



American Malacological Society

81ST ANNUAL MEETING

University of Michigan Biological Station
Pellston, Michigan
August 28-31, 2015

Program compiled and edited by Linda Garcia, Taehwan Lee,
Amanda Haponski, Ryutaro Goto and Tom Duda

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Welcome to AMS 2015

Welcome to northern Michigan and the 81st Annual Meeting of the American Malacological Society! The setting of the UMBS should afford a fantastic backdrop to the excellent schedule of presentations being offered. The meeting includes a Keynote Address by Alison Sweeney, an AMS-sponsored symposium ('Early Career Malacologists'), several organized and contributed sessions, and a poster session. An auction will take place after the poster session to raise funds for student research awards; thanks to all of those who contributed items! Two receptions with food and beverages will take place the first two nights of the meeting (a 'Welcome Reception' on 8/28 and a reception during the poster session and auction on 8/29). The AMS banquet and awards ceremony will occur the last night of the meeting (8/30). Two fieldtrips will be take place on the final afternoon of the meeting (8/31).

Many AMS members (Alvin Alejandrino, Beth Davis-Berg, Dan Graf, Ken Hayes, Paul Johnson, Pat Krug, Jingchun Li, Chuck Lydeard, Fabio Moretzsohn, Dianna Padilla, Ellen Strong, Norine Yeung, and Dave Zannata) very graciously volunteered to organize symposia and sessions and, along with all participants who agreed to present, assembled the exceptional line-up of talks and posters that is being offered. Efforts by the AMS 2015 organizing committee (Cindy Bick, Peter Cerda, Alexandria Friedman, Ryutaro Goto, Amanda Haponski, Alyssa Lawler, Taehwan Lee, Paula Teichholtz, and Andrew Wood), staff associated with the University of Michigan Department of Ecology and Evolutionary Biology (EEB) (Linda Garcia, John Megahan, Robbin Murrell, Dan St. Pierre, and Amber Stadler) and University of Michigan Biological Station (UMBS) (Laurie Brooke, Peggy Meade, Lisa Readmond and Bob Vande Kopple), and various former AMS presidents and current council members (Amanda Lawless, Peter Marko, Paula Mikkelsen, Diarmaid Ó Foighil, Gary Rosenberg, Charlie Strum, and Paul Valentich-Scott) helped enormously and offered advise that helped to make this

meeting possible. Tim Pearce and Dan Zanatta kindly offered to lead fieldtrips on local land snails and freshwater molluscs. Moreover, the University of Michigan Office of Research, Museum of Zoology and its Mollusk Division, and EEB contributed funds for student travel awards, the Keynote Speaker and additional meeting amenities.

Tremendous thanks goes to all participants and to those mentioned above who helped make this meeting happen! I sincerely hope that the meeting generates discourse, discovery, collaborations, friendships and enlightenment. Although I learned much in coordinating this meeting, the highlight that I take away is the extraordinary commitment, devotion and sincerity of all those involved with our society—you are certainly an impressive lot!

Tom Duda

President, American Malacological Society, 2014-2015

Miscellanea

- Files associated with your oral presentations should be uploaded to the computer in your session room prior to the session. Personnel should be present to assist.
- In the schedule, student award presentation competitors are indicated with the symbol ‘†’.
- In the schedule and abstracts, presenters of presentations with multiple co-authors are denoted with an asterisk.
- The AMS 2015 group photo will take place at 5:30 PM on 8/30 outside of the Gates Lecture Hall. Please meet to be included with the photo!
- The Poster Session will occur at 7:00 PM on 8/30. Snacks and refreshments will be served!
- The AMS auction of books and molluscan paraphrenalia will occur from 8:00 - 10:00 PM on 8/30. Please come to bid on and purchase books, reprints and other fun items to raise funds for student research awards! Snacks and refreshments will be served!
- The AMS Business Meeting (7:00 - 8:00 PM on 8/30) is open to all AMS members.
- The Banquet will take place immediately following the AMS Business Meeting (8:00 - 10:30 PM on 8/30). Winners of the student presentation award competition will be announced and after-dinner food and beverages will be served!
- Please be on time for meals in the dining hall. Breakfast: 7:00 - 8:00 AM. Lunch: 11:30 AM - 12:30 PM. Dinner: 6:00 - 7:00 PM.
- Coffee breaks occur from 10:00 - 10:30 AM and 2:00 - 2:30 PM during sessions.
- Please meet for field trips at 1:00 PM on 8/31 at the Chatterbox.

Schedule at a Glance

Friday, August 28

AMS Council Meeting, 4:00 – 6:00 PM
AMS Welcome Reception, 8:00 – 10:00 PM

Saturday, August 29

Welcome address, 8:10 AM
Keynote address, 8:20 AM
Early Career Malacologists symposium, 9:00 AM – 2:00 PM
Great Lakes Malacology session, 2:30 – 4:10 PM
Marine Molluscs session, 2:30 – 4:10 PM
Poster session set-up, 4:30 PM
Poster session, 7:00 PM
AMS Auction, 8:00 – 10:00 PM

Sunday, August 30

Great Lakes Malacology session (continued), 8:40 – 10:00 AM
Marine Molluscs session (continued), 8:40 – 10:00 AM
Invasives session, 10:30 AM – 2:00 PM
Phylogenetics session, 10:30 AM – 2:00 PM
Pacific Island Land Snails session, 2:30 – 5:10 PM
Contributed Talks session, 2:30 – 5:30 PM
AMS Business meeting, 7:00 – 8:00 PM
AMS Banquet, 8:00 – 10:30 PM

Monday, August 31

Conservation session, 8:00 – 11:30 AM
Fieldtrips, 1:00 – 5:00 PM

Friday, August 28, 2015

4:00 - 6:00 PM ~ AMS Council Meeting (Alumni Room)

6:00 - 7:00 PM ~ Dinner (Dining Hall)

8:00 - 10:00 PM ~ Welcome Reception (Gates Lecture Hall/Alumni Room)

Saturday, August 29, 2015 (Gates Lecture Hall sessions)

7:00 - 8:00 AM ~ Breakfast (Dining Hall)

8:10 AM ~ Welcome Address (Gates Lecture Hall)

8:20 - 9:00 AM ~ Keynote Address by Alison Sweeney (Gates Lecture Hall)
"Photosymbiotic giant clams are transformers of solar flux"

Early Career Malacologists (Organizers: Alvin Alejandrino & Jingchun Li)

9:00 AM Molluscan biomineralization: Ancient proteins with novel functions
Bishoy Kamel^{†*}, PangKou Chang & Monica Medina

9:20 AM The eye-independent response of Octopus chromatophores to light may rely on the same deeply conserved r-opsin phototransduction genes used in octopus eyes
M. Desmond Ramirez^{†*} & Todd H. Oakley

9:40 AM Building snail shells: The role of *dpp* in shell coiling of a caenogastropod
Darcy L. Ross^{†*}, Kimberly J. Perry, Jonathan Q. Henry & Neil H. Shubin

10:00 - 10:30 AM ~ Coffee Break

10:30 AM Flashing in Ctenoides ales "disco" clams - predators and prey
Lindsey F. Dougherty^{†*}, Alexandria K. Niebergall, Katherine E. Meyer & Roy L. Caldwell

10:50 AM Evolutionary significance and roles of the mantle margin in Pteriomorphian bivalves
Jorge A. Audino^{†*}, José Eduardo & A.R. Marian

11:10 AM Particle surface properties and their effect on particle capture in suspension-feeding bivalve molluscs
Maria Rosa^{†*}, J. Evan Ward, Sandra E. Shumway & Ashley Frink

11:30 AM - 12:30 PM ~ Lunch (Dining Hall)

1:00 PM Phenotypic variation in the dog whelk, *Nucella lapillus*: An integration of ecology, karyotype, and phenotypic plasticity
Katie E. Vazquez^{†*} & Peter S. Petraitis

1:20 PM Comparing the gene flow pattern of the endangered scaleshell (*Leptodea leptodon*) with widely distributed fragile papershell (*Leptodea fragilis*) and their host fish
Jer Pin Chong^{†*} & Kevin J. Roe

1:40 PM Phylogenomics of Cladobranchia (Gastropoda: Heterobranchia: Nudibranchia)
Jessica A. Goodheart^{†*}, Adam L. Bazinet, Allen G. Collins & Michael P. Cummings

2:00 - 2:30 PM ~ Coffee Break

Saturday, August 29, 2015 (Gates Lecture Hall sessions) cont'd

Great Lakes Malacology, part I (Organizers: Dan Graf and Dave Zanatta)

- 2:30 PM Genetic isolation and homogenization: potential effects of waterfalls and man-made canals on the population genetic structure of freshwater mussels (Family Unionidae)
Isabel Porto-Hannes^{†*}, Howard Lasker & Lyuba Burlakova
- 2:50 PM Michigan's fluvial habitat suitability for 11 listed unionids
Wesley M. Daniel*, Arthur Cooper, Pete Badra & Dana Infante
- 3:10 PM Assemblage response of freshwater mussels to dams: Are all dams the same?
Shaughn E. Barnett & Daelyn A. Woolnough*
- 3:30 PM Environmental drivers of shell shape in *Pleurocera livescens*: Comparing small inland lakes and Lake Michigan
Kandis R. Cazenave & David T. Zanatta*
- 3:50 PM Biogeography of the freshwater mussels (Unionida: Unionidae & Margaritiferidae) of Wisconsin, USA
Daniel L. Graf*, Charles Jordan, Ryan Pappas & Madalyn Zimbric

4:30 - 5:30 PM ~ Poster set-up (Gates Lecture Hall)

6:00 - 7:00 PM ~ Dinner (Dining Hall)

7:00 - 8:00 PM ~ Poster Session (Gates Lecture Hall)

8:00 - 10:00 PM ~ AMS Auction (Gates Lecture Hall)

Saturday, August 29, 2015 (Alumni Room sessions)

Marine Molluscs, part I (Organizer: Fabio Moretzsohn)

- 2:30 PM What do we know about the marine bivalve fauna in western South America?
Paul Valentich-Scott*, Eugene V. Coan & Diego G. Zelaya
- 2:50 PM Cannibalism, autotomy, and the sensory ecology of prey detection in the intertidal olive shell, *Agaronia propatula*
Winfried S. Peters* & Ariel Z. Cyrus
- 3:10 PM The *Ischnochiton* problem: A widespread species-rich genus of similar appearing chitons is supported as polyphyletic
Douglas J. Eernisse
- 3:30 PM The Colin Redfern Collection at the Bailey-Matthews National Shell Museum
José H. Leal* & Colin Redfern
- 3:50 PM Extremophile marine bivalves at ancient methane seeps
Carole S. Hickman

4:30 - 5:30 PM ~ Poster set-up (Gates Lecture Hall)

6:00 - 7:00 PM ~ Dinner (Dining Hall)

7:00 - 8:00 PM ~ Poster Session (Gates Lecture Hall)

8:00 - 10:00 PM ~ AMS Auction (Gates Lecture Hall)

Sunday, August 30, 2015 (Gates Lecture Hall sessions)

7:00 - 8:00 AM ~ Breakfast (Dining Hall)

Great Lakes Malacology, part II (Organizers: Dan Graf and Dave Zanatta)

- 8:40 AM A contrast of population structure of *Pyganodon grandis* between Lake Erie and its tributaries
Robert A. Krebs
- 9:00 AM Phylogeography and genetic structure of two freshwater mussel species (Bivalvia: Unionidae) along hypothesized post-glacial dispersal routes into the Laurentian Great Lakes
Trevor L. Hewitt* & David T. Zanatta
- 9:20 AM Genetic structure of the mapleleaf mussel (*Quadrula quadrula*) on the Niagara Peninsula, Ontario, Canada: Inferring effects of canal and dam construction over the last 200 years
Jordan R. Hoffman*, Wendy L. Paterson, Todd J. Morris & David T. Zanatta
- 9:40 AM Terrestrial gastropods of South Fox Island, Leelanau County, Lake Michigan, Michigan, USA
Timothy A. Pearce*, Christen M. Drescher & Leigh H. Deuter

10:00 - 10:30 AM ~ Coffee Break

Invasives (Organizers: Beth Davis-Berg & Dianna Padilla)

- 10:30 AM Can invasive molluscs replace ecological function of lost freshwater biodiversity?
Dianna K. Padilla*, Alexander Y. Karatayev & Lyubov E. Burlakova
- 10:50 AM To invade as fast as a slug!
Érik L'Heureux*, François-Joseph Lapointe & Bernard Angers
- 11:10 AM Two for the price of one: inadvertent introduction of cryptic *Euglandina* species during failed biocontrol efforts in Hawaii
Kenneth A. Hayes*, Wallace M. Meyer III, Norine W. Yeung & John Slapcinsky

11:30 AM - 12:30 PM ~ Lunch (Dining Hall)

- 12:40 PM Invasive molluscs: Why do we keep repeating the same mistakes?
Elizabeth C. Davis-Berg
- 1:00 PM City of immigrants: The slugs of Chicago
Jochen Gerber & Rachel Sommer*
- 1:20 PM Preliminary analysis of records of non-native *Bulimulus* spp. (Gastropoda, Bulimulidae) in the continental United States – Taxonomy, distribution, and trends
Francisco J. Borrero*, Abraham S. H. Breure & David G. Robinson
- 1:40 PM The snail also rises: Desiccation tolerance of *Pomacea* spp. (Gastropoda: Ampullariidae)
Paul Glasheen*, Clementina Calvo, Mariana Meerhoff, Kenneth A. Hayes & Romi L. Burks

2:00 - 2:30 PM ~ Coffee Break

Sunday, August 30, 2015 (Alumni Room sessions)

7:00 - 8:00 AM ~ Breakfast (Dining Hall)

Marine Molluscs, part II (Organizer: Fabio Moretzsohn)

- 8:40 AM Comparative ecological approach to habitat and food use: *Conus* diversity on Seychelles reefs
Alan J. Kohn
- 9:00 AM Molecular phylogeny of the columbellid gastropods
Marta J. deMaintenon* & Ellen Strong
- 9:20 AM How does the eastern oyster cope with living as an almost closed system during winter?
Elise Mayrand*, Luc A. Comeau & André Mallet
- 9:40 AM Cryptic and pseudocryptic speciation masks heterobranch sea slug diversity
Ángel Valdés

10:00 - 11:00 AM ~ Coffee Break

Phylogenetics (Organizer: Ellen Strong)

- 10:30 AM A molecular phylogeny of the Tonnoidea
Ellen E. Strong*, Nicolas Puillandre, Magalie Castelin, Alan G. Beu & Philippe Bouchet
- 10:50 AM Evolution of parasitism in *Caledoniella montrouzieri* Souverbie, 1869 (Littorinimorpha), a unique marine snail living on gonodactylid mantis shrimps
Ryutaro Goto*, Tsuyoshi Takano & Yasunori Kano
- 11:10 AM The living solar panel - Evolution of photosymbiosis in marine cockles
Jingchun Li*, Sarah Lemer, Lisa Kirkendale, Gonzalo Giribet, Rudiger Bieler & Colleen Cavanaugh

11:30 AM - 12:30 PM ~ Lunch (Dining Hall)

- 12:40 PM Reconciling morphology and molecules: Developing a comprehensive phylogeny for the Pectinidae (Bivalvia) to accurately assess biological diversity in the Indo-Pacific
Jeanne M. Serb
- 1:00 PM A new bivalve phylogeny -- a revised bivalve classification
Rüdiger Bieler*, Paula M. Mikkelsen, Gonzalo Giribet & the BivAToL team
- 1:20 PM Phylogeny, morphology and species limits of Neotropical apple snails (Caenogastropoda: Ampullariidae)
Kenneth A. Hayes
- 1:40 PM Phylogenetic systematics of Hawaiian Succineidae
Norine W. Yeung*, Robert H. Cowie, Brenden S. Holland & Kenneth A. Hayes

2:00 - 2:30 PM ~ Coffee Break

Sunday, August 30, 2015 (Gates Lecture Hall sessions) cont'd

Pacific Island Land Snails (Organizers: Ken Hayes & Norine Yeung)

2:30 PM Pacific Island Land Snail Conservation: Case studies from the Hawaiian Islands

Kenneth A. Hayes* & Norine W. Yeung

2:50 PM The phylogenetics and conservation status of the Hawaiian Helicinidae

Kelley Leung[†]*, Norine W. Yeung & Kenneth A. Hayes

3:10 PM Diversity of Hawaiian Microcystinae (Gastropoda: Stylommatophora: Helicarionoidea) 75 years after H. B. Baker

John Slapcinsky*, Norine W. Yeung, Deena T.A. Gary & Kenneth A. Hayes

3:30 PM Systematics and conservation of Hawaiian orthurethrans

Norine W. Yeung* & Kenneth A. Hayes

3:50 PM Build-up of diplommatinid land snails and conservation context in the western Pacific Micronesian islands of Belau (Republic of Palau, Oceania)

Rebecca J. Rundell

4:10 PM Survival of *Partula* species after a mass extinction event: A phylogenomic perspective using museum specimens

Amanda E. Haponski

4:30 PM Differential survival among Tahitian tree snails during a mass extinction event: Persistence of the rare and fecund

Cindy S. Bick[†]

4:50 PM Some thoughts on the long-term survival prospects of Partulidae

Diarmaid Ó Foighil* & Cindy S. Bick

5:30 PM ~ Group photo (meet outside Gates Lecture Hall)

6:00 - 7:00 PM ~ Dinner (Dining Hall)

7:00 - 8:00 PM ~ AMS Business Meeting (Alumni Room)

8:00 - 10:30 PM ~ AMS Banquet and Awards Ceremony (Gates Lecture Hall)

Sunday, August 30, 2015 (Alumni Room sessions) cont'd

Contributed Talks

- 2:30 PM Green eggs and hulls: DNA barcoding of southern Australian chitons and their plankton-collected embryos
Richard B. Emler & Douglas J. Eernisse*
- 2:50 PM Analysis of morphological variation of the shells of *Argonauta argo* Linnaeus, 1758 and *Argonauta nouryi* Lorois, 1852 (Cephalopoda: Argonautidae) using geometric morphometrics
Héctor G. Suriano^{†*} & Brian Urbano Alonso
- 3:10 PM Effect of high gene turnover on intraspecific variation of a venom gene family composition in *Conus*
Peter A. Cerda^{†*} & Thomas F. Duda, Jr.
- 3:30 PM Differentiation of olfactory receptor genes of *Conus* species from different dietary guilds
Andrew Wood^{†*}, Alyssa Lawler & Thomas F. Duda, Jr.
- 3:50 PM A tale of two species: Comparative phylogeography and genetic diversity of *Pomacea canaliculata* and a putative cryptic congeneric in the Rio de la Plata Basin
Sofia R. Campos^{†*}, Cristhian M. Clavijo, Fabrizio Scarabino, Romi L. Burks & Kenneth A. Hayes
- 4:10 PM Phylogeographic patterns in some Thai freshwater mussels
John M. Pfeiffer[†]
- 4:30 PM Phylogeography of the rock shell *Thais clavigera* (Mollusca): Evidence for long-distance dispersal in the northwestern Pacific
Daewui Jung & Joong-Ki Park*
- 4:50 PM The distribution of commonness and rarity in the freshwater gastropod fauna of U.S. Atlantic drainages
Robert T. Dillon, Jr.

