, and a subordinate female. A total of 3 trials were conducted per colony, for a maximum of 46 trials (one colony had only 2 trials), using 32 individuals in total (females: n=16; males: n=16). Statistical analysis of the video tracking found no significant preferences of breeding males toward the queen (pregnant or non-pregnant) or the subordinate female. However, there was apparent (although not statistically significant) preferential behaviour seen among subordinate males, in which they preferred the non-pregnant queen for a much longer time than which they preferred the subordinate female, but had no apparent preference for either the subordinate female or the queen when the latter was pregnant. This study breaks ground on a new area of research in the naked mole-rat. However, future studies with a larger number of colonies, as well as a greater number of trials, should be conducted in order to validate this study's results in a statistically significant manner, and determine the underlying causes of the preferential behaviour observed.
**Stress Response of Starved *Tetrahymena thermophilia***

Ghazaleh Goldar, Costin Antonescu and Jeffrey Fillingham

Keywords: Tetrahymena thermophilia, Starvation, Stress response, Cell signalling, Membrane trafficking

The plasma membrane is the surface through which all cells communicate with their environment. As such, the cell surface membrane harbors proteins responsible for nutrient uptake, intercellular signaling and adhesion. In order to appropriately respond to the environment, the cell surface proteins, collectively called the cell surface protein, must be tightly regulated. To learn more about the way membrane proteins are altered and regulated during cellular starvation (a form of stress that requires organism adaptation), *Tetrahymena thermophilia*, unicellular ciliated protozoan was used as a model organism. The purpose of this research project was to study how the cellular stress of starvation (metabolic stress) control the cell surface proteome in *T. thermophilia*. We used a strategy involving labeling of extracellular-exposed proteins with a membrane-impermeant biotinylation reagent followed by purification of biotinylated proteins. Using this method we aim to identify how these organisms control the membrane trafficking and membrane protein composition in order to survive the starvation state. Following SDS-PAGE and silver stain, we observed that starvation induced a substantial change in composition and abundance of the cell surface proteins compared to what was seen in non-starved cells. Future work will examine how the cell surface abundance of specific proteins is altered during starvation stress, allowing a better understanding of the regulation of membrane traffic and cellular adaption.

**In Vivo Functional Characterization of Human Mdm2 and MdmX RING Domains***

Heather Lau, Olga Egorova, and Yi Sheng

York University

Keywords: E3 ligase, protein:protein interactions, RING domain, immunoblotting, colony formation assay, flow cytometry

The tumour suppressor p53 plays a critical role in cell cycle arrest and apoptosis. Mdm2 and MdmX are negative regulators of p53, and work by binding and inhibiting its transcriptional activity. Mdm2 also targets p53, MdmX, and itself for proteasomal degradation. A conserved C-terminal RING domain is believed to be primarily responsible for this E3 ligase activity. However, despite the presence of a RING domain in MdmX, the protein possesses no intrinsic E3 ligase ability and its regulation of p53 may be primarily mediated by its interaction with Mdm2 – also via their RING domains. Previous studies involving site-directed mutagenesis found certain amino acid differences between the MdmX and Mdm2 RING domains. These alterations are believed to be the source E3 ligase ability differences, though the exact function of the MdmX RING domain has yet to be characterized. Here, in vivo studies involving ectopically expressed Mdm2-RING and MdmX-RING fusion domains were conducted in the U2OS mammalian cell line. FLAG-tagged Mdm2-RING and MdmX-RING were ectopically expressed in U2OS cells and their effects on p53 levels and activation were examined. Results showed that Mdm2-RING and MdmX-RING stabilized both endogenous Mdm2 and MdmX, but had little effect on p53 levels in the cell. MdmX-RING overexpression also reduced p21 levels, suggesting its inhibitory effect on p53 activation. U2OS colony formation assays showed higher growth with the MdmX-RING constructs and fewer colonies with the Mdm2-RING construct, implying MdmX-RING possessed more oncogenic potential. This study provides new insight into the function of the Mdm2 and MdmX RING domains and their role in p53 regulation.
Determining the Role of Src Family Kinases on EGF-Stimulated Akt Phosphorylation

Stefanie Lucarelli and Costin Antonescu

Ryerson University

Keywords: EGFR, SFK, Akt, Cancer, Clathrin

Akt is a kinase activated by several mechanisms, including stimulation with epidermal growth factor (EGF), and is a critical regulator of cell survival, metabolism and proliferation. EGF binding its receptor (EGFR) results in EGFR phosphorylation, leading to the recruitment of signaling intermediates to the receptor including Gab1 and PI3-Kinase resulting in the production of phosphatidylinositol-3,4,5-trisphosphate (PIP3). Akt is recruited to the membrane by PIP3 binding, resulting in its activation through phosphorylation at T308 and S473. Src-family kinases (SFKs) contribute to EGF-stimulated EGFR phosphorylation, and may also be required for EGF-stimulated Akt activation, yet this molecular mechanism remains unclear. Concurrent to activation of signaling pathways, EGF binding EGFR results in receptor recruitment to clathrin-coated pits (CCPs), protein assemblies at the plasma membrane involved in endocytosis. Our laboratory has identified that clathrin, the core scaffolding protein within CCPs, is required for EGF-stimulated Akt phosphorylation. We aim to determine the mechanism by which SFKs participate in clathrin-dependent activation of Akt by EGFR. Treatment of cells with SFK inhibitor Dasatinib resulted in the virtually complete loss of c-Src activity. Dasatinib treatment also inhibited EGF-stimulated phosphorylation of Akt at S473 and T308, Gab1 at Y627, and EGFR at Y845. These results confirm previous studies that used other SFK inhibitors (e.g. PP1), and seem consistent with a role for SFKs in EGF-stimulated Akt phosphorylation. However, drug titration experiments reveal that c-Src autophosphorylation is more sensitive to Dasatinib than Akt phosphorylation. This suggests that Dasatinibs effect on EGF-stimulated Akt phosphorylation is independent of c-Src. This indicates a possible role for other SFKs (e.g. Fyn) or non-SFK kinases in this pathway. Experiments using gene silencing of SFKs will further reveal the nature of SFKs involvement in clathrin-dependent EGFR signaling. Since EGFR and SFKs are commonly disrupted in human tumors, this research may reveal novel cancer treatment therapies.

Common Requirement for Clathrin in Signalling by distinct Receptor Tyrosine Kinases

Rohan Pandey and Costin Anontescu

Ryerson University

Keywords: Clathrin, Clathrin coated pits, Akt, EGFR, c-Met, Pitstop2

Akt is an important signalling kinase that plays a variety of roles within the cell, including regulation of metabolism, proliferation and survival. Akt is activated by several different Receptor Tyrosine Kinases (RTKs) like the epidermal growth factor (EGF) receptor (EGFR), c-Met and Insulin Receptor (IR). Upon binding to EGF, the activated EGFR recruits and phosphorylates GAB1, in turn leading to activation of phosphatidylinositol-3-kinase (PI3K) and Akt. Our lab has shown that the activation of this pathway probably requires Clathrin, a scaffold protein essential for receptor endocytosis. The EGF stimulated activation of GAB1 and Akt occurs concomitantly to EGFR localization within the Clathrin Coated Pits (CCPs). This suggests that Clathrin probably has a signaling role in EGFR signalling separate from its role as a scaffold in endocytosis. In c-Met signalling, the activation of Akt occurs directly through GAB1 and through Insulin Receptor Substrate (IRS) in IR signalling. Since these RTKs differ in the mechanisms by which Akt is activated, it is not known whether they all require Clathrin to activate Akt upon ligand binding. To address this question, we established a model to study the activation of Akt by activation of either EGFR, c-Met or IR in the same cellular background. This model was used in combination with selective perturbation of Clathrin using Pitstop or siRNA gene silencing to determine how each RTK may uniquely require Clathrin for ligand-stimulated Akt activation. Thus far, our results suggest that Clathrin has a signalling role in all three RTK pathways in RPE cells. Since Akt is up regulated in human tumors, understanding the activation of Akt by RTK related pathways has implications for developing novel therapies to treat cancer.
Structural and Functional Characterization of the Interaction between Ubiquitin Binding Domains of Arf-BP1 and Ubiquitin

Raghav Ramabadran, Rahima Khatun, and Yi Sheng
York University

Keywords: Ubiquitin, Protein:protein interaction, Protein Ubiquitination, NMR and X-ray Crystallography, Fluorescence Anisotropy and Isothermal Titration Calorimetry

Ubiquitination as a post-translational modification serves as a cellular signal, governing a variety of cellular processes such as cell cycle regulation, DNA damage response and protein degradation. Ubiquitin Binding Domains (UBDs) are modular units found as a part of ubiquitin receptors involved in ubiquitination and de-ubiquitination processes. They interact with Ubiquitin (Ub), and act as the readers and decoders of various ubiquitin signals in the cell. The structural diversity of UBDs provides functional specificity in transducing different Ub signals (mono, multiple mono, or poly-ubiquitination) in a multitude of ubiquitin mediated cellular events. Elucidating the mechanisms of action and the function of UBDs in different biological contexts is vital to our knowledge of ubiquitin signaling in cellular regulation. However, the structural and mechanistic understanding of the interactions between different UBDs and Ubiquitin is largely uncharacterized. ARF-BP1 is a 482 KDa multi-domain modular E3 ligase that is located on the short arm of the X-chromosome. It is known to ubiquitinate multiple substrates including p53 and Myc. ARF-BP1 inactivation in neuronal stem cells in mice caused postnatal lethality and cerebellar abnormalities as discovered through a series of point mutations in highly conserved regions. One such mutation is located in one of the three UBDs of ARF-BP1. This study characterized the UBDs of ARF-BP1 through structural and biophysical approaches. We cloned three putative UBDs and established their interaction with Ub. Moreover, we found that they have micromolar affinities to single Ub or Ub chains without distinction. Our studies show that the reported X-linked mutation within the first UBD disrupts the interaction and affinity to Ub. The experimental outcome of this project will shed light on the role of UBDs in Ub signalling as well as functional importance in E3 ligase activity.

RBM5 and RBM10 mRNA and Protein Expression in a Small Cell Lung Cancer Cell Line

Sarah Tessier and Leslie Sutherland
Laurentian University

Keywords: RBM5, RBM10, small cell lung cancer, apoptosis, alternative splicing

RBM5 is an RNA binding protein that has been shown to play a role as a putative tumor suppressor and modulator of apoptosis, a type of programmed cell death. The gene encoding RBM5 is one of many tumor suppressor genes that are frequently deleted or mutated in lung cancer. As a result, RBM5 expression is often decreased or absent in lung cancer tumour cells. RBM5 shares approximately 50% homology with another RNA binding protein, RBM10. RBM10 is frequently mutated in lung cancer and, like RBM5, has been associated with apoptosis. To date, the majority of lung cancer research concerning both RBM5 and RBM10 has been performed in non-small cell lung cancer samples, and so it remains to be determined if similar results are seen in small cell lung cancers. The objective of my project was to examine RBM5 and RBM10 mRNA and protein expression in small cell lung cancers using the GLC20 small cell lung cancer cell line. Previous work has shown that GLC20 cells have a homozygous deletion of RBM5. RBM10, however, was expressed at the mRNA and protein level in GLC20 cells, and at quite similar levels as in other cell types. To determine if the expressed RBM10 was functional, we sequenced the transcript. This revealed that GLC20 cells expressed a novel RBM10 variant, likely the result of alternative splicing, differing in only one amino acid from published full-length RBM10 transcript sequence. Interestingly, this amino acid is located in one of RBM10’s two RNA-binding domains, which could mean it may have serious functional implications in small cell lung cancer progression.
Session 8 - IB 235

Ecology

Saturday March 22
3:00 - 4:30 pm
Does Garlic Mustard density have an impact on native species' richness? A review of the literature and a long term dataset

Harsimrat Rataul
York University

Keywords: Alliaria petiolata, invasiveness, species richness, diversity, allelochemicals

Garlic Mustard (Alliaria petiolata) is a well studied species on many invasive plant lists. It has invaded forests throughout the Northeast and Northwest in the United States and Southern Canada. Previous studies have noted that its life history traits e.g. 1. rapid population growth rate, 2. short life cycle, 3. increased allocation of resources towards reproduction, 4. ability to produce allelochemicals are some of the mechanisms underlying the invasiveness of garlic mustard. Numerous studies have been performed to study the direct and indirect impacts of Garlic Mustard on the diversity and physiology of native species present in the North American forests. Of great interest is research into the impact of Garlic Mustard allelochemicals on mycorrhizal fungi of native species such as sugar maple, Acer saccharum. My literature review is aimed to assess the evidence for the extent to which the presence of Garlic Mustard in a disturbed or an undisturbed area is likely to be the sole cause of declines in the native plant species richness and diversity. I also reviewed the literature with respect to the relative number of short-term and long-term research studies on garlic mustard impacts. The findings of my literature review were applied to a case study of a long-term data set from 1995-2009 examining the density and disturbance of garlic mustard in two different parks in Southwestern Ontario: Point Pelee National Park and Rondeau Provincial Park. I asked whether garlic mustard density was significantly correlated with native plant species richness and if not, why not.

Health Survey of Street Trees in London Ontario, with Special Focus on Fungal Infections

Vlad Deboveanu, R.G. Thorn, B. Rubin, and R. Gardiner
University of Western Ontario

Keywords: native vs non-native trees, fungal infections, tree health, London Ontario, biodiversity

Street trees are valuable economically to the cities where they are planted because they save money, but are subject to a variety of stressors, including water stress, salt damage, air pollution, and heavy pruning that can lead to tree disease, decay and death. Trees, especially native ones, serve an important ecological role, allowing for larger biodiversity. Knowing tree status is important because they cannot serve their ecological role if they are unhealthy and tree falling can lead to damage, which is made more likely if infected by decay fungi. I surveyed street trees in London Ontario in terms of their health and decay status. I assessed which fungi were present on each tree, and what the differences in health and decay were between tree genera or species. I compared diameter at breast height (dbh) to disease among and between trees sampled. It was found that neighborhoods that contained more non-native trees were more diseased on average. Non-native trees experienced more fungal infections than native ones. This has important implications ecologically, as native trees are better promoters of biodiversity.
Litter position effects on the decomposition of *Bromus inermis* and *Poa pratensis* litter during the winter

Rosa Del Giudice and Hugh A.L. Henry

Western University

Keywords: decomposition, Bromus inermis, Poa pratensis, litter position, winter

Decomposition of plant litter plays an important role in ecosystem carbon storage and nutrient cycling. However, studies of litter decomposition typically overlook the influence of depth within the litter layer, and in particular, the latter has not been explored over winter, when snow cover may further influence decomposition. I examined the influence of litter position on the decomposition of litter from two grasses, Bromus inermis and Poa pratensis, over winter. I assigned each mesh litterbag to one of five treatments: below the soil surface, on the soil surface with no litter cover (both with and without snow removal), on the soil surface with litter cover and suspended above the litter layer. After 14 to 15 weeks of incubation in the field, the litterbags were collected. There were no significant differences in percentage mass loss among treatments for B. inermis leaves (F=0.364, p=0.79) and B.inermis stems (F=1.96, p=0.15). However, for P. pratensis leaves, mass loss for the litter suspended above the snow and for litter exposed to an overlying snow and litter layer was significantly higher than that of the other treatments (F=7.817, p=0.001). My results imply that the effects of litter depth on the microbial decomposition of grass litter over winter may be low, whereas photodegradation may accelerate decomposition for standing litter that remains above the snow.

Long-term Avian Migratory Data Reveal Differential Responsiveness to Climate Variation

Rachel Hasson, Christine Madliger, Chris Harris, Rick Ludkin, and Oliver Love

University of Windsor

Keywords: avian migration, climate variation, phenology, NAO, temperature

Abstract: Proper timing of life history events such as emergence from hibernation, return from migration, flowering and insect emergence, are crucial for maximizing reproductive success and survival. Increased average temperatures in the springtime can lead to an advance of these and many other events in an organism's life, requiring the organism to shift its phenology accordingly. However, there is a significant amount of variability in the degree to which animals can adjust their phenology in response to environmental variables. If animals do not have the capacity to adjust their phenology to match that of their food supply and other habitat needs, there can be negative impacts upon fitness, leading to population declines. With current predicted and ongoing changes in global climate, assessment of differential responsiveness is needed. We examined whether nine broadly-represented migratory passerine species were able to shift their spring arrival dates in response to local and broad-scale climate variables using a 16-year banding dataset from Southern Ontario. We obtained mean monthly temperatures (March-May) and the winter North Atlantic Oscillation to represent local and regional climatic indices, respectively. In addition, we investigated whether migratory distance could explain the degree to which species were able to alter their arrival dates in relation to climate. Variation in winter NAO was not predictive of arrival date in any of the species. However, we found a significant negative relationship between local temperatures and arrival date in all species, indicating earlier arrivals in years with warmer local temperatures. Although species responses differed, migratory distance did not influence the degree to which a species adjusted arrival date in relation to local temperature. Our results indicate that the nine species chosen have varying degrees of capacity to track changes in local temperature and adjust spring migration phenology accordingly.
Developing a standardized field-based approach to monitoring the effects of water quality on wetland plants

Kevin MacColl and Kevin Stevens
Wilfrid Laurier University

Keywords: wetlands, water-quality, germination, seedling, assay

Wetland ecosystems are important Canadian resources offering ecological and economic value. Since the many ecosystem services provided by wetlands are facilitated by wetland plants, understanding the responses of wetland plants to changing water quality is essential to maintaining these functions. While standardized laboratory-based assays exist to quantify the effects of water quality on plants, they are unable to capture the temporal heterogeneity that field-grown plants experience. Currently there are no standardized field-based approaches for monitoring the effects of water quality on wetland plants that offer the same amounts of control as laboratory assays (i.e. genetic control, prior conditioning, age). As part of a broader goal to establish standardized field-based approaches, this study: i) compared germination rates among five wetland plant species (Echinocloa crus-galli, Phalaris arundicaceae, Persicaria pensylvanica, Bidens frondosa and Alisma triviale) under standardized growth room conditions ii) optimized sterilization procedures to minimize fungal contamination on germinating seeds of three wetland plant species (E. crus-galli, P. arundicaceae and P. pensylvanica) and iii) quantified the effects of various exposure systems on seed germination of E. crus-galli. The highest rates of germination were found in of E. crus-galli, P. arundicaceae (77 ± 22.0% and 95 ± 5.0% respectively), germination in P. pensylvanica was 27 ± 16.4%. There was no germination in B. frondosa or A. triviale. Soaking E. crus-galli seeds in 50% bleach for 10 minutes increased the rate of germination from 51.7 ± 15.1% in controls to 73.3 ± 2.3% and reduced fungal contamination from 46.7 ± 16.7% to 10.7 ± 11.5%. Germination of P. arundicaceae was reduced in all exposures from 73.3 ± 2.31% and reduced fungal contamination from 46.7 ± 16.7% to 10.7 ± 11.5%. Germination of P. arundicaceae was reduced in all exposures from 60.0 ± 10.6% in controls to 15.3 ± 10.4%. P. pensylvanica did not germinate in any treatments. There was no significant effect (p>0.05) of the delivery system on E. crus-galli seed germination, and averaged 51.9 ± 13.1% across treatments.

The role of plant communities and plant quality on Dicyphus hesperus population growth

Lida Nguyen-Dang, Meghan Vankosky, and Sherah VanLaerhoven
University of Windsor

Keywords: Dicyphus hesperus, plant community, nitrogen, biological control, population

Biological control using predatory insects is used as an alternative to pesticides due to resistance development and environmental issues arising from chemical insecticide use. Native omnivores and generalist predators represent cost-effective biological control choices, as populations of these species tend to persist in the environment when their target prey are absent or rare. Omnivorous insects such as Dicyphus hesperus Knight (Heteroptera: Miridae) consume insects pests such as Trialeurodes vaporariorum Westwood (Hemiptera: Aleyrodidae), the greenhouse white fly, as well as plant tissues. To maintain the population of these omnivorous insects, it is important to consider the composition of plant communities. The objective of this study was to determine how plant community structure and tomato plant quality affect D. hesperus nymph survival and resultant adult populations. Fifteen D. hesperus (ten females, five males) were added to enclosures housing high or low quality tomato plants (Solanum lycopersicum L., Solanaceae) and an alternative host plant for seven days. The alternative host plants include Verbascum thaspus L. (Scrofulariaceae), Capsicum annuum L. (Solanaceae), Solanum melongena L. (Solanaceae) and Nepeta cataria L. (Labiatae). Nymphs and adults were counted upon emergence and the intrinsic rate of increase (r), developmental time, longevity, and reproduction rate were calculated. To determine the effect of plant community and tomato plant quality, a two-factor an analysis of variance (ANOVA) will be done. The preliminary results have shown that high nitrogen tomato paired with eggplant have yielded a higher F1 and F2 adult generations with nymphs that develop faster compared to the low nitrogen tomato paired with eggplant. This suggests that nitrogen is important in the overall development of D. hesperus. Both high and low pepper treatments did not enable F1 adults to survive to reproduce. Overall, the composition of plant communities is a vital consideration when maintaining populations of omnivorous predatory insects for biological control.
Session 9 - IB 250

Cell & Molecular Biology

Saturday March 22
3:00 - 4:30 pm
Shroom3 is required for nephron development

Hadiseh Khalili, Alexandra Sull, Thomas Drysdale, and Darren Bridgewater

McMaster University

Keywords: Shroom3, Kidney Development, Nephron number, Cystic glomeruli, Glomerular diseases

Background: Formation of nephrons, the filtration units of the kidney, is essential for kidney function. Defects in nephron formation result in reduced nephron number and can lead to chronic kidney disease and hypertension. Shroom3, a cytoskeletal effector protein, regulates cell shape changes during embryogenesis, events that are observed in nephron formation. Numerous Genome Wide Association Studies (GWAS) have linked Shroom3 to kidney disease and function. However, the role of Shroom3 in kidney function and nephron formation is completely unknown. We hypothesized that Shrm3 is required for nephron formation.

Results: Analysis of Shroom3-/- mice containing a gene trap β-galactosidase reporter gene demonstrated Shroom3 expression in specific cells of the developing nephron (condensing mesenchyme cells and podocyte cells). Shroom3 expression was maintained in podocyte cells and also observed in collecting duct epithelial cells in mature kidneys. The spatial and temporal pattern of Shroom3 expression was confirmed by immuno-staining using Shroom3 specific antibodies. The analysis of Shroom3-/- mutant kidneys demonstrated 3 major abnormalities. (1) Histological analysis of kidneys from Shroom3-/- mice demonstrated numerous condensed and cystic glomeruli at E13.5, E14.5, and E16.5. (2) Glomerular counting at E18.5 demonstrated a 1.6-fold reduction in glomerular number in Shroom3-/- mice when compared to wild type (n=3). (3) Analysis of postnatal Shroom3+/-- mice revealed focal segmental glomerulosclerosis (FSGS) and glomerular hypercellularity.

Conclusion: The absence of Shroom3 leads to early defects in nephrogenesis resulting in reduced glomerular number and postnatal glomerular diseases.

Determining the requirement for Shroom3 in epidermal morphogenesis in the mouse

Jennifer Fish, Thomas Drysdale, Alexandra Sull, and Brittany Binnington

Western University

Keywords: Shroom3, epidermis, morphogenesis, actin binding protein, stratum granulosum

The process of tissue morphogenesis requires proper regulation of the cytoskeleton in individual cells of that tissue. This study investigates the cytoskeletal binding protein, Shroom3, and its involvement in epidermal epithelium morphogenesis in mice. I utilize a mouse model with a LacZ gene trap insertion in the Shroom3 gene that disrupts Shroom3 function and mice homozygous for the gene trap have severe exencephaly. Shroom3 is necessary for promoting cell shape changes in the neural tube through apical constriction and apical-basal elongation. Preliminary evidence suggests that Shroom3 is expressed in the epidermis and I hypothesize that Shroom3 is required for proper epithelial morphogenesis in the epidermis. We will use the mouse model to compare epidermal epithelial morphogenesis in wild type, heterozygotes, and homozygous mutant mice. Epidermal sections were stained with Haematoxylin and Eosin to visualize morphology. Other sections were used for immunocytochemistry using antibodies against Filaggrin and beta-galactosidase to better define the epidermal layers and determine sites of Shroom3 expression. To conclude my data collection I plan to use morphmetrics to compare layer width in the epidermis, as well as stain the samples with antibodies against Keratin-14 and Involucrin to enable further comparison of the morphology of epidermal layers between genotypes.
A piece of the CCN puzzle: the role of CCN1 in dermal fibroblast adhesion to the extracellular matrix

Melissa Gaskas, Katherine Thompson, and Andrew Leask

University of Western Ontario

Keywords: CCN1, adhesion, integrins, matrix contraction, matricellular protein

Within the current literature, highly adhesive and contractile myofibroblasts are the cell type present in connective tissue that is essential for normal wound repair, and that persist in fibrosis. There is limited understanding of the role of CCN1, one of the six members of the CCN family of matricellular proteins, in promoting fibroblast adhesion to the extracellular matrix during a wounding or fibrotic response. CCN1 has been found to interact with the integrin β1 subunit, promoting contraction of the actin cytoskeleton leading to scar formation during wound healing, and also induces downstream expression of genes that contribute to an adhesive and contractile phenotype. Consequently, CCN1 mediates the differentiation of dermal fibroblasts into myofibroblasts. An adhesion assay of cultured mouse fibroblasts with a fibroblast-specific genetic knockout of CCN1 showed a significant decrease in total cell adhesion to fibronectin when observed at time points of 30, 90, and 120 minutes after plating (P<0.05). To confirm these data, immunocytochemistry was conducted to specifically detect actin stress fibres that showed less extensive spreading in CCN1-deficient cells compared to wild type cells. Analysis of the cultured fibroblasts using qPCR showed a significant decrease in CCN1 mRNA levels, thus confirming the knockout (P=0.0187). In addition, qPCR was conducted to analyze mRNA expression of integrins β1, α4, and α5, the cell surface receptors for fibronectin, and showed no significant difference when either in the presence or absence of CCN1. While the exact mechanism of CCN1 facilitation of adhesion is still unknown, it can be concluded that it is required for optimal fibroblast adhesion that is important to maintain skin integrity. Further investigation of the mechanism of CCN1 in promoting adhesion is necessary, nonetheless the data are consistent with the hypothesis that CCN1 may contribute to fibrotic responses in vivo.

Evidence for the presence of the alternative oxidase (AOX) pathway in the copepod Tigriopus californicus

Jaspreet Singh and Allison McDonald

Wilfrid Laurier University

Keywords: alternative oxidase, Tigriopus californicus, environmental stressors, energetic demand, animal evolution

The electron transport chain (ETC) in animals is comprised of various electron carriers and complexes that generate a proton motive force, which yields energy in the form of adenosine triphosphate (ATP) through oxidative phosphorylation. The alternative oxidase (AOX) pathway is an alternative route that catalyzes the oxidation of ubiquinol and the reduction of oxygen to water in the ETC; thereby by-passing Complexes III and IV. AOX reduces the number of protons pumped across the inner mitochondria membrane and is therefore seen as energetically wasteful. Previous work has demonstrated that AOX is present in some animals, but is limited to sessile or slow species. The assumption has been that AOX is not compatible with an active lifestyle due to energetic constraints. Recent DNA database searches using bioinformatics revealed an AOX sequence in the marine copepod Tigriopus californicus. This species lives in tidepools along the west coast of North America and is subject to a wide variety of environmental stresses on a daily basis and likely has high energetic demands. This research project uses molecular biology and physiological techniques to confirm the presence and examine the role of AOX in this organism. T. californicus may prove to be a model organism for the study of AOX in animals and may aid in providing an explanation for the loss of AOX in some other animal species. The study of animal AOX may eventually contribute to the treatment of mitochondrial dysfunctions and disorders in humans using AOX gene therapy.
Pokeweed Antiviral Protein is Regulated by a Small RNA

Alexander Klenov, Lydia Burns, Gabriela Krivdova, Kira Neller, and Katalin Hudak
York University

Keywords: glycosidase, small RNA, pathogen defense, post-transcriptional regulation, mRNA cleavage

Plants have evolved many strategies to evade pathogen attack and glycosidases are one group of enzymes thought to be involved in defense. Glycosidases remove purine bases from RNA, thereby inhibiting their translation. Pokeweed antiviral protein (PAP), synthesized by the pokeweed plant Phytolacca americana, inhibits the replication of several plant and animal viruses by removing purines from viral RNAs. Most of the studies investigating PAP’s mode of action have relied on its expression in heterologous systems. Very little is known about the regulation of PAP in the native plant. We report here that PAP mRNA is regulated by a small RNA that targets its open reading frame (ORF). By primer extension and 5' RACE, we show that PAP mRNA is cleaved 192 nt from its 5’ end. Electrophoretic mobility shift assay indicated the presence of a small RNA complementary to the region spanning the cleavage site. qRT-PCR showed that by scrambling the small RNA target site, PAP mRNA levels increased 23-fold compared to the wild type target site. Subsequent sequencing of the small RNA pool of pokeweed confirmed that it aligned completely with the target site within the PAP ORF. Work is underway to confirm the in vivo significance through a small RNA sponge. As well, an Argonaut pulldown will test the link between the small RNA and the silencing pathway in plants. We are currently investigating the physiological relevance of the small RNA and our initial results suggest that it is down-regulated by jasmonic acid. Jasmonic acid is a plant hormone that has been implicated in controlling plant response to stress. This down-regulation would likely increase PAP levels and supports our hypothesis that PAP defends against pathogens. This is the first report of a plant defense protein being regulated by a small RNA.

