4th Annual

Biology Graduate Research Forum

Agenda

Presented By

The Department of Biology and

The Society of Biology Graduate Students

Saturday, October 19th, 2013

University Community Centre Room 56

The University *of* Western Ontario

www.uwo.ca/biology/bgrf/index.html

Biology Graduate Research Forum 2013 Agenda

Saturday, October 19, 2013 • University Community Centre (UCC) Room 56

8:30 – 9:00 am	Poster set-up and load presentations
9:00 – 9:05 am	**Welcome and Opening Remarks** Mark Bernards - Chair, Department of Biology
	Platform Session I - Long oral presentations
9:05 – 9:20 am	**Combined effects of altered nitrogen availability, temperature, and CO_2 on nitrogen fixation by the cyanobacterium *Nostoc punctiforme*** Danielle Griffith
9:20 – 9:35 am	**Migratory condition, but not flight, increases in muscle oxidative enzymes in yellow rumped warblers** Morag Dick
9:35 – 9:50 am	**Functional characterization of microRNA156 in *Medicago sativa*** Banyar Aung
9:50 – 10:05 am	**Periphyton growth as an indicator of agricultural impacts in low-order streams in the Beaver Valley watershed, Ontario, Canada** Catherine Dieleman
10:05 – 10:20 am	**Investigating the role of PDK1 in mediating amyloid-beta resistance in a transgenic mouse model of Alzheimer's disease** Richard Harris
10:20 – 10:35 am	**Why I study rapid evolution in salmon** Steve Sharron
10:35 – 10:50 am	Morning break
	Platform Session II - Short oral presentation
10:50 – 10:57 am	**Increasing atmospheric nitrogen deposition: Implications for tallgrass prairie restoration** Jennifer McPhee
10:57 – 11:04 am	**Factors influencing migration chronology by Lesser Scaup (*Aythya affinis*) and Mallards (*Anas platyrhynchos*) during spring** Taylor Finger
11:04 – 11:11 am	**An eye to the future: identifying early disease mechanisms in a mouse model of retinal degeneration** Eric Dolinar
11:11 – 11:18 am	**The adaptive capacity of thermal tolerance: Reintroduction of Atlantic salmon into Lake Ontario** Kayla Gradil
11:18 – 11:25 am	***Arabidopsis* response to spider mite feeding: Perception, Signaling and Response** Kristie Bruinsma
11:25 – 11:32 am	**Effects of changing ocean acidity on the growth and toxicity of the marine raphidophyte *Heterosigma akashiwo*** Julia Matheson

11:32 – 11:39 am	**Habitat selection during the nonbreeding period by Eastern Population Tundra Swans** Katelyn Weaver
11:39 – 11:46 am	**Olfaction-related copy number variants, important for mate selection, are predominant in wild mice but infrequent in inbred laboratory mice** Maja Milojevic
11:46 – 11:51 am	**Redundant role of cytokinin receptors during symbiotic root nodule organogenesis in *Lotus japonicus*** Mandana Miri
11:51 – 11:58 am	**A genetic basis for plasticity in thermal tolerance within a coastal population of Chinook salmon** Nicolas Muñoz
12:00 – 1:00 pm	Lunch break
	Laudenbach Memorial Lecture
1:00 – 2:00 pm	Dr. Melissa Holmes, University of Toronto
2:00 – 3:00 pm	Poster Session
3:00 – 3:20 pm	Closing Remarks and Award Presentations

2. Platform Presentations – Long Oral Presentations

L1. **Combined effects of altered nitrogen availability, temperature, and CO2 on nitrogen fixation by the cyanobacterium *Nostoc punctiforme***

Danielle Griffith and Zoë Lindo

Nitrogen (N) fixation is a critical ecosystem-level process, particularly in boreal forests, in which productivity is strongly N limited. Nitrogen inputs from moss-associated cyanobacteria contribute a substantial amount of N to these systems; however, few studies describe the response of the cyanobacteria from the moss system to global environmental change. Here, we quantify N fixation activity by the cyanobacterium *Nostoc punctiforme* in response to increases in N availability, atmospheric CO_2 concentrations, and temperature using a factorial study design in a controlled greenhouse setting for a 90 day period. Measurements of N fixation activity were taken every ten days beginning at day 30, with carbon fixing vegetative cells and N fixing heterocyst cells quantified at day 90. Nitrogen availability was the main factor influencing N fixation, with heterocysts and N fixation virtually absent in available N treatments. In conditions without N, elevated CO_2 and increased temperature had combined effects on N fixation rates that differed at day 30 and day 90: elevated CO_2 and temperature were initially stimulatory, but become inhibitory by the end of the study. We posit that the observed changes result from altered cyanobacterial growth rates and nitrogenase activity, rather than differences in heterocyst densities. Collectively, our findings suggest that short-term increases in CO_2 and temperature may increase N fixation rates and, potentially, alter the N budget in boreal forest ecosystems.

L2. **Migratory condition, but not flight, increases in muscle oxidative enzymes in yellow-rumped warblers**

Morag F. Dick and Christopher G. Guglielmo

The migratory flights of birds are extreme and intense feats of endurance lasting hours to days. To help meet this challenge, physiological and biochemical changes occur in the flight muscles to help power and sustain energy supply. These changes include increases in fatty acid oxidative capacity and flight muscle size. The degree and extent to which birds seasonally prepare in advance for migratory flights versus during flight is unknown. In a preliminary analysis of a transcriptomic study, we examined the effect of migratory condition and endurance exercise on flight muscle metabolic enzymes. Muscle samples were taken from captive yellow rumped warblers (*Dendroica coronata*) from three treatments: 1) fall migrants at rest, 2) fall migrants after a 4 hr endurance flight and 3) from wintering non-migratory condition birds at rest. Compared to wintering birds, migrants had significantly higher carnitine palmitoyl transferase activity, with a trend for higher activity levels of citrate synthase and 3-hydroxyacyl CoA dehydrogenase. Lactate dehydrogenase activity was lower in migrants. Endurance exercise had no effect on metabolic enzymes. These results suggests that migrant birds increase their fatty acid oxidative potential and decrease anaerobic capacity in advance of migratory flights and sustain this capacity during endurance flight.