5:30 PM ~ Group photo (meet outside Gates Lecture Hall)

6:00 - 7:00 PM ~ Dinner (Dining Hall)

7:00 PM ~ AMS Business Meeting (Alumni Room)

8:00 - 10:30 PM ~ AMS Banquet and Awards Ceremony (Gates Lecture Hall)

POSTERS

A survey to assess the potential for dispersal along America's burning river

Rachel E. Andrikanich[†] & R.A. Krebs

Taxonomic reevaluation of *Ostrea johnsoni* Aldrich, 1886 (Bivalvia: Flemingostreidae)

Michael J. Bolton

The Paul Hesse Collection at the Academy of Natural Sciences of Philadelphia

Francisco J. Borrero & Gary Rosenberg

Conservation and phylogenetics of the endodontoid land snails of Belau (Republic of Palau, Oceania)

David A. Bullis[†] and Rebecca J. Rundell

Mussel, sex and mitochondria

Charlotte Capt[†], Sebastien Renaut, Nathan Johnson & Sophie Breton

The role of life history strategy in predicting extinction risk of freshwater mussels

Amanda J. Chambers[†]

The California Helminthoglyptidae Project

Lance Gilbertson, David Goodward & Douglas J. Eernisse

Mitochondrial inheritance and sex determination in bivalve species

Arthur Gusman[†], Marco Passamonti, Christiane Hudon & Sophie Breton

Urbanization impacts on land snails: Abundance, diversity and community composition

Mackenzie N. Hodges[†] & Michael L. McKinney

Shell banding indicates increased growth rate in modern freshwater mussels from human impacts

Kristin L. Irwin^{†*} Michael L. McKinney, Gerald Dinkins & Matthew P. Reed

Marine Mollusk Resource Bank of Korea (MMRBK)

Daewui Jung[†], Yeongjae Choe, Youngheon Shin, Soyeong Jin, Sora Kong & Joong-Ki Park

Development of a DNA microarray-based identification system for commercially important Asian oyster species

Daewui Jung, Yeongjae Choe, Youngheon Shin, Jiyeon Kim, Won Sun Lee & Joong-Ki Park

Distribution of sphaeriid slams in Western Lake Erie twenty-five years after invasion of *Dreissena*

Michael E. Keller[†] & Robert A. Krebs

POSTERS, cont'd

Reproductive aspects of *Siphonaria lessoni* (Gastropoda: Heterobranchia) from the southwestern Atlantic Ocean

Henrique Knack de Almeida[†] & Juliana Giménez

Molecular and morphometric data suggest the presence of a neglected species in the marine gastropod genus *Conus*

Alyssa Lawler[†] & Thomas F. Duda, Jr.

Great Lakes Invasives TCN: Documenting the occurrence of invasive molluscs threatening the Great Lakes Basin

Taehwan Lee & Thomas F. Duda, Jr.

Population genetics and phylogenetic placement of the federally endangered Iowa Pleistocene snail *Discus macclintocki* (Mollusca: Gastropoda)

Jermaine Mahguib[†] & Kevin Roe

The Biodiversity of the Southern Gulf of Mexico Project: Filling gaps and establishing baselines

Fabio Moretzsohn, Nuno Simões & J. W. Tunnell, Jr.

Incongruencies between geometric morphometrics and DNA barcodes in delineating species of *Pyganodon* mussels (Bivalvia: Unionidae)

Baleigh E. Schuler[†] & David T. Zanatta

InvertEBase: Digitizing land and freshwater mollusks of the eastern United States

Elizabeth K. Shea, Rüdiger Bieler, Taehwan Lee, Diarmaid Ó Foighil & Petra Sierwald

Population genetic congruence between six freshwater mussels and their host, freshwater drum (*Aplodinotus grunniens*)

Ashley Smith[†] & Andrew Simons

The Sphaeriidae Collection of Victor Sterki at the Carnegie Museum of Natural History

Charles F. Sturm & Timothy A. Pearce

Size of first sexual maturity in *Brachidontes rodriguezii* (d'Orbigny, 1846) from the southwestern Atlantic Ocean

María Eugenia Torroglosa, Mariel Ojeda, Henrique Knack de Almeida & Juliana Giménez

[†] Student presentation award competition

Monday, August 31, 2015 (Gates Lecture Hall sessions)

7:00 - 8:00 AM ~ Breakfast (Dining Hall)

Conservation (Organizers: Paul Johnson & Chuck Lydeard)

- 8:00 AM Mollusks of Michigan's Upper Peninsula
John B. Burch & Huateng Huang
- 8:20 AM Land snail conservation in Mid-Atlantic USA states: Imperilment ranks and recovery plans
Timothy A. Pearce
- 8:40 AM Terrestrial gastropods of Illinois
Jochen Gerber
- 9:00 AM Review of the Helicodiscidae of North Carolina
Amy S. Van Devender* & Robert W. Van Devender
- 9:20 AM Update to the conservation status of freshwater gastropods of Canada and the United States
Paul Johnson, Arthur Bogan, Kenneth Brown, Noel Burkhead, James Cordeiro, Jeffrey Garner, Paul Hartfield, Dwayne Lepitzki, Gerry Mackie, Eva Pip, Thomas Tarpley, Jeremy Tiemann, Nathan Whelan & Ellen Strong
- 9:40 AM West Coast aquatic molluscs
Stephanie A. Clark

10:00 AM ~ Coffee Break

- 10:30 AM Hidden diversity in plain sight: Genetic confirmation of putative Louisiana fatmucket in Illinois
Alison P. Stodola, Charles Lydeard*, James T. Lamer, Sarah A. Douglass & Kevin S. Cummings
- 10:50 AM Freshwater mussel reintroduction and recovery in Alabama
Paul D. Johnson*, Jeffrey R. Powell, Michael L. Buntin, Todd L. Fobian, Jeffrey T. Garner, Jesse T. Holifield & Thomas A. Tarpley
- 11:10 AM Conservation status of North American freshwater mussels
James D. Williams, Arthur E. Bogan, Jayne Brim Box, Noel M. Burkhead, Robert S. Butler, Alberto Contreras-Arquieta, Kevin S. Cummings, Jeffrey T. Garner, John L. Harris, Robert G. Howells, Sarina J. Jepsen, Nathan A. Johnson, Todd J. Morris, Terry L. Myers & Jason M. Wisniewski

11:30 AM - 12:30 PM ~ Lunch (Dining Hall)

1:00 - 5:00 PM ~ Field Trips (Meet at the Chatterbox)

6:00 - 7:00 PM ~ Dinner (Dining Hall)

A survey to assess the potential for dispersal along America's burning river

Rachel E. Andrikanich^{†*} & Robert A. Krebs

Cleveland State University, 2100 Euclid Avenue, Cleveland, OH 44115, USA
Jadekis10@aol.com

The Cuyahoga River, an American Heritage River, has long been an area of environmental interest. Throughout the 1970's the lower Cuyahoga was viewed as one of the most polluted aquatic ecosystems in the country, largely devoid of faunal diversity, not just of freshwater mussels, but also their respective host fish. The upper Cuyahoga River (above Cuyahoga Falls) currently maintains a historical number of 10 different Unionid species, however, the lower Cuyahoga River has experienced a dramatic decline in species number, reducing a historical count of as many as 30 to only 4 unionid species of mussel confirmed today. There are no historic surveys of mussel diversity concerning the Middle Cuyahoga River, which became the focus of the current project. Surveying portions of the Cuyahoga River between the city of Kent and the Cuyahoga National Park is necessary to understand diversity within the whole watershed. More recently, through extensive investment by the Northeast Ohio Sewer District to reduce combined sewage overflow and widespread public support, water quality of the Cuyahoga River continues to improve, becoming suitable habitat for the once extirpated species. Still regions within the lower Cuyahoga show few mussels and little indication of the reason for their absence. Through proper survey methods of the Middle Cuyahoga River, data collected on species type and population numbers will be vital to both create a current catalogue of mussel diversity along the river and address which species have been lost from the whole watershed. Once known, an assessment will be completed to ascertain which species may migrate downstream or how best to create a plan for any reintroductions or augmentations of species into the river, with a goal to create a more viable aquatic habitat.

† Student presentation award competition

* Presented by

Poster Session

Evolutionary significance and roles of the mantle margin in Pteriomorphian bivalves

Jorge A. Audino^{†*}, José Eduardo & A.R. Marian

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University of São Paulo, Rua do Matão, Travessa 14, 101,
Postal code 05508-090, São Paulo, SP, Brazil
jorgeaudino@ib.usp.br*

The bivalve mantle margin corresponds to the free portion of the mantle lobes, underneath the shell edges, usually bearing muscular, sensory or secretory structures in tissue projections commonly named pallial folds. In the Bivalvia, this specific region displays several adaptive traits and functions associated with different lifestyles. Particularly in the Pteriomorphia, a clade regarded as the most extensive radiation of epifaunal life habits, the mantle margin comprises several singularities involving pallial fold organization, associated structures and functions displayed. Mantle margin development has been studied in detail for a scallop species, casting light on the understanding of mantle fold differentiation and pallial organ formation. For example, the middle mantle fold is the last one to be formed, but several pallial features are originated during larval period and retained after metamorphosis. While the first steps were made in attempt to elucidate mantle margin development in Pteriomorphians, its extensive diversity of form and functions is still not well understood. For instance, different sorts of tentacular organs are found in the middle or inner mantle folds (or even in both) of numerous families, e.g. Pteriidae, Ostreidae, Limidae, and Pectinidae. Complex variation in mantle fold number and division is also present in the Arcidae and representatives from other families. Despite great contributions to the mantle margin morphology for several taxa, the complex diversity of this anatomical region still addresses broad questions to bivalve evolutionary biology. Can we talk about homologous pallial structures among those bivalves? How might mantle margin evolution be correlated with diversification of life habit and form in those lineages? The first insights to those questions should be raised by an analysis of mantle margin diversity, including ancestral character reconstructions in a phylogenetic framework and detailed anatomical studies.

Early Career Malacologists Session

Assemblage response of freshwater mussels to dams: Are all dams the same?

Shaughn E. Barnett & Daelyn A. Woolnough*

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Central Michigan University, Mt. Pleasant, MI, 48859, USA
wooln1d@cmich.edu*

Large-scale modifications of rivers in the United States, including dams, have drastically impacted the richest areas for freshwater mussels. Dams are extremely variable from their structure and function, to their history. Dam removals are common nationwide due to maintenance costs and dam use around the country. However, comparisons of dam types and removals on aquatic fauna, especially Unionidae, are largely understudied. In fact, <10% of removals have had any follow up studies. The purpose of this study was to determine the downstream impacts of low-head dams, controlled low-head dams (i.e., hydro-electric), and low-head dam removals on freshwater mussel assemblages. Quantitative surveys were conducted at 15 sites in the Lake Michigan watershed from 2014-2015 (i.e., 5 uncontrolled low-head dam sites, 5 controlled low-head dam sites, and 5 low-head dam removal sites). Our study considers the change in mussel diversity along a longitudinal gradient downstream of the dams and removals. In 2014, we did not find a difference in mussel diversity between our low-head dam and low-head dam removal sites nor a change in diversity from upstream to downstream at the sites. All diversity indices, when we separated our sites into controlled dams, uncontrolled dams, and dam removals, did show significant differences (Kruskal-Wallis; $p < 0.05$). In 2014 uncontrolled low-head dams had higher species richness and evenness than low-head dam removals (Dunn's test; $p < 0.05$). We will present 2014 and 2015 results, assessing mussel assemblage response to low-head dams and removals in the Lake Michigan drainage basin. These data are valuable for management decisions about dam removals and mussel assemblages in the Great Lakes region.

Great Lakes Malacology Session, Part I

Differential survival among Tahitian tree snails during a mass extinction event: Persistence of the rare and fecund

Cindy S. Bick[†]

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The deliberate introduction of the carnivorous Rosy Wolf Snail (*Euglandina rosea*) to the Society Islands in the 1970's led to a mass extirpation of its rich Partulidae fauna. On Tahiti, ongoing field surveys have encountered remnant populations of two closely related endemic species, *Partula clara* and/or *Partula hyalina*, in 38 valleys. *Euglandina rosea* is responsible for the extinction of terrestrial snail species across Oceania and understanding why these Tahitian taxa have survived may have conservation implications across the region. A null hypothesis states that they endured because they were the most abundant and/or widespread species and that they too, will eventually be driven to extinction. Although we lack demographic data contemporaneous with *E. rosea*'s introduction, an early 20th century study by H. E. Crampton contains a wealth of demographic information about intact Tahitian *Partula* populations. His data show that *P. clara* and *P. hyalina* were widespread in valleys but were consistently much rarer than now-extirpated co-occurring congeners. Crampton also recorded clutch sizes for individual gravid snails and his data show that *P. clara* and *P. hyalina* consistently had higher instantaneous mean clutch sizes. Higher fecundities may have contributed to their persistence in Tahiti's valleys and I am currently looking at the possible role of ecological factors in that survival.

Pacific Island Land Snails Session

A new bivalve phylogeny -- a revised bivalve classification

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BivAToL team⁴**

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Recent investigations based on detailed morpho-anatomical, ultrastructural, molecular sequence, and transcriptomic (RNA-seq) data of bivalves have provided the basis for a thorough re-evaluation of the relationships among the major bivalve lineages. Six major monophyletic lineages have been identified to comprise modern Bivalvia: (Protobranchia (Pteriomorpha (Palaeoheterodonta (Archiheterodonta (Anomalodesmata + Imparidentia))))). Research history and key findings are presented and translation of the new evolutionary hypothesis into Linnaean hierarchy is discussed. The Bivalve Assembling the Tree-of-Life project (BivAToL) is supported by the U.S. National Science Foundation (NSF) AToL program (DEB-0732854/0732903/0732860)

Phylogenetics Session

Taxonomic reevaluation of *Ostrea johnsoni* Aldrich, 1886 (Bivalvia: Flemingostreidae)

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The oyster *Ostrea johnsoni* Aldrich was described in 1886 from the middle Eocene of Alabama and Mississippi, U.S.A. Since then it has been placed in the genera *Alectryonia* and “*Lopha*”. Examination of the shell morphology using recent advances in supraspecific oyster taxonomy has found *O. johnsoni* to be consistent with the genus *Nicaisolopha* Vialov, 1936 (Bivalvia: Flemingostreidae) (type species *Ostrea nicaisei* Coquand, 1862, from the Campanian-Maastrichtian of Algeria).

This genus is characterized by: shell small to medium in size; outline circular, oval or triangular; subequivalve and biconvex, left valve usually more convex and capacious; both valves with few plicae, at least in older individuals; commissure wavy or zigzag; exterior surface with concentric growth lamellae; chomata usually observable, ostreine type and restricted to near the hinge; adductor muscle imprint kidney to comma shape and situated postero-ventrally to subcentrally; microstructure of shell simply-foliated with some empty and mocret lenses. Species in Lophini (Bivalvia: Ostreidae) may have a similar appearance, however, *N. johnsoni* does not fit well in Lophini because Lophini do not form growth lamellae which *N. johnsoni* does, Lophini sometimes form claspers which *N. johnsoni* does not, Lophini usually form lophine chomata which *N. johnsoni* does not, and Lophini do not form mocret shell lenses which *N. johnsoni* does.

The earliest clearly identifiable Lophinae are from the Miocene. Ten species are currently assigned to *Nicaisolopha*. Eight from the Cretaceous (Albian-Maastrichtian) of North and South America, Africa, the Middle East, southern Europe, and India; one species, *N. clotbeyi* (Bellardi, 1854), from the Eocene of Africa; and one species, *N. tridacnaeformis* (Cox, 1927), from the Pliocene and the present Indian Ocean and the present southwestern Pacific Ocean.

Poster Session

Preliminary analysis of records of non-native *Bulimulus* spp. (Gastropoda, Bulimulidae) in the continental United States – Taxonomy, distribution, and trends

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The genus *Bulimulus* Leach 1814 comprises arguably over 100 species and subspecies of mainly Neotropical distribution, occurring in Central and South America, as well as in most Caribbean Islands. The majority of the species are ground dwellers, being common on rock surfaces, as well as among vegetation and leaf litter on the ground. Many species are at least partially arboreal, occurring mainly on low vegetation. Species recognition of several taxa in the genus is not easily accomplished on the basis of shells alone, due to similarities in size, shape, dull or brown coloration, and general lack of conspicuous conchological characters. When specimens of such taxa occur outside of their natural ranges, and when original provenance data is uncertain, species recognition can be difficult. In this study, we analyzed records collected by the USDA-APHIS program across the United States, to assess which taxa of the genus *Bulimulus* have been found in interceptions of cargo (maritime, aerial, land borders) and baggage, as well as surveys of selected locations within the USA where snails have been found, and which have been preliminarily identified as *Bulimulus* spp. In addition, we have been able to incorporate additional records from other collectors and researchers. Altogether, the initial conclusion is that at least one species has become established in the continental USA, and appears to be spreading, at least locally. Additional species may be considered as with the potential to become established, based on the frequency of their detection. A preliminary analysis of temporal and spatial patterns of distribution is given for selected species in the southern USA.

Invasives Session

The Paul Hesse Collection at the Academy of Natural Sciences of Philadelphia

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The Paul Hesse Collection, purchased by ANSP in 1926, focused on non-marine mollusks of Europe and countries bordering the Mediterranean and Black Seas. It contains about 7,500 lots totaling about 50,000 specimens and is thus an important resource for studying Palearctic mollusks. Type lots of at least 40 European authors are included therein. Type localities represented by the Hesse type material at ANSP are in Central Asia, as well as in Bulgaria, Cyprus, Georgia, Greece, Morocco, Syria and Tunisia. Born in Germany, Hesse was an influential malacologist, whose expertise was sought after by many specialists of his time, with whom he maintained correspondence and exchanged material. Hesse introduced available names for 62 species-group, 62 genus-group and 4 family-group taxa, all of them gastropods and most terrestrial. Five additional species-group names were introduced by other authors in Hesse's works. Among Hesse's species-group names, 7 were replacements for preoccupied names of other authors. We found type specimens for 32 Hesse taxa in the ANSP collection. H. B. Baker listed primary type material at ANSP for 22 of these and designated lectotypes where ANSP held more than one specimen. For the 10 names not treated by Baker, it has not been previously reported that ANSP holds type material, and for several species, the material at ANSP is the only type material of those names. Hesse's collection is unusual in that he wrote sources and dates of receipt on most of the labels, which not only was helpful in determining what specimens he had at hand when he named taxa, but provides latest possible collecting dates for samples, information which could be used in reconstructing faunal baselines.

Poster Session

Conservation and phylogenetics of the endodontoid land snails of Belau (Republic of Palau, Oceania)

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The morphologically exquisite endodontoid land snails (Pulmonata: Charopidae and Endodontidae), have suffered extinction and extirpation across Pacific islands. The western Pacific archipelago of Belau (Republic of Palau, Oceania) still has several extant, endemic endodontoids. However, of the fifteen known, described species and subspecies of endodontoids on Belau, one species is endangered (*Semperdon uncatus*) and eleven are critically endangered (*Aadonta angaurana*, *A. constricta babelthuapi*, *A. c. constricta*, *A. c. komakanensis*, *A. fuscozonata depressa*, *A. f. fuscozonata*, *A. irregularis*, *A. kinlochi*, *A. pelewana*, *Semperdon kororensis*, *Semperdon xyleborus*), based on IUCN criteria. Our goals are: (1) to better understand the evolution and biogeography of the Belau endodontoids using molecular phylogenetic approaches and COI (mtDNA) sequences; and (2) to compare species' presence or absence on Belau islands relative to past distributions, in order to target forest areas for future protection and management. We found that neither *A. f. fuscozonata* nor *Semperdon xyleborus* have been found on the island of Oreor since Yoshio Kondo's (Bishop Museum, Honolulu, Hawaii) Micronesian Expedition surveys of Belau in 1936. These results represent our preliminary findings which will be used to inform potential future conservation efforts.

