



6<sup>TH</sup> ANNUAL

## BIOLOGY GRADUATE RESEARCH FORUM

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# AGENDA

PRESENTED BY

THE DEPARTMENT OF BIOLOGY AND  
THE SOCIETY OF BIOLOGY GRADUATE STUDENTS

FRIDAY, OCTOBER 16<sup>TH</sup>, 2015

PHYSICS AND ASTRONOMY BUILDING  
THE UNIVERSITY OF WESTERN ONTARIO

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## SCHEDULE

8:00 – 8:30 am	Registration / Poster set-up / Load presentations
8:30 – 8:45 am	Opening Remarks, <b>Mark Bernards</b> - Chair, Department of Biology Overview of BGRF 2015, <b>Aniruddho C. Hoque</b> - Chair, Organizing Committee, BGRF 2015
EVENT	Session I - Long Talk (10 minute talk + 2 minute Q/A)
8:50 – 9:02 am	Arachnids of the Arctic: cold tolerance and water immersion survival in Arctic spiders and pseudoscorpions: <b>SUSAN ANTHONY</b>
9:05 – 9:17 am	Characterizing the Genetic Basis of Behavioural Isolation Between Drosophila Species: <b>CARYN DOONER</b>
9:20 – 9:32 am	Decomposition Dynamics in Boreal Peatlands Under a Future Climate: <b>ROSA DEL GUIDICE</b>
9:35 – 9:47 am	Porcine Epidemic Diarrhea Virus: Producing a Preventative Solution Using the Membrane Protein: <b>ZAYN KHAMIS</b>
9:50 – 10:02 am	Androgens and immunity in bluegill sunfish: <b>JOHN LOGGIE</b>
10:05 - 10:45 am	POSTER SESSION / BIOBOOTH / COFFEE BREAK
EVENT	3- MINUTE THESIS
10:50 – 11:13 am  (PARTICIPANTS WILL BE CALLED IN A RANDOM ORDER)	<p>Death from the shadows: Assessing perceived predation risk effects on juvenile survival: <b>MARK CHARLES ALLEN</b></p> <p>The influence of plant growth form on porewater DOC concentration and character in northern peatlands: <b>CATHERINE DIELEMAN</b></p> <p>The Green (Immuno-)Gobulin: Development of a plantibody to prevent colonization of Escherichia coli O157:H7 in the bovine gastrointestinal tract: <b>ADAM SCOTT CHIN FATT</b></p> <p>Climate change impacts on communities of fungi in boreal peatlands: <b>ASMA ASEMANINEJAD HASSANKIADEH</b></p> <p>Genomic correlates to kin recognition and invasiveness in a subterranean termite: <b>TIAN WU</b></p>
11:15 am - 12:10 pm	POSTER SESSION / BIOBOOTH / LUNCH

## SCHEDULE

EVENT	Session II - Long Talk (10 minute talk + 2 minute Q/A)
1:45 - 1:57 pm	Flight performance in a migratory songbird exposed to elevated dietary methyl-mercury: <b>YANJU MA</b>
2:00 - 2:12 pm	Regulation of mitochondrial metabolism during hibernation by reversible suppression of electron transport system proteins: <b>KATE MATHERS</b>
2:15 - 2:27 pm	Candidate genes involved mate-preference in Drosophila: <b>JALINA BIELASKA DA SILVA</b>
2:30 - 2:42 pm	Soybean root suberin and resistance against the pathogen Phytophthora sojae: <b>TRISH TULLY</b>
2:45 - 2:57 pm	Individual diversity at MHC as a predictor of survival and a correlate of neutral-locus heterozygosity in free-living Song Sparrows: <b>MATTHEW JAMES WATSON</b>
EVENT	KEYNOTE SPEAKER
3:15 - 4:00 pm	<b>DR. BOGUMIL KARAS</b> President and CSO at Designer Microbes Inc. & Adjunct Scientist at J. Craig Venter Institute
EVENT (4.05 - 4.30 pm)	PRIZES/CLOSING REMARKS

## LONG TALK PRESENTERS

### Arachnids of the Arctic: cold tolerance and water immersion survival in Arctic spiders and pseudoscorpions

Susan Anthony,  
Supervisor: Dr. Brent Sinclair

Arctic arthropod species have to cope with extreme winter temperatures, short summer season, and intermittent flooding. The mechanisms of coping with cold (cold tolerance strategies) and limits of thermal activity have never before been explored in Canadian Arctic arachnids. This past summer, I collected four species of Pardosa wolf spiders (*P. moesta*, *P. lapponica*, *P. sodalis*, and *P. glacialis*), and one species of pseudoscorpion (*Wyochernes asiaticus*) from 60° to 70° latitude in the Yukon Territory. I determined their freezing temperatures (supercooling point, SCP), critical thermal maxima and minima (CT<sub>max</sub>, CT<sub>min</sub>; temperatures beyond which normal locomotion ceases), and lower lethal temperatures. Arctic spider species have significantly lower CT<sub>mins</sub> than spider species from warmer climates (*Latrodectus hesperus* California), but CT<sub>max</sub> is relatively similar across all species. The pseudoscorpions are as cold hardy as the other Arctic arachnids, but have a CT<sub>max</sub> that matches other Sub-polar pseudoscorpions, but is lower than the other arachnids I have collected. Further, the pseudoscorpion lives at the river's edge and likely experiences seasonal immersion in flooded water. I found that this species can survive over a week immersed in oxygen-rich and de-oxygenated water, and has the same death rate as non-immersed individuals. These preliminary results show that there is much left to be learned about Arctic species, and whether they can adapt to the drastically changing climate in the North.

### Characterizing the Genetic Basis of Behavioural Isolation Between Drosophila Species

Caryn Dooner  
Supervisor: Dr. Amanda Moehring & Dr. Susanne Kohalmi

Behavioural isolation is one of the mechanisms through which speciation can occur. Behavioural isolation typically involves divergence in aspects of courtship and mating, leading to reproductive isolation. In general, the genetic basis of male courtship is better understood than that of female rejection behaviour, yet the latter more often determines whether copulation occurs. *Drosophila* is a commonly-used model for studies of behavioural isolation. *Drosophila simulans* and *D. melanogaster* are found in overlapping regions, but are behaviourally isolated from one another as *D. simulans* females will not mate with *D. melanogaster* males. A previous mapping study identified *Mekk1* as a gene that contributes to female rejection behaviour. The purpose of this study is to determine how *Mekk1* contributes to female rejection behaviour. The two lines where this behaviour was observed (*D. melanogaster* and *D. simulans*) were sequenced for *Mekk1*. Both coding and non-coding sequence differences were found. While it is possible that coding differences contribute to the behaviour, there were no differences in functional domains, meaning that differences in *Mekk1* expression levels are more likely responsible for the behavioural phenotype. I assayed levels of gene expression using reverse transcription polymerase chain reaction (RT-PCR) in four sample types: female adult heads, female adult bodies, female pupal heads and female pupal bodies. While behaviour is likely to be controlled by a neural process, bodies were also assayed since other physiological mechanisms and feedback loops could affect the behaviour. Two different lifecycle stages were included as neural development occurs during pupation, and the behaviour is observed in adult flies. Although no significant difference was

found with RT-PCR between species, there is a trend that Mekkl is more highly expressed in pupae bodies in *D. melanogaster* compared to *D. simulans*. This trend in RNA expression will be explored further using more sensitive analysis.