L3. **Functional characterization of microRNA156 in *Medicago sativa***

Banyar Aung, Margie Gruber, Lisa Amyot, Nusha Keyghobadi, and Abdelali Hannoufa

MicroRNAs (miRNAs) regulate members of the *Squamosa Promoter-Binding Protein-like* (*SPL*) genes and play important roles during vegetative to reproductive phase transition in plants. Here we conducted a study to investigate the function of miR156 in *Medicago sativa* (alfalfa), a forage and potential bioenergy crop. To determine the number of loci encoding miR156 paralogs in alfalfa, an *in silico* search was conducted using publicly available sequences. Alfalfa plants overexpressing *M. sativa* miR156 and *Lotus japonicus* miR156 were generated, and the miR156 cleavage targets were validated using a modified 5′-RACE technique. *In silico* analysis shows that some alfalfa sequence reads (~ 60 bp) are similar to the miR156 precursors but the hairpin secondary structure could not be produced from these short sequences. Of the five predicted target *SPLs* genes, three (*SPL*6*, SPL*12 and *SPL*13) contain miR156 cleavage sites and their expression is downregulated in transgenic lines overexpressing *M. sativa* miR156 and *L. japonicus* miR156. These transgenic alfalfa lines had reduced internode length and enhanced shoot branching, as well as elevated biomass production though no significant effects of miR156 are observed on plant height and root length. Although *M. sativa* miR156 has little effect on nodulation and flowering time, *L. japonicus* miR156 causes a range of reductions in nodule numbers and delays flowering time by up to 45-50 days compared to wild type. Our observations imply that miR156 could be employed as potential tool to enhance biomass production and quality in alfalfa.

L4. **Periphyton growth as an indicator of agricultural impacts in low-order streams in the Beaver Valley watershed, Ontario, Canada**

Catherine Dieleman and Pat Chow-Fraser

Agricultural runoff is rich in nitrogen, phosphorus, and sediments, which are pollutants that can accumulate in rivers and lakes and, in high concentrations, can lead to eutrophication events and ultimately cause habitat loss and degradation. To protect downstream ecosystems from agricultural impacts it is paramount that farmers have an effective and inexpensive method to monitor nutrient runoff into their streams. Previous work by McNair & Chow-Fraser (2003) demonstrates a strong relationship between phosphorus levels and measured periphyton growth on clear acrylic rods in wetlands. By sampling 23 sites we tested the relationship between periphyton growth and common water chemistry variables in low-order streams to example the applicability of this method as an agricultural tool. Samples were taken between June and July in 2012 and 2013, from nine first-order, five second-order, and nine third-order streams. The rods were colonized with periphyton over a two-week incubation period. Surprising, periphyton growth did not significantly respond to any water chemistry parameter measured, but instead increased with increasing stream order. These results suggest that periphyton growth in low-order streams, unlike most other freshwater environments, is likely determined by stream morphology and not water chemistry. Based on these findings this method is not recommended as an indicator of agricultural impacts in low-order streams.

L5. **Investigating the role of PDK1 in mediatingAmyloid-Beta resistance in a transgenic mouse model of Alzheimer's Disease**

Richard Harris and Robert Cumming

Alzheimer's disease (AD) is principally characterized by the accumulation of senile plaques in the brain comprised of aggregates of a small neurotoxic protein called amyloid-beta (Aβ). A recent study showed that cultured nerve cells selected for resistance to Aβ toxicity display a unique form of metabolism termed aerobic glycolysis, whereby glucose is preferentially broken down into lactate instead of being processed through the mitochondria. This switch in metabolism diminishes the production of harmful oxygen free radicals, prevents apoptotic signaling, and increases the production of lactate; a metabolite that enhances memory and is neuroprotective. One of the key enzymes in mediating this effect is pyruvate dehydrogenase kinase 1 (PDK1). Nerve cells resistant to Aβ exhibit elevated levels of PDK1, whereas chemical or genetic inhibition of PDK1 results in re-sensitization to Aβ toxicity. In this study, I am examining the Aβ resistance mechanism in transgenic AD mice by administering a PDK inhibitor in the drinking water and monitoring disease progression over time using the Morris water maze to test memory, and magnetic resonance spectroscopy to examine brain metabolites, including lactate. Cultured primary cortical neurons will also be used to directly measure the effects of PDK1 inhibition on Aβ sensitivity. These experiments will test the hypothesis that elevated PDK1 activity is required to protect brain cells from Aβ toxicity *in vivo* and *in vitro*. These results will help explain how the brain can resist neurodegeneration and cognitive decline, and may contribute to the design of effective treatments for memory loss in AD patients.

L6. **Why I study rapid evolution in salmon**

Steve Sharron

Pacific salmon and rainbow trout (*Oncorhynchus* spp) have a long history of global relocation, invasion and naturalization. They are prized both as sportfish and an inexpensive protein source for peoples around the world. From their sprawling native range in the North Pacific, Oncorhynchids can be found today in temperate regions of all continents except Antarctica. They are reeled in from the highest navigable lake in the world, rivers of rugged Patagonia, the fiordland of Southern New Zealand, and from the fresh waters of the Laurentian Great Lakes. As Charles Darwin knew well, salmon make excellent study systems for evolutionary biologists because of their extensive history of colonization and local adaptation; along with their myriad variations in life history traits within and between populations. Naturalized populations provide opportunistic researchers like me a chance to explore the phenomenon of rapid or contemporary adaptation, documented numerous times in introduced salmon. While the adaptive capacity of introduced salmon has been studied for decades, there are still many traits that remain unexamined or the evidence remains sparse and conflicting. To me, the introduction of anadromous Pacific salmon to the adfluvial environment of the Great Lakes is particularly intriguing. Specifically, I want to explore how they have adapted to a novel environment where their canonical juvenile migration no longer leads to salt water. I will convince you of the importance of Pacific salmon to the study of rapid adaptation and discuss how research on naturalized Great Lakes populations can contribute to our understanding of this phenomenon.