Role of Spy1 in Functional Differentiation

Ellen Laurie, Bre-Anne Fifield, and Lisa Porter
University of Windsor

Keywords: lactogenesis, functional differentiation, Spy1, c-Myc, cell cycle

Normal mammary gland development is dependent on proper regulation of the cell cycle, which allows the gland to progress through cyclic stages of proliferation, differentiation, and apoptosis. Misregulation of the cell-cycle can lead to irregular development of the mammary gland, a potential trigger for oncogenesis. Data from our lab has shown that Spy1, a cell-cycle regulator, increases mammary tumorigenesis in vivo. Spy1 mimics the developmental expression profile of the potent mammary oncogene c-Myc and, like c-Myc, overexpression of Spy1 results in premature expression of early differentiation genes in mammary epithelial cells. The purpose of this study was to determine if mammary gland epithelial cells overexpressing Spy1 or c-Myc functionally differentiate. Using virally manipulated mouse mammary epithelial cells that are capable of differentiating in vitro, we are measuring markers of functional differentiation. Our early results suggest that overexpression of Spy1 and c-Myc support functional differentiation but that Spy1 overexpression results in very early expression of these markers. Since increased lactation decreases the risk of developing breast cancer, it is important to understand the mechanisms of normal mammary gland development and the role that Spy1 plays.
Session 10 - IB 260

Evolution

Saturday March 22
3:00 - 4:30 pm
Hemiclonal analysis of direct and indirect fitness and its associations with female choosiness
Leah DeJong and Tristan Long
Wilfrid Laurier University
Keywords: hemiclonal, genetic variation, fitness, Drosophila melanogaster, female choosiness

Classical sexual selection theories predict that females evolve and maintain choosiness in order to maximize the benefits and minimize the costs of mating. Previous studies have established a genetic basis for variation in female choosiness in fruit flies (Drosophila melanogaster) through the hemiclonal approach, which allowed researchers to 'control' male and female genotypes in order to understand the role of genetic variation in a population's phenotypic mating patterns. Here, I use these previously quantified Drosophila melanogaster lines to examine if genetic individual variation in female choosiness is correlated with variation in direct fitness (number of eggs produced) or indirect fitness (reproductive success of sons and daughters). It was predicted that 'choosier' females would have higher direct and/or indirect fitness than their 'less choosy' conspecifics. Contrary to these expectations, our results indicate a potential role for sexual conflict in our laboratory population (and perhaps beyond) in shaping the selection acting on the evolution of female preferences.

The evolution of low-complexity regions in protein sequences
Sonya Elango and Brian Golding
McMaster University
Keywords: LCRs, Bioinformatics, Genomics, MCMC, Microsatellites

Low-complexity regions (LCRs) are common features of the eukaryotic genome that are characterized by a compositional bias towards a small number of different amino acids. While these regions typically form an unstructured protein product, they have been implicated in a number of functional roles, ranging from mRNA stability to circadian rhythm duration. Despite their ubiquity and diverse functions, LCRs are poorly understood. However, these regions share certain features with microsatellites, a relatively well-characterized class of sequences. The similarities between the two types of sequences can therefore provide some insight into the characterization of LCRs. In particular, a number of different models of microsatellite evolution have been proposed and can potentially be applied to the study of LCRs. This project seeks to provide some insight into LCR evolution by performing computer simulations that apply these models to LCRs. In order to do this, the Approximate Bayesian Computation (ABC), a statistical technique, will be used to determine which models of microsatellite evolution are relevant to LCRs. Two parameters that the ABC manipulates in this study are the rates of replication slippage and point mutation. The performance of these simulations in the C programming language will yield certain values for these parameters in each model. Certain models can therefore be eliminated based on the biological feasibility of these parameter values. Based on previous experimental results, we predict that models that take into account factors such as length dependency and rate asymmetry will be better at describing LCR behaviour. These models include Kruglyak's proportional slippage model and Walsh's linear birth death chain. In applying these models to LCRs, we can gain some insight into the characterization of these regions. As LCRs are so ubiquitous and functionally diverse, learning more about their evolution and dynamics is very important.
Cross-generational effects of male attractiveness on offspring immunocompetence

Ashley Guncay and Tristan Long

Wilfrid Laurier University

Keywords: sexual selection, immunocompetence, Drosophila melanogaster, bacterial load, survivorship, weight, Pseudomonas aeruginosa, sexual conflict

While the fitness benefits promoting the evolution and maintenance of female choosiness (where females "prefer" to mate with males of increased "attractiveness") is clear in those species where males provide their mates with direct benefits (resources, protection, shared parental responsibilities), in many species where males do not contribute directly to a female's lifetime reproductive success, females still exert strong preferences. It has been proposed that in such species, that females are instead choosing "attractive" mates based on the anticipated benefits manifested in their offspring. One of the traits that may be involved in this sexual selection is that of immunocompetence (the ability to mount an immune response following exposure to a pathogen), but previous work on the link between this trait and male attractiveness has been ambiguous. Here, using the model species, Drosophila melanogaster, I examine whether father attractiveness indirectly influences sired offspring immunocompetence and other relevant traits (survivorship, bacterial load and adult weight). I found support for the "immunocompetence handicap hypothesis": attractive males (studs) sired male offspring with better immunocompetence than did less attractive males (duds). However, I also found evidence that sexual conflict promoted immunological difference in males and females sired by the same father or exposed to the same pathogen.

A population genetics study of Boletus edulis isolates from the Czech Republic

Stephanie Zahorka and Jianping Xu

McMaster University

Keywords: biogeography, Boletus edulis, Czech Republic, genetic markers, population genetics

Boletus edulis is a mushroom with a multi-million dollar market in the food industry, significant cultural importance throughout Europe, and increasing implications in the healthcare industry. Despite its apparent global importance, there have been relatively few studies of its biology and almost nothing is known about its population biology and biogeography. This study uses multilocus DNA sequencing to analyze populations of B. edulis from the Czech Republic where over 90% of the population collects and consumes wild edible mushrooms including B. edulis. A total of 110 fruiting bodies from nine subpopulations are analyzed in this study. The internal transcribed spacer (ITS) was sequenced to confirm species identity and five single copy species-specific markers were sequenced for population genetic analyses. Preliminary results show differences in strains based on the geographic separation of the populations. The results from this study will help with understanding the population biology of this and other ectomycorrhizal fungal populations.
Using flow cytometry to assess the genetic and environmental factors influencing unreduced gamete production in Brassicaceae spp

Dylan Sora and Brian Husband

University of Guelph

Keywords: Unreduced, Gamete, Flow, Cytometry, Brassicaceae

Polyploidy, the possession of more than two complete sets of chromosomes, is widespread among angiosperms. The most common mechanism of polyploid formation is believed to be though the union of unreduced (2n) gametes produced through a meiotic non-reduction event during gametogenesis. Although the cytological mechanisms of unreduced gametes formation are well understood, the genetic and environmental conditions promoting unreduced gamete production are unclear. Here we test the hypothesis that genetic (hybridity) and environmental (nutrient deficiency, leaf wounding) stressors will disrupt typical meiotic division in plant pollen cells increasing unreduced gamete production. We use flow cytometry to estimate unreduced gamete production on Brassica napus, Sinapis arvensis and backcrossed hybrids to compare the effects of hybridity, nutrient limitation and wounding treatments from pollen collected in two time intervals (blocks). Unreduced gamete formation was low ranging from 0-4.79% with a mean of 0.69%, however there were several biologically relevant trends. Hybrids produced increased amounts of unreduced gametes in the first block only, indicating hybrids may achieve increased rates of polyploidization though unreduced gamete formation early in development, potentially explaining a high abundance of polyploid hybrids. Nutrient limitation and wounding did not affect unreduced gamete production in either block. The second sampling block had increased percentages of unreduced gamete compared to the first, indicating unreduced gamete production may increase with plant age. This study is the first of its kind to estimate unreduced pollen gamete production using flow cytometry in a manipulative experiment. Results indicating hybrids and increased plant age may increase unreduced gamete production may further our knowledge of polyploidzation events in plants providing a more comprehensive background in plant evolutionary biology.

Evolutionary History of the Class A Scavenger Receptors

Nicholas Yap, Brian Golding, Dawn Bowdish, and Johnathon Stone

Keywords: Evolution, Immunology, Scavenger Receptors, SRCR domain, MARCO

The Scavenger Receptors are a class of innate immune system protein receptors that were originally discovered for their ability to bind modified low-density lipoprotein. These receptors were later shown to bind a variety of host-modified ligands such as oxidized LDL, acetylated LDL, and various bacterial ligands including Streptococcus mutans, Escherichia coli, and Mycobacterium tuberculosis. The class A Scavenger Receptors (cA-SRs) are one of eight classes of SRs, and are phagocytic receptors on the surface of macrophages with an intracellular N-terminus, an extracellular C-terminus and are composed of trimers of collagenous domains. However, the five protein family members also contain a large amount of diversity. Three of the family members contain a Scavenger Receptor Cysteine-Rich (SRCR) domain, while one family member lacks the domain and the other possess a C-type Lectin domain. Despite these differences, previous work by Whelan et al., (2012) showed how these five proteins may have emerged through a gene duplication event. However, their study was unable to firmly identify the origin of several of the domains, including the SRCR domain, within the protein family. With newly available sequence data from more ancient organisms, the relationship between these proteins can now be better characterized. This study attempts to utilize various bioinformatic programs and newly available sequences in order to elucidate the possible evolutionary history of the cA-SRs. Bayesian analysis showed that the three SRCR containing receptors were more closely related to each other than the two non-SRCR containing receptors. These results differed from those in Whelan et al., (2012) where the Macrophage Associated Receptor with Collagenous domain (MARCO) grouped with the non-SRCR containing receptors. Therefore it seems plausible that the SRCR domain of the cA-SRs was acquired in the early development of the vertebrate immune system.
Session 11 - IB 270

Genetics

Saturday March 22
3:00 - 4:30 pm
The role of retrotransposable sequences on the evolution and individuality of the human genome

Courtney Gendron, Shiva Singh, Beth Locke, and Kathleen Hill

Western University

Keywords: Retrotransposable elements, HERV, LINE-1, Monozygotic twins, Bioinformatics

Although variation has been well established for human retrotransposable elements (REs) across diverse human populations, genetic variation on an individual level has yet to be researched. REs are genetic repeat elements ubiquitous to many eukaryotic organisms able to amplify themselves within a genome. Although most of these human REs have been deactivated, some still maintain functional open reading frames. Genetic variation of the HERV-W, HERV-K and LINE-1 species were studied using the full genomic sequences of two pairs of monozygotic twins discordant for schizophrenia and the parents of one of the twin pairs. Using the BLAST-like alignment tool, genomic locations of REs were compared across all genomic sequences, which are aligned to the human reference sequence by Comparative Genomics software. Since the repeat elements under study have the ability to recombine and some actively mobilize within human genomes, there is potential for novel variation across and within generations. The presence or lack of variation will further the understanding of HERVs and their contribution to the evolution and individuality of the human genome.

Nmt: a candidate gene for behavioural isolation between Drosophila melanogaster and D. simulans

Soundarya Selvam and Amanda Moehring

University of Western Ontario

Keywords: female mate preference, speciation, reproductive isolation, behavioural isolation, Drosophila melanogaster

The biodiversity observed in nature is in part a byproduct of speciation, which is maintained via reproductive isolation mechanisms that prevent gene flow between species. Behavioural isolation is often considered to be the most important reproductive isolation mechanism since it arises early in the speciation process and minimizes the costs that would be associated with creating unfit offspring. Recent studies in Drosophila have identified Mekk1 as a candidate behavioural isolation gene between D. melanogaster and D. simulans. Mekk1 expression in the two species may underlie female mate preference in D. simulans that isolates this species from D. melanogaster. This project uses bioinformatics and molecular genetic techniques to compare Mekk1 expression in the two Drosophila species.
Investigation on de novo Structural Variant (SV) mutations using complete genome sequences in families with monozygotic twins

Jane Gui
Western University

Keywords: complete genome sequence, twins, alu, structural variant, SV, copy number variant, CNV, de novo mutation, monozygotic, family, inversions, deletions, duplications, germline, somatic, genetic, genomic, non-allelic homologous recombination

Copy Number Variants (CNVs) and Structural Variants (SVs) including inversions, deletions, duplications, and complex rearrangement are genetic elements that can be defined as ranging from 50 bp to 3 Mb in size. They are responsible for a large proportion of genomic individuality and have profound implications for phenotypic differences and disease susceptibility. However, few studies have investigated de novo germline and somatic CNV and SV mutations that may explain their formation and possible contribution to sporadic diseases. This project investigates de novo genomic structural changes in families with monozygotic twins (MZTs) using complete genome sequences. It focuses on copy number variants (CNVs) and five types of structural variants (SVs). We hypothesized that the number of shared CNVs and SVs is directly correlated with the degree of relatedness; and a major portion of the newly formed CNVs and SVs are facilitated by genomic repeats (Alu in particular) that denotes mutational hotspots. The results showed that the number of shared CNVs and SVs often correlates with relatedness. So far, three CNVs (involving TPO and CES1 genes) discordant between the MZT pairs have been confirmed using real-time PCR. Using UCSC RepeatMasker, the presence of Alu near the SV break points was found to vary across different types of SVs. There was also one-third more Alu elements present near the break points of post-twinning deletions than that of pre-twinning deletions. This observation indicated different replicating mechanisms were employed during meiosis and mitosis and the genome was subjected to different rates of SV formation. This finding may help us predict the likelihood of certain SV mutations before conception and after conception as well as their potentials in causing genetic disease. Future research should focus on elucidating the exact mechanistic differences of Alu-facilitated non-allelic homologous recombination between meiotic and mitotic DNA replications.

Examination of obesogenic related methylation changes of the POMC promoter in female CD1 mice neonatally exposed to bisphenol-A

Trevor Deley, Harry Mackay, John Stead, Alfonzo Abizaid, and Alex Wong
Carleton University

Keywords: epigenetics, obesity, bisphenol-A, energy intake, environmental toxins

Bisphenol-A (BPA) is an environmental contaminant found ubiquitously throughout North America. Previous studies indicate that BPA acts as an obesogen to perinatally exposed rodents. BPA is also categorized as a xenoestrogen that has been shown to bind to NPE1; an enhancer upstream of the proopiomelanococortin (POMC) promoter. POMC codes for a prohormone that has been increasingly implicated in energy balance in vertebrates and humans. A previous study conducted by Mackay et al. showed that female CD-1 mice exposed to BPA perinatally were heavier, ate more, and had reduced POMC expression in the arcuate nucleus of the hypothalamus (ARC). The purpose of this study was to examine the effect of BPA on the methylation status of the POMC promoter in female CD-1 mice on a high fat diet. The promoter region was analyzed using bisulfite sequencing for changes in methylation status of CpG islands to determine if the xenoestrogen BPA was involved in epigenetic changes regulating energy intake.
Analyzing Gene Expression to Aid in the Quantification of Development Within the Pupal Stage of *Lucilia sericata*

J. Garabon, A. Tarone, M. Boffa, and S. VanLaerhoven

University of Windsor

Keywords: gene expression, post mortem interval, *Lucilia sericata*

Entomology is widely used in forensics to determine the chronology of an event, most frequently regarding the time since death or post-mortem interval (PMI). Upon death and decomposition of a body, various insects, such as blow flies, identify the corpse as a nutritional source. Under normal conditions, blow flies locate the body and oviposit within minutes after death. Due to the rapid egg allocation, the time of oviposition is accepted as the approximate time of death. This parameter is exceptionally useful, as forensic entomologists can then use the age of the blow fly to estimate the PMI. Traditionally, the age of an immature blow fly is estimated via length measurements that are ultimately used to create linear regression models. Many issues arise when using this strategy, particularly within the pupal stage of the fly lifecycle. Alternatively, one may use the unique temporal expression patterns of various genes to aid in quantification of the development of a blow fly. In this study, I have generated expression profiles for six candidate genes within the pupal stage of the blow fly *Lucilia sericata*. Each gene was chosen based on its unique orthologous expression pattern within *Drosophila melanogaster*. These results may be compiled with other gene expression data in order to ultimately develop a subset of genes that can be used to quantify developmental progression within each pre-adult stage of this blow fly. Consequently, this would allow for more accurate and precise estimations of the PMI. The use of gene expression data has many additional advantages, including uncomplicated legal acceptance; effortless integration into current forensic laboratories; potential for implementation of robotic analytical tools; and the possibility for generation of error rates and confidence intervals. Quantitative gene expression analysis of blow fly development could therefore prove to be an indispensable tool for modern forensic investigations.

Investigating the Conservation of Metabolic Function within Prokaryotic Species

Thomas Hemmy and Dr. Moreno-Hagelsieb

Wilfrid Laurier University

Amongst microbial ecologists, it is widely presumed that if several bacteria are the same species, they will have highly similar, if not identical metabolic functions. This notion is contrasted by the prevalence of horizontal gene transfer amongst prokaryotes, and recent pan-genomic studies, which suggest that individual bacterium within a prokaryotic species can possess a wide range of genes, proteins, and metabolic processes. When determining the species of a bacterium, the prokaryotic 16s ribosomal RNA genes are commonly analyzed, as they are highly conserved, and present within almost all bacteria, making them the ideal marker genes. To test the ability of prokaryotic 16s ribosomal RNA genes to accurately represent bacterial metabolic function, we have clustered the 16s ribosomal RNA sequences from prokaryotic species within the NCBI database together, placing sequences that share a >97% similarity into species like groups known as operational taxonomic units. The metabolic function of each organism was then contrasted to the metabolic function of the other organisms within its operational taxonomic unit, allowing us to determine the degree of variation between the metabolic pathways of the species within each cluster. We found that although most operational taxonomic units contained only one species, a wide range of metabolic pathways could be observed within each cluster, suggesting that metabolic function is variable within bacterial species.
Session 12 - IB 280

Genetics, Cell & Molecular Biology

Saturday March 22
3:00 - 4:30 pm
Quality Control Removing Quality During Copy Number Variant Detection

M. Coumans, M. Milojevic, N. Patel, M.E.O. Locke, A. Edge, and K.A. Hill
Western University

Keywords: CNVs, duplication, outlier, provirus, nucleoskeleton

Copy number variants (CNVs), a form of structural variation, involve large duplications or deletions of genomic DNA and have great potential to affect phenotype. When analyzing CNVs in a large number of samples using the Mouse Diversity Genotyping Array and subsequent CNV detection software (PennCNV), stringent filtering criteria (log r ratio standard deviation > 0.35 or a b allele frequency drift > 0.10) are applied within the detection algorithms to identify experimental outliers. CNV characteristics, such as base pair length, chromosome location, GC content and genes affected, were analyzed in all outliers. Herein, I report an inbred strain of mice, MA/MyJ, with a novel insertion of a mouse mammary tumour virus into the genome not present in other inbred strains. Moreover, the provirus, Mtv-43, has inserted upstream of the gene CORO2A, an actin binding member of the nuclear receptor corepressor complex that remains inadequately characterized, which has been shown to cause an improper gene expression profile. The nuclear receptor corepressor complex incorporates transcription factors which alter chromatin structure and gene expression important in cell cycle regulation, homeostasis, and development. Recent findings revealing nuclear actin’s role in chromatin remodelling complexes generate great interest in CORO2A and warrants future studies to elucidate novel insights into the mechanisms underlying CNV formation.

Molecular analysis of ATRX-deficient mice

Emily Grant, Yan Jiang, and Nathalie G. Berube
Western University

Keywords: ATRX, gene regulation, Musk, Folr1, brain development

Disruptions in alpha thalassemia mental retardation X-linked (ATRX), a chromatin remodeling protein, cause a neurodevelopmental disorder associated with memory and learning defects. To study the effects of ATRX deficiency on brain function, the loxP/Cre system was used to conditionally delete Atrx in the mouse brain. Two different mouse strains were analyzed. In AtrxNestinCre mice, ATRX is absent throughout the developing brain from embryonic day 11 (E11) while in AtrxCamKIIICre mice it is deleted only in postmitotic neurons of the forebrain. Microarray analysis of the AtrxCamKIIICre mice hippocampus at 3 months of aged revealed that many genes are differentially expressed. In this study, I focus on muscle skeletal receptor tyrosine kinase (Musk) and folate receptor 1 (Folr1) because these genes were previously linked to learning and memory processes. Musk is a receptor tyrosine kinase that plays a key role in the learning-dependent activation of the CREB/C/EBPβ pathway that mediates memory consolidation and Folr1 is an important player in the synthesis of neurotransmitters. Expression of these genes in the hippocampus of AtrxNestinCre, AtrxCamKIIICre, and control mice were analyzed by real-time PCR. Results indicate that Musk and Folr1 are indeed expressed at lower levels in the hippocampus of both mutants. Data collected suggests that inactivation of the chromatin remodeling protein leads to a decrease in transcription of genes involved with memory and learning in the hippocampus. In the future, determining whether MUSK and FOLR1 protein levels are also reduced and the downstream effects could help understand the spatial memory deficits observed in these mice and guide the development of therapies for intellectual disability.
Ammonia toxicity may be an early trigger of neurodegeneration in the harlequin mouse, a model of premature neurodegeneration

Anson K.C. Li, Eric A. Dolinar, and Kathleen A. Hill

University of Western Ontario

Keywords: neurodegeneration, ammonia toxicity, retina, cerebellum, quantitative-PCR

Purpose: Early mechanisms that initiate retinal and cerebellar neurodegeneration are largely unknown and can be studied in the harlequin (hq) mouse. Vision deficits in the retina begin at 2 months of age, and progress to a complete loss of function by 10 months. In the cerebellum, neurite degeneration begins at 2 months, and cerebellar size is decreased by 10 months. The hq mouse contains a mutation in the Apoptosis-inducing factor (Aif) gene and the downregulation of Aif leads to decreased ATP production. The detoxification of excess ammonia in neurons is energetically expensive. It is hypothesized that ammonia build-up is toxic to neurons and may trigger neurodegeneration in the hq mouse.

Methods: Using an inclusion criteria of minimum fold change=1.5 and p<0.05, there were 6513 and 296 differentially-expressed genes in the 4-month old hq retinal and cerebellar microarray data respectively. Ingenuity Pathway Analysis and KEGG Pathway Analysis of microarray data identified potential pathways associated with neurodegeneration. Retinal and cerebellar tissues from hq and wild-type mice at two, three, and four months of age (n=10 in all cohorts) were harvested. Twelve key genes were selected for gene expression confirmation using Applied Biosystems ViiA7 quantitative-PCR.

Results: Pathways involved in amino acid metabolism and ammonia detoxification via the urea cycle were differentially-expressed, such as the twenty genes involved in the arginine and proline metabolic pathways (p=0.009). Preliminary quantitative-PCR results on cerebellar samples have found key genes to be differentially-expressed, such as Asparagine synthetase (Fold=1.27; p=0.027) which catalyzes ammonia removal from glutamine and is important for neuronal function.

Conclusion: Decreased ATP production may lead to ammonia toxicity in neurons, thus initiating downstream retinal and cerebellar neurodegeneration. Confirmation of differentially-expressed genes represents the first step in identifying neurodegenerative mechanisms. Future studies using immunohistochemistry will localize the specific cell type initiating neurodegeneration within the retina and cerebellum.

Characterization of downstream elements of the miR156-SPL regulatory network in Arabidopsis thaliana root

Spencer Jones, Yang Wang, and Abdelali Hannoufa

Western University

Keywords: Arabidopsis, MicroRNA, Overexpression, Regulatory Networks, Development

The Arabidopsis thaliana microRNA MicroRNA156 (miR156) has been demonstrated to silence the Squamosa Promoter Binding Protein-like (SPL) family of genes. Together, miR156 and the SPL family form a regulatory network that influences plant development as well as secondary metabolism; however the downstream elements of this system have not been extensively documented. This study’s intention is to confirm that three candidate genes interact with SPL proteins and are involved in the miR156 regulatory network. Thus far, root tissue has been collected from three Arabidopsis genotypes, SK156, RS105 and wildtype. RNA has been extracted from this tissue for use in real-time quantitative PCR to gauge relative expression levels. Chromatin immunoprecipitation-qPCR will be conducted in the near future to ensure that these genes do interact with SPL proteins. This report touches on results obtained thus far and future objectives. Further knowledge of the miR156 regulatory network will advance our understanding of plant development and can provide improvements to future agriculture.
Discovery of Protein Motifs in the Macrophage Scavenger Receptor Using MSA-PRP and APC

S. Han, P. Bharadwaj, K. Novakowski, A. Lee, A. Wong, and D. Bowdish

McMaster University

Keywords: Macrophage, Immunology, Bioinformatics, Pneumonia, Receptor

Class A scavenger receptors, including scavenger receptor A and macrophage receptor with collagenous structure, are surface proteins that bind modified endogenous ligands and bacterial components. As these receptors play a key role in innate immunity, they are associated with a range of infectious diseases such as pneumonia. Thus, understanding the physical properties of these receptors will provide insight for the development of novel therapeutics. Macrophage receptor with collagenous structure is amongst the least well-characterized members of this family and is expressed in macrophages to mediate pathogen recognition. Our investigation addresses the development of an efficient and highly accurate bioinformatics technique through combinatorial usage of Aligned Pattern Clustering, and Multiple Sequence Alignment Pattern Retrieval Program for novel motif discovery in the macrophage scavenger receptor. By utilizing scavenger receptor A and its validated motifs as a model, we successfully validated the feasibility of this bioinformatics technique with a minimum sensitivity of 54% and positive predictive value of 60%. As a subsequent validation of the newly discovered motifs, the top sub-sequences of macrophage receptor with collagenous structure, selected by both programs, were analyzed for their biological functionality. Here, we propose that RGRAE, VFCRMLG, EDAGVE and WGTICDD motifs in the scavenger receptor cysteine-rich play an important role in pathogen recognition. To validate the findings, an arginines residue within VFCRMLG was mutated to glycine through site-directed mutagenesis. After confirming its expression, functional assays were conducted to validate its functionality. Here, we report that R461G does not alter MARCO's signalling capacity.