Poster Session

Mollusks of Michigan's Upper Peninsula

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Of the 84 counties into which the state of Michigan is divided, 15 of these counties are in Michigan's Upper Peninsula. The Upper Peninsula of Michigan is bounded on the north by Lake Superior, on the east by Whitefish Bay and the Saint Mary's River (which separates it from Ontario, Canada), on the south by Lake H

uron and Lake Michigan, the Straits of Mackinac and Wisconsin, and on the west by Wisconsin. The northern part of Michigan, including the Upper Peninsula, is rugged, with hills and mountains, and is not completely worn down by erosion. Our mollusk surveys in Michigan's Upper Peninsula have included Sugar Island, the Huron Mountains, and the eastern part of Hiawatha National Park. Surveys of Sugar Island and the Huron Mountains were initiated by our own interests. We surveyed the eastern area of the Hiawatha National Park at the request of the United States Forest Service. The mollusks of Michigan's Upper Peninsula are represented by the same gastropod and bivalve families that occur in Michigan's Lower Peninsula. The land snails include several prosobranchs [Endontidae, Euconulidae, Haplotremotidae, Helicinidae (*Hendersonia occulta*), Limacidae, Philomycidae, Polygyridae, Stropilipsidae, Succinidae and Zonitidae] and pulmonates [Carychiidae (*Caryclinum exiguum*), Cionellidae (*Cionella lubrica*), Pupillida and Valloniidae (*Zoögenetes harpa*). The freshwater gastropods also include representatives of prosobranchs (Ampularidae, Bithyniidae, Hydrorbiidae, Pleuroceridae, Pomatiopsidae and Valvatidae) and pulmonates (Ancylidae, Lymnaeidae, Physidae and Planorbidae). The freshwater bivalves include unionacean and sphaeracean clams. One of our interests in our Huron Mountains mollusk survey is to write a book on the mollusks of the Huron Mountains and the surrounding area. Working in the Huron Mountains is more difficult now that our friends have since passed away, and getting access to the area, which has to go through the Huron Mountain Club, creates some obstacles, and is not altogether satisfactory.

Conservation Session

A tale of two species: Comparative phylogeography and genetic diversity of *Pomacea canaliculata* and a putative cryptic congeneric in the Rio de la Plata Basin

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Knowledge of Earth's biodiversity remains insufficient for understanding and conserving it as evidenced by the Linnean and Wallacean shortfalls, which respectively refer to the fact that only a small portion of the planet's species have been described, and to our woefully incomplete understanding of the distributions of known species, especially invertebrates. Phylogenetic studies seek to examine evolutionary relationships and clarify species identities, while phylogeography provides a clearer understanding of the distribution of intraspecific diversity across the geographic landscape. Together, these fields provide insights into fundamental processes shaping biodiversity and help address both the Wallacean and Linnean shortfalls. In South America, high diversity and abundance combined with presumed wide distributions make apple snails (*Pomacea* spp.) good candidates for studies of biodiversity and evolution. Recent studies of ampullariids revealed cryptic species in southern Brazil and Uruguay and preliminary data suggest hydrogeological events played a major role in shaping ampullariid biodiversity in this region. To examine patterns of apple snail biodiversity in the Rio de la Plata Basin and the role that marine incursions may have had in shaping these patterns, we collected snails from 32 sites across Uruguay, sequenced a fragment of the COI gene from 260 individuals of two *Pomacea* species to date, and analyzed these sequences in combination with others previously obtained from snails in Brazil and Argentina (N=550). Phylogenetic analyses confirmed previous findings of a putative cryptic species closely related to *Pomacea canaliculata*, and recovered 35 *P. sp.* (N=201) and 54 *P. canaliculata* (N=349) haplotypes. Haplotype network analyses revealed closer relationships among *P. sp.* haplotypes compared to *P. canaliculata*, potentially indicating a recent range expansion of the former. Uruguayan *P. sp.* did not share any haplotypes with Brazil, but Uruguayan *P. canaliculata* shared several haplotypes with Argentina; a pattern consistent with range expansion following marine incursions during the Pleistocene.

Contributed Talks Session

Mussel, sex and mitochondria

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Mitochondrial DNA is typically strictly maternally inherited (SMI) in animals. However, one taxon has a radically different inheritance system known as doubly uniparental inheritance (DUI). Indeed, in some bivalve molluscs, two distinct mitochondrial lineages exist and are transmitted in a sex-specific manner. The female genome (F mtDNA) is inherited from the mother by both sons and daughters, which is what is found in a SMI case. However, the male genome (M mtDNA) is inherited from the father by only sons (males do not transmit the F mtDNA to their progeny). This represents a “mother-to-daughter” and “father-to-son” mitochondrial inheritance system.

Interestingly, two novel protein-coding genes have been discovered in these particular mtDNA lineages; f-ORF in the F mtDNA and m-ORF in the M mtDNA. These proteins, exported from the organelle, have been hypothesized to play a role in sex determination. Specifically, in freshwater mussels, a perfect correlation has been observed between gonochorism (= separate male and female sexes) and the presence of DUI, whereas closely-related hermaphroditic species lack the M mtDNA (= possess SMI) and have macromutations in the f-ORF gene, suggesting a loss or a modification of its function. DUI likely represents the first case of sex determination involving the mitochondrial genome in animals, and this would explain its long-term persistence in bivalves (as heteromorphic sex chromosomes are absent in this taxon). However, the link between DUI and sex determination still remain to be elucidated.

For this purpose, we compared the transcriptome of gonadic tissues from three kinds of individuals; males and females (from the gonochoric and DUI-possessing *Utterbackia peninsularis*) and hermaphrodites (from the SMI-possessing *U. imbecillis*). These samples enable comparing males vs. females vs. hermaphrodites but also DUI vs. SMI species. These analyses will allow us to identify potential candidates linked to this atypical mitochondrial transmission and to sex determination.

Poster Session

Environmental drivers of shell shape in *Pleurocera livescens*: Comparing small inland lakes and Lake Michigan

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Pleurocera livescens [= *Elimia livescens* (Menke 1830)] is a freshwater gastropod common in the Laurentian Great Lakes region. Geometric morphometric analysis was conducted to determine the variation in shell shape among sites along the shoreline of Lake Michigan (4 sites) and three inland lakes on Beaver Island and Manitou Island (8 sites) in Michigan, U.S.A. Canonical Variates Analysis (CVA) showed significant variation in shell shape among the sites sampled from inland lakes and those on the Lake Michigan shoreline. An assignment test based on the CVA found that individual snails could be 82.5% correctly assigned to their lake of origin and 62.8% correctly assigned to their site of origin. CVA axes were tested for correlations with the environmental variables. Shell shape in *P. livescens* correlated most significantly with fetch length and specific conductance. Higher fetch lengths produce higher energy wave action and may result in snails with a larger aperture, more globose shape, and lower spire in individuals (better for anchorage). Lower fetch lengths produced lower energy wave action and may result in snails with a smaller aperture, more elongate shape, and higher spire (better for navigating above soft sediment). It appears that similar environmental processes to those documented in classic studies on marine snails affect shell shape in freshwater snails in similar ways. This suggests that shell shape plasticity is a critical factor in regional adaptation and success in this widely distributed gastropod.

Great Lakes Malacology Session, Part I

Effect of high gene turnover on intraspecific variation of a venom gene family composition in *Conus*

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Understanding the impacts of species interactions on evolution is a key aim in biology. Venom, a toxic substance used for prey capture and/or defense, can be used to evaluate the role of molecular genetic processes related to an organism's ecology due to it containing direct gene products and its use in species interactions. The diverse group of cone snails (family Conidae), a venomous predatory marine gastropod, has a venom composition that varies greatly among and within species. Venom components ('conotoxins') are expressed by members of many gene superfamilies and subject to strong positive selection. Conotoxin gene family composition is effectively restructured by high levels of gene turnover (i.e., high rates of gene duplication and gene loss). Nonetheless, while all previous studies of venom gene family composition have focused on patterns of variation among species, no work has yet addressed the effect of high rates of gene turnover on patterns of variation within species. Here we evaluate the composition of A-superfamily conotoxins of individuals of populations of *Conus*. In particular, we used general primers to amplify regions of A-superfamily loci from genomic DNA and sequenced these amplicons to determine the presence/absence of loci in individuals. We quantified and compared levels of variation in gene family composition within and among populations. Results may indicate the importance of gene turnover in generating and maintaining diversity of venom genes within species.

Contributed Talks Session

The role of life history strategy in predicting extinction risk of freshwater mussels

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The inability to predict which species are at the greatest risk of extinction is one of the fundamental weaknesses of the field of conservation biology. Resolution of this issue should be of paramount importance among researchers considering the current extinction crisis and the anticipated levels of species loss due to human-induced climate change. Some studies have been able to successfully link the extinction vulnerability of a species to its life history strategy. Linking the life history strategies of freshwater mussels (*Bivalvia*: Unionidae) to their susceptibility of extinction is an area of research that has only recently begun to receive attention, and may be exceedingly important for these critically imperiled organisms. Therefore, the objective of this study was to determine if a relationship exists between the life history strategy of at-risk freshwater mussel species in counties in the state of Michigan, U.S.A. and the intensity of anthropogenic land use. Non-metric multidimensional scaling (NMDS) revealed that the occurrence of at-risk mussels was positively associated with urban and agricultural land use and negatively associated with forested, grassland, and wetland land use. There appeared to be no discrimination between high levels of urban and agricultural land use and the type of life history strategy exhibited by mussels, possibly indicating that disturbance levels might be so intense as to render irrelevant certain evolutionary adaptations which should maximize survival and reproductive success. Although life history strategy alone may be a relatively poor predictor of extinction risk, recent studies suggest that life history strategies in combination with the spatial traits of a species may be better able to forecast extinction vulnerability, even with regard to climate change.

Poster Session

Comparing the gene flow pattern of the endangered scaleshell (*Leptodea leptodon*) with widely distributed fragile papershell (*Leptodea fragilis*) and their host fish

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Most freshwater mussels are obligate parasites on fishes. Because mussels are infaunal and largely sessile, it is reasonable to assume that the majority of gene flow between mussel populations relies on the dispersal of glochidia by host fishes. If a mussel species only infests a single species of host fish, the genetic structure of the mussel populations should be congruent with the genetic structure of the host fish. I examined the correlation between the genetic structure of two closely related species, *Leptodea leptodon* and its sister species *Leptodea fragilis* with their sole host fish, freshwater drum *Aplodinotus grunniens*. *Leptodea leptodon* is a federally endangered species while *L. fragilis* is common and widely distributed. It is of conservation interest to uncover the mechanisms allowing one species to be widely distributed while the other is endangered, when these closely related species share their lifecycle with the same host fish. We non-destructively collected about 110 samples for all three species from the Gasconade, Meramec, and Bourbeuse rivers in Missouri. Both mtDNA and microsatellites data indicated high levels of gene flow between sample sites in all three species, although weak population structure was detected in both mussel species but not in host fish. Despite its imperiled status, *L. leptodon* showed similar levels of gene flow as *L. fragilis*. These results implied that dispersal of larvae by *A. grunniens* had similar effects on maintaining the connectivity between mussel populations, and gene flow among imperiled *L. leptodon* populations was not as limited as previously assumed. Evidence for a bottleneck was indicated for *L. leptodon* but not for the other two species. Our findings suggested that the rarity of *L. leptodon* is perhaps due to other factors such as habitat specificity rather than limited host dispersal.

Early Career Malacologists Symposium

West Coast aquatic molluscs

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Recent genetic and morphological studies has revealed that the aquatic molluscan faunas of northern California, Oregon and Washington are more diverse than previously thought. A summary of the discovery's will be presented along with the conservation implications.

Conservation Session

Michigan's fluvial habitat suitability for 11 listed unionids

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In Michigan, 62% of unionid species are considered endangered, threatened, or of special concern. To aid in management of these unionid species, ten state listed/special concern species and one federally listed endangered species (*Epioblasma triquetra*) were modeled using ecological parameters necessary to characterize habitat suitability within the Upper and Lower Peninsulas of Michigan. Habitat suitability values were proportional to likelihood of occurrence. Mussel data came from a combination of recent site occurrences (1990-2012) from the Michigan Natural Features Inventory unionid assemblage surveys and Natural Heritage Database. We utilized Maximum Entropy Modeling (MaxEnt) that employed natural (n=13) and anthropogenic (n=11) landscape variables including dam metrics, streamflow variables, and water temperature. Since potential host fishes are important biological determinants of mussel distributions, host fish distributions were modeled with MaxEnt with the same set of landscape variables, and then the results were integrated into the mussel's models. The model predicted that between 1,274 to 11,205 km of habitat (1.7 to 15% of the state's lotic reaches) would be suitable for species occurrence. Highly suitable habitat (defined as a logistic value greater than 0.5; a very conservative value for this model parameter) included between 330 to 3,241 km (0.4 to 4.3%) of lotic reaches. Natural variables were the strongest indicators of suitable habitat for all species, but *E. triquetra* that had strong influences from dams and agricultural land uses. The top four variables determining suitable habitat for unionids include stream discharge (QA50), host richness distribution, urban land use, and upstream dam density. The integration of all eleven models of suitable habitats can provide information on best available habitat in the state for multiple listed species. The combination of modeled unionid distributions along with the statewide important ecological parameters can allow for more informed decisions in conservation planning and management of Michigan's listed unionids.

Great Lakes Malacology Session, Part I

Invasive molluscs: Why do we keep repeating the same mistakes?

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Humans have translocated molluscs around the planet for much of our history. Despite thirty years of discussion of the worst molluscan invaders within the field of malacology, the problem of invasive molluscs is worsening. We are repeating the same mistakes of introducing these invaders to other ecosystems, to the detriment of native flora and fauna. This talk is a high-level discussion of some of the most damaging invasive molluscs across the planet, and their impact on local ecosystems. Species discussed include members of the Invasive Species Specialist Group's 100 worst list, the giant African snail (*Lissachatina fulica*), and other invasives such as apple snails, zebra mussels, Asian clams, Pacific oyster and rosy wolf snails. I will discuss specific pathways of invasion, touching on the new fad of using snails as facial treatments, invasive species impacts on human health issues, and the role of the giant African snail throughout the globe, as well as its current status in the USA. I will address ways to teach this material in a variety of biology classes so that as scientists and educators we can hopefully avoid these mistakes in the future.

Invasives Session

Molecular phylogeny of the columbellid gastropods

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With 725 living species in over 65 nominal genera, columbellids are a successful group of small to medium-sized (mostly 5 to 25 mm) neogastropods, distributed in temperate to tropical waters worldwide. Extensive polychromatism has caused the establishment of a plethora of names currently treated as synonyms. Although columbellids can be found from the intertidal to depths of 2,000 meters, maximum diversity is in the 0-100 m interval in the tropics, where 40-50 species commonly co-occur at single West Pacific sites, with syntopic occurrences of up to 10-12 species. Species vary widely in habitat, feeding, larval development and adult anatomy, and provide many potential avenues for studying macroevolutionary trends. Membership in the family is traditionally confirmed using the unique morphology of the radula and, as in all shelled gastropods, species are typically defined and identified by conchological characters, which are unfortunately not particularly diagnostic for establishing supraspecific classifications. The monophyly of the group and its constituent genera have never been rigorously tested. To reconstruct columbellid phylogeny, we assembled a mitochondrial and nuclear gene data set, based on multiple representatives each of over 80 species in 25 genera and representative outgroups from the buccinoid and muricoid neogastropods. Correspondence of the resulting phylogeny with the traditional classification based on anatomical and morphological data will be assessed.

Marine Molluscs Session, Part II

The distribution of commonness and rarity in the freshwater gastropod fauna of U.S. Atlantic drainages

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The database of the Freshwater Gastropods of North America project currently contains 11,471 records of 67 species inhabiting Atlantic watersheds from Georgia to the New York line. Information theoretical analysis suggests that this list of 67 is complete, no additional species apparently so rare as to have been missed entirely. The distribution of species incidence appears bimodal, with one peak around 20-30 records and a second peak in the 200-400 range. Then adopting the quartile system of Gaston, we suggest that the $0.25 (67) = 17$ species in the left tail of this incidence distribution be defined as “rare,” specially designating the leftmost 5% as rank I-1 and the next 20% as rank I-2. The remaining $0.75 (67) = 50$ of the species we divide equally into ranks of increasing incidence I-3, I-4, and I-5. Focusing on the $0.50 (67) = 34$ species in ranks I-1, I-2, and I-3, our review of the published literature suggests that 2, 5 and 10 of them likely demonstrate above-median incidence elsewhere outside of our study area, respectively. We define these species as “peripheral” in U.S. Atlantic drainages, appending a subdesignation “p.” Then following Gaston, 7 species are “pseudorare” in our study area, being designated I-1p and I-2p. And an equal number of I-3 species must therefore demonstrate the phenomenon that Gaston terms “non-apparent rarity.” The relationship between the objective system of incidence rarity here proposed previous subjective systems of ranking by “conservation status” is explored.

Contributed Talks Session

Flashing in *Ctenoides ales* “disco” clams - predators and prey

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The “disco” clam *Ctenoides ales* is known for its vivid flashing display which results from light-scattering silica nanospheres. How the light display affects predators of the disco clam, as well as its prey, is unknown. Observations of predation events in the wild are extremely rare, so known clam habitats on coral reefs were searched in order to identify shells of deceased clams that showed predation damage. The type of damage was then linked to potential predators identified on the reef, and their visual capability was examined to determine whether they are capable of perceiving the flashing display. To assess whether the light display serves as a lure for phototactic prey items, including phytoplankton and zooplankton, water samples were collected directly from inside clams in both high-light (flashing visible) and low-light (flashing not visible) conditions underwater. The volume and diversity of plankton was compared between the two conditions, as well as against a control water sample taken 10cm (± 2 cm) away from the clam. Additional samples were collected using plankton nets and exposed to two treatments, including video playback of a screen mimicking the spectra of the clam with two lines – one constant and one flashing. The second treatment utilized artificial clams made from *C. ales* valves with LED strips of light that were off, on, or flashing. Samples were again compared for volume and diversity. Preliminary results did not indicate any differences between the varying treatments.

