Non-model Model Organisms in the Era of Large Scale Genomics.

The advent of NextGen sequencing technology has facilitated the development of large-scale sequencing projects for a broad array of species. NextGen sequencing has the capacity to generate tremendous amounts of data on the patterns of gene expression making it highly attractive tool for the masses. However, there can be several difficulties with the analysis and interpretation of large-scale transcriptomic datasets, particularly with non-model organisms for which a complete genome sequence is not available. Research in my lab has been investigating the stress-induced patterns of gene expression for blue mussels in the genus *Mytilus*. Blue mussels are a foundational species within intertidal and shallow subtidal communities in temperate and sub-polar regions of the world’s oceans. They provide structure and ecosystem services that numerous other species in these communities rely upon and thus are considered a “model” organism from an ecological perspective. On the other hand, despite 40 complete genome sequences for eukaryotic organisms on Genbank and some 665 projects in progress, there are no plans to sequence the genome of any blue mussel species. I will present results from our research that seeks to identify key pathways of gene expression in blue mussels exposed to osmotic stress in the absence of a complete genome sequence.
Keynote speaker: Paul Rawson, Ph.D.
Non-model Model Organisms in the Era of Large Scale Genomics.

** Coffee break

10:15-11:00 am

High mutation rates in the mitochondrial genomes of *Daphnia pulex*.
Sen Xu

Genetic and expression changes in Lactate dehydrogenase as potential mechanisms for promoting local adaptation in the *Daphnia pulex* species complex (Cladocera, Anomopoda).
Bora Demiri

The effects of declining calcium levels on the gene expression of *Daphnia pulex*.
Ianina Altshuler

11:15-12:15 pm

Bioamplification and selective depletion of POPs during the critical period of larval Chinook salmon.
Jen Daley

Patterns of bioaccumulation of Lake Huron lake trout (*Salvelinus namaycush*).
Mark Ryder

Assessing Lake Simcoe food web contaminant dynamics under the influence of multiple stressors.
Michael Thibert

The chemical and biological evolution of mature fine tailings in oil sands end-pit lakes.
Michael Chen

12:15-1:30 pm LUNCH (not provided)
1:30-2:15 pm

Niche width differences for guppy populations experiencing contrasting predation intensity.
Caroline Dennis

Movement and behaviour of deep-water fish species in Arctic marine ecosystems.
Iva Peklova

Seasonal Patterns in Fatty Acids and Stable Isotopes of *Calanus hyperboreus* (Copepoda, Calanoida) from Cumberland Sound, Baffin Island, Nunavut.
Bailey McMeans

** Coffee break **

2:30-3:15 pm

Validating the use of Fs-LA-ICP-MS to analyze the chemical composition of elasmobranch vertebral centra to aid in determining movement ecology.
Heather McCann

Speciation in ancient lakes: the calanoids of Sulawesi.
James Vaillant

The Reductive Dissolution of Tl(I)-jarosite by *Shewanella putrefaciens* CN32: Providing new Insight into Thallium(I) Biogeochemistry.
Christina Smeaton

Friday, April 15th, 2011

9:15-10:00 am

Patterns of selection and genetic drift in the gene expression of the immune response in Rainbow Trout of Babine Lake, BC.
Kyle Wellband

The analysis of genetic load and inbreeding depression in Chinook Salmon (*Oncorhynchus tshawytscha*).
Kendra Komsa

Genetic structure and gene flow among populations of the threatened eastern sand darter (ammocrypta pellucida) in two canadian rivers.
Robert Ginson
10:00-11:15 am

Sperm Traits in Wild and Farmed Chinook salmon (*Oncorhynchus tshawytscha*)
Sarah Lehnert

Effects of chlorine treatment in reducing viable organism populations in ballast water tanks.
Marco Hernandez

Vector-based risk assessment for ship-mediated biological invasions in the Canadian Arctic.
Farrah Chan

Domestic Ballast as a Potential Vector of Nonindigenous Species to the Great Lakes.
Remi Adebayo

Multiple introductions and invasion pathways for the invasive ctenophore *Mnemiopsis leidyi* in Eurasia.
Sara Ghabooli

