2016 FMCS Workshop

POPULATION GENETICS AND FRESHWATER MOLLUSK CONSERVATION

National Conservation Training Center – Shepherdstown, WV

February 16-19, 2016

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The Freshwater Mollusk Conservation Society (FMCS) is dedicated to the advocacy for public education about, and conservation science of freshwater mollusks, North America's most imperiled fauna.

This is the 10th Biennial FMCS Workshop

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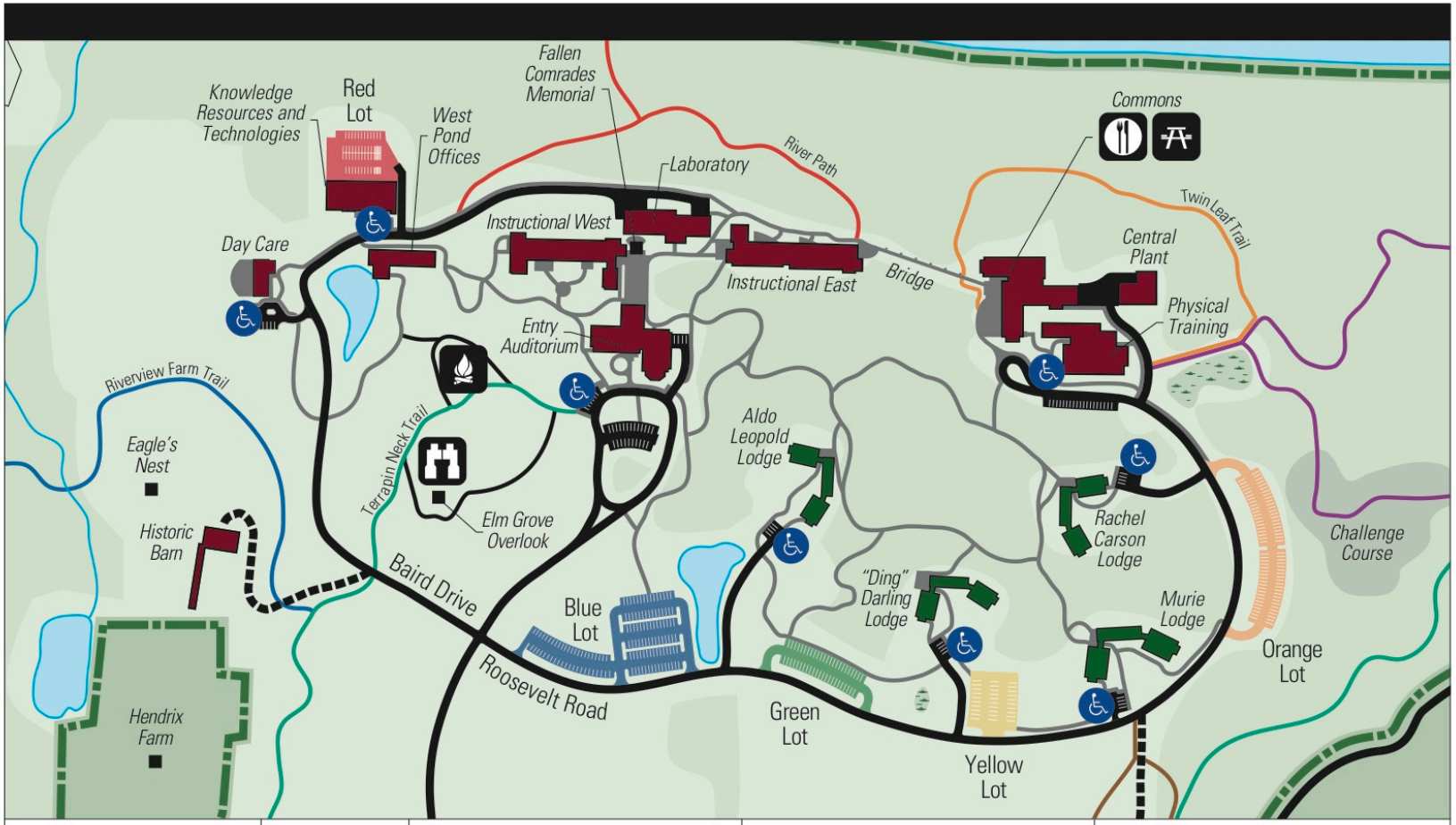

National Conservation Training Center

Campus Map

- Accessible Parking
- Firepit
- Elm Grove Overlook
- Dining Hall
- Picnic Area
- Paved Trails
- Paved Roads
- Gravel Roads
- Points of Interest