The *Ischnochiton* problem: A widespread species-rich genus of similar appearing chitons is supported as polyphyletic

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Out of about 950 recognized species of chitons, over 100 belong to the widespread genus, *Ischnochiton* Gray, 1847. At a species-level it is relatively well known and, like other members of its suborder, Chitonina Thiele, 1909, which collectively includes over half of all extant chiton species, its greatest diversity is in the tropics and cooler seas to the south. In southern Australia, *Ischnochiton* is especially diverse and ecologically important and can be larger bodied than is normal for *Ischnochiton*. I have gradually been able to sequence collections of *Ischnochiton* and other Chitonina with mitochondrial 16S and COI. Most genera of Chitonina, including *Ischnochiton*, have scaly girdles of flexible armor. The other similarly ornamented Chitonina genera tend to have more distinctive dorsal valve sculpturing whereas *Ischnochiton* is a genus with many small generic chitons without much distinctive sculpture. My results from the better sampled and more slowly evolving 16S gene region are not adequately resolving deep nodes within Chitonina, but they do robustly support the phylogenetic hypothesis of “*Ischnochiton*” as a polyphyletic assemblage of between four to seven independent lineages, scattered across Chitonina. Despite their similar appearance, separate geographically restricted phylogenetic lineages apparently have either plesiomorphic or superficial similarity of weak valve sculpturing. Most worldwide species do not belong to the lineage that includes the type species for *Ischnochiton* from South Africa, currently known as *I. textilis* (Gray, 1828), and this implies that substantial generic reassignment across Chitonina will eventually be necessary. Partly because of the *Ischnochiton* problem, a detailed phylogenetic analysis across Chitonina is needed. With collaborators, we are undertaking phylogenomic and morphological approaches with dense taxon sampling that could not only resolve *Ischnochiton* lineages but should also allow us to evaluate the evolution of specific traits and previously unrecognized biogeographic affinities within Chitonina.

Marine Molluscs Session, Part I

Green eggs and hulls: DNA barcoding of southern Australian chitons and their plankton-collected embryos

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We obtained mitochondrial COI and 16S sequences as DNA barcodes for 24 morphology-identified adult chiton (Mollusca: Polyplacophora) species collected from mostly Victoria, Australia, which represents the first broad molecular survey of the southern Australian chiton fauna. Each voucher was documented with macro-photography; images and taxonomic details have been organized into a still-unreleased web site that includes not only species we observed but also other species known from this region. We then used the adult COI sequences to distinguish 21 species of eggs or embryos collected as plankton that had already been documented with photomicroscopy. We obtained genomic DNA from single embryos and amplified a partial COI sequence to match with sequences from adults. Chitons often have distinctive species-specific egg hull sculpturing patterns and certain other embryonic or larval traits and their presence in the plankton can reveal reproductive characteristics resulting from natural spawning events that are difficult to otherwise observe. We matched embryos to adults for 10 species from multiple genera and identified 11 additional genetically distinct chiton embryos for which we can only identify provisionally to genus. This linking of benthic adults to their planktonic embryonic stages allows the construction of hypotheses on phylogenetic relationships of species and radiations of taxa within this fauna. Our results have revealed endemic patterns of speciation that are obscured by conventional classification, especially for the species-rich genus *Ischnochiton* Gray, 1847. We have also discovered a novel category of egg hull morphology that, together with sequence results, support the elevation of *Frembleya* H. Adams, 1867 to full generic status, rather than as a recognized subgenus of *Plaxiphora* Gray, 1847.

Contributed Talks Session

Terrestrial gastropods of Illinois

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While much of Illinois is today occupied by agricultural land, urban, suburban and industrial development, the great geographic and climatic diversity of the state continues to support a diverse land snail and slug fauna. About 128 terrestrial gastropod species are known to live or have lived in the state since the early 1800s. A number of species were recorded in the early 20th century from isolated locations immediately at the state's borders and have, despite efforts made, not been confirmed for Illinois in many decades. They may have been temporary advances from neighboring states. Other species that are dependent on continuous availability of high-quality forest habitat have become exceedingly rare over the last century, especially in the Chicago area and adjacent NE Illinois.

Conversely, 18 non-native species (or 14% of the total) live in Illinois, a number that increased considerably due to recent surveying. In the slugs the proportion of non-native species is as high as 62% (10 of 16 species). The influx of non-native species is expected to continue.

Conservation Session

City of immigrants: The slugs of Chicago

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The first discovery in the Americas of the slug *Tandonia kusceri*, native to SE Europe, in a Chicago suburb in 2013 led to an opportunistic survey of slugs in Chicago and its collar counties. Slugs from this area in the Field Museum of Natural History were also examined. Twelve slug species in five families (6 Arionidae, 2 Agriolimacidae, 2 Limacidae, 1 Milacidae, 1 Philomycidae) were identified based on external appearance and genital anatomy. All of these species, except the philomycid *Philomycus carolinianus* and the agriolimacid *Deroceras laeve*, are introduced from the Palaearctic. While *D. laeve* is not uncommon even in the city, the *P. carolinianus* population has been reduced to mere vestiges in isolated forest remnants. The Chicago records of *Arion distinctus*, *A. fasciatus*, *A. fuscus*, *A. hortensis* and *Ambigolimax valentianus* constitute considerable range extensions.

The California Helminthoglyptidae Project

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Our project goal is to advance the still limited understanding of the diversity, anatomy, distribution, and phylogeny of California's native helminthoglyptid land snails, including exploring species diversity and estimating phylogenetic affinities for *Cahuillus* and *Eremarionta*, genera that are common in the Mojave Desert and surrounding arid lands. Are these desert snails most closely related to the coastal or offshore island genera, including *Helminthoglypta*, *Plesarionta*, *Micrarioranta*, or do they have closer affinities to the east, for example with members of a better studied genus common in the Sonoran Desert, *Sonorella*? Our studies could be extended to better characterize the tempo and mode of land snail diversification in California. We are: (1) observing and photographing live specimens, (2) analyzing shell structure, especially embryonic whorl ornamentation with SEM, (3) dissecting and preparing permanent, stained, slide-mounted reproductive systems for enhanced viewing of internal structures including dart morphology, and (4) sequencing and performing molecular phylogenetic analysis for combined data sets from two mitochondrial gene regions, COI and 16S. We are completing such studies on multiple species illustrated here that represent five of the six above-mentioned helminthoglyptid genera. Our preliminary molecular results have indicated that species diversity has likely been underestimated, even though there are many species currently recognized as valid. Our results have so far not resolved the affinities of the Mojave Desert snails, which we expect might eventually be resolved with more thorough sampling of taxa, the addition of nuclear gene markers, and the integration of morphological characters in a combined data set analysis.

Poster Session

The snail also rises: Desiccation tolerance of *Pomacea* spp. (Gastropoda: Ampullariidae)

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Climate change will dramatically affect freshwater ecosystems in future decades. Frequent, severe droughts punctuated by flooding events will increase water-level fluctuations. Freshwater mollusks that utilize aquatic-terrestrial habitats, if affected, may show higher susceptibility to drawdown or increased survival due to specialized adaptations that other taxa lack. Apple snails, *Pomacea* spp. (Ampullariidae), live in freshwater, but deposit egg clutches on terrestrial substrates. These species may show both resistance to desiccation, and resilience after dry-down events, because they possess opercula, burrow, and estivate; all traits that prevent water loss. We buried 156 snails of assorted sizes (*Pomacea* spp.) beneath dry sand to test their tolerance to water loss, simulating drought and the burrowing response. Mixed groups of snails collected from four permanent waterbodies in Uruguay remained buried for 47 days, during which we recorded daily survivorship. We found that 36% survived the entire period. Mortality curves indicated a higher lethal exposure time for 50% of *Pomacea* (LT50) than those observed for mollusks that were not buried, in other studies. Additionally, we found sex-related differences, with fewer males surviving than females. After 47 days, most survivors placed in water resumed normal activities within 24 hours, including eating and mating. Snails from two sites laid eggs during the revival period. These results indicate that *Pomacea* spp. can survive long drying periods, quickly recover, and are capable of reproduction shortly after. These traits were probably key to their adaptation to ephemeral habitats, as both resistance to and resilience after water-level fluctuations are critical to population persistence. In addition, desiccation tolerance and high reproductive rates after dry-down may confer an advantage to these species in non-native habitats, as drought frequency increases with continued climate change. Increased understanding of how organisms respond to such changes will allow us to better mitigate the impacts to biodiversity.

Invasives Session

Phylogenomics of Cladobranchia (Gastropoda: Heterobranchia: Nudibranchia)

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Cladobranchia (Gastropoda: Nudibranchia) is a diverse (~1000 species) but understudied group of sea slug mollusks. In order to fully understand the ecological and morphological character evolution as well as the potential importance of nudibranchs within Cladobranchia, a solid understanding of the evolutionary history of this group is necessary. This goal has yet to be achieved, as to date there have only been two direct attempts at resolving the evolutionary relationships of members within this group, with neither identifying a well-supported topology. In addition to these studies, multiple others addressed some of the relationships within this clade while attempting to resolve the evolutionary history of parent groups to Cladobranchia (namely Nudibranchia and Euthyneura). However, all of these phylogenetic studies support different topologies and groupings of taxa within Cladobranchia. Even at the most fundamental level, it is unclear whether the three traditional groupings within Cladobranchia (Euarminida, Dendronotida and Aeolidida) are monophyletic. In our research, we have successfully addressed some of these long-standing issues in resolving the evolutionary history of Cladobranchia utilizing RNA-Seq data (transcriptomes). We sequenced 16 transcriptomes of cladobranchs from 16 different genera *de novo* and combined these with three transcriptomes from the NCBI Sequence Read Archive (SRA). Transcript assembly using Trinity and orthology determination using HaMStR yielded 839 orthologous groups for phylogenetic analysis under a maximum likelihood framework. These data provide a well-supported and almost fully resolved phylogenetic hypothesis of the sampled taxonomic groups in Cladobranchia. Our results support the monophyly of Cladobranchia and the sub-clade Aeolidida, and show that Dendronotida is paraphyletic. The data collected also resolve the position of the problematic genus *Melibe* among taxa previously assigned to Dendronotida, the affinities of which were called into question in previous analyses. Some interesting familial level relationships were revealed, including a monophyletic Aeolididae being derived from within a paraphyletic Facelinidae. However, broader taxon sampling will be necessary before we propose any taxonomic modifications within Cladobranchia.

Early Career Malacologists Symposium

Evolution of parasitism in *Caledoniella montrouzieri* Souverbie, 1869 (Littorinimorpha), a unique marine snail living on gonodactylid mantis shrimps

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Origin of parasitic lifestyle is one of the most attractive issues in evolutionary biology. *Caledoniella montrouzieri* is a marine snail living on the abdominal side of mantis shrimps of the genus *Gonodactylus* (Gonodactylidae), which are carnivorous predators that use their powerful raptorial claws to snap up prey. *Caledoniella* is usually found as a male-female pair on the host and the female lays numerous egg capsules on the host abdomen. Rosewater (1969) suggested the possibility that *C. montrouzieri* sucks the body fluids of the host and Reaka (1978) found that the parasitism by the snail has serious negative effects on the hosts (e.g. decreased growth rate and reproductive failure). The genus *Caledoniella* was previously assigned to its own family Caledoniellidae (Rosewater 1969) and then transferred to Vanikoridae (see Bouchet & Rocroi 2005), but its phylogenetic position remains contentious. Our preliminary molecular analysis suggests that *C. montrouzieri* (type of the genus) belongs to the superfamily Truncatelloidea, not to Vanikoroidea. To decipher its more detailed position, we performed a molecular phylogenetic analysis using four genes (18S, 28S, 16S and COI) from 16 representatives of truncatelloideans. Results show that *C. montrouzieri* is nested among species of *Sigaretornus* (Tornidae), commensals in the burrows of various marine invertebrates, and forms a clade with an undescribed *Sigaretornus* from the burrow of the mantis shrimp *Bigelowina phalangium*. This topology suggests the evolutionary acquisition of parasitic lifestyle of *C. montrouzieri* in the following order: (1) exploitation of the marine invertebrate's burrow, (2) specialization to mantis shrimps and (3) colonization of the abdomen of the mantis shrimp. We will discuss the morphological and ecological specialization of *C. montrouzieri* to ectoparasitic lifestyle by comparing with the closely related species of *Sigaretornus*.

Phylogenetics Session

Biogeography of the freshwater mussels (Unionida: Unionidae & Margaritiferidae) of Wisconsin, USA

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The fresh waters of Wisconsin are biogeographically significant because 1) the state straddles the divide between the Mississippi and Great Lakes/St. Lawrence basins, and 2) much of the state was only recently colonized following ablation of late Pleistocene glaciers. Current disjunctions of freshwater mussels among basins are strong evidence for past confluence, and this study set out to describe the distributions of mussel species of the state in that context. Species distributions were determined from a literature review as well as analysis of more than 8600 Wisconsin species-locality records from 6 databases of museum specimens and observations. Each species-locality record was georeferenced to river drainage and county or township (when possible). At least 49 species have been reported from Wisconsin, although there is evidence for more. The counties of greatest species richness are those along the western border of the state, adjacent to the Mississippi, St. Croix, and Wisconsin rivers. Six overlapping faunal assemblages were identified: 1) 7 or 8 species are known from all major basins including Lake Superior; 2) 9 or 10 species are known from all major basins except Lake Superior; 3) 1 species is known only from Lake Superior; 4) 3 species are known from only from eastern Wisconsin in tributaries of Lake Michigan and the Rock-Fox (Illinois); 5) 12 species are known from the Mississippi basin and the Fox (Lake Michigan); and 6) the remaining 16 species are restricted to the western part of the state in the Mississippi Basin. Species assemblages are indicative of the chronology of post-glacial colonization. Moreover, the species patterns uncovered in this study are hypothesized to be indicative of patterns of gene flow within species.

Great Lakes Malacology Session, Part I

Mitochondrial inheritance and sex determination in bivalve species

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Mitochondria are semi-autonomous organelles, mostly known for their role in energy production. Several characteristics make them unique: they have their own genome, the mitochondrial DNA (mtDNA), and contrary to the nuclear genome, they are inherited uniparentally by Strictly Maternal Inheritance (SMI) in most animal species.

Exceptionally, one model of mitochondrial heredity found in bivalve molluscs goes against the rule of SMI: the Doubly Uniparental Inheritance (DUI) of mtDNA. Species with DUI have two mitochondrial lineages: one transmitted through eggs (F-type), the other through sperm (M-type). By promoting the presence of two distinct genomes inside an organism, a harmful situation that can lead to severe pathologies in humans, this model of heredity has raised concerns about its evolutionary origins and functions. Actually, one main hypothesis to explain the evolution and persistence of DUI involves its role in sex determination. If true, the DUI system would represent the first known animal sex determination system soliciting the mtDNA.

The elucidation of this hypothesis depends on a widened study of different DUI systems (How widespread is DUI, and does it have a single or multiple origins?). For this purpose, I am studying the taxonomic distribution of DUI in bivalve mollusks by testing for its presence in families where no investigation has been done yet. It is expected that DUI evolved once in the ancestral bivalve lineage and is broadly distributed within the Bivalvia. To date, DUI has been found in 9 families out of ~105 bivalve families. My preliminary results confirm the discovery of the DUI system in a new family of bivalves (i.e. in the species *Scrobicularia plana*, family Semelidae) and sustain the hypothesis of a single origin of DUI.

Poster Session

Survival of *Partula* species after a mass extinction event: A phylogenomic perspective using museum specimens

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The Partulidae is a tree snail family endemic to Oceania that represents one of the most infamous recent examples of oceanic island mass extinctions. Approximately 120 species are recognized with the center of their distribution in a single hotspot archipelago, the Society Islands. The Society Islands had 61 endemic partulid species, half of the entire clade, until their catastrophic mass extinction due to the introduction of the carnivorous rosy wolf snail *Euglandina rosea*. There are a small number of Society Island *Partula* species that still survive in the wild either in montane cloud forest >1,000m in elevation (*P. otaheitana* on Tahiti), where the predator is relatively ineffective, or in Tahitian (*P. clara* and *P. hyalina*) or Moorean (*P. taeniata*) valleys. This pattern of differential survival in the valleys is not understood, especially in light of predation models predicting their extirpation within three years of contact with the predator. Additionally, these valley populations experience fluctuations in abundance from year to year with individuals not being sighted for several years. Previous results found these valley survivors to be genealogically linked based on mitochondrial DNA cytochrome oxidase c subunit I sequences with surviving *P. taeniata*, *P. clara*, and *P. hyalina* comprising nominal sister species. These results also showed most *P. clara* and all *P. hyalina* comprise a single founding lineage on Tahiti. However, these results were based solely on a single marker. Here, I analyze high-resolution nuclear genomic data by employing the double digested Restriction Associated DNA (ddRAD) sequencing method to examine the relationships among these survivors. I utilize lyophilized and alcohol preserved tissue samples that are archived at the University of Michigan's Museum of Zoology to address the question: Are *P. clara* and *P. hyalina* distinct species?

Pacific Island Land Snails Session

Two for the price of one: inadvertent introduction of cryptic *Euglandina* species during failed biocontrol efforts in Hawaii

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Among the most publicized biocontrol cases gone awry is the introduction of the predatory land snail *Euglandina rosea* from Florida to Hawaii to control the giant African snail, *Lissachatina fulica*. Not only did *Euglandina rosea* fail to reduce *A. fulica* populations, it also became a major factor in the decline and extinction of native land snails in Hawaii and elsewhere in the Indo-Pacific. Phylogenetic analyses of COI and 16S mitochondrial genes from 110 individuals collected throughout the main Hawaiian Islands indicate that *E. rosea* populations in Hawaii consist of two robustly supported monophyletic lineages, with a mean genetic distance of 16% and 8% between them for COI and 16S respectively. Sequences from *E. rosea* individuals collected throughout its native range (Florida, Georgia, Mississippi, Alabama) revealed levels of genetic differentiation (12%, COI; 6%, 16S) that is far greater than those seen within other congeners, and equivalent to distances among species. These genetic data in combination with anatomical characters support the recognition of at least 10 distinct species of *Euglandina* within a complex of species recognized as one. The high levels of genetic diversity, typically correlated with geographic isolation, may indicate possible underlying ecological differences (e.g. arboreal vs. epigeal behavior) among the two species that were introduced to Hawaii and elsewhere. Such differences may have contributed to the success of *Euglandina* spp. invasion and may also explain the greater than initially anticipated impacts on native snail populations. Too few biocontrol programs assess levels of genetic variation or ecological plasticity in introduced organisms. As such, numerous divergent lineages with distinctive life histories and behaviors have probably been inadvertently introduced, and may continue to have unpredicted ecological interactions with non-target species.

Invasives Session

Pacific Island Land Snail Conservation: Case studies from the Hawaiian Islands

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Islands comprise only 5% of the earth's landmass, yet the study of island biota has contributed substantially to understanding ecology and evolution broadly. Huge local diversity is the hallmark of what has made Pacific islands, Hawaii particularly, our finest natural laboratories for evolutionary study. Nowhere, in relation to land area, does land snail diversity reach that of the Pacific islands, with >6,000 species, mostly single island/archipelago endemics. But, this legacy is vanishing fast and we have yet to unlock many of its secrets. The Hawaiian Islands support one of the world's most spectacular radiations of land snails, which have distinctive evolutionary, ecological and cultural legacies and play an important role in our understanding of evolution in general and island biology in particular. Snails provide key ecosystem services (e.g. litter decomposition and nutrient cycling), are indicator species for intact mid-elevation rain forests, and key to watershed maintenance. They provide insights into historical processes, since their shells can provide a record of colonization and evolutionary events. The Hawaiian land snail fauna is disharmonic, with only 10 of the ca. 90 recognized land snail families, with estimates of more than 750 species. The real number is unknown as most have not been studied comprehensively for 60+ years. Despite this uncertainty, even the most conservative estimates indicate that Hawaii is an incontrovertible gastropod diversity hotspot. Even more spectacular is that >99% of the species are endemic, many to single islands. Using an integrative approach, we have begun cataloging the remaining Hawaiian land snails and placing them within a larger evolutionary framework. Unfortunately, much has been irretrievably lost, but there remains a great deal of diversity, including undescribed species, that may still be saved. Insights from these remaining taxa will be invaluable for understanding how we can conserve land snails across the Pacific.