3. Platform Presentations – Short Oral Presentations

S1. **Increasing atmospheric nitrogen deposition: implications for tallgrass prairie restoration**

Jennifer McPhee, Hugh Henry, and Laura Borden

Agricultural activity and the combustion of fossil fuels will continue to increase rates of atmospheric nitrogen deposition over the next century. Nitrogen is typically a limiting resource for terrestrial plants, and many native species are well adapted to low-nitrogen conditions. As the rate atmospheric deposition increases, elevated nitrogen can affect both plant biomass and species composition. These effects may be especially important in the context of ecological restoration projects, where the end product relies on achieving and/or maintaining a particular community composition. Increased atmospheric nitrogen deposition might increase competition from highly productive, nitrogen-demanding, non-native species, decreasing the success of native species chosen for restoration projects. We used a field experiment in Norfolk County, Ontario, to examine how nitrogen addition affects the success of tallgrass prairie restoration. We predicted that nitrogen addition would increase the abundance of plant species not included in the original seeding. In the first year following seeding, there was an abundance of the weedy species *Erigeron canadensis* L. in the nitrogen addition plots. However, the abundance of this species was greatly reduced by the second year. Contrary to our original prediction, there was an increase in the relative biomass and cover of native species with nitrogen addition, but not a significant increase in non-native, highly competitive species. The latter species were scarce at the site. Dispersal limitation may potentially delay the invasion of non-native species into tallgrass prairie restoration sites with increased nitrogen deposition.

S2. **Factors influencing migration chronology by Lesser Scaup (*Aythya affinis*) and Mallard (*Anas platyrhynchos*) during spring**

Taylor A. Finger, Scott A. Petrie, Irena F. Creed, Michael L. Schummer, Alan D. Afton, Michael L. Szymanski, and Michael Johnson

Exogenous factors reflecting changing weather conditions may influence the timing of spring migration of lesser scaup migrating from winter grounds in the southern United States to spring nesting locations in Canada and Alaska. I used satellite implanted Lesser scaup and annual spring migration surveys to compare the influence that spring weather conditions have on migration chronology. On a broad scale analysis, weather variables were averaged across regions located in the US and Canadian Prairies, the Great Lakes, and eastern Boreal Forests, and tested to determine their influence on rate of migration and date of arrival at survey stratums and breeding grounds. Implanted Lesser scaup using the traditional migration route, date of arrival and rate of migration to a Waterfowl Breeding Population stratum and breeding ground varied positively with temperature and available water on the landscape. On an individual migration analysis, weather conditions were used to determine which variables predicted a migratory movement. After removing non-significant variables, thawing degree days was the only variable that significantly predicted a migration movement. Lastly, using annual spring migration surveys from North Dakota, I observed the differences in dates of arrival by scaup and mallards into North Dakota and tested the same weather variables to observe their effect on the differences in timing of migration between the two species. Lesser scaup on average arrived earlier than Mallards however, difference in arrival were not influenced by the weather variables in my analysis. I recommend adjustments in WBPHS survey techniques and estimates for Lesser scaup breeding population.

S3. **An eye to the future: identifying early disease mechanisms in a mouse model of retinal degeneration**

Eric Dolinar, Justin Wagner, Mohammad Ali Faraz, Adam Cadesky, and Kathleen Hill

Within 25 years, when our graduate student cohort reaches middle-age approximately $30 billion will be spent annually on the devastating impacts of vision loss in Canada. Understanding early mechanisms of retinal degeneration is vital for prevention and treatment and therefore we study the *harlequin* (*hq)* mouse which carries an X-linked mutation in the *Apoptosis-inducing factor* (*Aif*) gene resulting in mitochondrial dysfunction and retinal cell loss by 4 months of age. Previously, we characterized chronic microglial activation in the *hq* retina leading to the toxic accumulation of reactive oxygen species and cytokines. The triggers of *hq* microglial activation are unknown and may be either the response of an exogenous antigen crossing a compromised blood-retina-barrier (BRB) or an endogenous photoreceptor malfunction resulting from ATP deficiency. To test the first hypothesis, cohorts of wild-type (WT) and *hq* mice at two ages (>4, and <7 months of age) received an intravenous injection of Evans Blue dye (EB). Post-mortem excavation of EB from tissues was performed in a novel formamide small-scale EB extraction. Comparisons of EB concentrations were assessed by a two-way ANOVA ($p < 0.05$). The sensitivity of our assay was confirmed with detection of EB in injected mice and not in uninjected WT mice with more EB in liver than retina. Higher EB levels were not found in the *hq* mouse retina at either age, indicative of high integrity of retinal immune privilege. These findings suggest that endogenous factors may lead to chronic microglial activation and fixes our focus towards internal photoreceptor malfunction.