11:30 LUNCH (provided)
ABSTRACTS

High mutation rates in the mitochondrial genomes of Daphnia pulex
Sen Xu

Despite the great utility of mitochondrial DNA (mtDNA) sequence data in population genetics and phylogenetics, key parameters describing the process of mutation (e.g. the rate and spectrum of mutational change) are supported by few direct estimates. Furthermore, the variation of the mtDNA mutation process within species, e.g. between lineages with contrasting reproductive strategies, remains poorly understood. In this study, we directly estimate the mtDNA mutation rate and spectrum in Daphnia pulex mutation-accumulation (MA) lines derived from cyclical parthenogenetic (CP) and obligate parthenogenetic (OP) lineages. The nearly complete mitochondrial genome sequence of 82 CP and 47 OP Daphnia lines reveals that its mtDNA mutation rate on a per-generation basis (1.37 × 10⁻⁷ and 1.73 × 10⁻⁷ per nucleotide per generation for CP and OP clones, respectively) is among the highest in eukaryotes. The Daphnia mtDNA mutation spectrum is dominated by insertions and deletions (70%), largely due to the presence of mutational hotspots at homopolymeric nucleotide stretches. Maximum-likelihood estimates of the Daphnia mitochondria effective population size reveals that between five and ten copies of mitochondria genomes are transmitted per female per generation. Comparison between sexual and asexual clones reveals highly similar mutation spectrum but higher mtDNA mutation rate in asexual than in sexual lineages.

Genetic and expression changes in Lactate dehydrogenase as potential mechanisms for promoting local adaptation in the Daphnia pulex species complex (Cladocera, Anomopoda)
Bora Demiri

Understanding the genetic basis of adaptation is a central task for evolutionary biology. Previous studies indicate that the Lactate dehydrogenase (LDH) gene plays an important role in local adaptations to ecologically different habitats in a number of species. Here I investigate how LDH contributes to local adaptations of Daphnia pulex and Daphnia pulicaria, two sister species. D. pulex lives in shallow ephemeral pond habitats, while D. pulicaria inhabits lakes. I use a controlled acclimation experiment and RT-qPCR to test whether there is correlation between the expression of LDH and environmental conditions such as different temperature and oxygen levels that usually characterize the pond and lake habitats. This study will expand our understanding of how differences in gene expression levels of metabolic genes contributes to local adaptation in divergent natural populations.
The effects of declining calcium levels on the gene expression of *Daphnia pulex*
Ianina Altshuler

Canadian lakes and ponds are under many environmental stressors such as acid rain, metal contaminants, invasive species, climate change, eutrophication, and other pollutants. Recently we have become aware of a sharp calcium decline in the Canadian Shield lakes as an emerging environmental stressor. This decline is partially caused by natural, long-term process of soil acidification, but has been unnaturally hastened by anthropogenic factors. Gene expression profiling can be used to understand an organism’s response to environmental stressors. Using *Daphnia pulex* as a model organism, I explore changes in the expression of target genes under a gradient of calcium concentrations to determine the effects of this stressor on native biota. Genes involved in maintaining calcium homeostasis and cell proliferation were chosen as target genes. In addition, I conducted a phylogenetic analysis on one of the target genes, SERCA, to understand its evolutionary history and explore any gene duplication events that may affect its expression pattern. Results show up and down regulation of several genes coding for different calcium pumps in animals under calcium stress. These finding could be used to understand how the animals cope with declining calcium concentration in the environment.

Bioamplification and selective depletion of POPs during the critical period of larval Chinook salmon
Jen Daley