Campus Store
Extension 7350
11:00 AM – 2:00 PM

Conservation Library
Extension 7304

Dining Services
Extension 7353

Breakfast	6:30 AM – 9:00 AM *Hot Food until 8:30 AM*
Lunch	11:30 AM – 1:30 PM *Hot Food until 1:00 PM*
Dinner	5:30 PM – 7:30 PM

Commons Lounge
Extension 7351
5:30 PM – 11:00 PM

Physical Training Center *Extension 7341*
Sunday – Thursday 6:00 AM – 10:00 PM
Friday 6:00 AM – 4:30 PM

DAY 1, ARRIVAL & REGISTRATION Tuesday, February 16, 2016	
1200 – 1900 Auditorium Lobby	WORKSHOP REGISTRATION
1300 – 1500 Auditorium Lobby	STUDENT WORKER TRAINING
1730-1930 Commons	DINNER
1830 – 1930 Commons	WORKSHOP INSTRUCTORS MEETING
1900 – 2200 Roosevelt Room Commons	WELCOME RECEPTION

DAY 2, SESSIONS I, II, III Wednesday, February 17, 2016	
0630 – 0745 Commons	**Breakfast**
Session I 0800 0950 Auditorium	**INTRODUCTION TO CONSERVATION GENETICS** Dr. David J. Berg[1] and Dr. Kentaro Inoue[2] [1]Department of Biology, Miami University, Hamilton, Ohio, USA [2]Department of Ecology and Ecosystem Management, Technische Universität München, Munich, Germany This session will cover 1) a review of basic genetic terms such as allele, locus, genotype, etc.; 2) mechanisms generating variation (mutation, independent assortment, crossing over) and purging it (natural selection, genetic drift); 3) different types of genetic data such as mitochondrial and nuclear sequences, microsatellites, and other markers; and 4) principles of population genetics including Hardy-Weinberg equilibrium and Mendelian versus quantitative traits. We will assume that participants have no knowledge of genetics beyond that presented in General Biology courses. After this refresher, we will focus on understanding how one describes genetic variation as it is distributed within and among populations. This will include measures describing within-population variation such as allele frequencies, haplotype sequences, and allelic richness. Among-population variation will be considered using the framework of fixation indices (F_{ST}). Conservation implications of this material will be considered as well.
1000 – 1030 Auditorium Lobby	**Break**
Laboratory I 1035 – 1150 Auditorium & Classrooms (Instructional East)	**USE OF GENALEX TO DESCRIBE GENETIC VARIATION AND STRUCTURE** Dr. David J. Berg and Dr. Kentaro Inoue The laboratory session will provide participants with the opportunity to describe genetic variation within populations and analyze genetic structure among populations using Genetic Analysis in Excel (GenAlEx). This MSExcel add-in allows one to conduct widely used population genetic analyses from a spreadsheet. Participants will have the opportunity to analyze microsatellite data for several species of freshwater mussels. BRING YOUR LAPTOP!
1150 – 1250 Commons	**Lunch**

Session II **1300 – 1450** **Auditorium**	**BIG TROUBLE IN LITTLE POPULATIONS** Dr. Curt L. Elderkin[1] and Dr. Emy M. Monroe[2] [1]Department of Biology, The College of New Jersey, Ewing, New Jersey, USA [2]Whitney Genetics Laboratory, US Fish & Wildlife Service, LaCrosse, Wisconsin, USA This session will cover 1) the importance of maintaining genetic diversity within populations; 2) how populations evolve by random chance, known as genetic drift; 3) the hazards encountered in small populations including inbreeding; and 4) how to calculate genetic diversity and inbreeding within small isolated populations. During the session we will walk through many studies previously done on threatened and endangered species and then focus closely on some previous work done on freshwater mussels.
1500 – 1530 **Auditorium** **Lobby**	**Break**
Laboratory II **1535 – 1650** **Auditorium &** **Classrooms** **(Instructional East)**	**GENETIC DRIFT AND BOTTLENECKED FERRETS** Dr. Curt L. Elderkin and Dr. Emy M. Monroe This laboratory will provide a hands-on experience in conservation genetics of small populations. The module we will use revolves around a real-life example using Black Footed Ferrets. The module consists of three parts where we will look at how allele frequencies change in small populations; discuss what the effective population size is, and how it can change genetic diversity; and finally how to best maintain heterozygosity of a managed population. BRING YOUR LAPTOP!
Session III 1700 – **1730 Auditorium**	**UNIOBARCODE: BUILDING A COMPREHENSIVE DNA BARCODE LIBRARY FOR FRESHWATER MUSSELS** Nathan A. Johnson Southeast Ecological Science Center, US Geological Survey, Gainesville, Florida, USA This session will provide participants with an understanding of DNA barcoding methods and applications. We will review the traditional methodologies for identifying freshwater mussels and learn how DNA barcoding is being used to build an alliance between molecular and morphological taxonomy. We will end the session exploring barcode workflows and analytical tools while discussing applications in freshwater mollusk ecology, taxonomy, and conservation.
1730 – 1900 **Commons**	**Dinner and Casual Discussion**