### **Decomposition Dynamics in Boreal Peatlands Under a Future Climate**

Rosa Del Giudice  
Supervisor: Dr. Zoë Lindo

Climate change is expected to increase atmospheric carbon dioxide (CO<sub>2</sub>) levels and global temperatures. In Boreal peatlands, these changes are expected to indirectly affect decomposition through changes in litter input and decomposability associated with changes in plant species composition. Specifically, observed changes in plant community composition have been a decrease in the abundance of peat-forming mosses (*Sphagnum* spp.) and an increase in graminoid and shrub species. I used *Sphagnum* spp., *Carex magellanica* (graminoid) and *Chamaedaphne calyculata* (woody shrub) litter to quantify the decomposability and carbon release of these three species. Initial decomposability metrics were measured during leaching and were namely: mass loss during leaching, dissolved organic carbon release, respiration and carbon lability analyses. *Sphagnum* spp. released the least amount of dissolved organic carbon, while *Ch. calyculata* released the most amount of dissolved organic carbon. Dissolved organic carbon released by *Ch. calyculata* was the most recalcitrant, while dissolved organic carbon released by *Sphagnum* spp. was the most labile. For microbial respiration during 48-hour leaching, *C. magellanica* and *Sphagnum* spp. had the greater average microbial respiration compared to *Ch. calyculata*. These results suggest that possible changes in plant community composition from *Sphagnum* mosses to woody shrub vegetation may accelerate carbon loss from northern peatlands.

### **Porcine Epidemic Diarrhea Virus: Producing a Preventative Solution Using the Membrane Protein**

Zayn Khamis  
Supervisor: Dr. Rima Menassa

Porcine epidemic diarrhea (PED) has caused widespread economic losses due to the death of neonatal pigs and the weight loss of fattening pigs. A subunit vaccine against its causative agent, porcine epidemic diarrhea virus (PEDv) could help protect herds through vaccinating sows, providing passive lactogenic immunity to suckling newborns. The membrane (M) and spike (S) proteins of PEDv have epitopes that can stimulate neutralizing antibodies, giving effective immunogenic protection. Research to date has focussed on building subunit vaccines with the S protein – however, in contrast to S, M is less susceptible to mutations, and also plays a critical role in viral assembly and budding. Using plants as a platform to produce the protein allows for feeding the leaves to sows without processing or extracting the protein, a method that has been shown to illicit a strong immune response. It is hypothesized that the M protein of PEDv can be produced transiently in *Nicotiana benthamiana* at high levels. Little research has been done on producing M, and it has never been produced in plants. My research has successfully shown that high levels of M expression can be achieved in *N. benthamiana* once the challenges of membrane protein production and extraction are overcome. To overcome production challenges, different constructs have been tested to find the construct that expresses most highly, and several extraction buffers have been used to fully appreciate how much protein is being produced. Having successfully expressed M in plants allows the opportunity to test for its abilities to bind with other proteins to form virus-like particles, and opens up possibilities for scaling up production.

## **Androgens and immunity in bluegill sunfish (*Lepomis macrochirus*)**

John Loggie

Supervisor: Dr. Bryan Neff

Androgens such as 11-keto testosterone (11-KT) are known to mediate the expression of many traits and behaviours associated with male reproduction, but the immunocompetence handicap hypothesis posits that androgens also play a role in immune system regulation. Here, I test the prediction that male bluegill sunfish (*Lepomis macrochirus*) will demonstrate a negative relationship between circulating 11-KT concentration and innate immune system activity. Male fish were captured either immediately prior to spawning or between bouts of spawning activity: circulating 11-KT concentrations were determined along with measures of neutrophil respiratory burst activity and leucocyte concentrations in blood. I found no relationships between circulating 11-KT and any of my immunity measures, although measures of innate immunity correlated with one another. Ongoing work will aim to determine whether or not circulating 11-KT concentration is related to the induction of cytokine gene expression following an experimental vaccination. Together, these studies are among the first to test the predicted immunosuppressive effect of androgens in fish.

## **Flight performance in a migratory songbird exposed to elevated dietary methyl-mercury**

Yanju Ma

Supervisor: Dr. Christopher G. Guglielmo

Many songbirds migrate long distances and may be exposed to different dietary methyl-mercury (MeHg) concentrations during their annual cycle. There is ample evidence that environmental MeHg exposure can cause reductions in avian fitness, particularly in aquatic species during breeding. However, recent work indicates that terrestrial songbirds that live in association with MeHg contaminated environments can bioaccumulate significant MeHg in tissues. How the MeHg levels we observe in migratory songbirds affect flight performance and migration is still unknown. We conducted a MeHg dosing experiment (0.5ppm in wet weight, relevant to contaminated environment) with yellow-rumped warblers (*Setophaga coronata*) while they were in a hyperphagic, migratory state. Warblers rapidly bioaccumulated dietary MeHg to 10 to 20 fold in blood, approximately 60 fold in liver, 40 fold in brain and muscle, and over 100 fold in kidneys over after 2 weeks. There was no significant effect of MeHg on vertical takeoff ability. In 2-hour wind tunnel flights, MeHg treated warblers had a greater median of numbers of strikes (landing or losing control), longer strike duration, and shorter flight duration than control birds. There was also a positive correlation between total blood Hg concentration and the median of strikes in the MeHg treated warblers. In terms of energetics MeHg treated warblers had a nearly significant greater cost of transport (2-tailed  $P = 0.065$ ), which may have been caused by their poorer control in flight. In conclusion, hyperphagic migratory birds rapidly accumulate MeHg from the diet which has the potential to affect flight performance and migration ability.