S4. **The adaptive capacity of thermal tolerance: reintroduction of Atlantic salmon into Lake Ontario**

Kayla Gradil, Christopher C. Wilson, and Bryan D. Neff

Global climate change is projected to have widespread effects that could threaten the viability of natural populations. The ability of a species to adjust to climate change is modulated by its adaptive capacity, some of which involves an evolutionary response. Physiological processes of aquatic ectotherms critically depend on their thermal environment, such that the optima for performance often correspond to historic temperatures. In the face of impending climate change, conservation managers must consider augmenting or reintroducing individuals that have high thermal tolerance or those from a population with high adaptive capacity for temperature. Current restoration efforts for Atlantic salmon (Salmo *salar)* in Lake Ontario are focused on three source populations as candidates for reintroduction. In this study, I will evaluate the thermal tolerance and its underlying adaptive capacity in these candidate source populations using maximum heart rate measurements. The goal of my research is to identify which populations will have the highest relative survival and thereby greatest likelihood for long-term restoration success in the face of projected warming temperatures.

S5. ***Arabidopsis* response to spider mite feeding: perception, signaling, and response**

Kristie Bruinsma and Vojislava Grbic

Herbivores deriving nutrients at a plant host's expense represent a major biotic factor in both natural ecosystems and agricultural settings. Much research has been pursued in the attempt to unravel the factors affecting the interaction between arthropod herbivores and their plant hosts. From the plant's perspective, this interaction begins with perception of attack, initiating a signalling cascade involving phytohormones and resulting in transcriptomic and metabolic defence responses. To date, most molecular-genetic studies of plant-arthropod interaction have focused on insects; however, herbivorous mites feed on a variety of plant species. The two-spotted spider mite, *Tetranychus urticae*, feeds on over 1000 plant species, one of which is *Arabidopsis thaliana*, a model plant species previously used in studies of plant-arthropod interaction. Using these two model organisms, my research focuses on using microarray data from two *Arabidopsis* accessions with drastic differences in susceptibility to spider mite feeding to identify how *Arabidopsis* defends itself against spider mites using pre-existing differences in defensive states as well as induced plant defences. I used this microarray data to: study how *Arabidopsis* perceives attack, utilizing Damage Associated Molecular Pattern receptors, PEPR1 and PEPR2, to aid in perceiving plant tissue damage; identify Jasmonic acid as the key phytohormone involved in orchestrating the defence response following perception; and identify secondary metabolic compounds, Indole Glucosinolates, that affect mite performance and development, leading to enhanced plant resistance. Thus, my findings provide insight into how plants defend themselves against this major class of arthropod herbivores.

S6. **Effects of changing ocean acidity on the growth and toxicity of the marine raphidophyte *Heterosigma akashiwo***

Julia Matheson and Charles Trick

Harmful algal blooms (HABs) are a global issue that have been garnering the attention of scientific studies, industries, and coastal communities in the past 20-30 years. Negative impacts of these blooms on coastal waters include: toxin production, disruptions to marine food chains, and altered ecological relationships. Despite an increasing frequency of HABs, these harmful relationships are generally poorly defined and not fully understood. This is especially true in the case of the marine raphidophyte *Heterosigma akashiwo*, whose fish-killing toxic mechanism remains a mystery. My project addresses the variable toxicity from *H. akashiwo* and its relation to environmental changes. Specifically, I will examine whether acidification of coastal waters and high carbon dioxide levels (the driver of ocean acidification) stimulate toxicity from *H. akashiwo*. I hypothesize that acidified ocean waters with low pH will increase the level of toxicity in *Heterosigma akashiwo*. By closely examining the connection between pH, CO_2, and the variable toxicity in *H. akashiwo*, this project will provide insight on this species' toxic mechanism and enhance the current understanding of HAB dynamics as a whole.

S7. **Habitat selection during the nonbreeding period by Eastern Population Tundra Swans**

Katelyn H.A. Weaver, Michael L. Schummer, Scott A. Petrie, and Hugh A.L. Henry

Around 1970, wetland loss, conversion to agriculture necessitated Eastern Population (EP) Tundra Swans (TUSWs) to incorporate waste agricultural grains into their diets in addition to traditional foods. Identifying how TUSWs select wetland and terrestrial (agricultural fields) habitats in these altered landscapes will enable conservation strategies to ensure adequate foraging habitats are available for these birds. Further, understanding habitat selection is essential to assess TUSWs' biological requirements, predict effects of further habitat change, and test hypotheses underlying ecological processes. Our study will use satellite telemetry data from 55 EP TUSWs to investigate seasonal selection of agricultural and wetland habitats during the nonbreeding period. I hypothesize that diurnal habitat selection will differ seasonally at the Atlantic Coast, Great Lakes and Prairies due to nutritional requirements, food availability and habitat accessibility. I predict that TUSWs will select wetland habitats during autumn, shifting to agricultural habitats during late autumn and early winter and continue using agricultural habitats throughout spring. When swans occur in aquatic habitats we hypothesize that they will select wetlands based upon food availability and accessibility. We predict that swans will select palustrine and estuarine wetlands during autumn and winter and lacustrine wetlands during spring. We also predict that swans will select habitat with greater wetland coverage and density. I will compare independent habitat variables at used locations to random locations using mixed conditional logistic regression models. Information about habitat selection obtained from our study will help inform conservation strategies for EP TUSWs and other waterfowl at staging and wintering areas.

S8. **Olfaction-related copy number variants, important for mate selection, are predominant in wild mice but infrequent in in bred laboratory mice**

Maja Milojevic, Beth Locke, Mark Daley, and Kathleen Hill

Copy number variants (CNVs) are major contributors to genetic and phenotypic diversity but the degree to which CNVs are affected by different selective pressures is not well known. CNVs involve the duplication and deletion of genomic regions and can contain dosage-sensitive genes that affect phenotypic expression. Wild-caught and laboratory-bred mice are an ideal experimental framework to study the impact of natural and artificial selective pressures on CNVs. These two pressures are hypothesized to impact structural variation differently across a mouse genome. CNVs can be detected using the Mouse Diversity Genotyping Array (MDGA). MDGA probes bind to fluorescently labelled target DNA fragments, releasing fluorescence light at intensities proportional to the number of target DNA fragments. A publically available dataset of 351 MDGA fluorescence intensity files allowed the hypothesis to be tested by comparing genome-wide CNV profiles in wild-caught mice and laboratory-bred mice. The 351 mice were found to have 10,895 CNVs, containing over 5,000 genes. Wild-caught mice had 37 and 41 more CNVs per mouse than the C57Bl/6J and C57Bl/6NJ inbred strains, respectively. Major biological pathways affected by CNVs in wild-caught mice were involved in olfaction, pheromone response and immunity. Biological pathways affected in C57Bl/6J mice were immunity and nucleosome assembly while in the C57Bl/6NJ strain, the major pathway was immunity. Inbred mice are not isogenic and have a bias for immunity-related CNVs. Wild mice contain a greater number and diversity of CNVs, mimic human genetic diversity and show a strong bias for olfactory phenotype diversity, relevant to mate selection.