Salmon provide significant maternal resources to eggs in order to allow over-wintering incubation and survival of larvae before the transition to exogenous feeding. The maternal provisioning of yolk to eggs also deposits significant quantities of persistent organic pollutants (POPs), where the eggs achieve chemical fugacities that reflect the maternal tissues. As yolk utilization progresses there is potential to realize further increases in POP fugacities if yolk lipids are depleted at a faster rate than POPs, a condition known as bioamplification. This study investigated the bioamplification of POPs in Chinook eggs and larvae. Chinook eggs were incubated in heath trays using a flow through system receiving Detroit River water at in-situ temperatures. No change in chemical mass or fugacity occurred in eggs from fertilization to hatch-out and POP depuration rates in larvae were slow from days 0-135. However, commencement of spring warming between days 135-168 resulted in $K_{ow}$ dependent elimination. Lipids declined from 8.6±0.2% in fresh eggs to 1.2±0.1% after 168 days. Bioamplification was maximized for the highest $K_{ow}$ POPs, with a 7-fold increase in larval fugacities compared to fresh eggs. This study demonstrates that Chinook larvae are exposed to higher chemical fugacities of POPs than predicted by maternal deposition alone.
Patterns of bioaccumulation of Lake Huron lake trout (*Salvelinus namaycush*)
Mark Ryder

Steady state theory has been used in recent years to describe the accumulation of organic contaminants, particularly super hydrophobic chemicals (log Kow > 6), in the tissue of an organism. Recent studies have shown that not all chemicals achieve steady state within an organism's lifetime. This is especially true for larger organisms and top predators. My study investigates the accumulation of polychlorinated biphenyls (PCB's) in lake trout (*Salvelinus namaycush*) from Lake Huron to test the assumption of a steady state model. Lake trout are a long lived, top predator and should therefore achieve steady state within their lifetime. Micro-extraction methods were used to extract both lipids and 24 individual PCB congeners from lake trout. Whole body homogenates were used rather than specific tissues to better estimate total body burden. Preliminary results indicate that compounds of high hydrophobicity (log Kow > 6.5) were less likely to achieve steady state, and continue to accumulate in the body of the fish. These results are important for fisheries management as currently a steady state model is being utilized for fish consumption advisories. My data suggests using a steady state model can underestimate the level of contaminants present in fish and therefore under predicts the levels of those who consume them.

Assessing Lake Simcoe food web contaminant dynamics under the influence of multiple stressors
Michael Thibert

The Lake Simcoe cold-water fishery, which is an excellent indicator of water quality and overall ecosystem health, has seen dramatic declines under the influence of multiple stressors. These stressors include a greater frequency in algal blooms from increased nutrient loading and the introduction of invasive species. My research goal is to examine contaminant dynamics in the warm and cold-water food webs of Lake Simcoe and to assess the influence of multiple stressors on contaminant exposures experienced within each subsystem. This will be achieved through data compilation, supplemental field studies, and comparative food web modeling on two independent systems: Lake Simcoe and Sharbot Lake. The information generated from this research will be useful in assessing the benefits of various actions taken by the Ministry and will assist in the Ontario government’s initiatives on improving the health of Lake Simcoe.
Processing oil sands for the extraction of bitumen produces a large amount of mine waste. The current practice involves gravity settling and subsequent storage in large basins. The denser slurry material, termed mature fine tailings (MFT), is then transferred to end-pit lakes (EPLs). An ongoing sustainable strategy is creating a containment region by combining previously quarried areas, (i.e. West in Pit mine) into a series of EPLs. A key factor to the implementation of a successful EPL design is how the underlying sediment will develop over time. Sediment Oxygen Demand (SOD) is a major contributor to oxygen depletion. Biochemical processes occurring at the sediment-water interface can influence ecosystem function and sustainability. The biochemical reactions associated with natural sediment can be altered by the presence of Oil Sands Processed Material (OSPM), which can affect SOD and ecosystem viability by limiting oxygen concentrations in the overlying water. Establishing the biotic and abiotic controls of SOD is imperative in assessing and developing current EPL remediation prediction models to be effective at restoring productivity to that observed during premining conditions.