## **Regulation of mitochondrial metabolism during hibernation by reversible suppression of electron transport system proteins**

Kate Mathers  
Supervisor: James Staples

During hibernation, small mammals cycle between periods of torpor ( $T_b=5^{\circ}\text{C}$ ) and interbout euthermia (IBE;  $T_b=37^{\circ}\text{C}$ ). Mitochondrial metabolism is rapidly ( $<2\text{hrs}$ ) suppressed by 70% in torpor relative to IBE, though the mechanisms of this transition are unknown. We investigated flux through electron transport system (ETS) proteins in intact liver mitochondria of 13-lined ground squirrels (*Ictidomys tridecemlineatus*) sampled during torpor and IBE to give insight into the regulation of mitochondrial suppression. We also measured maximal enzyme activity in homogenized mitochondria and whole liver tissue. Our results show that complexes I and II are significantly suppressed in torpor relative to IBE, but complexes III, IV, and V do not differ. While complexes I and II show dramatic differences in activity, the amount of each protein remains constant between torpor and IBE. Because of this rapid and reversible suppression, we suggest that complexes I and II may be regulated by post-translational modification during hibernation.

## **Candidate genes involved mate-preference in Drosophila**

Jalina Bielaska Da Silva  
Supervisor: Dr. Amanda Moehring

Behavioural isolation occurs when individuals mate with their own species and avoid mating with individuals from another species. This form of reproductive isolation is usually determined by female preference, but the genetic basis for female preference remains largely unknown. A previous genetic mapping study identified eight potential candidate genes for female species-specific mate preference that contribute to female *Drosophila simulans* rejection of *D. melanogaster* males. I tested seven of these eight potential candidate genes using hybrids with various gene disruptions using 'no choice' mating assays. This study identified that three of the genes; transformer 2, doublesex, and gasket, are likely candidate genes (G-test statistic:  $P=0.014$ ;  $P=0.027$ ;  $P=0.023$ ), while transformer appears to be following a similar trend and may also be a candidate gene. This study identified candidate genes that contribute to female species-specific mate preference in *Drosophila*.

## **Soybean root suberin and resistance against the pathogen Phytophthora sojae**

Trish LA Tully  
Supervisor: Dr. Mark A 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  $\omega$ -hydroxyalkanoic acids are predominant and most strongly correlated with resistance to *P. sojae* in soybean. These  $\omega$ -hydroxyalkanoic acids are synthesized by a subfamily of cytochrome P450 enzymes collectively known as the fatty-acid  $\omega$ -hydroxylases (FA $\omega$ Hs).

In soybean, the FA $\omega$ H genes show a tissue specific expression pattern with only genes GmFA $\omega$ H-5 and GmFA $\omega$ 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 $\omega$ 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.

### **Individual diversity at MHC as a predictor of survival and a correlate of neutral-locus heterozygosity in free-living Song Sparrows**

Matthew James Watson

Supervisor: Dr. Beth MacDougall-Shackleton

Genetic diversity is critical in shaping the adaptive capacity of natural populations and the fitness of individuals. Genome-wide diversity is often assessed using selectively neutral markers such as microsatellites, but neutral-locus diversity may not accurately reflect heterozygosity at functional loci that are subject to natural selection. The major histocompatibility complex (MHC) is the most polymorphic region in the vertebrate genome: in many species, MHC diversity provides a survival advantage through enhanced resistance to infectious disease, consistent with balancing selection. I measured genetic diversity of adult and juvenile Song Sparrows (*Melospiza melodia*) at 12 microsatellite loci and at MHC class II  $\beta$ , to assess correlations between diversity at different marker types and associations between genetic diversity and survival. Neutral-locus (microsatellite) diversity did not predict MHC diversity, and neither type of diversity predicted overwinter survivorship. MHC diversity is high in this population (296 alleles found in 69 individuals, 15-33 alleles per individual) and I am now screening candidate “good-gene” alleles that may predict overwinter survivorship and disease status in this population. This information will aid in conservation and management decisions, for example in determining how to best assess genetic diversity and adaptive potential of wild populations.

### **3-MINUTE THESIS PRESENTERS**

#### **Death from the shadows: Assessing perceived predation risk effects on juvenile survival**

Mark Charles Allen

Supervisor: Dr. Lianne Zanette

Recently, predators have been credited with having a more profound effect on prey population dynamics than previously predicted in wildlife ecology. This may be attributable to recent evidence suggesting that predators not only kill prey, but through the 'fear' of predators (i.e. perceived risk of predation) induce anti-predatory responses that may incur energetic or physiological costs among individuals. These anti-predatory costs among prey individuals, may scale up to effects on prey population growth/size as a whole, through effects on prey reproduction (i.e. number of offspring produced), juvenile survival, and/or adult survival. We previously demonstrated that increasing a females perceived risk of predation during the breeding season can cause a 40% reduction in the number of offspring that songbirds can fledge (i.e. leave the nest). Expanding on those findings, my thesis focuses on how the perceived risk of predation affects prey population dynamics through effects on juveniles, a critical but often an understudied life-history stage in wildlife demography. We monitored the survival of juvenile song sparrows (*Melospiza melodia*) and found that juveniles reared in a high perceived risk predation environment have lower survival compared to juveniles reared in a perceived low predation risk/control environment. Thereby demonstrating that the fear of predators has a greater net effect on

wildlife prey population growth/size then previously shown, through effects on both prey reproduction and juvenile survival.

### **The influence of plant growth form on porewater DOC concentration and character in northern peatlands**

Catherine Dieleman

Supervisor: Dr. Brian A. Branfireun

Peatlands are the most efficient terrestrial ecosystem at storing carbon in the world, purportedly due to the prevalence of decomposition inhibiting Sphagnum moss species. Under future climate change conditions, however, many peatlands are expected to have vascular vegetation as the dominate growth form, with unclear ramifications for key fractions of the carbon budget such as dissolved organic carbon (DOC). In fact, little is known regarding the effects of differing plant growth forms on porewater DOC production and character, despite DOC's role in C cycling and water quality. To address this knowledge gap we determined DOC quantity and quality, plant productivity, and ecosystem respiration in intact, replicated peat monoliths dominated solely by Sphagnum moss, graminoids, or bare peat (control). During periods of high productivity graminoids had significantly lower porewater DOC concentrations than Sphagnum moss and bare peat mesocosms; however, these trends did not correspond to a change in porewater DOC quality. Instead, Sphagnum moss mesocosms were associated with significantly higher DOC lability. These values were very constant temporally and did not reflect Sphagnum moss productivity. We also noted significantly higher ecosystem respiration in the graminoid mesocosms, particularly when plant productivity was maximized – suggestive of enhanced microbial activity contributing to the observed lower DOC concentrations. Specific plant growth forms are indicative of differing porewater DOC concentrations during periods of high productivity; however, belowground processes, such as microbial breakdown and peat matrix leaching, are a stronger determinant of the resultant porewater DOC quality in northern peatlands.