1900 – 2200 Roosevelt Room Commons	***ADVANCES IN FRESHWATER MOLLUSK CONSERVATION*** **Poster Session and Concurrent Social**

DAY 3, SESSIONS IV, V, VI, VII Thursday, February 18, 2016	
0630 – 0745 Commons	**Breakfast**
Session IV 0800. – 09:50 Auditorium	**PHYLOGENETICS AND SPECIES DELINEATION** Dr. Kevin J. Roe[1] and Dr. David M. Hayes[2] [1]Department of Natural Resource Ecology & Management, Iowa State University, Ames, Iowa, USA [2]Department of Biological Sciences, Eastern Kentucky University, Richmond, Kentucky, USA This session will cover 1) the use of phylogenetic trees and the relationship between phylogenetic trees and taxonomic classifications and the delineatior of species; 2) a review of the use of terminology associated with phylogenetic trees and the basics of phylogenetic theory; 3) a discussion of different approaches for generating phylogenetic trees including algorithmic approaches and optimality criteria.
1000 – 1030 Auditorium Lobby	**Break**
Laboratory IV 1035 – 1150 Auditorium & Classrooms (Instructional East)	**USE OF MEGA TO DETERMINE PHYLOGENETIC RELATIONSHIPS.** Dr. Kevin J. Roe and Dr. David M. Hayes The laboratory session will provide the opportunity for participants to complete all the basic stages of phylogenetic analysis using DNA sequences and the software package Molecular Evolutionary Genetics Analysis (MEGA) including data acquisition, DNA sequence alignment and editing, testing for the appropriate model of sequence evolution, generation of phylogenetic trees, and reliability estimation. BRING YOUR LAPTOP!
1150 – 1250 Cafeteria	**Lunch**

Session V **1300 – 1450** **Auditorium**	**NEW DIRECTIONS IN CONSERVATION GENETICS** **ENVIRONMENTAL DNA (EDNA) FOR DETECTING BIODIVERSITY** Dr. Emy M. Monroe & Dr. David Hayes This presentation will update participants on the rapid development and application of environmental DNA (eDNA) in freshwater systems. Managers may be interested in using this new tool in the genetic toolbox, so this session will present critical considerations when using eDNA and summarize ecology of eDNA in aquatic systems. A couple of interactive exercises will illuminate some of the less obvious technical challenges for eDNA analyses. We will consider important limitations managers need to understand with the implementation of this tool in a management context. **GENETICS AND CAPTIVE PROPAGATION OF FRESHWATER MOLLUSKS** Dr. David J. Berg This presentation will consider the ways in which principles of conservation genetics can inform propagation and management of species of conservation concern. The questions to be addressed are "How do we maximize "good" variation while minimizing "bad" variation?" when creating a program of captive propagation and "How do we manage reintroduction of propagated individuals into natural settings?" We will discuss strategies for characterizing natural variation, founding, expanding, and managing captive populations, choosing individuals for reintroduction, and managing reintroduced populations.
1500 – 1530 **Auditorium Lobby**	**Break**

