



2021 Annual Meeting



# American Malacological Society

*Program and Abstracts*



# Program and Abstracts



87<sup>th</sup> Annual Meeting  
American Malacological Society  
Cape Breton, Nova Scotia, Canada

June 14–18, 2021

*Compiled and edited by:*

*Timothy A. Rawlings, Jeff C. Clements, Rod Beresford, Kellie White*

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# Welcome to the 87<sup>th</sup> Annual AMS Meeting

Kwe' pjila'dik! / Dia dhaoibh agus fáilte! / Hello and welcome!

We are thrilled to have you join us for the 87<sup>th</sup> Annual Meeting of the American Malacological Society. Steeped in the deep cultural traditions of the Mi'kmaq people, it is an honour to host the 87<sup>th</sup> AMS meeting at Cape Breton University in Nova Scotia, Canada. We look forward to presenting a stimulating meeting filled with interesting talks and posters and to providing you with a framework for sharing information and ideas, strengthening ongoing collaborations and making new connections, and learning more about molluscs.

We have an exciting program planned, with more than 195 attendees and 108 contributions (talks and posters). The Plenary Session at this year's meeting is being delivered by Dr. Roxanne Beinart from the University of Rhode Island, who will present her current research on the ecology and evolution of symbiotic snail species from hydrothermal vents in the western Pacific. This year's President's Symposium "Freshwater Mussels of the North Atlantic Drainage", organized by André Martel, Kellie White, and David Zanatta, also looks to be very interesting, bringing together a broad group of scientists with research interests spanning the ecology, distribution, evolution, conservation, and restoration of North Atlantic freshwater mussels.

In addition to the President's Symposium, the meeting will feature three other themed symposia:

- 1) "Modern Advances in Molluscan Behaviour" (organized by Jeff Clements and Russell Wyeth) will underscore contemporary advancements in our understanding of complex molluscan behaviours, from chitons to cephalopods.
- 2) "Mollusc-Microbe Interactions" (organized by Suzanne Dufour) will showcase current research examining the interactions between molluscs and microbes.
- 3) "Showcasing Molluscan Research at the Undergraduate Level" (organized by Tim Rawlings, Jeff Clements, and Russell Wyeth) will promote the outstanding research that can be undertaken at the undergraduate level from the perspective of supervisors and students, with a keynote presentation from Dr. Patricia Kelley.

In addition to these symposia, we have several contributed sessions incorporating a wide variety of topics spanning the anatomy and morphology, contemporary and historical diversity, ecology, systematics, and evolution of molluscs. An EDI Discussion will also provide attendees with the opportunity to voice their opinions on how AMS can move towards becoming a more equitable, inclusive, and diverse society.

Despite being virtual, there is no shortage of events to maintain attendee engagement! Following the Plenary talk on Monday, there is a student social, which will provide an opportunity for our student attendees to get to know one another. In addition, we have retained the always-entertaining AMS auction to support student research. And, for the first time ever, we are including a locally-themed trivia event. Think you know a lot about Atlantic Canada - eh? We shall see! The conference will close with student awards on Thursday evening and the AMS Business meeting on Friday.

We hope you all enjoy the intellectual and social stimulation that this virtual conference is set to provide!

Wela'lin,

Your AMS 2021 local organizing committee

Tim Rawlings (AMS President), Jeff Clements, Kellie White, and Rod Beresford

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# Equity, Diversity, and Inclusion at AMS

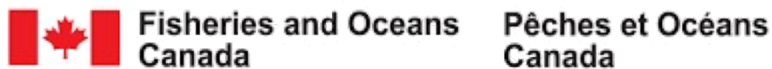
## American Malacological Society Statement on Equity, Diversity and Inclusivity

Members of the American Malacological Society spend their lives studying and appreciating the wonderful diversity of form, function and ecological breadth of mollusks. We recognize that certain aspects of malacological research and collections have benefitted from historical associations with colonization and systems of oppression, such as slavery, and that societies such as AMS, have not been equally accessible to all people. We acknowledge this history and commit to the future of our Society by finding and supporting the next generation of malacologists with this in mind, as we look to advance our field through an inclusive lens. AMS welcomes all malacologists regardless of culture, ethnicity, race, sex, gender identity and expression, sexual orientation, nation of origin, age, languages spoken, veteran's status, religion, or disability. We expect our members to respect the diverse perspectives that come together at our meetings and take every opportunity to help the Society become more diverse, equitable, and inclusive through recruiting, supporting and encouraging new people of all backgrounds.

May, 2021



# Wela'lin to our sponsors



# Schedule at a Glance

Time (EDT)	MONDAY	TUESDAY	WEDNESDAY	THURSDAY	FRIDAY
11:00					
11:30					
12:00					
12:30					
13:00					
13:30	<b>AMS Council Meeting</b> AMS Councillors/Committee Chairs only				
14:00					
14:30					
15:00					
15:30					
16:00	<b>Welcome to AMS 2021</b> AMS President - Tim Rawlings	<b>Session 2</b> Special symposium <i>Mollusc Microbe Interactions</i>			
16:30	<b>Plenary Lecture</b> Dr. Roxanne Beinart <i>"The impact of microbial symbionts on the ecology and evolution of hydrothermal vent snails"</i>				
17:00					
17:30					
18:00					
18:30	<b>Student social</b> Organizers: Tricia Goulding and Chandra Earl	<b>Poster session I</b>	<b>Poster session II</b>		
19:00					
19:30					
20:00		<b>AMS Auction</b> Organizer: Paul Callomon	<b>Quiz</b> So You Think That You Know About Atlantic Canada, Eh?		
20:30					

All times in EDT

MONDAY, JUNE 14	
1:00 - 3:00	AMS Council Meeting
4:00 - 4:30	<b>Welcome to AMS2021</b> AMS President: Tim Rawlings
4:30 - 5:30	<b>Plenary Lecture: Dr. Roxanne Beinart</b> Graduate School of Oceanography, University of Rhode Island "The impact of microbial symbionts on the ecology and evolution of hydrothermal vent snails"
6:00 - 7:30	<b>Student Mixer</b> Organizers: Tricia Goulding and Chandra Earl

\*Eligible for the Constance Boone and/or Charlie Sturm Awards

## TUESDAY, JUNE 15

### SESSION #1

#### President's Symposium - Freshwater Mussels of the Atlantic Drainage

Moderators: André Martel, David Zanatta

11:00 - 11:10	André Martel; David Zanatta	Opening remarks
11:10 - 11:30	Ree Brenninn Houston; Donald Pirie-Hay	Implementing the Management Plans for the Brook Floater and Yellow Lampmussel
11:30 - 11:45	Kellie White	Population Demographics, Reproductive Life History and Conservation Threats of <i>Lampsilis cariosa</i> in Nova Scotia
11:45 - 12:00	Ilya Vikhrev	Massive Northward Expansion of the Alien Asian Pond Mussels ( <i>Sinanodonta</i> spp.) in European Russia
12:00 - 12:30	Keiko Nakamura*	Last Chance for <i>Pseudunio auricularius</i> in Spain: Results from Translocation and Captive Breeding Programs
12:30 - 12:45	<i>Break/Discussion</i>	
12:45 - 1:00	Mariah Scott*	What Can The Shells Tell Us? Understanding Changes in the Community Composition of Freshwater Mussels (Bivalvia: Unionidae) in Great Lakes Region Through Comparison of Living Community and Dead Shell Assemblages
1:00 - 1:15	André Gomes-dos-Santos*	The Crown Pearl: A Draft Genome Assembly of the European Freshwater Pearl Mussel <i>Margaritifera margaritifera</i>
1:15 - 1:30	Andrew McElwain	Histological Changes to the Mantle of Normal and Truncated Freshwater Mussels (Unionidae and Margaritiferidae) from the Nashua River, Massachusetts
1:30 - 1:45	Rebekah Rogers	Gene Family Amplification Facilitates Adaptation in Freshwater Unionid Bivalve <i>Megaloniais nervosa</i>
1:45 - 2:15	Donald Stewart	Can Molecular Signatures Be Used to Detect Cryptic Hermaphroditism in Freshwater Mussels? A Case Study Using <i>Pyganodon</i> in Atlantic Canada
2:15 - 2:30	Louise Lavictoire	Designing a reinforcement programme for the freshwater pearl mussel ( <i>Margaritifera margaritifera</i> ) in the River Irt (NW England)
2:30 - 3:00	<i>Discussion and closing remarks</i>	

### SESSION #2

#### Mollusc-Microbe Associations

Moderators: Suzanne Dufour, Wallace Meyer

2:45 - 3:00	Wallace Meyer	Plants and Associated Microbial Communities Critical to Hawaiian Arboreal Snail Conservation
3:00 - 3:15	Bridget Chalifour*	Characterization of the Gut Microbiome in Wild Rocky Mountainsnails ( <i>Oreohelix strigosa</i> )
3:15 - 3:30	Tyler Griffin*	Developing <i>Mytilus edulis</i> as an Experimental System for Bivalve Gut Microbiome Research
3:30 - 3:45	Rod Beresford	The Oyster ( <i>Crassostrea virginica</i> ) Parasite MSX ( <i>Haplosporidium nelsoni</i> ) in the Bras d'Or Lake, Cape Breton, Nova Scotia – Efforts to Re-establish a Vital Industry to Rural Cape Breton
3:45 - 4:00	Brooke Long-Fox*	Discerning a <i>Ctena</i> Species (Bivalvia: Lucinidae) from San Salvador Island, The Bahamas, through Phylogenetic DNA Barcoding Coupled with Host Morphologic and Endosymbiont Diversity Variations
4:00 - 4:15	<i>Break/Discussion</i>	
4:15 - 4:30	Ruiqi Li*	Insights into the Transcriptomic Response of Photosymbiotic Marine Cockles (Subfamily Fraginae)
4:30 - 4:45	Bridget Vincent*	Cephalopod Photophores: Estimating the Origins of Complex Convergent Traits
4:45 - 5:00	Melissa Betters*	Rethinking Informative Traits: Environmental Influence on Shell Morphology in Deep-Sea <i>Provanna</i> sp.
5:00 - 5:15	Susan Kidwell	Using Time-Averaged Dead-Shell Assemblages of Lucinids to Reveal 20th-Century Changes in Coastal Ecosystems

**SESSION #3****Marine Gastropods (mostly): Physiological Ecology, Genetics, Evolution, and Diversity***Moderator: Tom Duda*

3:00 - 3:15	Jan Pechenik	Intertidal <i>Crepidula fornicata</i> Do Not Lose Biomass During Massachusetts Winters
3:15 - 3:30	Tom Duda	Mutation Rates of Mitochondrial and Nuclear Genomes of Gastropods
3:30 - 3:45	Matthew Penney*	Population Genetic Structure of the Waved Whelk ( <i>Buccinum undatum</i> ) on the Scotian Shelf Using Two Mitochondrial Genes
3:45 - 4:00	Tricia Goulding	A Molecular Phylogeny of the Epitoniidae: Estimating Evolutionary Relationships with Broad Taxon Sampling and Genomic Data
4:00 - 4:15	Vanessa Knutson*	Most Cephalaspidea Have a Shell, but Transcriptomes Can Provide Them With a Backbone (Gastropoda: Heterobranchia)
4:15 - 4:30	Timothy Campbell	Conoids of the Lower Waccamaw Formation: Why Are There So Many of Them?
4:30 - 4:45	Timothy Campbell	Increase the Known Diversity with One Weird Trick: Look Closely: Heterobranchs of the Lower Waccamaw Formation

**POSTER SESSION I****Symposium: Mollusc-Microbe Associations**

1	Emily Kunselman*	Comparison of Microbial Communities in the Olympia Oyster Gut Across the Puget Sound to Define Resident Bacteria and Explore Potential Dysbiosis
2	François Lallier	Are Lucinid Bivalves Strictly Dependent on their Chemotrophic Endosymbionts for their Carbon and Nitrogen Requirements?
3	Meagan Haubner	Hawaiian Land Snails Gut Microbiome Sequencing: A Review and Proposed Methodology
4	Nichole Giani*	Genetic and Functional Diversity of Clade A Lucinid Endosymbionts from the Bahamas and Florida
5	Nova Hanson*	Effects of Hydrothermal Vent Chemistry on Reproductive Allocation in Symbiotic Punk-Rock Snails
6	Russell Minton	Differences in Gut Microbiome Composition and Function Between Two Polygyrid Land Snails, <i>Polygyra cereolus</i> (Muhlfeld, 1816) and <i>Praticolella mexicana</i> Perez, 2011 (Gastropoda: Polygyridae)

**Symposium: Showcasing Molluscan Research at the Undergraduate Level**

7	Lauren Douglas	An Evaluation of Muskrat Middens as Tools for Monitoring Freshwater Mussel Populations
8	Meghan Fraser*	Ecological Thresholds of the Chinese Mystery Snail ( <i>Cipangopaludina chinensis</i> ) in Relation to Nova Scotia Environments
9	Rory MacNeil*	Mantle-flap Lure Morphology and Behavior of <i>Lampsilis cariosa</i> (Bivalvia: Unionidae)
10	Tori Field*	The Impact of the Freshwater Mussel <i>Elliptio complanata</i> on Water Quality

**Contributed Posters**

11	Kathryn Perez	Building a DNA Barcoding Library of Western Texas Spring Snails (Gastropoda: Caenogastropoda: Cochliopidae & Hydrobiidae)
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## WEDNESDAY, JUNE 16

### SESSION #4

#### Symposium: Modern Advances in Mollusc Behaviour

*Moderators: Jeff Clements, Russell Wyeth*

11:00 - 11:15	Jeff Clements	Mussels in Hot Water: The Behavioural Ecology of Temperate Mussels Under Ocean Warming and Acidification
11:15 - 11:30	Laura Steeves*	Temporal Mismatch Between Pumping Rate and Food Availability in <i>Mytilus edulis</i>
11:30 - 11:45	Trevor Hewitt*	Behavioral Component of Host Infection Strategy in the Polymorphic Lures of <i>Lampsilis fasciola</i> (Bivalvia: Unionidae)
11:45 - 12:00	Sabine Roussel	Understanding Behaviour for Improving Stock-Enhancement Success of the European Abalone, <i>Haliotis tuberculata</i>
12:00 - 12:15	Eduardo Sampaio*	Collective Behaviour and Social Dynamics During Interspecific Hunting Between Octopus ( <i>Octopus cyanea</i> ) and Multiple Fish Species
12:15 - 12:30	<i>Break/Discussion</i>	
12:30 - 12:45	Robyn Crook	Nociception and Pain in Cephalopods
12:45 - 1:00	James Newcomb	Circadian Rhythms and the Influence of Light on the Behavior of Nudibranchs
1:00 - 1:15	Xochiti Vital*	Light Preference of a Photosynthetic Animal: <i>Elysia crispata</i> Rejects Red and Intense Lights
1:15 - 1:30	Allison Irwin*	Using Visual Behaviour and Retinal Ultrastructure to Explore Visual Function in the Marine Gastropod <i>Conomurex luhuanus</i> (Strombidae)
1:30 - 1:45	<i>Break/Discussion</i>	
1:45 - 2:00	Jillian Detwiler	Context Dependence of Parasite-Modified Behavior for Freshwater Planorbid Snails
2:00 - 2:15	Olwyn Friesen	Parasite Impacts on Snail Chemical Communication: Implications for Behavioural Modification and Defence Priming
2:15 - 2:30	Ken Lukowiak	<i>Lymnaea</i> Are Competent to Undergo Both Configurational Learning and a Garcia-like Effect and Form Long Term Memory
2:30 - 2:45	Russell Wyeth	Sensory Modulation of Odour-Based Navigation in the Freshwater Gastropod, <i>Lymnaea stagnalis</i>
2:45 - 3:30	<i>Discussion and closing remarks</i>	

