



7TH ANNUAL

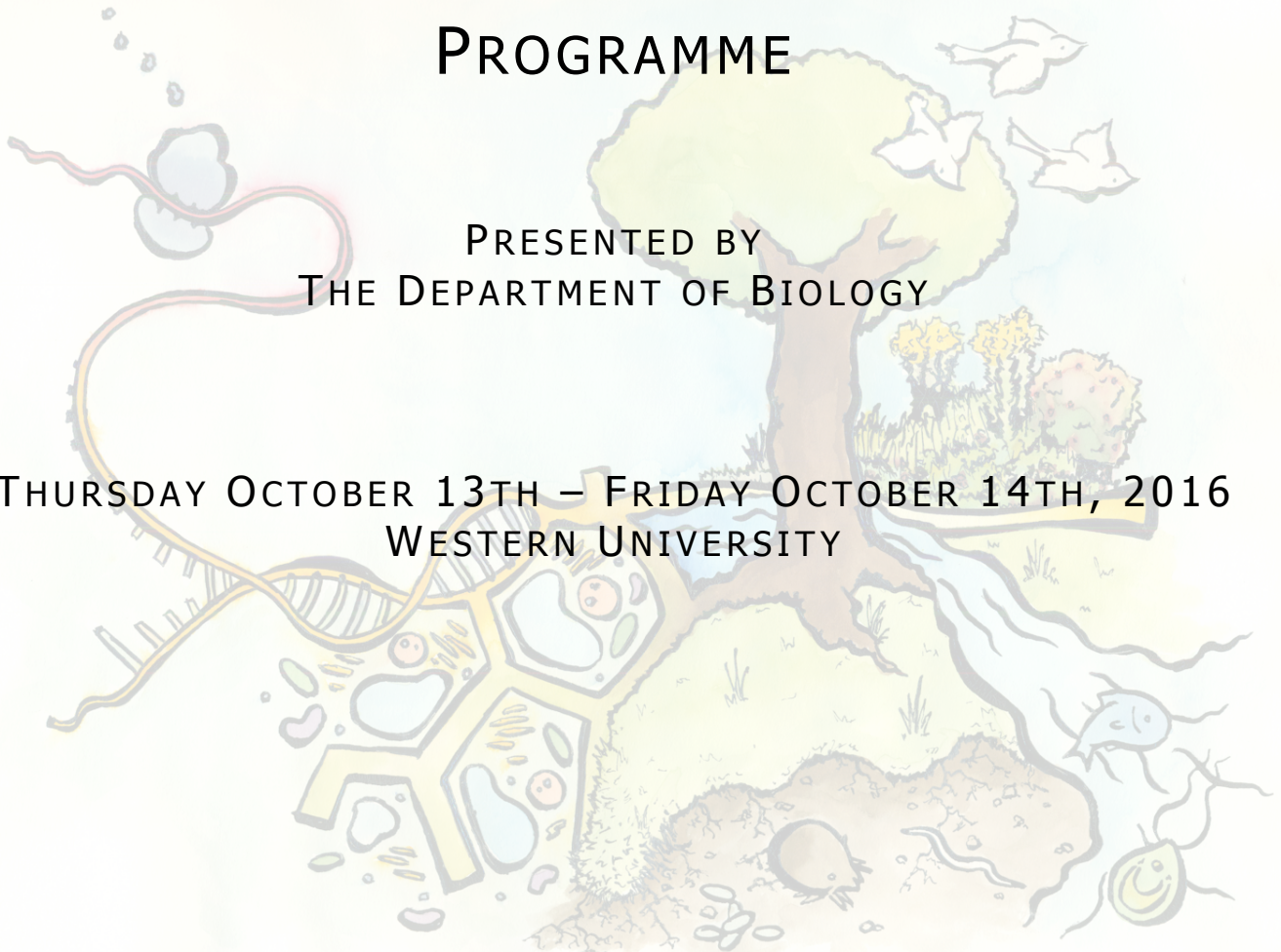
BIOLOGY GRADUATE RESEARCH FORUM



PROGRAMME

PRESENTED BY
THE DEPARTMENT OF BIOLOGY

THURSDAY OCTOBER 13TH – FRIDAY OCTOBER 14TH, 2016
WESTERN UNIVERSITY



Biology Graduate Research Forum 2016 Agenda

Thursday October 13th - Friday October 14th, 2016

Thursday October 13th

- 4:00 – 5:00 pm **Poster setup**
PAB Atrium
- 5:00 – 5:30 pm **Pre-lecture reception**
PAB Atrium
- 5:30 – 5:45 pm **Welcome and Opening Remarks**
Dr. Mark Bernards – Chair, Department of Biology
Matheus Sanita Lima – Chair, BGRF 2016
PAB 148
- 5:45 – 7:00 pm **David Laudenbach Public Lecture**
Dr. Rachael Morgan-Kiss – Associate Professor, Department of Microbiology, Miami University (*introduced by Dr. Norman Hüner – Professor, Department of Biology*)
PAB 148
- 7:00 – 9:00 pm **Post-lecture reception**
Grad club

Friday October 14th

- 8:30 – 9:30 am **Poster setup / Registration**
PAB Atrium
- 9:30 – 11:00 am **Standard talks**
Concurrent sessions – AHB 2B02 & 2B04
- 11:00 - 11:15 pm **Coffee break**
AHB Atrium
- 11:15 – 12:35 pm **Lightning talks**
Concurrent sessions – AHB 2B02 & 2B04
- 12:35 – 1:15 pm **Lunch break**
PAB Atrium
- 1:15 – 2:30 pm **Poster session**
PAB Atrium
- 2:30 – 4:00 pm **Panel discussion**
PAB Atrium
- 4:00 – 5:00 pm **Awards and closing remarks**
PAB Atrium
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Biology Graduate Research Forum 2016 Schedule of Talks

AHB 2B02		10 minute talks – Concurrent session A1	
9:30 – 9:45 am	S1A. Mapping Patterns of Phosphorylation of Proteins Important in <i>Drosophila melanogaster</i> Development Anirban Banerjee		
9:45 – 10:00 am	S2A. Plant-Herbivore Interaction: Dissection of the Cellular Pattern of <i>Tetranychus urticae</i> Feeding on the Host Plant Nicolas Bensoussan		
10:00 – 10:15 am	S3A. <i>MiR156</i> OE improves drought resilience in <i>Medicago Sativa</i> in a SPL13-dependent manner Biruk A. Feyissa		
10:15 – 10:30 am	S4A. Long-term salinity stress leads to attenuation of state transition response in <i>Chlamydomonas</i> spp. Isha Kalra		
10:30 – 10:45 am	S5A. The adaptor protein p66SHC regulates metabolism, ROS production, and Amyloid-beta sensitivity in CNS cells Asad Lone		
10:45 – 11:00 am	S6A. Antarctic <i>Chlamydomonas</i> spp. exhibit differential restructuring of the photosynthetic apparatus in response to iron Gregory Cook		
AHB 2B04		10 minute talks – Concurrent session B1	
9:30 – 9:45 am	S1B. Tracking behavioural and neuronal responses to social pheromones: Insight from a pre-social model Justin Croft		
9:45 – 10:00 am	S2B. Plant traits elucidate ecosystem engineering in peatlands Julia Palozzi		
10:00 – 10:15 am	S3B. Phylogenetic analysis of the <i>Rhodniini</i> tribe (<i>Insecta: Hemiptera: Heteroptera: Reduviidae: Triatominae</i>) Carlos Barreto		
10:15 – 10:30 am	S4B. Chemical composition of preen oil reflects MHC similarity in songbirds Joel Slade		
10:30 – 10:45 am	S5B. Energetics of Migratory Bats during Stopover: A Test of the Torpor-Assisted Migration Hypothesis Dylan Baloun		
10:45 – 11:00 am	S6B. Water-Fat MRI Suggests an Endogenous Rhythm of Brown Adipose Tissue Proliferation in a Hibernator Amanda MacCannell		
AHB Atrium		11:00 – 11:15 am	
11:00 – 11:15 am	Coffee break		

AHB 2B02**Lightning talks – Concurrent session A2**

11:15 – 11:23 am

L1A. Characterizing the genetic basis of behavioural isolation in *Drosophila simulans* using CRISPR/Cas9

Jalina Bielaska Da Silva



11:23 – 11:31 am

L2A. All you need is cryoprotection: Cold tolerance of the Colorado potato "Beetle"

Jacqueline Lebenzon



11:31 – 11:39 am

L3A. The association between oxidative stress and cellular differentiation with upregulation of galectins in HL-60 cells

James Vinnai

11:39 – 11:47 am

L4A. Sequence-function relationships of AROGENATE DEHYDRATASE promoters from *Arabidopsis thaliana*

Emily Cornelius

11:47 – 11:55 am

L5A. Gatekeepers of rhizobia entry: cytokinin-ethylene crosstalk might take us towards nitrogen-fixing crops

Mandana Miri

11:55 – 12:03 pm

L6A. Expression Studies of Human Metallothionein Isoform 2a

Devika Jayawardena

12:03 – 12:11 pm

L7A. The SWI/SNF chromatin remodeling complex is essential in the regulation of *Drosophila* short-term memory

Max Stone

12:11 – 12:19 pm

L8A. Detection of de novo somatic mutations arising with normal development, tumorigenesis and metastasis achieved with cost efficiency and high resolution

Maja Milojevic

12:19 – 12:27 pm

L9A. Detecting arogenate dehydratase activity *in vivo*

Emily Clayton



12:27 – 12:35 pm

L10A. Spirodiclofen resistance in Ontario greenhouse populations of two-spotted spider mite

Hooman H. Namin

AHB 2B04**Lightning talks – Concurrent session B2**

11:15 – 11:23 am

L1B. Thermal tolerances of Arctic spiders

Susan Anthony

11:23 – 11:31 am

L2B. Unravelling organelle genome evolution architecture using RNA-sequencing data

Matheus Sanita Lima

11:31 – 11:39 am

L3B. MHC diversity, parasitism, and olfactory-based mate choice in a migratory songbird

Leanne Grieves

11:39 – 11:47 am

L4B. Frost Stress in an Old Field Plant Community

Curtis Lubbe

11:47 – 11:55 am

L5B. The Genetic and Environmental Basis for CHC Biosynthesis in *Drosophila*

Heather Ward



11:55 – 12:03 pm

L6B. Effect of thiamine deficiency on reproductive traits in three populations of Atlantic salmon

Kimberly Mitchell

12:03 – 12:11 pm

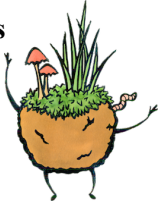
L7B. Vertical distribution of fungi in hollow and hummock of boreal peatlands

Asma Asemaninejad

12:11 – 12:19 pm

L8B. The young progeny of aged parents are less social

Dova Brenman



12:19 – 12:27 pm

L9B. Assessing the long term effects of perceived predation risk on the avian brain

Lauren Witterick

11:27 – 12:35 pm

L10B. Fatal attraction: the volatile influences that will lead whiteflies to deadly encounters and the dsRNA responsible

Kaitlyn Ludba

Oral Presentations – Standard Talks

S1A. Mapping Patterns of Phosphorylation of Proteins Important in *Drosophila melanogaster* Development

Anirban Banerjee, Anthony Percival-Smith

During formation of the anterior-posterior axis, HOX proteins determine the identity of body segments in *Drosophila*. A HOX-derived protein, Fushi tarazu (FTZ), a HOX co-factor, Extradenticle (EXD) and the HOX proteins are transcription factors that regulate target gene expression during development. Besides a highly conserved DNA-binding homeodomain, HOX proteins also contain other conserved motifs called Short Linear Motifs (SLiMs) whose sequences when altered have an effect on overall HOX activity. SLiMs are proposed to be sites of phosphorylation and this is thought to regulate the activity of HOX proteins. The primary aim of this work is to develop a comprehensive, unbiased catalogue of the phosphorylation sites for FTZ, EXD and all HOX proteins extracted from developing *Drosophila melanogaster* embryos. Then, the hypothesis that HOX SLiMs are sites of phosphorylation will be tested by analyzing whether SLiMs are phosphorylated and whether SLiMs are preferential sites of HOX phosphorylation. The *Drosophila* embryos were transformed with the triple-tagged Hox cDNAs by P-element mediated transformation and multiple germ-line transformant fly lines were established. As controls, it was shown that the heat-shock ectopic expression system produces more tagged protein than the traditional GAL4-UAS system and that the tagged HOX proteins are biologically active. Heat-shocked embryos were collected and purified under denaturing conditions using Nickel beads which have affinity towards the His tag. Tagged SCR purified from embryos was successfully detected using MS/MS and few phosphates were also mapped which needs further confirmation. This will be extended to other HOX proteins too.