S9. **Redundant role of cytokinin receptors during symbiotic root nodule organogenesis in *Lotus japonicas***

Mandana Miri, Mark Held, Hongwei Hou, Christian Huynh, Loretta Ross, Shushei Sato, Satoshi Tabata, Jillian Perry, Trevor Wang, and Krzysztof Szczyglowski

Cytokinins are essential plant hormones that control many aspects of plant development. They participate in responses to endogenous cues and play an important role as messengers for external stimuli related to diverse biotic and abiotic conditions. During beneficial root symbiosis between legumes and nitrogen-fixing rhizobia, cytokinin signaling constitutes the key endogenous signal for the nodule structure organogenesis. In *Lotus japonicus*, activation of the LHK1 histidine kinase cytokinin receptor is required and also sufficient for this process to occur. However, the fact that some nodulation still occurs in *lhk1-1* loss-of-function mutants indicates the presence of an LHK1-independent signaling pathway. In this study, we have tested a hypothesis that additional *L. japonicus* cytokinin receptors, such as LHK1A, LHK2 and LHK3, might function in at least a partially redundant manner to mediate nodule formation. We show that unlike *lhk1-1*, the triple mutant plant carrying deleterious mutations in all three cytokinin receptor genes, *Lhk1*, *Lhk1A* and *Lhk3*, does not form nodules. On the other hand, ectopic application of cytokinin to wild-type roots increases the steady-state level of all of the cytokinin receptor mRNAs but fails to do so in the *lhk1-1* mutant. Based on the obtained data, a working model is presented in which LHK1 has a unique function in the root epidermis but acts partially redundantly with LHK1A and LHK3 in the root cortex to mediate differentiation of nodules in *L. japonicus*.

S10. **A genetic basis for plasticity in thermal tolerance within a coastal population of Chinook salmon**

Nicolas J. Muñoz, John W. Heath, Anthony P. Farrell, and Bryan D. Neff

With global temperatures projected to surpass the limits of thermal tolerance for many species, evaluating the genetic architecture underlying thermal tolerance is critical for understanding the potential for evolutionary responses to climate change. For aquatic ectotherms, such adaptive responses will likely involve adjustments of their critical thermal maximum (CT_{max}) as well as their ability to deliver oxygen to tissue in high temperatures. This study used a quantitative genetic breeding design coupled with multiple rearing environments to evaluate the heritability as well as the plasticity of thermal tolerance within a coastal population of Chinook salmon (*Oncorhynchus tshawytscha*) from the Quinsam River, British Columbia. Families of fish were reared in both current and elevated (+5°C) temperatures, and the CT_{max} and hematocrit (Hct) of offspring from each family and temperature treatment were measured. Plastic adjustments of thermal tolerance were detected, with the mean ± S.D. CT_{max} and Hct significantly increasing from 24.9 ± 0.6°C to 26.1 ± 0.5°C and 37.2 ± 5.6% to 39.9 ± 5.4% in the current and elevated treatments, respectively. Additive genetic (i.e. heritable) variation for both CT_{max} and Hct was negligible, although there were significant interactions between paternal ID, maternal ID and temperature treatment for both measures, indicative of a genetic basis for plasticity. Although adaptation from standing genetic variation for CT_{max} and Hct may be limited, these results suggest that plasticity and genetic variation for plasticity may provide adaptive mechanisms by which Pacific salmon populations can cope with rising temperatures.

4. Poster Presentations

P1. **Expression of fatty acid ω-Hydroxylase (*GmFAωH*) genes in soybean (*Glycine max*) roots**

Trish Tully, Jessica Koteles, Pooja Sharma, and 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. 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 (FAωHs). In soybean, the FAωH genes show a tissue specific expression pattern with only genes *GmFAωH-5* and *GmFAωH-6* being expressed in root tissue. A model system of hairy roots will be used to further explore the relationship between these two genes, suberin deposition, and pathogen resistance. In conjunction with a bioinformatics analysis of the two FAωH genes expressed in roots, hairy roots can be transformed using an *Agrobacteriium rhizogenes*-based gene transformation system where the expression of these two genes can be modulated using over-expression and RNAi vectors. The proposed downstream change in suberin deposition pattern can be analyzed using GC-MS, and pathogen resistance can be tested using a pathogenicity assay.