### SESSION #5

#### Freshwater Molluscs: Taxonomy, Species Diversity, and Temporal Dynamics

*Moderator: Tim Rawlings*

11:00 - 11:15	Jonathan Todd	Tales From Living and Dead Snails: Faunal Dynamism in Lake Tanganyika, East Africa
11:15 - 11:30	Ellinor Michel	The Neothauma Shell Beds of Lake Tanganyika: Palaeoecology, Patchy Ecosystems and Divergence in a Rift Lake
11:30 - 11:45	Emma Rempel*	Insights from Integrative Taxonomy on the Limits of Morphological Delimitation and Species Diversity in Freshwater Snails (Planorbidae: <i>Planorbella</i> and <i>Helisoma</i> )
11:45 - 12:00	Eric Wagner	<i>Limnophysa</i> , not <i>Ladislavella</i> for the North American Stagnicoline Snail Genus
12:00 - 12:15	Daniel Graf	Good, Clean Family Fun: Biodiversity Informatics of Freshwater Bivalves Above the Species Level
12:15 - 12:30	<i>Break/Discussion</i>	

**SESSION #5 (continued)**

**Land Snails: Species Delimitation, Evolution, Geographic Distribution, and Conservation**

*Moderators: Tim Pearce, John Slapcinsky*

12:45 - 1:00	Jared Tomie	Cape Breton Highlands National Park: Opportunities for Research on Terrestrial Gastropods
1:00 - 1:15	Kathryn Holcomb	Conservation for an Endemic Springsnail in Utah's West Desert
1:15 - 1:30	David Bullis	Molecular Phylogenetics, Biogeography, and Premating Isolation in the Punctoid Land Snails of Belau (Republic of Palau, Oceania)
1:30 - 1:45	Teresa Rose Osborne*	Does Fortune Favor the Small? Immigrant Selection on Pacific Island Land Snails
1:45 - 2:00	Chandra Earl	Pacific Island Land Snail Biodiversity Repository (PILSBRY) Portal
2:00 - 2:15	<i>Break/Discussion</i>	
2:15 - 2:30	John Slapcinsky	Anatomical Data Supports Only Four Species of Partulid Tree Snails in Papua New Guinea and the Solomon Islands, One with an Extraordinary, Multi-Archipelagic Distribution
2:30 - 2:45	Norine Yeung	Integrative Systematics of the Hawaiian Achatinellidae
2:45 - 3:00	Andy Huang	Current and Historical Distributions of <i>Amastra cylindrica</i> (Amastridae)
3:00 - 3:15	Taylor Maruno*	Mapping <i>Euglandina rosea</i> : Evaluating the Distribution of the Rosy Wolfsnail in Hawai'i
3:15 - 3:30	<i>Break/Discussion</i>	

**POSTER SESSION II**

**Showcasing Molluscan Research at the Undergraduate Level Symposium**

1	Anastasia Morrison*	Tubercle Construction in <i>Graneledone boreopacifica</i> (Octopoda: Megaleledonidae)
2	Camilo Muñoz Schuler*	Evaluating the Putative Role of Exosomal Pathways in the Process of Shell Formation in <i>Crassostrea gigas</i>
3	Donica Larade*	Tyrosine Hydroxylase-Like Immunoreactivity in the Nervous System of <i>Tritonia exsulans</i>
4	Gabriela Villamonte-Cab*	Flashback Through ARMS: A Study of Mollusks Assemblages in Sisal Reef, Mexico
5	Lilly Thomey	Developing an Alternative, Lab-Based Diet for Hawaiian Ground Snails – Food Preference Research and Nutrient Analyses
6	Sarah Stagnone*	Quantification of Connective Tissue vs. Spicule Content in Dorid Nudibranch Mantle Networks
7	Victoria Allen	Holey Shell: Quantifying Bioerosion in <i>Tridacna derasa</i> Shells

**Contributed Posters**

8	Abdelwaheb Ben Othmen	Genetic differentiation between populations of <i>Tridacna maxima</i> (Bivalvia: Cardiidae: Tridacninae) Across the Saudi Arabian Coast: A Phylogeographical Approach
9	Carmen Cobo*	New Data on Abyssal Solenogastres (Mollusca, Aplacophora) with the Study of a Collection from the Clarion-Clipperton Fracture Zone
10	Fernanda Silva	Brazilian Troglobitic and Troglophilic Snails
11	Jordon Detlor	New Record of <i>Zoogenetes harpa</i> (Say, 1824) in Utah, USA
12	Kathryn Holcomb	Conservation Agreement and Strategy for Springsnails in Nevada and Utah
13	Kathryn Perez	Working Towards a Phylogeny of Central Texas Cavesnails (Gastropoda: Caenogastropoda: Cochliopidae)

## THURSDAY, JUNE 17

### SESSION #6

#### Showcasing Molluscan Research at the Undergraduate Level Symposium

*Moderators: Brian Penney, Michael Middlebrooks, Glenys Gibson*

11:00 - 11:45	<b>Keynote Presentation: Making the Most of Molluscs: Course-Based Undergraduate Molluscan Research Benefits a Broad Range of Student</b> Dr. Patricia Kelley	
11:45 - 12:00	<i>Break/Discussion</i>	
12:00 - 12:15	Alexandra Nockengost	Solar-Powered Sea Slug <i>Elysia papillosa</i> Prefers a Diet That Reduces Photosynthetic Longevity
12:15 - 12:30	Daniela Gutierrez Andrade	Effectiveness Of Ceratal Autotomy In Sacoglossan <i>Placida kingstoni</i> as a Defense Mechanism Against a Crustacean Generalist Predator
12:30 - 12:45	Michael Middlebrooks	What To Do When Things Go Wrong: Engaging Undergraduates in Malacology Research During Pandemics and Other Disasters
12:45 - 1:00	<i>Break/Discussion</i>	
1:00 - 1:15	Shreya Chalapalli	Comparing Freshwater Mollusks from Big Lake, Indiana Across 94 Years (1926 and 2020)
1:15 - 1:30	Pamela Tapia	Benthic Micromolluscs And Juveniles From Arrecife Alacranes National Park
1:30 - 1:45	Jann Vendetti	Diversity in Two <i>Deroceras</i> Land Slug Species in Southern California
1:45 - 2:00	Kyra Madunich*	Water Subsidies Enhance Gastropod and Isopod Species Richness in Southern California
2:00 - 2:15	Tamara Ledoux*	Effects of Anthropogenic Sounds on the Behaviour and Physiology of the Eastern Oyster ( <i>Crassostrea virginica</i> )
2:15 - 2:30	<i>Break/Discussion</i>	
2:30 - 2:45	Glenys Gibson	Effects of Petroleum-Based and Biodegradable Microplastics on Tissue Structure in the Eastern mudsnail <i>Tritia obsoleta</i>
2:45 - 3:00	Caitlin Ball*	The Impacts of a Combination of Thermal and Air Stress on the Survival and Respiration of Winter-Acclimated <i>Crepidula fornicata</i>
3:00 - 3:15	Himani Patel*	Investigating the Interplay of Genetics and Thermal Stress on Energy Metabolism in Invasive Mollusk, the New Zealand Mud Snail <i>Potamopyrgus antipodarum</i>
3:15 - 3:30	MacKenzie Ryan	Validation of Environmental DNA (eDNA) Protocols for Conservation of Freshwater Mussels <i>Alasmidonta varicosa</i> , <i>Margaritifera margaritifera</i> , and <i>Lampsilis cariosa</i>
3:30 - 3:45	William Bauer	A Tale of Two Mussels: DNA Barcoding of Unionids from Guanacaste, Costa Rica
3:45 - 4:00	Timothy Rawlings	Science Atlantic and the Science Undergraduate Research Experience in Atlantic Canada
4:00-4:15	Liz Shea	Using Digital Natural History Collections in Course-Based Undergraduate Research Experiences (CUREs)

### SESSION #7

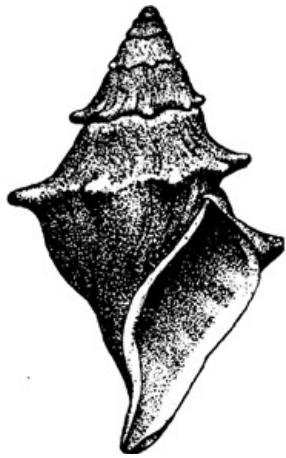
#### Shell Biomineralization, Shell Colour, and Scallop Visual Systems

*Moderator: Kathryn Perez*

11:45 - 12:00	Suzanne Williams	Evolution of Shell Colour
12:00 - 12:15	Michael Whiteside*	Shell Pigmentation in the Eastern Oyster, <i>Crassostrea virginica</i>
12:15 - 12:30	Kanmani Chandra Rajan*	Oyster Biomineralisation in Acidifying Oceans: From Genes to Shells
12:30 - 12:45	Jorge Audino	Who Has More Eyes? Life habits and Allometry Explain Variation in Eye Abundance Among Scallop Species (Pectinidae)
12:45 - 1:00	<i>Break/Discussion</i>	

**SESSION #7 (continued)****Cephalopods: Species Discrimination, Ecology, and Phylogenetic Relationships***Moderator: Liz Shea*

1:15 - 1:30	Abigail Pratt*	Finding a Home for the Ram's Horn Squid ( <i>Spirula spirula</i> ) Using Phylogenomics
1:30 - 1:45	Mariana Díaz Santana Iturrios	Statolith shape of Loliginid Squids: Discriminant Power and Ancestral State
1:45 - 2:00	Renata Pacheco-Ovando	Identification of Loliginid Squids Based on Beak Shape Obtained by Geometric Morphometrics
2:00 - 2:15	Maria Moreno-Alcántara*	Seasonal and Interannual Variation of Atlantidae (Pterotracheoidea) in the Pacific Coast of Baja California, México
2:15 - 2:30	<i>Break/Discussion</i>	
<b>Digitizing Natural History Collections</b>		
2:30 - 2:45	Gary Rosenberg	Telescopes for Malacology
<b>Marine Bivalves - Living, Boring, and Taxonomically Confusing</b>		
<i>Moderator: Kevin Kocot</i>		
2:45 - 3:00	Sarah MacLean	Boring Bivalves: Using Molecular Phylogenetics to Resolve Species Identities in <i>Botula</i> (Mytilidae)
3:00 - 3:15	Kelli DeLeon	Taxonomic Teredinidae Turmoil and the Effort to Resolve Shipworm Relationships in the Pacific
3:15 - 3:30	Nancy Treneman	Brooding on Dispersal: Shipworms in the Hawaiian Islands
3:30 - 3:45	Marina Güller	Distribution and Zoogeography of the Bivalvia of the Eastern Pacific Ocean - 40 Years Later
3:45 - 4:00	David Campbell	Will the Real <i>Mytilus incrassatus</i> Please Stand Up?



# Abstracts



## Plenary lecture

### **The Impact of Microbial Symbionts on the Ecology and Evolution of Hydrothermal Vent Snails**

Beinart, Roxanne A.

Graduate School of Oceanography, University of Rhode Island, RI, USA

[rbeinart@uri.edu](mailto:rbeinart@uri.edu)

Molluscs in many marine ecosystems have formed symbiotic associations with microbes that allow them to capitalize on the relative diversity of microbial physiology. At hydrothermal vents, many invertebrates, including molluscs, host symbiotic, chemosynthetic bacteria that provide their nutrition in the otherwise food-limited deep sea. Here, I present work on the ecology and evolution of symbiotic snail species from two sympatric sister genera that dominate hydrothermal vents in the western Pacific (*Alviniconcha* and *Ifremeria*). Using genomics to assess variation in symbiont gene content and physiological experiments to compare chemosynthesis among these species, we are building evidence indicating that the particular traits of their specific bacterial symbionts impact the geochemical habitats occupied by these species. This provides insight into their current distribution within and between vent sites, as well is important for understanding speciation processes in this group. Altogether, this work advances knowledge about the role that symbiotic microbes can play in molluscan ecology and evolution.

## SESSION 1

### President's Symposium: Freshwater Bivalves of the North Atlantic Drainage

# Implementing the Management Plans for the Brook Floater and Yellow Lampmussel

Brennin Houston, Ree\*<sup>1</sup>; Pirie-Hay, Donald\*<sup>2</sup>

1. Department of Fisheries and Oceans – Maritimes Region, Bedford Institute of Oceanography, Dartmouth, NS, Canada; 2. Department of Fisheries and Oceans – Gulf Region, Moncton, NB, Canada

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Nova Scotia and New Brunswick are home to two freshwater mussel species, the brook floater (*Alasmidonta varicosa*) and yellow lampmussel (*Lampsilis cariosa*), which have been listed under Canada's Species at Risk Act (SARA) as Special Concern. This status designation requires the development of a management plan that sets the management objective, broad strategies, and measures for the conservation of the species. Fisheries and Oceans Canada's (DFO) Species at Risk Program plays an important role in coordinating and collaborating with partners to implement the management plans for both mussel species. In this presentation, we provide an overview of some of the key actions DFO has undertaken to assist partners in advancing the conservation of these freshwater mussels. Among actions taken, DFO has helped lay the groundwork for surveys necessary to develop a more accurate understanding of the distribution and occupancy of these at-risk freshwater mussels in Canada. Since 2015, DFO has funded a number of workshops on mussel identification and field survey techniques to train local partners such as Indigenous groups, environmental organizations, and academic researchers. DFO has also developed educational and outreach materials to support local organizations in their efforts to survey and locate at-risk freshwater mussels, as well as to engage the general public on the importance of freshwater mussels and protecting their habitat. Recently, DFO has supported local groups and academic laboratories to further develop and implement environmental DNA surveys for brook floater, yellow lampmussel, and the extirpated dwarf wedgemussel (*Alasmidonta heterodon*), whose habitat is currently undergoing restoration. DFO also continues to support stewardship and restoration projects led by partner organizations through various federal funding programs.