Investigating Nodal expression in mouse models of Duchenne muscular dystrophy

Ratna Varma, Kelly Gutpell, and Lisa Hoffman

University of Western Ontario

Keywords: Duchenne muscular dystrophy, fibrosis, TGF-beta, nodal, skeletal muscle

Duchenne muscular dystrophy (DMD) is a neuromuscular disorder for which stem cell therapy has been ongoing since 1980s. While transplanted muscle progenitor cells (MPCs) can engraft within damaged muscle tissue, little/no significant improvement in muscle contractile strength has been demonstrated. Studies attribute this to the limited ability of transplanted MPCs to survive, migrate and engraft within dystrophic muscle tissue. This is believed to be due to a poor microvascular environment and presence of fibrotic/scar tissue that inhibit effective muscle repair. Nodal, a TGF-β superfamily member, has been implicated as a potential regulator of fibrosis, however its expression in DMD models and potential role in muscle repair are unknown. This study compared Nodal expression in diaphragm and gastrocnemius tissues of old mdx:utrn+/- mice and young mdx:utrn-/- mice with their age-matched wildtype mice via immunohistochemistry. Nodal's impact on C2C12 myoblast cell viability was also assessed through MTT assays. Nodal expression was present in some but not all diaphragm tissues, and it was absent in all old mdx:utrn+/- gastrocnemius tissues. Nodal was expressed in young mdx:utrn-/- diaphragm tissue. It is inconclusive whether Nodal is differentially expressed with DMD progression. Due to Nodal's role in maintaining pluripotency of human embryonic stem cells, Nodal treatment was expected to increase myoblast cell viability. Nodal, however, did not significantly affect myoblast cell viability, therefore it appears to be dispensable for survival of MPCs in DMD mouse models. This suggests that Nodal can be targeted in severely affected models for treatment of DMD.
Sunday March 23
Session 13 - IB 245

Cell & Molecular Biology

9:00 - 10:30 am
The vacuolar pH in yeast phosphoinositide mutants

Christina Wattson, Cheuk Y. Ho, and Roberto J. Botelho

Ryerson University

Keywords: phosphatidylinositol-3,5-bisphosphate; vacuolar acidification; quinacrine; cDCFDA; Fab1

The endocytic pathway functions to internalize molecules from the plasma membrane and recycle them back or sort them for degradation. Those destined for degradation culminate in the lysosome or vacuole (yeast). The lysosome is the principle hydrolytic compartment of the cell and it serves to break down cellular wastes products, fats, carbohydrates, proteins and other macromolecules into their monomeric components and then recycle these constituents back to the cytoplasm. Proper acidification of this cellular compartment is essential for its hydrolytic function as many of the enzymes responsible are acidic hydrolases which optimally function at lower pH values. Phosphatidylinositol-3,5-bisphosphate [PI(3,5)P2] is primarily restricted to the endolysosomal/vacuolar system and is generated from PI(3)P by a PI3P 5-kinase known as PIKfyve (mammalian) or Fab1 (yeast). Despite few identified effector molecules, PI(3,5)P2 has been linked to the regulation of many cellular functions including stress responses, autophagy, exocytosis and activity of transporters, Ca2+ signaling functions, membrane fusion (endosome to lysosome), membrane fission (recycling) and finally endolysosome acidification. This final link to acidification stems from previously published experiments done with yeast cells deficient in PI(3,5)P2 using the qualitative dye quinacrine. Quinacrine is thought to accumulate in acidic compartments, yet failed do so in the vacuoles of fab1Δ mutants, thus suggesting a regulatory function for PI(3,5)P2 in vacuolar acidification. In an effort to quantitatively measure the vacuolar pH in these mutants, our lab developed a novel protocol using the pH-sensitive dye cDCFDA. Interestingly, our measurements show that there is actually no significant difference in vacuolar pH between wild type (pH 4.8) and fab1Δ (pH 5.0) yeast cells. Measuring the vacuolar pH in mutants of the proton pump V-ATPase (vma4Δ and vph1Δ) showed that the assay can detect alkaline vacuolar pH, supporting its accuracy.

Orthology versus functional redundancy among selected genes in the Skp1-like gene family of Arabidopsis thaliana

Florida Doci, Mohammad Dezfulian, Evgeni Gentchev, Curtis Foreman and William L. Crosby

University of Windsor

Keywords: Arabidopsis thaliana, ASK gene family, loss of function alleles, phenotype, functional redundancy

Plants require functionally sophisticated mechanisms to regulate patterning and development in a rapidly changing environment. Unbiased genetic analyses have revealed that plants have highly elaborated targeted protein degradation mechanisms for the regulation of diverse plant-specific processes. In Arabidopsis thaliana, the Arabidopsis SKP1-like (ASK) genes are essential subunits of the SCF class of multi-protein E3 ubiquitin-ligase complexes, which are largely responsible for driving ubiquitin-dependent protein degradation.

Unlike humans or yeast which possess a single Skp1 gene, Arabidopsis expresses 21 ASK genes. Structural analysis of ASK genes indicates high primary amino acid sequence similarity although sequence-based phylogenetic relationships within the family is a poor predictor of shared or redundant functionality. Although many genes in this family remain uncharacterized, evidence suggests that some are functionally redundant (e.g. ASK1 and ASK2). It is unclear however the extent of such redundancy across all members of the ASK gene family. In order to examine the degree of functional redundancy within the ASK gene family, loss of function alleles in select genes were examined for gross patterning and development phenotypes. In this study knockdown mutants of ask11/12, generated by ectopic expression of artificial microRNAs (amiRNAs), were examined. A series of phenotypic screens were employed to survey for aberrant patterning and development at different stages of growth. Depending on the transcript targeted by individual amiRNAs, the levels of transcription abundance and suppression differ. This study looked at two independent lines of ask11/12 mutants (designated a and b), each with different levels of transcription suppression.

Germination rate, root elongation, response to gravitropism, and rosette leaf morphology were assessed for both mutant lines. Results indicated a significant difference in germination rate, root elongation and bolt length between the mutant and wildtype. The results described here suggest that these two loci encode different functions in support of development in Arabidopsis.
ALS regulatory subunits, AIP1 and AIP3, play evolutionarily conserved albeit divergent roles in growth and development of Arabidopsis

Curtis Foreman, Mohammad Dezfulian, and William L. Crosby

University of Windsor

Keywords: acetolactate synthase (ALS), ALS interacting protein (AIP), Arabidopsis thaliana, aberrant phenotype, sodium ion homeostasis

The functional contribution of the acetolactate synthase catalytic enzyme (ALS) to the biosynthesis of branched chain amino acids (BCAA) is well understood, yet current literature lacks a comprehensive understanding of the molecular regulation of this pathway. In bacteria, ALS-interacting proteins (AIP) are known to mediate feedback-inhibition of the pathway through interaction with the catalytic subunits of all 3 isozymes. AIP1 and AIP3 are evolutionarily conserved orthologues of bacterial feedback-regulatory proteins and are implicated in the regulation of ALS activity as the first enzymatic step in the BCAA synthesis pathway. To investigate the molecular role of ALS and AIPs in BCAA synthesis, we examined aip1-2 and aip3-1 knockout alleles in Arabidopsis. These mutants were subject to gross phenotypic assays, BCAA profile, hormone response assays, transcript abundance quantification and protein localization studies using fluorescent microscopy. Surprisingly, loss of function genetic backgrounds involving aip1-2 and aip3-1 exhibited a chlorotic phenotype and aberrant growth responses in sodium chloride and valine-supplemented media, respectively. Transcript abundance of AIP1 and AIP3 differs substantially across various tissues, suggesting differential roles in growth and development. Subcellular localization studies revealed the novel finding that AIP1 and AIP3 are localized to the peroxisome, although the functional significance of this finding is unknown. Despite the phenotypic differences observed in aip1-2 and aip3-1 backgrounds, important functional redundancy between these loci was suggested by the finding that aip1-2/aip3-1 double knockout mutants are synthetically lethal. Taken together, the data suggests a role for ALS and/or AIP proteins in pathways unrelated to BCAA synthesis, including Na-ion homeostasis, together with broader aspects of patterning and development. Further investigations into the molecular role of AIP in Na-ion homeostasis and valine response would provide valuable insight into the molecular mechanisms that co-regulate these diverse physiological functions in plants.

Defining the Mechanism of SCF-dependent SLBP Degradation: Finding the Magic F-box

Ashley. Chin and E. Lécuyer

McMaster University

Keywords: Stem Loop Binding Protein, Histone mRNA, SCF, Ubiquitination, Drosophila melanogaster

The regulation of histone messenger RNA (mRNA) metabolism is of great significance in eukaryotes, as it is intimately linked to DNA synthesis and cell cycle progression. Unlike other metazoan mRNAs, histone transcripts are non-poly adenylated, but contain a highly conserved stem–loop (SL) element in their 3’untranslation region. The histone SL is recognized by the Stem Loop Binding Protein (SLBP), a specialized RNA binding protein that controls histone transcript maturation, nuclear export and translation. Interestingly, the expressions of histone mRNAs and SLBP are tightly regulated during the mammalian cell cycle, showing restricted expression during S-phase. In human cells, SLBP clearance at the end of S-phase has been shown to involve a Cyclin-Dependent Kinase 1 (CDK1) phosphorylation of SLBP, resulting in Skp1-cullin-F-box (SCF) E3 ligase complex mediated degradation of SLBP. However, the specific F-box proteins involved in targeting SLBP for ubiquitination and subsequent proteasomal degradation remains unknown. Moreover, it is unclear whether a similar SLBP degradation mechanism is conserved in Drosophila. Based on preliminary data, we hypothesized that SCF-mediated degradation of SLBP is conserved in Drosophila and that would represent an attractive model for identifying conserved F-box proteins involved in targeting SLBP for SCF-mediated degradation. RNA interference experiments involving Drosophila cell lines were used to confirm whether SCF-mediated degradation of SLBP is conserved in Drosophila and to screen for putative F-box candidates. In vivo experiments involving transgenic flies expressing inducible hairpin RNAs targeting F-box factor genes were conducted to validate the in vitro hits. Results suggest that SCF-mediated degradation of SLBP is conserved in Drosophila and that one or more F-box factors may be involved in SLBP degradation. By defining the mechanism of SCF-mediated degradation of SLBP, this project sheds light on the regulation of histone mRNA metabolism and aids in the much needed discovery of substrates for F-box proteins.
Characterization of the Role of Cockayne Syndrome Group B (CSB) in Telomerase-Negative Cancer Cells

Angus Ho, Nicole Batenburg and Xu-Dong Zhu

McMaster University

Keywords: Telomeres, Cancer, Cockayne Syndrome, ALT cells, Telomerase-negative

The integrity of telomere length is vital for cell survival and proliferation. Over 80% of human cancers activate telomerase to maintain their telomere length in order to achieve unlimited growth potential, whereas up to 15% of cancers maintain their telomere length through a telomerase-independent mechanism known as alternative lengthening of telomere (ALT) (Cesare et al., 2010; Bryan et al., 1997).

Cockayne syndrome (CS) is a devastating autosomal recessive disorder characterized by a multitude of developmental defects including growth failure, vision degeneration, and UV-sensitivity (Lagerwerf et al., 2011). The majority of CS is caused by mutations in the CSB gene encoding the Cockayne syndrome group B protein (CSB). CSB has been implicated in DNA repair, chromatin remodeling, transcription and telomere maintenance. It has been reported that CSB regulates telomerase-dependent telomere lengthening (Batenburg et al. 2012), however its role in telomere maintenance in telomerase-negative cancer cells has yet been characterized. In this study, we examined the role of CSB in regulating the formation of the ALT-associated PML bodies, also known as APBs, which are subnuclear structures found exclusively in telomerase-negative cancer cells. We find that overexpression of CSB impairs the formation of APBs, suggesting for the first time that CSB plays a role in regulating the ALT activity. As a result, studying the role of CSB in tumorigenesis and in telomere regulation in ALT cells may help elucidate new potential treatments for cancer patients.

Repression of hypoxia-inducible factor-1 alpha gene expression by the transcription factor Kaiso

Joseph Longo, Christina C. Pierre, Blessing Bassey, and Juliet M. Daniel

McMaster University

Keywords: Hypoxia, HIF-1α, Kaiso, Epigenetics

Hypoxia is a common characteristic of many solid tumours and is associated with poor prognosis and resistance to treatment. In response to hypoxia, the hypoxia-inducible factor-1 (HIF-1) heterodimer orchestrates a cascade of transcriptional events that activates genes involved in cell survival, angiogenesis, and energy metabolism; however, this response is dependent on the stabilization of its oxygen-sensitive regulatory subunit, HIF-1α, which is only stabilized under hypoxic conditions. While the mechanisms governing the post-translational regulation of HIF-1α have been well studied, those that regulate HIF-1α at the transcriptional level are not fully understood. In this study, we demonstrate that the transcription factor Kaiso interacts with the methylated HIF1A promoter in hypoxia and that Kaiso depletion results in increased HIF-1α and HIF-1 target gene expression. Collectively, our data implicate Kaiso as a negative regulator of HIF-1α expression.
Session 14 - IB 235

Ecology

Sunday March 23
9:00 - 10:30 am
Estimation of bird mortality using comparative capture rates suggests decreased juvenile survivorship during migration

Ron Togunov and Alex Mills
York University

Keywords: migration, mortality, survivorship, age class, banding data

Avian population dynamics research has disproportionately focused on the stationary periods of adults, resulting in an incomplete understanding of age-related processes. We attempt to estimate survivorship of juvenile songbirds during the migratory periods using banding data from eastern North America for six Neotropical migrants: American Redstart (Setophaga ruticilla), Baltimore Oriole (Icterus galbula), Black-throated Blue Warbler (Setophaga caerulescens), Rose-breasted Grosbeak (Pheucticus ludovicianus), Swainson's Thrush (Catharus ustulatus), and Veery (Catharus fuscescens). We compared the proportion of juveniles to adults between the autumn and spring migration seasons and also along the migration flyway during autumn to identify differential mortality. The proportion of juveniles between autumn and spring decreased on average from 0.80 to 0.58 in males and from 0.73 to 0.61 in females. The weighted regression along the autumn flyway showed that the proportion of juveniles among males decreased -1.6% per degree latitude on average and -1% for females. Decrease in proportion of juveniles was higher in peripheral flyway sites (-1.5%) compared to interior sites (-0.8%). The results show that juvenile survivorship is significantly lower than adults and near the periphery of the migration route.

Climate-growth relationship in snapping turtles (Chelydra serpentina): development of an innovative approach

M. Perron, K. Sasaki, J. Dech, and J. Litzgus
Laurentian University

Keywords: climate change, snapping turtles, long-term growth data, crossdating, climate-growth relationships

Ectothermic animals, specifically chelonians, are among the most vulnerable to climate change, yet the sensitivity of turtle populations to these effects is still relatively unknown. Since growth rates of turtles are related to their fitness, long-term growth data are fundamental to predicting responses to changing climate. Part of the challenge is that long-term growth data on turtles is scarce due to their life history, which includes great longevity. Conventional methods to obtain these data, including mark and recapture, are costly and time-consuming. To address this issue, an alternative method is proposed that involves the analysis of annual growth increments visible on the carapace scutes, which if correctly dated, can provide multi-decadal growth data. A dendrochronological (tree-ring study) technique, crossdating, was applied to the growth increments present on the scutes of snapping turtles (Chelydra serpentina) from a population in Algonquin Park, Ontario, Canada. Crossdating allows for accurate dating of annual growth increments by cross-matching the synchronous growth response of individuals in a population to local climate variables. Such synchronicity was present among a subset of individual female turtles from the population, indicating the potential application of crossdating to this species. Age-related growth trends were statistically removed from crossdated increment data to elucidate climate-related annual variability in growth chronologies. Average growth of those individuals (1950-1984) was significantly correlated with several monthly climate variables, including summer drought, January, May and July precipitation, as well as February temperature. Such growth responses suggest that the predicted future increase in drought at the study site could negatively affect the studied population. Overall, results suggest that crossdating may be applied to other populations to provide long-term growth data and establish climate-growth relationships.
Vegetative Analysis of Six Main Roadways in Greater Sudbury, Ontario, Canada

Sabrina J. Rainville and Sabah Nasserulla

Laurentian University

Keywords: Greater Sudbury, roadside vegetation, vegetative analysis, ruderal, quadrat sampling

Roadsides are known to be polluted due to salting and vehicle exhaust fumes, in addition to mechanical disturbances. Such an environment is inhabited by plant species which can survive and reproduce under those conditions. This study attempts to initiate documentation of such species through the vegetative sampling of six main highways which pass through Greater Sudbury, Ontario, Canada. List quadrat method (1x1m) was used to sample twenty quadrats in each of three spots along the six highways selected. Species quantity, density, dominance, frequency and cover were analysed. While soil analysis results are pending, so far the study has concluded that 83 species were encountered, belonging to 25 families. Poaceae, Asteraceae, and Fabaceae were most frequently represented, with 23, 20, and 7 species respectively.

Effects of temperature and atmospheric carbon dioxide on microbe-mediated nitrogen and carbon dynamics of the boreal bryosphere

Margaret Sawatzky and Zoe Lindo

University of Western Ontario

Keywords: climate change, nitrogen, carbon, moss-associated microbes, decomposition

Moss-associated microbes such as N2-fixing cyanobacteria and heterotrophic decomposers play key roles in boreal forest nitrogen and carbon dynamics, contributing to processes such as the provisioning of biologically available nitrogen (through N2 fixation and organic matter decomposition) and respiratory CO2 release. However, it is unknown how these processes will be affected by single and combined aspects of climate change, such as elevated temperature and CO2. We used a full factorial experiment to examine the effects of temperature (11.5°C, 15.5°C, 19.5°C), CO2 (400 ppm, 750 ppm), and cyanobacterial density on N2 fixation rates, heterotrophic respiration rates, microbial biomass, and inorganic N availability in a boreal feather moss system. Heterotrophic respiration rates (although not microbial biomass) increased with temperature, and nitrogen availability increased with temperature when atmospheric CO2 was also elevated. Nitrogen availability was correlated with heterotrophic respiration rates, suggesting that heterotrophic decomposers actively release inorganic N to the boreal system as a whole. Cyanobacterial densities declined during the experiment, and the N2-fixing potential of remaining cyanobacteria was likely not realized, due to the continuing release of biologically available N by decomposers. As such, N2 fixation was marginal in all systems, and no relationship between cyanobacterial N2 fixation, cyanobacterial densities, or system-wide N availability was observed.
The production of canola and sunflower on thick versus thin compost layers over desulfized Ni-Cu Tailings

K.M. Stewart, P. Beckett, and D. Campbell

Laurentian University

Keywords: Tailings, Phytoremediation, Metals, Organic residues, Crops, Biomass, Roots

In areas like Sudbury where mining plays an important role in the economy, appropriate care and treatment of tailings and the metals found within them is crucial. The mining industry in Sudbury has produced thousands of hectares of "unusable" tailings. Tailings are a by-product of the milling process from refining nickel/copper mineral rich rock. One of the main mining companies in Sudbury is using layered system of desulfurized tailings and organic residues/compost towards the proper treatment of their tailings. Developments in phytoremediation techniques have led to the use of "crop species" such as Brassica napus (canola) and Helianthus annuus (sunflower) to aid in tailings remediation. This presentation will focus on production of both species grown on either thick or thin organic compost, as well as looking at whether or not rooting systems will avoid the underlying desulfized tailings and remain in the compost.

Data collected included depth of compost, depth and extent of roots for both species. Above ground biomass was calculated for each species grown either on thick or thin composts. A significant difference was observed between species (P<0.05) for above ground biomass. There was also a significant difference (P<0.05) between compost depth, species and interaction for root depth. Root width showed no significant difference (P>0.05). Low amounts of bioavailable metals were found in either thick or thin composts. Results show a successful application of organic compost covers to phytoremediate mine tailings in Sudbury. Growing crop species provides a use for tailings, as well as providing a possible source of income by using both species as a biofuel option.

The effect of declining calcium concentration in freshwater biota on fitness of Daphnia and Bosmina species

Rebecca Van Kempen, France Lapointe and Charles Ramcharan

Laurentian University

Keywords: daphnia, zooplankton, Bosmina , calcium decline, acid deposition, boreal shield, freshwater biota

Cladocera (a taxonomic group of zooplankton) are at the base level of many aquatic food webs and are considered to be keystone group. The crustaceans require calcium for hormone regulation as well as to maintain and replace their carapaces. In Boreal Shield lakes, the level of calcium is decreasing in many freshwater ecosystems due to a naturally low buffering capacity as well as large scale acidic deposition and inadvertent calcium extraction by humans. We attempted to determine the potential effect of calcium decline on five different species of cladocera: Daphnia schodleri, Daphnia parvula, Daphnia catawba, Daphnia ambigua and Bosmina longispina. Animals were collected from Nepahwin and Ramsey Lakes in the region of Sudbury, Ontario. These species are parthenogenic thus individual mothers could be used as initiators of clonal lines,. The different clonal lines were then exposed to four different calcium concentrations (0.0 mg•L-1, 1.5 mg•L-1, 3.0 mg•L-1, 15 mg•L-1), to determine the effects of Ca on fitness and longevity. The results demonstrated that for Daphnia spp., lower calcium concentrations affected not only longevity but also age at first reproduction and maximum body size. Low Ca also reduced reproductive output. Daphnia species seemed adapted for increased fitness at higher calcium concentrations, while Bosmina had increased fitness at lower calcium concentrations. Our work expands the number of species that have been evaluated in terms of tolerance of low Ca, and also suggests that as Ca decline progresses; lake food webs will see a shift away from Daphnia spp. which are primary sources of food for fish, towards the smaller-bodied Bosmina spp. which are difficult for fish to feed upon.
Session 15 - IB 250

Ecology

Sunday March 23
9:00 - 10:30 am
Effect of Coxiella burnetti Infection on Body Mass of Rodent Hosts

Trisha Hewitt
Laurentian University

Keywords: zoonoses, pathogen, body mass, rodent, Coxiella burnetti

Pathogenic zoonoses are characterized by their ability to transfer disease from animals to humans, and understanding the epidemiology of these organisms is important for the monitoring, control and overall understanding of zoonotic related health issues. Zoonoses often use wild animal populations as reservoirs, and pathogenic infections of a host may come at an energetic cost resulting in decreased body condition, leading to reduced host fitness. Coxiella burnetti is a re-emerging, highly virulent zoonotic bacterium that infects a variety of host species. The presence of this bacterium has been confirmed in wild populations of Northern flying squirrels (Glaucomys sabrinus), deer mice (Peromyscus manicuatus), Southern red-backed voles (Clethrionomys gapperi), woodland jumping mice (Napaeozapus insignis) and North American red squirrels (Tamias striatus) in Algonquin Provincial Park. The effect on body condition upon infection with C. burnetti in wild rodent populations is currently unknown. The objective of this study was to determine the impact of infection on host body mass and body condition. There were significant differences found in masses of infected versus uninfected hosts.

Geometric morphometric analysis of skulls of wolverine Gulo gulo and fisher Martes pennanti using digital calipers and a 3D Scan

Johanna Christy Alabré
Laurentian University

Keywords: geometric morphometrics, skull morphology, sexual size dimorphism, linear measurements, 3D scanner

For the longest time, biologists have been intrigued about comparing anatomical and morphological features in organisms, to do so several methods have been invented. Recently, geometric morphometrics have been one of them. Geometric morphometrics is considered a new methodological approach for studying shape variations of landmarks configuration in species. It provides information about where parts of the organisms are with respect to each other. In this study, shape variations in skulls were analyzed in both wolverines Gulo gulo and fishers Martes pennanti, each separated into two sex classes consisting of adult males and adult females. Thirteen measurements were done using digital calipers with direct data entry to the nearest 0.01mm for linear measurements and a 3D scanner which gave us the surface area and volume of the skulls. A total of 117 skulls with 67 wolverines and 50 fishers were measured. Using SPSS software, multivariate discriminant analysis showed considerable differences in skull size between both, species and sex. The skull of a male fisher was approximately 16 % larger than that of a female, whereas the skull of a male wolverine was approximately 8 % larger than that of a female. As expected, the results were all male biased (males being bigger than females) with p < 0.001 in all cases. These results were expected and supported all sexual size dimorphism hypotheses. Multiple tests were done to find variables with the strongest discriminating ability and three out of the thirteen variables were found to be significantly strong. By using a 3D scanner, the surface area and volume of the skulls were estimated, which was impossible to achieve by using linear measurements. Hence, we conclude that methodologically, both the digital calipers and 3D imagery can be used, because both provide useful information that will allow scientists to design new studies of shape variability in several organisms.
Effects of Mining on the Physiological Ecology and Morphology of Herpetofauna in Sudbury, Ontario

Camille Tremblay Beaulieu, Kiyoshi Sasaki, David Lesbarrères, Glen Watson, and Jacqueline Litzgus

Laurentian University

Keywords: mining, conservation physiology, fluctuating asymmetry, body condition, metabolic rate

A century of Sudbury's mining operations has created barren landscapes with high levels of heavy metals and acidity. Our previous population-level studies of amphibians and reptiles found that severely affected sites (barren), despite their superficial recovery in vegetation cover, had lower numbers of species and lower abundances compared to reference sites. The purpose of the current study is to investigate the mechanisms behind these differences in population ecology. To test whether population-level effects are driven by individual-level variation resulting from mining impacts, we investigated the morphology and physiology of individuals from barren and reference sites. We measured bilateral asymmetry in sculation (snakes), limb deformation (frogs), body condition and standard metabolic rate (SMR, snakes). We predicted that animals from the barren sites would display poorer body condition, higher levels of asymmetry, and elevated metabolic rates as compared to animals from reference sites. We found that the proportion of individuals with limb deformities was higher in barren sites for both mink frogs (9.0%) and green frogs (4.2%) compared to reference sites where no frogs with deformities were found (0%). Limb deformities can impact fitness and the higher proportion of frogs with deformities in the barren sites may explain the lower abundances of anurans observed in these sites. Patterns of snake sculation differed between our two target species; red-bellied snakes had more asymmetries in barren sites whereas garter snakes had more asymmetries in reference sites. Preliminary analyses of metabolic rates indicate that there were no differences in SMR of snakes between barren and reference sites. Additional data on the physiological variables will be presented. These findings are important because they shed light on the mechanisms underlying impacts at population- and community-levels, and will thus help to develop more targeted restoration strategies in the context of mining operations.

Use of paraffin embedded larvae in studying feeding biology of two forest defoliating Lepidoptera

Erin Van Breda

Laurentian University

Keywords: entomology, histology, gypsy moth, spruce budworm, comparison

Examining the contents of the digestive system of the larvae of Lepidoptera using histological techniques provides a novel approach to understanding insect feeding biology. Fixing and sectioning larvae embedded in paraffin allows one to see pieces of host tissues as they occur within the gut of live larvae at the moment of collection. Sections were obtained for the digestive tract of larvae of spruce budworm, Choristoneura fumiferana, which had fed on white spruce, Picea glauca and balsam fir, Abies balsame; and gypsy moth, Lymantria dispar, which had fed on white birch, Betula papyrifera, and red oak, Quercus rubra. Using Image-J computer programming, the area of pieces of ingested plant tissues in the midgut, rectum, and internal fecal pellet were measured. It was hypothesized that plant tissues would be digested as they passed from the midgut to the anus; however, it was found that the size of the plant tissues within the gut undergo little reduction in area suggesting that cell walls are not digested.
Root structure and growth of wetland plants with contrasting root turnover strategies

Dominique Gagnon and Peter Ryser

Laurentian University

Keywords: root turnover, dry matter content, specific root length, relative growth rate, leaf economics spectrum

Plants with different ecological strategies possess different methods of resource investment. The above-ground characteristics can be aligned along a gradient of leaf economics spectrum, but the concurrent below-ground relationships remain relatively unknown.

Fine roots of most herbaceous wetland plants in northern Ontario survive the winter, but in some perennial species the roots senesce in the fall. This study is part of investigations aiming to understand the ecological constraints determining adaptive advantages of these two root turnover strategies, focusing on root characteristics and growth, as well as relevant above-ground traits.

Fine roots of Dulichium arundinaceum, Carex stricta, Scirpus microcarpus, Carex oligosperma, Carex lasiocarpa, Eleocharis palustris, and Schoenoplectus acutus survive the winter, whereas roots of Alisma triviale, Sparganium androcladum, Rhynchospora alba, Calla palustris, Sagittaria latifolia, and Pontederia cordata senesce in the fall. We hypothesised that the result in resource investment of the opposing ecological strategies translates to differing root characteristics, in a similar manner known to that of the above-ground strategies along the leaf economics spectrum. The plants were garden grown for one season, and harvested in two separate pot experiments.

Results demonstrate that the species with roots senescing in the fall (annual) had a greater specific root length and a lower root dry matter content than species with roots surviving the winter (perennial). These species also demonstrated a greater above-ground relative growth rate in comparison, corresponding to the low root dry matter content. However, root length did not differ among contrasting root turnover strategies. Plants with annual root systems have a lower leaf dry matter content and a higher specific leaf area. This indicates that the strategy of perennial plants to produce new roots for each growing season is associated with root and leaf characteristics to be expected from the known economics spectrum.