Session VI **1545 – 1700** **Auditorium**	**PLENARY SESSION: THE EXPANDING ROLE OF GENOMICS IN CONSERVATION AND ECOLOGY** Dr Gordon Luikart Division of Biological Sciences, University of Montana, Missoula, Montana, USA Dr. Gordon Luikart is currently a Professor of Biological Sciences at the University of Montana's Flathead Lake Biological Station. After receiving his Ph.D. under Drs. Fred Allendorf and J.T. Hogg at the University of Montana, he held several postdoctoral fellowships and research scientist appointments at the National Center for Scientific Research in Grenoble, France. In 2005, Dr. Luikart assumed his current position at the University of Montana. In 2014, he was named one of "The World's Most Influential Scientific Minds" by Thomson Reuters for being one of the most highly-cited authors of peer-reviewed scientific papers published between 2002 and 2013. Continuing to collaborate with Fred Allendorf and other colleagues at Flathead Lake Biological Station, Dr. Luikart's research uses genetic principles and tools to address questions of conservation in natural, domesticated, and invasive populations. Recently, much of this work has focused on the application of genomics to questions of conservation. He has authored a seminal book, *Conservation and the Genetics of Populations*, the third edition of which will be released this year. Dr. Luikart has authored well over 100 papers in peer-reviewed journals such as *Science*, *Trends in Ecology & Evolution*, *Proceedings of the National Academy of Sciences*, *Conservation Biology*, and *Molecular Ecology*. This talk will explain why it is an exciting time to be using genetic/genomic approaches in conservation biology. The talk will provide an overview of recent advances in DNA sampling (eDNA), DNA genotyping (via "next generation sequencing", RADs, and RAPTURE), and recent statistical approaches for analysis of DNA data. Data analysis topics will cover population genomic approaches including the estimation of inbreeding using runs of homozygosity (roh), and estimation of effective population size (Ne) using linked loci. Data analyses topics will also include the delineation of adaptively-differentiated populations (e.g. ESUs) using candidate adaptive SNP loci.
Session VII **1700 – 1800** **Auditorium**	**Question and Answser Period with the Instructors and Presenters**
1800 – 1900 **Cafeteria**	**Dinner and Casual Discussion**
1900 – 2200 **Roosevelt Room** **Commons**	**Wrap Up Social**

DAY 4, DEPARTURE **Friday, February 19, 2016**	
0630 – 0900 **Commons**	**Breakfast**
	DEPARTURE AFTER BREAKFAST (sack lunch may be picked up from cafeteria by prior arrangement)

FMCS CONSERVATION GENETICS WORKSHOP – NATIONAL CONSERVATION TRAINING CENTER, SHEPHERDSTOWN, WV: FEBRUARY 16 – 19, 2016

POSTER SESSION ABSTRACTS

	ADVANCES IN FRESHWATER MOLLUSK CONSERVATION **Wednesday, February 17, 2016 | 7:00 p.m.** **Roosevelt Room** **Commons**
Poster 1	**NICHE AND LINEAGE DIVERSIFICATION IN A FRESHWATER MUSSEL SPECIES COMPLEX.** Ashley D. Walters[1], Kentaro Inoue[1], John L. Harris[2], & David J. Berg[3]. [1]Department of Biology, Miami University, Oxford, OH 45056; [2]Department of Biological Sciences, Arkansas State University, State University, AR 72467; [3]Department of Biology, Miami University, Hamilton, OH 45011.

We investigated the relationship between lineage divergence and niche differentiation within a freshwater mussel species complex. The morphologically defined *Obovaria jacksoniana* and *Villosa arkansasensis* form a species complex consisting of five clades in the lower Mississippi and Gulf Coast drainages of the USA. We employed ecological niche modeling to estimate niche space based on eight environmental layers, and multivariate statistics to estimate niche overlap. Additionally, we used a molecular clock method to estimate divergence time between clades. Our results indicate that a majority of clades occupy distinct environmental niches, indicating a pattern of niche divergence. We found a negative correlation between divergence time and niche overlap; thus, clades that diverged most recently occupied the most-similar niches. Recent speciation within this complex, likely due to geographic isolation, appears to have been accompanied by niche differentiation. Rather than two species, this complex consists of five species that are distinguishable both genetically and ecologically. While providing insight into the process of speciation, our study also suggests that niche differentiation may be a useful measure for identifying taxonomic units of conservation interest.

Poster 2	**DEVELOPMENT OF A STRATEGIC CONSERVATION PLAN FOR *QUADRULA* SPECIES OF THE GULF COAST PRAIRIE REGION.** Wesley M. Daniel[1], Dana M. Infante[1], Cynthia Edwards[2], Benjamin Kahler[2], and Elizabeth Throckmorton[1]. [1]Michigan State University, Department of Fisheries & Wildlife, East Lansing, MI 48823; [2]Gulf Coast Prairie Landscape Conservation Cooperative, National Wetlands Research Center, Lafayette, LA 70506