S2A. Plant-Herbivore Interaction: Dissection of the Cellular Pattern of *Tetranychus urticae* Feeding on the Host Plant

Nicolas Bensoussan, Vojislava Grbić

The two-spotted spider mite, *Tetranychus urticae* Koch (*Acari: Tetranychidae*), is one of the most polyphagous herbivores feeding on cell contents of over 1100 plant species including more than 150 crops. It is being established as a model for chelicerate herbivores with tools that enable tracking of reciprocal responses in plant-spider mite interactions. However, despite their important pest status and a growing understanding of the molecular basis of interactions with plant hosts, knowledge of the way mites interface with the plant while feeding and the plant damage directly inflicted by mites is lacking. Here, utilizing histology and microscopy methods, we uncovered several key features of *T. urticae* feeding. By following the stylet path within the plant tissue, we determined that the stylet penetrates the leaf either in between epidermal pavement cells or through a stomatal opening, without damaging the epidermal cellular layer. Our recordings of mite feeding established that duration of the feeding event ranges from several minutes to more than half an hour, during which time mites consume a single mesophyll cell in a pattern that is common to both bean and *Arabidopsis* plant hosts. In addition, this study determined that leaf chlorotic spots, a common symptom of mite herbivory, do not form as an immediate consequence of mite feeding. Our results establish a cellular context for the plant-spider mite interaction that will support our understanding of the molecular mechanisms and cell signaling associated with spider mite feeding.

S3A. MiR156 OE improves drought resilience in *Medicago Sativa* in a SPL13-dependent manner

Biruk A. Feyissa, Susanne E. Kohalmi, Abdelali A. Hannoufa

Climate change has resulted in more frequent extreme weather conditions causing major damage to crop productivity. Plants respond to these changes (abiotic stress) by developing different resilience mechanisms, such as phenotypic and/or gene level strategies. Being a forage crop and food supplement for humans, *Medicago sativa* L. (alfalfa) shares the same threats to its productivity. Recently, our research group reported enhanced vegetative yield in alfalfa by over expressing MicroRNA 156 (miR156-OE) that down-regulates seven SQUAMOSA-PROMOTER BINDING PROTEIN-LIKE (SPL) genes. In this study, I used three miR156-OE and MsSPL-6 & 13 RNAi genotypes under drought conditions at the juvenile vegetative phase. LC-ddMS2- and GC-MS-based metabolic profiling, as well as qRT-PCR- based transcript analyses were used to understand the response of miR156-OE plants to drought stress. Down-regulation of SPL13 expression, and moderately increasing miR156 enhanced secondary metabolite accumulation and associated gene transcripts, such as PHENYLALANINE AMMONIA-LYASE, DIHYDROFLAVONOL-4-REDUCTASE, MYB transcription factor Myb112, FLAVONOID GLUCOSYLTRANSFERASE2. Moreover, photosynthesis assimilation rate and efficiency were increased in accordance with leaf chlorophyll content, opened stomatal conductance and midday leaf water potential. In line with this, expression of photosynthesis-associated genes were also increased, including Photosystem I p700 chlorophyll A appoprotein APS I and Photosystem II Q (b) protein. Taken together, we conclude that a moderate increase in miR156 expression enhances drought resilience by modulating a network of genes and secondary metabolites.

S4A. Long-term salinity stress leads to attenuation of state transition response in *Chlamydomonas* spp.

Isha Kalra, Rachael Morgan-Kiss

The ability and efficiency to utilize light energy defines survival and productivity of all photosynthetic organisms. Plants and algae rely on numerous mechanisms to maintain energy balance. For example, light harvesting capacity increases in the presence of low light environment, while photoprotective mechanisms are activated under high light or high excitation pressure. In plants and algae, including the model green alga, *Chlamydomonas reinhardtii*, state transitions is major mechanism to counter high excitation pressure by redistributing energy from photosystem II to photosystem I (PSI) by phosphorylation of LHCII proteins. The Antarctic psychrophilic *Chlamydomonas* sp. UWO241, is a natural state transition variant which does not show the state transition response. Its native habitat is hypersaline (Lake Bonney, McMurdo Dry Valleys), thus consequently UWO241 is halotolerant. Recently we isolated a second psychrophilic alga from the shallow layers of Lake Bonney, *Chlamydomonas* sp. ICE-MDV. This alga is dominant in shallow layers of the lake that has low salinity. Interestingly this species exhibits normal state transition response when exposed to high light or chemical inhibitors. We hypothesize that adaptation or acclimation to long-term salinity stress attenuates state transition response across all strains. To test our hypothesis we acclimated *C. reinhardtii*, *C. sp. ICE-MDV* and *C. sp. UWO241* to high salt stress and measured their state transition response under high light stress and chemical inhibitors for the response. As predicted, low temperature chlorophyll fluorescence revealed that state transitions were also attenuated in *C. sp. ICE-MDV* and *C. reinhardtii*. Last, all strains acclimated to high salinity exhibited increased PSI-associated cyclic electron flow.

S5A. The adaptor protein p66SHC regulates metabolism, ROS production, and Amyloid-beta sensitivity in CNS cells

Asad Lone, Robert Cumming

A key pathological feature of Alzheimer's disease (AD) is the accumulation of extracellular deposits of amyloid-beta (A β) peptide within the brains of affected individuals. A β accumulation is associated with oxidative stress, neuronal death, and synaptic loss. However, 40% of the elderly have pronounced A β deposition within their brains, yet show no symptoms of dementia, indicating that some cells are resistant to A β toxicity. Several studies suggest that central nervous system (CNS) cells that are resistant to A β toxicity display a metabolic shift from mitochondrial-dependent oxidative phosphorylation (OXPHOS) to aerobic glycolysis. The adaptor protein p66SHC has been shown to play a definitive role in aging, as well as in regulation of redox balance and ROS levels. Recent studies have shown that p66SHC expression and activation can shift the cellular metabolic state from OXPHOS to aerobic glycolysis. Hence, we propose that the expression and activation of p66SHC in CNS cells promotes both increased OXPHOS and sensitivity to A β toxicity. Transient overexpression of p66SHC in a rodent neuronal cell line repressed glycolytic enzyme expression and increased mitochondrial ETC activity and ROS levels. The opposite effect was observed when endogenous p66SHC expression was knocked down in a rodent glial cell line. Exposure to A β promoted the activation of p66SHC, resulting in an upregulation of mitochondrial metabolism. Moreover, expression and activation of p66SHC increased sensitivity to A β toxicity. Our findings indicate that expression and activation of p66SHC renders CNS cells more sensitive to A β toxicity by promoting mitochondrial OXPHOS while repressing aerobic glycolysis. Thus, p66Shc may represent a therapeutically relevant target for the treatment of AD.

S6A. Antarctic *Chlamydomonas* spp. exhibit differential restructuring of the photosynthetic apparatus in response to iron

Gregory Cook, Rachael Morgan-Kiss

Although iron is the fourth most abundant element on Earth, most resides in a form unavailable for biological use or is often chronically limited, particularly in aquatic environments. Iron is an essential nutrient for all life forms; however, plants and algae have a high requirement for iron due to its abundance within chloroplasts. Photosynthetic protein complexes essential in the process of converting light into chemical energy, specifically photosystem I (PSI) and ferredoxin, utilize iron in oxidation-reduction reactions. As such, iron deficiency targets PSI relative to photosystem II (PSII) in the model alga *Chlamydomonas reinhardtii*. Early work on the Antarctic lake alga *Chlamydomonas* sp. UWO241 revealed that this extremophilic phototroph exhibits a permanent phenotype in iron-replete growth medium, which superficially resembles iron deficiency (i.e. downregulation of PSI). We hypothesized that adaptation to permanent iron deficiency in its native environment may contribute to this unusual phenotype. Here we report our findings on the effect of iron availability on the physiology and photobiology of the psychrophilic *Chlamydomonas* sp. UWO241, the model *C. reinhardtii* and a newly isolated Antarctic psychrophile, *Chlamydomonas* sp. ICE-MDV.

S1B. Tracking behavioural and neuronal responses to social pheromones: Insight from a pre-social model

Justin Croft, Graham Thompson and Alison Camiletti

Social insects often communicate reproductive roles through pheromones. For example, in colonies of European honey bees, drones and workers cue their reproductive behaviour from queen mandibular pheromone (QMP). Virgin queens that emit QMP attract drones with which to mate. Mated queens, by contrast, use QMP to attract workers with whom she cooperates to raise offspring. Studies in the Social Biology Group at Western University suggest that this reproductive signal may not be limited to conspecific recipients, but may elicit a comparable response from non-social insects, including *Drosophila melanogaster*. Remarkably, QMP seems to de-activate female ovaries, as it does in workers. QMP may also accelerate mating effort by males, as it normally does with drones. In the present study, I build on these bee-fly comparisons to test if male or female flies are positively attracted to volatile QMP, and further use the fly model to map the neural receptors that mediate this behavioural response. Results from a T-maze assay indicate that both sexes are attracted to QMP, suggesting that the physiological effects of bee pheromone on flies is not strictly pharmacological but are potentially functional. Moreover, I have established a nuclear factor activated T-cell (NFAT) fly line that will permit the fluorescent staining of specific neurons activated by QMP. My predominant goal is to exploit the fly model to map olfactory circuitry that coordinates social communication in honey bees.

S2B. Plant traits elucidate ecosystem engineering in peatlands.

Julia Palozzi, Zoë Lindo

Ecosystem engineers are organisms that have disproportionate effects on their environment given their abundance. Ecosystem engineers modulate the availability of resources to other species through changes to biotic or abiotic materials, which can cause an increase or decrease in species diversity. Peatlands are functionally important ecosystems acting as significant stores of carbon due to slow decomposition rates driven by cool and moist conditions and nutrient-poor plants. As peat is partially decomposed plant material, belowground peat properties are governed by aboveground plant species composition. Sphagnum mosses have always been hypothesized to be ecosystem engineers, but links to ecosystem-level processes such as decomposition rates remain to be established. My work uses a plant functional trait approach, linking aboveground plant traits to belowground spectral organochemical properties of peat that are indicators of decomposition. I demonstrate that both moss and sedge species play important roles as ecosystem engineers in their respective peatland type.