### **The Green (Immuno-)Gobulin: Development of a plantibody to prevent colonization of Escherichia coli O157:H7 in the bovine gastrointestinal tract**

Adam Chin Scott Fatt

Supervisor: Dr. Rima Menassa

Shiga toxin-producing Escherichia coli (STEC), particularly the most prevalent serotype O157:H7, is a potentially fatal zoonotic food-borne pathogen that is commonly associated with widespread and consistently recurring outbreaks of bloody diarrhea and abdominal cramps. Although transmission via other animals is possible, it primarily harbors in a bovine intestinal reservoir. This project seeks to produce a secretory antibody in Nicotiana benthamiana leaves that could be orally administered to cattle as part of their feed prior to slaughter that would reduce STEC colonization via passive immunization. More specifically, the objectives toward this end goal are to: 1) identify llama derived heavy chain variable regions (VHHs) that are specific for the C-terminal domain of the intimin protein, a previously established STEC antigen; 2) fuse the sequences of these identified VHHs to bovine Fc domains that will enable immunogenicity in the bovine gut; 3) to coexpress these fusions along with a joining chain and secretory component that will allow for complete assembly of dimeric secretory antibodies localized in the endoplasmic reticulum; 4) to optimize the transient expression of the VHH-Fc fusions, joining chain and secretory component to obtain the highest expression and binding possible; and 5) to assess the effect of the secretory antibody on in vitro adhesion and colonization of STEC.

This project is still in its infancy with the recent immunization of a llama with the C-terminal domain of intimin. We have already developed constructs for the joining chain, secretory component and some test VHH-IgA fusions and have them all expressing in *N. benthamiana* leaves. Ultimately, the development of this plant-based anti-STEC prophylaxis has the potential to improve food safety and be a viable alternative to antibiotics for the control of STEC colonization.

### **Climate change impacts on communities of fungi in boreal peatlands**

Asma Asemaninejad

Supervisor: Dr. Greg Thorn

Peatlands have an important role in global climate change through sequestration of atmospheric CO<sub>2</sub>. However, global climate change is already affecting a large part of these ecosystems, including both above- and below- ground communities and their functions. As a result, there is concern that altered fungal community function may turn peatlands from carbon sinks to carbon sources, greatly exacerbating the impacts of climate change. Fungi have a greater biomass than other soil organisms excluding plant roots and play a central role in these communities. In a factorial experiment established in Western's Biotron facility, I am assessing the impacts of the elevated temperature, CO<sub>2</sub> concentration and altered hydrology associated with Canada's predicted climate change on communities of fungi in peat cores at 3 different horizons. I have analysed the fungal communities in the upper horizon (0-5 cm), middle horizon (10-15 cm) and bottom horizon (20-25) of peat cores, and studied changes in the fungal communities over 18 months. During the experiment, there was no significant effect of CO<sub>2</sub>, hydrology or depth on fungal diversity, but under dry condition fungal richness increased with temperatures elevated 4 °C above ambient, and significantly decreased with increased temperatures of 8 °C in the middle horizons. Similar patterns were observed under wet hydrological conditions with the greatest species richness observed in the upper horizon under 4 °C above ambient, and lowest fungal richness observed at the bottom horizon under 8 °C above ambient. These results allow for a better understanding of changes in fungal communities in peatlands which is crucial to predicting consequences of global climate change more accurately.

### **Genomic correlates to kin recognition and invasiveness in a subterranean termite**

Tian Wu

Supervisor: Dr. Graham Thompson

As social insects, termites typically live in kin-based groups that are headed by a reproductive king and queen, but are otherwise populated by a large number of sterile workers and soldiers. Despite their sterility, these helper castes can gain indirect fitness by directing help toward their reproducing relatives and defending against unrelated intruders. For invasive populations of the Eastern subterranean termite (*Reticulitermes flavipes*), these kin-mediated behaviors can break down, leading to the formation of mixed kin supercolonies that spread over vast areas and contain a large number of reproductives. One explanation stems from the genetic consequence of the invasion itself; founding populations lose allelic variations essential for recognition due to founder effect. If so, invasive populations should be genetically less diverse and show poor recognition than similarly sized native populations. In our study, we use next-generation sequencing to test this explanation. We created RNA-sequence libraries that correspond to a series of invasive and non-invasive populations from North America. As we assemble these libraries, they serve as a reference assembly for this economically important pest species, and will likewise serve to contrast gene expression and allelic diversity across colonial and supercolonial

populations. If loss-of-recognition is preceded by loss-of-alleles, then we simply expect invasive supercolonies to be less diverse at most loci. Moreover, we expect the very genes involved in recognition to evolve via negative frequency-dependent selection that favours rare alleles and the maintenance of balanced polymorphisms. We aim to screen our assemblies against these criteria to test the genetic etiology of supercolonies, and to potentially identify genes for kin recognition in a subterranean termite.

## **POSTER PRESENTERS**

### **Metabolic rate, colony size and latitude, but not phylogeny, affect rewarming rates of bats.**

Dylan E. Baloun

Supervisor: Dr. Chris Guglielmo

Torpor is an energy-saving adaptation that allows many endotherms to save energy by abandoning the energetic cost of maintaining elevated body temperatures ( $T_b$ ). Although torpor can reduce overall energy expenditure, rewarming from torpor is energetically expensive. Thus, costs of rewarming can impact the overall costs of torpor. Rewarming rapidly is less energetically expensive than rewarming over a longer interval because of decreased heat loss to the environment. Ecological and behavioural factors influencing the rate of rewarming and the availability to rewarm passively could therefore influence the evolution of rewarming rates and overall energetic costs of arousal from torpor. Bats are a good model to assess the affects of ecological and behavioural correlates of rewarming because of the widespread expression of heterothermy and ecological diversity. We used comparative analyses to explore the relationship between basal metabolic rate (BMR) as a measure of thermogenic capacity, local climate (i.e., latitude) and maximum colony size as predictors for rewarming rate in 45 bat species. After controlling for phylogeny, high BMR was associated with rapid rewarming rates, with species living at higher absolute latitude, in smaller colonies, rewarming the fastest. This suggests that passive rewarming and social thermoregulation may help reduce energetic costs of rewarming. Our results show the diversity of adaptations to maintain a positive energy balance in a range of climates, as well as provide insight into possible mechanisms facilitating the evolution of heterothermy in endotherms.

### **Evaluating the effects of root exudates from buckwheat, *Fagopyrum esculentum*, on wireworms of the species *Agriotes sputator***

Yeritza Liliana Bohorquez Ruiz

Supervisor: Dr. Ian Scott

Generalist insect herbivores utilise visual, chemical and tactile cues to locate host plants. However, generalist soil-dwelling herbivores rely most on chemical cues in order to detect suitable and avoid unsuitable plants. Wireworms (Coleoptera: Elateridae) are generalists and are serious pests of many agricultural crops; thus requiring pest management strategies. Preliminary studies observed reduced wireworm densities after buckwheat (*Fagopyrum esculentum*) is used as a cover crop; potentially due to the plant releasing repellent, antifeedant and/or toxic chemicals into the soil. I will explore the different potential effects of chemicals from buckwheat roots on the behaviour of wireworm species *Agriotes sputator*, using a six arm olfactometer and small plot experiments. My results will be the basis for subsequent chemical analyses, as these compounds could offer an alternate management strategy.