The southeast United States' rivers and streams support the most diverse unionid (freshwater mussel) fauna on earth. These species are a focus of the Gulf Coast Prairie Landscape Conservation Cooperative (GCP LCC) because of their sensitivity to habitat degradation, fish community changes, and changes in water quality and quantity, making them an important indicator of environmental condition of freshwater habitats. The majority of the GCP LCC area is in eastern Texas, central Oklahoma, and southern Louisiana. Numerous threatened and endangered *Quadrula* species, including several endemics, occur throughout this region. The goal of this project is to combine current information from the literature with expert knowledge to be used in support of the development of a Conservation Plan for *Quadrula* species in the GCP LCC region. To meet this goal, we are working to consolidate information from peer-reviewed journals, state wildlife action plans (SWAPs) and grey literature from state and federal agencies on distribution, life history traits, conservation needs, and on-going conservations actions for *Quadrula* genus and other sympatric species including species of greatest conservation need within Louisiana, Oklahoma, and Texas. When possible, this information will be integrated with species distributions and management action locations into a spatially-explicit database. We are also working to seek feedback from regional experts, stakeholders, and malacologists from FMCS about the current and future threats to *Quadrula* species in the Gulf Coast Prairie region to provide to the GCP LCC. All this information will facilitate the development of the Conservation plan for *Quadrula* species in the GCP LCC region.

Poster 3	**RIVER SPECIFIC GENETIC DIVERSITY OF *MARGARITIFERA MARGARITIFERA* WITH RESPECT TO HOST FISH AND POPULATION SIZE.** Santtu Välilä[1], Jürgen Geist[2], Paul Erik Aspholm[3], Emily Knott[1] and Jouni Taskinen[1]. [1]Department of Biological and Environmental Science, University of Jyväskylä, 40500 Jyväskylä, Finland, [2]Technische Universität München, Aguatic Systems Biology Unit, 85354 Freising, Germany; [3]Nibio, Norwegian Institute of Bioeconomy Research, NO-1431 Ås, Norway.

Effective conservation approaches for endangered species require integration of ecological and genetic information. Low genetic diversity is a matter of concern, as it may reduce the ability of the species to adapt to environmental changes. We examined the genetic structure and diversity of 21 *Margaritifera margaritifera* populations located in Finland, Sweden and Norway. We used COI sequences and microsatellites to generate genetic information. From 18 observed COI haplotypes, 7 were restricted to certain populations. The number of observed haplotypes per population ranged from 1 to 10. An average of 5.2 alleles was observed for the 9 microsatellite loci. Hierarchical AMOVA revealed that 0% of the genetic variation was among drainage systems, 31% among populations within drainages, and 69% within populations. Pair-wise FST values spanned a wide range and 88% of differences in all pairwise comparisons were highly significant. The results of the Mantel test confirmed that there was no isolation by distance. A regression model was fitted to the four response variables, mean observed and expected haplotype (H) and allelic (A) richness, using the host species and the mussel population size as predictor variables, assuming asymptotic increase in the response variable with the increasing population size. *M. margaritifera* of salmon rivers had a higher asymptotic haplotype and allelic richness than *M. margaritifera* of trout rivers. Allelic richness was at its asymptotic level already in the smallest observed N of < 10.000 while haplotype richness reached its asymptote with N around 50.000 mussels for both species. The results show that current population differentiation does not match with current drainage systems. Most of the populations had relative high pairwise FST values, indicating that there is a strong differentiation between populations. Thus, no introductions should be carried out to increase genetic diversity without the information of the genetic structure of the populations.

Poster 4	**COMPARING LAB BASED HOST INFESTATION TRIALS TO NATURAL GLOCHIDIAL INFESTATIONS: GENERALIST MUSSELS MAY BE MORE SELECTIVE THAN EXPECTED.** Katie Bockrath[1], Robert Bringolf[2], John P. Wares[3]. [1]USFWS Midwest Fisheries Center, Whitney Genetics Lab, [2]University of Georgia, Warnell School of Forestry, [3]University of Georgia, Department of Genetics.