## **Population Demographics, Reproductive Life History and Conservation Threats of *Lampsilis cariosa* in Nova Scotia**

White, Kellie L.\*; Penney, Alicia; Douglas, Lauren; McPhee-Tomko, Elizabeth; MacNeil, Rory

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Yellow lampmussel (*Lampsilis cariosa*) occur along the Northeast Atlantic Slope of North America from Georgia to Nova Scotia. They are considered threatened and declining throughout much of their range in the United States. Listed as of "Special Concern" federally in Canada, they are found in only two provinces: New Brunswick and Nova Scotia. Yellow lampmussel are designated as "Threatened" in Nova Scotia and until recently were thought to be limited to the upper Sydney River and two small, connected lakes (Blacketts and Gillis) in the Sydney River watershed. The discovery of a second Nova Scotia population at Pottle Lake in 2015 prompted an extensive search of waterbodies in the region and the location of a third population at Forresters Lake in 2015. In collaboration with three levels of government, indigenous groups, and recreational anglers we did extensive sampling of all three Nova Scotia populations to fill knowledge gaps associated with population demographics, reproductive life history, and conservation threats. Filling these gaps is essential for developing effective management plans and predicting how the species will respond to management strategies intended to mitigate threats. Our sampling revealed that yellow lampmussel density was low in all three Nova Scotia populations at 0.45-0.95 mussels/m<sup>2</sup>. Life history and reproductive characteristics were similar across populations with maximum age estimated at 25 years. The minimum age of females becoming gravid and displaying mantle lures was four years with females brooding glochidia through spring and fall. Sex ratios were significantly ( $p < 0.05$ ) skewed toward males in all three populations. White perch (*Morone americana*) was the only fish species found to host yellow lampmussel glochidia and the recent illegal introduction of chain pickerel into Blacketts Lake poses a major threat to white perch in the Sydney River watershed. We found no evidence of recent yellow lampmussel recruitment in Blacketts Lake suggesting this population may be in jeopardy.



## **Massive Northward Expansion of the Alien Asian Pond Mussels (*Sinanodonta* spp.) in European Russia**

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Asian pond mussels are one of the most remarkable invaders among freshwater bivalves rapidly spreading throughout the world. There are two species in the genus documented as alien ones: *S. woodiana* (Lea, 1834) and *S. lauta* (Martens, 1877). The invasion of Asian pond mussels in Russia was firstly discovered in 2017 in the artificially heated section of the Yenisei River, Eastern Siberia. Later, invasive populations of both species were recorded in the Belovo Reservoir, Ob River basin, Western Siberia. Both of these sympatric invasive assemblages are associated with artificially heated waters discharged from thermal power plants (TPP) and further spreading of Asian pond mussels out of these thermal refugia is restricted by unfavorable temperature conditions of surrounding freshwater habitats. In contrast, invasive Asian pond mussels that were found in the downstream section of the Volga River have established rather abundant populations under natural environmental conditions. Furthermore, these species were recorded from the Kama River basin, where they inhabit the artificially heated Karmanovo Reservoir and native habitats in the Buy River. Conversely only *S. lauta* was found in the artificially heated Zainsk Reservoir and the Zay River. It was found that *S. lauta* from invasive populations shares a COI haplotype that is closely related to those from South Korea. Conversely, *S. woodiana* reveals the commonest invasive haplotype being recorded from European countries and northern Myanmar. We propose that the recent invasion of *S. woodiana* and *S. lauta* in Russia was associated with fish stocks imported from Kazakhstan. The rapid expansion of these mussels throughout Russia was caused by a human-mediated dispersal of infested fishes from a site(s) of initial invasion to other freshwater systems: the Lower Volga (at least since 2002), Yenisei (2004), Ob (2007), and Kama (1985) rivers. Our species distribution modeling (SDM) shows that most of European Russia north of the Don and Kuban River basins is unfavorable for *S. woodiana* under the current climatic conditions. This finding stresses the role of artificially heated water bodies in further northward expansion of *Sinanodonta* invasion in Russia.

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## **Last Chance for *Pseudunio auricularius* in Spain: Results from Translocation and Captive Breeding Programs**

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The giant freshwater pearl mussel *Pseudunio auricularius* (= *Margaritifera auricularia* Spengler, 1793) is classified as critically endangered in the IUCN Red List. The population of the Ebro River basin (Spain) has suffered a strong decline in recent years, registering high mortalities, especially in the Canal Imperial de Aragón (CIA) where it presents the highest densities. These high mortality rates were also registered in the other three species of freshwater mussels that used to live in the canal: *Potomida littoralis*, *Unio mancus* and *Anodonta anatina*, but the causes of these declines are yet to be uncovered.

To face this unusual mortality, the Aragón regional government drawn up in 2016 a plan to evaluate the recovery and survival of adults of the giant freshwater pearl mussel translocated from the CIA to the Ebro River. During 4 years 820 specimens have been translocated and the first results indicate that the river may allow a higher survival for *P. auricularius* than the canal. The overall survival of translocated mussels after one year was 41.58% for the first group (2017), 68.73% for the second (2018) and 48.65% for the third (2019). Conversely, the survival rate of the control group left in the canal was only of 19.70% after the first year.

Furthermore, a captive breeding program started to successfully produce juveniles in 2014, allowing the production of different cohorts that are maintained in laboratory facilities, but will be released into the natural environment in the near future to reinforce field populations.

Both translocation and captive programs together are probably the last chance to save *Pseudunio auricularius* from extinction in Spain and so guarantee the survival and recovery of this iconic invertebrate species.

## **What Can the Shells Tell Us? Understanding Changes in the Community Composition of Freshwater Mussels (Bivalvia: Unionidae) in Great Lakes Region Through Comparison of Living Community and Dead Shell Assemblages**

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Freshwater mussels in the family Unionidae have experienced numerous anthropogenic ecological changes in the Great Lakes region. These changes include, but are certainly not limited to, habitat disturbance, pollution, direct harvest for the historic button industry, and introductions of the invasive mussels *Dreissena polymorpha* and *Dreissena bugensis*.

This study utilizes data from the Unionid Refuge Project, comparing the discordance between living community and dead shell assemblages of freshwater mussels. The difference in species richness, community composition, evenness, and abundance will be compared within each site. Over 200 half-hectare sites throughout the Great Lakes region are part of the analysis, representing a mixture of sites with different ecological histories, a range of no presence to high intensities of dreissenid invasion, and different abiotic environmental variables. This study looks for changes in species richness and community composition in these locations. This information will help us better understand how substantially unionid communities have been altered over time. An additional focus is the investigation of what changes vary as a function of recent and historic anthropogenic impacts to this increasingly imperiled community.

## **The Crown Pearl: A Draft Genome Assembly of the European Freshwater Pearl Mussel *Margaritifera margaritifera* (Linnaeus, 1758)**

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Since historical times, the inherent human fascination with pearls turned the freshwater pearl mussel *Margaritifera margaritifera* (Linnaeus, 1758) into a highly valuable cultural and economic resource. Although pearl harvesting in *M. margaritifera* is nowadays residual, other human threats have aggravated the species conservation status, especially in Europe. This mussel presents a myriad of rare biological features, e.g. high longevity coupled with low senescence and Doubly Uniparental Inheritance of mitochondrial DNA, for which the underlying molecular mechanisms are poorly known. Here, the first draft genome assembly of *M. margaritifera* was produced using a combination of Illumina Paired-end and Mate-pair approaches. The genome assembly was 2.4 Gb long, possessing 105,185 scaffolds and a scaffold N50 length of 288,726 bp. The ab initio gene prediction allowed the identification of 35,119 protein-coding genes. This genome represents an essential resource for studying this species' unique biological and evolutionary features and ultimately will help to develop new tools to promote its conservation.

## **Histological Changes to the Mantle of Normal and Truncated Freshwater Mussels (Unionidae and Margaritiferidae) from the Nashua River, Massachusetts**

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Shell damage and deformities represent a mussel health problem that has received little attention over the years. Generally, the shell may become damaged or misshapened due to trauma to the shell or possibly as the result of an injury to the mantle. During a 2017 survey of the Nashua River, Massachusetts, some *Elliptio complanata*, *Lampsilis radiata*, *Strophitus undulatus* (Unionidae), and *Margaritifera margaritifera* (Margaritiferidae) exhibited abnormal shells characterized by a truncated posterior margin. We classify such malformations as either slight, moderate, or severe. Prevalence of truncated shells and sample sizes (whole mussels and empty shells) are as follows: *E. complanata*, 49%, n = 71; *Lampsilis radiata*, 33%, n = 3; *Strophitus undulatus*, 100%, n = 1, *M. margaritifera*, 57%, n = 7. Strayer (2008) documented a similar deformity among unionids in the Hudson River Valley and Southern Tier regions of New York. To the best of our knowledge, this phenomenon has not been reported elsewhere since. We used shell-thin sections to characterize changes in shell growth, and histology to describe cellular changes to the mantle. Herein we report preliminary histological results from *E. complanata*. The mantle edge consists of a simple columnar epithelium surrounding a meshwork connective tissue, and muscle fibers. All individuals sampled appeared to exhibit elevated levels of hemocytes throughout mantle tissues. Normal individuals tended to have robust and intact tissue layers, whereas truncated individuals tended to exhibit minor degradation to muscle and connective tissue. Although some literature suggests parasites or commensalistic organisms can interfere with shell formation, evidence of parasitic infections (e.g., eggs of *Unionicola* sp.) was only observed in the mantle of four *E. complanata*. Presently we are uncertain of the specific cause of these deformities, but it seems the mantle is stressed periodically such that new shell material builds up locally over many years.

## **Gene Family Amplification Facilitates Adaptation in Freshwater Unionid Bivalve *Megalonaias nervosa***

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As organisms are faced with intense rapidly changing selective pressures, new genetic material is required to facilitate adaptation. Among sources of genetic novelty, gene duplications and transposable elements (TEs) offer new genes or new regulatory patterns that can facilitate evolutionary change. With advances in genome sequencing it is possible to gain a broader view of how gene family proliferation and TE content evolve in non-model species when populations become threatened. Freshwater bivalves (Unionidae) currently face severe anthropogenic challenges. Over 70% of species in the United States are threatened, endangered or extinct due to pollution, damming of waterways, and overfishing. We have created a reference genome for *Megalonaias nervosa* to determine how genome content has evolved in the face of these widespread environmental challenges. We observe a burst of recent transposable element proliferation causing a 382 Mb expansion in genome content. Gene family expansion is common, with a duplication rate of  $1.16 \times 10^{-8}$  per gene per generation. Cytochrome P450, ABC transporters, Hsp70 genes, von Willebrand proteins, chitin metabolism genes, mitochondria eating proteins, and opsin gene families have experienced significantly greater amplification and show signatures of selection. We use evolutionary theory to assess the relative contribution of SNPs and duplications in evolutionary change. Estimates suggest that gene family evolution may offer an exceptional substrate of genetic variation in *M. nervosa*, with  $P_{sgv}=0.185$  compared with  $P_{sgv}=0.067$  for single nucleotide changes. Hence, we suggest that gene family evolution is a source of "hopeful monsters" within the genome that facilitate adaptation.

## **Can Molecular Signatures Be Used to Detect Cryptic Hermaphroditism in Freshwater Mussels? A Case Study Using *Pyganodon* in Atlantic Canada**

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Many freshwater mussels (Unionida) have an unusual system of doubly uniparental inheritance (DUI) of mitochondrial DNA. In DUI positive species, males possess a female-transmitted (F-type) mt genome and a male-transmitted (M-type) mt genome. These genomes contain open reading frame (orf) genes referred to as f-orf and m-orf, present in F and M mt genomes, respectively. These genes have been implicated in sexual development in Unionida. When gonochoric species evolve hermaphroditism, they lose their M-type mt genome, and f-orf genes evolve rapidly. Resulting F-ORF proteins are highly divergent in primary nucleotide sequence, inferred amino acids, and hydrophobic properties. These modified genes (and proteins) are referred to as hermaphroditic orfs or h-orfs (and H-ORFs). We investigated patterns of hydrophobicity divergence for H-ORF proteins in hermaphrodites versus F-ORF proteins in closely related gonochoric species against cytochrome c oxidase subunit 1 (cox1) divergences. This approach was used to assess whether cryptic hermaphrodites can be detected. We did not detect evidence for a transition of any populations of Eastern Floaters, *Pyganodon cataracta* (Say, 1817) to hermaphroditism, but our analyses demonstrate that molecular signatures in mtDNA can be used to detect hermaphroditism in freshwater mussels.

## **Designing a Reinforcement Programme for the Freshwater Pearl Mussel (*Margaritifera margaritifera*) in the River Irt (NW England)**

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Propagation programmes for the freshwater pearl mussel (*Margaritifera margaritifera*) are now common throughout the mussel's European range; an unfortunate consequence of their continued rapid population decline. Many of these breeding programmes are now attempting conservation translocations in to the wild (i.e., reintroductions or reinforcements), using a variety of different methods. I will describe the strategy employed for planning and undertaking reinforcements in the River Irt, Cumbria (UK), as part of the River Irt Reintroductions Research Project.

Juveniles have been propagated at the Freshwater Pearl Mussel Ark since 2007. Several cohorts are now ready for release over the next few years. One of the key early objectives of the project was to investigate whether offspring are genetically representative of the wild population, in order to inform our release strategy. I discuss initial results here. We have also begun annual broodstock rotation of wild-fertilised mussels to attempt to ensure high broodstock genetic diversity.

Juvenile habitat mapping<sup>1</sup>, slope analysis, current land use practices and historic/anecdotal evidence of mussel distributions have been used to select potential mussel release sites for further consideration. A mussel silo trial using mussels >15 mm length commenced in July 2020 to assess if water quality at several candidate sites within the river Irt was suitable for juveniles. We discuss our results so far and outline how this method will continue to be used to assess water quality limitations of juvenile mussels within this catchment. We are also planning multiple stressors and metabolomics investigations for 2021 and 2022 to better understand what the potential effects of stress may be on juvenile mussels during translocations.

In this project we are using a suite of tools to try and better understand the effects of propagation and conservation translocations on mussels at both the individual and population levels.

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## SESSION 2

### Special Symposium: Mollusc-Microbe Interactions

#### **Plants and Associated Microbial Communities Critical to Hawaiian Arboreal Snail Conservation**

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Despite calls to protect and expand habitat for native Hawaiian snails, conservation remains hampered by a lack of foundational ecological information. For example, until recently, habitat requirements for most Hawaiian arboreal snails, e.g., what plants they require, remained unknown. We investigated native arboreal snails' plant preferences in wet montane areas (Kohala, Hawai'i; Mt Ka'ala, O'ahu, and Pu'u Kukui, Maui) across the Hawaiian archipelago. Despite the study including snails endemic to different islands, concordant patterns emerged. Across islands and species, snails preferred a subset of patchily distributed understory plants (*Broussaisia argute*, *Ilex* spp., and *Clermontia* spp.), and avoided the two most abundant plants at all sites studied: the dominate tree, *Metrosideros polymorpha*, and the mid-story ferns *Cibotium* spp. Using these results as a guiding framework, we employed a metagenomic approach to test the hypothesis that epiphytic fungal and bacterial assemblages, the primary food for these snails, differed among preferred and non-preferred plant species. Analyses uncovered differences in microbial assemblages among preferred and non-preferred plant species and support the idea that protecting and restoring diverse understory plant assemblages with a focus on key plant species for snails may enhance native Hawaiian arboreal snail conservation. These data also provide opportunities for research to elucidate effective snail conservation strategies. Future research should explore if (1) snail fitness is enhanced when feeding on preferred plants, and if (2) certain fungi and bacteria may enhance or inhibit snail fitness. Attention to foundational ecological information may provide the vital insights required to preserve the remaining species.