S3B. Phylogenetic analysis of the *Rhodniini* tribe (*Insecta: Hemiptera: Heteroptera: Reduviidae: Triatominae*)

Carlos Barreto, Alexandre Silva de Paula

“It is most disgusting to feel soft winged insects, about an inch long, crawling over one's body” (Charles Darwin, Voyage of the Beagle). The *Rhodniini* tribe (*Heteroptera: Reduviidae: Triatominae*) are small winged insects considered for their hematophagous habit (blood-sucking) and potential transmission of *Trypanosoma cruzi*. In Brazil, information about these important disease vectors is limited. The tribe is comprised of two genera, each proposed as a monophyletic group by Pinto (1962). However, recent evidence has questioned the validity of these two genera. I present a phylogenetic analysis of 18 species from South and Central America using morphologic and molecular 16S rDNA data; two species, *Dipetalogaster maximus* (*Triominini* tribe) and *Reduvius personatus* (*Reduviinae*) were used as outgroups. My results strongly suggest that the two genera *Psammolestes* and *Rhodnius* are not monophyletic groups, and should be considered as a single genus (*Rhodnius*). This work contributes to the knowledge of distribution and identification of *Rhodniini* which can aid Brazilian public health decisions.

S4B. Chemical composition of preen oil reflects MHC similarity in songbirds

Joel Slade, Matthew J. Watson, Tosha R. Kelly, Gregory B. Gloor, Mark A. Bernards, and Elizabeth A. MacDougall-Shackleton

In jawed vertebrates, genes of the major histocompatibility complex (MHC) play a key role in immunity by encoding cell-surface proteins that recognise and bind non-self antigens. High variability at MHC suggests that these loci may also function in social signalling such as mate choice and kin recognition. This requires that MHC genotype covaries with some perceptible phenotypic trait. In mammals and fish, MHC is signalled chemically through volatile and nonvolatile peptide odour cues, facilitating MHC-dependent mate choice and other behaviours. In birds, despite evidence for MHC-dependent mating, candidate mechanisms for MHC signalling remain largely unexplored. However, feather preen oil has recently been implicated as a potential source of odour cues. We examined whether the chemical composition of preen oil correlates with MHC class IIB genotypes of wild song sparrows (*Melospiza melodia*). Pairwise chemical distance reflected amino acid distance at MHC for male-female dyads, although not for same-sex dyads, and chemical diversity did not reflect MHC diversity. We used gas chromatography-mass spectrometry (GC-MS) to characterize preen oil compounds, and identified four wax esters that best reflect MHC similarity. Provided songbirds can detect variation in preen oil composition, this cue may allow individuals to assess MHC similarity and compatibility of potential mates.

S5B. Energetics of Migratory Bats during Stopover: A Test of the Torpor-Assisted Migration Hypothesis

Dylan Baloun, Chris Guglielmo

The torpor-assisted migration hypothesis posits that migratory bats use torpor during daytime roosting to minimize refueling requirements and preserve fuel stores for nocturnal flights. Field studies indicate that bats regulate body temperature and time in torpor so that daily energy expenditure is independent of ambient roosting temperature. However, direct measurements of total roosting energy expenditure in relation to ambient and body temperature are lacking. Our objective was to measure full-day body composition change and energy expenditure of bats roosting at different temperatures to test the prediction of the torpor-assisted migration hypothesis that fat and energy use by bats is independent of ambient roosting temperature. We further tested whether torpor use is affected by migration season, sex and age. We predicted that bats would use less fat during the spring than the fall, on account of the colder spring weather, especially in females that are gestating and facing imminent lactation. We predicted that juvenile bats would use more torpor than adults in the fall to ensure sufficient fat stores for migration. We captured silver-haired bats (*Lasionycteris noctivagans*) at Long Point Bird Observatory, Long Point, Ontario. We used quantitative magnetic resonance analysis to measure change in fat and lean mass and to calculate total energy expenditure during roosting at 10, 17, 25 degrees C for 12 hours (the length of a daytime stopover). Body temperature was monitored with radio-transmitters. This study will test predictions of the torpor-assisted migration hypothesis and further our understanding of energy management at stopovers for migratory bats species.

S6B. Water-Fat MRI Suggests an Endogenous Rhythm of Brown Adipose Tissue Proliferation in a Hibernator

Amanda MacCannell, Kevin Sinclair, Lanette Friesen-Waldner, Charles McKenzie, and James Staples

Hibernating mammals spend most the winter torpid with body temperatures near 5°C. Individual bouts of torpor last for several days and are interrupted spontaneously by arousal periods during which body temperature increases to approximately 37°C in just a few hours. During these arousals brown adipose tissue (BAT) is the primary source of heat production. In non-food-caching hibernators, including ground squirrels, body mass and white adipose tissue proliferation are controlled by an endogenous rhythm, allowing animals to store food energy to fuel the hibernation season. The seasonal rhythms of BAT quantity are less well studied. In non-hibernating eutherians, BAT proliferation requires acclimation to cold temperatures. In hibernators, however, BAT genes related to thermogenesis are upregulated in autumn, even when animals are housed at warm temperatures. We predicted that the total volume of BAT would also increase as the hibernation season approached, even in the absence of cold acclimation. We used water-fat MRI to measure total BAT volume in ground squirrels, housed at 23°C, at intervals of approximately 10 days from late spring until hibernation began in late autumn. During that period BAT volumes increased significantly from 0.59% to 4.44% of total body volume. Moreover the proportion of the MRI signal related specifically to lipid in BAT decreased over that period, suggesting a relative increase in BAT water content. Our data demonstrate that BAT quantity and, probably, mass-specific thermogenic capacity, increase in hibernators without cold acclimation. This raises the possibility that BAT function and amount are also controlled by an endogenous rhythm.

Oral Presentations – Lightning Talks

L1A. Characterizing the genetic basis of behavioural isolation in *Drosophila simulans* using CRISPR/Cas9

Jalina Bielaska Da Silva, Amanda J Moehring

Behavioural isolation is a prezygotic mechanism that keeps two different species reproductively isolated from each other due to differences in courting and mating behaviour. This form of reproductive isolation is usually determined by female preference, such as the rejection-like behaviour exhibited by *Drosophila simulans* females to *D. melanogaster* males. Though female rejection behaviour has been characterized, the genes that contribute to this behaviour are still largely unknown. In order to confirm the genetic basis of behavioural isolation, CRISPR/Cas9 will be used to disrupt a gene, previously linked to female rejection behaviour, in both *D. melanogaster* and *D. simulans*. This will allow for the formation of two *D. melanogaster/D. simulans* hybrids, one with the *D. melanogaster* allele disrupted and one with the *D. simulans* allele disrupted. A reciprocal hemizygoty test will then be used to score the behavioural phenotype of the hybrid females. This experimental approach will confirm the genetic basis of female rejection behaviour, helping to bridge the understanding of speciation at the molecular level.

L2A. All you need is cryoprotection: Cold tolerance of the Colorado potato "Beetle"

Jacqueline Lebenzon, Brent Sinclair

Overwintering insects risk freezing of their body fluids when exposed to temperatures below zero. By lowering their supercooling points (SCP; temperatures at which they would normally freeze), some insects are able to avoid freezing altogether. Lower SCPs are often correlated with the accumulation of small cryoprotectants (such as polyols or amino acids) via fat body metabolism. Despite the importance of cryoprotectants on the overwinter survival of insects, the extent to which cryoprotectants increase cold tolerance still remains unclear. Using the Colorado potato beetle (*Leptinotarsa decemlineata*; CPB), I investigated the role of cryoprotectants in freeze-avoidant insects. First, I used molecule-specific spectrophotometric assays and quantitative direct injection mass spectrometry to identify putative cryoprotectants in cold-tolerant CPB. Having identified possible cryoprotectants, I then used quantitative PCR to identify metabolic enzymes involved in cryoprotectant synthesis that are transcriptionally up regulated in cold-tolerant CPB. With cryoprotectant molecules and their matched metabolic enzymes as targets, I plan on manipulating enzyme mRNA abundance of up regulated target enzymes using RNA interference. I predict that knocking down mRNA abundance of metabolic enzymes (and therefore decreasing whole animal concentrations of cryoprotectants) will decrease cold tolerance of CPB. These results will help us understand the link between cryoprotectants, supercooling capacity, and increased cold tolerance in insects.

L3A. The association between oxidative stress and cellular differentiation with upregulation of galectins in HL-60 cells.

James Vinnai, Alexander Timoshenko

Galectins are a group of β -galactoside binding proteins that are involved in different cellular processes including stress responses and differentiation. The specific role of differential galectin expression across many tissues and cell types has not been fully characterized. To examine the role of galectins we used a model cell line HL-60, which is easily differentiated into neutrophil-like cells and express stress-sensitive galectins. I hypothesize that oxidative stress sensitive galectins are mediators for HL-60 cell differentiation. Dimethyl sulfoxide-induced differentiation and menadione-induced oxidative stress promoted upregulation of galectins-1, -3 and -10. Moreover, menadione treatments in combination with antioxidant N-acetylcysteine rescued control expression levels but only partially rescued galectin expression mediated by the dimethyl sulfoxide treatment. Interestingly, menadione treatment decreased LGALS9 expression whereas dimethyl sulfoxide treatment reduced LGALS12 expression. OTX008 and thiodigalactoside decreased cell proliferation and inhibited cell differentiation. While oxidative stress showed a trend toward enhanced HL-60 cell differentiation, N-acetylcysteine significantly attenuated it. Treatment with 5-aza-2'-deoxycytidine increased expression of LGALS1, LGALS3, LGALS10 and LGALS12. JNK signaling is increased during oxidative stress while decreased during neutrophilic differentiation. Finally, JNK activation increased galectin transcript expression while inhibition of this pathway decreased galectin expression. Modification of the cellular redox environment of HL-60 cells during differentiation potentially impacts galectin expression resulting in either enhanced or diminished levels of differentiation. DNA methylation and JNK signaling represent regulatory mechanisms for galectin expression that may be, in part, present during cellular stress responses, considering manipulation of these regulatory mechanisms also produced similar galectin expression profiles.

L4A. Sequence-function relationships of AROGENATE DEHYDRATASE promoters from *Arabidopsis thaliana*

Emily Cornelius, Susanne Kohalmi

The phenylpropanoid pathway is among the most important secondary metabolic pathways in plants, as it allows the synthesis of lignins, pigments and defense compounds. The precursor is phenylalanine (Phe), an aromatic amino acid synthesized only by bacteria, fungi and plants. The final step of Phe synthesis in plants is catalyzed by the enzyme arogenate dehydratase (ADT). The *Arabidopsis thaliana* genome encodes six ADTs, annotated ADT1 to ADT6. It is known that ADTs are differentially expressed during different developmental stages and when grown under different environmental conditions, suggesting unique roles for each ADT. Different gene expression levels suggest that ADTs are transcriptionally regulated, and since promoters play a key role in initiating transcription, this research focuses on ADT promoters. The first objective was to identify predicted or known regulatory elements present in each ADT promoter and categorize them based on their predicted function. Not surprisingly, a large number of elements are related to stress response and development, complementing the evidence that ADTs are differentially regulated during these situations. The second objective is to clone each ADT promoter into a vector 5' to eGFP and GUS to create ADT-GFP/GUS promoter sequences that will be introduced into the *Arabidopsis* genome using *Agrobacterium*-mediated stable transformations. This will allow an in planta analysis of ADT expression in all tissues under various growth conditions. Not only is this research an excellent opportunity to study sequence-function relationships for the regulation of expression in a small gene family, but also has potential applications in crop biotechnology.