The influence of physiological traits on climatic niche occupancy and competitive ability in the polyploid plant, Chamerion angustifolium

Ken A. Thompson, Brian C. Husband, and Hafiz Maherali

University of Guelph

Keywords: Polyploidy, Competition, Climatic Niche, Drought Tolerance, Ecological Niche Modelling

Polyploidy—the possession of more than two copies of each chromosome in the nucleus—has significant physiological consequences, but little is known about how the altered physiology of polyploids influences their ecology. Here, we present results from two studies investigating how physiological traits influence (i) the climatic niche and (ii) competitive ability in Chamerion angustifolium, a polyploid plant. Tetraploid C. angustifolium have physiological adaptations to tolerate drought relative to diploids and are less tolerant of freezing.

To investigate differences in the climatic niches of diploids and tetraploids, we compiled a dataset of 134 C. angustifolium populations of known ploidy across North America. We extracted climate data associated with these populations and found that tetraploids occupy a drier niche than diploids, while diploids occupy a colder niche than tetraploids. Using ecological niche models, we demonstrate that the climatic niches of diploid and tetraploid C. angustifolium are very similar to their geographic distributions.

To investigate differences in the competitive abilities of diploid and tetraploid C. angustifolium, we conducted a competition experiment in the greenhouse where we grew both cytotypes together at different densities and relative proportions across a soil-moisture gradient. We found that cytotypes did not differ in their competitive abilities across the soil-moisture gradient.

Collectively, our results suggest that physiology is at least partially responsible for differences in the realized climatic niches of diploid and tetraploid C. angustifolium, but do not enable tetraploid C. angustifolium to outcompete diploids when water is limited.
Session 16 - IB 260

Microbiology

Sunday March 23
9:00 - 10:30 am
Tunable protein expression system in bacteria

Ayat Kinkar, Eyad Kinkar, Mazen Saleh, and Pejman Hanifi-Moghaddam
Laurentian University

Keywords: inducers, IPTG, L-Rhamnose, tunable, periplasmic expression, E. coli, vector

Optimization of protein expression platform is important in academia and pharmaceuticals, which is still a challenge. Many labs are striving to express a protein for therapeutic purposes but fail, as it requires the optimization of several variables such as expression system and expression conditions. One of these variables is the optimal rate of expression, which can be controlled by varying codons, temperature, nutrition or the type of inducer. Inducers play a major role in an inducible expression system. They can turn on and off the expression of the protein. The most popular one is IPTG. However, IPTG can be toxic to the cells at high concentration and is not "tunable". This is very important if the protein has to be folded in the periplasmic space. Choosing the right inducer may allow the host cells to maintain and control protein expression. We have hypothesized that a tunable system would greatly increase the chance of periplasmic expression in bacteria. We have chosen L-Rhamnose's tunable inducing system and compared it to that of IPTG. To test our hypothesis we first chose 4 clones that could not be expressed with IPTG system and one control, which was expressed with IPTG. We examined the expression of these five different genes cloned into L-Rhamnose vector and induced with different L-Rhamnose concentrations. Our results show that two of the four proteins could be expressed in our tunable system but at various inducing concentration. In conclusion we show that the rate of the protein expression plays an important role in the expression of the proteins in E.coli, especially for the expression of periplasmic protein.

Characterization and Elucidation of Enterococcal and Clostridial Biofilms Under Environmental Stressors

Jason Byron Perez, Robin M. Slawson, and Joel T. Weadge
Wilfrid Laurier University

Keywords: Enterococcus, Clostridium, Biofilm, Environmental Stress, Biofilm-associated protein

Abstract: Most bacteria preferably grow within biofilms, which are matrices encasing multicellular communities of bacteria. Bacterial growth within biofilms infers an increase in protection from environmental conditions that may aid pathogens in persisting under variable conditions. Enterococcus and Clostridium are well-known pathogens, but their ability to produce biofilm has not been thoroughly assessed. The biofilm forming capabilities of eight isolates of Enterococcus spp. from storm water retention ponds (associated with floating islands and cold-temperatures) were assessed. Initial studies with enterococci and clostridia strains focused on establishing the optimal growth conditions (eg. anaerobic clostridial growth) as a basis for further evaluations. Biofilm potential was assessed in the laboratory and under conditions mimicking environmental stress conditions (eg. temperature, shear stress). Clostridial experiments are ongoing, but enterococcal studies have progressed enough to demonstrate that growth of enterococci at 37°C for 120 hours leads to the greatest biofilm production of control strains. Deviations from this temperature to have shown variances in the amount of biofilm formed and type of biofilm (eg. biofilms and pellicles). Stress exposure experiments involving shear stress resulted in the production of pellicles (air-liquid interface biofilm), and temperature shock (ie. a sudden shift to different temperatures) has demonstrated variability in biofilm production. The biofilm and pellicles have been used for determining what specific matrix components are leading to biofilm formation. While still preliminary, we are utilizing spectrophotometric and plate based colorimetric assays to probe for the presence of specific carbohydrates or fimbriae that may be present in these biofilm types. Characterization of enterococcal and clostridial biofilms may further help understand their environmental survival mechanism and virulence associated with biofilm production within the host.
Structural and Functional Characterization of the Role of BcsG in Bacterial Cellulose Biosynthesis

Erum Razvi, Laura Kell, and Joel T. Weadge
Wilfrid Laurier University

Keywords: biofilms, cellulose, crystallization, enterobacteriaceae, protein function

Bacteria commonly live in multicellular communities, such as biofilms. The extracellular matrix of a biofilm, which surrounds and supports bacteria, is predominantly composed of exopolysaccharides produced by the encased bacteria. For example, Escherichia and Salmonella spp. produce the exopolysaccharide, cellulose. This exopolysaccharide leads to the formation of a biofilm that helps these bacteria elude detection by the immune system, and increases their tolerance to antimicrobial agents and harsh environmental factors. Genetic studies have demonstrated that at least four genes, bcsABZC, are essential for the biosynthesis of cellulose in bacteria. However, enteric pathogens, such as E. coli and Salmonella spp., possess an additional three genes, bcsEFG, proven critical to the proper synthesis of the polymer. BcsG is predicted to play a role in the release of growing cellulose chains from bacterial cells, but biochemical verification of this hypothesis is lacking. The goal of the present research is to overcome this deficit of understanding through the cloning, overexpression, purification and structure-function characterization of BcsG. Two protein constructs of BcsG, the entire polypeptide sequence and a truncated derivative lacking the N-terminal transmembrane region have been generated. Purification of both constructs has been successful using immobilized-metal ion affinity chromatography, but only the soluble truncated derivative of BcsG can be isolated to high yields. Extensive protein crystallization trials with this truncated construct have led to the identification of promising conditions that are currently being optimized. Biochemical exploration of the predicted enzymatic activity is also being conducted through cellulase assays to confirm and characterize BcsG. Combined, these structural and functional analyses will improve our understanding of the role BcsG has in the cellulose biosynthetic complex and increase our overall knowledge of how biofilms develop in E. coli and Salmonella spp.

Isolation and characterization of viruses infecting the freshwater algae Chrysocromulina parva

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University of Toronto Mississauga

Keywords: algal viruses, phycodnaviridae, NCLDV, Chrysocromulina parva

In the following study, water samples from the Bay of Quinte, an embayment of Lake Ontario, were tested for lytic activity against the prymnesiophyte algae Chrysocromulina parva and cell lysis was observed upon addition of 0.45 μm-filtered water samples from the bay. Microscopic and molecular studies were conducted to determine morphological properties of the lytic agent and determine its taxonomic affiliation. The genome size was estimated at 485 kbp, and transmission electron microscopy revealed 145 nm diameter virus particles assembled within the cytoplasm; characteristic features of a broad group of viruses termed NCLDVs (nucleocytoplastic large DNA viruses). Amplification and sequencing of the virus's partial DNA polymerase (polB) gene and comparisons with sequences from cultivated algal viruses suggest that this newly isolated virus (henceforth termed CpV) is a member of the Phycodnaviridae; a class of NCLDVs that infect marine and freshwater algae. Phylogenetic analyses related CpV most closely to the virus genera Pyrmnesiovirus that includes viruses that infect the marine algae Chrysochromulina brevefilum and Phaeocystis globosa. Multiple Major Capsid Protein (MCP) fragments were also amplified, but their sequences were closely related to cultivated prasinoviruses and Mimivirus-like viruses. The isolation of the freshwater Chrysocromulina parva virus presented here marks the first isolation of algal viruses infecting freshwater species other than Chlorella-like algae. Contrasting phylogenies of CpV genes, and its exceptionally large genome size may suggest the virus is a hybrid linking the NCLDV classes Phycodnaviridae and Mimiviridae. Future studies combined with whole-genome sequencing are needed to determine whether CpV represents a new category of species within the NCLDVs.
Investigating the effect of anaerobic shock on the antibiotic resistance profiles of environmentally isolated pathogens

Sarah Asselin and Robin M. Slawson

Wilfrid Laurier University

Keywords: Yersinia enterocolitica, Enterococcus faecalis, Antibiotic resistance/susceptibility, Zone of inhibition, Anaerobic shock, Temperature stress

The increasing prevalence of antibiotic resistance expression within the environment has become very concerning. With no means of removing antibiotics from waste wastewater from water treatment facilities and industrial and agricultural practice, ecological microorganisms have a greater opportunity for the incorporation of these antibiotics into their genome, altering their natural antibiotic resistance profiles. The antibiotic resistance/susceptibility profiles of four bacterial isolates were measured under anaerobic shock and temperature stress as a means of better understanding their physiological stress responses. Environmental Yersinia spp. and Enterococcus spp. were placed under anaerobic shock at various temperature stresses and the results were compared with the control microorganisms, Yersinia enterocolitica and Enterococcus faecalis, under the same conditions of physiologic stress. The isolates were grown up subject to temperature stress and combined anaerobic shock and temperature stress until they reached the late log phase of their growth cycle, at which point the antibiotic resistance/susceptibility of each isolate was measured using specific antibiotics. The growth of these isolates were measured by recording the optical density (at 600nm) periodically and corresponding the estimated cell density with colony-forming units (CFU/mL) that were calculated for the inoculum before exposure to the conditions of stress and at the time of antibiotic testing. The results show that exposure to combined temperature stress and anaerobic shock, the estimated cell density of the Yersinia spp. decreased with the decrease in temperature, whereas Enterococcus faecalis estimated cell density increased, and the estimated cell density of the Enterococcus environmental isolate remained constant. This indicates the Yersinia spp. were expiring with the decrease in temperature while the Enterococcus spp. were able to flourish and survive. The antibiotic resistance/susceptibility tests varied and no observable pattern was detected regarding the control isolates and the environmental isolates of the same genus.

Evaluation of water quality indicators in amended and un-amended stormwater retention ponds

Jessica Beckett and Robin M. Slawson

Wilfrid Laurier University

Keywords: Stormwater Ponds, Coliforms, E. coli, Water Quality, Floating Island

Floating Islands are plastic rafts inoculated with aquatic plants the offer an ideal growth environment for microorganisms in the water. They are an effective means of lowering the biochemical oxygen demand and chemical oxygen demand of the water. Less investigation has been done on how these changes affect water quality indicators within the water column, and how they compare to small untreated ponds. This study aims to gain some insight into the levels of cultureable heterotrophic bacteria, fecal coliforms, and E. coli in both types of ponds. Samples representative of water bodies treated with floating island technology were provided from two locations near Lindsay Ontario, while untreated ponds were sampled from three locations in the Kitchener-Waterloo area. Samples from treated and untreated locations were subjected to community level physiological profiling (CLPP), heterotrophic plate counts (HPC), and membrane filtration for the isolation of fecal coliforms (mFC). Among the floating island sample locations there did not seem to be a consistent relationship between the amount of root material in the sample and the levels of fecal coliforms/E. coli. However the average CFU/mL was greater in samples containing root material than samples without, highlighting the important role that aquatic plants play in offering stable habitats for microorganisms. Although the untreated locations had lower coliform levels and CFU/mL it must be notes that the samples were gathered in significantly colder weather. Out of the three untreated locations the third site consistently displayed the highest average CFU/mL, likely due to its smaller size and shallower depth. Further studies should be performed investigating seasonal changes in water quality at each location to gain a better understanding of the impact of the floating islands.
Session 17 - IB 270

Animal Physiology

Sunday March 23
9:00 - 10:30 am
Long-term stress of domestic and wild American mink (*Neovison vison*)

Paula Di Benedetto, Jeff Bowman, Gabriela Mastromonaco and Albrecht Schulte-Hostedde

Laurentian University

Keywords: cortisol, domestic, enzyme immunoassay, fur farm, mink

Stress can be beneficial to an animal when reacting to a short-term stressor by stimulating the flight-or-flight response, however long-term stress can be maladaptive. Domesticated animals demonstrate elevated stress levels when living conditions required in captive habitats are not met. American mink (*Neovison vison*) have been domesticated on fur farms within their native North American range since the late 1800s. If domestic mink are more stressed than wild mink, then domestic mink should have higher hair cortisol concentrations than wild mink. We collected hair samples from wild and domestic mink from Ontario and Nova Scotia, and performed enzyme immunoassay to determine cortisol levels. Domestic mink had significantly higher hair cortisol concentrations than wild mink. We also found that hair cortisol concentrations were significantly higher for mink from Nova Scotia than Ontario. Sex had no significant effect on cortisol levels, and there was no interaction between mink type (domestic, wild) and location (Ontario, Nova Scotia). Analyzing long-term stress of domestic mink may help to improve the welfare of these animals on fur farms. Future studies should assess habitat features of fur farms such as water pool availability and size.

Development of an artificial diet for gut loading in the fall field cricket (*Gryllus pennsylvanicus*)

Jacqueline Lebenzon and Brent Sinclair

Western University

Keywords: ion homeostasis, osmotic homeostasis, chill coma, artificial diet, gut loading

At low temperatures most insects will enter a state of reversible muscle paralysis called chill coma. The onset of chill coma is characterized by the migration of sodium and water from the hemolymph to the gut, disrupting ion and water homeostasis. Disruption of homeostasis is driven by ion gradients, thus manipulating ion gradients between the hemolymph and gut should affect the insect’s ionic response to low temperature. An artificial, lab synthesized diet with ingredients in known concentrations could be used to load the insect gut with a target ion and thus affect recovery from chill coma. In this study, I developed a controlled artificial diet for the fall field cricket, *Gryllus pennsylvanicus*, that is easily manipulated, eaten by adult fall field crickets, loads the gut, and does not adversely affect ion and osmotic homeostasis between the hemolymph and gut. In future studies, this artificial diet can be used as a tool to manipulate ion gradients in the gut of G. pennsylvanicus before low temperature exposure and therefore test hypotheses about the relationship between gut contents and insect cold tolerance.
Relevance of SNARE Protein Syntaxin-1A in Cardiac Function and ANP Release

Arash Boroumandi, Xiaodong Gao, and Robert G. Tsushima

York University

Keywords: syntaxin-1A, heart, atrial natriuretic peptide, transgenic mouse, SNARE proteins

SNARE (soluble N-ethylmaleimide sensitive factor attachment protein receptor) proteins are important for the transportation and coordination of intracellular vesicles, as well as regulating the release of neurotransmitters and hormones, such as atrial natriuretic peptide (ANP). ANP is a peptide hormone released primarily from the adult atria, and is responsible for lowering blood pressure. The main stimulus of regulated ANP release in the heart is mechanical stretch of the atrial cells, which occurs during increased atrial load, and hormone (e.g. endothelin) stimulation. ANP release and expression are enhanced under pathological conditions, such as ischemic heart disease and hypertension. It has been shown the SNARE proteins syntaxin-4, VAMP-2, and SNAP-23 form a complex that facilitates the release of ANP in a regulated and stimulus driven fashion. However, the Tsushima lab has observed the expression of the SNARE proteins, syntaxin-1A and SNAP-25, in the heart.

Syntaxin-1A has been shown to regulate voltage gated L-type calcium channels in the brain and endocrine cells. In my project, I studied the role of syntaxin-1A on heart function and ANP release using a heart-specific conditional knockout mouse model. ANP release and cardiac function were measured in the isolated perfused mouse heart model. My results indicate that knocking out syntaxin-1A had the following outcomes: 1) there was significant decrease in the heart rate of the knockout mouse heart in comparison to the wild type heart; and 2) there was significant increase in the ventricular end systolic pressure, which translated into an increase in develop pressure. I did not observe any significant difference in the functional recovery of wild type and knockout syntaxin-1A hearts subjected to ischemia and reperfusion injury. I am currently measuring the release of ANP release from hearts subjected to hypotonic stress. My studies will identify novel roles of syntaxin-1A in the heart, and it regulates myocardial contraction, heart rate, and ANP secretion.

Modulation of the retinoic acid signalling pathway during the expansion of hematopoietic progenitor cells

Tyler T. Cooper

University of Western Ontario

Keywords: hematopoiesis, hematopoietic stem/progenitor cells (HSPC), aldehyde dehydrogenase (ALDH), retinoic acid (RA)

During embryogenesis, tissue patterning and development is influenced by retinoic acid, a lipophilic signaling molecule whose production is mediated by the intracellular enzyme aldehyde dehydrogenase (ALDH). ALDH activity also plays a central role during hematopoiesis in vivo, and ALDH inhibition has been shown to promote the expansion of primitive hematopoietic progenitor cells (HPC) in vitro. We have previously shown that transplantation of HPC retaining high ALDH-activity (Ahi HPC) can stimulate islet regeneration in STZ-treated diabetic mice. Therefore, we documented differences in ALDH activity as fresh ALDHhi umbilical cord blood cells (Ahi UCB) are expanded in hematopoietic culture conditions for 3, 6, or 9 days. Moreover, the expression primitive surface markers (CD34+, CD38-, CD133+) is reduced as Ahi UBC cells expand ex vivo. It was determined that six days of ex vivo expansion gave rise to the largest fold-increase of Ahi HPC expressing primitive surface markers. By modulating the retinoic acid pathway during HPC expansion, by using an ALDH inhibitor (DEAB), we expect to increase the production of islet regenerative hematopoietic progenitor cells. We hypothesize that inhibition of ALDH activity will reduce HPC differentiation resulting in an increased number of Ahi HPC with primitive surface marker expression.
Implications of Consuming a Western Diet following an adverse in utero environment upon the fructose metabolic pathway in the Sk

Jia Liu, Lin Zhao, and Timothy Regnault

Western University

Keywords: western diet (WD), fructose, ATP, in utero, metabolic syndrome

The contribution of high amounts of fats and processed sugars, typical of the infamous Western Diet (WD), to the rapid rise in the prevalence of the metabolic syndrome is an increasingly important area of research. Given the increasing incidence of metabolic disorders, especially insulin resistance (IR) in early life in those born following an adverse in utero environment, it is critical to understand how WD impacts later life disease processes. We investigated how consumption of WD in postnatal life may augment markers of fructose metabolism and alter energy balance (pre-determinants of IR), following an adverse in utero environment. To study this, the gastrocnemius muscle, a primary site of IR, of male guinea pigs (Cavia porcellus) fed either a Control Diet (CD; 6% fructose/kg feed and 18% fat) or a WD (18% fructose/kg feed and 46% fat) were harvested from both Control Birth Weight (CBW) and Low Birth Weight (LBW) animals at young adulthood (140 days, ~ 18 human years).

Real-Time PCR results indicate that the transcript levels of fructose metabolizing enzymes triokinase, ketohexokinase-A, and ketohexokinase-C were significantly (p<0.05) reduced in LBW animals, and transcript levels of triokinase was further reduced (p<0.01) due to WD. Interestingly, muscle of LBW offspring fed a CD for life, had significantly (p<0.05) reduced concentrations of ATP relative to CBW/CD (fold difference relative to CBW/CD = 0.53:1; LBW/CD:CBW/CD); however, in WD animals, LBW lead to increased ATP levels compared to CBW (fold difference relative to CBW/CD = 1.03:0.88; LBW/WD:CBW/WD). While WD reduced triokinase expression, it had no impact upon ATP unless coupled to a LBW phenotype. These data demonstrate that a poor in utero environment down-regulates the postnatal fructose metabolic pathway and ATP synthesis ability in muscle. Further, we speculate in CBW, possible reductions in ATP production, often cited as an effect of excessive fructose intake, may be overcome when fructose is fed in combination of high levels of fats.

The Regulation of Ghrelin Secretion from Pancreatic Epsilon Cells

Amanda Mohabeer, Xiaodong Gao and Robert Tsushima

York University

Keywords: endocrine pancreas, epsilon cells, ghrelin, SNARE proteins, voltage-gated calcium channels

Abstract: Discovered in 1999, ghrelin, a 28 amino-acid peptide hormone has been found to be secreted from the stomach and pancreas. Within the endocrine pancreas it is secreted from epsilon cells, which make up less than 1% of the islet of Langerhans. In 2010, Goldstein’s lab derived a pancreatic ghrelinoma cell line (PG-1 cells) and showed that the β-adrenergic receptor agonist, norepinephrine, stimulated ghrelin secretion from these cells. I have been investigating the cellular components responsible for mediating the secretory processes of ghrelin release from these cells. Specifically, I am determining the expression of the exocytotic protein machinery in PG-1 cells, and whether extracellular calcium is needed to facilitate ghrelin secretion. Immunoblot analysis was carried out for various SNARE (soluble N-ethylmaleimide sensitive attachment factor receptor) proteins. I observed the presence of the core SNARE complex SNAP 25, syntaxin 1A and VAMP-2, as well as the SNARE-associated proteins, Munc. The dependence of extracellular calcium on norepinephrine-stimulated ghrelin secretion was performed in the presence or absence calcium in the external solution. I observed reduced stimulated ghrelin secretion when external calcium was absent. To further explore the dependence of extracellular calcium, cells were treated with voltage-dependent calcium channel blockers to inhibit the activity of L-type, P/Q-type, N-type and T-Type channels. Preliminary results suggest a potential role of L-type and N-type channels in facilitating calcium influx needed for stimulated secretion. Lastly, to further determine which SNARE proteins are essential for ghrelin secretion, cells are currently being transfected with botulinum A, botulinum C, and tetanus toxin which proteolytically cleave SNAP-25, syntaxin 1A and VAMP-2 respectively. The cells would then be subjected to secretion assays to determine if they are vital to this pathway. My studies will demonstrate the importance of voltage-gated calcium channels and SNARE proteins in mediating the secretion of ghrelin from pancreatic epsilon cells.
Session 18 - IB 280

Physiology

Sunday March 23
9:00 - 10:30 am
Reproduction, Stress and Feather Quality in Tree Swallows

Kenneth Sarpong, Pierre Paul-Bitton, Christine Madliger, Chris Harris, Stephanie Doucet, and Oliver Love

University of Windsor

Keywords: corticosterone, condition, exaggerated ornaments, mechanism, reproductive investment

In a variety of species, exaggerated ornaments such as large horns or bright plumage are indicative of condition and can influence mate choice. Despite considerable evidence that the production and maintenance of high quality ornaments is positively related to condition and reproductive performance, few studies have investigated the mechanisms linking ornament quality and condition. Physiological measures such as baseline glucocorticoids (e.g. cortisol and corticosterone) represent ideal candidates for investigating this mechanistic link due to their reflection of energetic status (i.e. individual state) and growing evidence that glucocorticoids can influence feather growth and quality. We investigated the relationship between plumage quality attributes, baseline corticosterone (CORT), and reproductive investment in adult female tree swallows (Tachycineta bicolor) breeding in Cayuga, Ontario. We found that past reproductive investment predicted plumage coloration, and that past CORT levels were negatively related with plumage quality. In addition, plumage quality predicted current year condition and reproductive investment. Overall, these results provide evidence that female plumage coloration is indicative of female quality and reproductive investment. Furthermore, our results support the idea that CORT may be an important mechanistic link between an individual’s condition, reproductive performance, and ornament quality.

Effect of heavy metals and drought stresses on the stem conductive structure, leaf area and stomatal density of Dodonaea viscosa

Andrea P. Rayon R.

Laurentian University

Keywords: drought stress, heavy metals, Dodonaea viscosa, drought tolerance, heavy-metal tolerance

Vegetation on metalliferous soils, either of natural or anthropogenic origin, faces besides metal-stress also other stresses such as drought. Some plants growing on nickeliferous laterites with millions of years of adaptive evolution can tolerate high metal concentrations, such as certain specialized vegetation in New Caledonia, which also often experiences prolonged periods of drought. The nature of the interaction between these two stresses, heavy-metals and drought, has been investigated in plant species with a short evolutionary history on metal polluted substrates, but has not been investigated in plants which have acquired drought and heavy-metal tolerance on natural metalliferous soils. In order to understand long-term evolutionary adaptation to multiple stresses, the interaction between simultaneous metal and drought stresses in a species naturally occurring on sites with these stresses was investigated. Dodoneae viscosa is such a species, with natural adaptation to nickeliferous laterites in New Caledonia, where it is used as a pioneer species in mine-site restoration. Seedlings were grown in a greenhouse under drought and Cu-Ni-slag-induced heavy-metal contamination in a factorial combination. The results showed that the two stresses have an additive effect, similar to the combined effect of these stresses previously observed in red maple with shorter evolutionary history on contaminated substrate. Leaf area, and xylem, phloem and total stem cross-sectional areas showed significant reduction under both heavy-metals and drought treatments in an additive manner. The results suggest that presence of heavy-metals aggravates drought stress even for naturally metal- and drought-tolerant species, in a similar manner as known e.g. for red maple. However, it is possible that under natural conditions the mycorrhizal symbiosis of D. viscosa improves its tolerance to these stresses, as found with many plant species in New Caledonia.
Influence of sound direction on auditory midbrain response to novel sound

Huiming Zhang, Chirag Patel, and Blake White
University of Windsor

Keywords: neurophysiology, auditory neuroscience, auditory midbrain, field potential recordings

Novel sounds are acoustic events occurring infrequently in the environment. The detection of novel sounds is of importance to the biological fitness of animals. Novel sounds may originate from locations different from those of repetitive/continuous background sounds (named as standard sounds elsewhere). Studies in our laboratory indicate that neurons sensitive to novel sounds exist in the auditory midbrain. For some midbrain neurons, this sensitivity is dependent on the angle of separation between novel and standard sounds. The topographic location of these neurons has yet to be revealed. Furthermore, it is unknown how this separation dependence of sensitivity to a novel sound is reflected by responses of neural populations in the structure. This study was designed to address these questions using the rat as an animal model. An oddball paradigm consisting of a train of tone bursts was used to elicit auditory responses. Each tone burst had one of two frequencies, with one tone higher and the other tone lower than the characteristic frequency of a neuron. Tone bursts with two frequencies were presented at different probabilities to mimic standard and novel sounds. Standard and novel sounds were presented from either one or two loudspeakers, with the location of each loudspeaker controlled independently. Auditory responses to an oddball paradigm were recorded from single neurons (unit recordings) or a population of neurons (local field potential recordings). Recording locations were verified by using a dye upon completion of an experiment. Our results reveal that neurons with spatial separation dependence in sensitivity to novel sound are located in the dorsal and lateral regions of the auditory midbrain. The effect of spatial separation on the sensitivity to novel sound is reflected in population responses as revealed by local field potentials. This research contributes to understanding how novel sounds are processed in the auditory midbrain.