## Characterization of the Gut Microbiome in Wild Rocky Mountainsnails (*Oreohelix strigosa*)

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The Rocky Mountainsnail (*Oreohelix strigosa*) is a terrestrial gastropod of ecological importance in the Rocky Mountains of western United States and Canada. Across the animal kingdom, including in gastropods, gut microbiomes have profound effects on the health of the host. Current knowledge regarding snail gut microbiomes, particularly throughout various life history stages, is limited. Understanding snail gut microbiome composition and dynamics can provide an initial step toward better conservation and management of this species. We employed 16S rRNA gene amplicon sequencing to examine gut bacteria communities in wild-caught *O. strigosa* populations from the Front Range of Colorado. These included three treatment groups: (1) adult and (2) fetal snails, as well as (3) sub-populations of adult snails that were starved prior to ethanol fixation. Overall, *O. strigosa* harbors a high diversity of bacteria. We sequenced the V4 region of the 16S rRNA gene on an Illumina MiSeq, and obtained 2,714,330 total reads. We identified a total of 7,056 unique operational taxonomic units (OTUs) belonging to 36 phyla. The core gut microbiome of four unique OTUs accounts for roughly half of all sequencing reads returned and may aid the snails' digestive processes. Significant differences in microbial composition, as well as richness, evenness, and Shannon Indices were found across the three treatment groups. Comparisons of gut microbiomes in *O. strigosa* adult, fetal, and starved samples provide evidence that the host internal environments influence bacterial community compositions, and that bacteria may be transmitted vertically from parent to offspring. This is the first comprehensive report on the structure and membership of bacterial populations in the gastropod family Oreohelcidae and reveals similarities and differences across varying life history metrics. Strong differentiation between these life history metrics demonstrates the need for wider sampling for studies of dynamics of the snail gut microbiome.

## **Developing *Mytilus edulis* as an Experimental System for Bivalve Gut Microbiome Research**

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Bivalves have ecological and economic importance, but information regarding their associated microbiomes is lacking. It has become evident that gut-associated microbiomes contribute significantly to host physiological processes. For decades, blue mussels (*Mytilus edulis*) have been used as model suspension-feeding bivalves in laboratory studies of anatomy, behavior, and physiology. This species also has enormous potential to serve as an experimental system for evaluation of hypotheses about bivalve-microbe interactions. The aims of the present studies were to develop mussels as an experimental system by 1) evaluating fecal sampling as a reliable proxy for gut microbiome assessment and 2) evaluating antibiotic administration as a method for perturbing the gut microbiome. In one experiment, mussels were collected from the natural environment and placed into microcosms to allow for fecal egestion. Feces and gut homogenates from the same individuals were sampled and subjected to 16S sequencing. Fecal communities of different mussels resembled each other but did not resemble gut communities. Fecal communities were significantly more diverse, in terms of richness and evenness, than gut communities. Results suggested a mostly transient nature for fecal microbiota. The use of fecal sampling as a nondestructive substitute for direct sampling of the gut, therefore, is strongly discouraged. In a separate experiment, mussels were delivered an antibiotic mixture for 21 days to probe effects on microbial abundance, diversity, and taxonomic composition. Mussels were administered antibiotics in isolation, and stringent sterilization methods were employed, which included sterilized seawater and microalgal food. Antibiotics significantly lowered microbial abundance and species richness, and significantly altered community composition. This protocol for disturbing the gut microbiome will likely work on other suspension-feeders, and the resulting animals are eligible for use in subsequent experiments. Taken together, these findings help strengthen *M. edulis* as a tool for future endeavors investigating the symbiosis between bivalves and their gut microbiome.

**The Oyster (*Crassostrea virginica*) Parasite MSX (*Haplosporidium nelsoni*) in the Bras d'Or Lake, Cape Breton, Nova Scotia – Efforts to Re-establish a Vital Industry to Rural Cape Breton**

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The oyster parasite, *Haplosporidium nelsoni*, was first detected in the Bras d'Or Lake, Cape Breton, Nova Scotia in the early 2000s following catastrophic oyster mortality on multiple oyster lease sites and in the wild population. *H. nelsoni* is found in oyster beds from Florida to Maine and usually causes mortality rates of 90% or higher. The parasite cannot be eradicated and oyster populations are slow to recover. Despite being first detected in the Delaware Bay area in the late 1950s, the life cycle of the parasite is still not known. Once the Bras d'Or Lake was designated *H. nelsoni* positive there were very little efforts to try and rebuild the oyster industry within the Bras d'Or Lake and efforts were focused on detection outside of the Bras d'Or Lake. Presently, there are two areas outside of the Bras d'Or Lake designated *H. nelsoni* positive because oysters were transferred to these areas from the Bras d'Or Lake. For decades, including the years prior to, during, and after the disease outbreak, oysters were transferred from the Bras d'Or Lake across Atlantic Canada. The presence of Malpeque disease outside the Bras d'Or Lake means no oysters can be transferred in and with *H. nelsoni* in the Bras d'Or Lake no oysters can be transferred out. The Bras d'Or Lake oyster industry will have to become its own industry. I will share what we have observed and learned and what we are doing to re-establish this important industry for the communities around the Bras d'Or Lake and the health of the waters of the Bras d'Or Lake.

## **Discerning a *Ctena* Species (Bivalvia: Lucinidae) from San Salvador Island, The Bahamas, through Phylogenetic DNA Barcoding Coupled with Host Morphologic and Endosymbiont Diversity Variations**

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Lucinidae are the most diverse bivalve family to host chemosynthetic endosymbionts. Here, we examine host shell variability and endosymbiont diversity in a well-supported *Ctena* clade. *Ctena* molecular data support species delineations aligning with geography: *C. orbiculata* in Florida, the Gulf of Mexico, and northern Caribbean, *C. imbricatula* in the Caribbean and Central America, and *C. mexicana* in the eastern Pacific. Published molecular data for the group is minimal, with few specimens sequenced and little DNA barcoding data available, i.e. cytochrome c oxidase subunit I (COI).

*Ctena* from three inland anchialine ponds and a shallow coastal lagoon on San Salvador Island, the Bahamas were used in Bayesian analyses of one nuclear (28S rRNA) and two mitochondrial (cytochrome b (cytb) and COI) genes. A highly-supported clade of San Salvador *Ctena* phylogenetically distinct from both *C. orbiculata* and *C. imbricatula* was recovered. Cytb pairwise distance analyses indicate this clade has an 11.0% sequence divergence from *C. mexicana*, 15.4% from *C. imbricatula*, and 18.5% from *C. orbiculata*. Within the San Salvador *Ctena* clade, no patterns of population-level phylogenetic variation were found among localities and there was little divergence among individuals.

Geometric morphometric analysis describing internal shell morphology and outline shape revealed that San Salvador *Ctena* overlap in shape space with Floridian *C. orbiculata*, although both shape (MANOVA,  $p=0.001$ ) and size (Mann Whitney,  $p=3.48 \times 10^{-12}$ ) differed significantly. San Salvador *Ctena* are larger (tidal lagoon exception) than *C. orbiculata*, have a more predominant anterior shell extension, and a longer, more ventrally detached anterior adductor muscle scar. Morphologic separation among localities occurs and indicates environmental influence on morphology. Endosymbiont taxonomic diversity show few locality-specific Operational Taxonomic Unit (OTUs) that may be associated with vegetation at localities. In summary, both host morphology and symbiont composition may be highly influenced by environmental factors independent of host phylogeny.

## Insights into the Transcriptomic Response of Photosymbiotic Marine Cockles (Subfamily Fraginae)

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Photosymbiosis is a mutualistic relationship between a host organism and photosynthetic microbes. It has independently evolved in diverse marine lineages. However, molecular mechanisms behind such symbioses remain less understood, especially in mollusks. This study aims to investigate the expression of photosymbiotic related genes in mollusks using a group of diverse but less studied marine cockles (Subfamily Fraginae), which establishes photosymbioses with algal lineages from the family Symbiodiniaceae. They adapted a wide range of lifestyles in diverse habitats, ranging from shallow reef sediment to deeper sandy bottoms. In this study, we used three photosymbiotic species including highly adapted species *Fragum fragum*, *F. whitleyi* from shallower waters ( $\approx 1\text{m}$ ), and *F. sueziense* from deeper lagoon bottoms ( $\approx 5\text{m}$ ). We kept each species under three different light intensities (normal, reduced, and dark), and obtained a total of 176 transcriptomes from both mantle (symbiont containing) and foot (no symbionts) tissues of the three bivalves through RNAseq. We accessed regulations of genes related to nitrogen metabolism, glucose metabolism, and reactive oxygen species in the three light intensities. We also compared the gene expression patterns from those three pathways of the species that differently relies on photosymbiosis.

## **Cephalopod Photophores: Estimating the Origins of Complex Convergent Traits**

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Convergent traits arise when distantly related taxa independently develop similar phenotypes. However, by a single gene. Determining where these traits originate is key in understanding their evolutionary history and how patterns of convergence persist in multiple levels of biological organization. Bioluminescence is a convergent, complex trait present across taxa in both marine and terrestrial species, including the class Cephalopoda. The organ producing bioluminescence (photophores) shows extensive morphological diversity across both taxa and biological levels. Different species of cephalopods may have bacteriogenic photophores (organs whose symbiotic bacteria produce light) or autogenic photophores (organs that produce light using their own cells) in varying degrees of complexity. Though we know cephalopod bioluminescence is convergent, the number of independent origins of these complex traits is a mystery. We created a species-level phylogeny using published short-read genetic data and transcriptomes to assess whether a higher resolution affects our estimates of evolutionary origins. After gathering morphological data for each species' photophore, we used ancestral state reconstruction to determine the number of evolutionary origins for bacteriogenic photophores, autogenic photophores, and common components of autogenic photophores. In future work, this will help us determine if patterns of convergence remain consistent across biological levels in a complex trait.

## **Rethinking Informative Traits: Environmental Influence on Shell Morphology in Deep-Sea *Provanna* sp.**

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Marine gastropod mollusks within deep-sea, chemosynthetic environments present unique challenges to taxonomic study because they are chronically under-sampled, yet are anomalously biodiverse along the ocean floor. While classifying gastropod diversity often relies on shell morphology, the accuracy of shells in delineating species is no longer clear, as genetic evidence increasingly confirms intraspecific morphological variation. Chemosynthetic environments, for instance, may present a uniquely heterogenous landscape where abiotic factors can affect gastropod shell formation and maintenance. In examining a snail species from the genus *Provanna* (Dall, 1918) (Gastropoda) from three hydrocarbon seeps along the Costa Rica Margin, preliminary data have found variation in traits that would typically be considered taxonomically informative. Evidence of shell morphology varying within a single gastropod species is not unheard of, however, the extent of this variation within *Provanna*, and what drives this variation, is still poorly understood. My current research addresses the question: Does the environment in which marine gastropods live have a significant effect on their intraspecific morphological variation? This project will examine how shell morphometry within a species of *Provanna* varies along environmental parameters associated with active hydrocarbon seepage, such as biogenic substrate, oxidative reductive potential, dissolved oxygen, and alkalinity. This research may elucidate the impact of heterogeneous chemosynthetic landscapes on gastropod morphology, and critically assess the reliability of shells in diagnosing chemosynthetic gastropod species.



## Using Time-Averaged Dead-Shell Assemblages of Lucinids to Reveal 20th-Century Changes in Coastal Ecosystems

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Lucinid bivalves are good targets for paleoecological evaluation of coastal ecosystems and especially for detecting human impacts, given the preference of some taxa for sensitive habitats, such as seagrass meadows, and the tolerance of others for relatively noxious ones, such as seabeds affected by high organic loads. Importantly, such species are often common or even dominant in such settings, i.e. are reliably and abundantly present, and their shells, although aragonitic rather than calcitic, are moderately thick and low in organic content, imparting high post-mortem durability. Thus, lucinid shells can persist within the surface mixed layer as testaments to former local populations and can be dated using geological methods, allowing us to establish the timing and magnitude of past changes and the trajectory of present-day populations. We will describe two such studies on urban shelves, using radiocarbon-based amino-acid racemization dating of individual shells. (1) In southern California, age-dating of hundreds of *Parvilucina tenuisculpta* shells serves as a proof-of-concept: dead shells record the huge middle-shelf populations present in the 1970s-80s and their subsequent decline with improved wastewater treatment; assemblages also show that populations did not increase significantly until the onset of wastewater release in the 1930s, and that they should revert to <20% of bivalve individuals once conditions are fully natural. (2) In the tropical Gulf of Eilat, northern Red Sea, our live-dead analysis of bivalve assemblages in 30-60m water depths revealed that *Ctena divergens* occurs ~only as dead, but very abundant, shells, even in seagrass-covered areas, signaling otherwise unsuspected changes in that habitat. Our new <sup>14</sup>C results show that this decline has occurred entirely within the 20th century, concomitant with urbanization and industrialization, after a millennium of high abundance. Lucinids are thus exceptionally revealing subsamples of molluscan death assemblages for tracking anthropogenic changes, both positive and negative.

## SESSION 3

### Contributed Talks: Marine Gastropods (mostly): Physiological Ecology, Genetics, Evolution, and Diversity

#### **Intertidal *Crepidula fornicata* Do Not Lose Biomass During Massachusetts Winters**

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A number of marine bivalve species have been found to lose substantial tissue mass during mild winters, probably because of relatively high rates of energy expenditure in times of limited food availability. In this study we set out to determine whether the suspension-feeding marine gastropod *Crepidula fornicata* also loses tissue mass during the winter. Individuals over a wide size range (about 5.5 to 49 mm in shell length) were collected intertidally in Massachusetts several times per year during 7 years between 2009 and 2019 (mean sample size ( $\pm$ SD) =  $33 \pm 14.5$  individuals collected per sampling period). In the laboratory, shell lengths were measured to the nearest 0.1 mm and dry tissue weights were determined. Seasonal sample comparisons were made using a body mass index (BMI): g dry weight/shell length<sup>3</sup>. Over the seven winters included in our study, we detected no significant declines in BMI. To investigate the impact of low food availability and the physiological impact of short-term temperature stress, we conducted laboratory studies with live individuals. We first determined the extent to which snails lost biomass while being starved for 3 weeks at a winter seawater temperature of 6°C. We also assessed the impact of a 3-hr elevated temperature stress on feeding and respiration rates for winter-acclimated individuals 24 and 48 h after the stress period had ended. Surprisingly, individuals starved at 6°C for 2 or 3 weeks in the laboratory showed no significant declines in tissue biomass. In addition, both respiration rates ( $\mu$ l oxygen consumed h<sup>-1</sup> mg tissue<sup>-1</sup>) and mean feeding rates (ml filtered h<sup>-1</sup> individual<sup>-1</sup>) declined following thermal stress for at least the subsequent 48 hr. Future studies with *C. fornicata* should document the energy budgets of these animals at low winter seawater temperatures, and the impact of short-term elevated temperatures on those energy budgets.