L5A. Gatekeepers of rhizobia entry: cytokinin-ethylene crosstalk might take us towards nitrogen-fixing crops

Mandana Miri, Krzysztof Szczyglowski

Like animals, plants produce a number of substances and hormones that coordinate growth and development. Understanding how hormones interact to coordinate plant growth is a major challenge in developmental biology. Leguminous plants particularly thrive under nitrogen-limited conditions because of their ability to develop a specialized symbiotic organ on their roots, the root nodule, in response to rhizobial infection. The signaling pathways for nodule development are divided into two major events, rhizobial infection (epidermal program) and nodule organogenesis (cortical program). Cytokinin signaling is one of the key endogenous signals in the inception of root nodule organogenesis. In the model legume *Lotus japonicus*, one of the key processes in nodule organogenesis is mediated by the Lotus Histidine Kinase (LHK) cytokinin receptors. However, the role of cytokinin in mediating rhizobial entry into roots is less clear. Our data indicate that the cytokinin-dependent signaling events which promote the development of infection threads in the cortex also appear to stimulate a negative feedback mechanism that restricts subsequent infections at the root epidermis. The feedback loop presumably is the result of cytokinin-ethylene crosstalk. As the rate-limiting step in ethylene biosynthesis is mediated by ACC synthase (ACS), we hypothesize that increased cytokinin activity in the root epidermis, enhances the ACS activity. This is presumed to elevate the ethylene level, which subsequently inhibits bacterial infection. By using a combined approach involving reverse genetic and expression analyses the role of cytokinin-ethylene crosstalk in regulating the extent of bacterial infection in legume plants was further investigated.

L6A. Expression Studies of Human Metallothionein Isoform 2a

Devika Jayawardena, Martin Stillman

Acute metal toxicity is easily diagnosed by a patient's symptoms. However, chronic low-level exposure to toxic metals cannot be easily identified until later in life, when the damage has already been done. Most toxic metals such as mercury (Hg), cadmium (Cd), lead (Pb), and arsenic (As) are sulfhydryl-reactive metals, which bind to the sulfhydryl groups of the proteins and disrupt their function. One such metal binding protein that has been shown to bind to metals is human liver metallothionein (MT), which forms metal-thiolate complexes. MT protects other proteins from dysfunction as well as binding to essential metals like zinc (Zn) and copper (Cu). Human MT2a (the predominant isoform in livers) is a very difficult protein to express in *E. coli*. My research is being carried out to determine the optimal growth conditions to make *E. coli* express the maximum yield of MT2a and to investigate how Zn being displaced by As, when it is bound to MT2a, in vitro.

L7A. The SWI/SNF chromatin remodeling complex is essential in the regulation of *Drosophila* short-term memory.

Max Stone, Jamie Kramer

The SWI/SNF ATP-dependent chromatin remodeling complex has been identified through gene ontology analyses as the most enriched protein complex amongst all genes implicated in the dominant genetic forms of intellectual disability (ID). Despite these implications, most studies on the SWI/SNF complex have focused on its role in differentiation and tumor suppression. In my research, I systematically investigate the role of this highly conserved protein complex in memory, using *Drosophila* as a model system. *Drosophila* is an excellent model due to the transgenic techniques and established behavioural assays available. I use the UAS-Gal4 system with RNAi technology to perform cell-type-specific knockdown of individual SWI/SNF genes in the mushroom body, which is the memory centre of the fly brain. Knockdown flies are tested for short-term memory using courtship conditioning, an established memory assay in flies. From these experiments, six of the 15 SWI/SNF complex genes were identified as essential genes in the formation of short-term courtship memory, while seven more genes have been identified as candidates. This is the first systemic analysis of the SWI/SNF complex in the context of learning and memory. These results demonstrate that SWI/SNF plays a critical role in the regulation of neurological processes, and have identified genes and phenotypes that should be further studied in order to determine the specific role of SWI/SNF-mediated gene regulation in complex brain function. Due to the high level of conservation between flies and humans, these results provide essential steps in understanding the role of genes involved in SWI/SNF-associated forms of ID.

L8A. Detection of de novo somatic mutations arising with normal development, tumorigenesis and metastasis achieved with cost efficiency and high resolution

Maja Milojevic, MEO Locke, C Tolg, AK Edge, M Daley, E Turley, KA Hill

New appreciation for the prevalence of somatic mosaicism is due to technological advances and exquisite experimental designs. The Mouse Diversity Genotyping Array (MDGA) contributes cost-effective and high-throughput assessment of copy number variant (CNV) and single nucleotide polymorphism (SNP) diversity. We applied this technology in a C57BL/6J mouse “parents-plus-sons” experimental design with multiple tissues sampled from each individual to obtain a baseline for mosaicism arising with development. We identified tissue-specific differences in de novo mutations and putative programmed deletions arising in certain tissues. We also examined de novo genetic diversity between tumor and metastatic tissue within an individual. CNVs and SNPs were identified in 12 primary mammary tumours and metastatic lung samples, from six MMTV-PyMT mice. Three mice also had a Rhamm knockout genotype which we have shown increases the number of small deletions in primary tumours. CNV occurrence is elevated across all cancer samples and with greater inter-mouse variation and more deletions, compared to CNV profiles observed with normal development. Primary tumour samples have more inter-animal variability in CNV incidence than do metastasis samples. On average, RHAMM^{-/-} primary tumours have 15-fold more CNVs than observed with normal tissue development. The difference in SNP heterozygosity between primary tumors and metastatic tissue ranges from 2,754 to 18,829 loci. In contrast, the difference is 739 to 4,590 loci in pairwise comparisons of normal tissues within a mouse. The MDGA approach to tracking in vivo somatic mosaicism with normal development, tumorigenesis and metastasis is successful in providing quantitative and qualitative assessments of somatic mosaicism.

L9A. Detecting arogenate dehydratase activity in vivo

Emily Clayton, Susanne Kohalmi

Phenylalanine (Phe) is an essential amino acid that can be synthesized through two pathways: the arogenate and the prephenate pathway. The prephenate pathway involves converting prephenate to phenylpyruvate in a decarboxylation/dehydration reaction by a prephenate dehydratase (PDT), followed by a transamination of phenylpyruvate to Phe by a phenylpyruvate aminotransferase (PPAT). The arogenate pathway requires the transamination of prephenate to arogenate by a prephenate aminotransferase (PAT), then a decarboxylation/dehydration of arogenate to Phe by an arogenate dehydratase (ADT). ADTs and PDTs catalyze the same type of reaction and are very similar in sequence. PDT activity can be easily determined in vivo using a yeast complementation test in the PDT knockout *Saccharomyces cerevisiae pha2* strain. There currently is no in vivo test for ADT activity, and biochemical assays are problematic as the substrate of an ADT, arogenate, cannot be purchased. We have developed a method to detect ADT activity in vivo. ARO8 and ARO9 encode the two *S. cerevisiae* PPATs required for Phe synthesis via the prephenate pathway. Mating single knockout strains and sporulating the diploid generated a haploid double knockout strain. As predicted, the Δ aro8 Δ aro9 knockout is Phe requiring. This yeast strain will be transformed with an AtPAT to introduce the arogenate pathway. In the presence of a PAT, an ADT will complete the pathway to synthesize Phe in this yeast strain. This assay is in the same genetic background as the PDT complementation assay currently in use, and will be the only in vivo test of ADT activity.

L10A. Spirodiclofen resistance in Ontario greenhouse populations of two-spotted spider mite

Hooman H. Namin, Ian Scott, Vojislava Grbic, Miodrag Grbic

Two-spotted spider mite, *Tetranychus urticae* (Koch) is a major agricultural pest, feeds on over 1100 plant species and causes considerable yield losses in field and greenhouse crops. Although application of synthetic acaricides remains the main method for global mite control, *T. urticae* has developed resistance towards many registered acaricides (currently 93 acaricides). This arthropod develops resistance against a novel pesticide within two to four years, and is considered as one of the most resistant arthropod pest worldwide. In recent years many research efforts have focused on determining the mechanisms of acaricide resistance as an essential part of effective integrated pest management. Spirodiclofen belongs to the acaricidal group of spirocyclic tetronic acid derivatives that disrupts lipid biosynthesis by direct inhibition of acetyl coenzyme A carboxylase (ACCase). Spirodiclofen is mainly effective against all developmental stages of spider mites with a strong effect on female fecundity and fertility. This acaricide adheres to the waxy cuticle of leaf surface, and is one of the most active commercialized contact acaricides to control most of the economically important mite species. However, resistance to Spirodiclofen in *T. urticae* can be developed by insensitivity at the target site due to point mutations, or increased activity of major detoxification enzymes including esterases, P450 monooxygenases and glutathione-S-transferases. The objective of this research is to investigate the key enzymes in detoxification pathways of Spirodiclofen, and to identify the genes involved in Spirodiclofen resistance mechanism in *T. urticae*.

L1B. Thermal tolerances of Arctic spiders

Susan Anthony, C. M. Buddle, T. T. Hoye, N. Hein and B. J. Sinclair

Spiders are dominant arthropods predators in the Arctic. At such high latitudes, spiders and other ectotherms are subjected to many months of winter when temperatures are well below zero (c. -60C). To cope with such low temperatures, some ectotherms become tolerant of freezing (ex. wood frog), whereas most other ectotherms adjust their physiology to prevent freezing, and many ectotherms seeking snow buffered microhabitats (Tair= c. -13C). However, we do not know much about Arctic spiders, and how they cope with winter. This is of particular importance as most climate change models predict increases in yearly temperatures, as well as reductions in snow cover, in the coming century. My PhD research will focus on the thermal tolerances of Arctic spiders (their supercooling point, SCP, critical thermal maximum, CTmax, and their cold tolerance strategies). Thus far, I have collected data from field fresh species of the genus *Pardosa* from the Yukon, Greenland, as well as those acclimated to warmer (20C) and cooler (4C) temperatures. My studies have concluded that lab-acclimated and summer field fresh individuals have similar SCPs (c. -7C), and are therefore incapable of surviving winter without physiological adjustment. I therefore propose to continue my research by measuring SCP and low temperature physiology on spiders acclimatized to an Arctic winter, to elucidate their winter strategy, and further discover their underlying mechanism of low temperature survival.

L2B. Unravelling organelle genome evolution architecture using RNA-sequencing data

Matheus Sanita Lima, David Smith

Mitochondria and plastids genomes are extremely diverse in size. Mitochondria genomes vary from 11 Mb to 6 kb, while plastids can vary from 1 Mb to 30 kb. Non-coding DNA (intergenic and intronic regions) accounts for most of this size variation, but the mechanistic and evolutionary reasons for that are still unknown. Next generation sequencing has generated unprecedented amounts of genomic and transcriptomic data (DNA and RNA reads) that can be used for organelle genome evolution studies. However, most of these data is used only for the study of cell nucleus, being the organelle reads even discarded in such investigations. Therefore, I decided to use this untapped data source to investigate the transcription of organelle genomes in plastid-bearing protists. I mapped the transcriptomes over the genomes of 116 protist species to verify what is transcribed and what it is not. 77 out of 116 species had their organelle genomes nearly entirely (> 90%) recovered from transcripts. These genomes come from diverse protists and vary immensely in size and structure. Therefore, RNA-seq data generated for cell nucleus studies can be used to investigate organelle genome transcription. Even though organelle genomes can exhibit large portions of non-coding DNA, these regions are still actively transcribed and might play a role in post-transcription regulation. In this talk, I will give an overview of the state of the art of organelle transcriptomics, argue how RNA-seq can be used to explore this field and speculate how transcription can interfere in the genome size evolution.