Phylogeny, morphology and species limits of Neotropical apple snails (Caenogastropoda: Ampullariidae)

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The Ampullariidae (apple snails) are freshwater gastropods and a key group of basal caenogastropods. They play important ecosystem, disease vector and agricultural pest roles and have great potential as models in evolutionary biology. The family is composed of two reciprocally monophyletic lineages, Old World taxa, and the more diverse New World ampullariids. The family has not been fully revised and knowledge of the real levels of species diversity remains uncertain, particularly among New World taxa with >250 available species-group names in four genera: *Asolene*, *Felipponea*, *Marisa* and *Pomacea*. Historically ampullariid evolutionary relationships were poorly understood, especially regarding *Pomacea*, which has implications for research on many aspects of ampullariid evolutionary biology. To better understand Neotropical ampullariid diversification and the processes that shaped contemporary diversity samples were collected from more than 200 populations in South and Central America, concentrating heavily on Brazil, the center of ampullariid diversity. Phylogenetic analyses of two mitochondrial and three nuclear loci from more than 1500 snails representing 65 species indicate that New World Ampullariidae are a robustly supported monophyletic group with respect to Old World ampullariids. Of the four Neotropical genera, only one, *Asolene*, was recovered as monophyletic, nested within a clade consisting of all species of *Marisa* and *Felipponea*. Most species of *Pomacea* cluster into four distinct groups irrespective of geography. Relationships supported by the phylogeny are consistent with patterns of anatomical variation, and despite the lack of monophyly among genera the overall tree topology consistently supports the hypothesis that diversification within the Ampullariidae has been, in part, driven by key innovations for exploiting ephemeral habitats and concomitant reproductive adaptations. Moving forward, this robust phylogeny will provide the basis for comparative studies of the evolution of anatomical, physiological, behavioral and molecular traits involved in macroevolutionary processes driving diversification and adaptation in these snails.

Phylogenetics Session

Phylogeography and genetic structure of two freshwater mussel species (Bivalvia: Unionidae) along hypothesized post-glacial dispersal routes into the Laurentian Great Lakes

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Understanding genetic diversity of imperiled freshwater mussel species across large spatial scales is necessary for developing appropriate conservation strategies. Genetic data is important for investigating population connectivity, uniqueness (e.g., Evolutionarily Significant Units), and testing biogeographic hypotheses. Mitochondrial sequences and microsatellite loci were used to analyze the phylogeography of two common and widespread unionid species (*Lampsilis cardium* and *Lasmigona costata*) from the Great Lakes and the historically connected Wabash, Illinois, and Wisconsin river drainages; which may have acted as conduits for mussels from refugia south of the Pleistocene glacial maximum. Approximately 30 individuals of each species were collected 17 sampling locations with a mantle clip being removed from each specimen for genetic analysis. Using standard methods, a fragment of the mitochondrial gene COI was sequenced and a suite of microsatellite loci were genotyped. Using mitochondrial DNA haplotype data and microsatellite allele frequencies, multiple analyses suggest two distinct genetic populations for both *Lam. cardium* and *Las. costata*. A total of seven hypothesized post-glacial dispersal scenarios were compared using an Akaike Information Criterion to test the various models of isolation-by-distance. For both *Lam. cardium* and *Las. costata*, evidence was strongest for multiple post-glacial dispersal routes into the Great Lakes. Ten of the putative *Lam. cardium* haplotypes found in the Maumee (Great Lakes) and Wabash (Ohio River) drainages were revealed to be more similar to *Lampsilis ovata* sequences available on GenBank rather than *Lam. cardium*. Multiple assignment tests using microsatellite allele frequencies were conducted to determine if *Lam. cardium* and *Lam. ovata* are interbreeding. Assignment tests failed to accurately classify individuals to their respective species, suggesting *Lam. cardium* and *Lam. ovata* in this region interbreed freely.

Great Lakes Malacology Session, Part II

Extremophile marine bivalves at ancient methane seeps

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High-profile research on living bivalves at deep-water methane seeps has centered on obligate symbioses with thiotrophic and methanotrophic Bacteria and Archaea. The scope of research on ancient cold seeps is broader because paleontologists have the advantage of easier access to sites at which bivalves are preserved in situ with the geochemistry and three-dimensional stratigraphic record of fluid migration pathways and sites of effluent discharge. Zonation at ancient seep sites also reveals (1) non-chemosymbiotic bivalves that thrived opportunistically on chemosynthetic fixation of carbon by free-living microbes and (2) bivalves tolerant of hypoxia and toxic metalliferous compounds.

Cold seeps in the deep-water upper Eocene Keasey Formation in Oregon include species of Solemyidae, Lucinidae, Thyasiridae, Lasaeidae, and Basterotiidae – families in which chemosymbioses have been documented. The bivalves are zoned, with articulated thyasirids in the seep carbonates (chemoherms, limestone blocks, layers of carbonate concretions, nodules and blebs) and articulated lucinids and solemyids in surrounding mudstone and siltstone. Of particular interest is evidence of diffuse methane seepage through sediments preserving extremophile bivalves that were not part of the core chemosymbiotic community. Seep associates include (1) taxa that thrived opportunistically as deposit-feeders (Nuculidae and Nuculanidae), taking advantage of enhanced anaerobic oxidation of methane by the free-living microbiota, and (2) taxa with tolerance for toxic geochemistry and adaptations for life in hypoxic sediments. A new and locally-abundant carditid bivalve at one seep site represents an ancient archiheterodont family with a clade-specific oxygen binding protein.

Study of fossil bivalves and ancient deep-water seeps assumes new significance as global warming causes expansion of oxygen minimum zones into shallow water and human activities cause oxygen depletion through pollution and eutrophication. The observed onshore-offshore migration of marine taxa over geologic time is subject to reversal if extreme offshore conditions become more pervasive onshore.

Marine Molluscs Session, Part I

Urbanization impacts on land snails: Abundance, diversity and community composition

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Urbanization has tremendous impact on most native species. Urban ecosystems are becoming increasingly prevalent, while urban ecology is a relatively underdeveloped field. This is especially true in land snails, which are a surprisingly understudied organism. Due to their low mobility and dispersal potential, land snails are valuable indicators of ecosystem disturbance. Little is known of land snail distribution or community composition in the urban setting. This study examines the role of urbanization on land snail abundance, diversity, and community similarity in 60 parks across three cities in Tennessee. Sampled parks include small extensively landscaped downtown parks, neighborhood and community parks, district athletic parks, and large nature preservation parks, each with variable vegetation, soil characteristics, disturbance and use. Three collection methods were used to measure snail species composition: extensive scouring of 3m² quadrants for macro snails, soil sampling for micro snails, and opportunistic visual searches in niche habitats. Preliminary results suggest that intensely disturbed urban ecosystems such as small downtown parks often have low snail species richness, dominated by one or two superabundant native species like *Triodopsis* sp. or *Ventridens* sp. These small parks sometimes harbor large populations of non-native species, including *Oxychilus* sp.; many of which represent first reports from the state of Tennessee. In contrast, less disturbed areas, such as nature parks, typically have a much higher species richness, and more evenly distributed abundance patterns, with little to no non-native species. This evidence suggests that urbanization promotes homogenization among land snail communities. It is unknown what influence this may have on other organisms in urban ecosystems.

Poster Session

Genetic structure of the mapleleaf mussel (*Quadrula quadrula*) on the Niagara Peninsula, Ontario, Canada: Inferring effects of canal and dam construction over the last 200 years

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Alterations to watercourses have numerous effects on connectivity in aquatic systems, and thus can majorly influence the dispersal abilities of aquatic biota. Canals create connections between waterbodies, which can be used as corridors for dispersal by opportunistic invaders, while dams act as isolating barriers, fragmenting populations. The Niagara Peninsula of Ontario, Canada has a 200-year history of dam and canal construction, resulting in the major alteration of the watercourses of the region. These modifications have allowed the entry of numerous invasive species into the upper Great Lakes (e.g., sea lamprey, alewife) and have likely facilitated dispersal in native species as well. The purpose of this study is to explore the effects of canal and dam construction on the genetic structure of Mapleleaf mussels (*Quadrula quadrula*). While they native to much of the upper Great Lakes and Mississippi drainage system, *Q. quadrula* have recently been found in an eastern Lake Ontario harbor, where the species was not known to occur. The establishment of *Q. quadrula* in Lake Ontario may have been a recent event, facilitated by connections made throughout the Niagara Peninsula's history of canal construction. Additionally, previous research indicates the Dunnville Dam on the Grand River, ON (a Lake Erie tributary) acts as an upstream barrier to fish movement. It is possible that this near 200 year old dam may also act as an upstream barrier to dispersal and gene flow for *Q. quadrula*. In this study, analyses of microsatellite DNA genotypes were used to evaluate these hypotheses, examine the effect of different watercourse alterations on the genetic structure of mussel populations, and uncover the history of *Q. quadrula* dispersal in the Niagara Peninsula. Ultimately, this information has the potential to improve conservation strategies for this and other unionid species at risk.

Great Lakes Malacology Session, Part II

Shell banding indicates increased growth rate in modern freshwater mussels from human impacts

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Growth banding in freshwater mussels can be relatively accurate indicators of growth rate. We measured external and internal growth bands on the shells of modern mussels in Tennessee and compared the growth rates to the same species of mussels from archaeological middens that were dated to the Middle to Late Woodland Period. Our goal was to compare the growth rates between modern and archaeological specimens to see if modern anthropogenic impacts such as massive water pollution and river impoundments were affecting mussel growth rates. The species used for external growth band analysis were: *Quadrula metanevra*, *Elliptio crassidens*, *Cyclonaias tuberculata*, and *Fusconaia subrotunda*. Our results indicate that there is indeed a visible signature of modern human impacts: recently collected specimens are generally significantly ($p = 0.05$) larger than specimens from the Middle to Late Woodland Period (~ 2200 - 1000 years old), when specimens of similar developmental age are compared. Internal growth band analysis was performed through detailed microscopic examination of thin sectioned shells of modern and archaeological *Q. metanevra*. Results from this analysis suggest the same conclusion, that modern individuals are growing faster. Further internal growth band studies are planned using more species. While our study cannot prove what specific impacts are causing this accelerated growth rate, previous work indicates that increasing water temperature from river impoundments and climate change, and especially increasing nutrients from farm runoff may be implicated. If accelerated growth from human impacts is a general pattern in many mussel species, this may have significant implications for conservation.

Poster Session

Freshwater mussel reintroduction and recovery in Alabama

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With a historical diversity comprising 182 species, representing 20% of the global species richness (≈ 890 species), Alabama is home to the greatest diversity of freshwater mussels on the planet. Species diversity is primarily the result of 10 separate river basins occurring within the state. Over the last century, wholesale physical modification and water quality degradation drove 24 species to extinction and resulted in extirpation of another 26 species from state waters. Additionally, some 63 species are now listed as federally endangered or threatened by the US Fish and Wildlife Service (USFWS). To address this significant conservation challenge, the Alabama Department of Conservation and Natural Resources (ADCNR) created the Alabama Aquatic Biodiversity Center (AABC) to lead recovery efforts through propagation and reintroduction. Following a 5-year construction effort, the AABC became fully operational in late 2010. Working cooperatively with USFWS and other state and federal agencies, regional recovery planning documents were also completed the same year. AABC mussel recovery efforts have two main areas of focus: 1. reintroduction of exceptionally rare species; 2. reintroduction of other rare but easily propagated species to evaluate scaling and possible site suitability. Reintroductions have taken place over multiple localities and/or years including 14 species to date. Since 2010, 25 separate releases of seven Tennessee River Basin species (four T&E) totaling 16,561 individuals have been carried out in areas of their former ranges. Reintroduced individuals have persisted at all recipient localities except one, and gravid females were detected at three localities. Since 2010, 15 separate releases of seven Mobile River Basin species (four T&E) totaling 6,855 individuals have been carried out in areas of their former ranges. All recipient localities are persisting and gravid females were detected at three localities. Additionally, host fish relationships have been determined for six species. Restoration of unionid populations is a decade-long endeavor. It is anticipated that recruitment of new individuals to some or all of the new populations will be detected within the next three years.

Update to the conservation status of freshwater gastropods of Canada and the United States

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An update of the recent American Fisheries Society (AFS) freshwater gastropod conservation assessment evaluated 709 species of freshwater gastropods representing 16 families and 93 genera. We found a total of 69 species as extinct or possibly extinct, 282 endangered, 102 threatened, 73 vulnerable, 157 currently stable, and 26 species have uncertain taxonomic status. Of the entire fauna, approximately 74% of freshwater gastropods are imperiled (vulnerable, threatened, endangered) or extinct, which exceeds imperilment levels reported for fishes (39%) and crayfishes (48%), but is identical to the current AFS mussel assessment (74%). Despite the high imperilment rate, the US Fish and Wildlife Service currently recognizes only 29 species as federally endangered, and 6 threatened, with another 6 as current candidates. However several environmental advocacy groups have filed petitions to list dozens more species across the United States. During the assessment process, conservation status reviews were hampered by a paucity of current distributional information and taxonomic uncertainties for many species. Nevertheless, successful recovery efforts have been developed for numerous species and a single Alabama gastropod has been down-listed by USFWS from endangered to threatened. This represents the first down listing of a freshwater mollusk under the Endangered Species Act due to recovery. Research on several fronts including basic biology, physiology, conservation best practices, life history, and ecology is needed, but systematics and digital curation of museum collections and databases, coupled with comprehensive status surveys (geographic limits, threat identification) should be prioritized to promote future conservation efforts.

Conservation Session

Marine Mollusk Resource Bank of Korea (MMRBK)

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The Marine Mollusk Resource Bank of Korea (MMRBK) was accredited in 2010 by the Ministry of Oceans and Fisheries of Korea with financial support from the government. The MMRBK houses approximately 600 marine mollusk species collections (wet collections preserved in 70% ethanol) collected from Korean sea coast as well as northwestern Pacific including Japan, and China Sea coasts. Comprehensive inventory information such as GPS data, specimen images, number of specimens are available online and curated under the specimen database system of the MMRBK. Currently the MMRBK has undertaken multiple missions that include (1) research for taxonomy, biodiversity and phylogeny of northwestern Pacific mollusk species, (2) management of mollusk collections and taxonomist education program, and (3) providing taxonomic information and specimen loan to researchers, environmental NGOs, and the general public. The current state (including major tasks) of the MMRBK will be presented in detail in this report.

Poster Session

Development of a DNA microarray-based identification system for commercially important Asian oyster species

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The correct identification of oyster species is essential for both aquaculture and taxonomic study, but it has often been a challenging task due to enormous morphological variation in shell morphs with ecophenotypic origins. The difficulty of species identification based entirely on shell characters has raised the need for developing an accurate, rapid tool for the identification and discrimination of oyster species. In this study, we established a DNA microarray-based identification system for eight commercially important Asian oyster species (*Crassostrea ariakensis*, *C. gigas*, *C. sikamea*, *C. nippona*, *C. angulata*, *Ostrea circumpecta*, *O. denselamellosa*, and *Saccostrea kegaki*). Sixteen species-specific probes developed in this study unambiguously distinguished eight target oyster species with no false-positive or false-negative signals. Of the eight oyster species examined, three *Crassostrea* species, *C. angulata*, *C. gigas* and *C. sikamea*, that are indistinguishable by morphology, could be precisely identified using species-specific hybridization probes. The DNA microarray-based identification system developed in this study offers a fast, reliable and simple-to-use tool for eight Asian oyster species, most of which are of commercial value and/or ecological significance in the macro-benthic community of offshore marine environments.

Poster Session

Phylogeography of the rock shell *Thais clavigera* (Mollusca): Evidence for long-distance dispersal in the northwestern Pacific

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The present-day genetic structure of a species reflects both historical demography and patterns of contemporary gene flow among populations. To precisely understand how these factors shape current population structure of the northwestern (NW) Pacific marine gastropod, *Thais clavigera*, we determined the partial nucleotide sequences of the mitochondrial COI gene for 602 individuals sampled from 29 localities spanning almost the whole distribution of *T. clavigera* in the NW Pacific Ocean (~3,700 km). Results from population genetic and demographic analyses (AMOVA, F_{ST} -statistics, haplotype networks, Tajima's D , Fu's F_s , mismatch distribution, and Bayesian skyline plots) revealed a lack of genealogical branches or geographical clusters, and a high level of genetic (haplotype) diversity within each of studied population. Nevertheless, low but significant genetic structuring was detected among some geographical populations separated by the Changjiang River, suggesting the presence of geographical barriers to larval dispersal around this region. Several lines of evidence including significant negative Tajima's D and Fu's F_s statistics values, the unimodally shaped mismatch distribution, and Bayesian skyline plots suggest a population expansion at marine isotope stage 11 (MIS 11; 400 ka), the longest and warmest interglacial interval during the Pleistocene epoch. The lack of genetic structure among the great majority of the NW Pacific *T. clavigera* populations may be attributable to high gene flow by current-driven long-distance dispersal of prolonged planktonic larval phase of this species.

Contributed Talks Session

Molluscan biomineralization: Ancient proteins with novel functions

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Biom mineralization is the process by which living organisms construct hard skeletons, creating magnificent structures such as Coral Reefs, Bone, Teeth and Shells. While mostly formed of minerals, biominerals contain proteins giving them extra hardness or special abilities different from naturally occurring mineral forms. Molluscs are key-organisms in studying biomineralization due to their complex shells. We have employed a comparative genomics approach to study the evolutionary origin of this complex trait. In order to test different hypotheses related to the evolution of the biomineralization toolkit we developed a bioinformatics pipeline that we used to identify shared protein families involved in biomineralization related processes across cnidarians, mollusks, echinoderms, arthropods and vertebrates. A web-based database was constructed to cater for all the data generated through the pipeline and is available at <http://biomine.net/>. Our analysis has allowed the identification of a shared biomineralization toolkit as well as molluscan specific innovations. In addition we are developing *Biomphalaria glabrata* as a model system to investigate the functional role of biomineralization proteins.

Early Career Malacologists Symposium

Distribution of sphaeriid slams in Western Lake Erie twenty-five years after invasion of *Dreissena*

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Clams in the family Sphaeriidae are widespread native mollusk species that are often overlooked. The distribution of these organisms in Lake Erie has not been examined in the 25 years since the initial invasion of the zebra mussel, *Dreissena polymorpha*. Carr and Hiltunen identified 10 species of Sphaeriidae in Western Lake Erie in 1961, of which *Pisidium casertanum*, *P. compressum*, *P. nitidum*, *Sphaerium corneum*, and *S. striatinum* and *Musculium transversum*, contributed 89.7% of all fingernail and pea clams sampled and were considered common. Four other species were reported as rare. Our research examines whether the distribution of Sphaeriid clams in western Lake Erie have declined similar to unionid mussels, as a step to enhancing the overall picture of impacts from the invasive dreissenids. Strayer has reported for the Hudson River that sphaeriid diversity initially declined after the dreissenid invasion, but after a significant die-off of *D. polymorpha*, a condition present in Lake Erie, densities of native species rebounded. Multiple standard ponar samples of Sphaeriid clams were made by the Ohio Environmental Protection Agency at 12 Western Basin stations and several more from the Central Basin as by-catch from mayfly-larva sampling in the summers of 2012-2014. Preliminarily, members of *Sphaerium* are rare, *M. transversum* are common as are at least several species of *Pisidium*.