## **Mutation Rates of Mitochondrial and Nuclear Genomes of Gastropods**

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For many invertebrate groups, mutation rates of mitochondrial DNA (mtDNA) are typically two to ten times greater than mutation rates of nuclear DNA (nuDNA), but some land snail species show up to a 40-fold difference in rates. To better understand patterns of variation in mutation rates of mtDNA and nuDNA of gastropods and evaluate potential factors that may be associated with the apparent excessive level of rate variation among clades, I examined mtDNA and nuDNA sequence datasets from 121 published phylogenetic studies of gastropods that included various members of Caenogastropoda, Heterobranchia, Patellogastropoda, and Vetigastropoda. I used these data to infer differences between mutation rates of mtDNA and nuDNA by calculating the ratio of the total molecular divergence of mtDNA and nuDNA as estimated from gene trees. Ratios show nearly two orders of magnitude difference among datasets, with values ranging between 1.4 and 91.9, although average values calculated for most higher-level taxa (i.e., suborders and above) were less than 20. Datasets with exceptionally large ratios, which included various clades of Caenogastropoda, Heterobranchia, and Vetigastropoda, exhibit relatively low levels of nuDNA divergence (as opposed to relatively high levels of mtDNA divergence). Nonetheless, these outlier datasets also tend to include members of gastropod genera that had radiated recently. Moreover, datasets with little taxonomic breadth (i.e., contain members of single genera or families) exhibit significantly larger ratios than those with greater breadth. These results suggest that calculated values of mutation rates of nuDNA of recently diverged species are underestimated because these species show only very few if any fixed differences at nuDNA.

## **Population Genetic Structure of the Waved Whelk (*Buccinum undatum*) on the Scotian Shelf Using Two Mitochondrial Genes**

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The Waved Whelk, *Buccinum undatum* L., 1758, is a carnivorous marine gastropod broadly distributed within the North Atlantic Ocean. The life cycle of *B. undatum*, in contrast to many marine invertebrates, does not have a pelagic stage. Fertilization occurs internally and eggs are laid in large masses attached to the benthos. Adults also have limited mobility and show movement speeds of 15cm/min only when in the presence of food or predators. This limited mobility likely accounts for significant genetic structuring between whelk found between Europe and North America found in previous studies, but finer structuring of Canadian whelk has not been thoroughly assessed due to insufficient sampling. For this study, 242 whelk were sampled from eight sites on the Scotian Shelf to assess population genetic structuring using the COI and 16S mitochondrial gene regions. Sequences were concatenated for individual samples. In total, 40 haplotypes were identified. One haplotype was dominant across all sampling sites, ranging from about 45-75% of haplotype composition for individual sites. 75% of haplotypes occurred in one sampling site. Overall  $F_{st}$  was 0.024 and pairwise  $F_{st}$  was significant between one site and six others. Tajima's  $D$  values ranged from -1.33 to -1.96 and were significant for six sites, indicating a possible population expansion. Mantel Test results did not indicate that Isolation By Distance was significant ( $r^2 = 0.002776$ ,  $p = 0.295$ ), indicating that distance at this scale does not cause reproductive isolation. Results indicate a population that has likely undergone a recent expansion.

## **A Molecular Phylogeny of the Epitoniidae: Estimating Evolutionary Relationships with Broad Taxon Sampling and Genomic Data**

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The Epitoniidae is a moderately diverse family of gastropods that feed on anemones and corals, with approximately 785 species currently recognized from the intertidal to depths of more than 1,000 meters. A large number of epitoniid species and genera have been described but understanding their evolutionary relationships has been impeded by convergence in shell characters. In addition, both the Janthinidae and Nystiellidae have been recently synonymized with Epitoniidae, but whether these lineages or other large clades might merit recognition as distinct subfamilies has not been tested with dense taxonomic sampling. We used barcode sequence data (COI, 16S) from 620 specimens representing approximately 220 species from the Indo-West Pacific, Caribbean, and Mediterranean, and nuclear loci (28S, 18S, H3) from selected representatives as the first step towards an improved understanding of evolutionary relationships of these snails. Our phylogeny indicates that the genus *Epitonium* is polyphyletic and is represented by at least three distinct lineages. In addition, our preliminary results support the synonymy of Nystiellidae and Janthinidae with Epitoniidae. However, the relationships between many deep-sea taxa remain poorly resolved. To investigate these relationships further, we are obtaining genomic data with a sequence capture approach. We used published transcriptomes and genomes to identify ultra-conserved elements and exons in caenogastropods and developed a universal probe set for sequence capture. Our probe set includes 29,441 baits to target 2,896 loci via anchored-hybrid enrichment. In-silico analyses of 19 available transcriptomes indicate that our probe set recovers several hundred to more than a thousand loci from a diversity of caenogastropods, and that these data are phylogenetically informative in analyses of deep phylogenetic relationships. The recovery of loci and the utility of our bait set in resolving epitoniid relationships at the subfamily, genus and species level are now being evaluated *in vitro*.

## **Most Cephalaspidea Have a Shell, but Transcriptomes can Provide Them with a Backbone (Gastropoda: Heterobranchia)**

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Cephalaspidea comprises marine heterobranch gastropods commonly known as headshield slugs, bubble snails and their relatives. The cephalaspidean shell—which can be external and robust, internal, or altogether absent in the adult—is of particular interest in this group, and a well-resolved phylogeny can give us greater insight into the evolution of this character. Molecular data have clarified many relationships within Cephalaspidea, but studies involving few Sanger sequenced phylogenetic markers remain limited in the resolution they provide. Here we take a phylogenomic approach, the first to address internal cephalaspidean relationships, sequencing and assembling transcriptomes de novo from 22 ingroup taxa—representing the five currently accepted superfamilies, 10 of the 21 currently recognized families, and 21 genera—and analyzing these along with publicly available data. We generated two main datasets varying by a minimum taxon occupancy threshold (50% and 75%), and analyzed these using maximum likelihood, Bayesian inference and a coalescence-based method. We find a consistent, well-supported topology, with full support across most nodes including at the family and genus level, which also appears to be robust to the effect of compositional heterogeneity among amino acids in the dataset. Our analyses find Newnesioidea as the sister group to the rest of Cephalaspidea. Within the rest of the order, Philinoidea is the sister group to a clade that comprises (Bulloidea (Haminoeidea, Cylichnoidea)). There is strong support for several previously suggested, but tenuously supported relationships such as the genus *Odontogljaja* nesting within the family Aglajidae, and a sister group relationship between Gastropteridae and Colpodaspididae, with Philinoglossidae as their sister group. We discuss these results and their implications in the context of current cephalaspidean taxonomy and evolution. Genomic-scale data give a backbone to this group of snails and slugs, and hold promise for a completely resolved Cephalaspidea.

## **Conoids of the Lower Waccamaw Formation: Why are there so many of them?**

Campbell, Timothy, D.\*<sup>1</sup>; Campbell, David C.<sup>2</sup>; Campbell, Lyle D.<sup>3</sup>

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The lower Waccamaw Formation contains a rich basal Pleistocene fauna with an extreme abundance of mollusks. This diverse subtropical fauna is found in southeastern North Carolina and eastern South Carolina. Roughly 40% of the taxa are extant, and roughly 50% overlap with the Upper Pliocene Duplin Formation of the Carolinas. This study has collected and identified 744 species from a single quarry, increasing the known diversity for the lower Waccamaw from 650 to 1050 species. In my most speciose superfamily, Conoidea, I have found 95 species. There are published records of 58 species. Out of the 95, 60 are unidentified to species level, and presumed undescribed. 74 of them are additions to the known conoidean fauna. About 40 of my conoideans are known from a single specimen. I have found four conoids, six clathurellids, 29 drilliids, one strictispirid, 28 mangeliids, one mitromorphid, 14 pseudomelatomids, 11 terebrids, and one taxon of uncertain familial placement. My conoidean taxa range from a 74 mm *Conus adversarius* Conrad, 1841, to the 2 mm (full adult) *Vitricythara micromeris* (Dall, 1903). The median maximum size is 9 mm. *Conus oniscus* Woodring, 1928 is likely the gastropod with the highest biomass at this site. The three most common, and the three largest species of “turrids” are previously unreported from the formation. One undescribed species is second largest, and among the most common.

## Increase the Known Diversity with One Weird Trick: Look Closely: Heterobranchs of the Lower Waccamaw Formation

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The lower Waccamaw Formation contains a rich basal Pleistocene fauna with an extreme abundance of mollusks. This diverse subtropical fauna is found in southeastern North Carolina and eastern South Carolina. Roughly 40% of the taxa are extant, and roughly 50% overlap with the Upper Pliocene Duplin Formation of the Carolinas. This study has collected and identified 744 species from a single quarry, increasing the known diversity for the lower Waccamaw from 650 to 1050 species. In Heterobranchia, I have found 114 species. There are published records of 39 species. Out of the 114, 56 are unidentified to species level, and presumed undescribed. 101 of them are additions to the known heterobranch fauna. Nine of my non-Pyramidellid heterobranchs are known from a single specimen. In my most speciose family, Pyramidellidae, there are published record of 20 species. I have 92. 50 of them are unidentified to species level, and presumed undescribed; and 90 are additions to the known pyramidellid fauna. About 40 of my pyramidellids are known from a single specimen. I have found one cimicid, two murchisonellids, one mathildid, one architectonicid, one acteonid, two ringiculids, one retusid, six tornatinids, one limacinid, one creseid, 92 pyramidellids, two amathinids, one physid, one ellobiid, and one taxon of completely unknown placement. My heterobranch taxa range in size from *Chemnitzia atlasi* (Bartsch, 1955), *Chemnitzia cerberusi* (Bartsch, 1955), an undescribed *Chemnitzia*, and two undescribed *Strioturbonillas* at ~15 mm to the 0.92 mm (full adult) *Cyclostremella humilis* Bush, 1897. The most common taxa include *Ringicula*, *Acteocina*, *Iolaea millium* (Lea, 1843), *Ondina emeryi* (Bartsch, 1955), *Chrysallida weberi* Bartsch, 1955, and *Chemnitzia atlasi* (Bartsch, 1955). All of the largest and most common pyramidellids, except the *Iolaea*, are previously unreported.



## SESSION 4

### Special symposium: Modern Advances in Mollusc Behaviour

# **Mussels in Hot Water: The Behavioural Ecology of Temperate Mussels Under Ocean Warming and Acidification**

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Global climate change is anticipated to have wide ranging effects on ecologically and economically important marine biota. Two global change stressors of contemporary interest in the marine realm are ocean acidification and warming (OAW). Herein, the potential effects of OAW on animal behaviour can act as important mediators of ecological impacts. In this talk, I will discuss some of our research regarding effects OAW on valve gaping behaviour of temperate marine bivalves (mussels). Using empirical evidence from laboratory experiments, I will demonstrate that warming, but not acidification, has the potential impact mussels' behavioural responses to predators (valve closures). By combining our behavioural results with previous research regarding OAW effects on mussel ecophysiology, I will argue that the observed effects of warming on mussel behaviour likely contribute to negative effects on mussel ecophysiology. I will close by discussing ways in which these impacts on behaviour and ecophysiology can translate into population- and community-level impacts and lay the groundwork for future work in this arena.

## **Temporal Mismatch Between Pumping Rate and Food Availability in *Mytilus edulis***

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Feeding rates in bivalves are influenced by a suite of environmental conditions including food quantity and quality; however, feedbacks between feeding and digestive processes are not well understood. The purpose of this study was to explore feedbacks between feeding and digestive processes, as well as interindividual variability in feeding rates, in the blue mussel *Mytilus edulis*. Over the course of five days, physiological rates related to feeding (pumping and ingestion) and digestive processes (gut passage time) were measured every 20 minutes, and 24 hours, respectively using natural seawater and individuals of 50mm in length. Preliminary results suggest high interindividual variability in feeding rates, with some individuals continually pumping at high rates ( $\approx 5 \text{ lh}^{-1}$ ) and some at low ( $\approx 1 \text{ lh}^{-1}$ ), despite being exposed to the same conditions. Gut passage time also varied both between individuals, and temporally throughout the experiment. To explore feeding-digestive feedbacks, pumping rate was correlated to food availability (Fluorescence ( $\mu\text{g l}^{-1}$ )) using temporal mismatches informed by gut passage time. Results indicate that there is a higher degree of correlation when pumping rates are matched to food availabilities from 10 hours prior. This result suggests that digestive processes may play a role in the feeding activity of bivalves, and that current feeding rates may reflect a previous food environment. These findings contribute to our mechanistic understanding of feeding-digestive relationships and may be informative for *in situ* measurements of feeding, as well as individual growth models.

## **Behavioral Component of Host Infection Strategy in the Polymorphic Lures of *Lampsilis fasciola* (Bivalvia: Unionidae)**

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Mimicry and deception are ecologically and evolutionarily significant phenomena that have been observed and studied across a wide range of biological systems. A good mimic involves the adaptive resemblance of the mimic to a model, and can incorporate multiple different criteria including morphology, pigmentation, behavior, and olfactory cues. In bivalves, mimicry is utilized by many species of freshwater mussel in the family Unionidae to exploit host fish as part of a complex parasitic life cycle where the unionid larvae are obligate parasites on fish. The gravid females of some species produce mimetic lures from their mantle tissue or release mimetic aggregates of larvae called conglutinates. *Lampsilis fasciola* is a species of North American unionid mussel that produces a mantle lure with well documented polymorphisms. Some individuals create lures that closely resemble darters (*Etheostoma* and *Percina*), while others create bright orange lures with smooth margins, possibly resembling a leech. Within single populations, striking differences in lure coloration and shape have been observed. However, the behavioral component of this lure is poorly understood. We collected video data of lure behavior from 69 *L. fasciola* from two sites in Southeast Michigan. The behavior in a subset of videos (35) was quantified by hand using Adobe Premiere and recording specific frames in which lure movements begin and end. We also recorded lure behavior from a small number of *Lampsilis cardium*, a congener that co-occurs with *L. fasciola*. Preliminary analyses suggest that there are strong quantitative and qualitative differences between *L. fasciola* and *L. cardium*, but not between *L. fasciola* morphs. *L. fasciola* behavior is characterized by highly variable behavior within individuals, while *L. cardium* behavior is highly regular. Within *L. fasciola*, the behavior of the lure does not seem to correlate with what we presume the lure is trying to mimic.