Freshwater mussels are a species rich but threatened group of aquatic invertebrates. Their parasitic larval stage makes them dependent on a suitable fish host to complete their life cycle. With over 70% of mussel species threatened, endangered, or extinct, it is important to understand the interactions mussels have with their fish hosts. Lab based host infestation trials allow us to investigate the breadth of fish species glochidia can use as a host, and though the information gained through these tests is highly informative, it does not reflect natural mussel-fish interactions. By collecting fish across a stream community while both generalist and specialist mussels are releasing glochidia, we can directly relate lab host trials to natural infestations. In general, lab based host infestation trials suggest that successful metamorphose of glochidia from specialist mussels should be limited to small groups of fish (ie: family or genus) while generalist glochidia from mussels should metamorphose on fish across families or genera. I allowed glochidia from naturally infested fish to complete metamorphose in an AHAB unit and in doing so, determined the breadth of a sampled fish community that was acting as ecologically important host for three mussel species. I used two mitochondrial genetic barcodes, COI and FORF, to identify glochidia collected from naturally fish. I found the information gathered from lab based host infestation trials for specialists mussels were reflected in natural populations, but generalist mussels functionally use far fewer fish as hosts than expected with lab based host infestation trials and can may primarily associate with a single fish species.

Poster 5	***MARGARITIFERA MARGARITIFERA* DISTRIBUTION AND HABITAT CHARACTERISTICS IN PENNSYLVANIA STREAMS.** Mary Walsh, Pennsylvania Natural Heritage Program, Western Pennsylvania Conservancy, 800 Waterfront Drive, Pittsburgh, Pa 15222

Since the pearl hunters depleted populations and coal mine effluent polluted many of the streams in the limited range in Pennsylvania, the known habitat of *Margaritifera margaritifera* (Eastern Pearlshell) has shrunk since its occurrences in the Commonwealth were first documented in the early 20th century. In order to meet the Eastern Pearlshell Species Action Plan's goals for informed conservation, the project filled in distribution information gaps, documented population density, and characterized habitats for the Pennsylvania-endangered *Margaritifera margaritifera*. We searched for previously unknown populations of *Margaritifera margaritifera* in streams prioritized as potential habitats in the Little Schuylkill River, Schuylkill River, Maiden Creek, Lehigh River, White Clay Creek, and upper Delaware River watershed in Pennsylvania. At 58 locations in 33 streams, snorkelers conducted timed-searches, measured relative abundance, and evaluated habitats and water quality. Additionally, we used quantitative survey methods at four locations in two creeks to assess population densities. Seven species of Atlantic Slope freshwater mussels (Margaritiferidae and Unionidae families) were found in 22 survey sites in twelve streams. Besides documenting the up and downstream bounds of habitat in streams with existing populations, we also documented *Margaritifera margaritifera* in two streams with previously unknown populations. *Margaritifera margaritifera* occurred with four Unionid species at one stream, but it was the only freshwater mussel species in three other streams. The density of *Margaritifera margaritifera* ranged from "not detectable" to 0.897 /m2 (95% CI 0.624-1.29) among the four sites. Streams with extant *Margaritifera margaritifera* habitats had low conductivity, alkalinity, hardness, slightly acidic to neutral pH, and low concentrations of nitrogen, phosphorus, and iron. The results of EPA Rapid Bioassessment Habitat evaluations at *Margaritifera margaritifera* sites indicated that locations with extant populations surveyed for this study had minor siltation, but had high quality habitats overall. Stream reaches supporting *Margaritifera margaritifera* habitats were prioritized for conservation actions.

Poster 6	**IMPROVEMENTS IN JUVENILE *IO FLUVIALIS* SURVIVAL USING POND WATER AND POND SYSTEMS.** Sarah L. Colletti, Megan E. Bradley and Joseph F. Ferraro. Aquatic Wildlife Conservation Center, Virginia Department of Game and Inland Fisheries, Marion, Virginia 24354.

Freshwater gastropods are the most at-risk group of animals in North America with over 319 species listed as imperiled and an estimated 60 already extinct. *Io fluvialis* used to range over the Tennessee River basin from Muscle Shoals, Alabama to the headwaters of the Clinch, Powell and Holston Rivers but has been restricted to only the headwaters of these Rivers in Virginia. It is listed as a Virginia Species of Concern due to catastrophic spills, changes in water quality and habitat alterations. *Io fluvialis* have been propagated and cultured at the Virginia Department of Game and Inland Fisheries' Aquatic Wildlife Conservation Center since 2005 and approximately 11,500 released into the Upper Clinch and Powell Rivers. Broodstock are collected from the Clinch River, VA and transported to the lab for spawning. Broodstock are held in 0.93 meter fiberglass tanks with flow through South Fork Holston river water where eggs are laid. Using the previous culture protocol, adults were moved after eggs are laid and juveniles remained in the fiberglass tanks; aquariums filled with pond water were also tested. In 2012 survivorship of juveniles was <1%. In 2013 survivorship was 0. In 2014 and 2015, newly hatched juveniles were put directly into pond-fed troughs which dramatically increased post-hatching survival. In 2015, mean survivorship was 59% across 5 troughs and varied from 37% to 90%. The pond-fed troughs are warmer and higher in nutrients than unadulterated river water resulting in faster algae growth and provide increased surface area for feeding. Improved juvenile survival in the hatchery results in a greater likelihood for restoration of the species to the Upper Clinch River and eventually to its historic range.