L3B. MHC diversity, parasitism, and olfactory-based mate choice in a migratory songbird

Leanne Grieves, Elizabeth A. MacDougall-Shackleton

The major histocompatibility complex (MHC) is a highly polymorphic gene family that is crucial to the vertebrate immune system. MHC diversity is maintained largely by pathogen-mediated selection and, as beneficial mate choice decisions are important to reproductive success, sexual selection should favour the ability to assess MHC. In birds, chemical communication has been largely overlooked but MHC genotype can be assessed via olfaction in other taxa. Most birds secrete preen oil for feather maintenance. This oil also contains volatile compounds. There is a positive link between MHC-genotype and preen oil composition, but whether birds use this information to assess potential mates is unknown. High MHC allelic diversity has also been linked to disease resistance. Preen odour thus provides a compelling potential mechanism for both MHC-based mate choice and disease avoidance. To assess MHC-based mate choice, I will design choice trials to test whether birds prefer MHC-dissimilar over MHC-similar individuals of the opposite sex. Odour cues can also be used to detect and avoid sick conspecifics. In birds, the MHC is vital to the immune response against avian malaria. I will test whether preen odour changes with infection status by comparing preen oil from captive birds pre- and post- malaria infection. I will conduct additional choice trials to test whether birds avoid preen odour from infected individuals. Chemical communication in birds may be more common than previously believed and my PhD research could shift our perspective on sexual selection, mate choice, and communication in birds.

L4B. Frost Stress in an Old Field Plant Community

Curtis Lubbe, Hugh Henry

Frost is a major stress that greatly impacts the distribution of plant species. Herbaceous species can only survive areas with regular frost if they can avoid or tolerate freezing stress. Many plants avoid freezing stress by placing buds at or below ground level where they are insulated by snow, litter, or soil. Although it can protect, increased depth may have a cost when frost stress is absent; deeper placement may delay growth and put plants at a competitive disadvantage relative to their neighbours. To explore this tradeoff, I conducted a snow removal experiment in a self-assembled field community, examined by species and perennating structure. Although the winter was comparatively mild, there was a significant decline in red clover (*Trifolium pratense*), a species with buds at the soil surface on a branched taproot. This study will contribute to better understanding of frost tolerance and community dynamics, a greatly under-studied field, with the inclusion of belowground traits. The decline of red clover indicates that even mild frost can alter the relative abundances of plant species.

L5B. The Genetic and Environmental Basis for CHC Biosynthesis in *Drosophila*

Heather Ward, Amanda J Moehring

The type and quantity of cuticular hydrocarbons (CHCs) expressed by *Drosophila* are determined by the complex interplay between the fly's genetic background, its diet, and the commensal microbes that colonize its gut. Since the CHC profile of a fly is intrinsically linked to its reproductive fitness, alterations to the fly's profile due to input from any of these mechanisms can potentially lead to reproductive isolation and eventual speciation. Using genetic and molecular techniques, this study aims to separate out and independently examine each of the factors contributing to CHC variation in *Drosophila* in order to better understand the mechanisms that give rise to behavioural isolation and speciation in insects.

L6B. Effect of thiamine deficiency on reproductive traits in three populations of Atlantic salmon

Kimberly Mitchell, Bryan Neff

The extirpation of species from their historical range is a major issue in conservation biology. Atlantic salmon were once abundant in Lake Ontario, but were extirpated more than a century ago. There have been multiple attempts to reintroduce Atlantic salmon into Lake Ontario, but these attempts have not yet produced a self-sustaining population. One potential obstacle is the introduction of invasive species in Lake Ontario, which has altered the prey fish community. The current diet of salmonids in Lake Ontario is composed primarily of the introduced alewife and rainbow smelt, which contain high concentrations of the enzyme thiaminase. This enzyme breaks down an essential vitamin thiamine (B1), and induces thiamine deficiency. Within the Great Lakes basin, thiamine deficiency in salmonids is associated with a high mortality of juveniles. This study aims to look at the effect of thiamine deficiency on reproductive traits in three Atlantic salmon populations (LaHave, Lac Saint-Jean, Sebago), which have previously been used in reintroduction efforts. Experimental feeds will mimic either the historical (low-thiaminase) or current (high-thiaminase) diet of salmonids in Lake Ontario. Several metrics, including thiamine levels, sperm performance, egg quality and mortality, will be used to determine if a diet high in thiaminase affects the reproduction of Atlantic salmon. In addition, it will be determined if any of the three populations have a greater tolerance to a high-thiaminase diet. The results from this study may provide insight into managing the Atlantic salmon reintroduction effort in Lake Ontario.

L7B. Vertical distribution of fungi in hollow and hummock of boreal peatlands

Asma Asemaninejad, Greg Thorn, Zoe Lindo

Hollow and hummock of Boreal peatlands differ in water table position, pH, plant community composition and biochemical properties that might affect the structure of their fungal communities. The community composition of fungi in three different depths (0-5 cm, 15-20 cm, 30-35cm) of hollow and hummock of a nutrient-poor fen in northern Ontario were assessed by Illumina sequencing of D1 variable region of large subunit of rDNA. Our metabarcoding results revealed statistically distinct fungal community composition between hollow and hummock. Hollow contained more diverse fungal community than hummock in general. However, within each microscale, middle horizon of hollow and bottom horizon of hummock were comparable in terms of fungal biodiversity. These peat layers were identified as an optimum area bearing the most diverse and heterogeneous community composition of fungi. This study is the first to characterize the optimum zone of high fungal diversity in hollow and hummock of Boreal peatlands.

L8B. The young progeny of aged parents are less social

Dova Brenman, Anne Simon

Parental and grandparental age can alter the fitness of the progeny. Here we studied the effect of aging on neurodevelopment in the progeny in terms of changes to basic social behaviors like social spacing and social avoidance. We also investigated the trans-generational effect on social behavior on progeny whose parents have been aged. We found that at older ages (30 days old, 90% survival and 50 days old, 50% survival) *Drosophila* were less social and worse at avoiding *Drosophila* stress odorant (dSO) and even the young progeny of these aged flies were less social and worse at avoiding dSO than those with young parents, suggesting that the aging process can contribute heritable change to neurodevelopment and social behavior. Interestingly, it was enough to only have an aged father for the sons to be less social. We recapitulated the effect of old parental age on social spacing of their progeny by accelerating the aging process through increased metabolism (aging flies at 29C) or reactive oxygen species exposure (paraquat). In contrast, delaying aging of the parents through caloric restriction resulted in more social progeny. Although it is still unclear how the aging process affects gametes leading to changes in neurodevelopment and specific social behaviors, the powerful model system *Drosophila* and its underused ability to display simple social interactions will allow us to identify the underlying mechanisms.

L9B. Assessing the long term effects of perceived predation risk on the avian brain

Lauren Witterick, Scott MacDougall-Shackleton, Michael Clinchy, Liana Zanette

Predators affect prey populations not only through direct killing, but also through the perception of predation risk. Responding to predator threats is critical for prey survival, however perceived predation risk can have lasting effects ranging from individual changes in neurobiology up to the population level. My research focuses on the lasting effects of predator 'fear' on the avian brain. I will be using auditory playbacks to manipulate predation risk in black-capped chickadees (*Parus atricapillus*) in acoustic isolation and brown-headed cowbirds (*Molothrus ater*) in large outdoor aviaries. I will be looking for long lasting changes in brain morphology and activation in regions thought to be involved in the avian fear network. My research aims to connect laboratory methods used to quantify the effects of fear in the brain with behavioural and physiological changes found from perceived predation risk in the field.

L10B. Fatal attraction: the volatile influences that will lead whiteflies to deadly encounters and the dsRNA responsible

Kaitlyn Ludba, G Thompson, C Donly, I Scott

With global food security becoming increasingly important, and insecticide resistance on the rise, new insect pest management strategies need to be considered. One technology that is becoming increasingly utilized in pest management research is RNA interference (RNAi), which exploits the cellular mechanism for gene regulation; exogenous double-stranded RNA (dsRNA) introduced to cells silences the complimentary endogenous messenger RNA of a target. This can result in development delays, decreases in insecticide resistance, and lethality to pests. Other alternatives to chemical insecticides are pest-specific trap crops, which attract target pest species using either visual or olfactory cues. By targeting the olfactory senses in insects, an attractant or arrestant effect, depending on the insect species, can be observed. This has been seen in transgenic Micro-Tom tomatoes (*Solanum lycopersicum*), which have enhanced carotenoid cleaving deoxygenase gene activity, resulting in an increased release of volatile organic compounds (VOCs). As a result of these enhanced genes, the VOC profile in transgenic Micro-Tom tomatoes has increased oviposition preference by *Trialeurodes vaporariorum* (Westwood) compared to wild-type tomato. By combining these attractive plants with RNA interference, a novel lethal trap crop model, which first lures, and then kills by silencing vital gene targets, can be developed. This model can be used in future research in lethal trap crop development, which can benefit greenhouse production by decreasing chemical insecticide use and decreasing destructive pest populations, thereby increasing crop yield.

Poster Session

P1. Investigating the Protective Effects of Mitochondrially Targeted TERT on Neuronal Metabolism and Resistance to Amyloid- β

Olivia Singh, Robert Cumming

Telomerase consists of two main components that function as dimers; the telomerase RNA component (TERC) and the telomerase reverse transcriptase (TERT). TERT catalytically adds TTAGGG hexanucleotide repeats to the 3' end of the lagging strand of chromosomes thereby preventing telomere shortening during DNA replication in mitotic cells. While telomerase is highly expressed in germ line cells, embryonic stem cells, and malignant cancer cells, there is increasing evidence of a non-telomeric function of TERT in post-mitotic neural cells. Studies show that when cells experience oxidative stress, TERT can translocate from the nucleus to the mitochondria and promote a decrease in mitochondrial reactive oxygen species (ROS) production while increasing mitochondrial membrane potential. Mitochondrial dysfunction is a prominent feature of many neurodegenerative diseases including AD. A major pathological feature of AD is the progressive accumulation of amyloid-beta ($A\beta$) peptide within the cortex and hippocampus. It has been shown that $A\beta$ oligomers directly interfere with mitochondrial respiration by binding to alcohol dehydrogenase (ABAD) thereby promoting mitochondrial dysfunction, ROS production, and cell death. Hence, we hypothesized that TERT may protect neurons from mitochondrial dysfunction and $A\beta$ toxicity via metabolic reprogramming. We have created stable cell cultures with doxycycline inducible expression of TERT in the murine hippocampal neuronal cell line HT-22. Induction of TERT expression in HT22 cells resulted in altered glycolytic enzyme activity. We are currently determining if TERT localizes to mitochondria and confers neuroprotection against $A\beta$ toxicity via metabolic reprogramming. The results from this study may lead to a novel potential therapy for the treatment of AD.

P2. Adaptation of two-spotted spider mite *Tetranychus urticae* to *Arabidopsis* indole glucosinolates

Golnaz Salehipour-shirazi, Kristie Bruinsma, Huzefa Ratlamwala, Vojislava Grbić

The generalist herbivore, two-spotted spider mite (*Tetranychus urticae*) has the capacity to develop resistance to a wide variety of pesticides and defense compounds of the host plants. Rapid development of resistance to several classes of pesticides in *T. urticae* necessitates introduction of alternative management strategies to control *T. urticae*. Indole glucosinolates (IGs), a plant secondary metabolite found in the plants of the family *Brassicaceae* is shown to negatively affect the performance of spider mites. In this study, it is examined whether the spider mites can develop adaptation to IGs and what would be the mechanism of adaptation. The results showed that compared to bean-reared spider mites, those that were reared on IGs-containing *Arabidopsis* for several generations better performed, and induced more damage on *Arabidopsis*. This partial adaptation to *Arabidopsis* could be due to suppression of plant defense or detoxification of IGs by spider mites. The results showed that suppression of the plant defense was not the reason of spider mites adaptation to *Arabidopsis*, since mite adaptation did not change expression of genes required for IGs biosynthesis in *Arabidopsis*. However, higher expression of detoxification genes in spider mites and lower performance of adapted mites that were treated with detoxification enzymes inhibitors on *Arabidopsis* represents involvement of the spider mites detoxification enzymes in adaptation of spider mites to *Arabidopsis* IGs. This implies that to apply IGs against *T. urticae*, the spider mites potential to detoxify IGs should be considered to be able to avoid development of resistance in spider mites and control them successfully.