Integrin’s Role in Maintaining Adhesions during Drosophila Heart Remodeling and Aging

Simina Bogatan and Roger Jacobs
McMaster University

Keywords: Drosophila, integrin, heart, talin, longevity

Proper cardiac muscle function is critical for optimal health. Thus as individuals age, and their cardiomyocyte performance declines, the risk of debilitating heart diseases increases. Heart cells and the adhesions holding them together remodel as individuals grow. Little is known about what happens to the adhesions during remodelling and aging, but it is known that Integrins are responsible. Integrins, and their turnover, are necessary for heart remodelling. The Drosophila melanogaster heart model is being used to study this problem, since it is a simple genetic organism that has developmental and functional homology to the vertebrate heart. We used the GAL4/UAS system is used in conjunction with RNA interference to decrease Integrin function during heart growth in Drosophila. My experiments demonstrate that Integrins are necessary for heart remodelling and maintaining cardioblast adhesions. To test the requirement of Integrin during heart function, Integrin levels were reduced at various stages of development. The adult flies were then assessed for changes in morphology and longevity. Confocal microscopy analyses of adult hearts illustrated various degrees of heart malformation for each treatment. In particular, muscle cells could not regenerate contractile fibres subsequent to a transient loss of Integrin adhesion. The longevity assays revealed drastically decreased lifespans for those flies whose levels of Integrin were decreased in the heart during metamorphosis. Further discoveries of what happens to cardioblast adhesions during remodelling could lead to treatments for human heart diseases like cardiac hypertrophy.
Physiological validation of infrared thermography (IRT) for measuring the presence of brown adipocyte activity in health, male adults

Anton Rogachov
McMaster University

Brown adipose tissue (BAT) is a unique organ found in mammals that has evolved to dissipate large amounts of chemical energy in the form of heat in mammals. This hallmark thermogenic feature of BAT is facilitated through the expression of a unique protein, UCP1, which uncouples oxidative phosphorylation from ATP production, producing heat instead of ATP. It is now well established that catecholamines released by the SNS are the primary activators of the β-3 adrenergic receptors found on the membrane of BAT. Therefore, our study designed aimed at manipulating the activation of BAT and attempted to capture its activity within the supraclavicular (SCV) region in lean, adult males. As cold exposure is considered the traditional activator of BAT, we wrapped a surgical blanket, set to 12°C, around the waste of participants and this served as our control exposure. Likewise, the ingestion of caffeine citrate, a known SNS activator, on a separate week served as our positive control. On the contrary, propranolol, a clinical β-blocker, was administered the following week before cold stimulation, serving as the negative control. A follow up energy expenditure test was also completed to supplement the thermography. Thermal images of the SCV area were taken over a course of 40 minutes, overlain, and the 10% temperature readings were taken from our ROI. Of the subjects tested (N=4), three showed to have active BAT, while one did not. Early findings suggest that caffeine does in fact elicit a similar BAT response as cold however, significant suppression, with propranolol, of this response has not yet been demonstrated. These results are limiting due to the inadequate sample size and the study is currently ongoing.

Characterization of ion channel expression and function in pancreatic epsilon cells

Aryan Abadeh, Xiaodong Gao, and Robert Tsushima
York University

Keywords: epsilon cells, ghrelin, ion channels, pancreatic islets

The endocrine pancreas is composed of the islets of Langerhans, which play an important role in glucose homeostasis. The islets consist of five cell types: beta (β)-cells which secrete insulin, the body’s blood-glucose lowering hormone; alpha (α)-cells which secrete glucagon, the body’s principal blood-glucose increasing hormone; somatostatin-producing delta (δ)-cells; pancreatic polypeptide (PP)-containing cells; and ghrelin-secreting epsilon (ε)-cells, which comprise less than 1% of the total islet cell population. Recently, a suitable model for studying the underlying cellular and biochemical properties of ε cells was developed. Expression of SV40 (Simian vacuolating virus 40) large T-antigen under the control of preproghrelin promoter by Goldstein’s group resulted in the creation of an immortalized cell line, pancreatic ghrelinoma or PG-1 cells. Islet cells develop from a common embryonic precursor cell, thus I hypothesized that many of the same ion channels participating in the generation of electrical activity in β-and α-cells play an important role in the excitability of PG-1 cells. To characterize the ion channels expressed in PG-1 cells, I first performed whole-cell patch clamp measurements. I observed the presence of two kinetically different voltage-gated Ca2+ currents corresponding to low-voltage activated (LVA) and high-voltage activated (HVA) Ca2+ channels. A non-inactivating voltage-gated K+ channel was observed. I occasionally observed in some cells voltage-gated Na+ currents. Lowering the intracellular ATP concentration in the cell, I was able to measure ATP-sensitive K+ channels. To gain more insight into the type of ion channels that are expressed in PG-1 cells, I performed RT-PCR analysis. My preliminary results showed the presence of all four HVA voltage-gated Ca2+ channel isoforms; CaV1.2 (L-type), CaV2.1 (P/Q-type), CaV2.2 (N-type), and CaV2.3 (R-type). The LVA T-type voltage-gated Ca2+ channel isoforms, CaV3.2 and CaV3.3, were also detected. Lastly, PCR results demonstrated the presence of the following voltage-gated Na+ channel isoforms in PG-1 cells, NaV1.1, 1.2, 1.3, 1.6, and 1.9. I am currently determining the specific voltage-gated K+ channel isoform expression profile in the PG-1 cells. My studies are the first to characterize the electrical properties of PG-1 cells, and provide new insight into the potential cellular mechanisms that control ghrelin secretion from ε cells.
Session 19 - IB 245

Cell & Molecular Biology

Sunday March 23
10:45 - 11:45 am
Does HST3 have a role in double strand break repair?

Behnam Manavi Tehrani and Jeffrey Fillingham

Ryerson University

Keywords: checkpoint recovery, chromatin, double strand break repair (DSBR), Hst3, H3K56ac

Double strand breaks (DSBs) in DNA are serious problems that if unrepaired can lead to the loss of the centromere distal segment of the chromosome. The budding yeast, Saccharomyces cerevisiae, serves as an excellent model for identifying fundamental mechanisms of double strand break repair (DSBR). Importantly, DSBR occurs in a chromatin context in eukaryotes. Post-translational modification of amino acids in the histone proteins that compose chromatin have been demonstrated to have important roles in both the physical repair of the DSB, as well as in signalling the successful completion of repair. Both DNA repair, and checkpoint activation and subsequent exit, are crucial steps in maintaining genomic stability.

On DSBs formation checkpoint kinase Mec1 phosphorylates the carboxy-terminal of the histone H2A (forming H2AX in mammals) on chromatin flanking the damage site which signals for DSB recognition and repair. Separately, Mec1 induces DNA damage checkpoint causing cell cycle arrest which persists until DSB is repaired. Without such system in place, the cell will replicate its genome causing gross mutations within the cell, leading to detrimental results such as cancer and autoimmune disorders.

In addition, it is known that histone H3 acetylation at lysine 56 (H3K56ac) is required for post-repair chromatin reassembly at sites of DNA double-strand breaks (DSBs), a process necessary for re-entrance to the cell cycle through exit of a DNA damage checkpoint. The histone deacetylases Hst3 and Hst4 are known to deacetylate H3K56ac in yeast, but it is not known whether their deacetylation is also required for completion of DSBR and subsequent exit from DNA damage checkpoint. The aim of my undergraduate thesis project is to engineer a specialized strain of S.cerevisiae in order to test the hypothesis that expression of Hst3 and/or Hst4 is required for exit from DNA damage checkpoint after an engineered induction of a DSB.

Roles of Cyclins A, B, and, B3 in Drosophila Female Meiosis

Ketki Rana

University of Windsor

Keywords: cyclin A, cyclin B, cyclin B3, CDK, meiosis, redundancies, cyclins-CDK complexes

Meiosis is a type of cell division that produces four haploid cells through two nuclear divisions, without an intervening S phase. In mitosis, however two genetically identical diploid cells are produced through one nuclear division. Meiosis is studied to gain a better understanding of diseases that result in human infertility and birth defects, and to acquire further insight on cell cycle regulation. Cell cycle control in mitosis and meiosis is facilitated through regulatory proteins known as cyclins that function with cyclin-dependent kinases (CdkS). Drosophila melanogaster have three major mitotic cyclins, Cyclins A, B, and B3, that regulate mitosis and meiosis. Previous work in mitosis showed that cyclin A mutants are lethal. Cyclin B and cyclin B3 single mutants are viable whereas, their double mutants are lethal suggesting some redundancies between them in mitotic progression. Also, cyclin A and cyclin B have redundant functions such as, nuclear envelope breakdown and mitotic entry. More information about Cyclins-Cdk complexes’ roles and redundancies are known in mitosis, in comparison to meiosis. Preliminary work in meiosis showed that Cyclin A is important for nuclear envelope breakdown, Cyclin B is important for spindle assembly, and Cyclin B3 is important for the degradation of other cyclins. We use mutant analysis to study the roles of the individual cyclins as well as the redundancies between them. Preliminarily there are no redundancies between cyclins in meiosis. Unlike mitosis, there does not appear to be redundant roles between the cyclins in meiosis. More work is needed to conclusively determine the roles of each cyclin in meiosis. Future studies on the roles of cyclins-Cdk complexes can help understand cell cycle regulation in meiosis.
Almost all organisms have evolved cyclic rhythms of biological activity in response to the daylight cycle. The consequence of such rhythm is adaptation to, and anticipation of, daily changes in the organism’s environment. These biological processes have endogenous origins and periods of about a day, and thus referred to as circadian rhythms. These rhythms are driven by a biochemical mechanism known as a circadian clock or oscillator. Found in all eukaryotes and even some prokaryotes, circadian oscillators are self-sustaining and are able to generate rhythms in the absence of environmental time-cues. The ubiquitous nature of circadian oscillators, as well as their conservation among a wide array of organisms, make chronobiological research not only intriguing but also essential in unravelling the rhythm observed in biological processes from cellular to whole organism levels. Neurospora crassa is the ideal model organism to study circadian rhythms particularly because its clock mechanism is analogous to that of mammals. Peroxiredoxins (Prxs) are a highly conserved and ubiquitous family of proteins that function as peroxidases as well as sensors and regulators of local peroxides. The oxidation-reduction cycles of Prxs are highly conserved among all domains of life, making them universal biomarkers of rhythmicity. I used Prxs to assay for rhythmicity in Neurospora strains with a mutated non-functioning central oscillator (FRQ-null mutants). Previous work on FRQ-null mutants has shown that despite having a non-functioning central oscillator, they still express rhythms of spore formation and Prxs oxidation; supporting the presence of a second central oscillator that expresses rhythm in Neurospora FRQ-null mutants. Currently, I am using Prxs to assay for oxidation rhythms in FRQ-null Neurospora strains that contain novel mutations that render both known oscillators non-functioning to determine if more than two oscillators exist in Neurospora.
The Importance of the Disulphide Bond in the Carboxysomal Y-Carbonic Anhydrase, CcmM

Alexandre Paquette, George Espie, and Charlotte de Araujo
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Keywords: cyanobacteria, carboxysome, carbonic anhydrase, rubisco and disulphide bond

Carbonic anhydrase (CA) is a ubiquitous enzyme that catalyzes the reversible inter-conversion between HCO3- and CO2. There are three distinct evolutionary lineage of CA found in living organism, designated α, β and Y, found mainly in animals, plants and eubacteria and eubacteria and Archea, respectively. In photoautotrophic cyanobacteria, CA is essential for photosynthetic CO2 fixation, but unlike in higher plants this enzyme is confined to a structure known as a carboxysome which also houses the cellular compliment of the Calvin cycle enzyme Rubisco. The carboxysomal HCO3- dehydration complex of the diazotrophic cyanobacterium Nostoc PCC 7120 contains a unique multi-domained Y-CA, CcmM, that binds to Rubisco while at the same time delivering CO2 to Rubisco’s active site. CcmM also has a unique disulphide bond not found in other CAs that is apparently involved in both the catalytic mechanism and regulation of CA activity in the carboxysome. To understand the role of this disulfide bond we have created a number of recombinant CcmM proteins with specific substitutions and/or deletions and evaluated their enzymatic activity. Wild-type CcmM209 Cys194-Cys200 was a moderately active CA with a kcat of 2x104 s-1 and a kcat/Km of 4.1x106. Removal of the C-terminal 8 amino acids had no appreciable effect, but CcmM196 displayed a kcat of only 320s-1, a 63 fold reduction in activity. The CcmM209 C194L and C194L-C200L displayed a kcat around 4.8 x 103 while CcmM201 C194S –C200S displayed only 23% OF wild-type activity. The data indicated that the C194-C200 disulfide bond is required for maximum activity. Conservative amino acid substitutions results in a 4 fold decrease while changing the region from hydrophobic to hydrophilic results in dramatic reduction in activity. Thus, unlike most other enzymes, CcmM appears to be activated under oxidizing conditions.

Role of 40 S ribosomal proteins in cell cycle control: characterization of Schizosaccharomyces pombe mutants

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Keywords: Schizosaccharomyces pombe, 40S ribosomal proteins, regulatory checkpoint, cell cycle progression, cytokinesis

Regulatory checkpoints ensure the proper completion of cell cycle events. One such checkpoint – referred to as the cytokinesis checkpoint – functions to delay cell cycle progression upon perturbation of the cellular machinery responsible for cell division. Deactivation of the cytokinesis checkpoint can result in the formation of genetically unstable cells with multiple nuclei. A genome-wide screen of Schizosaccharomyces pombe gene deletion mutants showed that cells lacking a subset of 40S ribosomal proteins (rps402, rps502, rps901, rps1601) are defective in the cytokinesis checkpoint. Imaging via fluorescence microscopy revealed that these S. pombe mutants accumulated multiple nuclei and failed in cytokinesis when challenged with the actin depolymerizing drug, Latrunculin A. While ribosomal proteins have been implicated in growth and cell cycle control, the exact mechanisms of function remain unknown. In this study we hope to provide further insight into the role of these proteins with respect to control of the cell cycle.
Role of Intracellular Calcium in Ghrelin Secretion from Mouse Pancreatic Epsilon Cells

Pirunthan Perampalam, Xiaodong Gao, and Robert Tsushima

York University

Keywords: ghrelin secretion, fluorescence, microscopy, hormones, noradrenaline, norepinephrine, calcium, ryanodine, IP3, pancreas, endocrine, PG-1

The pancreatic islets of Langerhans play an important role in regulating glucose homeostasis in the body. There are 5 main endocrine cell types in the islets; alpha, beta, delta, epsilon and PP, which secrete glucagon, insulin, somatostatin, ghrelin, and pancreatic polypeptide, respectively. The cellular control of insulin, glucagon and somatostatin secretion has been well established, and it is known the elevation in intracellular Ca2+ is the critical factor in the initiation of hormone vesicle exocytosis. In islet alpha and beta cells, the primary source of Ca2+ for hormone secretion is from the extracellular space via the influx through voltage-gated calcium channels. However, it is not known if this is true in islet epsilon cells for ghrelin secretion. I have been investigating the modulation of intracellular Ca2+ in the epsilon clonal cell line, PG-1, by confocal epifluorescence measurements. Noradrenaline was used to stimulate ghrelin secretion. PG-1 cells were loaded with the Ca2+-sensitive dye, fluo-4. The dependence of extracellular Ca2+ was investigated by removing Ca2+ from the extracellular solution. The release from intracellular Ca2+ stores was blocked using ryanodine (ryanodine receptor inhibitor) or xestospongin C (IP3 receptor inhibitor). Calcium was observed to be released in waves in response to stimulation by noradrenaline. Interestingly, even within the same treatment group, different oscillatory patterns of calcium release into the cytosol were observed. It was also found that extracellular calcium is required for intracellular calcium release in response to noradrenaline stimulation.

These studies will provide new mechanistic information on how ghrelin secretion is regulated in epsilon cells, and will determine if these cells share similar properties in hormone release as other islet cells.

Exposure to Endocrine Disrupting Chemicals: Implications for Human Health

Brandon Tang, Tyler Pollock, and Denys deCatanzaro

McMaster University

Keywords: Endocrine disrupting chemicals, Bisphenol A, Triclosan, Health, Estradiol

The World Health Organization published a report in 2013 which highlighted the possible threat of endocrine disrupting chemicals (EDCs) to human health. Humans are ubiquitously exposed to these substances, which interfere with the regular metabolism and activity of hormones. Bisphenol A (BPA) is an EDC found in plastics which distributes across the tissues of rodents after exposure to human-relevant doses. BPA uptake into tissues is exacerbated by triclosan, a common EDC found in soaps. Triclosan can also increase exposure to exogenous doses of the natural sex hormone estradiol. By disturbing endocrine homeostasis, EDCs could have significant implications for human health.
Session 21 - IB 235

Ecology & Evolution

Sunday March 23
10:45 - 11:45 am
Comparison of Ectoparasites from North American Red Squirrels and Northern Flying Squirrels Using DNA Barcoding

A.J. Sajatovic and A.I. Schulte-Hostedde

Laurentian University

Keywords: fleas, host specificity, cryptic species, host race formation, morphology

Accurately and efficiently identifying biological diversity is of great importance, yet relying on morphological species identification alone can result in incorrect identifications due to genetic variability, phenotypic plasticity, sexually dimorphic traits, morphologically cryptic taxa, and differences in life stages. The use of a DNA barcoding approach to taxonomy, which uses a 648 base pair region of the mitochondrial cytochrome c oxidase I (COI) gene as a standardized genetic marker, has proven to accurately identify species-level genetic divisions. Fleas (Siphonaptera) are obligate blood-sucking ectoparasites whose survival depends on their host. The genetic structure of parasite populations is driven by the evolution of host specificity. Previously, the identification of ectoparasites such as fleas has been based on a combination of host use and morphology, and the formation of ectoparasite host races and the presence of cryptic ectoparasite species among host species have been observed in ectoparasite populations. This study used DNA barcoding to determine the population genetic structure of fleas found on North American Red Squirrels and Northern Flying Squirrels in Algonquin Park, Ontario, followed by subsequent flea morphological identification. This study was conducted to: i) compare flea populations between host species; ii) determine if the formation of flea host races exists within the studied squirrel populations, and; iii) determine if cryptic flea species are present within the studied squirrel populations. Three genetic clusters of fleas were observed each demonstrating high host specificity, with very few fleas in a cluster being found on the same host species, supporting evidence of host race formation. Morphological identification of flea specimens is pending, but will aid in determining the presence of cryptic flea species. These findings may contribute to better understanding the host-parasite interactions which play a role in the structuring of ectoparasite populations.

Fungal endophytes of Festuca rubra increase in frequency following experimental exclusion of herbivores

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Keywords: species interactions, mutualisms, competition, herbivory

Plant-fungal endophyte interactions are common in nature and they can have important impacts on the ecology of plants. Vertically transmitted endophytes are hypothesized to serve as mutualists, protecting plants from herbivores. If this hypothesis is true then we expect endophytes to be most abundant in the presence of herbivores and least abundant in the absence of herbivores. We tested this prediction by studying the effects of intense rabbit grazing (Oryctolagus cuniculus) on grass-endophyte interactions at Silwood Park, UK. We examined seeds of red fescue (Festuca rubra) collected from 15 natural populations that had been protected from rabbits for 4 months to 21 years. Contrary to our prediction, mean endophyte frequency increased from 45% to 83% following 21 years of rabbit exclusion. To better understand the mechanisms driving this increase in frequency, we conducted a fully factorial greenhouse experiment where we crossed F. rubra infection status (i.e. E+ or E-), competition (i.e. presence or absence of intraspecific competitors) and simulated grazing (i.e. damaged or undamaged). In both damaged and undamaged treatments, infected plants produced approximately twice more total biomass than uninfected plants, and endophytes did not influence tolerance to herbivory. These results suggest that endophytes change plant growth but not compensatory responses to damage. The endophyte and competition treatments interacted such that the presence of competitors reduced total biomass of infected plants by 38%, while there was no effect of competition for uninfected individuals. In this system, grazing is known to reduce F. rubra abundance and seed production. Thus, our results suggest that by increasing plant growth and biomass, endophytes may be benefiting host plants only in the absence of grazing.
Multi-Level Selection in a Plant Capable of Kin Recognition

Christopher Moser-Purdy and Susan Dudley
McMaster University

Keywords: multilevel selection, kin recognition, density manipulation, competition, garlic mustard

Some plants exhibit kin recognition; that is, phenotypic plasticity to growth with kin versus to stranger plants. Though trait responses to kin have been measured in some plant species, the competitiveness and fitness consequences of these traits remain largely unknown. In order to determine the fitness consequences of plant kin recognition, we performed a density manipulation study in wild populations of garlic mustard (Alliaria petiolata), a biennial plant known to exhibit kin recognition. Our goal was to answer: (1) are pre-manipulation individual and group traits in A. petiolata under natural selection in manipulated density environments, (2) what are the competitiveness and fitness consequences of these traits, and (3) how do these traits compare to those seen in other studies when A. petiolata is exposed to kin versus strangers? Plants were separated into high and low density treatments in the field and selection on traits was estimated using multilevel selection models. Results were compared across density treatments with plants in high density treatments expected to experience more competition than plants in low density treatments. In low density populations, a positive effect of individual blade weight and a negative effect of group petiole length on final biomass and survival were found. In high density populations, a positive effect of group blade weight and a negative effect of group petiole length were found on survival and a positive effect of group blade weight on final biomass was found. This indicates that group selection operates on A. petiolata in high and low densities, but perhaps on more traits in high densities. Furthermore, the competitiveness and fitness of A. petiolata may depend more on the group it belongs to than its individual traits. These results indicate that groups of kin may benefit more from having shorter petiole lengths and increased blade weights.

The Effect of Accessory Proteins on Sperm Survivability in Drosophila pseudoobscura

Caryn Dooner
University of Western Ontario

Keywords: antagonistic co-evolution, heteromorphic sperm, accessory gland proteins (ACPs), female reproductive tract proteins (FRPs), reproduction

Antagonistic co-evolution between males and females to control reproductive success may give rise to a variety of reproductive strategies, such as female spermicides and male accessory proteins. The interplay between male sperm morphology (fertilizing eusperm versus non-fertilizing parasperm), male accessory gland proteins (ACPs), and female reproductive tract proteins (FRPs) has not been assessed. Three aspects of these reproductive traits within Drosophila pseudoobscura will be discussed: (1) the effect of ACPs and parasperm proportion on sperm survivability when in the presence of FRPs; (2) the effect of ACPs and parasperm proportion on sperm survivability when not in the presence of FRPs; and (3) the effect of conspecific vs heterospecific ACPs on sperm survivability when in the presence of conspecific FRPs.
Session 22 - IB 250

Environment

Sunday March 23
10:45 - 11:45 am
Effect of Pesticides on Honey Bee Survivorship, Foraging and Immunocompetence

Jamie Lee Martin and Graham Thompson

Western University

Keywords: bee, pesticide, immunity, neonicotinoid, survival

The honey bee, Apis mellifera, is a highly social insect that has been domesticated into a key pollinator of agricultural crops. In southern Ontario, honey bees are vital to the agro-food industry, yet honey bee populations continue to decline. Here I test the impact of a locally deployed pesticide on forager performance and health. I exposed foragers to an agriculturally relevant dose of conventional and new nicotine-like pesticides, and measured their effects on worker survivorship, foraging behaviour and immune response. Topical exposure to pesticides had an immediate effect on worker survivorship, with neonicotinoid-treated workers most likely to die within 24-hrs. Bees surviving this period continued to die, but the long-term treatment effect on survivorship was less pronounced. Surviving bees also showed altered foraging behaviour, with neonicotinoid-treated workers of foraging age being less likely to return to the hive. Finally, I assayed immune-gene expression at five loci, but it remains unclear whether pesticides of any type alter the immunity of individual bees.

Survival and productivity of Daphnia mendotae in recovering acid and metal stressed lakes

M. Heerschap and J. Bailey

Laurentian University

Keywords: freshwater, acidification, bioassay, Sudbury, mining

Extensive mining activity in both Sudbury, Ontario as well as Elliot Lake, Ontario have had a profound impact on the freshwater environments surrounding these centers. Over 100 years of metal mining in Sudbury has contaminated many of the lakes in close proximity and left more than 7000 lakes in a 17 000 km2 area acidified to a pH<6, the point at which organisms experience significant biological damage. Four decades of Uranium mining in the town of Elliot Lake have had similar effects on the close by Serpent River Watershed. Improperly managed tailings have led to 4 decades of contamination and acidification from low pH effluent. This study utilizes a 14 day bioassay on clones of the acid sensitive Daphnia mendotae to determine the current status of lakes in both of these regions. The lack of pre-mining data from these lakes requires the use of a reference medium that simulates reference conditions for soft water Canadian Shield lakes. A soft water medium specifically designed for Cladocerans such as D. mendotae known as FLAMES medium was utilized both as a control and to replicate reference lake conditions. Bioassay treatments from 3 study lakes from the Sudbury area and 2 study lakes from the Serpent River Watershed were compared with each other and to FLAMES using Mann-Whitney U and Spearman correlation analyses. These results as well as water chemistry data from the spring and summer of 2013 show a relationship between low survival and reproduction and low pH, low ambient calcium availability, and heavy metal contamination.
The Effects of Benzo-a-pyrene on the Transcriptome of Brown Bullheads

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Keywords: contaminant, NextGen sequencing, polycyclic hydrocarbon, Brown bullhead, mRNA

Abstract: Aquatic contaminants often accumulate in the sediments thus having large effects on bottom dwelling organisms. Brown bullhead (Ameiurus nebulosus), a bottom dwelling catfish, is reported to have high tumor rates within contaminated regions. To investigate their response to polycyclic aromatic hydrocarbons (PAHs; a common class of contaminants in sediments), we inter-peritoneally injected brown bullhead with 50 mg/kg of benzo-a-pyrene (BaP), a carcinogenic PAH, and others with a sham injection. After 24 hrs, we euthanized the fish, sampled liver tissue and later extracted total RNA, synthesized cDNA performed massively parallel (“NextGen”) sequencing on 4 challenged and 4 control fish. Each of the 4 samples contained pooled RNA from two individuals. The RNA-Seq data for each replicate were de-novo assembled using Trinity RNA-Seq Software and individual genes were tested for up-regulation and down-regulation in response to the PAH challenge by running decideTest on the edgeR analysis. Gene sequences that showed a significant response were annotated for putative function using Blast analyses. The data was analyzed for the response of suspected genes involved in contaminant exposure and then for identification of unexpected responses. A total of 108 sequences were found to have been up-regulated and 294 down-regulated in response to the PAH challenge. The majority of up-regulated genes were associated with metabolic function, as expected; however other genes associated with endogenous stimuli response, morphogenesis and cancer related genes were also up-regulated. Of the down-regulated sequences, the majority possessed functions involving molecular binding properties, while other down-regulated genes included members of the cytochrome p450 family perhaps reflecting the organism’s response to the carcinogen. Majority of responding genes were down-regulated likely due to severe stress. Many of the responding functions were expected but a number of genes that did not have a known function in contaminant response were also identified.

The effects of toxicity modifying factors on the acute toxicity of samarium to Hyalella azteca

Alyssa Verdin and James McGeer
Wilfrid Laurier University

Keywords: Toxicity, Samarium, Rare earth elements, Hyalella azteca, toxicity modifying factors

The rare earth elements (REEs) are a group of metals with highly valued optical, catalytic and magnetic properties. The growing demand for REEs for use in clean-energy technologies has placed importance on the development of water quality guidelines in Canada. Samarium (Sm) is an example of an REE for which there is increasing concern but very little data. This research project focused on developing an improved understanding of the toxicity of Sm and in particular the influence of water chemistry. Water chemistry parameters known to influence the toxicity of other metals were tested at concentrations that covered the typical variation that occurs in natural waters. Toxicity modifying factors (TMFs) were tested in short term tests at Sm concentrations of 2.6, 5.3, 10.6, 21.3, 42.6 and 66.5 µM Sm. TMFs evaluated included: Ca, Mg, Na, Cl, dissolved organic matter (DOM) and pH. Acute (96h) tests were conducted according to Environment Canada standard methods (EPS RM/33) at 23°C using the freshwater amphipod Hyalella azteca. In culture waters (no TMFs, 23°C, pH 7.7, and hardness of 62.5mg CaCO3/L) the LC50 for Sm was 5.3µM (±1.1 SEM, n = 3 tests) and this was similar to a previously published study. Additions of Ca (2mM) and DOM (8mg dissolved organic carbon/L) provided significant protection against Sm toxicity, however there were no ameliorative effects observed for Na and Mg. There were also no differences between Sm toxicities across a range of pH values from 6.5 to 8.2. Overall, the main objective was to examine the interaction between the aqueous free metal ion Sm3+ and TMFs with the aim of contributing to the development of toxicity prediction models that can be applied for site specific water quality guidelines and criteria. Understanding the ecotoxicity of Sm (and all other REEs) in freshwaters will contribute to the establishment of environmental thresholds/regulations.
Session 23 - IB 280

Ecology & Evolution

Sunday March 23
10:45 - 11:45 am
The effects of non-consumptive predation on encapsulation in dragonfly larvae (Libellulidae: Odonata)

Minh Tam Duong and Shannon J. McCauley

University of Toronto Mississauga

Key words: encapsulation, predator, stress, melanization, immune response

The effects of predators on prey can go beyond consumptive interactions. Visual and chemical predatory cues can be enough to induce plastic responses including changes in behaviour, morphology, and physiology, which can be costly. In dragonfly larvae, the presence of caged invertebrate predators has been shown to increase rates of mortality. In this study, we investigated the potential relationship between predator-induced stress and diminished immune response; a potential mechanism that may underlie the observed mortality patterns. A diminished immune response can have various consequences such as increased susceptibility to infection, inability to close wounds, and inability to encapsulate foreign bodies (internally), all of which may lead to increased mortality. We used dragonfly larvae (Leucorrhinia intacta) injected with nylon monofilaments to assess the level of encapsulation, a common assay for immune response in insects. We hypothesized that in the presence of a caged predator, larval immune response would decrease, resulting in decreased encapsulation and melanization of the monofilament. We also investigated whether temperature modified this interaction and combined this with our predator treatments to create a full 2x2 factorial experiment, crossing predator exposure and two temperatures. In contrast to our hypothesis, we found that larvae exposed to caged predators encapsulated the monofilament significantly more than those without predators. Also, temperature did not affect the rates of encapsulation, nor did it interact with predator exposure; however this may be due to the limited range at which we tested. Our results suggest that increased mortality in L. intacta in the presence of predators is not related to the suppression of immune response. A possible reason for this may be that when larvae detect predatory cues their immune response increases in preparation for further injury, which is a costly process and may lead to the stress response in which we see increased mortality.