Niche width differences for guppy populations experiencing contrasting predation intensity
Caroline Dennis

Understanding interspecific interactions and the consequences of these interactions within a system is of profound importance to ecologists; of particular interest are predator-prey relationships. In the rivers of Northern Trinidad, waterfalls restrict the movement of guppy (Poecilia reticulata) predators resulting in low predation pressure at upstream sites and high predation pressure at downstream sites. Guppies, potential prey items, and predators were collected for stable isotope analysis (δ¹⁵N and δ¹³C) from up- and down-stream sites in five river systems (Aripo, Turure, Quare, Tunapuna, and Tacarigua). Trophic position and isotopic niche width were estimated and analyzed using linear mixed effects models. Results suggest that trophic position did not differ between high low predation guppy populations (Z = -0.17, df=1, P = 0.865) but niche width was greater at the high predation sites compared to the low predation sites (Z = -0.6023, df= 1, p < 0.001). Guppies may be less selective and feed on a wider variety of food items when predation is intense. Alternatively, differences in other variables between high and low predations sites, including resource availability and guppy density, may contribute to the differences in isotopic niche width.
Movement and behaviour of deep-water fish species in Arctic marine ecosystems
Iva Peklová

Animal movement plays a key role in determining the spatial, demographic and genetic structure of populations, and ultimately underpins species management. Quantifying movements can reveal behavioral patterns that provide insight into habitat preferences and responses of animals to environmental or human-induced changes. Considering climate changes and exploitation of Arctic marine resources, it is critical to expand our knowledge of the movements of largely unstudied deep-water Arctic fishes. To do so, satellite and acoustic movement tracking technologies were employed in Greenland Halibut (*Reinhardtius hippoglossoides*) and Arctic Skate (*Amblyraja hyperborea*) in Cumberland Sound, Nunavut. Satellite data obtained between August and November 2010 showed the mean water temperature encountered was 2.4 ± 0.001 °C for halibut and 2.1 ± 0.007 °C for skate. In general, skates showed higher vertical activity levels and traversed a larger depth range (400-1400 m) than halibut (800-1400 m). This also implies that skates moved repeatedly across the Sound between deep and shallow waters, while halibut remained in deep water pockets for the entire period. Depth and temperature profiles provide evidence for overlapping habitats but also suggest differences in activity levels and behavioral patterns in these two species. These data will contribute to regional species-specific management plans.

Seasonal Patterns in Fatty Acids and Stable Isotopes of *Calanus hyperboreus* (Copepoda, Calanoida) from Cumberland Sound, Baffin Island, Nunavut
Bailey McMeans

*Calanus hyperboreus* forms an important link between phytoplankton and higher trophic levels in northern oceans. In the present study, values of δ\(^{15}\)N, δ\(^{13}\)C and fatty acids were compared among *C. hyperboreus* sampled during August ("summer") and April ("winter") across two consecutive years in Cumberland Sound, Baffin Island, Canada. *C. hyperboreus* did not switch to a higher trophic position during winter based on δ\(^{15}\)N values, but significantly higher δ\(^{13}\)C in summer 2007 versus 2008 could indicate differences in phytoplankton species composition. Several fatty acid proportions and concentrations were similar within seasons between both years (summer: higher 18:2n-6, 18:3n-6, 20:5n-3, \(\sum\)polyunsaturated fatty acids; winter: higher 18:1n-9, \(\sum\)monounsaturated fatty acids). However, several fatty acid proportions and concentrations (i.e. 18:1n-9, 20:1n-9, 22:1n-9) varied inter-annually between summer-sampled *C. hyperboreus*, which could be attributed to differences in phytoplankton species composition and the timing of ice break-up between summer 2007 and 2008. Results from the present study stress the need to monitor changes in *C. hyperboreus* fatty acids over time, and have implications for studies focused on the diet of higher trophic level animals in Cumberland Sound and in other arctic marine ecosystems.
Validating the use of Fs-LA-ICP-MS to analyze the chemical composition of elasmobranch vertebral centra to aid in determining movement ecology  
Heather McCann

Understanding ontogenetic shifts in habitat and migration patterns of threatened apex predators is important for conservation and management strategies. Current methods used to determine these key life-history characteristics do not provide data throughout all of ontogeny. The elemental profiles of elasmobranch vertebral centra may present a unique tool to examine habitat usage and migration patterns over ontogeny. To utilize the elemental profiles of vertebral centra two conditions must be met (i) elements contained within the vertebral centra must be present above detection limits and (ii) the inorganic portion of the vertebral centra and associated elements must undergo no reworking. To test this tool, the vertebral centra from 9 white sharks (Carcharodon carcharias) were analyzed using femtosecond laser ablation inductively coupled plasma mass spectrometry (Fs-LA-ICP-MS). A total of 19 elements were measured, including major (3), minor (3), trace (9) and rare earth (4) elements. Elemental profiles characteristic of juvenile animals were seen in the juvenile portion of adult animals indicating reworking within the vertebral centra was minimal. Elements that have well-established relationships in the environment (e.g. Sr, Ba) can therefore be used as chemical markers for examining seasonal and size based habitat preference and movement ecology over ontogeny.