Poster 7	**AMERICA'S NEWEST INVADER? - DISCOVERY OF A THIRD *CORBICULA* SPECIES IN ILLINOIS.** Jeremy S. Tiemann[1], Sarah A. Douglass[1], Mark A. Davis[1], and Kevin S. Cummings[1]. [1]Illinois Natural History Survey, Prairie Research Institute at the University of Illinois, Urbana-Champaign, IL 61820

Corbicula, a "hyper-invasive alien" with great biofouling capabilities, was first recorded in North America in 1924 in British Columbia and breached the Continental Divide in the late 1950s. Since then, it has spread throughout the continent. *Corbicula* taxonomy is muddled and unclear, as is the number of species that have become established. Literature reports vary from an invasion of but a single species to invasions of multiple species. The Midwest has long been recognized as having only *Corbicula fluminea*. However, in 2008, a tentative second species, *Corbicula largilllierti*, began appearing in the navigable rivers of Illinois. It has purple nacre with more compressed, tighter ridges when compared with *C. fluminea*. A third Corbulid species was discovered in Illinois while sampling the Illinois River near Marseilles on 15 October 2015. Over 200 individuals were collected in conjunction with *C. fluminea* and *C. largillierti*. This undetermined species has fuchsia colored rays radiating from the umbo and white nacre with purple lateral teeth. It is currently unknown in North America, and we have no information for what the species is or its potential impact on aquatic ecosystems. In collaboration with the University of Michigan - Museum of Zoology, genomic and morphometric assessments are being employed to confirm the identity of this undocumented Corbulid and also that o *C. largillierti*. Accurate species delimitations are essential for informing adaptive management, developing predictive invasion/dispersal models, and assessing potential effects on aquatic ecosystems. We request that our colleagues to please alert us to the presence of unusual Corbulids in your study areas if encountered.

Poster 8	**PRELIMINARY FINE-SCALE ANALYSES OF GENETIC DIVERSITY, COLONIZATION HISTORY, AND POPULATION STRUCTURE OF THE EASTERN PONDMUSSEL, *LIGUMIA NASUTA*, IN THE GREAT LAKES REGION.** Mariah W. Scott[1], Todd J. Morris[2], David T. Zanatta[1]. [1]Central Michigan University, Institute for Great Lakes Research, Biology Department, Brooks Hall 217, Mount Pleasant, MI 48859, U.S.A.; [2]Fisheries and Oceans Canada, Great Lakes Laboratory for Fisheries and Aquatic Sciences, 867 Lakeshore Rd., Burlington ON L7S 1A1, Canada

Ligumia nasuta (Bivalvia: Unionidae) has colonized and persists in the Atlantic slope and Great Lakes regions of North America, but is considered imperiled in many of the states and provinces it inhabits. This expansive range was colonized through *L. nasuta* dispersing into the Great Lakes region, following retreat of the Wisconsin glaciers. While many of the known populations appear to have followed natural colonization routes, populations in some small inland lakes in the Great Lakes region are hypothesized to be the result of anthropogenic introductions via fish stocking. Using newly developed microsatellite DNA loci for *L. nasuta*, the genetic diversity and structure of remaining populations will be assessed to inform future management projects, examine the colonization history of the species, and determine if the remnant populations have experienced genetic bottlenecks or founder effects. Samples from 54 sites in 22 waterbodies across the range of *L. nasuta* (n=295) have already been collected for this study, with additional sampling planned. Ten to 15 of the newly developed microsatellite loci will be genotyped and scored. Genetic diversity estimates will be used to determine population structure between sampling locations and test for significant differentiation within and between populations. Mantel tests of genetic isolation will be compared for water, road, and Euclidean distances between sampling locations to assess likelihood of natural or anthropogenic colonization history. Also, genetic diversity indices and models will be used to test if a past genetic bottleneck event or founder effect has occurred. The presented material will focus on the preliminary progress and future plans for the project.

Poster 9	**CURRENT AND EMERGING ISSUES IN BIVALVE ECOTOXICOLOGY.** Gagné, F., André, C., Auclair, C., Gagnon, C. Aquatic Contaminants research division, Environment Canada, 105 Mc Gill, Montréal, QC, Canada H2Y 2E7.