Poster Session

Reproductive aspects of *Siphonaria lessoni* (Gastropoda: Heterobranchia) from the southwestern Atlantic Ocean

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Structural characterization and reproductive cycle of *Siphonaria lessoni* were investigated in Villa Gesell at Buenos Aires Province (37°16'S 56°58'W). *S. lessoni* is an herbivore gastropod commonly found inhabiting hard substrates in the intertidal zone of rocky shores along the South-western Atlantic Ocean. Artificial structures such as fishing docks introduced in sandy beaches like Villa Gesell, provides a new substratum for this species settlement. Histological study of the gonad shows simultaneous hermaphroditism in this species. The stage of gonadal development and oocytes size frequency in the female portion as the presence of sperm in the male portion were used to estimate reproductive events. The gametogenesis was observed synchronous for both female and male portions. The oogenesis stages were defined by vitellogenesis process. Previtellogenic oocytes and early vitellogenic were found within gonad throughout the year. The mature oocytes, ripe of vitello, were also found along the year but in high frequency during the beginning of the austral summer. Spermatogenesis was continuous along the year. The spawning period in this species at the sampled site extended from November to February (end of austral spring and summer). This reproductive period was associated with changes in temperatures and photoperiod.

Poster Session

Comparative ecological approach to habitat and food use: *Conus* diversity on Seychelles reefs

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Conus is the largest genus of marine animals with nearly 700 species currently recognized, and individual coral reef-associated habitats support 5-36 congeners. How stable these assemblages are over time is not known, but their high species diversity suggests the evolution of mechanisms that reduce or avoid interspecific competition. This comparative ecological study of 33 species in Seychelles will be the final of eight short-term or “rapid assessment” reports of *Conus* assemblages throughout the Indian Ocean. It emphasizes variation in species composition, diversity, and population density with environmental attributes, and use of food and space resources by co-occurring congeners. In general, species specialized more on different prey taxa than different microhabitats. These results are generally consistent with those previously reported for *Conus* assemblages in similar habitats elsewhere in the tropical Indo-Pacific, and they corroborate several hypotheses of expected adaptive strategies proposed and supported in earlier reports in the series: 1. Topographically complex, physically benign habitats support more diverse species assemblages than topographically simpler, physically harsher habitats. 2. *Conus* body size is smaller and less variable in the latter habitats and ranges more broadly in the former. 3. Population density of all co-occurring species is inversely related to species diversity, and ranges up to an order of magnitude higher in topographically simpler habitats. 4. Resource partitioning, especially of food resources but also of microhabitats, facilitates assemblages of numerous co-occurring *Conus* species and their avoidance of interspecific competition.

These results also support the hypothesis that differential specialization on habitat space and food resources has contributed importantly to the striking Cenozoic adaptive radiation of *Conus*. As the field research for this as yet unpublished study was carried out in the mid-20th century, it also provides baseline data for future studies of how changing marine environmental conditions affect coral reef-associated biotas.

Marine Molluscs Session, Part II

A contrast of population structure of *Pyganodon grandis* between Lake Erie and its tributaries

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Freshwater mussels (Bivalvia: Unionoida) have declined throughout their range, highlighting the need to better characterize genetic structure, as for many species, evidence of divergence or inbreeding may be masked by the longevity of mussels and large historical population sizes. Thus, studies are needed on species that remain abundant. Here I report preliminary population genetic results for a fast breeding common species, *Pyganodon grandis*, for which population sizes remain good, but variable, and often of low abundance in flowing water. The area of study was the numerous small southern tributaries of Lake Erie, where this species is ubiquitous. Recent results on a fragment of the mtDNA CO1 gene suggest that Lake Erie composed a historically continuous population dominated by a single haplotype, even though extant populations are now reduced. The same common haplotype occurs at a frequency near 50% in the tributary rivers compared to 85% in Lake Erie. Haplotype diversity is therefore greater in rivers, possibly from multiple entry points to streams, such as headwater capture from the Ohio River watershed. Differentiation among river populations is suggested even in this species, for which abundant host fish may create some of the highest levels of gene flow in the family. Of note is the sporadic occurrence of an anomalous and highly divergent haplotype lineage, termed “type A” in contrast to the standard “type B”, suggesting that multiple jump dispersal events contribute to a complex population structure in the region. Microsatellite loci, presently under development, may soon help characterize whether isolation among streams is accompanied by reduced genetic variation within populations.

Great Lakes Malacology Session, Part II

To invade as fast as a slug!

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When thinking about the invasions of North America, slow dispersers such as slugs are definitely not the first species that come to mind. Nevertheless, the European species complex of *Arion subfuscus* - *A. fuscus* has had an impressive invasion history. This complex is composed of the most common exotic slugs of North America and occupies multiple habitats but identities, origins and distribution of its members are unknown in a large part of the territory. This study aims therefore to assess the diversity of mitochondrial lineages of this species complex to determine if we are facing a single lineage or multiple. Additionally, their ecology is unknown; members of the complex could either be habitat generalists or habitat specialists. More than 400 specimens collected throughout Québec were analysed and their mitochondrial genome compared to known European genomic sequences. Several mitochondrial lineages of *A. subfuscus* were detected, revealing punctual introductions from distinct European regions. By contrast, *A. fuscus* is widespread and only two haplotypes differing by a single mutation were detected, suggesting a common origin prior to introduction. In a systematic sampling across a region, this invasive species was present in all types of habitats, ranging from natural to disturbed. From the 60's when only a few localized populations were found, this slug is now widespread and common throughout Québec. This study is a front-runner in revealing the impressive expansion of its range within the last 45 years.

Molecular and morphometric data suggest the presence of a neglected species in the marine gastropod genus *Conus*

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Understanding patterns of marine diversity is critical in shaping evolutionary theory. However, interpreting relationships of marine taxa is challenging and many groups remain poorly understood. In the course of evaluating patterns of genetic diversity of members of the marine gastropod family Conidae, I discovered that individuals of *Conus flavidus* from Hawaii possess mitochondrial haplotypes that are more similar to haplotypes of *C. frigidus* than to those of *C. flavidus* from elsewhere in the Indo-West Pacific. In particular, for gene trees constructed from sequences of mitochondrial gene regions, members of these three groups (i.e., *C. flavidus* from Hawaii and *C. frigidus* from American Samoa, Vanuatu, Madagascar, and Reunion and *C. flavidus* from Guam, American Samoa, and French Polynesia) occur in reciprocally monophyletic clades. On the contrary, sequences of a region of a nuclear gene are identical among all examined *C. flavidus* individuals and these are distinct from sequences of *C. frigidus*. In addition, sequences of another nuclear gene region and morphometric characters of individuals of *Conus flavidus* from Hawaii are more similar to those of *C. flavidus* from other locations than *C. frigidus*. Taken together, these results suggest that the population of *C. flavidus* at Hawaii represents a distinct species that may have already been (aptly) described in 1861 by Pease as *Conus neglectus* (and later renamed by Brazier in 1877 as *Conus peasei*). Moreover, based on the contradictory relationships inferred from analyses of mitochondrial and nuclear sequences (and morphometric data), *C. peasei* may have originated through past hybridization among the ancestral lineages that gave rise to *C. flavidus* and *C. frigidus*.

Poster Session

The Colin Redfern Collection at the Bailey-Matthews National Shell Museum

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In early 2015, Colin Redfern (CR) completed the donation of his collection of Bahamian mollusks to the Bailey-Matthews National Shell Museum (BMSM) on Sanibel Island. Material donated comprises 9046 lots of dry (7942) and preserved (1604) marine mollusks, all collected by CR and collaborators in Abaco and neighboring areas over a period of at least four decades. The collection certainly represents a substantial portion of the shallow-water molluscan diversity of the northeastern Bahamas. All lots have been cataloged by CR into the BMSM catalogue. The collection's importance is enhanced by the fact that part of the material has been illustrated in CR's *Bahamian Seashells* books (1161 species in the 2011 version): the books constitute a veritable illustrated catalogue of the CR collection. The collection also includes a number of species in need of formal descriptions and a large number of types of taxa named in recent decades. The material is available for study and BMSM is already sending lots on loan to specialists in the US and abroad.

Marine Molluscs Session, Part I

Great Lakes Invasives TCN: Documenting the occurrence of invasive molluscs threatening the Great Lakes Basin

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Invasion of non-indigenous species including molluscs represents one of the greatest threats to the health of Great Lakes ecosystems. Not only have catastrophic impacts of several invasives been well documented (e.g., Asiatic clams and zebra mussels), but the number of taxa on the invasives “watchlist” has also grown steadily. Voucher specimens held in natural history museums are a primary source of data for tracking and monitoring the spread of invasives. As part of a collaborative effort involving more than 25 institutions and more than 1.73 million specimens representing 2,550 species of exotic fish, clams, snails, mussels, algae, plants, and their congeners, the UMMZ Mollusk Division is currently digitizing approximately 25,000 catalogued lots that roughly comprise 390,000 specimens of molluscs. Data derived from digitized historic specimens and high-resolution images will be available through a national resource (iDigBio.org). This information will improve the ability of both experts and the general public to more accurately distinguish invasive species from their native congeners.

Poster Session

The phylogenetics and conservation status of the Hawaiian Helicinidae

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Hawaii features an extraordinary diversity of land snails, with over 750 species that are 99% endemic. Like most of the ten land snail families of Hawaii, the Helicinidae are severely imperiled and poorly studied. Marie C. Neal monographed the Hawaiian Helicinidae in 1934, recognizing 14 species and 43 varieties in *Pleuropoma* and *Orobophana*. Since then, almost no data on their distributions, systematics or conservation status have been published. Many Hawaiian land snails have declined precipitously, and Solem hypothesized that most Hawaiian Helicinidae were extinct as of 1990. To investigate this claim, we surveyed 884 sites across the six main Hawaiian Islands, including sites where Helicinidae were historically recorded. Live populations were recorded at nine sites (two on Kauai, six on Oahu, and one on Maui). Phylogenetic analyses of mitochondrial (COI, 16S) and nuclear (28S) markers in combination with analyses of type materials, original descriptions, and morphology were used to identify distinct lineages and place names on taxa. We recovered nine taxa belonging to *Pleuropoma*: *P. kauaiensis*, two varieties of *P. oahuensis*, and five varieties of *P. laciniosa*, some of which may be distinct species. Examination of evolutionary relationships indicates a need for systematic revision of the family in Hawaii. If we consider described varieties as distinct species, an assumption supported by our analyses, as much as 83.9% of species are extinct. There has also been a massive contraction in range, with complete extirpation occurring for islands of Lanai, Molokai, and Hawaii, and distributions being far smaller than historically recorded for Kauai, Oahu, and Maui. Because the conservation status of the Hawaiian Helicinidae's is critical, immediate action is needed to protect them, such as listing and management of all extant taxa under the Endangered Species Act. However, additional data are needed to have these taxa and many others considered for listing.

Pacific Island Land Snails Session

The living solar panel - Evolution of photosymbiosis in marine cockles

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Photosymbiotic associations between invertebrate hosts and photosynthetic dinoflagellates are crucial to the trophic and structural integrity of marine ecosystems. Although extensive efforts have been devoted to study the short-term ecological interactions between animal hosts and their symbionts, long-term evolutionary dynamics of photosymbiosis in many marine metazoans are less well understood. The marine bivalve family Cardiidae contains two lineages that include photosymbiotic taxa: the infamous giant clams (Subfamily Tridacninae) and the heart cockles (Subfamily Fraginae). To date, it is unclear whether photosymbiosis in Tridacninae and Fraginae resemble convergent evolution or shared ancestral characters. Both groups host zooxanthellae intercellularly in an elaborate network of primary, secondary and tertiary zooxanthellar tubes. However, shell morphologies in giant clam species are relatively uniform whereas photosymbiotic taxa in Fraginae exhibit diverse adaptations to photosymbiosis, including greatly flattened, solar-panel-like shells and lens-like microstructural shell features. In this study, we established a backbone phylogeny for Cardiidae utilizing novel transcriptome data from 4 Tridacninae species, 8 Fraginae taxa and 7 other cardiids. We used phylogenomic approaches to resolve the phylogenetic relationship between *Tridacna* and Fraginae, and to demonstrate how photosymbiosis evolved within the marine bivalve family Cardiidae.

Phylogenetics Session

Population genetics and phylogenetic placement of the federally endangered Iowa Pleistocene snail *Discus macclintocki* (Mollusca: Gastropoda)

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Biological diversity is an important component of ecosystems, affecting their health and stability. Although loss of diversity via local extinction can occur naturally because of environmental changes, such as the climatic shifts that accompanied glacial recessions in North America at the end of the Pleistocene Epoch, diversity loss has increased today due to contributions from anthropogenic factors. Some relictual species experience both climatic and human pressures, such as the Iowa Pleistocene snail (*Discus macclintocki*), which is currently on the Federal endangered species list. *Discus macclintocki* maintains an extremely narrow temperature tolerance compared to closely related and more widespread congeners. It is currently only found in the Driftless Area of Iowa and Illinois, on north-facing algal (cold air) talus slopes, and is most active between 10° and 15°C. *Discus macclintocki*'s habitat restrictions, small size (5 – 8 mm) and limited dispersal ability have been sources of concern over the viability of the remaining 38 known populations. Our lab is in the process of conducting population genetic analyses of known populations of *D. macclintocki* using both mitochondrial DNA and nuclear microsatellite markers. Presented here are preliminary population genetic analyses using mitochondrial 16S DNA sequences, as well as a preliminary phylogenetic assessment of the placement of *D. macclintocki* relative to other species of *Discus*.

Poster Session

How does the eastern oyster cope with living as an almost closed system during winter?

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At its northernmost range limit (48°N), the eastern oyster *Crassostrea virginica* spends about four months a year in water < 0°C. Due to the difficulty of sampling under a thick ice cover, little is known on the physiology and behavior of oysters living in cold water. Oysters held in tanks in water < 0°C showed bouts of minimal shell opening (mean gape angle of 0.49°) every few days and therefore lived as almost closed systems. Oysters held under the ice on the bottom of a bay in New Brunswick (Canada) showed signs of increasing energy demands as winter progressed: the concentration of lipids and proteins in the digestive gland decreased, as did the mass of this organ. Even though minimal, shell opening appeared to allow some exchanges with the surrounding water. Indeed, changes in pH (from 7.7 to 7.0) and ammonia concentration (from 0.12 mM to 0.80 mM) in the intra-pallial fluid were moderate, considering the prolonged exposure to winter conditions. Acidification of the intra-pallial fluid and mobilization of lipids respectively suggest that both anaerobic and aerobic pathways were solicited. Albeit moderate, the drop in pH would be sufficient to accelerate the dissolution rate of the shell. The increasing use of energy reserves could be partly due to the intensification of detoxification mechanisms as ammonia accumulated. When water warmed up to 5°C, in mid-April, the oysters abruptly opened their valves to maximum angles (about 5.88°). Ammonia concentration and pH returned to early winter values and protein concentration rose from 59 to 81 mg/g wet digestive gland. This northern population of *C. virginica* showed no adaptation of gaping behavior to cold temperature. However, its ability to use various nutrient substrates and to minimize the deleterious effects of catabolic by-products would allow survival in prolonged extreme cold conditions.

Marine Molluscs Session, Part II

The biodiversity of the southern Gulf of Mexico project: Filling gaps and establishing baselines

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The Gulf of Mexico is a semi-enclosed, large marine ecosystem, with warm-temperate waters (Carolinian Province) in the north and tropical waters (Caribbean Province) in the south. A comprehensive biotic inventory of the entire Gulf sponsored by the Harte Research Institute (HRI) completed in 2009 revealed a diverse biota, with 15,419 species, of which 2,455 were mollusks. However, the current inventory of mollusks suggests that the southwest quadrant is the least diverse in the Gulf, despite of having the most extensive coral reefs in the Gulf. Nearly half of the mollusks are not reported from SW. Crustaceans, sponges, and other taxa have similar biodiversity patterns, while a few taxa such as rotifers and tardigrades are entirely missing or seriously underreported (e.g., platyhelminthes) from the SW quadrant.

A new project, also sponsored by HRI and in collaboration with researchers from Mexico, Brazil, Colombia, USA, and other countries, aims to fill gaps of knowledge and to establish biodiversity baselines in the southern Gulf, focusing on the Campeche Bank region, among other goals. The effort is particularly timely because Mexico is getting ready to greatly expand oil and gas exploration in the region. Several expeditions to reefs and banks in the Campeche Bank are planned over the next three years to collect marine invertebrates in the following taxa: sponges, hydrozoans, anthozoans, platyhelminthes, mollusks, echinoderms, crustaceans, bryozoans, and ascideans. Among the mollusks, it is expected that particularly nudibranchs and micromollusks may yield many new records from the region.

Poster Session

Some thoughts on the long-term survival prospects of Partulidae

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The current status of partulid tree snails epitomizes both the worst and the best aspects of human conservation impact. In recent decades, partulids have experienced dramatic population reduction and, in many cases, extirpation/extinction across much of their vast collective range. This has been largely driven by the deliberate introduction of continental predators as misguided biological control agents across Oceania – a process that has continued to unfold in an unregulated fashion long after its harmful effects have been documented. On the other hand, partulids have benefited from the establishment of the exemplary International Partulid Programme (one of the first invertebrate captive breeding programs) that has undoubtedly saved a number of species from extinction. Nevertheless, captive breeding is a stopgap measure that has not been uniformly successful and that is unlikely to be sustainable indefinitely. Given that, how might this endemic Pacific Island radiation be conserved? Present reintroduction events aim to reintroduce captive snails to artificially protected “predator enclosures” in their endemic ranges that may be politically attractive but are clearly unsustainable (at least on biologically-meaningful timescales). New ecological data on persistence of partulids in the wild, and lessons from parallel conservation efforts involving other taxa, provide some clues on how it might be possible for at least some partulids to persist in Oceania.

Pacific Island Land Snails Session

Can invasive molluscs replace ecological function of lost freshwater biodiversity?

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Freshwater molluscs are among the most endangered species in freshwaters. At the same time, we see that molluscs are overrepresented among invading species relative to their biodiversity. Most scientists agree that the impacts of introduced species can be harmful to ecosystems, and carry large economic costs for society. Recently, there has been a movement to suggest that the impacts of introduced species has been overemphasized, and that there is substantial value to adding introduced species to communities. We tested whether invasive molluscs can replace the ecosystem functions that are being lost as we continue to lose freshwater molluscan biodiversity. Our analysis revealed that for both bivalves and gastropods, the families of recently extinct, endangered, and imperiled species differ from those for exotic species (Table 2). While the unique North American diversity of Unionidae (Bivalvia), and Pleuroceridae and Hydrobiidae (Gastropoda) are rapidly declining, common exotic species of Ampullariidae (Gastropoda), *Dreissena* spp., and *Corbicula* (Bivalvia) are spreading at extremely high rates. We also found that exotic and native transplanted molluscs are not only phylogenetically different than recently extinct, endangered, and imperiled species, but also occupy different habitats. Therefore, the introduction of exotic species cannot compensate for the loss of biodiversity; extinctions of native species has largely occurred in streams and rivers, while introductions are typically in lakes and reservoirs.