Speciation in ancient lakes: the calanoids of Sulawesi  
James Vaillant

Ancient lakes have revealed much about speciation processes and are becoming increasingly popular for evolutionary studies. The island of Sulawesi, Indonesia, is home to the ancient Malili lakes which represent an ideal study system for studying speciation in zooplankton, a poorly understood process, because of their varying interconnectedness. In this study, we use a combination of molecular and morphological data to characterize the evolutionary history and speciation patterns of the island’s calanoid species. Copepod samples were gathered from 20 sites of 5 of the island’s lakes. Neighbour-joining and Bayesian phylogenetic reconstructions were conducted using both mitochondrial and nuclear markers. Large divergences in morphology and molecular data reveal that different genera have colonized distant lakes. Within the Malili lake system, the two headwater lakes share two closely related mitochondrial clades, while the most downstream lake maintains a highly divergent lineage. However, homogeneity across nuclear markers and morphology suggests that gene flow occurs between all three hydrologically connected lakes. This pattern is very curious and suggests unidirectional hybridization may be occurring between the lakes. The results of this study will provide valuable insights into the evolutionary forces that drive speciation in pelagic invertebrates and generate biodiversity in aquatic ecosystems.
The Reductive Dissolution of Tl(I)-jarosite by *Shewanella putrefaciens* CN32: Providing new Insight into Thallium(I) Biogeochemistry
Christina Smeaton

Jarosite minerals \( \text{MFe}_3(\text{SO}_4)_2(\text{OH})_6 \) are precipitated in the metallurgical industry to scavenge iron, alkali metals and sulfate ions from processing solutions and contain toxic metals such as Pb, Ag and Tl. During this process, large volumes of jarositic wastes are produced and often confined to large capped tailings ponds, thereby creating potential for anaerobic reductive dissolution by dissimilatory metal reducing bacteria. Despite the high toxicity of thallium, very few studies exist on the abiotic and biotic dissolution of thallium mineral phases. In this study we examined the reductive dissolution of synthetic Tl(I)-jarosite \( \text{TlFe}_3(\text{SO}_4)_2(\text{OH})_6 \) by *Shewanella putrefaciens* CN32 using batch experiments under anaerobic circumneutral conditions. Cell viability and solution chemistry including pH, Eh, Fe speciation and Tl concentrations were measured over time and demonstrated an increase in Fe(II) and Tl concentrations in samples inoculated with bacteria compared to control samples. Environmental scanning electron microscopy showed alteration of the Tl-jarosite and secondary Fe mineralization in both the control and inoculated samples. In contrast to previous studies with Pb and Ag-jarosite, *S. putrefaciens* CN32 did not show precipitation of Tl nanoparticles associated with the cell surface thus suggesting a different mechanism for Tl detoxification. The results of this study provide new insight into the biogeochemical cycling and potential for increased mobility of Tl(I) in reducing environments.
Patterns of selection and genetic drift in the gene expression of the immune response in Rainbow Trout of Babine Lake, BC.

Kyle Wellband

Sub-divided populations that are exposed to different environments will experience different selective pressures potentially leading to local adaptation. Locally adapted populations present a challenge for the conservation and management of populations as introgression between previously isolated populations can result in less fit offspring via out-breeding depression. Because of this, it is important to investigate the potential for local adaptation in genetically sub-divided populations that exist across heterogeneous environments. Rapid evolution of gene expression of fitness related traits in Pacific salmonids has been reported and may be appropriate for investigating local adaptation in recently diverged populations. I will present results of a study using reverse-transcriptase quantitative-PCR to compare gene expression of immune and metabolic stress response traits among genetically sub-divided populations of rainbow trout from Babine Lake, BC.