P3. Investigation of genetic mutants displaying synthetic lethality/sickness with *tsc1* and *tsc2* loss of function mutations in *Schizosaccharomyces pombe*

Ashyad Rayhan, Jim Karagiannis

Tuberous sclerosis complex is an autosomal dominant disorder characterized by hamartomas in multiple organs. The disease results from the loss of function mutations in either the TSC1 or TSC2 genes. While not conserved in budding yeast, orthologous genes (*tsc1* and *tsc2*) do exist in the fission yeast, *Schizosaccharomyces pombe*. Using this genetically tractable model, we sought to exploit recent advances in genetic interaction biology to examine genes that modulate the phenotypic effects of *tsc1* and *tsc2* mutations. Our ongoing study has identified two genes, *fft3* (a SMARCAD1 family ATP-dependent DNA helicase) and *ypa1* (a peptidyl-prolyl cis/trans isomerase) as strong candidates for further analysis. While complete deletion of either gene has little phenotypic effect in normal cells, their loss in either *tsc1*Δ or *tsc2*Δ backgrounds results in severe growth inhibition. Furthermore, we show that the strains bearing mutations in the *fft3* ATPase domain display similar growth-suppression effects. Thus, inhibition of either *fft3* (through targeting the ATPase domain) or *ypa1* may represent an “Achilles’ heel” of cells with defective *tsc1* or *tsc2*. Lastly, we demonstrate that the *tsc2*-R1296P allele (an allele of *tsc2* bearing a mutation orthologous to that found clinically) is also synthetically sick with both *ypa1*Δ and *fft3*Δ.

P4. Effects of DOM on N-fixing cyanobacteria in oligotrophic lakes

Erika Freeman, Irena Creed

Nutrient limitation has long been recognized as a vital factor controlling the formation and maintenance of harmful cyanobacteria blooms in freshwaters. Nutrient management efforts have traditionally focused on the contributions of inorganic forms of nutrients, specifically the macronutrients phosphorus (P) and nitrogen (N). Although both P and N play an important role in regulating phytoplankton production in freshwater systems, it is now understood that the combination of nutrients that promote high levels of growth and the dominance of potentially harmful toxin-forming cyanobacteria are much more complex. Here we investigate both macronutrient and micronutrient conditions that promote the dominance of N-fixing cyanobacteria (i.e., diazotrophs). First, we present the results from a survey of 40 freshwater oligotrophic lakes that form a gradient from low to high P, N, and dissolved organic matter (DOM) concentrations (which influence micronutrient availability). Then, we explore relationships between P, N, and DOM and the dominance of diazotrophic cyanobacteria in Ontario lakes.

P5. Assessing landscape effects on genetics and dispersal of the Rocky Mountain Apollo Butterfly *Parnassius smintheus* using a resistance mapping approach

Helen Chen, Nusha Keyghobadi

The effect land cover has on dispersal is a key question in landscape ecology and is often assessed indirectly using genetic data. Because of this, it is important to understand just how well genetic variables and dispersal correspond. I will compare separately the relationships of dispersal and population genetic structure to underlying landscape features using a resistance mapping approach, and test the validity of using genetic structure as a proxy for dispersal. I will analyze genetic and dispersal data from a network of populations of the Rocky Mountain Apollo butterfly, *Parnassius smintheus* on Jumpingpound Ridge in Alberta. I am generating a resistance surface map of the study area in ArcGIS that combines aerial imaging, land classification, and elevation data. This surface will be analyzed in Circuitscape to derive resistance distances that will be correlated separately with dispersal and genetic data from this landscape. With a better understanding of how resistance surfaces reflect dispersal and genetic differentiation, we can better interpret the results of landscape genetic studies, which are increasingly used to determine and mitigate the effects of habitat fragmentation on species.

P6. Identifying the neural basis of female receptivity within drosophila species

Priya Mahabir, Amanda Moehring

The complex processes that regulate mate preference have been widely studied. Most studies to date have focused on the mechanisms that drive male mate choice, while those that underlie female mate preference remain largely unknown. Recent studies show that females in most species are the primary discerners of reproductive receptivity. In order to address the existing knowledge-gap, a combination of genetic tools will be employed, including temperature-sensitive gene disruption, in both *D. melanogaster* and *D. simulans* to isolate regions of the brain responsible for female sexual receptivity or rejection. Identifying the neural basis of female receptivity, while of interest in its own right, will also contribute to our understanding of the origin of speciation and how neuronal circuits integrate multiple sources of information from various modalities to subsequently produce directed behaviour.

P7. Regulation of suberin biosynthesis in a wound-healing potato (*Solanum tuberosum* L.) tuber model

Katie Woolfson, Alexandra Kachura, Anica Bjelica, Meghan Haggitt, Yanni Zhang, Mark A. Bernards

Suberin is a complex biopolymer prevents water loss and microbial infection in specific plant tissues. The suberin macromolecule comprises two domains: the poly(phenolic) domain, which is assembled from hydroxycinnamic acids and their derivatives, and the poly(aliphatic) domain, which consists of modified fatty acids and glycerol. In potato, the deposition of each domain is coordinately regulated, where the deposition of phenolics precedes that of the aliphatic domain. Abscisic acid (ABA) plays a regulatory role in wound-induced suberization. In this work, potato tubers that were wounded and treated with the ABA biosynthesis inhibitor fluridone (FD) demonstrated an attenuation of phenolic product biosynthesis and a reduction in aliphatic suberin monomers relative to controls. Gene expression analyses in wound-healing tubers demonstrated earlier expression of genes involved in phenolic suberin biosynthesis than the majority of aliphatic metabolism genes and genes involved in linkage and deposition, which were highest 3-4 days post-wounding. While FD treatment did not have a pronounced effect on phenolic-related genes, it delayed wound-induction of aliphatic and linkage pathway genes and led to lower expression levels in these two subsets of genes across wound-healing. Treatment with ABA restored normal gene expression patterns. These findings support a role for ABA in the regulation of genes involved in aliphatic suberin metabolism, but not phenolic suberin biosynthesis. The roles of transcription factors that may orchestrate the differential timing of suberin biosynthetic pathway induction are currently being explored in order to elucidate the regulatory link between phytohormone signaling and the downstream induction of stress-responsive suberin biosynthetic genes.

P8. Photosynthesis in the cold: characterization of photosynthetic ferredoxin from the Antarctic alga *Chlamydomonas* sp. UWO241 reveals novel features of cold adaptation

Marina Cvetkovska, David Smith, Norman Huner

Chlamydomonas sp. UWO241 is a unique, psychrophilic green alga isolated from Lake Bonney, Antarctica. Despite the importance of polar algae as the primary source of organic carbon in cold environments, relatively little is known about how physiological processes function at low temperatures. The objective of this work is to characterize chloroplastic ferredoxin, a key enzyme involved in the distribution of photosynthetic reducing power. Typically, cold-adapted enzymes possess a range of features that confer a high level of structural flexibility and high activity at low temperatures. This is usually accompanied by low stability at moderate temperatures. By isolating ferredoxin from UWO241 and observing its biochemical and structural properties, we show that this protein has both high activity at low temperatures and high stability at moderate temperatures. Thus, it represents a novel class of cold-adapted enzymes. Photosynthetic organisms encode multiple ferredoxin isoforms, where typically only one is highly abundant and involved in photosynthetic electron transport. The primary protein sequence of photosynthetic ferredoxin is highly conserved among algae, and we determine that subtle differences in sequence can lead to significant changes in activity at low temperatures. We also show evidence for a duplication of the main ferredoxin gene in the UWO241 genome, which results in the presence of two highly similar and functional photosynthetic ferredoxins. The presence of two proteins in UWO241 could provide an adaptive advantage for survival at cold temperatures. In conclusion, our study on ferredoxin from the psychrophile UWO241 reveals novel insights on the functioning of photosynthesis in the cold.

P9. The Role of Glial Lactate in Memory and Neuroprotection in *Drosophila*

Ariel Frame, Robert Cumming

The dynamic relationship between neurons and astrocytes has been a sought-after topic of investigation for years. Astrocytes in the brain, which outnumber neurons, were originally thought to simply glue neurons together and maintain the extracellular milieu. Importance of the astrocytic contribution to neuronal function and survival is becoming increasingly appreciated. One way in which astrocytes may support neurons is by supplying them with metabolic substrates. There has been evidence emerging to support the hypothesis that astrocytes produce lactate through aerobic glycolysis and shuttle it to neurons. A few studies have shown that this phenomenon, termed the Astrocyte-Neuron Lactate Shuttle (ANLS), is involved in memory in vertebrates such as chickens, mice and rats. A paper published recently reported that glial glycolysis is required for the survival of neurons in the brain of fruit flies, *Drosophila*. They found that if glycolysis is inhibited in glial cells, neurodegeneration occurs and life span is drastically reduced. My project aims to validate the ANLS and its conserved role in memory and neuroprotection by elaborating on this finding in *Drosophila*. I will be testing the hypothesis that glial cells provide lactate as a metabolic substrate to neurons which is required for learning and memory as well as survival with age. To do this I will be using *Drosophila* which have genetic alterations causing lactate production to be increased or decreased specifically in glial cells. I will be assessing multiple forms of memory in these flies and checking for changes in survival as well as neurodegeneration with age.

P10. Effects of the Brain Nonapeptides on Shoaling Behaviour in the Guppy (*Poecilia reticulata*)

Babak Ataei Mehr, Shawn Garner, Bryan Neff

Research into neuro-behavioural mechanisms influencing social behaviour suggests an important role for nonapeptides across vertebrate taxa. The general pattern that has emerged is that arginine–vasopressin (AVP)/arginine–vasotocin (AVT) increases ‘anti-social’ behaviour (aggression) whereas oxytocin (OT)/isotocin (IT) increases ‘pro-social’ behaviour (affiliation). Many fishes readily form social groups, referred to as shoals, but few studies have specifically addressed the effects of nonapeptides to differences in shoal formation across different life stages (juvenile and adult), sexes and populations. Several decades of research on the Trinidadian guppy (*Poecilia reticulata*) have established the species as a model system for understanding social behaviour because of evolved differences in shoaling propensity across populations, largely in response to differences in predation regimes. I will discuss my research on the guppy that: (1) characterizes differences in shoaling behaviour across multiple populations, sexes, and life history stages; (2) quantifies the distribution of AVT and IT neurons in the brains of individuals that exhibit high and low shoaling behaviour; (3) compares expression of AVT and IT receptor genes in individuals that exhibit high and low shoaling behaviour; and (4) determines whether administration of AVT/IT and their antagonists influence shoaling behaviour.

P11. Western Science Writers in Residence

David Smith

Over the past three years, Western Science Writers in Residence have published over 20 popular-science articles, including pieces for Canada’s Arctic Journal, Guru Magazine, Western News, and Western’s Faculty of Science Homepage. Now we have our own online magazine called Hipademic. This poster highlights the Writers in Residence Program and provides details for how to get involved.