## **The Progeny of Old Parents are Less Social**

Dova B Brenman

Supervisor: Dr. Anne F Simon

Many aspects of behavior such as courtship behavior, odor avoidance and motor activity are affected by advanced parental age and can be measured in *Drosophila melanogaster*. Social behavior can also be analyzed through the preferred distance between individuals, which can be abnormal with alterations in neurodevelopment. To assess preferred distance, we used the social space assay to quantify the distance between neighboring flies – individuals usually rest ~2 body lengths apart and deviations from this are considered abnormal. Our question is therefore: what impact does aging have on social behavior and is this impact heritable over several generations? To investigate the effect of parental age on social behavior, *D. melanogaster* were aged 30 days, as this is when our strain (Canton-S) shows a decline in fertility and survivability (90% survival), and at 50 (50% survivability). Older flies are less social when tested with the social space assay as compared to seven-day-old flies. Moreover, the progeny of aged flies are also less social, demonstrating the heritability of this defect. However, when subsequent generations of flies are tested, the defect dissipates in three generations, and social distances return to normal. Interestingly, it is not necessary for both parents to be aged, as an effect is seen through having only old fathers. In summary, we have identified a stronger alteration in social space in the progeny of aged flies versus the aged flies themselves, with a paternal effect. This may indicate different aging mechanisms in germ cells versus somatic tissues resulting in a stronger effect in the progeny of aged parents than in the parents. Additionally, the loss of altered social space in subsequent generations indicates an increase in heterozygosity that counteracts the effect of aging and damage and restores the social distances to normal levels.

## **Confirmation of a candidate gene for behavioral isolation in *Drosophila***

Tabashir Chowdhury

Supervisor: Dr. Amanda J. Moehring

As one of the major tenets of speciation, reproductive isolation maintains species boundaries by preventing gene flow. Among the numerous reproductive isolating mechanisms, behavioral isolation is one of the earliest acting barriers. This mechanism involves discordance in mating strategies between diverged taxa, with females exhibiting a preference for conspecific male traits. *Drosophila* is ideally suited for studying the genetic mechanisms underlying complex behaviors due to its stereotypic multimodal courtship ritual, and a comprehensive genetic toolkit. Although several candidate genes have been linked to behavioral isolation in *Drosophila* the genetic basis for species-specific female preference remains unclear. My work is on a candidate behavioral isolation gene for species-specific female preference. By using deficiency mapping and mating assays involving multiple gene mutants, I have confirmed that this candidate gene plays a significant role in female preference for conspecific males.

## Development of an in vivo assay to determine arogenate dehydratase activity

Emily J. Clayton

Supervisor: Dr. Susanne E. Kohalmi

The essential amino acid phenylalanine (Phe) can be synthesized via the arogenate or prephenate pathway in plants, bacteria or fungi. This requires the transamination of prephenate to arogenate by a prephenate aminotransferase (PAT), followed by a decarboxylation/dehydration of arogenate to Phe by an arogenate dehydratase (ADT) or the reverse enzymatic steps: a decarboxylation/dehydration of prephenate to phenylpyruvate by a prephenate dehydratase (PDT), followed by a transamination of phenylpyruvate to phenylalanine by a phenylpyruvate aminotransferase (PPAT). Amino acid sequences of PDTs and ADTs are highly similar and cannot be used to determine which of the two enzymatic activities a protein has. Currently it is possible to assess the PDT activity in vivo using a yeast complementation assay, but it is not possible to determine ADT activity without a complex and expensive in vitro biochemical assay. It is therefore desirable to develop a cheap and simple assay to test for ADT activity in vivo. As it is the presence of either the PAT or the PPAT that determines which pathway is used in these species, a PPAT knockout yeast strain stably transformed with a plant PAT could potentially be used to assess ADT activity of subsequently expressed proteins. Two PPAT genes were identified in *Saccharomyces cerevisiae*: ARO8 and ARO9. However, neither knockout line for these genes lacks the ability to grow in absence of Phe. Therefore, the haploid strains must be mated to generate a diploid that is heterozygous for both the *aro8* and *aro9* knockout. This diploid can then be sporulated to identify haploid progeny which are homozygous for both deletions. If successful, the haploid,  $\Delta aro8 \Delta aro9$  strain can be used in a simple in vivo complementation assay to efficiently assess ADT activity of any transformed putative PDT/ADT enzyme.

## Reactive Oxygen Species in mouse F9 cells due to increase in NOX1 activity

Benjamin Dickinson

Supervisor: Dr. Greg Kelly

Mouse teratocarcinoma F9 cells differentiate into primitive endoderm (PrE) when treated with retinoic acid (RA) and these changes are accompanied by an up-regulation of Wnt6 and activation of the canonical WNT/ $\beta$ -catenin pathway. Data from our lab shows PrE differentiation is accompanied by an increase in reactive oxygen species (ROS), which induces a conformational change in Nucleoredoxin (Nrx) preventing its ability to bind and inhibit dishevelled. This in turn positively impacts on the WNT/ $\beta$ -catenin signaling pathway leading to differentiation. Treating F9 cells with H<sub>2</sub>O<sub>2</sub>, in the absence of RA, is sufficient to induce F9 cells to differentiate into PrE. Furthermore, treating cells with antioxidants attenuates this RA-mediated differentiation. The source of endogenous ROS seen following RA treatment was investigated and members of the NADPH oxidase (NOX) family were identified as candidates. Nox1-4 and Duox2 genes are up-regulated by RA and in silico analysis revealed the Nox1 promoter is regulated by Gata6, a master regulator of extraembryonic endoderm differentiation. Interestingly, Nox1 and Nox4 are up-regulated when Gata6 is overexpressed in F9 cells. Furthermore, the pan-NOX inhibitor VAS2870 and NOX1-specific inhibitor ML171 significantly reduced the ability of RA to induce PrE differentiation. However, overexpression of Nox1 or Nox4 in F9 cells is not sufficient for differentiation. Thus, the data suggests that the ROS produced during the differentiation of F9 cells into PrE is the result of an increase in NOX1 activity; however, overexpressing Nox1 alone is not sufficient.