P2. **Canada's forests in a changing climate impacts, responses, and unanswered questions**

Joseph R. Stinziano and Danielle A. Way

Air temperatures are expected to increase to a greater extent at high latitudes this century, mainly due to anthropogenically-driven increases in CO_2. Warming is expected to positively influence Canada's boreal forests by lengthening the growing season, advancing the treeline, and increasing productivity and growth. Combined with the expected effects of CO_2 fertilization on tree growth, Canada's forests are expected to become a greater carbon sink this century. However there are other environmental factors such as photoperiod, edaphic features, water, and nutrient availability that may constrain tree responses to global change. Further, the interactive effect of increased temperature and CO_2 on Canadian boreal species as a whole is relatively unknown. Using a meta-analysis of studies involving temperature and CO_2 manipulations on Canadian boreal tree species, we find that Canadian boreal forest species as a whole show a decline in biomass with increasing growth temperatures, which is ameliorated by elevated CO_2. Photosynthetic CO_2 assimilation tends to respond positively to increased temperatures and CO_2, while there is insufficient data on the effects of temperature on photosynthetic capacity in Canadian boreal species to draw conclusions. The constraint that photoperiod imposes on seasonal changes in photosynthesis in Canadian boreal evergreen species is currently unknown, but my on-going work aims to elucidate whether photoperiod impacts the autumnal decline in photosynthetic capacity in a dominant Canadian tree species, white spruce (*Picea glauca*).

P3. **Factors influencing autumn-winter distribution of dabbling ducks in the Atlantic and Mississippi Flyways of North America**

Lena M. Vanden Elsen, Scott A. Petrie, Christopher G. Guglielmo, and Michael L. Schummer

In migratory birds, evidence suggests northward latitudinal shifts in distribution during winter for a variety of species in North America (La Sorte and Thompson 2007). Severity of weather necessary to cause southern migration by waterfowl may differ among species. Also, some duck species may migrate independently of weather severity, where migration results from endogenous rhythms related to photoperiod (Gwinner 1996). Because wildlife habitats are predicted to change with changing climates, species of dabbling ducks that use weather cues to migrate may remain spatially linked to habitat resources relative to those using photoperiod cues. A Weather Severity Index (WSI) was developed for mallards (*Anas platyrhynchos*; Schummer et al. 2010) that used temperature and snow cover data. The WSI explained change in relative abundance of mallards at mid-latitude staging areas during autumn and winter. However, in mallards, photoperiod explained substantially less variation in migration activity during the same period. We aim to investigate the relative contribution of weather and photoperiod cues for other species of dabbling ducks using data from standardized waterfowl surveys conducted through eastern North America, September – February. Developed WSIs for each species of dabbling duck will be modeled with future climate change scenarios to determine how dabbling duck distributions may vary under climate change. Preliminary results suggest that migration thresholds differ between northern and mid-latitude sites, with mallards leaving Long Point, Ontario approximately two weeks earlier than they would leave Missouri, USA. Investigations are still ongoing.

P4. **The use of two Great Lake islands by migrating bats**

Toby J. Thorne

Flight allows bats to migrate over relatively large distances, in order to follow food resources and favorable weather climate. The difficulties of tracking migrating bats means most studies have used alternative methods such as stable isotope analysis, and the passage of bats though 'pinch points' when migrating. An example of this would be at Long Point Nature Reserve, where a spit of land extends into Lake Eire. The distance between the end of the spit to the other side of the lake represents the shortest crossing at the center of the lake and so a concentration of migrating bats, and birds, is found at Long Point. As well as spurs of land, islands can also be important sites where a concentration of migrating animals occurs. I will look at two such islands in the Great Lakes; Amherst and Peele islands are found at the northeast of Lake Ontario and the southwest of Lake Erie respectively. The two islands differ in their setting; Amherst is approximately 2km from the mainland, whereas Peele is 10-12km from the nearest landfalls, and potentially represents a more significant stopping point for bats migrating via Peele point to the north. I plan to test the importance of these sites for migrating bats and look for differences between them. This will primarily involve long-term monitoring by bat detectors and call analysis to identify species, supplemented by mist-netting and other fieldwork as appropriate.

P5. **Inheritance of virulence in the root rot pathogen *Phytophtora sojae***

Sirjana Devi Shrestha and Mark Gijzen

The interaction of pathogen avirulence (*Avr*) and host resistance (*Rps*) genes determines the disease outcome of the root and stem rot pathogen *Phytophthora sojae* on soybean plants. The messenger RNA transcript levels of the *Avr3a* gene of *P. sojae* are variable among strains. Strains with detectable *Avr3a* mRNA transcript are avirulent and strains lacking *Avr3a* mRNA transcript are virulent on soybean plants carrying the *Rps3a* gene. A genetic out-cross between the virulent strain (ACR10) and avirulent strain (P7076) of *P. sojae* showed that all F1 and F2 progeny were virulent on soybean plants carrying *Rps3a* gene, despite that the *Avr3a* gene itself segregated normally. The presence of *Avr3a* mRNA transcripts were detected in the avirulent strain P7076 but not the virulent strain ACR10 nor in any of the progeny. To determine whether silenced alleles of *Avr3aP7076* from F1 (ACR10 X P7076) progeny have the capacity to silence expressed alleles of other strains of *P. sojae*, the F1 hybrid was test-crossed with strain P6496. A total of 110 oospores were isolated and hybrids identified using three different co-dominant DNA markers. From these, 31 hybrids (*Avr3aP6497* /*Avr3aP7076* = 14 and *Avr3aP6497* /*Avr3aACR10*= 17) were detected. Analysis by RT-PCR of hybrids showed that silenced alleles of *Avr3aP7076* do not appear to have the ability to silence *Avr3aP6497* alleles, since all hybrids were found to express *Avr3a* transcripts and to be avirulent towards soybean plant carrying *Rps3a*.