Land snail conservation in Mid-Atlantic USA states: Imperilment ranks and recovery plans

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Land snails are one of the most endangered groups of organisms worldwide. In 2002, more than 50% of mollusks on the IUCN Red List of Threatened Species were land snails. This talk describes efforts toward conserving land snails in the Mid-Atlantic USA states of Pennsylvania and Virginia. Priority for conservation of land snails differs among states. Virginia has long recognized and supported research and conservation efforts on its imperiled land snails. In contrast, Pennsylvania only recently began to recognize its imperiled land snails. These differences between the two states might reflect real differences in degree of imperilment of the snail fauna. Pennsylvania lacks any endemic or federally recognized land snail species of concern. In contrast, the greater number of recognized land snails of concern in Virginia (five endemic species, one of which is federally endangered) is likely due to its rugged topography, abundant limestone, and less extensive glacial history. However, differences also likely reflect contrasting priorities among state agencies. While the Virginia Department of Game and Inland Fisheries takes responsibility for terrestrial invertebrates, none of Pennsylvania's three state biotic agencies takes responsibility for terrestrial invertebrates. Recent efforts have dramatically improved knowledge of land snail distributions in Pennsylvania and collaboration with the Natural Heritage Program produced, for the first time, justifiable imperilment ranks for land snails. Consequently, land snails of concern have been included in the state wildlife action plan, from which funding can help prevent species from becoming endangered through research, management, and recovery efforts. In Virginia, land snail conservation efforts are ahead of those in Pennsylvania. Recovery plans are being written and updated. Recovery plans summarize distribution and survival status of species of concern and list actions to be taken. Possible actions can include protecting habitat, surveying potential habitat for new populations, monitoring existing populations, and establishing new populations.

Conservation Session

Terrestrial gastropods of South Fox Island, Leelanau County, Lake Michigan, Michigan, USA

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Published papers about land snails on the islands of the Great Lakes exist for only six islands, although more than 565 islands exist in the upper three Great Lakes (Lakes Superior, Michigan, and Huron). No publications exist on the land snails of the 12 main islands of the Beaver Island archipelago off the northwest coast of Michigan's Lower Peninsula, despite regular ferry access and permanent human habitation on two of them. Ongoing biogeographical investigation comparing land snails on these islands and the adjacent mainland addresses how glacial history of the area influenced snail occurrences. This talk contributes to this larger biogeographical study by presenting information on land snails from one of the islands of the Beaver Island Archipelago, South Fox Island. Visual search and leaf litter sampling found more than 37 species at 14 stations. The three main habitats were beech and sugar maple forest, white cedar forest, and meadow. Some species appeared to be restricted to certain habitats. South Fox Island contains some of the northernmost occurrences of two minute species: *Carychium nannodes* and *Guppya sterkii*. Perhaps climate tempering by the surrounding lake could keep the area warmer in the winter and could contribute to these northerly distributions. As has been noted for some other islands in northern Lake Michigan, certain larger (>15 mm) species found on the adjacent mainland are absent from South Fox Island. While the more cold-adapted *Anguispira alternata* and *Neohelix albolabris* are present on both the adjacent mainland and South Fox Island, the more warm-adapted *Haplotrema concavum* and *Mesodon thyroideus* are present on the mainland but absent from the Island. These patterns of distribution are consistent with a hypothesis that the sequences of glacial history, island development, and snail colonization influenced modern snail distributions.

Great Lakes Malacology Session, Part II

Cannibalism, autotomy, and the sensory ecology of prey detection in the intertidal olive shell, *Agaronia propatula*

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Olive shells (Olividae; Caenogastropoda) are scavengers and/or predators in tropical and subtropical coastal marine environments. Their prey capture behavior is complex and includes the deposition of the prey in a pouch formed transiently by the posterior metapodium. Members of the genus *Oliva* are the best-known species, but the direct observation and the performance of experiments in their natural environment is hampered by their preferred location in the subtidal zone. In contrast, members of the genus *Agaronia* have specialized for life in the intertidal zone of sandy beaches, and therefore lend themselves to behavioral and ecological field studies. In this presentation, we summarize our recent and ongoing research on *Agaronia propatula* in El Salvador and Costa Rica, and demonstrate their characteristic behavior in videos. We characterized the tidal migrations and the sensory abilities that enable *A. propatula* to find, identify, and subdue potential prey. In contrast to *Oliva* species, *A. propatula* voluntarily sheds parts of its foot when molested (autotomy). Since cannibalism is frequent in the species, we tested the hypothesis that autotomy is a defense against intraspecific aggression, but found no conclusive support. The role of *A. propatula* as an opportunistic key predator on Central American beach ecosystems will be discussed.

Marine Molluscs Session, Part I

Phylogeographic patterns in some Thai freshwater mussels

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The contemporary river systems of Thailand are a reflection of a series of historic rearrangements driven by various climatic fluctuations and geological events. Sea level rise and fall dramatically changed the size of watersheds, while tectonic uplifts caused major watershed to reverse their flow. We used a molecular approach to explore how such historical events may have shaped freshwater mussel diversity and distribution. Preliminary data resolve a mosaic of phylogeographic patterns some of which may be explained by historic and modern-day river connections, while others may be products of differences in life history. Our results are discussed in the context of the geological, climatic, and ecological factors that shaped freshwater mussel diversity and distributions in Thailand.

Contributed Talks Session

Genetic isolation and homogenization: potential effects of waterfalls and man-made canals on the population genetic structure of freshwater mussels (Family Unionidae)

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Dispersal, the movement of individuals from their natal population to their breeding population, has important ecological and evolutionary consequences. Dispersal of freshwater species like mussels (Family Unionidae) that spend most of their lifetime buried in sediments can be limited. However, unionids have a unique life history that involves parasitism on host fish species for larval development and dispersal. Dispersal is also affected by river connections and barriers like dams and waterfalls. The configuration of natural waterfalls, canals and dams of the lower Great Lakes watershed illustrates how landscape structures affect dispersal. The objectives of this project were to: 1) assess the spatial scale of dispersal of the common unionid species *Lampsilis siliquoidea* in the western Lake Ontario watershed, 2) describe genetic diversity within populations, 3) determine the effects on dispersal of natural barriers such as waterfalls and 4) corridors such as man-made canals. Seven microsatellite loci were used to determine genetic diversity and population structure. Populations above waterfalls were genetically differentiated from the population within the same stream below waterfalls and had lower genetic diversity. Waterfalls may serve as natural experiments to assess the long term effects of dams on species dispersal and genetic diversity. There was low genetic differentiation among populations below waterfalls from different streams suggesting that canals such as the Erie Canal may provide a corridor for dispersal between streams that otherwise would be isolated. Canals that connect waterways that were isolated in the past can cause genetic homogenization which may have positive or negative ecological and evolutionary impacts on aquatic species. Determination of gene flow and genetic diversity at the population level can provide an understanding of the natural populations' genetic variability and therefore, their ability to withstand environmental perturbations, their potential for resistance to local extinction and their natural rate of recovery.

Great Lakes Malacology Session, Part I

The eye-independent response of *Octopus* chromatophores to light may rely on the same deeply conserved r-opsin phototransduction genes used in octopus eyes

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How do novel behaviors evolve? Do they use newly evolved underpinnings, or are pre-existing components repurposed for novel behavioral functions? Cephalopods like octopuses and squids use novel pigmented organs embedded in their skin, called chromatophores, to rapidly change the color and pattern of their skin for camouflage and communication. While changes in body patterning rely on eyesight, we have also found that light causes the chromatophores in isolated *Octopus bimaculoides* skin to expand without eye or CNS input. We call this behavior Light-Activated Chromatophore Expansion or LACE. To identify potential molecular mechanisms that may underlie LACE, we found that the same r-opsin phototransduction genes used in eyes are expressed in octopus skin, and identified peripheral sensory neurons in the skin that express r-opsin. LACE is maximally sensitive to blue light (~470-480 nm) and has a λ max of 480, very close to the known spectral sensitivity of opsin in octopus eyes. LACE suggests that octopus skin is intrinsically sensitive to light, and that this dispersed light sense could contribute to their unique and novel camouflage abilities. Further, r-opsin phototransduction gene expression in octopus skin and similar spectral sensitivities between octopus eye opsin and the light sensitive protein underlying LACE suggests that a common molecular mechanism for light detection in eyes may have been co-opted for light sensing in octopus skin.

Early Career Malacologists Symposium

Particle surface properties and their effect on particle capture in suspension-feeding bivalve molluscs

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The capabilities of suspension-feeding bivalve molluscs to ingest or reject certain particles selectively are well known. Recently, physicochemical properties of particles have been shown to play a role in mediating post-capture selection in these molluscs. In particular, surface charge and particle wettability, a proxy for surface hydrophobic forces, can be used by different bivalve species as qualifiers for selection. Although the role of surface properties in post-capture selection is being defined, how these physicochemical factors affect capture has been little studied. The goal of this project was to address how non-specific chemical interactions affect particle capture. To this end, a series of adhesion assays and particle capture experiments were designed to assess the mechanisms of particle discrimination at the time of capture. First, mucus from the pallial organs of the blue mussel, *Mytilus edulis*, and the eastern oyster, *Crassostrea virginica*, were separately isolated and fixed onto microscope slides. Slides with adhered mucus were then incubated with a solution containing previously characterized particles whose surface properties have been manipulated. Adhesion of the particles to each type of pallial mucus was then quantified. Preliminary results suggest some particles are more likely to adhere than others. Multivariate analyses are ongoing to determine if certain particle types differentially adhere to the mucus extracted from each pallial organ. Secondly, previously characterized particles of different sizes (2, 3, 4.5, 6, 10- μm), both unbound and covalently bound with different neoglycoproteins (N-acetyl-glucosamide, D-mannose), or bovine serum albumin (BSA) were directly delivered to the inhalant siphon of mussels. The exhalent water was then sampled, and capture efficiencies calculated. Preliminary results suggest that in the smaller size ranges, the surface characteristics and presence of epicellular sugars can affect capture efficiency.

Early Career Malacologists Symposium

Building snail shells: the role of *dpp* in shell coiling of a caenogastropod

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The gastropod shell has evolved diverse forms and is well preserved in the fossil record, inspiring a century of research on the rules that guide shell coiling. To understand how selection has shaped the diversity of shell forms over time, we must link models of morphology to the shell's underlying genetic basis. Shimizu et al. (EvoDevo 2013, 4:15) noted that *dpp* (BMP2/4 homolog) expression was enriched in the direction of shell coiling in the shell gland of pond snails, but was expressed equally around the gland in limpets, a lineage of gastropods characterized by their secondarily derived non-coiling shells. Shimizu and colleagues hypothesize that changes in *dpp* activity may underlie the numerous evolutionary transitions from coiled to limpet-like shells seen across Gastropoda. Functional tests of their model remain to be performed, and *dpp* needs to be examined across gastropod lineages to test for the generality of this mechanism. The developmental model system *Crepidula fornicata* (the common slipper shell) belongs to Caenogastropoda, a species-rich branch of gastropods that have not yet been examined for *dpp* expression. Like the distantly related non-coiling limpets of Shimizu et al.'s 2013 study, *Crepidula* has convergently evolved a flattened limpet-like shell morphology, yet it does have a coil of less than one whorl. We characterize *dpp* expression in *Crepidula* using in situ hybridization from the earliest stages of shell gland development through growth of the larval shell and the early post-metamorphic shell. Effects of knock-down on *dpp* signaling are reported as well as a preliminary assessment of the proposed role of cell proliferation in shell patterning. Future work includes more detailed perturbations of *dpp* signaling, expansion to a sister species of *Crepidula fornicata* with a different shell morphology, and characterization of other shell patterning genes by leveraging new RNA-seq data.

Early Career Malacologists Symposium

Build-up of diplommatinid land snails and conservation context in the western Pacific Micronesian islands of Belau (Republic of Palau, Oceania)

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About half of the known land snail fauna of Belau are diplommatinids: minute leaf litter- or limestone karst-dwelling species perhaps best-known from Belau's famous mushroom-shaped "Rock Islands." Molecular data suggest that species have not shifted between general habitat types (leaf litter vs. rocks) within islands, as would be predicted in adaptive radiation, but rather have built up within each of these two habitat types. Diplommatinids' geographic distributions bear the imprint of extinction on a geological timescale. Ongoing human development over the last hundred years has also left its mark on diplommatinids, but a combining data from endemic partulids and other more readily assessed snails is important for moving forward with a land snail conservation program in Belau, and elsewhere in Micronesia.

Incongruencies between geometric morphometrics and DNA barcodes in delineating species of *Pyganodon* mussels (Bivalvia: Unionidae)

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Conservation of the imperiled diversity of freshwater mussels (unionids) is paramount to preserving the health and quality of North American freshwater ecosystems. An impediment to conserving this diversity remains the correct identification of closely related species. Two inland lakes on Beaver Island in Lake Michigan house thriving populations of *Pyganodon grandis* (Giant Floater) and *Pyganodon lacustris* (Lake Floater). *Pyganodon grandis* and *P. lacustris* in these lakes have only been easily distinguishable through use of DNA barcoding. Using geometric morphometric techniques, morphological differences between these two morphologically similar species of *Pyganodon* were measured. Procrustes superimposition of twenty-two landmarks along the dorsal and ventral margins of the shells yielded two distinct morphometric groupings using principal components analysis and cluster analysis. Mitochondrial DNA barcoding (COI) was used to confirm the species identity of a subset of the mussels collected. The results of the mtDNA barcoding were largely consistent with the morphometric analysis; however, there was evidence of possible hybridization between these two species. The utility of modern morphometric techniques combined with DNA barcoding holds great promise in assessing species identifications and revealing cryptic diversity and hybridization among closely related unionid species.

Poster Session

Reconciling morphology and molecules: Developing a comprehensive phylogeny for the Pectinidae (Bivalvia) to accurately assess biological diversity in the Indo-Pacific

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Scallops (Pectinidae Rafinesque, 1815) are one of the most morphologically, behaviorally, and biologically diverse family of bivalved molluscs, but lack a well-supported, comprehensive phylogenetic hypothesis. While the results from early molecular phylogenetic analyses of the Pectinidae appeared to be congruent with morphologically-based classification systems and gave researchers a false sense that the relationships within the scallops were predictable and robust, as molecular phylogenetic studies have increased the number of species sampled and taxon density, lineages that appear to share similar morphological traits formed unanticipated relationships with other species, indicating a great deal of morphological convergence. My lab developed a global molecular phylogeny for 148 species of scallops using two mitochondrial (12S rRNA, 16S rRNA) and three nuclear (18S rRNA, 28S rRNA, Histone H3) genes. We compared our phylogenetic hypotheses to the most widely used classification system. While we found congruence between the morphological-based classification system and our molecular phylogenetic hypothesis for many of the subfamilies and tribes of the Pectinidae, the subfamily Chlamydinae and its tribes were not monophyletic. This finding has great implications for our understanding of pectinid evolution because the Chlamydinae contains the majority of named species and the greatest diversity of shell shape. Furthermore, we found that convergence in shell shape masks biological diversity, especially Indo-Pacific lineages. Finally, our analyses uncovered increased levels of endemism for Australian and East African Coastal biogeographic provinces of the western Pacific Ocean.

Phylogenetics Session

InvertEBase: Digitizing land and freshwater mollusks of the eastern United States

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North America is projected to experience profound biodiversity change that will have extraordinary and unpredictable consequences for all U.S. ecosystems. Understanding the scope of that change requires a high-resolution picture of preexisting biodiversity levels. Natural history museum collections contain that information, but not in a form that is readily accessible to a broad variety of end users. InvertEBase is a new Thematic Collections Network in iDigBio, the National Resource for Advancing Digitization of Biodiversity Collections (ADBC) and is comprised of 10 mollusk and arthropod collections in six major U.S. natural history museums. The shared goal of all InvertEBase participants is rapid data entry and networking of georeferenced locality data to form a solid foundation for distribution mapping and to examine change over time due to large scale perturbations (*e.g.*, climate change, land-use change). Over 3 million specimens of terrestrial and freshwater mollusks and arthropods of eastern North America will be digitized and mobilized on the web via the Symbiota webportal (invertebase.org). Freshwater mollusks are the focus of Project Year 1 at the Field Museum (emphasis on unionids), the University of Michigan Museum of Zoology (emphasis on gastropods), and the Delaware Museum of Natural History (emphasis on unionids). This collaborative National Science Foundation award (NSF EF 14-02667, EF 14-02697, EF 14-04964, and others) is made as part of the National Resource for Digitization of Biological Collections through the Advancing Digitization of Biological Collections program and all data resulting from this award will be available through the national resource (iDigBio.org).

Poster Session

Diversity of Hawaiian Microcystinae (Gastropoda: Stylommatophora: Helicarionoidea) 75 years after H. B. Baker

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Despite its isolation in the North Pacific, Hawaii has an extraordinarily diverse land snail fauna with 750+ species, 99% of which are endemic. One of the best studied groups of Hawaiian land snails are the 60 endemic species of Microcystinae which were the subject of an extensive monograph by H. B. Baker in 1940 which used shell, radular and genital morphology to define species and species groups. Hawaiian species were placed in three of four Pacific genera, although Baker expressed some doubts in these groupings because of several presumed homoplasies. To better understand the diversity and phylogenetic relationships of extant species of Microcystinae we surveyed more than 800 sites, recording approximately 1500 specimens from the six largest islands. A preliminary phylogeny reconstructed using a fragment of COI and 16S from these specimens recovered more than 40 monophyletic lineages that have unique morphological characters and are interpreted as distinct species. However, not all of these lineages can be referred to named species and some are likely to be new cryptic species. Of the three genera present in Hawaii *Kaala* is monophyletic, while *Hiona* appears to be polyphyletic with respect to *Philonesia*. Microcystinae appear to be among the more resilient of Hawaii's native snails which have suffered estimated extinction rates of 50-90%. Continued sampling in Hawaii and additional nuclear markers will help to more fully resolve the diversity, phylogenetic relationships and evolutionary history of this group of snails in Hawaii. Uncovering this diversity remains important because populations appear to be declining as a result of introduced species, especially predators as well as other environmental perturbations which continue to impact the Hawaiian Islands.

Pacific Island Land Snails Session

Population genetic congruence between six freshwater mussels and their host, freshwater drum (*Aplodinotus grunniens*)

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Unionid mussels disperse via the use of a fish host. As such, their population structure should mirror that of the host, but studies have found this to not always be the case. In my work, I use a group of mussel species that parasitize only one fish - the freshwater drum (*Aplodinotus grunniens*). This single host system should provide a clearer signal of the effect of host movement on mussel dispersal. I use variation in microsatellite markers to compare population genetic structure in six mussel species: *Potamilus alatus*, *Potamilus ohioensis*, *Truncilla truncata*, *Truncilla donaciformis*, *Ellipsaria lineolata*, and *Leptodea fragilis*), as well as freshwater drum. My work takes place in the state of Minnesota and spans 4 major drainage systems: St. Croix, Minnesota, Mississippi and Red River. I first look for the presence of structure within a species, and then compare the structure within mussel species to their host and to each other. I present here the results of my first field season and preliminary findings.