## **Understanding Behaviour for Improving Stock-Enhancement Success of the European Abalone, *Haliotis tuberculata***

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Stock-enhancement programs can be an efficient method to restore collapsed natural populations or preserve fishing activities. This practice consists in releasing hatchery-reared juveniles from wild or farmed broodstock into natural environments. However, success is often low with less than 12% abalone survival measured worldwide. Several factors such as predation, habitat quality, abalone age, shell length or the use of protective structure have already been assessed for their potential impact on mortality rates. However, the role of factors such as domestication, stress and nutrition status before implantation are far less known. In addition, a fine analysis of abalone behavioural response to predator might be an interesting way to understand the high mortality observed mainly the first month after implantation. A project (Ourmel FEAMP) is currently conducted to study 1) the impact of domestication process on adult and juvenile abalone behaviour 2) the role of stress and nutrition status just before implantation. We focused mainly on prey-predator responses using different spatial and temporal scales: short-term response to predator and stressful events, diurnal rhythm in the presence or absence of predator during trials of one or two weeks, and survival in large mesocosms. We showed that domestication might impact adult abalone response to predator after only one generation. However, these results were not confirmed in juveniles indicating this effect might be age-dependant. Stress and nutrition during the preparation that precedes implantation are probably two of the major stressors that strongly impact the abalone behaviours and response to predator in the wild. In addition, we showed that the hiding behaviour and activity during night is determinant for the survival during the first week post-implantation. The next step of this project will be to design a release system adapted to the ethological characteristics of abalone juveniles to avoid high mortalities due to predators.

## Collective Behaviour and Social Dynamics During Interspecific Hunting Between Octopus (*Octopus cyanea*) and Multiple Fish Species

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In collective behaviour, complex coordination and individual/group decision-making can emerge from simple, localized rules of interaction, considering every individual as identical. However, in biological systems, variation amongst individuals can alter the “weight” of specific individual’s decision within a group, creating a dynamic network of attraction-repulsion forces driving individual and group movement. Parallely, sociality has the potential to drive brain evolution and cognition, but the role of individual cognition on collective movement and group decision-making constitutes a largely unexplored field. Using SCUBA, we recorded interspecific coordinated hunting events between *Octopus cyanea* and multiple partners (i.e. various fish species), and obtained animals tracks over a 3D reconstructed habitats, which enables multi-scale analyses gauging novel and key parameters in interspecific collectives, e.g. movement synchrony between *O. cyanea* and fish partners; leader-follower dynamics; social and individual level factors influencing leadership; and presence/absence of social rules. From individuals to collective, understanding the underpinnings of these interspecific interactions can potentially deepen our knowledge on cephalopod cognition in a social context, mechanisms of intentional/unintentional communication, and the influence of higher order traits (morphological, behavioural, and cognitive) on collective movement and decision-making in naturally-occurring heterogenous groups.

## **Nociception and Pain in Cephalopods**

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Cephalopods are the most neurologically complex of all the molluscs, with large brains and high densities of receptor organs all over their soft bodies. Cephalopod nociceptors, neurons tuned specifically to noxious or injurious stimuli, exhibit characteristics that are intermediate between those typical of other molluscs and those of vertebrates. Similarly to nociceptors found in other molluscs, cutaneous nociceptors in cephalopods are polymodal, relatively high threshold, and normally silent. After tissue injury, cephalopod nociceptors display robust and long-lasting plasticity with many of the same molecular hallmarks to those of molluscs', but lack site-specificity and instead show widespread hyperexcitability at sites both close to and distant from the injury site. In contrast to other molluscs (and all other invertebrates), cephalopod nociceptors enter a persistently hyperexcitable state long after injury which is characterized by ongoing, spontaneous firing. In vertebrates, spontaneous firing of nociceptors drives ongoing, spontaneous pain. Whether cephalopods experience vertebrate-like pain after injury is a subject of ongoing debate – the extensive peripheral processing of sensory inputs in cephalopods casts doubt on whether any nociceptive signal is processed in the higher cognitive centers of the central brain. Recent work from our lab shows that cephalopods exhibit behavioral changes after noxious stimulation that closely resemble pain behavior in mammals, suggesting that the affective (suffering) component of pain has also evolved in cephalopods. This finding raises interesting questions both about the welfare of laboratory cephalopods (and other molluscs) and equally interesting questions about the evolution of nociception and pain in diverse clades.

## **Circadian Rhythms and the Influence of Light on the Behavior of Nudibranchs**

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Circadian ( $\approx 24$  hour) rhythms are ubiquitous across animals, enabling organisms to prepare for optimal environmental conditions for foraging, evasion of prey, finding mates, and other important behaviors. These rhythms are produced by endogenous molecular clocks, which are best understood in *Drosophila* and mammals. To better understand the evolution of these clocks, we have been investigating circadian rhythms of behavior, and the underlying clock mechanisms, in several species of nudibranchs, including *Melibe leonina* and *Berghia stephanieae*. Early experiments indicated that *M. leonina*, while somewhat active throughout a 24-hour period, was most active at night. In the absence of any external light cues, this “nocturnal” pattern of locomotion persisted, indicating circadian rhythms of locomotion and the presence of an internal clock. Preliminary data in *B. stephanieae* suggests that this species was also nocturnal and likely exhibited circadian rhythms of locomotion. In *M. leonina*, eyeless animals did not maintain circadian rhythms of locomotion in constant darkness, suggesting that the eyes are important for the clock. However, eyeless animals still exhibited nocturnal activity in the presence of light cues, indicating that extraocular photoreception may be important in mediating the effects of light on behavior. Additional experiments in both *M. leonina* and *B. stephanieae*, demonstrated that both species responded to illumination of posterior epidermal tissue. To eliminate the possibility that the eyes were detecting light from posterior illumination, further experiments were done in headless (and thus eyeless) *B. stephanieae*. Headless animals still responded to light, confirming the presence of extraocular photoreceptors. Light responses occurred with red light stimuli, as well as white light, indicating that extraocular photoreceptors were not restricted to short wavelengths of visible light. In summary, these species of nudibranchs exhibited circadian rhythms like most other animals and both the eyes and extraocular photoreception appear to be important in influencing behavior.

## Light Preference of a Photosynthetic Animal: *Elysia crispata* Rejects Red and Intense Lights

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Some sacoglossan slugs can obtain energy from the chloroplasts sequestered from the algae they consume (kleptoplasty). The relationship between slugs, chloroplasts and light, are central to understand these “photosynthetic” animal models. Too much light can damage the chloroplasts in photosynthetic organisms, and recent studies have described a photoprotective behavior in different species of *Elysia*. However, to better comprehend the advantages of this association and delimit the functionality of chloroplasts, behavioral studies under different light scenarios are still needed. Therefore, the aim of this study was to examine the preference of *Elysia crispata* for different light intensity and spectrum. To assess preference (active selection) and distinguish it from a passive association, two experiments were performed with organisms of *E. crispata* (N=75). Slugs were individually placed at the center of a cross maze with four different light conditions for 30 min: 1) the color choices offered simultaneously were green, yellow, red and blue light (n=31), and 2) the intensity choices presented simultaneously were 60, 180, 425 and 1400  $\mu\text{mol m}^{-2} \text{s}^{-1}$  light (n=27). A condition without light was the Control in both experiments (n=34 and n=29, respectively). The frequency, duration and sequence were recorded and considered dependent variables. At the end of the color experiment, 32.2-35.4% of the slugs selected yellow and blue, with a total duration (TD) of 4:00 h in both cases; 29% of the slugs chose green (TD 1:39 h) and only 3.2% were found in the red light (TD 8:43 min). Results of the intensity experiment showed that 48.1% of slugs preferred 60 (TD 4:23 h) and 37% preferred 180 (TD 4:44 h), whereas only 7.4% selected 425 and 1400 (TD 1:32 h and 48 min, respectively). Overall, results indicate that slugs actively reject both red and high light intensities (425-1400  $\mu\text{mol m}^{-2} \text{s}^{-1}$ ).



## Using Visual Behaviour and Retinal Ultrastructure to Explore Visual Function in the Marine Gastropod *Conomurex luhuanus* (Strombidae)

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All species within the conch snail family Strombidae possess extremely well-developed camera-type eyes of surprising sophistication compared to other gastropod groups. Although these eyes are known to be structurally complex, very little research on their visual function has been conducted. Here, we use isoluminant looming visual stimuli to test for behavioural evidence of high spatial resolution and luminance intensity contrast vision in a strombid, *Conomurex luhuanus*. Using these stimuli, we show that this species responds to objects as small as 1° in its visual field and can detect objects of a low luminance intensity contrast compared to the background, of Weber contrast -0.14. The defensive withdrawal response elicited by small, low-contrast visual stimuli suggests that conch use their high visual acuity and contrast sensitivity for early detection and avoidance of potential predators. We support these findings with calculations of spatial resolution and sensitivity from morphological data, and demonstrate a need for the integration of morphological and behavioural approaches in animal vision studies. Contemporary imaging techniques (serial block-face scanning electron microscopy, in conjunction with transmission electron microscopy) also reveal a greater complexity in *C. luhuanus* retina ultrastructure than previous studies of this species have found using TEM alone. We found the *C. luhuanus* retina is comprised of six cell types (including a newly identified ganglion cell and accessory photoreceptor), rather than the four cell types previously identified. These findings suggest conch have a remarkably complex visual system compared to those within other gastropod groups. This raises exciting new questions about how visual information is processed within strombids, and why this group has such fine spatial resolution for any gastropod, given that similar predator avoidance tasks in the periwinkle *Littorina* are supported by a spatial resolution nearly four times lower than that of *C. luhuanus*.

## Context Dependence of Parasite-Modified Behavior for Freshwater Planorbid Snails

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Many parasites with complex life cycles cause host behavioural changes that increase the likelihood of transmission to the next host. Parasite modification is often found in trophic transmission, but its influence on non-trophic transmission is unclear. In trematode parasites, transmission from the first to second intermediate host is non-trophic, suggesting that free-swimming larvae (cercariae) emerging in closer proximity to the next host would have higher transmission success. We performed two series of behavioural experiments with echinostome trematodes and their snail hosts to determine if potential second hosts (*Planorbella duryi*) were more attracted to parasitized first hosts. We took advantage of the parasite's broader specificity for second intermediate snail hosts and tested attraction to two heterospecific snail species: 1) *Stagnicola elodes*, 2) *Planorbella pilsbryi*. In a Y maze, a responding snail (*P. duryi*) was placed in the base and its response to treatments was assessed. Treatments were no stimulus, turion duckweed (*Lemna turionifera*; food item), non-parasitized first hosts, parasitized first hosts, and finally parasitized versus non-parasitized first hosts. Snails showed some attraction to uninfected *S. elodes* snails but had a stronger response to infected *S. elodes* snails. In contrast, there was no response to uninfected or infected *P. pilsbryi* snails. These results indicate that host behavioural modifications by echinostome trematodes are context dependent. Potential second host snails were more attracted to parasitized, heterospecific first host snails over non-parasitized heterospecific snails in one context (*Planorbella* and *Stagnicola*), but not the other (*Planorbella* and *Planorbella*). This work demonstrates that echinostome trematodes alter snail behaviour by changing navigational choices in uninfected potential hosts through a chemical communication mechanism. However, more work is needed to understand the context dependent nature of these behavioural modifications and their influence on non-trophic transmission to understand how host behavioural modifications influence freshwater ecosystem structure and function.

## **Parasite Impacts on Snail Chemical Communication: Implications for Behavioural Modification and Defence Priming**

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Host behaviour may be modified by their parasites to increase the likelihood of transmission, but the mechanisms underlying these interactions are not well understood. It is often suggested that chemical cues may be mediating these behavioural shifts, although through indirect evidence. Hosts and parasites produce signalling molecules, like oxylipins, that may play a role in transmission and behavioural modification. Parasites may also release their own oxylipins within hosts and/or manipulate host cues, representing a mechanism for parasite-modified behavior within some systems. Exposure to altered cues from infected hosts may also change behaviors in other individuals related to foraging, competition, and defense priming. Yet, the limited taxonomic and contextual scope of studies on signalling molecules, like oxylipins, limits our ability to understand their role in parasite-modified behaviour. We characterized the oxylipins of two snail species, Ram's horn snails, *Planorbella pilsbryi*, and Marsh pondsnails, *Stagnicola elodes*, both of whom are commonly infected with echinostome trematodes. We tested for differences in the diversity and amounts of oxylipins based on infection status and parasite activity. Overall, infected snails release different oxylipins than uninfected conspecifics, oxylipin cocktails vary by species, and increased parasite activity is correlated with the emission of higher amounts of oxylipins. In order to better understand the function of these oxylipins on snail defence priming, we exposed Marsh pondsnails to candidate oxylipins that have been found in higher amounts in infected snails. Exposure induced an immune response in naive snails, suggesting a role of oxylipins in inducing defence priming in naive hosts within a community. These results indicate that the alteration in oxylipin cocktails may play a role in altering transmission success and function as a possible mechanism for parasite-modified behaviour. More study is needed to further understand how the alterations in chemical cues may influence aquatic species interactions and ecosystem dynamics.

## ***Lymnaea* are Competent to Undergo Both Configural Learning and a Garcia-like Effect and Form Long Term Memory**

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Configural learning (CL) is a higher-order form of learning where snails develop a landscape of fear when they experience a predatory cue (e.g., crayfish effluent, CE) along with a taste of food (e.g., carrot, C). A 45 min one-time simultaneous exposure to CE+C results in a suppression of the food response to C; but the memory only persists for 3h. However, this intermediate form of memory (ITM) can be extended into long-term memory (LTM) by: 1) a second CL training session, 2) a flavonol (quercetin) and 3) a flavonoid (epicatechin). A Garcia-like learning and memory effect can also be demonstrated in *Lymnaea*. The Garcia-effect, known in human's as the Sauce Bearnaise-effect, occurs when a novel food substance is tasted and then the organism becomes nauseous (i.e. unwell) many hours later. It is a specialized form of conditioned-taste aversion. In *Lymnaea* the Garcia-effect occurs following the tasting of a novel food and then experiencing a heat shock (HS, 1h at 30°C) hours later. The snail suppresses feeding to only the novel food substance experienced before the HS and not to other food substances for up to days (i.e., LTM). Interestingly, quercetin which enhanced CL memory and which blocks the up-regulation of HSPs in *Lymnaea*, obstructs the Garcia-effect, if administered before the HS. Finally, the Garcia-effect is observed only if the snails are tested in a food-satiated state; food-deprived snails prefer to eat rather than exhibit LTM. Thus, *Lymnaea* exhibit far more complicated forms of associative learning and LTM than we initially thought.

## **Sensory Modulation of Odour-Based Navigation in the Freshwater Gastropod, *Lymnaea stagnalis***

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Many aquatic animals use olfactory-based navigation to move relative to prey and predators. Two common navigation strategies are used, depending on the flow in the animal's environment. Chemotaxis (moving up or down a chemical gradient) is used to move towards or away from odour sources in either no flow or laminar flow conditions. Meanwhile, odour-gated rheotaxis (moving up or downstream in the presence of an odour) is used in turbulent flow. Moreover, searching-for versus avoidance-of odour sources are distinct goals which need not require a simply inverted navigation strategy (there is only one odour source location to find, but many locations which could be sufficiently far from an odour source). Few studies have tackled this full complexity in one species. Navigation by the great pond snail, *Lymnaea stagnalis*, presents an interesting case in that they can experience both kinds of flow environments with both attractive (prey) and aversive (predator) odour sources. In a series of behavioural experiments, we are testing whether the snails can switch between chemotaxis and odour-gated rheotaxis, and how navigation differs relative to prey and predator odour sources. The results indicate that *L. stagnalis* can use either chemotaxis or odour-gated rheotaxis when moving towards at least some prey odour sources. Navigation relative to predator odour sources is categorically distinct, and seems to primarily involve upwards movement rather than horizontal movement away from the odour source. Furthermore, there is evidence that vision is integrated along with odour-based navigation, at least in environments without flow.