Characterization of an acid mine drainage site sediment microbial community

N. L. Valiquette, R. R. Auld, N. C. S. Mykytczuk, and T. J. S. Merritt

Laurentian University

Keywords: acid mine drainage, environmental sequencing, 16S rRNA, microbiological culture, microbial diversity

Acid mine drainage (AMD) sites are home to a suite of microorganisms with the capacity to damage, and possibly restore, mining affected environments. The bacterial oxidation of iron and sulfur compounds in mine tailings ponds creates an extreme environment characterized by low pH and high concentrations of toxic metals and is a prominent source of environmental damage worldwide. Although the microbial community structure of AMD environments is generally simple, dominated by only a few species of microorganisms, it is still poorly understood due to the lack of cultured organisms and relatively few genomic reference sequences available for study. Previous studies of the microbes that inhabit this environment have identified sulfur and iron reducing prokaryotes in anaerobic sediments and these organisms could possibly provide a solution in the remediation of toxic AMD sites. The organisms, and the diversity of this community, are particularly poorly studied reflecting a need to characterize the microbial communities of sites such as the Vale central tailings facility in Sudbury, ON.

Analysis of data sets of 16S rRNA gene sequences from direct sequencing of environmental samples has been shown to be effective in characterizing prokaryotic communities, particularly given that many microbial communities, including AMD communities, are predominantly composed of unculturable organisms. Analysis of an AMD sediment core using a bioinformatics approach following 454 pyrosequencing and geochemical analyses, including pH and oxidation-reduction potential, has allowed us to create a profile of the microbial community at varying depths of the pond’s sediment. As resolution of the community may only be possible to the genus level, culturing of organisms at the depths analyzed by direct sequencing has also complemented the pyrosequencing data by providing isolates of some of the community’s dominant microorganisms. Identification of cultured organisms via Sanger sequencing has also provided more detailed phylogenetic classification of these organisms and a substrate to work with for further analyses of species or community metabolism and physiology.
The Effects of Salinity and Dissolved Organic Matter on Copper Toxicity in a Euryhaline Hydroid (*Eudendrium carneum*)

James J. Duncan and Jim McGeer

Wilfrid Laurier University

Keywords: hydroid, euryhaline, acute toxicity, hydranth score, copper

Currently there are no water quality guidelines and criteria for estuarine environments, where freshwater rivers meet ocean water resulting in a range of intermediate salinities. To build water-quality criteria, organisms that inhabit these environments must be subject to toxicological tests with common contaminants found in these estuaries. The euryhaline hydroid *Eudendrium carneum* is found in estuaries around the world and is the test organism chosen for this study; while copper is a common contaminant in estuaries. This hydroid was exposed to nominal concentrations of 10, 20, 35, 50, and 100 μg/L of copper at salinities of 25.20 ppt and 15.06 ppt for 48 hours. These reflect the intermediate salinities in estuaries. Additionally, this hydroid was exposed to copper at a salinity of 25.20 ppt with 5 mg/L of dissolved organic matter for 48 hours. At 25.20 ppt, the lethal concentration of copper associated with 50% mortality (LC50) for copper at 48 hours was 40.24 μg/L of copper (nominal, with a 95% confidence interval (CI) [35.22, 45.98]); while the 48 hour LC50 at 15.06 ppt was 20.87 μg/L of copper (95% CI [16.37, 26.59]). The LC50 at 48 hours in 25.20 ppt with 5 mg/L of dissolved organic matter was 39.30 μg/L of copper (nominal, 95% CI [35.71, 43.26]). These results show that as salinity decreases, the sensitivity of this hydroid to copper increases. These results also indicate that this species of hydroid is sensitive to copper compared to other estuarine and marine organisms which makes it an excellent addition to marine and estuarine datasets.

DNA Signatures: An Alternative for Metagenomic Investigation of Microorganisms

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Wilfrid Laurier University

Keywords: bioinformatics, metagenomics, DNA Signatures, clustering, marker genes

DNA signatures, nucleotide sequences that possess distinguishing properties, have been shown to provide good representations of the microorganisms composing an entire genome. Clusters of microorganisms can be produced using the genomic information obtained using these signatures. Traditionally, marker genes are used to distinguish the presence of varying microorganisms in a sample. This information can then be used to produce clusters, which may illustrate the phylogenetic relationships of these varying microorganisms.

This project seeks to investigate whether DNA signatures can provide a significant representation of metagenomes, visualized using signature-similarity clusters. Metagenomic DNA sequences will be used to obtain DNA signatures. These signatures will then be used to produce clusters using the statistical programming language R. R will also be used for statistical computational analysis. It is expected that each cluster will represent specific phylogenetic groups. These clusters will be compared against those made with marker genes in metagenomes to examine whether the former provide good representations of phylogenetic relationships in metagenomes. FigTree will be used to visualize the trees representing phylogenetic data. If both trees are found to provide equivalent information, not only will the use of DNA signatures be applicable, but also species detection in large and diverse environments could be possible. This would further enable its use in several applications. For instance, this could aid in obtaining information about organisms present in metagenomes faster than using marker genes and than searching for homologous sequences in databases. Preliminary results show that clusters made from the DNA signatures display environmental relevance.
Session 24 - IB 270

Plant Physiology

Sunday March 23
10:45 - 11:45 am
The chemoattractant potential of ginsenosides from American ginseng for Pythium irregulare

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Dept. of Biology, Western University

Keywords: ginseng, Pythium, ginsenosides, pathogenicity, chemoattractant

American ginseng (Panax quinquefolius L.) is a native North American crop cultivated for its use as a medicinal plant. Ginsenosides, the triterpenoid saponins produced by P. quinquefolius, have been extensively studied for their medicinal value, however their function in the rhizosphere remains unknown. Ginsenosides, like other saponins, have demonstrated antifungal properties against root and non-root pathogenic fungal species in vitro. However, growth of Pythium irregulare, a major threat to commercial ginseng cultivation, is stimulated when exposed to ginsenosides. In addition, the pathogenicity of P. irregulare on ginseng roots correlates with the ability of this organism to partially deglycosylate ginsenosides into ginsenoside F2. In the present study, the chemoattractant potential of ginsenosides for P. irregulare was investigated by (1) monitoring what effect the in vitro exposure of purified ginsenoside extract and ginsenoside F2 have on the growth of the pathogen and (2) an in vivo assay development, which monitored the pathogenicity of P. irregulare toward ginsenoside-treated and untreated one-year old ginseng seedlings. Disease severity and Time to Infection (TTI) was evaluated by taking measurements of leaf fluorescence (Fv/Fm) as a proxy for stress, during a 15-day infection period. The in vitro exposure of P. irregulare to purified ginsenoside extract resulted in enhanced mycelial growth. In contrast, initial exposure of P. irregulare to ginsenoside F2 inhibited the growth of mycella, but this effect was not persistent. While both ginsenoside-treated and untreated ginseng plants showed signs of infection, TTI for the untreated plants was 2 days earlier. This suggests the presence of ginsenosides within the rhizosphere of the ginsenoside-treated plants was adequate enough to support the growth of the pathogen, potentially delaying its infection. These results support the hypothesis that ginsenosides secreted by American ginseng affect the growth of P. irregulare in vivo, potentially allowing the pathogen to find its host plant and promote infection.

Leaf anatomical acclimation of two boreal conifer species to growth in elevated atmospheric temperatures and [CO2]

Marin Mema

University of Western Ontario

Keywords: climate change, acclimation, conifer, leaf, anatomy

Boreal forest conifers are a major carbon sink for the biosphere, and their ability to acclimate to the conditions forecasted for the next century of climate change has become important to global change biology. A simple yet meaningful indication of their response may be in their anatomy, given the close relationship between structure and function in plants. In this study, saplings of two boreal conifer species, Scots pine (Pinus sylvestris) and Norway spruce (Picea abies) were grown for 18 months in sealed greenhouses set to outdoor temperature raised by +0, +4, or +8 °C and current or doubled outdoor CO2 pressure. The newest mature needles of the leading branch were studied for their stomatal density and cross-sectional anatomic proportions. Functionally distinct components (vascular tissue, photosynthetic mesophyll cells, and intercellular gas diffusion spaces) were manually delineated. These results will complement similar studies in the field, and further clarify how boreal conifers will be involved in the near-future global carbon balance.
Phenotyping a 3-ketoacyl-CoA Synthase 16 over expression line in *Arabidopsis thaliana*

Fiona Bergin  
University of Western Ontario

Keywords: *Arabidopsis thaliana*, very long chain fatty acids, KCS-16

The 3-ketoacyl-CoA Synthase 16 (KCS16) gene is one of twenty-one genes in the *Arabidopsis thaliana* genome involved in the biosynthesis of very long chain fatty-acids (VLCFA). VLCFA have chain lengths from 20 to 34 carbons and are important precursors to cuticular wax formation. During the course of prior work a transformed *Arabidopsis thaliana* plant demonstrated increased longevity and drought tolerance. Using TAIL-PCR, preliminary results suggested that a 35S enhancer element was found serendipitously inserted upstream of the KCS16 gene. In this study, we tested the hypothesis that over-expression of the KCS16 gene results in an increase in VLCFA, and that this would decrease non-stomatal water loss, thereby increasing overall drought tolerance and longevity. As the original plant failed to set seed, two new *Arabidopsis thaliana* KCS16 over-expression lines were created, one using the 35S constitutive promoter and the other using the *Arabidopsis thaliana* Act2 native constitutive promoter, in an attempt to replicate the originally observed phenotype. Using leaves from independent transformed T1 plants, GC/MS analysis confirmed that over expressing the KCS-16 gene resulted in an increase in VLCFA from C16 to C32 relative to wild-type plants. The next steps will be to obtain T2 seeds from plants accumulating increased VLCFA, from which plants will be grown and their drought tolerance assessed using relative water content assays to elucidate the effect of over expressing the KCS-16 gene on drought tolerance.

Diversity and Frequency of Fungal Species occurring in heavy metal polluted tailings in Sudbury, Ontario, Canada

Nneka Kagwachie  
Laurentian University

Keywords: acid-generating, tailing, soil, fungi, Sudbury

Soil is a very rich habitat comprising of many major groups of fungal species. The objective of this study is to determine the frequency and diversity of fungal species, occurring in the acid revegetated tailings at Vale INCO Sudbury, Ontario. Soil samples were collected at various area of two major acid-generating Vale INCO tailing sites. Fungal species had been isolated from the tailing substrate using the soil dilution method on Sabouraud Dextrose Agar, Malt Extract Agar and Potatoes Dextrose Agar media. A total of 28 species belonging 19 genera fungal species were identified. The most common species belong to Mycoderma sp., Actinomyces sp., Asperlligus sp., and Penicillium sp. This study suggests that revegetated acid-generating tailings do not provide suitable conditions for fungal activities.
Session 25 - IB 280

Science Education

Sunday March 23
10:45 - 11:45 am
Using Animations Combined with Active Learning to Overcome Student Misconceptions

Ananya Jhamb, Bryan DeBourbon, Marc Dryer, and Fiona Rawle

University of Toronto Mississauga

Keywords: active learning, genetics misconceptions, animations

Abstract: Common and deep-rooted misconceptions in genetics have been identified from the pedagogical literature. It is important to have students actively correct these misconceptions as they act as barriers to further understanding. In an attempt to correct these misconceptions, we have developed a targeted genetics module to be used in a tutorial or lecture setting. This module is comprised of both static and dynamic treatments of animations that are presented with or without active learning questions. The misconceptions targeted in this study include: the difference between a gene and allele, between a chromatid and chromosome, and between a homologous chromosome and a sister chromatid. Other targeted misconceptions are: the idea of “ploidy”, and chromosome structure in different cell cycle phases. The animation script was reviewed and validated by both scientific experts and students. An assessment instrument was developed and used for pre- and post-assessment of student knowledge regarding the genetic concepts being tested. Other forms of assessment include: focus groups, perspective surveys, and in-class clicker questions. Six “learning treatments” were employed in this study, the static treatments include: static illustrations alone, static illustrations with active learning questions, and static illustrations with active learning questions and formative feedback. Dynamic treatments include: animations alone, animations with active learning questions, and animations with active learning questions and formative feedback. The animation will be shown in this presentation, and early results will be discussed.

Revising Current Teaching Methods to Improve Student Learning in Introductory Science Courses

Kelsie Chasse, Sanja Hinic-Frlog, Christoph Richter, and Fiona Rawle

University of Toronto Mississauga

Keywords: desirable difficulties, blocking, interleaving, problem based learning, active learning

This study explores the possibility of using current cognitive psychology and pedagogical research findings to optimize student learning from novel course designs. Building on Robert Bjork’s theory of Desirable Difficulties, this research focused on how traditional, lecture-based teaching methods could be revised to improve students’ understanding of, and ability to apply, scientific concepts. Numerous studies have tested the effectiveness of blocking, interleaving, and problem based learning on student learning, however few initiatives have been taken to incorporate multiple new methods of teaching into one program. In order to devise an entirely revised syllabus, a meta-synthesis of existing literature was first conducted. Using the findings of the synthesis, an example syllabus was created for an introductory genetics course. Based on the results of current research in science education, the sample syllabus incorporated repetition of core genetic concepts, interleaving of multiple streams of science relating to genetic processes, and blocking of closely related topics in genetics. Together, these multiple approaches were used to create a problem based learning (PBL) structured syllabus that follows Blooms Taxonomy. Also, current introductory genetics students were surveyed on their opinions of the proposed syllabus. Survey results will be presented, and the limitations of this proposal and an avenue for future research into the effectiveness of the proposed syllabus will be discussed in the presentation.
Developing Better Principles for Misconception Targeted Animations

Bryan deBourbon, Ananya Jhamb, Marc Dryer, Fiona Rawle

University of Toronto at Mississauga

Keywords: misconceptions, pedagogy, animations

In order to optimize animation design towards correcting misconceptions, a thorough review of the literature was executed. The focus of this review was to identify (1) common misconceptions, (2) the best practices to correct misconceptions, and (3) the best practices of animation design in cognitive science.

The literature indicates that misconceptions are incorrect ideas derived from false assumptions. These ideas often form from the faulty understanding of threshold concepts, and become reinforced upon incorrect justification thereafter. Genetic sciences are especially subject to faulty understanding, and research specified that chromosomal organization was a core misunderstanding.

Investigations of misconception correction revealed that these reinforced assumptions are impossible to eliminate by mere disclosure alone, and instead must be addressed with a constructivist approach. Constructivism argues that students must identify their misconceptions independently, and acquire accurate experiences designed to build upon the truths of an existing misconception. Although some of the macroscopic or slow processes of genetics hinder constructivist methodology, animations act as a tool to form experience from virtual interaction and thus form proper schemas.

Research from cognitive science publications indicated that consideration for the cognitive structure of the audience was a necessity. Cognitive load theory states that learners have a limited working memory that becomes hindered if overwhelmed. When designing an animation it is imperative to limit this overload by minimizing intrinsic and extraneous load, while maximizing germane load.

Based upon this review, it was determined that the best practices of animation design include active learning, which consists of using questions intermittently in animations to identify misconceptions and foster proper schema retention. These practices also include consideration of visual literacy and salience, identification of the audience, exploitation of visual and phonological streams, along with consistent design.
Poster Session A - IB
Atrium

Saturday March 22
4:30 - 5:30 pm
1 - Bile salts induced resistance to CAMPS: A comparative study of EHEC and EPEC

Francis Aju-sue and Debora Foster

Ryerson University

Keywords: EHEC, EPEC, bile salts, polymyxin B, gastrointestinal tract

Enterohemorrhagic Escherichia coli O157:H7 (EHEC) and enteropathogenic Escherichia coli O127:H6 (EPEC) are food and water-borne pathogens that have been associated with severe illness such as diarrhea. EHEC is responsible for infections in mainly adults, whereas, EPEC is a common pediatric pathogen. They both use the same pathogenic mechanism to infect intestinal epithelial cells, however, they colonize different areas of the gastrointestinal tract. EHEC colonizes the large intestines and EPEC colonizes the small intestines. EHEC and EPEC encounter various stressors in the gastrointestinal tract including bile, an emulsifier of lipids that is made in the liver and stored in the gall bladder. Bile can also act like a detergent and disrupt the lipid bilayer of bacteria. Microarray analysis of bile salt treated EHEC shows the upregulation of various genes, including the arn operon, which is involved in the modification of the bacterial outer membrane. The arn operon encodes enzymes that modify the negatively charged lipopolysaccharide (LPS) by adding aminoarabinose, which reduces the overall negative charge on the LPS. Coincidentally, bile salt treatment has also been shown to enhance resistance to the cationic antimicrobial peptide, polymyxin B (PMB). This research aims at assessing bile salt induced resistance in EHEC and EPEC to PMB. Since, bile is released in the small intestines where EPEC colonizes, it is hypothesized that bile salts will more profoundly enhance EPEC resistance to PMB. Radial diffusion assays (RDA) showed enhanced resistance of both EHEC and EPEC to PMB when pre-treated with physiological concentrations of bile salts at 0.15% w/v and 1.5% w/v. In addition, bile salt treated-EPEC was more resistant to PMB than was bile salt treated-EHEC. These results suggest that EHEC and EPEC utilize bile salts to cue enhanced fitness and virulence. They also indicate that EPEC may benefit from a more robust response to bile salts.

2 - The Impact of Short Chain Fatty Acids on Motility and Flagella synthesis in Enterohaemorrhagic E.coli O157: H7

S. Jolley, D. Barnett Foster, Department of Chemistry and Biology, Ryerson University

Ryerson University

Keywords: Pathogenic, E.coli O157:H7, Flagella, Motility, Short-Chain Fatty Acids

Enterohaemorrhagic Escherichia coli O157:H7 strain 86-24 (EHEC) is a gram negative bacterium that colonizes the human intestinal tract. This foodborne pathogen exploits the natural human defenses to physiologically alter its phenotype to survive each local environment. During ingestion of EHEC, the pathogen encounters host defenses including low pH in the stomach, bile salts from the gall bladder, and short-chain fatty acids (SCFA) in the small and large intestines. These natural host defenses appear to cue the pathogen to upregulate genes that enhance pathogenicity by protecting against the stresses through acid resistance, efflux pumps, and increased motility. At the same time, EHEC simultaneously downregulates genes associated with colonization until reaching the large intestine. The SCFAs, primarily acetate, butyrate, and propionate in a 60:25:15 ratio, are formed during fermentation of dietary fibre by the communal flora and are naturally occurring metabolites of the gastrointestinal tract. The concentrations of SCFA range from 30 mM in the ileum up to 172 mM in the large intestine. This investigation explores the impact of EHEC treatment with concentrations of SCFA typically encountered in the small and large intestine on EHEC motility. This investigation also examines the role of the BarA-UvrY two component system as a potential sensor of SCFA in the regulation of motility. Results show that 30 mM SCFA mix increased EHEC motility relative to the 30mM NaCl control while the 172 mM SCFAs decreased motility relative to its 172mM NaCl control as determined by a soft agar motility assay. The results show that the 30 mM SCFA-induced increase in motility for the wild-type is lost in the isogenic ΔuvrY mutant under 30 mM SCFA mix. These results suggest that EHEC employs SCFAs to modulate motility and this motility regulation occurs in a uvrY-dependant manner. The results also highlight the significance of varying concentrations of SCFAs encountered in different regions of the gastrointestinal tract in modulating pathogen motility to drive locomotion to preferred niches.
As the terminal organelle of the endosomal system, lysosomes degrade material taken up from the extracellular region through fluid and solid phase endocytosis. Within immune cells, lysosomes also function in antigen presentation. Normal lysosomes are found to be small, dense, punctate structures dispersed uniformly throughout the cytoplasm. However, when professional phagocytes of the immune system, like macrophages and dendritic cells, respond to bacterial infection as part of the innate immune response, their lysosomes undergo a unique morphological change to dynamic, thin, radially dispersed tubular lysosomes. Based on results from prior research showing that when activated immune cells retain greater content of endocytosed material, it is hypothesized that the change in morphology from punctate to tubular lysosomes represents an increase in total lysosomal volume either through retention of membrane or lysosomal biogenesis. In an attempt to characterize the structural characteristics and physiological significance of this dynamic change in morphology, punctate and tubular lysosomes were imaged using spinning disk confocal microscopy and analyzed using a novel volumetric protocol to determine if bacterial LPS activation of macrophages causes an apparent increase in lysosomal volume. Indeed, we show that LPS-treatment caused a 70% increase in the apparent lysosomal volume. The results of this study suggest that tubulation of lysosomes may facilitate increased retention of exogenous antigens to upregulate antigen retention, processing and presentation or increasing phagocyte degradative capabilities by increasing lysosomal volume.

Cockayne Syndrome Group B protein (CSB) is a multifunctional protein involved in DNA damage repair, chromatin remodeling, telomere maintenance, and transcriptional regulation. CSB is required for the transcription-coupled (TC) subpathway of nucleotide excision repair (NER), as well as plays a role in base excision repair (BER). Mutations in CSB are associated with Cockayne syndrome (CS), a disorder characterized by growth and developmental failure, neurological deterioration, and UV-sensitivity. CSB is encoded by 4.5 kilobases (kb) over 21 exons from the ~90 kb CSB gene located at chromosome 10q11. Mutations in CSB typically result in loss of functional CSB, leading to deficient repair of UV and oxidative DNA damage, as well as telomeric aberrations. Elucidating the molecular mechanism underlying CS has been primarily focused on the TC-NER deficiency exhibited by loss of functional CSB, although other factors involved in the TC-NER pathway do not show as severe symptoms as CS when mutated. This suggests that other complications arising from the loss of CSB need to be investigated. The presence of a domesticated piggyBac transposon encoding a PGBD3 transposase in intron 5 of the CSB gene has resulted in three separate proteins to be expressed from this genomic locus: full-length CSB, a fusion protein consisting of exons 1-5 of CSB and PGBD3 (CSB-PGBD3), and the PGBD3 transposase. CSB-PGBD3 and PGBD3 show greater abundance than CSB. The CSB-PGBD3 fusion protein is also expressed in CS cell lines, even in the absence of CSB. Expression of CSB-PGBD3 alongside CSB induces an altered transcriptional profile compared to CSB expression alone, suggesting for a potential interaction between the two. Hypothesis: CSB-PGBD3 interacts with CSB and this interaction regulates the cellular function of CSB. To investigate CSB-PGBD3 interaction with CSB, I cloned Flag-tagged CSB-PGBD3, which was subsequently introduced into 293T cells through stable transfection.

This cell line has been used for examination of Flag-CSB-PGBD3 interaction with Myc-tagged CSB. In addition, I will also present data elucidating the cellular localization of Flag-tagged CSB-PGBD3 as well as Flag-tagged PGBD3.
5 - The Development of Myc-Targeting Cancer Therapeutics: Utilizing the Bacterial One-Hybrid Assay for Screening a Library of Binder

Sherif Saleh and Jumi A. Shin

University of Toronto Mississauga

Keywords: Myc, Bacterial One Hybrid, enhancer-box, cancer therapeutic agent, binder

The aberrant expression of Myc, a transcription factor and proto-oncogene that binds to the Enhancer box element (E-box, 5'-CACGTG-3'), is found in >50% of cancers. This makes Myc a target for developing cancer therapeutics. Our strategy is to construct a small unnatural hybrid protein that strongly binds the E-box with high specificity, to block Myc from initiating expression of its associated genes.

A library of 400 constructs was generated and evaluated for E-box binding using the Bacterial One-Hybrid (B1H) system. 16 constructs were found to be strong E-box binders. The specificity of those constructs to the E-box was evaluated by using the activator protein-1 binding site (Ap-1) and a non-specific site (NS) as targets. GCN4 and EmBP-1 were successfully cloned into the B1H system as controls. Four constructs (A2, B2, C7 and L8) were identified as strong and specific E-box binders. Of which, 2 constructs (B2 and L8) are currently undergoing expression and purification.

6 - Investigating cell viability when ERK pathway is inhibited during the ultrasound and microbubbles treatment

EunJee Park

Ryerson University

Keywords: ultrasound, microbubble, MAPK cascade, ERK, AML

Ultrasound is an efficient transporter of medication to specific areas using non-invasively transmitted energy. Ultrasound cavitation increases efficiency by injecting microbubbles. By combining both ultrasound and microbubble (USMB) treatment, called sonoporation, which creates temporary pores in cell membrane to increase permeability. Although USMB is an effective technique, previous studies found that it induces Extracellular Signal-Regulated Kinase (ERK) activation in Acute Myeloid Leukemia (AML) cells in response to mechanical damage and stress. ERK1 and ERK2 are cytoplasmic serine and threonine protein kinases that involve a Ras-Raf-MEK-ERK signal transduction cascade, also known as mitogen-activated protein kinase (MAPK) cascade. ERK signaling pathway may function as a cell adhesion, cell cycle progression, cell migration, cell survival, differentiation, metabolism, proliferation, and transcription.

Since ERK allows cells to survive via its signaling pathway, we hypothesized that when ERK is activated after a USMB treatment, ERK can regulate the cell survival pathway in order to recover from mechanical damage and increase cell viability. To test this hypothesis, AML cells were incubated with and without ERK inhibitor (U0126) before treating with USMB. These samples were treated with USMB for one minute for a 16 cycle pulse with a frequency of 0.5MHz at 400mV. After six hours of incubation in room temperature, Propidium Iodide (PI) was added into each sample to observe cell viability using the flow cytometry.

Using the paired t-test, there are significant difference and mean of cell viability decreased about 5% when ERK inhibitor was present during the USMB treatment. It can be concluded that since ERK pathway is an important response to cell survival including proliferation and differentiation, inhibiting ERK increased cell death during sonoporation. This work is significant to cancer therapies to increase targeted cell death by adding ERK inhibitor during USMB treatment.
7 - Application of FISH to detect Adherent Invasive 
*Eschericia coli* in a vitamin D deficient murine model of IBD

Emma Brun-Hayne, Kathene Johnson-Henry, Amit Assa, Philip Sherman,
Debora Foster, and Martina Hausner

Ryerson University

Keywords: fluorescence in situ hybridization (FISH), adherent-invasive 
*Escherichia coli* (AIEC), vitamin D, inflammatory bowel disease (IBD),
Crohn's disease

Background: The involvement of pathogenic microorganisms in the 
pathogenesis of Crohn's disease, inflammatory bowel disease (IBD) and 
ulcerative colitis is well documented. Adherent-invasive *Escherichia coli* 
(AIEC) is a pathogen associated with Crohn's disease. Vitamin D deficiency 
is implicated in patients with IBD and Crohn's disease. Previous studies 
using an animal model of vitamin D deficiency were unable to accurately 
quantify AIEC in colonic tissue isolated from mice infected with transmission 
electron microscopy. Aim: The aim of this study was to define whether AIEC 
can be detected qualitatively and quantitatively by Fluorescent in situ 
hybridization (FISH) in colonic tissue from a vitamin D sufficient and deficient 
murine model of IBD.