The analysis of genetic load and inbreeding depression in Chinook Salmon

*(Oncorhynchus tshawytscha)*

Kendra Komsa

There is strong evidence to show that inbreeding in many plants and animals is destructive and can lead to detrimental effects at the level of the organism as well as the population. Since inbreeding reduces genetic variation by decreasing heterozygosity and increasing genetic load the effects of inbreeding are often considered undesirable. Genetic load is a term used to describe the entire collection of deleterious alleles that can be expressed in an entire genome. The expression of deleterious recessive alleles occurs as a result of inbreeding through the increased homozygous allele combinations. Selection against deleterious recessive alleles, in a process referred to as purging, decreases their frequency within the population. It is because of this potentially beneficial outcome of inbreeding that conservation efforts have begun to focus on inbreeding depression and whether or not it is a suitable practice to allow inbreeding to naturally occur within populations. With the use of hermaphrodite Chinook salmon, we are able to perform the first quantitative study analyzing the effects of inbreeding depression and genetic load in vertebrate organisms at the most extreme level of inbreeding – selfing. Hermaphrodite offspring will be compared to outbred offspring and mixed parentage offspring to phenotypically determine any differences. Additionally, the offspring will be genotyped and deviations from Mendelian inheritance will be determined as evidence that purging of the genetic load is taking place.
Genetic structure and gene flow among populations of the threatened eastern sand darter (ammodrypta pellucida) in two Canadian rivers.
Robert Ginson

Eastern sand darters (Ammocrypta pellucida) have high dependence on fine, sandy substrate habitats throughout their species range. Conservation concerns for Canadian populations of A. pellucida include loss of preferred habitat and this can potentially increase population fragmentation and reduce gene flow among populations. Loss of gene flow can create isolated populations and negative genetic effects associated with this can result in loss of population fitness. Using ten recently developed microsatellite loci, this study focuses on determining the genetic structure and divergence among A. pellucida populations from two neighbouring watersheds (Thames and Grand Rivers) in south-western Ontario, Canada. Bayesian-genotype assignment tests found multiple genetic clusters in each watershed and FST estimates found high genetic divergence among clusters. Thames River genetic clustering revealed apparent spatial structuring; however, no pattern of isolation by distance was detected. A. pellucida in the Grand River had no geographic pattern among genetic clusters. Our results indicate that indeed A. pellucida in both watersheds experience population fragmentation promoting high genetic divergence, although each watershed had unique spatial genetic structuring. Further analysis to characterize the genetic structure of these populations is required before conservation strategies can be fully developed; however, future management must be implemented at the within-watershed level.

Sperm Traits in Wild and Farmed Chinook salmon (Oncorhynchus tshawytscha)
Sarah Lehnert

The potential impacts of escaped Chinook salmon (Oncorhynchus tshawytscha) from aquaculture sites on wild salmon populations are of concern along the west coast of Canada for a number of reasons. One is that the gene pool of farmed fish often diverges from that of wild populations, thus hybridization could be a threat to the genetic composition of the wild population. The potential for hybridization between farmed and wild stocks to occur will depend on the mating success of the escaped fish in the wild in which the role of behavioural factors such as male-male competition will be important. In fishes, sperm competition is important, as many fish species are external fertilizers and this allows several males to simultaneously fertilize the eggs of a single female. Farmed Chinook salmon are exposed, through domestication, to inbreeding, artificial selection and reduced gene flow. We hypothesize that farmed salmon would experience a decrease in sperm performance and hence competitive ability due to domestication compared to wild salmon. To test these predictions, a range of sperm related traits were measured in both farmed and wild Chinook salmon, including sperm longevity, sperm density, and sperm velocity. Our results provide insight into the potential impacts that escaping farmed salmon can have on spawning grounds of wild salmon populations.
Effects of chlorine treatment in reducing viable organism populations in ballast water tanks
Marco Hernandez