## **Evolution of kin recognition mechanisms**

Tim Hain

Supervisor: Dr. Bryan Neff

The extent to which phylogenetic history influences current traits has interested biologists for decades. Here I used recently-characterized variation in kin recognition mechanisms among six guppy populations to explore the phylogenetic history of this trait and its evolutionary lability. When a recognition mechanism is used by guppies, they can use phenotype matching, in which individuals are identified based on comparison to a recognition template, or familiarity, in which individuals are remembered based on previous interactions. Across the six populations I identified four transitions in recognition mechanism: phenotype matching evolved once and was subsequently lost in a single lineage, whereas familiarity evolved twice. Based on a molecular clock, these transitions occurred over timescales of hundreds of thousands of years, two orders of magnitude faster than previously documented changes in recognition mechanisms. A randomization test provided no evidence for phylogenetic signal, suggesting that kin recognition mechanisms are evolutionarily labile, though the specific selection pressures that may be contributing to variation in recognition mechanisms across the populations remains unknown.

## **Agaricomycetes of Ontario Tall Grass Prairies**

Chris Hay

Supervisor: Dr. Greg Thorn

Knowledge and understanding of fungal diversity is poorly known, particularly in non-woody ecosystems. Mushrooms and soil sequence data were collected from remnant tall grass prairies and restorations at various stages of recovery. Abundance of taxa within the Agaricomycetes were considered in light of potentially influential site conditions: years since major soil disturbance (tillage) and dominant vegetation cover. Comparisons were made between the results of aboveground (mushroom) and belowground (soil sequence) survey methodologies. Ontario tall grass prairies were found to hold a diversity of Agaricomycete fungi but seem to be dominated by three families: Entolomataceae, Clavariaceae, and Hygrophoraceae.

## **Connectivity rescues genetic diversity after a population collapse: empirical evidence from a butterfly population network**

Maryam Jangjoo

Supervisor: Dr. Nusha Keyghobadi

With climate change and associated climatic instability, natural populations are expected to experience more frequent and severe fluctuations in size. Fluctuations in population size can erode genetic diversity; however that diversity can be recovered through immigration. Connectivity of populations in the landscape enhances immigration and should facilitate genetic diversity recovery after a reduction in population size. While predicted in theory, and suggesting the importance of maintaining population connectivity in the face of climate change, the ability of connectivity to rescue genetic diversity after a population size collapse has not been clearly demonstrated in an empirical system. Here, we show that connectivity of populations in the landscape contributes to the maintenance of genetic diversity after a

severe demographic bottleneck. We were able to monitor genetic diversity in a network of populations of the alpine butterfly, *Parnassius smintheus*, before and after a severe reduction in population size that lasted three generations. We found that allelic diversity in the network declined after the demographic bottleneck, but there was a strong negative correlation between the connectivity of individual populations and the amount of allelic diversity lost. Our results demonstrate directly the ability of connectivity to mediate rescue of genetic diversity in a natural system.

### **Neonicotinoid resistance in the Colorado potato beetle**

Emine Kaplanoglu

Supervisor: Dr. Patrick Chapman

The Colorado potato beetle (*Leptinotarsa decemlineata*) is a significant pest of potatoes in most potato-growing areas of the world. Left unmanaged, the beetle is capable of completely defoliating potato plants and reducing the yield by up to fifty percent. Currently, the management of *L. decemlineata* heavily relies on use of insecticides, neonicotinoids in particular. However, emergence of insecticide resistance is a major concern. In insects, the most common cause of insecticide resistance is elevated detoxification, mainly caused by quantitative changes in protein levels of detoxifying enzymes such as cytochrome P450s, uridine 5'-diphospho-glucuronosyl transferases, esterases, glutathione S-transferases and ATP-binding cassette (ABC) transporters. Therefore, we hypothesize that elevated detoxification is the mechanism for neonicotinoid resistance in *L. decemlineata*. In order to address our hypothesis, we conducted RNA-seq and qPCR analyses and identified several detoxifying enzyme and ABC transporter genes which are transcriptionally upregulated in a neonicotinoid resistant strain of *L. decemlineata* compared to a sensitive strain. To demonstrate the function of these upregulated genes in neonicotinoid resistance, RNA interference (RNAi) will be used to silence their expression. This will be accomplished by producing double-stranded RNA specific for the upregulated genes in bacteria and feeding the bacteria to resistant insects. We will then evaluate the phenotypic effects of RNAi-based silencing of the upregulated genes on neonicotinoid resistance using bioassays. This work is significant as the results will lead to a better understanding of insecticide resistance in *L. decemlineata*, which may ultimately assist in developing novel strategies for its control.

### **Freezing Stress Memory Enhances the Growth Response of *Poa Pratensis* Under Drought**

Ricky S. Kong

Supervisor: Dr. Hugh A.L. Henry

Extreme climatic events are exposing herbaceous species in northern temperate regions to more intense and frequent stress. It has been observed that exposure to one stress may increase the tolerance to a second different stress, and this has been referred to as cross-adaptation. Both frost and drought stress cause cellular dehydration, and there are similar increases in protective compounds that include various sugars and amino acids. However, the effect of frost on drought tolerance has not been well characterized, and it is unknown whether the physiological changes that occur under freezing can in turn be linked to lower declines in biomass during periods of drought. *Poa pratensis* tillers were frozen in the late fall, early spring or late spring at 0 , -5 or -10 for 3d. Tillers that survived each freezing treatment were either well watered (-24kPa) or subjected to a moderate drought (-142kPa) or severe drought (-254kPa) for 3 weeks in the summer. Mortality was assessed after the drought and plants were harvested to determine total biomass. For plants that were not frozen, severe drought decreased survival by 61.1%. In comparison, severe drought decreased survival by 27.3% for plants that

were frozen in the fall and 16.7% for plants frozen in the spring. There was a significant interaction between freezing and drought, and the highest decline in biomass was observed for plants that were subjected to drought and not frozen (156mg). The decline in biomass was lower for grasses subjected to a severe drought and a fall (88mg) or spring freeze (33mg). Results suggest that plants can 'recall' previous stresses and this may result in faster and stronger responses when these plants are exposed to future stress. Drought tolerance is higher in plants that experienced a more recent frost suggesting that stress memory may be lost over time.

### **Pass the salt: Sodium gut loading enhances cold tolerance in the fall field cricket**

Jacqueline Lebenzon

Supervisor: Dr. Brent Sinclair

In the fall field cricket, *Gryllus pennsylvanicus*, sodium and water follow concentration gradients from the haemolymph to the gut during chill coma. Recovery from coma occurs upon reversal of this ion redistribution. We hypothesized that recovery time will be determined by the  $[Na^+]$  gradient between the haemocoel and gut, because that will determine the number of ions that must be redistributed during recovery.  $CT_{min}$  did not differ among crickets fed high (540 mM), medium (180 mM) or low (8 mM) sodium diets, or those with varying osmolality. Feeding crickets high sodium diets reduced chill coma recovery time, but diet osmolality did not affect recovery time, suggesting that it is the ion (not osmotic concentration per se) gradient that determines recovery time. Faster recovery time in crickets with sodium-loaded guts occurs because the reduced haemocoel-gut sodium gradient decreases the amount of ion redistribution required during recovery, thus speeding chill coma recovery.