P12. Engineering Plant O-Glycosylation

Israel Alfonso Ramirez-Alanis, Rima Menassa, Guy A. Cardineau

Plants have emerged as alternative expression platforms for the production of foreign proteins with pharmaceutical, nutraceutical or nutrimental properties. Among the advantages of using plant systems, in comparison to the well-established bacterial, yeast, or mammalian systems, plant platforms possess a lower production cost, absence of pathogens in common with humans, and capability to perform post-translational modifications. However, plant-specific post-translational modifications might also have a negative impact on the functionality of the foreign protein, thus leading to the production of plant-derived proteins with reduced or abolished activity, or allergenic effects in humans. Glycosylation is one of the most common post-translational modifications found in pharmaceutical proteins. In the present project, we aim to transiently express the recombinant human Granulocyte-Colony Stimulating Factor (rhG-CSF) in *Nicotiana benthamiana* plants, with the corresponding mucin-type O-glycosylation post-translational modification. The latter would be achieved by co-expressing the genes required for the synthesis of this specific post-translational modification, together with the gene of interest via *Agrobacterium* infiltration. The production of functional and safe human proteins in plants, with their respective native post-translational modifications, will prove the feasibility of using plants as expression platforms capable of imitating mammalian specific post-translational modifications of economically relevant proteins.

P13. Production of Dengue virus non-structural protein 1 for immunodiagnostic purposes in plant

Livia Marques, Bruno B. Silva, Maria Raquel L. Lacerda, Eridan O. Pereira, Rima Menassa, Maria Izabel F. Guedes

Dengue virus represents a major threat to global public health, billions of people are now at risk of infection by this mosquito-borne virus and thousands die each year. Dengue virus non-structural protein 1 (NS1) is a highly conserved glycoprotein involved in viral replication and the pathogenesis of dengue diseases. DENV NS1 levels can be found in the peripheral blood circulation for up to 9 days after illness onset, but can persist for up to 18 days in some cases. In this context, a plant expression system was chosen for recombinant antigen production, targeting a less expensive dengue diagnostic tool. In the present study Dengue virus non-structural protein 1 was transiently produced in *Nicotiana benthamiana* by targeting it to five different subcellular compartments. Analysis of transiently expressed protein in *N. benthamiana* was characterized by SDS-PAGE and western blot analysis of leaf total soluble protein extracts, using a monoclonal antibody Anti-Dengue Virus NS1 Glycoprotein antibody [DN3] ab 41616 (Abcam). After the presence of the NS1 heterologous protein was confirmed, a new test was evaluated using serum of patients positive for Dengue. The results show that the recombinant NS1 protein can be used as a diagnostic reagent, even when applied as a crude extract in the development of a serological diagnostic kit.

P14. Improving soybean cyst nematode (*Heterodera glycines* Ichinohe) resistance through controlling the expression of Rhg4, R30 and C32 genes in soybean

Farida Meerja, Yanjie Luo, Lining Tian, Danielle Way

Soybean is an important legume crop and is a good source of protein and oil worldwide. Soybean crop is heavily affected by pests, particularly soybean cyst nematode (SCN), which causes huge economic losses approximately \$1 billion in North America alone. SCN infects soybean roots causing symptoms called 'yellow dwarf' and it also increases vulnerability to other microbial pathogens by creating wounds in roots. SCN management in the fields by crop rotation, biological controls and applying nematicides are not very effective due to the fact that the nematode eggs can survive in soil up to a decade. A few partially resistant soybean cultivars are available but these cultivars cannot fully resist SCN infection. Therefore developing genetically resistant cultivars is a better management strategy to control SCN. Research has shown that some of the soybean genes are involved in SCN infection and controlling the expression of these genes may develop resistance in soybean. We are studying three of those genes including Rhg4, R30 and C32 using genome editing technology to achieve soybean resistant to SCN. Genome editing is a new technology that can precisely modify gene sequences within the organism without insertion of foreign genetic material, and subsequently improve traits. SCN susceptible cultivar Williams 82 is being used to carry out the research. After gene editing, SCN resistant lines will be identified and specific sequence modifications in the genes will be analyzed. Knowledge obtained from this research can be useful to develop SCN resistant soybean plants in different soybean cultivars.

P15. A cell-specific role of the *Lotus japonicus* LHK1 cytokinin receptor during symbiotic infection

Sina Gerayli, Krzysztof Szczyglowski

Leguminous plants selectively initiate primary responses to rhizobial nodulation factors which lead to symbiotic root nodule formation. Functioning downstream, cytokinin has emerged as the key endogenous plant signal for nodule differentiation but its role in mediating rhizobial entry into the root has also been suggested. The proposed work will define a cell-specific role for the *Lotus japonicus* LHK1 cytokinin receptor during rhizobial infection.

P16. It is more than just feeding the plant - Genetic analysis of nitrate transporter 2 family in *Brachypodium distachyon*

Jiang Wang, Norm Huner, Lining Tian

Agricultural productivity relies heavily on nitrogenous fertilizers. Excess N fertilizer application leads to lower nitrogen use efficiency (NUE) along with energy waste and environmental problems. Therefore, improving NUE in plants is of key importance. The small monocot plant *Brachypodium distachyon* (Brachypodium) is rapidly emerging as a powerful model system to study questions unique to the monocot crops (wheat, maize, rice, etc.). An exhaustive BLAST search was carried to identify putative orthologues of the Arabidopsis NRT2 genes in Brachypodium genome (Phytozome v11.0). Six genes encoding putative high affinity nitrate transporters (BdNRT2) were identified and were named BdNRT2.1, BdNRT2.2, BdNRT2.3, BdNRT2.4, BdNRT2.5, and BdNRT2.6. Analysis of individual BdNRT2 gene expression under different nitrogen sources and concentrations was performed. BdNRT2.1 and BdNRT2.2 were strongly induced by low nitrate concentrations and were classified as inducible genes, whereas other members were constitutively expressed. Interestingly, BdNRT2.5 was found to be repressed by higher concentration of both nitrate and ammonium. Furthermore, the high affinity transporter system (HATS) was reduced by 36% in *bdnrt2.1* T-DNA mutant and its overall NUE was also decreased by 37%. BdNRT2.1 over-expression lines showed a 24% NUE increase on average, and both HATS and NUE were able to be recovered in *bdnrt2.1* rescue lines. The work opens a gate for future investigation of these genes in monocot plants and also implicates the essential role of BdNRT2.1 in NUE related metabolism.

P17. Using *Brachypodium distachyon* as Model Species to Explore the Plant Genetic Involvement of *Gluconacetobacter diazotrophicus* Colonization in Monocots

Xuan Yang, Katleen Hill, Lining Tian

To study the nitrogen fixation of *Gluconacetobacter diazotrophicus* in different monocot crops, research was conducted to establish and optimize methods for introducing *G. diazotrophicus* into monocot model plant, *Brachypodium distachyon*. Inoculation was tested in liquid, semi-solid and solid media with or without a nitrogen supply. The colonization of *G. diazotrophicus* in *B. distachyon* was established through different inoculation methods and high level of colonization was achieved in liquid medium without nitrogen source. Furthermore, the results indicated the colonization of *G. diazotrophicus* can be stabilized in 2-3 weeks after inoculation in *B. distachyon*. The colonization displayed a “crack entry” pattern, which means *G. diazotrophicus* colonizes the root through the lateral root emergence sites. The total RNA from root tissues of colonized plants and control plants was extracted for next generation RNA sequencing to find out plant genes involved in the colonization process. The RNA sequencing result showed that 1,925 genes were differentially expressed in colonized root samples compared to the control, and among these, 1,076 genes were up-regulated and 849 were down-regulated. The gene ontology and pathway analysis of these differentially expressed genes revealed that jasmonic acid, ethylene, gibberellin, flavonoid biosynthesis and cell wall synthesis were highly regulated during *G. diazotrophicus* colonization. Therefore, the genes in these biosynthesis pathways potentially play important roles in the symbiotic relation between plant and *G. diazotrophicus* with respect to bacterial colonization as well potential nitrogen fixation in plant. The details about how each pathway contributes to the *G. diazotrophicus* colonization are under investigation.

P18. RNA interference of MDR genes in *Leptinotarsa decemlineata* and *Trichoplusia ni*

Grant Favell, Cam Donly

Leptinotarsa decemlineata (Colorado potato beetle) and *Trichoplusia ni* (cabbage looper) are two species of insects that plague the agriculture industry by consuming and damaging crops. These species are also well known for developing resistance to a variety of common pest control techniques including chemical pesticides, but the mechanisms of the resistance are still unclear. One possible mechanism is overexpression of multidrug resistance (MDR) genes which code for ABC transmembrane transporter proteins that actively transport toxic molecules out of a cell. Overexpression of these genes has been associated with toxin resistance in a variety of other species, but has not yet been investigated in either *L. decemlineata* or *T. ni*. The purpose of this project is to investigate how the expression of MDR genes in *L. decemlineata* and *T. ni* affects their susceptibility to a pesticide. The selected genes will be downregulated by feeding the insects double-stranded RNA (dsRNA) designed to cause RNA interference and then relative gene expression of the genes will be measured using qPCR. After proving successful downregulation, the insects will be fed a chemical pesticide in combination with the dsRNA to determine if the downregulation affects their susceptibility to it. The results will show whether or not the selected MDR genes are involved in pesticide susceptibility and if downregulation of MDR genes could serve as a pest control method.

P19. DNA-sequence-specific erasers of epigenetic modification

Chenlong Li, Yuhai Cui

How epigenetic regulators find their specific target genes in the genome remains a challenging question. Here we show that RELATIVE OF EARLY FLOWERING 6 (REF6), a plant-unique H3K27 demethylase, targets genomic loci containing a CTCTGYTY (Y represents T or C) motif via its zinc-finger (ZnF) domains and facilitates the recruitment of the chromatin remodeler ATPase BRAHMA (BRM). Genome-wide analyses showed that REF6 colocalizes with BRM at many genomic sites with the CTCTGYTY motif. Loss of REF6 results in decreased BRM occupancy at BRM-REF6 co-targets. Furthermore, REF6 directly binds to the CTCTGYTY motif in vitro, and deletion of the motif from a target gene renders it inaccessible to REF6 in vivo. Finally, we show that, when its ZnF domains are deleted, REF6 loses its genomic targeting ability. Thus, our work demonstrated that DNA sequence can provide the specificity for recruitment of chromatin-modifying proteins and answered a longstanding question regarding the recruitment of chromatin-modifying proteins in eukaryotes.

P20. Exploration of spatial and temporal changes in chlorophyll a of lakes in the northern temperate forest biome

Aleksey Paltsev, Irena Creed

Phytoplankton blooms are on the rise in the lakes of North America; however the fundamental question what factors contribute to these blooms has remained unanswered. To examine the influence of internal (lakes-specific) versus external (climate and landscape properties) factors on lake phytoplankton (1) a regression model that relates chlorophyll a (chl-a) to Landsat TM and ETM+ optical reflectance was developed for the Temporal Forest Biome (Ontario) and (2) two-way ANOVA that defines three types of variation (spatial, temporal, and space × time interaction) in chl-a was applied. Reflectance in Landsat band 3 showed the strongest correlation with in situ data explaining 85% of variance in chl-a ($p < 0.001$). Application of the regression model allowed to build a continuous detailed survey of chl-a in 6,410 lakes for 28 years. Application of the ANOVA revealed that internal type of variation (spatial x temporal interaction) explained the majority of the variance in chl-a (75%) for the study region. However, when the region was segregated into sub-regions (watersheds), a much larger proportion of the variance (more than 50% for 11 out of 12 watersheds) was related to external types (space and time). This suggests that the influence of external factors on chl-a is much more pronounced within regions that are relatively hydrologically homogeneous (watersheds) and not spatially extensive.