P6. **Study of the critical elements of protein body biogenesis in *Nicotiana benthamiana* leaves**

Reza Saberianfar, Jussi J. Joensuu, Sussanne Kohalmi, and Rima Menassa

Elastin-like polypeptides (ELP) and hydrophobin (HFBI) are two types of fusion tags that are shown to increase the accumulation levels of recombinant proteins when transiently expressed in *Nicotiana benthamiana*. ELP and HFBI fusion tags are capable of inducing the formation of protein bodies (PBs) in plant leaves. PBs are endoplasmic reticulum (ER) derived organelles originally found in seeds and required for accumulation of large amounts of protein. The mechanism by which the ELP and HFBI fusion tags induce the formation of PBs is not well understood. We have studied the critical elements of PB formation with the ELP and HFBI fusion tags. Our results show that: 1. A clear size difference was observed in distribution patterns of PBs induced by ELP or HFBI 2. PB formation is a concentration-dependent mechanism *in vivo* 3. Fusion tags positively affect the induction of PBs but are not necessary for PB formation 4. ER retrieval of proteins is required for PB formation, and 5. Secretory proteins can integrate to the PBs if co-expressed with the PB inducing proteins. In this study the potential of PB induction as a new approach to high-level recombinant protein production will be discussed.

P7. **Identification and characterization of a *Cysteine Protease* gene in tobacco for use in recombinant protein production**

Kishor Duwadi, Ling Chen, Angelo Kaldis, Rima Menassa, and Sangeeta Dhaubhadel

Plants are an attractive host system for pharmaceutical protein production. Many therapeutic proteins have been produced and scaled up in plants in a low cost compared to the conventional production systems. The main technical challenge during this process is to produce sufficient level of protein in plants. Low yield is generally caused by proteolytic degradation during expression and downstreaming of recombinant proteins. One approach to overcome proteolytic degradation involves creation of stable transgenic lines with reduced proteolytic activity. Recently, it has been found that Cysteine protease (CysP) inhibitors show protective effect on human immune- regulatory interleukin -10 (IL-10) production in plants. To identify *CysP* gene(s) involved in IL-10 accumulation, DFCI tobacco expressed sequence tag database was searched using 'Cysteine protease' as keyword. This search revealed a total of 55 putative *CysPs* out of which 32 are tentative contigs (TC) and 23 are singletons. Based on their expression in leaf tissue, 10 candidate *CysPs* were identified for further characterization. Overexpression and silencing constructs were made in order to study the effect of the selected *CysP* genes in tobacco lines that overexpresses IL-10 protein. Agrobacteria-mediated plant transformation technology was utilized to generate transgenic lines with reduced CysP and increased IL-10 accumulation. Using Enzyme linked immunosorbent assay (ELISA) an IL-10 fold increase upto1.6 was found in some T0 *CysP6* silenced plants compared to the levels present in wild type plants.

P8. **Analysis of the structural alterations in the genomes of the C57BL/6J inbred mouse line compared to 19 wild-caught mice**

Alanna K. Edge

Structural variations throughout the genome are more common than previously thought. Duplications and deletions of regions greater than 500 bp are called copy number variants (CNVs) and contribute to alterations in gene dosage and expression, affecting complex phenotypes. Here, CNVs in 8 C57BL/6J inbred mice and 19 wild-caught mice from diverse populations and of two subspecies were investigated. Since these mice represent extremes of genetic diversity, CNV profiles will likely differ: very few CNVs are expected in B6 mice, and wild-caught might are expected to have more CNVs, of which more are unique. CNVs were called from Mouse Diversity Genotyping Array (MDGA) data, and software called Hotspot Detector for Copy number Variants (HD-CNV) was used to identify CNVs shared between samples. A total of 232 CNVs were identified in B6 mice, averaging 29 per mouse, and a total of 1,298 CNVs identified in wild-caught mice, averaging 68 per mouse. For B6 mice there was more variation than expected for an isogenic line and 22.0% of CNVs in were unique. In wild-caught mice 44.3% of CNVs were unique and shared events indicate genomic hotspots or common origin. There was also strong contrast between the genes enriched in B6 and wild-caught mouse CNVs. Inbred mice are useful in scientific research due to their isogeneity, however they may contain more structural variation than previously seen. CNVs should therefore be taken into account when selecting mice for research. Also, since inbred mice are not genetically diverse, wild-caught mice may best mimic human population variation.

P9. **Salt stress affects accumulation of flavonoids and carotenoids in *Solanum nigrum***

Sasoussen Ben Abdallah, Lisa Amyot, Mokhtar Lachâal, Najoua Karray Bouraoui, and Abdelali Hannoufa

Medicinal plants accumulate a wide range of bioactive molecules, including secondary metabolites, such as flavonoids and carotenoids. These potent antioxidants are naturally occurring pigments that are ubiquitously present in *Solanum nigrum*, where they play important roles in the protection of the plant against biotic and abiotic stresses, including salinity. In this study, we set out to investigate the effect of sodium chloride on the production of carotenoids and flavonoids and the expression of their biosynthetic genes in leaves of the medicinal plant *Solanum nigrum*, which belongs to the Solanaceae family. Using different concentrations of NaCl (0, 50, 100 and 150 mM), we detected significant changes in flavonoid and carotenoid contents, and in the expression of key enzymes in the biosynthetic pathways of these compounds. We noted an up to 6-fold increase in total flavonoids, and quercitin- 3- glucoside in the leaves of plants treated with 150 mM NaCl. This increase in flavonoid accumulation was accompanied by enhanced expression of two flavonoid biosynthesis genes, chalcone synthase and flavonol synthase. In addition, phytoene synthase 1, phytoene synthase 2 and lycopene beta-cyclase were found to act synergistically to up-regulate carotenoid biosynthesis, as enhanced levels of beta-carotene and lutein were detected in leaves upon exposure to NaCl. Our analysis suggests that salinity stress induces expression of key genes involved in the biosynthesis of flavonoids and carotenoids resulting in the accumulation of these metabolites.