### **Female Mate preference in *Drosophila***

Priya Mahabir

Supervisor: Dr. Amanda Moehring

The complex processes that regulate mate preference is an area of research that has been universally studied. However, most studies to date have focused on the mechanisms that drive male mate choice, while those that underlie female mate preference remain largely unknown. This is a topic of interest as scientists have begun to understand that females are the primary discerners of reproductive receptivity. In order to address the existing knowledge gap we will be utilizing genetic tools in both *Drosophila melanogaster* and *Drosophila simulans* to isolate regions of the brain responsible for receptivity or rejection. We will be identifying these regions and corresponding genes for both conspecifics and heterospecifics. The three candidate genes of interest include, *Mekk1*, *fruitless* and *Katanin-60*. We will be recombining both temperature sensitive *ricin* and *shibire* to disrupt neuronal activity in specified brain regions. To flag the substrates we are interested in, we will exploit pre-existing genetic techniques which include the Gal-4-UAS system and the green fluorescent protein to demarcate activity. Examining female receptivity could begin to shed light on the more broad concept of how neuronal circuits integrate multiple sources of information from various modalities to subsequently produce directed behavior.

## **Tissue-Specific Copy Number Genotyping of Parents and Their Three Sons with Tracking of Developmental Dynamics of De Novo Mutagenesis**

Maja Milojevic

Supervisor: Dr. Kathleen Hill

Individual tissues are a rich mosaic of de novo copy number variants (CNVs) potentially relevant to tissue development, aging and disease but we understand little of the dynamics of these events. The Mouse Diversity Genotyping Array permits analysis of tissue-specific CNVs with a resolution of 915,951 loci queried by 493,290 single nucleotide polymorphism (SNP) and 421,905 invariant exonic probe sites. Applying this platform to an experimental design that assays the CNV genotype of four tissues (tail, hippocampus, lung and bladder) in a mouse family of three sons and their parents, and two additional tissues (pancreas and kidney) in the sons, we detected recurrent tissue-specific CNVs from a common developmental lineage. In total, 137 CNVs (77 gains and 60 losses) were detected (>500 bp, minimum marker call of three and probe density of 0.0003 probes per base pair), of which 25 are X-linked and all but one overlap a gene region. CNV burden averaged 5.27 per sample. Analysis of the parental consensus CNV genotype was used to identify 20 putative de novo somatic CNVs in the sons (6 gains and 14 losses). Recurrent de novo single copy deletions in the HoxA gene cluster were observed within multiple family members and within the endodermal developmental lineage giving rise to pancreas and bladder. Tissue-specific CNV genotyping within the context of the family unit is relevant to understanding spontaneous mutagenesis and selection that shape genome structure. Also, this experimental framework is well suited to provide insight into critical developmental periods of environmental mutagenesis.

## **Analyzing the possibility of piggy back targeting Arogenate dehydratase 5 into the nucleus in *Arabidopsis thaliana***

Sara Abolhassani Rad

Supervisor: Susanne E. Kohalmi

Arogenate dehydratases are a family of enzymes that catalyze the last step of phenylalanine biosynthesis in plants, which is the dehydration/decarboxylation of arogenate into phenylalanine. Since phenylalanine biosynthesis always happens in chloroplasts, all members of this family are targeted to chloroplasts using a transit peptide sequence. Surprisingly, one member of this family AROGENATE DEHYDRATASE5 (ADT5) in *Arabidopsis thaliana* is not only targeted to the chloroplasts, but also is found in the nucleus, the typical place for transcription factors. This unique localization pattern for this enzyme suggests that it has a non- enzymatic role in the cell. Such multifunctional proteins are usually referred as moonlighting proteins and they have different and unexpected roles in different parts of the cell. For targeting to the nucleus proteins need to pass through the nuclear membrane. One way is the “piggyback” system where importin proteins interact with proteins to import them in the nucleus. Using protein-protein interaction websites I found that ADT5 is proposed to interact with importin  $\alpha$ . To confirm this interaction I used two different protein-protein interaction assays: the in vivo Yeast-2-Hybrid (Y2H) assay and the in planta Bi-molecular Fluorescence Complementation (BiFC) assay. Results will be shown and discussed.

## **Identification and characterization of Isoflavonoid-specific prenyltransferase gene family in Soybean**

Arjun Sukumaran

Supervisor: Dr. Sangeeta Dhaubhadel

Soybeans are one of the most widely grown grain legumes worldwide because of its versatility as a food source and industrial use. However, one deterrent to maximizing yield is the pathogen, *Phytophthora sojae*, which can cause root and stem rot disease at any stage of soybean development. Many strategies have been implemented throughout the years to combat the pathogen such as use of pesticides, certain agricultural practises and implementing complete resistance. However, these have been largely ineffective in preventing *P. sojae* infection. An alternative strategy would be to improve the innate resistance of soybeans by promoting increased phytoalexin production. Glyceollins are soybean-specific antimicrobial agents which are derived from the isoflavonoid branch of the general phenylpropanoid pathway. Soybeans produce 3 forms of glyceollin: glyceollin I, glyceollin II, and glyceollin III. These forms are a result of differential prenylation on either the C2 or C4 carbon of glycinol. Currently, only the prenyltransferase (PT) responsible for glyceollin I production has been identified. Glycinol 4-dimethylallyltransferase (G4DT) is responsible for prenylating the C4 carbon of glycinol, however, the precursor to glyceollin II and glyceollin III is produced by the PT, G2DT, has yet to be identified. This research aims to identify all the PTs in soybean, and characterize isoflavonoid-specific PTs. Eleven GmPTs have been identified in this project, and they will be characterized by identifying their subcellular localization, gene expression in different tissues and in response to pathogen stress, and then through verification of their enzymatic activity. Better understanding of the isoflavonoid pathways will allow for more precise manipulation of glyceollin production, thus in effect, increasing resistance to *P. sojae* in soybean.