The lifestyle of bivalve populations makes them species at risk to anthropogenic stressors such as pollution, loss of habitats and climate changes. Indeed, mussels are sessile organisms and could live to relatively long periods in some species (up to decades if not centuries). It is anticipated that global changes are likely to have local impacts on biodiversity. In this sense, local mussel populations are directly impacted by upstream disturbances such as urban effluents discharges and loss/modification of habitats. They are filter-feeders from which they trap and concentrate micro-particles in the digestive gland which represent a major vector for contaminant exposure in mussel tissues. For these reasons, bivalves were selected as sentinel species to assess the toxicity of emerging contaminants such as nanotechnology, oil sand products, endocrine disrupters from municipal discharges and changes in the microbiome. The cumulative effects of complex mixtures and other stressors in these times of climate change were also examined at the molecular and cellular levels in the attempt to identify adverse outcomes pathways leading to the decline of mussel populations. Exposure to xenobiotics increase the susceptibility to temperature changes at the electron transport steps in mitochondria which could increase energy expenses in bivalves at polluted sites under thermal fluctuations. Exposure to municipal effluent and zinc oxide nanoparticles both elicit oxidative stress which could lead to inflammation and phagocytosis suppression. Recent studies also showed that air time survival could also be shortened in mussels exposed to nanoparticles and oil sand contaminated environments which support the contention that mussels are species at risk from urban activities.
Studies dealing on the cumulative effects of environmental stressors were also performed.

NCTC Frequently Asked Questions

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Yes, every room has its own direct-dial phone number. To give the number to someone off-campus, tell them to dial "304/876" and your 4 digit room number. For example, room 7403 would be 304/876 7403.

I have difficulty walking, and this is a walking campus. How can I move around the facility easily?
We have several motorized carts available for guests at the Front Desk. Simply dial "0" and let us know that you would like a cart, and we will deliver it to your door.

How do I control the heat in my room?
The lodges are centrally-controlled by our Maintenance Department's computer system. The lodges are set to one temperature (for example, 70 degrees,) and then the guest may fine-tune the temperature by about four degrees, warmer or cooler. There are two sets of controls in your room. The thermostat is located by the bed. It is a sliding lever that may be behind a plastic flip-cover. Do not push the lever to the absolute top or bottom position; this will turn the system off in your room. There is also a fan speed control located by the closet where you can control the amount of air coming into your room. If this is set to the OFF position, your room will not receive any heating or cooling. If you are uncomfortable, please dial "0" for Guest Services, and we will contact Maintenance to raise or lower the temperature in your room.

Does my room have high-speed Internet?
Yes! Wireless and wired Internet connections are in every room. We also provide a LAN cable for you in the room, in case you left yours at home.

Are there any laundry facilities on campus?
Yes, in every lodge, on the ground floor, you will find a laundry room with washer, dryers, and complimentary laundry detergent. We do ask that you try to finish your laundry before 10 pm, in order to avoid disturbing other guests who may be sleeping.

Where are the closest vending machines?
They are located on the ground floor of each lodge. In Instructional East and West, they are located in an alcove in the center of the buildings on the first floor.

Where can I go if I need to use a computer, print documents, or send a fax?
There are computers available for use, with Internet connections, along the hallways in Instructional East and West. The Conservation Library in the Commons also has computer stations available, and is open until 8 pm Monday, through Thursday. If you need to send a fax, or print documents, the Faculty Lounge, in room 106 Instructional East has a laser printer attached to the computer. There is a fax machine in the room as well.

I'm checking out very early in the morning on the day I'm departing. Should I check out the night before?
No need! We provide express check-out for you the night before you depart. We will slip a receipt for your stay under your door late in the evening, as well as a sheet with shuttle information if you are using this service. To check out in the morning, simply take your receipt with you, sign the outer envelope, and leave the envelope and room key in the room. Please dial "0" to let us know when you leave.

Where can I see the NCTC bald eagles?
If you are facing the Entry Auditorium building, you will be able to see their nest in the large sycamore tree to your far left. Since they are nesting and are sensitive to disturbances in their environment, we request that visitors do not walk too near the eagles' nest. If you would like a close-up view, we have a Web cam that is constantly keeping watch over the eagles, unobtrusively (it even has night vision.) Simply go to the following Web address in your browser:
http://training.fws.gov/eagle/

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