Methods: FISH was performed on paraffin embedded tissue from C57/BL6 
mice that were: Vitamin D-sufficient, Vitamin D-sufficient, LF82-infected, 
Vitamin D-deficient, Vitamin D-deficient, LF82-infected. Sections were 
dehydrated and hybridized with an *E. coli* specific oligonucleotide probe 
EC1531-Cy3 and counterstained with DAPI. Five images were collected for 
each treatment group and EC1531-Cy3 were quantified as a ratio of total 
cells visualized in the tissue culture.

Results: FISH using EC1531-Cy3 effectively detected invasive AIEC in 
colonic mucosal layers. Future studies utilizing an AIEC antibody in 
combination with FISH will allow for more specific localization and 
quantification of the pathogen. Developing techniques to visualize the extent 
of tissue infection-invasion from a pathogen such as AIEC will enhance our 
ability to quantify the extent of infection and contribute to our understanding 
of the role of AIEC in Crohn's disease.

8 - Bio-consolidated cellulosic ethanol production

Spencer Crook, Patrick Ronan, and Martina Hausner

Ryerson University

Keywords: ethanol, cellulose, fermentation, bio-fuel, climate

Abstract: In the face of rising oil prices, increasing atmospheric carbon 
dioxide levels, and climate change, it is clear that viable alternatives to fossil 
fuels which are sustainable, and cause minimal environmental impact are 
imperative to the progress of humanity and the wellbeing of the earth. 
Ethanol as a fuel source may in part, offer a possible solution. Specifically, 
ethanol produced efficiently, from cellulose, the most abundant bio-polymer 
on earth. This thesis seeks to investigate ethanol production from a variety 
of cellulosic substrates using a bacterial consortium isolated from nature. The 
bacterial consortia were grown in 100mL batch cultures with 1 gram of filter 
paper, switch grass, cardboard or newspaper provided as a cellulose source. 
The media became anoxic approximately 24 hours after inoculation. Within 
days, evidence of the cellulosic substrate being digested by the bacteria 
became apparent. Dry weight analysis of the cellulosic substrates was 
conducted 25 days after inoculation. Each of the cellulosic substrates 
exhibited some degradation with filter paper and cardboard displaying the 
highest levels at 0.407 grams and 0.340 grams respectively. Tri-weekly 
samples were taken from the cultures and analyzed via high pressure liquid 
chromatography (HPLC) to determine the concentration of ethanol and other 
metabolic end products. Preliminary data shows ethanol and acetate being 
the major end products produced. Further analysis of the HPLC data is 
currently underway. Additionally, samples of media and cellulosic material 
were taken at regular time intervals and are being viewed with confocal and 
fluorescent microscopy to visualize differences in cellulose attachment, as 
well as visible changes to the consortia across cellulose sources and time. 
The initial results of this project are encouraging. With more research, bio-
consolidated ethanol production from cellulosic waste products may one day 
contribute to a minimized dependence on fossil fuels.
9 - The influence of egg size and hatching time on growth of juveniles of rainbow trout (*Oncorhynchus mykiss*)

Bernardo Ramos Jose, Roy Danzmann, and Michael Burke
University of Guelph

Keywords: egg size, developmental rate, hatching time, life-history traits, rainbow trout

The relationship between egg size, developmental rate and life-history traits in rainbow trout (*Oncorhynchus mykiss*) is not clear and may vary depending on the strain. The present study verifies the effect of egg size and hatching time on growth in two cohorts of a hatchery strain of rainbow trout. The eggs were produced at Lyndon Fish Hatcheries and transported to be incubated in Alma research station (University of Guelph) for the trials. Mean hatching time, free-embryo length and growth rate were measured in 22 families obtained in 2012. Egg diameter, mean hatching time and growth rate were analysed in 25 families from 2013. Eggs were measured with a dissecting microscope equipped with a micrometer. Moreover, families were ranked and divided in three classes (early, middle and late) according to the chronological order of mean hatching time. The length of free-embryos was not correlated with mean hatching time for the 2012 group. However, families with a shorter mean hatching time grew significantly faster, up to 30 grams, than families which took longer to hatch. For the 2013 families, a correlation between egg diameter and mean hatching time suggests that larger eggs take longer to hatch when compared with smaller eggs. Growth data measurements are still pending for the 2013 families. Thus, these previous results can be used to provide a better understanding of the genetic influences regulating life-history traits and growth performance of rainbow trout.

10 - Delivery of RNAi against a gene of *Tetranychus urticae* via feeding on transgenic plants

Yasuko Togawa, Vladimir Zhurov, and Vojislava Grbic
University of Western Ontario

Keywords: RNAi, Tetranychus urticae, Arabidopsis thaliana

Two-spotted spider mite (*Tetranychus urticae* Koch) is a major pest that has a wide range of plant hosts, including commercially important species. *T. urticae* is known to rapidly develop acaricide resistance, thus there is an emerging need for a novel strategy to control this species. RNA interference (RNAi) delivered by transgenic plants that mites feed on is a great candidate for an alternative pest control due to its feasibility and target specificity. In this study, the RNAi is targeting the transcripts of the NADH dehydrogenase gene in *T. urticae*, whose protein product is essential for respiration. I hypothesize that feeding mites on dsRNA-producing Arabidopsis thaliana targeting NADH dehydrogenase transcripts will trigger RNAi in *T. urticae*, negatively influencing its performance and possibly causing mortality. The objective of the current study is to evaluate RNAi as an alternative pest control method. I selected three putative transgenic lines (25-2, 25-3 and 25-4); I conducted Basta resistance (BastaR) selection that is linked to an RNAi construct on all the seed stocks available and have identified homozygous, heterozygous and non-transgenic seed stocks among the selected lines. Subsequently, I performed reverse transcriptase quantitative PCR (qRT-PCR) on these lines and found that only samples from 25-3 had high expression of the transgene. These data, together with BastaR experiment, identified that only 25-3 line was homozygous for the single insertion of the transgene. I also measured the damage of transgenic and control plants due to feeding, and found no significant differences between transgenic and control lines. The assay on population performance of *T. urticae* on the transgenic line 25-3 and control plants is currently in progress. This study contributes to establishing a solid basis to assess the effect of RNAi on *T. urticae*. 
11 - Treatment of dry eye disease in a dry-eye rabbit model using a novel sulfadiazine-hyaluronic acid formulation

Kathleen Hoang, Ben Muirhead and Heather Sheardown

McMaster University

Keywords: Dry Eye Syndrome, Hyaluronic Acid, Sulfadiazine, Ocular Surface Treatment, Impression Cytology

Dry eye syndrome (DES) is a multifactorial disease that affects the ocular surface and tear film. DES is also known as dysfunctional tear syndrome and can lead to visual disturbances, inflammation, and potential scarring of the corneal surface resulting in permanent physical damage. Topical lubricants are by far the most widely used therapy for DES, but typically have a very low residence time on the ocular surface, and therefore provide transient relief. Other formulations are viscous gels that cause irritation and complications with administration and vision. We have developed a novel formulation which addresses many of the inadequacies of modern eye drops.

A series of novel formulations of covalently linked hyaluronic acid (HA) and sulphadiazine (SD) were prepared for testing. New Zealand White (NZW) rabbits were chemically induced to display dry eye symptoms by topically administering 0.1% Benzalkonium Chloride (BAC) twice daily for 14 days. These DES rabbits were rescued with our HA-SD formulations. This rescue was assessed using fluorescein and rose Bengal staining with slit lamp ophthalmoscopy, Schirmer’s testing, impression cytology, and conventional histology.

Results demonstrate the potential of HA-SD conjugates as a treatment for DES. Symptoms improved immediately after administration as monitored through ocular assessment and impression cytology with persistence of these beneficial effects longer than observed with commercial alternatives. DES symptoms disappeared completely much sooner when treated with HA-SD than when left untreated.

Therefore, this novel hyaluronic acid and sulphadiazine-based eyedrop formulation demonstrates potential for being an effective treatment for patients with DES and offers a great improvement on the current status quo.

12 - Analysis of the ENU-3 family proteins in C. elegans

Victoria Hipolito, Homai Anvari and M.T. Killeen

Ryerson university

Keywords: axon outgrowth and guidance, motor neurons, ENU-3, UNC-6/Netrin, paralogs

The research program in the Killeen lab at Ryerson is related to the identification and analysis of the molecules and mechanisms involved in the development of a functional nervous system. In particular, the work is related to the function of the ligand UNC-6/Netrin and its two receptors UNC-5 and UNC-40/DCC (deleted in colorectal cancer) in the establishment of the nervous system. The group is using the microscopic non-parasitic nematode, Caenorhabditis elegans as a model organism.

In C. elegans the DA and DB classes of motor neurons (MN) innervate the dorsal muscle cells that are responsible for forward and backward locomotion. The DA and DB classes have cell bodies along the ventral cord and send their processes dorsally along defined trajectories in response to the Netrin/UNC-6 signaling pathway. ENU-3 is a novel protein that was discovered through a genetic enhancer screen for enhanced motor neuron axon outgrowth defects in a putative null strain lacking UNC-5; unc-5(e53) (Yee et al., 2011). ENU-3 is a pan-neuronal protein predicted to be a trans-membrane protein whose true function is unknown.

Searches for homologues of ENU-3 have led to the identification of five highly similar proteins in C. elegans, all of unknown function: W03G9.3, W05F2.2, C38D4.1a, Y37D8A.12a and K01G5.3. The work described is directed towards finding a) whether all the members of the ENU-3 family of proteins are involved in motor axon outgrowth b) where and when the proteins are expressed.

Reduction of the mRNA level of each gene by RNA inhibition in an unc-5(e53) background showed significantly enhanced MN outgrowth defects, particularly of the DB4 and DB5 motor neuron axons. The proteins are therefore likely to be involved in MN outgrowth, possibly in redundant pathways.
13 - Engineering a Vector to Knockdown Expression of ASF1 using RNAi Methods

Rehman Ata, Jeffrey Fillingham

Ryerson University

Keywords: Tetrahymena, molecular biology, ASF1, proteomics, chromatin

The ciliate protozoan Tetrahymena thermophila is distinctive among eukaryotes as it has two nuclei, a macronucleus (MAC) and a micronucleus (MIC), within its single cell. T. thermophila reproduces asexually during vegetative growth and sexually during its mating. The highly fragmented polyploid (45n) MAC directs somatic functions and as such is transcriptionally active. The properties of the MAC makes T. thermophila an excellent model for chromosomes studies and therefore their chromatin assembly mechanisms. Many proteins play a part in chromatin assembly, including the highly conserved histone chaperone, Anti Silencing Factor 1 (ASF1). ASF1 is a H3-H4 histone chaperone protein that been associated with a variety of functions including: transcription activation, and deactivation, DNA repair, and DNA replication. The aim of this study is to engineer a vector with which ASF1 expression will be inducibly knocked-down using RNAi methods. This will be achieved by introducing a plasmid vector into T. thermophila. The REC8hpCYH plasmid, which was originally designed for the purposes of knocking down REC8 in T. thermophila, will be modified; the 500 bp REC8 inserts (reverse & forward) will be replaced with two identical, but inverted ASF1 500 bp sequences. Following molecular cloning, this vector will be used to transform T. thermophila by homologous recombination integrating the cassette into the RPL29 locus. Transcription will create a RNA hairpin, which will ultimately be recognized and processed by Dicer. Future studies will examine the phenotype of ASF1 knockdown in T. thermophila growth and development.

14 - GluA2-lacking AMPA receptor expression in homeostatic synaptic plasticity

Sébastien Maillé, Cary Soares, and Jean-Claude Béïque

University of Ottawa

Keywords: Stroke, Homeostatic synaptic plasticity, GluA2-lacking AMPA receptors, Recovery, Cobalt uptake staining

Neuroplasticity is a term that refers to the remodeling and reshaping of neural networks within the brain. This phenomenon has been extensively studied during the last few decades because of its crucial role in learning, memory and adaptation, as well as recovery from brain damage e.g. following stroke. Certain types of activity-dependent plasticity, such as long-term potentiation and long-term depression, are known to be tightly regulated by homeostatic plasticity mechanisms. Homeostatic synaptic plasticity stabilizes synaptic strength by, amongst other processes, adjusting the type and number of ionotrophic postsynaptic receptors. We have recently shown, using a variety of electrophysiological and biochemical methods, that long-term network silencing causes a homeostatic upregulation of GluA2-lacking AMPA receptors at cell surfaces of CA1 pyramidal neurons in the hippocampus. GluA2-lacking AMPA receptors, whose expression is normally limited in pyramidal neurons, are a class of ionotropic glutamate receptors that exhibit a higher conductance than other AMPA receptors as well as permeability to divalent cations, such as Ca2+ and Co2+. This study sought, by means of a cobalt uptake staining procedure, to gain a histological perspective of the number and identity of neurons of the hippocampus that are expressing GluA2-lacking AMPA receptors in response to long-term network silencing. We found that network silencing with tetrodotoxin caused an increase in the number of cells expressing GluA2-lacking AMPA receptors, although the cell types involved remain to be determined. The results of this study will broaden our understanding of the underlying cellular and molecular mechanisms driving neuroplasticity.
15 - Does Chronic Stress Exacerbate Noise-Induced Hearing Loss?

Julia M. Abitbol, Ashley Schormans, Marei Typlt, and Brian L. Allman

Western University

Keywords: Chronic Stress, Noise Exposure, Hearing Threshold, Auditory Brainstem Response, Rat

Hearing sensitivity can be influenced by exposure to factors in one's environment such as loud noise or psychological stressors. Noise exposure can damage sensory cells in the inner ear, leading to physiological changes in neurons in the auditory system, as well as permanent hearing loss. Acute exposure to psychological stressors can provide a protective function and hypersensitivity to the auditory system. At present, however, the impact of chronic stress on the auditory system is not fully understood. Interestingly, it has been found that neurons in the auditory system are particularly vulnerable to chronic stress. Consequently, a rat model was used to investigate the hypothesis that chronic stress prior to noise exposure will exacerbate noise-induced hearing loss. Male Sprague Dawley rats were divided into 4 groups: (1) chronic stress, (2) noise exposure (1h, 12kHz, 120dB, bilateral), (3) chronic stress plus noise exposure, and (4) controls. Based on a previously-established chronic stress protocol, rats were placed in a plastic restraint device (which painlessly limited their ability to move) for 6 hours/day for 21 consecutive days. Chronic stress was confirmed by monitoring changes in body weight; rats subjected to daily restraint gained the least percentage of their initial body weight compared to other treatments. Although chronic stress alone did not elevate final hearing thresholds, rats subjected to chronic stress prior to noise-exposure showed an elevation in final hearing thresholds for right and left ear clicks as well as 4- and 20kHz tonal stimuli compared to solely noise-exposed rats (16.3dB, 16.7dB, 14.17dB, and 11.67dB elevation, respectively). This supports the hypothesis that chronic stress exacerbates the degree of noise-induced hearing loss. The implication of these findings show that chronic stress represents a risk factor for hearing impairments in individuals that are also exposed to loud noise (e.g. military personnel and workers in heavy industry).

16 - Effects of SK Inhibitor Apamin and Cognitive Diet on Acheta Domesticus Cognitive Abilities and Possible Mushroom Body Impacts

Sheik Burkutoola and David Rollo

McMaster University

Keywords: Apamin, Cognition, Neurodegeneration, Mushroom Body, Learning

Cognitive processes, such as memory and learning, and the prevention of neurodegenerative disorders have been shown recently to benefit from an increase of certain nutrients in the diet. Many of the nutrients used in the cognitive diet are antioxidants which have been shown to improve cognition and prevent damage caused by free radicals and other reactive species. The use of neuroprotectants for increasing cognition and ameliorating neurodegeneration has also received considerable attention. Apamin has been shown to protect dopamine secreting neurons and increase the memory and learning abilities of the mouse model of Alzheimer's and Parkinson's. Apamin not only prevents damage but also decreases the threshold for synaptic plasticity by increasing the firing rate of neurons. Acheta domesticus was used in this study to determine whether apamin and a nutraceutical cocktail can increase cognition. The assay used to measure the cognitive changes was a variation of the Morris water maze called the dry Morris maze which was modified to be suitable for the crickets. This study also looked at the suitability of A.domesticus as a model for neurodegeneration and cognition. The cognitive cocktail caused a delay in the maturation of the crickets but the delay allowed them to grow for a longer period of time which caused them to also have a greater mass as adults. The preliminary results of the dry Morris maze show that the crickets that were fed the cognitive diet finished the maze faster than the control crickets even though they were not more active. Repeated trials showed that the cognitive crickets were more likely to finish with a better time during the next trial than the control crickets which on average did not improve.
17 - The effects of KATP channels on skeletal muscle fatigue and recovery are dependent on muscle stimulus frequency and fibre type

Mackenzie E. Charter and Coral L. Murrant

University of Guelph

Keywords: Skeletal Muscle, Potassium Channel, Submaximal, Fatigue, Recovery

ATP sensitive potassium (KATP) channels are hypothesized to protect against ATP depletion during maximal muscle contraction by decreasing force production, however their function in submaximal contractions and recovery is unknown. We sought to test whether KATP channels altered the force of contraction during fatigue and recovery of mouse slow (soleus; SOL) and fast (extensor digitorum longus; EDL) twitch muscle, in vitro, at maximal and submaximal stimulus frequencies. We fatigued SOL (60Hz, 60 contractions per minute (CPM) and 20Hz, 60CPM) and EDL (100Hz, 60CPM and 40Hz, 60CPM) for 5 minutes in the absence or presence of a KATP channel inhibitor (10-5M glibenclamide; GLIB) or a KATP channel opener (10-5M pinacidil; PIN) and then observed recovery (SOL: 60Hz 0.6 CPM and 20Hz, 0.6CPM; EDL:100Hz 0.6CPM and 40Hz 0.6 CPM). GLIB had no effect on fatigue or recovery of SOL or EDL at maximum stimulus frequencies but significantly attenuated force in SOL (12.2%) and EDL (6.9%) at submaximal frequencies. GLIB significantly enhanced force during recovery of SOL by 22.5% at submaximal stimulus frequencies. PIN did not affect fatigue of SOL or EDL at maximal stimulus frequencies or the recovery of SOL but significantly attenuated force of EDL during recovery by 8.9%. PIN had no effect on fatigue or recovery during submaximal contractions. Thus, the effect of KATP channels is dependent on both fibre type and stimulus frequency.

18 - Radiation tolerance and the bystander effect in the hydrated tardigrade species H. dujardini

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McMaster University

Keywords: Tardigrades, radiation tolerance, bystander effect, gamma radiation, survival

Tardigrades are known to be extreme tolerant organisms, being able to survive even after exposure to inhospitable environments such as space. Previous investigations have examined the survivorship of different species of tardigrades to various conditions but the radiation tolerance of this organism is an area of study that is still developing. In addition to direct contact with the radiation source, indirect contact through a mechanism of the radiation induced bystander effect is something that has been documented at lower levels of radiation, but tardigrades allow for testing at higher doses of radiation.

Due to this tolerance of extreme environments, we will be using the tardigrade species Hypsibius dujardini to investigate the survivorship and bystander effect of high doses of radiation on a colony of tardigrades. Hydrated animals will be exposed to 3kGy and 5kGy of radiation. Only one animal in the bystander groups will be exposed to radiation and transferred after to a colony of tardigrades that were not irradiated; their long term survival (every 48 hours) will be monitored until all the animals die. The results obtained will be analyzed using a logranked test allowing a comparison of survivorship between the control group, irradiated group and bystander group.

Preliminary results obtained have shown that the irradiated specimens have the lowest survivorship while controls demonstrate the highest survivorship and the bystanders showed intermediate survival. It is anticipated that this data will serve to further characterize the difference in levels of tolerance between tardigrade species and the possible differences in tolerance mechanisms.
19 - Influence of Royal Jelly and Methoprene on the Life History and Longevity of the Cricket, *Acheta domesticus*


McMaster University

Keywords: longevity, life history, royal jelly, juvenile hormone, methoprene

Target of ramamycin (TOR) is a growth regulatory pathway that is conserved across species (Seo et al. 2013). TORC1, a complex formed by the protein kinase TOR, upregulates protein synthesis and inhibits autophagy in response to the cellular environment to promote cellular growth and proliferation (Seo et al. 2013). In contrast, FOXO transcription factors (FOXO) are involved in a wide array of processes throughout development as transcriptional activators and repressors (Greer and Brunet, 2005). They promote cell cycle arrest at the G1/S boundary and delay the G2/M transition, inhibiting proliferation while potentially increasing DNA repair efficacy (Greer and Brunet, 2005). Royal jelly (RJ) is a food produced by the hypo-pharyngeal and mandibular glands of worker honeybees, Apis mellifera (Inoue et al. 2003). Honeybee larvae to be differentiated into queens are continuously fed RJ throughout their life and display distinct morphological and life history traits relative to worker honeybees, which include increased growth rate, larger body size and prolonged lifespan (Spannhoff et al. 2011). Juvenile hormone (JH) is a sesquiterpenoid secreted by the corpora allata, a pair of endocrine glands, in insects (Stoka et al. 1996 & Lim et al. 2005). The morphogenetic function of the hormone is the inhibition of metamorphosis and the conservation of larval characteristics (Stoka et al. 1996). In this study, Acheta domesticus was used to examine the effects of RJ and methoprene, a JH analog, on life history and longevity. The dietary treatment groups were as follows: control, royal jelly, methoprene and royal-jelly-and-methoprene combined. The following parameters were studied: survivorship, food consumption, maturation data, and body mass. The results indicate that methoprene treated males had a significant increase in mean growth rate. The methoprene and combined treatment groups had a significantly greater mean body mass in addition to undergoing an extra moult in the adult stage.

20 - Intestinal Urea Handling in the Freshwater Rainbow Trout (*Oncorhynchus mykiss*)

Joanna Smich, Julian Rubino, and Chris M. Wood

McMaster University

Keywords: teleost, rainbow trout, urea, ornithine, ammonia

Most teleost fish are ammoniotelic, meaning that these species excrete ammonia, a toxic metabolite of protein degradation, as their primary nitrogenous waste product. It has been shown that following a meal, teleost species experience high levels of ammonia production in the gut through natural degradation of dietary protein, which can be absorbed by the intestine. As an ammonia detoxification process, these species can excrete urea as well, although the role of urea synthesis is not well understood in teleost fish. Using glutamine as the primary nitrogen donor, teleosts use the Ornithine Urea Cycle (O-UC) to produce urea, although the genes for the enzymes are not always expressed. Previous research has shown that rainbow trout express many O-UC enzymes during early development, where urea synthesis is essential to prevent toxic accumulation of ammonia from the breakdown of the yolk sac. This environment may be compared to the high ammonia environment created by the chyme in the intestinal region. This gives reason to think that the capacity to produce urea may be retained in the rainbow trout intestine. Intestinal urea handling was observed in vitro in the intestine of the freshwater rainbow trout (*Oncorhynchus mykiss*). High luminal glutamine, glutamate, and ammonia were used to observe how intestinal urea handling is altered in each of these treatments. Overall, this research will aid in the establishment of a model of urea handling in the intestinal tract of freshwater teleost fish.
21 - Changes in physical health following an adapted physical exercise program for adults with autism and an intellectual disability

F. Azaizi, C.A. Sutherland, K. Carr, S. Horton, and N.R. Azar

University of Windsor

Keywords: exercise, physical fitness, Autism Spectrum Disorder, intellectual disability, adult

Relationship between energy expenditure and changes in physical health following a 12-week adapted physical exercise program for adults with autism spectrum disorder and an intellectual disability

Autism Spectrum Disorder (ASD) is a complex neurological disorder marked by persistent social communication and interaction deficits, and restricted or repetitive behaviours. According to recent surveys, only about half of North Americans are moderately active. Children and youth with ASD are often even less active than their typically developing peers, and these individuals tend to become less active as they age. The goal of this study is to increase the overall physical fitness of adults with ASD and an intellectual disability (ASD-ID), and to promote participation in physical activities. Fifteen adults with ASD-ID will participate in 90-minute adapted physical exercise (APEX) sessions, twice a week for 12 weeks. The APEX program will include cardiovascular and resistance training, and a group sports activity. Baseline measures of physical fitness (resting heart rate, blood pressure, cardiovascular fitness, muscle strength, flexibility) and functional movement (balance, reaction time, gait) will be taken at the beginning, middle, and end of the program. Energy expenditure (EE) levels during the exercise sessions will be monitored once per week using the BodyMedia Fit Armband. These data will be examined weekly to provide feedback to trainers regarding participants’ exercise intensity. Correlations of EE to measures of physical fitness and functional movement, particularly cardiovascular fitness, will also be examined. Because individuals with ASD often engage in more sedentary activities as they age, encouragement of vigorous exercise is of particular importance within this population. It is anticipated that participation in the APEX program will have a positive impact on participants’ health and fitness levels, as well as their attitudes towards exercise and their confidence in participating in physical activities in the future.

22 - Growth Responses of Tamarack to Recent Climate Warming: A Dendrochronological Study from Canada’s Northern Boreal Peatlands

Greg R. Lynch and Jennifer Balzter

Wilfrid Laurier University

Keywords: dendrochronology, tamarack, climate change, permafrost

The main objective of this study was to quantify any significant trends in the growth of tamarack under recent climate warming in Canada’s region of discontinuous permafrost. This region is proposed to be one of the most drastically affected by climate warming; therefore, understanding species-specific responses is a crucial step in understanding how landscape scale changes are influenced by abiotic conditions. Following dendrochronological sampling, growth-climate relationships were established using basal area increments and average annual seasonal temperatures (e.g., spring, summer, fall, winter, and annual average) as well as total annual precipitation (e.g., rain and snow). Preliminary results suggested that the majority (70%) of the sampled tamarack trees did not elicit any growth response to any of the selected climate variables. This result suggested that the growth-climate signal might be masked in these trees because of other physical (e.g., pest outbreak, permafrost dynamics, and nutrient availability) or physiological (e.g., water-use efficiency, water and nutrient uptake) drivers of growth. Currently, the focus of this study is to determine what factors are influencing the growth of tamarack at the study site. We expect to accomplish this by examining the tree cores for evidence of disturbance in the annual rings.
The African Migratory locust (Locusta migratoria L.) is an exceptional model for studying the mechanisms underlying insect flight due to its easily accessible nervous and muscular systems. Neuronal, muscular and metabolic mechanisms combine to promote and maintain the rhythmicity behind locust flight for long periods of time. A number of hormones, including the biogenic amine octopamine, are also involved during the initiation and maintenance of flight behavior. Octopamine has been shown to be important for other flight muscles such as dorsal longitudinal, pleuroaxillary, subalar and posterior tergocoxal muscles, through their direct supply of dorsal unpaired median (DUM) neurons. This study was performed to determine whether octopamine had an effect on activity of the forewing first basalar muscle (M97). I used electromyography to record M97 muscle depolarizations during tethered flight. Muscle activity was recorded before and after the injection of 50ml of $10^{-4}$ M octopamine into the locusts' hemocoel. Amplitude of the M97 action potential, duration, duration at half amplitude and maximum slope of the rising phase of the action potential were obtained for each flight sequence. No differences were observed in these parameters in the pre-octopamine and post-octopamine recordings. This suggests that M97 does not receive octopaminergic input or octopamine is unable to cross the blood-brain barrier surrounding the locusts’ central nervous system.
Poster Session B - IB
Atrium

Saturday March 22
5:30 - 6:30 pm
1 - Previous aggressive encounters and winning experience can predict aggression in subsequent fights in male Zebrafish

Oscar Chavez-Ibanez, Diane Seguin, Soaleha Shams and Robert Gerlai

University of Toronto Mississauga

Keywords: zebrafish, aggression, dominance, social behaviour

Male territoriality is key a factor for reproduction and survival of the species. Every species, including zebrafish, is subjected to selective pressures that have made males compete for a limited amount of resources such as food, mates, and territory. To characterize this social interaction, a behavioural paradigm was designed to test how previous fighting experience influences dominance patterns in subsequent aggressive encounters. Nine dyads composed of two size-matched males were paired twice to identify aggressive behaviours and to establish winners and losers. Dominance status was assessed through frequency and duration of the aggressive behaviours as well as overall fighting performance. Males that achieved a dominant status during the first pairing were more likely to win subsequent fights. In contrast, losing an aggressive encounter does not predispose males to behave in a certain way. Comparisons of the mean time engaged in a specific behaviour revealed that winners tend to spend more time chasing and striking as opposed to their subordinate counterparts. On the other hand, losers displayed higher levels of swimming, fleeing and freezing. Altogether these results show that: (1) aggressive encounters can be induced in mature males previously isolated for 24 hours. (2) Previous winning experience has a significant effect in modulating aggressive responses in future fights. (3) Subordinate males are not predisposed to a determined outcome, as previous losing experience has no significant effect in fighting experience.