## **Reproductive diapause alters stress tolerance in *Drosophila suzukii***

Jantina Toxopeus

Supervisor: Dr. Brent Sinclair

*Drosophila suzukii* (Diptera: Drosophilidae) is an invasive agricultural pest in southern Canada. Its ability to overwinter and therefore establish in this country could have severe implications for fruit crop industries. We demonstrate here that laboratory populations of Ontario *D. suzukii* larvae reared under short-day, low temperature, conditions develop into dark 'winter morph' adults similar to those reported globally from field captures, and observed by us on Pelee Island in Ontario. These adults have delayed reproductive maturity, enhanced cold tolerance, and can remain active at lower temperatures. Female *D. suzukii* have underdeveloped ovaries and altered transcript levels of genes associated with reproduction and stress. The traits of this 'winter morph' likely facilitate overwintering in Ontario, and have probably contributed to the global success of this fly as an invasive species.

## **Stress response profile of Galectins**

James Vinnai

Supervisor: Dr. Alexander Timoshenko

Galectins are a family of soluble  $\beta$ -galactoside binding proteins that serve as mediators of fundamental cellular processes including cell growth, differentiation, adhesion and others. The expression of galectins in different cells and tissues carries significance as evident by galectin profiling analysis of multiple cell lines (Lahm et al, 2001), normal (Than et al, 2014) and tumor tissues (Laderach et al, 2013). We hypothesized and explore a conceptual point regarding the functional significance of stress-induced differential expression of galectins in human promyelocytic cell line HL-60 under a variety of cellular stress conditions including cobalt chloride (100  $\mu$ M), oxidative stress inducer menadione (10  $\mu$ M), ER stress inducer tunicamycin (1  $\mu$ g/mL) and cell differentiation inducer DMSO. To investigate the functional significance of galectins, potential galectin inhibitory sugars including lactose, methyl  $\alpha$ -D-mannopyranoside, mannose and thiodigalactoside (TDG) were used to assay the inhibition of galectin function of HL-60 proliferation, viability and differentiation. We found that 24h exposure of HL-60 cells to menadione induced upregulation of galectin-1/-3/-10, which was rescued in the presence of an antioxidant N-acetyl-L-cysteine (1 mM) at both transcript and protein levels. Similarly, DMSO-induced differentiation of HL-60 cells into neutrophil-like cells was accompanied by increased galectin-3/-10 transcript and protein level, however, these levels were not rescued using N-acetyl-L-cysteine. TDG (40 mM) effectively reduced HL-60 cell proliferation, however, was unable to prevent DMSO-induced HL60 cellular differentiation. All other sugars showed no effect on cell proliferation or differentiation. Together, these data provide insight to the galectin expression profile of HL60 in response to stress stimuli and their potential in regulating fundamental cellular events in HL-60. Additionally, these data show the potential interaction galectins play with ROS dependent and independent processes.

## **Role of GPCRs through the elucidation of its binding partners**

Drew Wallace

Supervisor: Dr. Greg Kelly

G-Protein Coupled Receptors (GPCRs) activate heterotrimeric G proteins by promoting the exchange of GDP for GTP on the G $\alpha$  subunit. G Protein Signaling Modulator 3 (GPSM3) acts as a guanine nucleotide dissociation inhibitor (GDI), inhibiting the exchange of GDP for GTP and thereby promoting the inactive state of G $\alpha$  and the active state of G $\beta\gamma$ . GPSM3 transcript and protein levels have been shown to increase with serum stimulation and decrease with serum deprivation in vascular smooth muscle cells (VSMCs) from spontaneously hypertensive rats. Using a mammalian 2 hybrid assay, we will next attempt to identify binding partners of GPSM3 to further elucidate its role.

## **Abscisic acid regulation of biosynthesis and deposition of suberin in wound-healing potato.**

Katie Woolfson

Supervisor: Dr. Mark Bernards

Suberin is a complex biopolymer that is deposited during a wound-induced response to prevent water loss and microbial infection of potato tubers. The suberin macromolecule comprises two covalently-linked domains that together contribute to its dual functionality: the poly(phenolic) domain, which is

assembled from hydroxycinnamic acids, hydroxycinnamoyl amides and monolignols, and the poly(aliphatic) domain, which consists of ester-linked  $\omega$ -hydroxy acids,  $\alpha,\omega$ -dioic acids, fatty acids, 1-alkanols and glycerol. In *Solanum tuberosum*, the deposition of each domain is coordinately regulated, where the phenolic domain is laid down first, followed by the aliphatic domain. The findings of various research groups led to the hypothesis that the hormone abscisic acid (ABA) plays a regulatory role in wound-induced suberin production in potato. For example, after potato wounding, ABA levels initially drop, then rise again during suberization, indicating de novo ABA synthesis during this process. In the presented work, potato tubers were wounded and treated with the ABA biosynthesis inhibitor fluridone (FD), FD and ABA, or water as a control. Suberin composition was monitored and subsets of genes involved in various aspects of suberin biosynthesis and deposition were analyzed by RT-qPCR across a 6 day wound-healing time course. Overall, wounding rapidly induced expression of most genes involved in phenolic suberin biosynthesis (PAL1, CCR, C4H, THT), whereas the majority of aliphatic (FAR3, KCS6, FA $\omega$ H1, CYP86B1) and convergent metabolism (GPAT5, GPAT6, FHT, ABCG1) genes were not highly expressed until 3-4 days after wounding. While FD treatment did not have a pronounced effect on phenolic-related genes, FD treatment delayed wound-induction of aliphatic and convergent pathway genes and led to lower expression levels in these two subsets of genes across 6 days of wound-healing, relative to controls. These findings were consistent with suberin metabolite analyses, suggesting that ABA regulates the expression of genes involved in aliphatic and convergent suberin metabolism, but not phenolic suberin biosynthesis.

### **BIOBOOTH PRESENTERS**

**Keyghobadi Lab:** Alpine butterflies and Climate Change

**Moehring Lab:** Speciation in *Drosophila*

**Smith Lab:** *Polytomella* and Plastid Genome Evolution

**Cumming Lab:** Mice and Memory

**Sinclair Lab:** Insects and Cold Tolerance

### **ART EXHIBIT PRESENTERS**

**Tosha Kelly** submitted a picturesque painting of a black and white Warbler.

**Curtis Lubbe** submitted four whimsically peculiar drawings.

**Susan Anthony** submitted a colourful cross-stitch of three beautiful butterflies.

**Victoria Simkovic** submitted two wonderful watercolor paintings. She also submitted a living work of art: a termite farm!

**Marek Allen** submitted three photos of hummingbirds hatching.

**Vi Bui** submitted a photo of a cool cross-section of a grass from Antarctica.

**Christopher Hay** submitted six photos. Four are magnificent mirrorgraphs. Two are unparalleled universes done using phase contrast.

**Kim Mitchell** submitted four photos of lustrous landscapes.

**Katie Woolfson** submitted three photos. Two are landscapes, one in each of black-and-white and in-colour. The third is a fantastic photo of flowers.

**Tian Wu** submitted a photo of some bodacious beetles in their natural habitat.



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