**SESSION 5(A,B)**  
**Contributed Talks**

**5A: Freshwater Molluscs: Taxonomy, Species Diversity,  
and Temporal Dynamics**

**Tales from Living and Dead Snails: Faunal Dynamism in Lake  
Tanganyika, East Africa**

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Lake Tanganyika is the second oldest and deepest lake on Earth, containing 18% of the world's unfrozen fresh water. Its hyperdiverse, largely endemic fauna (fish, molluscs, crustaceans etc.) is largely confined to the extremely narrow, bath-tub rim of this steep-sided, ancient rift lake. Here, diverse benthic faunas adapted to clear waters are under increasing threat from increased anthropogenic sedimentation and rising anoxic waters from the depths. Short sediment cores from the lake reveal profound environmental and microfaunal changes to have occurred over the past century on local and regional scales. Around this highstand rift lake sedimentary outcrops are too limited to establish the response of the endemic macrofauna to environmental change. However, an unexpected source of data is available. Around the lake large numbers of long-dead, reworked mollusc shells can be collected by SCUBA from the lake bottom and beaches with calibrated C14 dates as old as 3000 years. Recent taxonomic work combined with extensive collecting has elucidated the taxonomy and distribution of abundant and species-rich snail clades, with many highly localized taxa as well as species-poor widespread taxa. A common mismatch in live-dead occurrences attests to geographic range contractions and extinctions in the past few centuries. Our emerging view is of a taxonomically richer, more dynamic and volatile molluscan fauna than previously suspected and one in which both short-ranged and widespread species are under increasing extinction threat.

## **The *Neothauma* Shell Beds of Lake Tanganyika: Palaeoecology, Patchy Ecosystems and Divergence in a Rift Lake**

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Shell beds are full-circle, biologically generated habitats for living organisms and key windows on past environments in fossil outcrops and cores. Lake Tanganyika (LT), Africa, has huge carpets of shell beds; up to 30% of shallow soft substrate consists of densely packed shelly substrates dominated by dead shells of a single gastropod species (*Neothauma tanganyicense*). Like other biogenic habitats such as reefs, LT shell beds host a rich, endemic fauna of sponges, fish, molluscs, crabs and other organisms. Some of these appear not only to be specialised on this unique substrate, but to have speciated in situ.

We are assessing this geologic-biologic system to determine how origin and persistence of the shell beds relates to population and evolutionary history of shell bed organisms and to ecosystem structure. Our multi-disciplinary project includes a range of approaches, from genetics of *Neothauma* to structural and sedimentological geology of the depositional systems. COI sequences reveal significant population structuring among living *Neothauma*, implying restricted gene flow even in this ubiquitous species. Understanding the mechanism of formation and age of these shell beds is critical for a range of issues from rates of divergence to interpretations of paleoclimates.

These shell beds are impacted by increasing rates of sedimentation caused by anthropogenic land-use changes. Preliminary data indicate that modern sediment blankets on the shell beds are thick and extensive enough to 1) preclude sponge growth, 2) remove cryptic habitats and 3) fragment these ecosystems into isolated patches.

## **Insights from Integrative Taxonomy on the Limits of Morphological Delimitation and Species Diversity in Freshwater Snails (Planorbidae: *Planorbella* and *Helisoma*)**

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Species-level resolution is critical to understanding the ecological role and evolutionary history of taxa. However, confounding factors like cryptic species, phenotypic variation, and subjective interpretations of morphology have led to species misidentifications and poor taxonomic resolution. To test whether these factors have resulted in inaccurate estimates of species-level diversity in freshwater snails, we used integrative taxonomy to characterize the diversity of 5 nominal planorbid species (4 *Planorbella* and 1 *Helisoma* species). These species commonly occur in North America and have been subject to taxonomic controversy. We explore whether shell morphology is sufficient to reliably distinguish the 5 nominal species by comparing putative morphology-based identifications with phylogenetic and geometric morphometric analyses of shell shape. Snails were collected from 7 sites (n = 212) ranging across 2 watersheds in central North America. Specimens were digitally imaged and a subset (n = 55) were sequenced at the mitochondrial COI gene (586 bp). Phylogenetic analysis of 52 unique sequences (including 18 from GenBank) revealed 5 clades that were at least 5% different. However, multiple nominal species were assigned to 3 of the 5 clades according to both GenBank identifications and our putative shell-based identifications. Geometric morphometric analysis differentiated 3 of the 5 clades, while the remaining 2 overlapped. We have shown that the genetic and morphological differences among 3 nominal species are congruent and that shell-based identification of species is mostly reliable. In contrast, the best method to discriminate the remaining 2 species is DNA barcoding as morphological analyses did not reveal clear and reliable delimiting traits. The inability of phylogenetic and geometric morphometric data to reliably differentiate 2 species indicates that examinations of other biological traits are needed. We will discuss our use of genome skimming to test whether analysis with mitogenomes and some nuclear genes provides more resolution on planorbid species delimitation.



## ***Limnophysa*, not *Ladislavella* for the North American Stagnicoline Snail Genus**

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Recent changes in lymnaeid taxonomy were reviewed and adjustments are suggested after consulting the rules of the International Code of Zoological Nomenclature (the Code, hereafter). BARGUES *et al.* (2001), using IT2 sequences, demonstrated that North American *Stagnicola* were genetically distinct from the European species. Meier-Brook and BARGUES (2002) proposed putting their North American stagnicoline clade (and *S. occulta*) into a new genus, *Catascopia*. CORREA *et al.* (2010), using ITS-1, ITS-2, and 16S sequences and more lymnaeids species, also supported the clade as a distinct taxonomic group. Vinarski (2012) noted older lymnaeid genus names were available that should be used instead of *Catascopia*, such as *Polyrhytis* and *Ladislavella* Dybowski, 1913. Since *Polyrhytis kingii* Meek, 1876, is a fossil and can't be used for any genetics, this was ruled out. Vinarski (2012) proposed *Ladislavella* as the genus for the clade, with *Leptolimnaea terebra* var. *sorensis* Dybowski, 1913 as type. The type species is currently recognized as either *Stagnicola terebra* or *Ladislavella terebra* (Welter-Shultes 2012; Glöer 2019). Campbell *et al.* (2017) used *Polyrhytis* instead of *Ladislavella* as a replacement for North American *Stagnicola* in their recent publication on Lencinae, based on the date priority of *Polyrhytis*. However, the Code rules (Chap. 15, Article 68.2) indicate that the type species for the new genus created by Meier-Brook and BARGUES (2002) is *Lymnaea catascopium* Say, 1817, by original designation. The Code also states (Chap. 6, Article 23.1) the name for the genus must be the oldest available name applied to that type. A review of the literature shows that *Limnophysa* Fitzinger, 1833, was applied to *catascopium* by Beck (1837), a genus later synonymized with *Stagnicola* Jeffreys, 1830 (Dall 1905; Baker 1911). So, *Limnophysa* is the oldest name applied to the type species that is available. In this case, *Limnophysa* has date priority over both *Ladislavella* and *Polyrhytis* (both now junior synonyms) regardless of type species.

## **Good, Clean Family Fun: Biodiversity Informatics of Freshwater Bivalves Above the Species Level**

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The MUSSEL Project Database (<http://mussel-project.net/>) of taxonomy and specimen records for freshwater bivalves (especially the order Unionoida) differs from similar endeavors in the extent to which “taxonomic opinions” are reported. In databases, a taxonomic opinion is an associative entity relating three pieces of information: a taxonomic work, a named taxon, and a valid taxon that circumscribes the nominal taxon (at least according to the author). For the luddite, a taxonomic opinion is a line in a synonymy. For any taxon, the MUSSELpdb lists the history of use of a described taxon. These data are the basis for the classification in the MUSSELpdb while simultaneously providing users with information about alternative classifications.

For species, the implementation and interpretation of taxonomic opinions is intuitive. Species are real and discoverable natural entities, and even non-systematists are familiar with the concepts of binomial nomenclature and synonymy. It is the rare taxonomic work that doesn't mention species by name.

Capturing and reporting taxonomic opinions above the species level is more complex for several important reasons, including: 1) recognition of supra-specific taxa is based on tradition and authority; 2) while every mention of a binomial species implies a genus, the application may reflect useful taxonomic information or merely satisfy Article 5 of the ICZN; 3) authors have no obligation to express a formal taxonomic opinion above the genus level; 4) the Principle of Coordination (especially for the family-group level, Art. 36) stretches nominal taxa across multiple taxonomic ranks; and 5) all kinds of useful data relevant to classification are presented as phylogenetic trees that are not amenable to the traditional format of a synonymy.

I have been working to implement solutions to these issues in the Internet version of the MUSSEL Project Database, and my talk will discuss my results to-date.

## 5B: Land Snails: Species Delimitation, Evolution, Geographic Distribution, and Conservation

### Cape Breton Highlands National Park: Opportunities for Research on Terrestrial Gastropods

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Cape Breton Highlands National Park (CBHNP) was established in 1936 and consists of 950 km<sup>2</sup> of forest, wetland, aquatic, and coastal habitats in northern Cape Breton, Nova Scotia. Past faunal inventories of invertebrates within Park boundaries have focused largely on terrestrial arthropods and freshwater invertebrates; almost nothing is known about the diversity and distribution of land snails and slugs. An improved understanding of the terrestrial gastropods within the Park is important for several reasons: 1) to preserve and protect natural resources within the context of a changing climate; 2) to identify potential vectors of *Parelaplostrongylus tenuis*, a nematode worm that causes devastating neurological effects in moose, and 3) to increase our knowledge of terrestrial ecosystems within CBHNP. To estimate the diversity of land snails and slugs likely to be present within CBHNP, we examined collection records from Cape Breton Island based on inventories from the Nova Scotia Museum of Natural History, Canadian Museum of Nature, other searchable museum and citizen science databases (InvertEBase, iDigBio, iNaturalist), as well as the published literature. Search results were updated to reflect current classification and taxonomy. The land snails of Cape Breton represent a relatively impoverished fauna compared to other parts of the NE USA, reflective of the post-glacial colonization of these landscapes within the past 10,000 years. Our compiled species records comprised 57 species of terrestrial gastropods in Cape Breton, representing 22 families; 26% of these species are likely introduced. This diversity is lowered to 52 species when considering only collection records from the two counties (Victoria, Inverness) which include CBHNP. Eight species are known vectors of the brain worm, *P. tenuis*, in Atlantic Canada. We hope that this quick assessment of species records in Cape Breton highlights the opportunity for research within CBHNP and encourages future collaborative research on land snails in the region.

## Conservation for an Endemic Springsnail in Utah's West Desert

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**Prerecorded talk available at:** <https://www.youtube.com/watch?v=PRGUHtDquw>

The Sub-globose Snake Pyrg *Pyrgulopsis saxatilis* is a springsnail found only in one spring complex in the West Desert of Utah. It is considered a sensitive species in Utah due to its endemism and was petitioned for listing under the Endangered Species Act (ESA) in 2009. Springsnail surveys in 2019 found that the current abundance and distribution of this species had declined and non-native fishes were present for the first time. Biologists were concerned that armored catfish (Loricariid catfish, *Ancistrus* sp., most likely *A. cirrhosus*) could be directly consuming snails or indirectly competing for food, which could be contributing to the lower observed springsnail densities. In 2020 the Utah Division of Wildlife Resources, along with federal partners, developed a Conservation Agreement and Strategy (CAS) that committed all partners to conservation actions to help ensure the persistence of this springsnail. Efforts are already underway to implement the CAS. A total of 1,758 armored catfish have been mechanically removed from the spring complex since December 2020. Some of these armored catfish (568) were marked and released below a newly constructed barrier to assess its effectiveness at preventing upstream movement of non-native fishes. To date, none of the tagged fish have been found upstream of the barrier. Future rotenone treatments are planned for non-native fish eradication efforts, and bioassays suggest that a 4 ppm treatment over 8 hours should achieve 100% mortality of all non-native fishes. Examination of 56 armored catfish stomachs found seven springsnail shells in six stomachs. The Sub-globose Snake Pyrg was determined to be not warranted for listing under the ESA in 2020 due, in part, to the partner commitments identified in the CAS. The CAS partners plan to continue conservation efforts to ensure the persistence of this species into the future.

## **Molecular Phylogenetics, Biogeography, and Premating Isolation in the Punctoid Land Snails of Belau (Republic of Palau, Oceania)**

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The land snail faunas of Pacific Islands are well known for their high species diversity, high degree of endemism, and often exceptional morphological diversity. Many aspects of the evolution and biogeography of these remarkable land snail faunas remains unexplored or unresolved for all but the most charismatic families. This is especially true for species within superfamily Punctoidea, particularly the Charopidae and Pacific-endemic family Endodontidae, which have been decimated by human-induced extinction on many archipelagos. The Belau archipelago (Republic of Palau) with its extensive intact pristine lowland rainforest is home to many extant and archipelago- (and island-) endemic punctoids and presents a unique opportunity to better understand the diversification of one of the most diverse but also imperiled land snail lineages on Pacific islands. For the first time, the diversification of the endemic Pacific punctoid fauna of Belau was studied using Bayesian Inference (BI) and Maximum Likelihood (ML) methods on mitochondrial (COI) and nuclear genes (ITS2). Our results do not indicate any biogeographic signal in the relationships of Belau punctoid species. However, morphological disparification in subspecies of *Aaadonta constricta* may have been initiated by the vicariance of the archipelago since the last glacial maximum (approx. 18,000 ybp). In addition, shell morphologies traditionally interpreted as being adaptive (e.g. shell shape and apertural barriers) have arisen and have been lost without ecological divergence suggesting non-adaptive trait shifts. Finally, we report the first new punctoid species are reported from living individuals as well the first new genus record from the Belau archipelago in nearly half a century.

## **Does Fortune Favor the Small? Immigrant Selection on Pacific Island Land Snails**

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Dozens of land snail families have colonized and diversified among Pacific Islands, but relatively little is known about how these snails disperse from mainland to island systems or between islands. Immigration to oceanic islands is limited by species' passive dispersal abilities, i.e. probability of being carried to a new island and capacity to survive an over-ocean journey. Possible dispersal mechanism, such as wind- or bird-mediated dispersal, rafting on vegetation, or floating in open water, may place different selective pressures on dispersing snails. This study investigates traits that may be under immigrant selection to inform hypotheses about over-ocean dispersal mechanisms. I focus on land snail assemblages in three Pacific archipelagos of increasing isolation from mainland systems: Lord Howe Island and neighboring small islands, Mariana Islands, and Samoan Islands. Preliminary results show that across all three archipelagos, archipelago-endemic species are larger than widespread species, and, compared to pulmonates, operculate species are overrepresented among single-island endemics. Additionally, vegetation-dwelling species are more likely to be archipelago- or island-endemics, and single-island endemics tend to be associated with high-elevation habitats, whereas widespread species are more common at lower elevations. These results suggest that small-bodied, ground-dwelling, low-elevation pulmonates are most prone to inter-archipelago dispersal, while larger, vegetation-dwelling, high-elevation operculate species are more likely to be confined to a single island or archipelago. Findings are consistent with the hypothesis that small, epiphragm-building pulmonates may be more likely to be picked up by wind or birds, carried farther, and less likely to desiccate during long-distance dispersal. The results also support a prediction of the Taxon Cycle that more geographically restricted island taxa also tend to be restricted to higher elevations and more specialized habitats or diets (i.e., herbivorous species and species eating arboreal biofilms, as compared to presumably detritivores ground-dwelling species).