Poster Session

Hidden diversity in plain sight: Genetic confirmation of putative Louisiana fatmucket in Illinois

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The range of the Louisiana fatmucket (*Lampsilis hydiana*) spans watersheds in Texas, northward to southern Arkansas, and eastward to western Mississippi. However, specimens with morphological similarities to the Louisiana fatmucket have been collected in watersheds in southern and south-central Illinois for several decades and were presumed to be strangely shaped fatmuckets (*L. siliquoidea*). In order to determine if the two species occur in Illinois, specimens were collected from throughout the state and analyzed genetically using DNA sequences of the mitochondrial *cox1* and *nad1* genes. Phylogenetic analysis yielded two genetically distinct clades that support the recognition of two different species – *L. siliquoidea* and putative *L. hydiana*. The presence of *L. hydiana* in Illinois represents a substantial range expansion, so it is imperative that we obtain topotype material to determine if putative Illinois *L. hydiana* is indeed *L. hydiana* or another closely related species. General conservation implications are discussed.

Conservation Session

A molecular phylogeny of the Tonnoidea

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The Tonnoidea is a moderately diverse group, with a little under 400 species living mostly in (sub)tropical waters on the continental shelf, and with a few species living in depths in excess of 2,000 meters. Among biologists, they are known for their teleplanic larvae and for their ability to secrete sulfuric acid; many feed on echinoderms, famously including the crown-of-thorns starfish. Among shell collectors, the Tonnoidea are popular for including the tuns, frog shells, helmets, tritons and other collectables. Tonnoideans are classified in seven currently accepted families - the “classic” Tonnidae, Cassidae, Ranellidae, Bursidae and Personidae, and the little-known, deep water Laubierinidae and Pisanianuridae. We assembled a 4-gene (COI, 16S, 12S, 28S) mitochondrial and nuclear dataset for ~90 species, representative of the morphological diversity of the superfamily, including such rare and elusive genera as *Akibumia*, *Distorsionella*, *Distorsomina*, *Personopsis*, *Pisanianura*, *Oocorys* and *Thalassocyon*. Bayesian analysis of the concatenated dataset recovered a monophyletic Tonnoidea, with *Ficus* as its sister group; unexpectedly, *Thalassocyon*, currently also classified in the Ficidae, was nested within the ingroup. Among traditionally included families, Tonnidae, Cassidae, Bursidae and Personidae were also supported as monophyletic but, remarkably, the Ranellidae was not, with cymatiids, *Ranella* and *Charonia* dispersed among three distinct clades. The Laubierinidae and Pisanianuridae together form a monophyletic group. Although not all nominal genera, nor even all currently accepted genera, have been included in the analysis, we believe the new phylogeny is stable enough to establish a revised family-level classification of the Tonnoidea. Molecular characters will continue to impact the systematics of the Tonnoidea at genus and species level, and our preliminary results have already disclosed several species complexes. This suggests that, despite their teleplanic larvae, the circumglobal distribution of several tonnoidean species is the result of excessive synonymy.

The Sphaeriidae Collection of Victor Sterki at the Carnegie Museum of Natural History

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The Sphaeriidae (Mollusca: Bivalvia) is a family of freshwater mollusks with world-wide distribution and comprising 150-200 species. These species are well represented in the Palearctic and Nearctic regions. Victor Sterki (1846-1933) was a student of this family and, at the time of his death, was working on and intended to publish a revision of the North American forms. He corresponded with numerous collectors in North America and Europe and amassed a collection of over 12,000 lots of Sphaeriidae. This collection resides at the Carnegie Museum. Sterki rarely designated holotypes for his 160 described taxa so most of his type specimens are syntypes. Most of the type localities represent wide geographical areas with numerous lots. These type lots were not previously identified, separated, and cataloged separately from the bulk of his collection. Decades ago (1940s-1960s), Stanley Brooks and H. B. Herrington studied Sterki's collection and published a number of nude, manuscript names. While we were sorting Sterki's collection, we discovered many additional unpublished label names. Some of these specimens with label names were discovered in another museum's collection. We are currently separating type and potential type lots from the rest of Sterki's sphaeriid collection. To date we have found more than 1700 lots of types or potential types. Once the sorting has been completed, these will be incorporated in an anticipated, comprehensive catalog of type mollusks in the Carnegie Museum's collection. In addition, we anticipate publishing a list of all of Sterki's valid, nude, and label names, with their corresponding modern names. This will help personnel at other institutions to determine the status of their Sterki material and whether they possess type material.

Analysis of morphological variation of the shells of *Argonauta argo* Linnaeus, 1758 and *Argonauta nouryi* Lorois, 1852 (Cephalopoda: Argonautidae) using geometric morphometrics

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Argonauts are a family of pelagic octopuses that inhabit tropical and temperate oceans of the world; they are most commonly recognized by the white showy ‘shells’ of females, commonly known as ‘Paper nautilus’. The taxonomic determination of this group has been based on features of the shells that exhibit great variability. Two species are reported for Mexico: *Argonauta argo* Linnaeus, 1758 and *Argonauta nouryi* Lorois, 1852, both with great shell variability resulting in several synonymies that have been used for different morphotypes commonly treated as different species. However, we demonstrated that it is possible to analyze the morphological variation of these organisms analyzing photographs of argonaut shells with geometric morphometric tools. The objectives of this study are: analyze the morphological variation of the shell in some populations; identify if there are patterns of morphological variation and determine whether it is possible to use the geometric shape of the shell as a taxonomic character that facilitates identification. We analyzed 255 photographs of argonaut shells collected on different years and localities along the peninsula of Baja California Sur. Were used a landmark and semi-landmark-based methodology to obtain shape configurations for each shell and made a consensus shape for posterior analysis. A Principal Component Analysis showed that most of the intrapopulation variability is present on the ornaments of the lateral sides of the shells in both species. A regression analysis showed that the shape changes as size change. F-tests show significant differences in shell shape between years indicating they are temporally differentiated. Finally, a Canonical Variable Analysis grouped significantly one of the three views analyzed of the morphotypes of *A. nouryi* indicating they are not clearly differentiated therefore these are the same species. This work allowed us to obtain a wide view of the variation of the argonaut’s shell in their natural habitat.

Contributed Talks Session

Photosymbiotic Giant Clams are Transformers of Solar Flux

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Giant Tridacnid clams, like reef-building corals, harbor and exchange nutrients with the photosynthetic dinoflagellate Symbiodinium. These clams are also notable for their bright, iridescent color patterns, caused by clam cells called iridocytes. These cells are unusual compared to iridocytes in other taxa, having a structure that is a superposition of sub-wavelength scale layers with a super-wavelength scale sphere. We recently showed that, in combination with a pillared geometry of the dinoflagellates within the clam mantle tissue, these iridocytes function to reshape and propagate incident solar radiance deep into the the system. This phenomenon results in a remarkably deep photic zone inside the animal, producing even illumination at about 10% of the intensity of downwelling sunlight along the sides of the algal pillars. This down-regulation of solar flux relative to irradiances on shallow reefs is approximately what is needed to reduce or eliminate non-photochemical quenching in Symbiodinium. Algae in clam are therefore likely able to use all of the energy present in high-intensity downwelling sunlight for photosynthesis while avoiding the photodamage that would result without this evolved system in place. This talk will outline our initial description of the system, and our ongoing work on the species complex in Palau. We are currently investigating the ecological responsiveness of iridocyte/algal system in various tridacnid species, as well as possible Symbiodinium clade/iridocyte interactions. Insights gained from the clam system may also inform efforts to produce algal-based chemicals and fuels more efficiently

Keynote Address

Size of first sexual maturity in *Brachidontes rodriguezii* (d'Orbigny, 1846) from the southwestern Atlantic Ocean

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The mussel *Brachidontes rodriguezii* (d'Orbigny, 1846) is the most abundant rocky shore intertidal species on the Buenos Aires coast. The intertidal community complexity is related to the presence and development of this mussel. The temporal and space variation of the community structure depend on physical (e.g. temperature, salinity and wave exposition) and biological factors (e.g. reproductive cycle and growth). Reproductive aspects as gametogenesis, spawning events and size at maturity provide valuable information about the biology of species and changes through time and space. The objective of this study was to estimate the size at first maturity of *B. rodriguezii* at artificial hard substrates. A histological determination was done during two consecutive reproductive events during the summers of 2012 and 2013. A total of 335 specimens between 3 and 25 mm in total length were studied. Sexual maturity was related to gonadal activity. Two categories of immature stages were described: undetermined (without gonadal development) and determined (with earlier gonadal development) where the gonad was restricted to the dorsal region of the visceral mass. Meanwhile, gonad of mature males and females was completely developed in both lobes of the mantle and the visceral mass. At 4 mm shell length, oogenesis and spermatogenesis were observed. Minimum sizes at maturity were 6.99 mm for females and 6 mm for males. The size of first maturity for the population, defined as the shell length at which the 50% of the population reach the gonadal maturity, was 8.30 mm for both sexes.

Poster Session

Cryptic and pseudocryptic speciation masks heterobranch sea slug diversity

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Molecular data has revealed unexpected high levels of cryptic and pseudocryptic diversity in heterobranch sea slugs, suggesting that current diversity inventories are grossly underestimating the total numbers of species. Two types of studies have revealed the existence of cryptic or pseudocryptic taxa, 1) assessments of the taxonomic status of circumtropical species, and 2) in-depth revisions of endemic species, including well studied regions such as the Northeastern Pacific Ocean, or well studied taxa. The inability to recognize these taxa has not only resulted in the underestimation of the total diversity of sea slugs, but also in the failure to understand biogeographic patterns, detect invasive species, and possibly other issues with broader implications to other fields of science. In this paper several of this studies are examined and the repercussions for other fields of science are discussed.

What do we know about the marine bivalve fauna in western South America?

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Bivalve Seashells of Western South America is the third in a series of monographs on the eastern Pacific Ocean marine bivalve fauna. The scope of this monograph is the fauna from the Perú-Chile Province, an area that extends from Punta Aguja, Piura, Perú (5.8°S), and continues south to the southern tip of Isla Chiloé, Los Lagos, Chile (43.4°S), considering the species occurring from the intertidal zone to the deep sea. We do not include the Chilean possession of Isla de Pascua [Easter Island], which is very distant from the continent and has an altogether different and unique fauna. Through a literature review and direct examination of specimens in museum and university collections, a marked decrease in known bivalve diversity has been observed when comparing the fauna from the Perú-Chile Province with similar northern latitudes. In the Alaskan, Oregonian and Californian Provinces, we have documented over 470 bivalve species, and 892 species in the Panamic Province, whereas we currently only have records for 201 verified named species from the Perú-Chile Province. In addition we have isolated an additional 38 marine bivalve species that are potentially new to science in the Perú-Chile Province, along with another 26 species which might range into the northern or southern limits of the Province. If the potentially new species and marginally ranged species are included, we would still have only 265 species in the region, some 45% less than the temperate regions in the northern Pacific. One factor that could help to understand the observed decrease in the number of species present in the southeastern Pacific may be under-sampling, especially in deeper waters. This fact is clearly evidenced when considering the high number of new species discovered in the study area. In addition, a very narrow continental shelf throughout much of the Province affords fewer shelf habitats, and may also be leading to a much lower bivalve diversity.

Marine Molluscs Session, Part I

Review of the Helicodiscidae of North Carolina

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Helicodiscidae Pilsbry, 1927 is a family of land snails (Clade Stylommatophora, Superfamily Punctoidea) with small, flat shells with equally spaced whorls and a wide umbilicus. Their sculpture (when present) consists of spiral peripheral ridges called lirae. These lirae are elaborated into “fringes” in several species. Fresh shells are translucent yellow or pale green, and the living animal is completely white, lacking even eye spots. Older shells are chalky white. Various forms of internal teeth are usually present within the aperture; but these may be reabsorbed and replaced as the shell grows. The family as now accepted has only four genera: *Helicodiscus* and *Lucilla* from much of North America, northern Mexico and the Caribbean (and introduced at least as far as Ireland, England and probably Brazil); *Polygyricus* from Virginia, USA; and *Stenopylis* from northern Australia, Indonesia, the Philippines and possibly southern China. Ten of the 27 helicodiscid species known from North America were described by Leslie Hubricht. The eleven species that occur in North Carolina include essentially all the known range of variation in size, number of whorls, shell sculpture, size of umbilicus, as well as number and shape of teeth. These species show a wide range in geographical distribution and habitat specialization, which we will document with diagnostic characters and distribution maps. Two species are of special conservation concern in North Carolina and four others are sufficiently rare that they may be listed in the future.

Conservation Session

Phenotypic variation in the dog whelk, *Nucella lapillus*: An integration of ecology, karyotype, and phenotypic plasticity

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The dogwhelk, *Nucella lapillus*, is an intertidal predator that displays classic ecotypic variation. The divergent shell morphology of ecotypes is adaptive in their respective environments. Dogwhelks from exposed shores typically have small shells with large apertural openings while dogwhelks on protected shores have large, robust shells with thick apertural lips. This morphological variation has been attributed to wave exposure, site-specific and/or chromosomal factors, and phenotypic plasticity. Through morphological analyses we have documented extensive site-specific variation in five morphological traits. Specifically, we found that site-specific factors explain a greater proportion of the variance across the five shell traits we examined. We have also documented the presence of a chromosomal polymorphism in Western Atlantic populations of the dogwhelk that were previously believed to be monomorphically of the $2n = 27$ karyotype. We have found that chromosome number ranges from $2n = 26$ to $2n = 32$ in dogwhelk populations in Maine. Furthermore, we suggest that chromosome number is correlated with morphology and may contribute to the site-specific variation we observed in our morphological survey. Lastly, we transplanted snails of different karyotypes from exposed and protected shores to four different protected shores. The results of this experiment suggest that chromosome number plays a role in the phenotypic response of shell traits to environmental stimuli and that this response is variable depending upon which trait is being examined. We assert that the drastic morphological variation observed in *N. lapillus* is not simply due to wave exposure, but is instead a plastic response mediated by chromosomal factors.

Early Career Malacologists Symposium

Conservation status of North American freshwater mussels

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North America has the greatest diversity of freshwater mussels on Earth (360 taxa). The Mussel Subcommittee (AFS Endangered Species Committee) determined that 74% of the fauna is imperiled (vulnerable, threatened, or endangered) or extinct; only 26% of the fauna is considered currently stable. This assessment is the first to include the entire North American fauna (Canada, the United States, and Mexico), comprising 360 species and subspecies divided among three families: Margaritiferidae (5 taxa), Mycetopodidae (3), and Unionidae (352). The modern extinction rate of freshwater mussels is more than 6,000 times greater than the background extinction rate, the second highest modern extinction rate reported for aquatic biotas. Mussels are vulnerable to multiple threats, most notably habitat alteration and loss, degraded water quality, and effects of nonindigenous species. Although discovery of new species is approaching an asymptote, documentation of the continental fauna is incomplete. Additional research utilizing anatomical, reproductive, and molecular-based data are urgently needed to document phylogenetic and phylogeographic relationships, detect cryptic taxa, document natural host relationships, and ultimately to provide enhanced conservation of these remarkable animals.

Conservation Session

Differentiation of olfactory receptor genes of *Conus* species from different dietary guilds

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The marine gastropod genus *Conus* (cone snails) is notable for its extravagant diversity, a quality that is often attributed to rapid radiation. While *Conus* species have diverged in many aspects, feeding ecology is often the predominant axis of differentiation among species. Because cone snails use venom to capture their prey, it is possible that selection imposed on venom by prey assemblage has facilitated ecological diversification and driven the tremendous radiation for which *Conus* is well known. Chemosensation, however, functions earlier than venoms do in the chronology of prey capture, and may therefore play an equally important, likely complementary, role in ecological diversification. Cone snails rely primarily on their osphradium, an olfactory organ situated just posterior to the siphon in the inhalant current, for chemosensation. I will utilize transcriptomic approaches to characterize olfactory receptor genes of *Conus* species representing major dietary guilds: *Conus miliaris* (vermivore), *Conus ebraeus* (vermivore), *Conus textile* (molluscivore), and *Conus geographus* (piscivore). I will employ phylogenetic approaches to identify olfactory receptor genes and examine the molecular evolution of these genes to evaluate the role of chemosensory evolution in the ecological diversification of *Conus*.

Contributed Talks Session

Systematics and conservation of Hawaiian orthurethrans

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The Orthurethra comprises 19 families and is a derived Stylommatophoran clade, with the Pacific families representing independent colonizations. Orthurethrans in Hawaii are represented by the Amastridae, Achatinellidae, and Pupillidae, whose geographic origins and systematics have been historically poorly understood. The Amastridae, endemic to Hawaii, are the most diverse family of Hawaiian land snails with 325 species in eight genera and two subfamilies. Only 14 species in three genera have been recorded recently and phylogenetics analyses of these remaining taxa support close relationships with the Holarctic Cochlicopidae. About 95% of the amastrids are probably extinct. The Achatinellidae comprises 324 species in the Pacific, with 209 Hawaiian species. Two of the five Hawaiian achatinellid subfamilies are endemic, Achatinellinae and Auriculellinae. Only the former, has been extensively studied and relationships within and conservation status of the family have been neglected. Preliminary results support the monophyly of the family and each of the Hawaiian subfamilies. Although only ca. 50% of the known diversity has been recovered, which includes cryptic species, this indicates higher than previously estimated diversity. The Pupilloidea are Holarctic in origin and are a major Pacific island land snail group with 56 Hawaiian species in six genera and are placed either in Pupillidae or Vertiginidae. Family level classifications differ among authors as do placement of genera. Recent surveys found 23 species in three Hawaiian genera, and ten additional species that are phylogenetically closer to North American *Vertigo*. As several of these are conchologically similar to endemic Hawaiian *Lyropupa* species the provenance of these taxa remains uncertain. Recent surveys indicate that a great deal of diversity in these families is lost, but there remain glimmers of hope as we have rediscovered species previously thought extinct and discovered several new species that await description.

Pacific Island Land Snails Session

Phylogenetic systematics of Hawaiian Succineidae

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Succineids have a global distribution primarily in damp areas close to fresh water, but a few inhabit vegetated patches in dry areas. On Pacific islands, they range from xeric coastal dunes to high elevation rainforests. Estimates of species diversity ranges from 171 to 350 species, with 42 species in Hawaii. The Succineidae originated in the Eocene in an unknown region, although their sister group, the Athoracophoridae, is thought to have originated within the Pacific Islands. Together the two families constitute the monophyletic Elasmognatha within the Stylommatophora, supported by molecular and morphological analyses. The Succineidae are divided into two subfamilies based on the presence or absence of a penial sheath (Succineinae and Catinellinae, respectively), with both subfamilies represented in Hawaii. Surveys of more than 800 sites on six of the largest main Hawaiian Islands recorded more than 2600 individuals representing 26 species from 295 sites. Phylogenetic relationships were assessed through analyses of COI, 16S and 28S sequences from 384 Hawaiian and non-Hawaiian individuals. Preliminary results indicate that the Hawaiian succineids do not form a monophyletic clade and the Hawaiian genera, *Succinea* and *Catinella*, are not reciprocally monophyletic, supporting both multiple colonization of the islands and the need for systematic revision. Biogeographically, all Hawaiian species were found to be single island endemics with the exception of *Succinea caduca*, which occurs on six of the largest main Hawaiian Islands. More than half of the estimated diversity was recovered, but less than half of these have been referred to known described species, hinting that the historical diversity may have been much higher than initially estimated.

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