P10. **Effects of elevated CO_2 and growth temperatures on respiration rates in Norway spruce (*Picea abies*)**

Yulia Kroner

Future climate change scenarios will include carbon dioxide-based increases in temperature. Boreal forest ecosystem located in circumpolar region will experience the most dramatic change in temperature. Plants have the ability to acclimate to changes in temperatures and rising carbon dioxide and these physiological responses will likely change global carbon fluxes. To properly model future carbon fluxes from vegetation, major parameters affecting the carbon cycle, such as autotrophic day and night respiration, have to be better characterized. My study investigates the response of respiration rates and light-saturated photosynthesis in the dominant boreal evergreen species, Norway spruce, to predicted climate change scenarios (higher carbon dioxide levels and rising temperatures), and therefore provides essential information required for accurate modeling of forest carbon fluxes.

P11. **The effect of natal philopatry on parasite load and immune function in song sparrows (*Melospiza melodia*)**

Heather MacGillivray and Beth MacDougall-Shackleton

Parasites are a widespread and diverse group that can significantly reduce host survivorship and reproductive success. The more heterogeneous the environment an organism encounters, the more likely it is to encounter a wide variety of parasites. Thus animals that disperse to breed far from where they were born should encounter a wider variety of unfamiliar parasites, relative to more philopatric individuals. Previous work in our focal breeding population of song sparrows has shown that individuals of local origin have lower bloodborne parasite loads than non-local individuals. Host adaptation to the local parasite fauna has been suggested as a candidate mechanism for this pattern, but alternatively, philopatric birds (of local origin) may have more effective immune systems than less philopatric birds. To distinguish between these possibilities, I use genetic assignment tests to identify birds of local origin and I relate this to parasite loads and multiple measures of immune function. I will discuss predicted and observed differences between local and non-local birds in parasite load, innate and adaptive immunity.

P12. **Stable isotope analysis of migratory distance and its relationship to immune allocation in song sparrows *Melospiza melodia***

Tosha Kelly, Scott MacDougall-Shackleton, and Beth MacDougall-Shackleton

Animals are exposed to a diverse range of parasites, many which are pathogenic. Because such parasites can place strong selective pressures upon hosts, optimal allocation to immunity is an important determinant of fitness. Because immunity in general is costly, life history theory predicts that immune allocation should vary with the diversity and abundance of parasites that a host is likely to encounter. At the same time, migratory animals face trade-offs between investing in immune defence and performing strenuous exercise, such as migratory flight. Birds that migrate long distances may be particularly challenged because as flight distance increases, so does the energetic cost of migration; yet these same long-distance migrants presumably encounter a growing number of unfamiliar parasites than do individuals migrating shorter distances. To determine if immune allocation varies with migratory distance, I estimated variation in migratory distance in a breeding population of song sparrows (*Melospiza melodia*), using stable isotope analysis. I then assessed birds at a range of immune measures that address diverse aspects of the innate and adaptive immune response. I predicted that birds strategically allocate their immune response such that longer-distance migrant individuals invest more in innate immunity and shorter-distance migrant individuals invest more in adaptive immunity. Results will be discussed.

P13. Habitat use of two swallowtail butterfly species: testing for positive edge responses in a fragmented landscape

Jenna Siu, Nusha Keyghobadi, and Daria Koscinski

Landscapes are becoming increasingly fragmented and natural habitat is being lost, contributing to a global decline in biodiversity. Research on the impact of habitat fragmentation on wildlife populations has mainly focused on species that rely on the interior of one habitat type. However, species that respond positively to the boundary between two habitat types, or *edge species*, should also be considered to gain a full understanding of these landscape changes. The eastern tiger (*Papilio glaucus*) and the spicebush (*Papilio troilus*) swallowtails require two different, or *complementary*, resources (larval host plants and adult nectar sources) that occur in different habitat types (forest and meadow). They must cross habitat boundaries to obtain these resources, making them edge species. My behavioural study quantifies the edge response of these charismatic swallowtail butterfly species at forest/meadow edges by assessing the distribution of their relative abundance and flight orientation in both habitats and at the forest/meadow boundary. My work contributes to better understanding of the connectivity of populations in the fragmented landscape of southwestern Ontario.

P14. *Lotus japonicas AMP1* and *HAR1* act synergistically to regulate root architecture

Alexandre Tromas, Chong S. Kim, Mark Held, Takuya Suzaki, Bogumil Karas, Shusei Sato, Satoshi Tabata, Masayoshi Kawaguchi, and Krzysztof Szczyglowski

Deleterious mutations in the *L. japonicus HYPERNODULATION ABERRANT ROOT FORMATION 1* (*HAR1*) locus lead to hypernodulation and hypermycorrhization phenotypes but also restrict root length and significantly increase root branching of un-inoculated *har1-1* mutant plants. *HAR1* is a central regulator of symbiotic and non-symbiotic root development in *L. japonicus*. A search for genetic suppressors of the *har1-1* phenotype lead to the identification of a root branching hypermorph, called *L. japonicus cluster root-like1* (*crl1*; so named for its superficial resemblance to genuine cluster roots). Instead of wild-type root architecture, *crl1* forms one large cluster of short rootlets with limited growth capacity. Genetic analyses have shown that the *crl1* root phenotype is determined by two independently segregating recessive mutations, *har1-1* and *Ljamp1-1*. We show that the *L. japonicas AMP1* gene encodes a predicted homologue of the *Arabidopsis* ALTERED MERISTEM PROGRAM 1 protein. As in *Arabidopsis*, the *Ljamp1-1* mutation has a pleiotropic effect on *L. japonicus* as reflected by increased cotyledon number, low fertility and short and highly branched shoots and roots. Thus, root architecture seems to be regulated by a synergistic action between *HAR1* and *LjAMP1* and the simultaneous impairment of these two genes results in reduced apical dominance. Although the *Ljamp1* single mutant root phenotype resembles *har1-1,* the *Ljamp1* mutation does not affect the symbiotic properties of *L. japonicus* Gifu, which is unlike an allelic *Ljamp1* mutation in *L. japonicus* MG20. We are currently testing the root architecture and nodulation phenotype of two new Gifu null *amp1* mutants.

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