2 - Effects of Early Social Isolation on Zebrafish Behaviour in Response to Social Stimuli

Niveen Fulcher, Soaleha Shams, and Robert Gerlai

University of Toronto Mississauga

Keywords: zebrafish, social isolation, locomotion, social behaviour

Behavioural effects of social isolation on innately social species are intriguing. Zebrafish is one such innately social species and displays complex social behaviours. Naturally, zebrafish prefer swimming in groups to swimming alone, and the sight of conspecifics can induce the shoaling response: the aggregation of individuals to form a tight group. When testing social interactions in zebrafish, shoaling response may be induced when stimulus is presented in the form of a live fish shoal and/or an animated image of a shoal. Studies of the effects of early environment on subsequent zebrafish behaviour are sparse in the literature. In the few fish studies available, some stated that isolation-reared fish spent significantly less time with social stimuli compared to control fish, while other studies suggested that socially deprived zebrafish show no social preference. Here, we manipulated the presentation of the social stimuli (live vs. animated) and examined activity, anxiety-related behaviour and preference for social interaction in fully isolated fish (compared to control fish). We found that social isolation affected response (distance to social stimuli) to live but not animated social stimuli. In contrast, locomotor activity (total distance traveled) increased in isolated fish when exposed to animated social stimuli but not in response to live social stimuli. We measured bottom dwelling and relative change in turn angles to examine anxiety-related behaviours and found that bottom dwelling was increased in isolated fish when exposed to both live and animated social stimuli but relative change in turn angle decreased during exposure to animated social stimuli only. Therefore, early social isolation affected social and non-social behaviour in zebrafish, though these changes were dependent on the type of social stimulus presented.
3 - The genetic study of genes that regulate the larval foraging behaviour in *Drosophila melanogaster*

Jay Gajiwala
York University

Keywords: behaviour, foraging, polygenic trait, *Drosophila melanogaster*, foraging and chaser

*Drosophila melanogaster* genetics is an excellent tool for studying the complexity of animal behaviour. What makes the study of behaviour most complicated is that most behaviours are polygenic traits under the control of more than one genes and the quantification of this behaviour is rather difficult. The study of these genes and their regulation in *Drosophila melanogaster* allows us to deduce the mystery behind many physiological processes that are evolutionarily conserved. I studied the many genes that control the *Drosophila melanogaster* larval foraging behaviour.

One of the genes controlling this behaviour is known as the foraging (for) gene. One allele of foraging gene is Rover (forR), which causes the larva to larger distances and the other allele is Sitter (forS), which causes the larva to move shorter distances. At the molecular level, for encodes a cGMP-dependent protein kinase (PKG). The forR allele produces a higher PKG activity, whereas the forS allele has a reduced PKG activity. Because PKG is an important part of cell signalling throughout the organism, it is expected that the change in PKG levels will have an impact on longevity of the adult organism. To understand more about the differences between the two alleles, I studied the longevity in adult flies with varying amount of PKG. The longevity of rover flies (forR) was compared to that of sitter flies (forS/forS). The results were confirmed with ectopic expression of foraging gene in transgenic flies using the GAL4/UAS system and RNAi technology.

A second gene known as Chaser (Csr) was also studied. Chaser (Csr) gene discovered in the 1990s is known to have an effect on larval foraging behaviour, but the location of the gene within the genome is unknown. This study used deficiency mapping to narrow down the region in which Chaser can exist. Chaser mutants were crossed to many deletions throughout the *Drosophila* genome to check for complementation. If the phenotype persists when Chaser mutants are crossed with a deletion, then Chaser is likely to be within the region. Chaser has since been narrowed down to a smaller part of the genome.

4 - Quantification and Analysis of Complex Behaviors in Zebrafish Using Argus

M. Sciuluna, S. Shams, J. McCrae, and R. Gerlai
University of Toronto Mississauga

Keywords: high-throughput screening, behavior quantification, R, animal behaviour, Zebrafish

Zebrafish (*Danio Ranio*) are a model organism for vertebrate behavior due to the ease of their maintenance and their (relative) evolutionary closeness to humans. Since this species is reproductively prolific, it is an ideal choice to be used for experiments involving high throughput screening of behavioral patterns. They exhibit a range of quantifiable behaviors whose expression under various environmental manipulations can help us understand the functional relevance of vertebrate behaviour. It is for this purpose that we developed Argus, a computer program that recognizes complex behavioral patterns and quantifies them meaningfully. Argus utilizes a previously created program called the RealFishTracker, (built by James McCrae). The RealFishTracker tracks movement of each fish and outputs x and y coordinates indicating their location in 2-dimentions. Argus uses these coordinates to calculate behavioral variables such as speed, distance traveled, and distance to any specified stimulus. Argus can reproduce many of the standard behavioral quantification techniques used in current biomedical research. These include measures of locomotor activity, thigmotaxis and anxiety-related behaviours. Argus was made to work with large data sets consistent with high throughput sequencing, so it can handle large data sets with ease, producing result summaries for multiple trials simultaneously. Argus was written in R, which is a programming language specialized for developing statistical software. R’s popularity has grown among researchers in all fields due to its free GNU licence. Argus is a free, specialized alternative to more expensive and limited commercially available software packages. Its interface is also designed to be simple and user friendly. Here, we compared output from Argus to output from a commercially available software called Ethovision by Noldus, to provide evidence for Argus’ validity and usefulness.
5 - Observing “boldness” behaviour in Sea Lamprey (Petromyzon marinus) in relation to susceptibility to capture in a trap

Erikas Kamaitis, Adrienne McLean, and Rob McLaughlin
University of Guelph

Keywords: boldness-shyness, invasive species, personality, repeatability, risk taking, temperament, trappability

Erikas Kamaitis, Adrienne McLean and Dr. Rob McLaughlin
Abstract: The introduction of the Sea Lamprey (Petromyzon marinus) into Lake Erie and the further expansion of its range throughout the upper Great Lakes had detrimental effects on populations of native fish species important to the Great lakes fisheries, such as Lake Trout (Salvelinus namaycush). A number of control methods have been very important to the ongoing management of the Sea Lamprey population. One of the more common techniques has been removal by trapping; unfortunately, this has not been as successful as first anticipated and recent research has focused on understanding Sea Lamprey behaviour and determining if individual variance is connected to trappability. One of the behaviours assessed is the "boldness-shyness continuum", which is loosely defined as an individual's tendency to take risks or not. Previous studies have determined that bold fish are easier to capture than shy fish, and could be the reason for why some lamprey are easier to trap than others. Due to the low trapping success and previous studies determining that bold fish are easier to capture, it was hypothesised that individuals caught in traps would be more willing to take risks than individuals caught outside the traps. Lamprey caught with backpack electrofishing and traditional trapping were tested for risk taking. Individual lamprey were placed in test tanks divided lengthwise down the centre of the tanks in order to compare the risk taking between individuals caught in traps with individuals caught outside the traps. To determine the repeatability of the behaviour each individual was put through three trials. Those that ventured into the centre of the test tanks, rather than moving along the wall, were considered to be more inclined to take risks, thus, more bold. Preliminary results suggest no significant difference between risk taking and the method of capture, sex or length.

6 - The Tube Test: A Systematic Paradigm for Tracking the Social Hierarchy within a Naked Mole Rat Colony

Ilapreet Toor
University of Toronto Mississauga

Keywords: naked mole rats, social hierarchy, dominance, weight, pass-overs

Naked mole rats are an east African, subterranean species of rodent. They are eusocial and consist of three castes: queen, breeding males, and workers. Larger naked mole rats have been found to be more dominant and aggressive than smaller ones. They also might be able to recognize each other’s social ranks, although the specific mechanism is unknown. Since body size is proposed to be a characteristic of dominance, the purpose of this study was to find a stable and systematic method of recording the hierarchy of a colony in regards to the weight of the colony members. As naked mole rats live in underground burrows, it was hypothesized that if weight is a factor in social dominance, then larger naked mole rats will always pass over smaller ones when encountering each other in a tunnel. To test this, two small polycarbonate bins were attached using a polycarbonate tube. Two naked mole rats were released at both ends of the tube, and whichever animal completely passed over the other was recorded. This methodology was used in two different tests using the same colonies; the first test consisted of three trials occurring once a week. The second tests consisted of six trials conducted over a span of two weeks. Both tests demonstrated moderate to high positive correlations and rank consistencies. However, there was in improvement in correlation scores from the first test to the second test for two colonies. The results found that heavier naked mole rats completed more pass-overs than lighter ones. However, the 6 trialed test had stronger weight-to-pass-over percentage correlations. This implies that pass-overs may be an effective method of tracking individual ranks within the hierarchy of a colony, especially if conducted every other day for two weeks.
Effects of Habitat Fragmentation on the Spatial Ecology of Two Endangered Turtle Species

Christopher J.H. Neufeld
Laurentian University

Keywords: Spotted turtle, Blanding's turtle, Fragmentation, Spatial Ecology, Conservation

Habitat fragmentation occurs when a habitat is divided into smaller, non-continuous pieces. It can be caused by anthropogenic disturbances (roads, settlements, etc.) or by natural disturbances (forest fires, floods, etc.). Having a smaller habitat to live in can alter the behaviour of the species within that habitat, and such alterations can include changes in home range size and daily movement patterns. My study focused on how habitat fragmentation affects the spatial behaviour of spotted turtles (Clemmys guttata) and Blanding's turtles (Emydoidea blandingii), and the potential implications for the recovery of these at-risk species. I hypothesized that habitat fragmentation would decrease home range size and movement patterns of both species because it will restrict movement. I also hypothesized that Blanding's turtles would be less affected by habitat fragmentation than spotted turtles because of the mobile nature of Blanding's turtles. Therefore, I predicted to see smaller home range sizes and smaller daily movements in fragmented compared to non-fragmented habitats for both species, and I predicted that Blanding's turtle home ranges would be larger than those of spotted turtles in fragmented habitats. I found that home range size and daily distance moved were smaller in fragmented compared to non-fragmented habitats for both species, and I predicted that Blanding's turtle home ranges would be larger than those of spotted turtles in fragmented habitats. I found that home range size and daily distance moved were smaller in fragmented compared to non-fragmented habitats for spotted turtles, but there was no difference in spatial attributes between fragmented and non-fragmented sites for Blanding's turtles. These results indicate that Blanding's turtles are less susceptible to habitat fragmentation than spotted turtles. Knowing this is important in designing roads and other infrastructure that could affect the home range sizes of these endangered species, and thus could lead to better mitigation measures and conservation efforts.

Effects of Scale in Observations of Spatial and Temporal Variation in Natural and Disturbed Landscapes

Felix Chan, Matthew Hammond, and Jurek Kolasa
McMaster University

Keywords: scale, spatial, temporal, variation, landscape

Disturbance can produce a shifting mosaic of patches at different successional stages. Changing spatial and temporal scale of observation affects the perception of variation in ecosystems and the processes that cause that variation. Our study aims to determine the patterns of sensitivity of ecosystem variables to spatial scales of observation. Ecosystem parameters were derived from NASA's MODIS (Moderate Resolution Imaging Spectroradiometer) satellite to examine the spatiotemporal patterns of net primary productivity (NPP), land surface temperature (LST), leaf area index (LAI), fraction of photosynthetically active radiation (FPAR), evapotranspiration (ET), and integrated reflectivity (Albedo). The study area is a 41 km by 21 km plot in Targhee National Forest located near Yellowstone National Park in the States of Idaho and Wyoming. The landscape has a distinctive divide between a naturally forested area and a clear-cut area.

To assess scale-dependence, we aggregated values representing cells of 0.25 km2 and 1 km2 into larger block and compared resulting coefficients of variation. Our findings suggest that a natural landscape's intrinsic spatial variability is greater than that of a disturbed landscape. We also found that higher spatial variation may be associated with disturbed landscapes, relative to natural landscapes, at finer scales of observation; and lower spatial variation with disturbed landscapes, relative to natural landscapes, at coarser scales of observation.
9 - Monitoring bat populations on the University of Toronto Mississauga campus

Ariana Besik and Alyssa Brown

University of Toronto Mississauga

Keywords: Myotis lucifugus, Chiroptera, University of Toronto Mississauga, habitat distribution, forested riparian areas

Bats in North America play an important role in controlling insect pest populations. Unfortunately, bat populations face decline due to habitat destruction and disease. The purpose of this project was to study the distribution of Myotis lucifugus activity on the University of Toronto Mississauga campus and to study the effects of temperature, humidity, and precipitation on Myotis lucifugus activity. Bat activity was measured twice a week from May 16th, 2013 to August 22nd, 2013 using an ultrasonic detector. At each site, the number of bats, location, and time of detection were recorded. Weather data was obtained from the UTM Metrological Station. Bat density maps for each individual month and for the entire summer period revealed widely distributed bat activity with most activity occurring in open areas near water. Bats activity was found to decrease when the three-day precipitation total increased. Interestingly, no relationship was found between bat activity and temperature or between bat activity and humidity. The results suggest that lack of roosting sites around favorable bat habitat, such as riparian areas near forests, may not be a major problem on the UTM campus and that these areas are crucial for conserving the campus bat populations.

10 - Phylogenetic host-parasite-specificity in aphids of Churchill, MN

Daniel Gibson, M. Alex Smith, and LeeAnn Fishback

University of Guelph

Keywords: host-specificity, Aphidoidea, barcoding, co-speciation, host-switching

Associated plants and insects make up 50% of all known species and these interactions shape our environment. Host-specificity can often drive speciation and extinction events. Aphids (Hemiptera: Aphidoidea) are an example of a host-specific, phytophagous insect in which co-evolution and host switching are thought to drive co-speciation. I hypothesised that if co-evolution and co-speciation between host plants and phytophagous aphid species is a result of species-specific co-adaptations, then aphid species in Churchill, Manitoba will be highly host-specific both by association and by phylogeny. A section of the COI mitochondrial gene (the barcode region) was amplified and sequenced from aphids collected from Churchill, Manitoba, and from these sequences a maximum-likelihood phylogenetic tree was created. Similarly, DNA barcode sequences for the 10 plant species from which the aphids were collected, were mined from the BOLD project [MKPCH] and a maximum likelihood phylogenetic tree was created using a concatenation of a segment of these three genes: ITS2, rbcLa and MatK. I used R and Core-Pa to statistically assess the degree of specificity of the aphid:plant associations. The picante package in R revealed significant clustering of aphid species on two separate plants: Labrador tea (Rhododendron groenlandicum) and Blueberry (Vaccinium uliginosum), and significant dispersion of aphids species on Salix spp. The Core-Pa analysis did not show evidence of co-speciation, but there were significantly lower numbers of host switching events than were expected from random associations. These results suggest that aphids are host-specific by association, but not necessarily by phylogeny. Studying the phylogeny of host-parasite-specificity will allow us to make inferences about the specific adaptations that allowed for species radiations in the past and may inform us on the ongoing processes of present-day speciation.
11 - The influence of vegetation structure on avian habitat selection at Welgevonden Game Reserve, South Africa

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Keywords: savannah, avifauna, habitat selection, foliage height diversity, Loxodonta africana

Many studies have documented the influence of vegetation structure on bird diversity, particularly foliage height diversity (FHD) (MacArthur and MacArthur, 1961; MacArthur et al., 1962; Karr and Roth, 1971; Willson, 1974; Rice et al., 1983). Birds were monitored at 40 different sites at Welgevonden Game Reserve. Habitat assessments were conducted at these same sites and quantified tree abundances, tree heights, woody biomass at different heights, grass heights and levels of elephant impact. Lastly, the habitat type was classified. Regression models were used to determine the influence of vegetation factors as well as bird abundance, elevation, habitat type and elephant impact on bird diversity. The vegetation factors analyzed were tree density, tree height and foliage height diversity. FHD, bird abundance and elephant impact were found to positively impact bird diversity. Tree density was found to negatively impact bird diversity. FHD was a weaker predictor of bird diversity than in previous studies. It was speculated that this may be due to differences associated with savannah vegetation compared to the vegetation at previous study sites.

12 - Adapptive potential of populations: quantifying genetic variation at the MHC-1 locus in the guppy (Poecilia reticulata)

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Keywords: adaptive potential, MHC-1, guppy, balancing selection, temperature stress

Climate change refers to characteristic changes in global weather patterns, including the notable rise in surface temperature, which is predicted to negatively impact many species. In a previous study, experimental populations of guppies exposed to elevated temperatures for 2 years lost significantly more genetic variation at neutral loci than populations maintained at their native temperature. I tested whether similar declines in genetic variation occurred at a functional locus, the major histocompatibility complex (MHC). The MHC is a highly polymorphic immune gene family responsible for pathogen recognition, the high variability at the MHC is critical to a populations adaptive potential. I first characterized MHC expression in guppies to determine if all alleles are expressed. I then used next generation sequencing (Ion Torrent PGM) to sequence fifteen individuals from each of three control and three experimental populations. I will compare diversity at the MHC to neutral loci and discuss the MHC as a model describing how selection maintains important genetic diversity.
13 - Phenotypic plasticity in the shells of apple snails (Pomacea flagellata) under geometric constraint

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Keywords: phenotypic plasticity, apple snails, geometric constraint, shell morphology, shell models

Aquatic snails are known for the great diversity in their shells. Factors such as predation, temperature, density dependence and pH contribute to their variation. The objective of this study was to determine the effect of spatial restrictions on shell shape in Pomacea flagellata (apple snails). The snails in experimental group were raised in tanks containing perforated dividers, which caused restriction of movement and provided increasing constraint on shell growth. Shells from the control and experimental tanks were collected and sectioned to obtain aperture measurements which was later used for shell modelling. Directional selection towards smaller shells with reduced aperture size and tighter shell coiling were expected for snails in the experimental tank. This would provide support for the idea that geometric constraint is an environmental factor contributing to phenotypic plasticity. Such information can contribute towards a database of the connections between shell morphology and the corresponding stressor. This can later be used to provide novel solutions to problem of apple snails as an invasive species.

14 - Phenotypic response to inhibition of meridional growth in adult Arbacia punctulata

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Keywords: echinoids, phenotypic flexibility, growth, biomechanism, morphology

Analyzing changes in the morphology of organisms with great accuracy has been a daunting task for the scientific community. The variation in skeletal growth of echinoids can be a valuable source of information in the study of phenotypic flexibility (Piersma & Drent, 2003), which is an important factor to consider when designing models of growth (Ellers & Telford, 1992). The purpose of the experiment is to analyze the growth of echinoids in response to a physical barrier limiting increase in test height. Arbacia punctulata will be nourished to allow growth for 8 weeks in an aquarium fitted with a horizontal surface in direct contact with their aboral side. The majority of growth in the experimental group will remain exclusive to test diameter (lateral growth), leading to significant decrease in height to diameter ratio. Therefore, we will be expecting Arbacia punctulata to exhibit significant morphological changes in response to environmental modifications (Dafni, 1986).

The predicted morphology will resemble irregular echinoids, such as sand dollars. Data from this experiment can be implemented to improve the quality of current growth models of echinoids or support the theories between the evolutionary history between sand dollars and sea urchins.
15 - Skull Morphology of *Captorhinus aguti*

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Keywords: C. aguti, Reptilia, Captorhinid, Permian era, skull morphology

*Captorhinus aguti* is a well-known primitive reptile of the family Captorhinidae, which first emerged during the Late Carboniferous and became widespread during the Early Permian. *C. aguti* is characterized by its multiple-rowed dentition, swollen cheeks, and skull length. The specimen studied in this project was retrieved from the fissure fills of the Richards Spur Locality in Oklahoma, USA. It consists of the left posterior section of the skull in which the braincase is largely intact, along with two full and two partial pre-sacral vertebrae. The fossil was prepared for analysis over the course of a few months using pin vices and Micro-Jack 3 airscribes under a microscope to remove rock matrix and expose the underlying bone. Photographs were then taken of the dorsal, ventral, left lateral, right medial, and occipital views and further analysed for morphology using the current literature regarding *C. aguti*. Although this species has been relatively well studied, the well-preserved braincase of this specimen offers an important and informative view into the occipital region of the skull of *C. aguti*. Analyses of new specimens such as the one investigated in this project continue to provide critical morphological information on captorhinids, and Reptilia as a whole.

16 - Fossil Taphonomy in the Early Permian Richards Spur Locality, Oklahoma, USA

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Keywords: taphonomy, Richards Spur, Permian, paleontology, fossil

Abstract: The purpose of this project was to prepare and study a paleontological specimen obtained from a large cave system that is present at the Early Permian Richards Spur Locality in Oklahoma, USA. Preparation of the specimen revealed a wide assortment of well-worn skeletal elements from a variety of tetrapod species. Fossil specimens found within the Richards Spur cave system can be found in various states of articulation and wear. Research into cave taphonomy, which is the study of the deposition and fossilization of organisms, suggests a number of different mechanisms can result in skeletal elements being found in different states of articulation and with different levels of wear. Using information on matrix composition, weather patterns, skeletal element placement, and wear, the story of the fossilization of these elements can be inferred. The fossils found at Richards Spur are from organisms that fell into the caves and became trapped, or died outside the caves and were picked up and worn by water movement, and then deposited into the caves. The fossils obtained from the Richards Spur cave system demonstrate that organisms may continue to be affected by the forces of nature even after death.
17 - Morphology of the left humerus of a diadectid

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Keywords: Diadectid, humerus, morphology, fossil preparation, vertebrate form and function

The morphology of the left humerus of a diadectid is described based on a specimen recovered from the Lower Permian Mud Hill Locality in Taylor County, Texas. Being one of the earliest herbivorous tetrapods, the dentition and cranial morphology of the diadectids has been of primary research interest. Thus, despite being a well-studied species, little is known with regards to its postcraniale skeleton. Preparation of the specimen involved matrix removal using a Micro-Jack 3, Pneumatic Air-Scribe, and pin vices. Measured to be approximately 13 cm in length, the typical tetrahedral shape common to many large Permo-Carboniferous tetrapods was also observed. The widely expanded proximal and distal surfaces were arranged nearly perpendicular to one another allowing for effective muscular relations given the posture of the animal. Overall, the humerus was short and stout with a very short shaft and possessed large muscular processes, features that are indicative of slow but powerful movement. In contrast to another intact diadectid humerus discovered at the same locality, this specimen had many broken surfaces in which the entepicondyle had broken off completely. The bone surface also displayed numerous bite marks indicative of carnivore feeding behaviour, since these were concentrated in cartilaginous and fleshy muscle regions. Although it is difficult to identify the scavenger based solely upon the anatomy of the bite marks, it is hypothesized that it could be a dissorophoid since it was identified as the possible scavenger of a Varanops skeleton, which was recovered in the vicinity of this diadectid specimen.

18 - Curriculum Map of the University of Ottawa Biomedical Science Program

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Keywords: biomedical, curriculum, science, undergraduate, program objectives

The biomedical science program (BIM) (created in 2002) is an interdisciplinary program in the Faculty of Sciences offered in both official languages. Having gone through its first program evaluation, professors and administrators are now seeking additional information and ways to reflect on the curriculum. A curriculum map is being developed for the undergraduate BIM program to collect and record curriculum related data to identify the pedagogical approaches and tools used, to assess the alignment of course learning with the program outcomes within the different program course options, and to evaluate if the English and French courses of the program address the same program objectives. Four research questions were devised to focus the creation of this descriptive map. What are the pedagogical approaches and tools used to teach? Are the different science-based options cohesive with the core program? Are the program objectives being met? Are the French and English versions of the program meeting the same program objectives? To answer these questions, general program-level information from program review documents and course sequences was compiled, followed by data from syllabuses and meetings with professors for all courses comprising the curriculum. Curriculum mapping results show that a variety of pedagogical approaches and tools are being used to teach, including an array of technology tools and course activities. They also show that all of the program objectives are being met, despite some objectives not attaining the level of mastery. Areas of future research include obtaining students' perspective on the curriculum. Going-forth, this descriptive curriculum map can be used as a baseline which will allow measuring of the impact of changes to the curriculum.
Program assessment is a critical component of curriculum development within educational institutions. Curriculum mapping is a program assessment technique that can provide insight into how a given program is delivering the intended curriculum and provide a foundation to formulate evidence-based recommendations to enhance/modify the program to address needs, strengthen weak and strong elements, etc. In 2012 the University of Ottawa wrote a review of the Biopharmaceutical Science program. The document provides brief overviews of many aspects of the program such as the program learning outcomes, program structure, program coherence, curriculum and modes of delivery etc. It does not specify how the courses are enacting their curriculum. This study investigates in greater detail which courses are fulfilling the program-learning outcomes; what methods courses are utilizing to deliver the curriculum and engage students, and to what degree the faculty are utilizing the available teaching resources made available to them. This study used a descriptive cross-sectional study design based on the program learning outcomes documented in the 2012 Biopharmaceutical Science Program Review. Data was collected from course syllabi for the 2013-2014 academic year, and from conducting interviews with course educators within the Biopharmaceutical Science program. Results indicate there is sufficient coverage of the program learning outcomes with a small fraction of program learning outcomes exhibiting minimal coverage; later years of study are implementing fewer outside formal lecturing activities; teaching assistants are being utilized mostly as markers; and the majority of courses have course assessments requiring work outside of scheduled class time to complete account for less than 30% of the total course evaluation. These findings can now serve as a foundation to developing changes to the curriculum in order to have the enacted curriculum better reflect the intended curriculum.
21 - Effect of first year biology courses on the students’ understanding, and acceptance of evolution

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Evolution is an underlying theme that unites all fields of biology, and plays a crucial role in the understanding of how, and why life changes over time. Despite its importance, it continues to be the topic, which remains misunderstood by some students, and these have sometimes even ended up in some journal articles. In order to evaluate the impact of undergraduate biology courses on students’ opinions of evolution, a tracking study was initiated that aimed to comprehend how the understanding, acceptance, and perceived importance of evolution changes as students proceed through their undergraduate biology courses at UTM. The Evolution survey was carried out both at the beginning of the first semester (Fall survey), and during the end of the second semester (Spring survey). The Fall survey was taken up by 393 students, while the spring survey was taken by 69 students who even took the Fall survey. The Likert response corresponding to the score of 3, or 4 was considered as a positive response; while a Likert response corresponding to the score of 1, or 2 was considered an unfavourable response. For understanding of evolution, about 74% of the students taking the fall survey had a favourable response (indicated by the Likert response corresponding to the score of 3, or 4) as compared to 78% of the students taking the spring survey; a positive change of 4%. Understanding of evolution that had dichotomous choices instead of Likert scale were thus evaluated separately. The proportion of students who responded positively showed a shift from 87% to 88%. For acceptance of Evolution, the proportion of students who chose a favourable response went down from 89% in the fall survey to 85% in the spring survey. For the category Perceived Importance of Evolution, the proportion of students responding positively dropped from 85% to 84%. Overall, combination of all of the 25 questions indicated that the proportion of students responding positively increased from about 82% to 83.5%. Also, the students who scored under 60% on the first survey, showed improvement when taking the second survey. We also found that the question category, and the time the survey was taken (Fall vs. Spring) had a significant correlation with the response of the students, but the time the survey was taken had no correlation with the total response distribution between various questions types. This longitudinal study will be continued to investigate for any possible shifts in students’ understanding, acceptance, and perceived importance of evolution as they take higher level biology courses.