In the Great Lakes, the largest vector of non-indigenous species (NIS) is ballast water of transoceanic ships. Since 1993, Ballast Water Exchange (BWE) has been enforced for all transoceanic ships with filled ballast tanks. BWE has been adopted by the International Maritime Organization (IMO) as D-1 standard and it has been in place globally since 2005. There is another standard D-2, developed in 2005 but not yet ratified. Even under these new regulations, it is possible that larger ships may still transport high numbers of viable organisms. In the region, New York (NY) has been attempting to make standards more stringent. The proposed standard is 100 times more stringent than the IMO D-2 level for ships in service and 1000 times more stringent for ships under construction.
This study will evaluate control techniques that will combine BWE with subsequent chlorination treatment, in an attempt to gain additive or synergistic benefits to the existing D-1 standard. It will develop an adequate sampling technique that will probe with robust statistical analysis whether the new (NY) standard is achieved. Molecular techniques will be used to identify and quantify possible surviving organisms.

Vector-based risk assessment for ship-mediated biological invasions in the Canadian Arctic
Farrah Chan

Global warming is reducing Arctic sea ice, and may provide additional navigation routes and a prolonged shipping season in the future. Therefore, the Arctic may be exposed to greater ship traffic and thus greater risk for ship-mediated biological invasions. We used a two-step model to identify high risk ports in the Canadian Arctic based on ship traffic and environmental suitability. First, we summarized 2005-2008 shipping data from the Canadian Coast Guard and Transport Canada, and used vessel arrivals and ballast water discharge volume as proxy measures for propagule supply. We estimated 541 arrivals discharging 233,396 m$^3$ of ballast water annually. We then compared the environmental conditions of the recipient ports with those of the connected source ports and bioregions to estimate establishment probability for potential aquatic non-indigenous species (ANS). Churchill, MB was identified as a high risk port with Port Alfred, QC as a potential ANS source. These results can be used to develop early detection programs at high risk ports and as a baseline for long-term monitoring of biological invasions as climate conditions and shipping activities in the region change.
**Domestic Ballast as a Potential Vector of Nonindigenous Species to the Great Lakes**

Remi Adebayo

Great Lakes ports receive approximately equal amounts of transoceanic and domestic (St. Lawrence River – SLR) ballast. While transoceanic ballast is recognized as a historically important introduction vector of nonindigenous species (NIS) to the Lakes, it is now well managed by ballast water exchange regulations. Domestic ballast is generally considered to be lower risk vector and is currently unregulated. Here we examine the potential risk of ballast from the SLR as a dispersal vector of NIS to the Great Lakes. We conducted biological surveys at 6 Great Lakes’ ports, 16 SLR ports, and sampled ballast water of 29 vessels with transits originating from SLR ports. We compare the invertebrate communities and environmental similarity between SLR and Great Lakes ports and estimate colonization and combined propagule pressure to the Great Lakes. Species level identification is currently underway; to date, 18 species not indigenous to the Great Lakes have been found in samples. The comparative invasion risk posed by ballast moved from SLR ports to the Great Lakes will be discussed.

**Multiple introductions and invasion pathways for the invasive ctenophore Mnemiopsis leidyi in Eurasia**

Sara Ghabooli

Genetic analysis has proven useful in understanding the invasion history and dynamics of colonizing NIS and identifying their source population(s). Here we investigated sequence variation in the nuclear ribosomal Internal Transcribed Spacer (ITS) region of the ctenophore *Mnemiopsis leidyi*. We surveyed populations from the native distribution range along the Atlantic coasts of the United States and South America, as well as populations in the introduced range from the Black, Azov, Caspian, Baltic, and Mediterranean Seas. Allelic and nucleotide diversity of introduced populations were comparable to those of native populations from which they were likely drawn. Introduced populations typically exhibited less genetic differentiation (lower $F_{ST}$ values) than native populations. Population genetic analyses supported the invasion of Eurasia from at least two different pathways, the first from the Gulf of Mexico (e.g., Tampa Bay) to the Black Sea and thence to the Caspian Sea, the second from the northern part of the native distribution range (e.g., Narragansett Bay) to the Baltic Sea. The relatively high genetic diversity observed in introduced populations is consistent with large inocula and/or multiple invasions, both of which are possible given ballast water transport and the extensive native distribution of the ctenophore in the Atlantic Ocean.