P21. Genomic record of wild and laboratory environmental influences on genomic diversity in *Mus musculus*

Kathleen A. Hill, Milojevic M, Atherton C, Qi FW, Soni DH, Edge AK, Charron B, and Locke MEO*
**presenter*

Single nucleotide polymorphisms (SNPs) and copy number variants (CNVs) are major sources of genetic diversity. These variants may impact phenotype and therefore are sentinels of adaptive response to selection. Here, wild-caught mice and classical laboratory inbred lines were used to study the effects of natural and artificial selective pressures. SNP and CNV loci were determined using the Mouse Diversity Genotyping Array (MDGA) and annotated according to Ensembl's mouse primary assembly GRCm38.4. SNP loci in 17 genomic variant types of either protein altering, regulatory, or neutral effects were examined. Variation at each genomic variant type was compared to the variation at synonymous SNP loci to determine genetic diversity between wild and laboratory-bred mice. As expected, SNP diversity across wild-caught mice subspecies is greater than SNP diversity across classical laboratory mouse lines. Genes affected by diversifying selection in wild-caught mice were associated with GTPase activity, DNA metabolic processes, and extracellular matrix gene ontologies. The top biological pathway with diversifying selection affecting gene regulation in wild-caught mice is lipid metabolism, molecular transport, and small molecule biochemistry, whereas in classical laboratory inbred lines, the top pathway is related to cancer, hematological disease, and immunological disease. Likewise, CNV gains and losses affect different pathways in wild-caught mice than classical laboratory inbred lines. Our results thus far suggest that different environments result in different genes and pathways impacted by SNP and CNV diversity. Next, I will identify F_{ST} – outlier SNPs and CNVs to determine candidate genes under diversifying selection.

P22. Behavioural mechanisms of avian protandry in the Black-throated Blue Warbler (*Setophaga caerulescens*)

Jessica Deakin, Yolanda Morbey, Chris Guglielmo

Protandry, meaning “males first”, is a common pattern of sex-biased timing that is seen across a diverse range of animal taxa (insects, amphibians, fish, mammals, and birds). In migratory birds, protandry is the norm, and is apparent in many events leading up to and including arrival at breeding sites. The evolutionary theory of protandry is well understood but there is currently little empirical evidence on the proximate causes of protandry. This study focuses on the behavioural sex differences in Black-throated Blue Warblers (*Setophaga caerulescens*), nocturnal neo-tropical long distance migrants, during the spring migration period. Migratory restlessness, an indicator of the eagerness to migrate, was observed in captive Black-throated Blue Warblers during spring 2016. Preliminary results indicate that males initially have a greater intensity of migratory restlessness, suggesting that males of this species depart the wintering quarters before females. The birds were then radio-tagged and released at a known stopover site to determine sex differences in their departure. Currently, the birds’ stopover behaviour and timing of departure are being analyzed and correlated to their behaviour in captivity.

P23. Soybean root suberin and resistance against the pathogen *Phytophthora sojae*

Trish Tully, Mark Bernards

Soybean (*Glycine max* [L.] Merr.) is a globally cultivated crop that is important to the sustainability of many industries. However, soybean is known to sustain a high level of crop loss due to infection by the oomycete pathogen, *Phytophthora sojae*. In soybean, aliphatic suberin deposition in roots has been correlated with defense against *P. sojae*. A deeper understanding of the interaction between suberin deposition and pathogen defense would shed light on the ability to engineer a highly resistant form of soybean, based on enhanced, innate defenses. Aliphatic suberin is comprised of a series of fatty-acid derived monomers, wherein the ω -hydroxyalkanoic acids are predominant and most strongly correlated with resistance to *P. sojae* in soybean. These ω -hydroxyalkanoic acids are synthesized by a subfamily of cytochrome P450 enzymes collectively known as the fatty-acid ω -hydroxylases (FA ω Hs). In soybean, the FA ω H genes show a tissue specific expression pattern with only genes GmFA ω H-5 and GmFA ω H-6 being expressed in root tissue. Using a model system of hairy roots, suberin levels are being manipulated through knock down and over-expression of GmFA ω H genes. Changes in suberin deposition will be measured and quantified by GC/MS and a pathogenicity assays used to determine whether resistance levels are affected by modification to suberin levels.

P24. Is there a role for stromules in ADT5 trafficking to the nucleus?

Sara Rad, Susanne Kohalmi

Arogenate dehydratases are a family of six enzymes with the main role of catalyzing the last step of phenylalanine biosynthesis. Since biosynthesis of phenylalanine happens in chloroplasts all members of this family are targeted from the cytosol to the chloroplast by an N-terminal transit peptide sequence. Through localization studies in *Arabidopsis thaliana* we found that within chloroplasts all ADTs localize to filled extensions stroma called stromules. Surprisingly, we found that one member of this family, AROGENATE DEHYDRATASE 5 (ADT5), is not only targeted to stromules, but also is found in the nucleus. Nuclei visualized with ADT5 are often surrounded with chloroplasts and they seem to be connected to the nucleus using stromules. Since ADT5 is too big to diffuse into the nucleus and no Nuclear Localization Signal (NLS) has been found in the sequence of this protein we hypothesize that it is targeted to the nucleus through stromules. To test this hypothesis ADT5-GFP was transformed to the chloroplast genome of *Nicotiana tobaccum* by particle bombardment. As this fusion proteins are only translated in the chloroplasts and not in the cytosol appearance of the fusion protein in the nucleus can only happen through stromules. Constructs were designed to express full length and partial ADT5. Stromule morphology, phenotype of plants and the nuclear ADT5 localization was analyzed. Results will be shown and discussed.

P25. Functional and biochemical characterization of a putative β -glucosidase from *Pythium irregulare*

Scarlett Puebla-Barragan, Mark Bernards

A putative β -glycosidase gene denominated PiGH1-x, isolated from the oomycete *P. irregulare* will be expressed in a recombinant system (*Escherichia coli* BL21 (DE3)). The purified recombinant protein will be characterized for glycosidase activity and substrate specificity, in order to confirm its identity. Once the enzyme has been characterized, gene expression will be induced in *P. irregulare* and quantified using qRT-PCR in order to identify whether its expression is triggered by the presence of ginsenosides.

P26. The SWI/SNF complex is required for axon morphogenesis in the Drosophila mushroom body

Melissa Chubak, Jamie Kramer

Defects in epigenetic regulation represent one of the most common causes of Intellectual disability (ID). In particular, the SWI/SNF chromatin remodelling complex is the most statistically over represented protein complex among the known dominant ID genes. The SWI/SNF complex is known to play a role in cellular differentiation and cancer, but recent studies have revealed a role for this complex in neurons. Genetic screens in *Drosophila* have identified several components of the SWI/SNF complex that are important for the regulation of dendrite morphogenesis. However, the role of this complex in axon morphogenesis remains unexplored. Furthermore, little is known about the role of this complex in the development of brain regions important for learning and memory. We have addressed these gaps by investigating the role of the SWI/SNF complex in the development of the *Drosophila* mushroom body (MB), a complex brain structure that is required for learning and memory in the fruit fly. Using targeted RNA interference (RNAi), we have knocked down the expression of each of the 15 SWI/SNF components specifically in the MB. Following knockdown, gross MB morphology was assessed using confocal microscopy to identify morphological defects. Initial results from this study have shown that several components of the SWI/SNF complex are essential for axon morphogenesis in the *Drosophila* MB, providing novel insight into the biological role of this core epigenetic regulatory complex. The results from this study will be used as a basis for further understanding the molecular mechanisms that are disrupted in the MB upon SWI/SNF knockdown. These findings may provide insight into the mechanisms that are disrupted in ID disorders that are caused by mutations effecting SWI/SNF components.

P27. Comparative analysis of essential genes in prokaryotic genomic islands

Xi Zhang, Feng Gao

Essential genes are thought to encode proteins that carry out the basic functions to sustain a cellular life, and genomic islands (GIs) usually contain clusters of horizontally transferred genes. It has been assumed that essential genes are not likely to be located in GIs, but systematical analysis of essential genes in GIs has not been explored before. Here, we have analyzed the essential genes in 28 prokaryotes by statistical method and reached a conclusion that essential genes in GIs are significantly fewer than those outside GIs. The function of 362 essential genes found in GIs has been explored further by BLAST against the Virulence Factor Database (VFDB) and the phage/prophage sequence database of PHAge Search Tool (PHAST). Consequently, 64 and 60 eligible essential genes are found to share the sequence similarity with the virulence factors and phage/prophages-related genes, respectively. Meanwhile, we find several toxin-related proteins and repressors encoded by these essential genes in GIs. The comparative analysis of essential genes in genomic islands will not only shed new light on the development of the prediction algorithm of essential genes, but also give a clue to detect the functionality of essential genes in genomic islands.

P28. Phytoplankton vs. Forests, who is feeding aquatic food webs?

Oscar Senar, Irena Creed

Dissolved organic matter (DOM) is a complex mixture of compounds with different chemical properties and susceptibility to biological breakdown. Traditionally, limnological research considers only the concentration of DOM. In lakes with high concentrations of labile DOM, heterotrophic bacteria dominate incorporating terrestrial carbon into the aquatic food web. In contrast, in lakes with relatively high concentrations of refractory DOM, bacterial productivity is low. As a result, the refractory DOM can influence competition among primary producers by modulating macro- and micro-nutrients. Our survey of 46 oligotrophic Ontario lakes set out to define the DOM conditions that promote cyanobacterial growth by sampling lakes with a range of DOM quality. We characterized DOM using Excitation Emission Matrices (EEMs) to define the DOC quality and compared this analysis with phytoplankton biomass and the contribution of cyanobacteria to the biomass. We then used stable isotopes to determine the main carbon source of zooplankton (which preferentially consume algae and bacteria over cyanobacteria). As DOM conditions changed from refractory to labile, zooplankton diet shifted from phytoplankton (autochthonous carbon) to heterotrophic bacteria (allochthonous carbon), and there was a concurrent increase in the proportion of cyanobacteria in the phytoplankton community. These findings suggest that cyanobacteria have a competitive advantage under intermediate DOM quality characteristics, providing support for a conceptual model that cyanobacteria can access nutrients that are not tightly bound to DOM. Climate change and its expected influence on DOM loadings to lakes may have significant consequences for aquatic food webs.

P29. HABs toxicity measurement by using yeast cells.

Malihe Mehdizadeh Allaf, C Dulal-Whiteway, CG Trick

Harmful algal blooms (HABs) are significant environmental problems. Cells that bloom are often associated with intercellular or dissolved toxins that are a grave concern to human. But cells may also excrete compounds that are beneficial to their competition allowing the cells to establish or maintain cells in bloom conditions. Here, we develop a yeast cell assay to assess if bloom forming species change the toxicity of the water environment. Current methods to assess toxicity involve whole-organism. Here, yeast cells are used as a bioassay model to evaluate eukaryotic cell toxicity. Yeast is a commonly used, easy to maintain bioassay species, free from ethical concerns but sensitive to a wide array of metabolic and membrane-modulating agents. Compared to using the whole-organism, this method offers rapid and convenient cytotoxicity measurements using a lower volume of samples. The flow cytometer was employed in this toxicology assessment to measure the number of dead cells using alive/dead stain analysis. The results show that yeast cells were metabolically damaged after 1 hour of exposure to our model toxin-producing euryhaline flagellates (*Heterosigma akashiwo* and *Prymnesium parvum*) cells or extracts. The mortality rate of yeast cells was almost 50% after 1 hour of exposure and increased to 70% after 3 hours.

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