## **Pacific Island Land Snail Biodiversity Repository (PILSBRY) Portal**

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Containing more than 6,000 species across 25,000 islands, Pacific Island land snails (PILS) are extraordinarily diverse due to their long, isolated evolutionary histories. Mostly composed of narrow-range, single island endemics, this fauna is increasingly threatened by habitat destruction, climate change and invasive species. Having succumbed to these threats, these snails account for nearly half of all documented animal extinctions since the 1500s. Unfortunately, a lack of research and easily available data, such as species names, collection dates and their location has limited the development of current PILS knowledge needed for conservation efforts. Fortunately, much of this information can be obtained from specimens and their associated data housed in museum collections. A coalition of six museums holding the majority of PILS information in the United States consequently developed the Pacific Island Land Snail Biodiversity Repository (PILSBRY) web portal, mobilizing their valuable resources for use by researchers, organizations and community scientists. Data for 3,681,279 specimens across 369,092 collecting events have been made publicly available, significantly contributing to biodiversity and systematic assessments. A comprehensive taxonomic authority file and a Pacific Island wide gazetteer are in development and will facilitate synthesis of data from across all collections. Images of type material, ledger entries and other associated metadata will also be linked to specimen records. This quick sharing of accurate, reliable data is necessary if we are to understand PILS evolution dynamics and make effective decisions regarding their conservation.

## **Anatomical Data Supports Only Four Species of Partulid Tree Snails in Papua New Guinea and the Solomon Islands, One with an Extraordinary, Multi-Archipelagic Distribution**

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Partulid tree snails of Papua New Guinea (PNG) and the Solomon Islands (SI), have remained relatively understudied and their taxonomy unstable. Surveys by Yoshio Kondo in the 1960's led him in an unpublished manuscript to reevaluate and greatly reduce the number of species he considered valid in the region, a trend that continues (Gerlach, 2016). We are engaged in a detailed taxonomic review of this regional assemblage that involved extensive regional field sampling from 2000-2016 followed by comparative conchological, anatomical, and molecular analyses. Morphological results support the presence of only two species of *Partula* in Near Oceania: *P. grisea*, and the Rennell Archipelago endemic *P. cramptoni*. Two more species are found in the Santa Cruz Islands (SI), one of these a single island endemic *P. vanikorensis* and another, *P. auraniana*, is found in both the Santa Cruz Islands and Vanuatu. *P. grisea* is highly atypical in its ecology and its distribution. It is restricted to the littoral zone of islands including small low islands and is frequently synanthropic, being found in coastal villages and absent from native forest. *P. grisea* has by far the widest distribution of any known partulid (most species are single island endemics); it is distributed across Near Oceania, including one record from a coastal village on the PNG mainland, in addition to a single island record from Vanuatu. Despite its extraordinary multi-archipelagic distribution, possibly linked with regional prehistoric trading exchange networks, this species exhibits modest levels of conchological and anatomical variation among its scattered island populations, the former consisting primarily of changes in shell size rather than shell shape. Local populations are typically small and fragmented and many may be declining; we were successful in finding survivors in less than half of Yoshio Kondo's 1960's locations.



## **Integrative Systematics of the Hawaiian Achatinellidae**

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The Achatinellidae, with about 330 species, are distributed throughout islands of the Pacific Ocean, reaching their highest diversity in Hawaii with 210 species (64%). The Hawaiian taxa represent 12 genera and includes representatives of five of seven subfamilies: Achatinellinae, Auriculellinae, Tornatellidinae, Pacificellinae and Tornatellininae. All Hawaiian species within two subfamilies (Achatinellinae, Auriculellinae) and all but two species from the other three subfamilies are endemic to the archipelago, with most restricted to a single island or mountain range. But the current taxonomy of Achatinellidae is outdated and only one subfamily, the Achatinellinae, has been evaluated within a modern molecular framework. To guide a systematic revision of the family, we used an integrative taxonomic approach incorporating shell morphology, anatomy, biogeography, original descriptions, and mitochondrial and nuclear DNA sequences from museum and recently collected specimens (n = 1679) of all Hawaiian achatinellid genera except the monotypic *Gulickia*, which may be extinct. Multi-locus phylogenetic analyses recovered strong support for all subfamilies, with most readily differentiated with conchological and anatomical data, but currently the genera within Achatinellinae are not supported with any data other than biogeography, and conchological data do not support *Gulickia* as distinct from *Auriculella*. Herein we present a provisional generic level taxonomic revision to provide a robust foundation from which to interpret the evolutionary patterns, biogeography, and ecology of this iconic Hawaiian land snail family. Most importantly, these data will inform conservation of the remaining species, all of which are threatened with imminent extinction.

## **Current and Historical Distributions of *Amastra cylindrica* (Amastridae)**

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As a result of speciation, primarily from its geographic isolation, Hawai'i is home to over 754 species of endemic land snails, many of which play vital roles in ecosystem functions. These services include nutrient cycling and maintenance of microbial communities that contribute to native forests' productivity. Unfortunately, land snail populations have been and continue to be negatively impacted by habitat destruction, invasive species, and climate change. Depending on the family, an estimated 65-100% of Hawaiian land snail species are already extinct with the remaining fauna imperiled. Compiling and comparing current species distributions to their historical ranges will provide an understanding of range reductions, habitat preferences, and prevention of additional loss. The Amastridae, an endemic family of Hawaiian land snails once comprising 325 species, now consists of only 22 extant species, including *Amastra cylindrica*, whose wild populations have dramatically dwindled in recent years according to records at the Bishop Museum. The museum's malacology collection holds records of an estimated 30,000 Amastridae lots representing approximately 254 species (counting 1,000 *Amastra cylindrica* lots), including when and where specimens were found, with most collected between 1864-1948. These historical records will be compared with recent surveys (post-2000) to assess changes in distribution of *Amastra cylindrica* using maps developed with CoGe and qGIS. Furthermore, because this species is captively reared at Bishop Museum and the Hawai'i Department of Land and Natural Resources' Snail Extinction Prevention Program, there is opportunity for reintroduction into the wild, potentially to areas where their historical locations coincide with protected state and federal managed lands. As Hawaiian land snails and other endemic species' populations rapidly continue to decline, understanding how their populations have been affected over time is crucial to not only mitigate losses, but also to assist in expanding populations and saving these imperiled species.

## Mapping *Euglandina rosea*: Evaluating the Distribution of the Rosy Wolfsnail in Hawai'i

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*Euglandina rosea*, also known as the Rosy Wolfsnail, is a carnivorous land snail introduced from Florida to Hawai'i in 1955 as a biocontrol agent for the Giant African Snail (*Lissachatina fulica*). Listed on IUCN's "100 of the World's Worst Invasive Alien Species", *E. rosea* has since been implicated in the extinction of over one hundred Pacific Island land snail species, and continues to threaten Hawai'i's imperiled native snail fauna, which is renowned for its diversity and endemism. Originally considered a single species, integrative studies have confirmed the presence of three distinct clades of *Euglandina* in Hawai'i, each representing a different species. However, little is known about their ecology, behavior, and spread, or if any disparities exist in their distributions. To assess the distribution of *Euglandina* spp. across the main Hawaiian Islands, we used data collected from extensive surveys and developed maps using QGIS with post-2000 locational records of both live and shell specimens from the Bishop Museum Malacology Collection and their partners. *Euglandina* spp. has been recorded on all of the main Hawaiian Islands except for Ni'ihau and Kaho'olawe. Initial results indicate clade 1 has the broadest distribution, present on Kaua'i, O'ahu, Maui, Lana'i, and Hawai'i, while clade 2 is absent from Lana'i. Clade 3 is only on Maui. Clades 1 and 2 have similar elevational ranges, but occur sympatrically in only three locations. Accurate taxonomy and distribution data are key to controlling and eliminating *Euglandina* spp. Knowledge of any distributional differences among the three clades allows further evaluation of each species' ecological requirements and can help identify the native snail populations at risk from this highly invasive snail. These data are informing effective, island-specific management approaches to help conserve Hawai'i's native land snail fauna and to develop control strategies for non-native *Euglandina* spp.

## SESSION 6

### Special symposium: Showcasing Molluscan Research at the Undergraduate Level

#### Keynote Address

### **Making the Most of Molluscs: Course-Based Undergraduate Molluscan Research Benefits a Broad Range of Students**

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Benefits of undergraduate research experiences (UREs) are broadly acknowledged to include enhanced research skills, life skills (problem solving, critical thinking, communication), and personal development (self-confidence, ability to work independently and in teams). UREs often follow an apprenticeship model; an individual student, frequently selected based on academic achievement, works with a faculty member on a project related to the mentor's research program. To extend the benefits of UREs to a wider range of students, more faculty are choosing to teach courses with embedded student research (often designated CUREs = course-based undergraduate research experiences). CUREs are consistent with current pedagogical emphases on inquiry, experiential/applied learning, and project-based learning. Faculty also benefit by advancing their research while enjoying a more interesting mode of teaching.

Molluscs are particularly amenable to study by undergraduates conducting individual, small-group, or course-based research projects. Abundant in modern and fossil settings, molluscs often can be collected as large samples, identified, and analyzed in meaningful ways by undergraduates. To illustrate how a CURE can incorporate molluscan research, I will present a case study: an invertebrate paleontology course I taught 9 times from 2003 to 2015, in which the laboratory primarily consisted of a team research project on molluscs. Although developed independently, my approach was consistent with principles articulated in a 2017 U.S. National Academies URE report. I have learned that a successful CURE requires clear understanding of learning goals and research goals by faculty and students, appropriate relevant and important questions driving the research, detailed planning, intensive mentoring of students in the practices of the discipline, effective collaboration, communication of results beyond the classroom, and appropriate assessment, including reflection. Despite challenges such as student inexperience, time constraints, and issues related to working in teams, the approach was beneficial to participants, as indicated by performance assessment measures, retention, and student reflections.

## **Solar-Powered Sea Slug *Elysia papillosa* Prefers a Diet that Reduces Photosynthetic Longevity**

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Most sacoglossan sea slugs are specialized herbivores which feed on siphonaceous green algae. Some sacoglossans sequester chloroplasts from their algal food and become photosynthetic in a process known as kleptoplasty. The duration for which photosynthesis can be maintained varies for different sacoglossan species, however, diet can have a significant impact. *Elysia papillosa* is a short-term kleptoplastic sea slug which feeds on algae in the genus *Penicillus*. Previous field studies have found that the slug is primarily found associated with *P. capitatus* although they are also less commonly found on *P. lamourouxii*. To assess the effect of diet on the duration of photosynthesis in *E. papillosa*, slugs were split into two diet treatment groups based on the algae from which they were collected. Prior to photosynthesis measurements, slugs were allowed to feed on their assigned diet ad libitum for two weeks at which point food was removed. Slugs were measured using a PAM fluorometer every two days as a proxy value for photosynthesis. *E. papillosa* fed *P. capitatus* had a significantly faster decline in photosynthetic activity compared to *E. papillosa* fed *P. lamourouxii*. Additionally, *E. papillosa* fed *P. lamourouxii* survived longer than slugs fed *P. capitatus*. A second group of slugs was then tested for chemotactic behavior using a Y- maze with algal cues from each species of *Penicillus*. Slugs collected from *P. capitatus* were significantly more likely to choose *P. capitatus* than *P. lamourouxii*. Slugs collected from *P. lamourouxii* did not show a significant preference. This combination of results is surprising because slugs would be expected to prefer the algal diet which promotes longevity in photosynthesis. This suggests that other factors such as larval preference, value as a cryptic refuge, or other unexplored factors may be responsible for the patterns observed in the preferences and distribution of *E. papillosa*.

## **Effectiveness of Ceratal Autotomy in Sacoglossan *Placida kingstoni* as a Defense Mechanism Against a Crustacean Generalist Predator**

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Sacoglossan sea slugs lacking a shell have developed a variety of chemical and physical defense mechanisms to respond to predation. Research on these mechanisms has centered around their chemical defenses, but little information is available on physical modes of defense such as autotomy, the voluntary detachment of bodily structures at a determined breakage point in response to danger or stress. Different sacoglossan species can cast off a variety of structures, but the effectiveness of the behavior against predator attacks has seldom been evaluated. *Placida kingstoni* is a small sacoglossan native to Florida and the Caribbean that can autotomize large dorsal projections called cerata. The objective of this study was to assess the relationship between ceratal autotomy and survival of *P. kingstoni* to the attack of a generalist predator. Shrimp of the *Lysmata wurdemanni* species complex were selected as model predators due to habitat overlap with the slug, generalist diet, and their aggressive nature. Each *P. kingstoni* was exposed to a starved shrimp for a ten-minute interaction. Most slugs were attacked by the shrimp, but the majority autotomized their cerata and survived. The predators often consumed the detached structures, which were often surrounded by a cloud of secreted mucus. Many slugs were able to survive the predator attacks by crawling away as the shrimp's attention was diverted to the cluster of mucus and cerata. The results of this study suggest that autotomy is an effective defense mechanism of *P. kingstoni* against predation. In the future, effectiveness of autotomy against a variety of predators should be tested because the behavior might not ensure survival if the slugs encounter predators with different modes of attack. Furthermore, autotomy should be studied in other sacoglossan species to determine if the behavior is exclusively defensive or if it might have an additional or alternative function.

## **What to Do When Things Go Wrong: Engaging Undergraduates in Malacology Research During Pandemics and Other Disasters**

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Hands on engagement in scientific research is a high impact experience for undergraduate biology students. Although not without its own unique challenges, the field of malacology offers many opportunities for successful undergraduate research due to the sheer diversity of mollusks many of which are greatly understudied. There are a variety of successful strategies for engaging undergraduate students in malacology research created for ideal conditions, including tactics for attracting and screening potential research students, building student excitement, growing their background knowledge, and creating a sense of student ownership in research projects. But what happens when things do not go as planned? Professional scientists and to a lesser degree graduate students can often deal with disruptions by delaying research projects, but undergraduates are usually severely limited in the time they have until graduation. Here, a variety of real-life scenarios are explored which can significantly disrupt the course of research including hurricanes, population disruptions, red tides, and a global pandemic. Methods to adjust undergraduate research under challenging and changing conditions are discussed with the goal of forging undergraduate student researchers into resilient scientists. Although research may not always go as planned, creative adaptations can be employed to build valuable undergraduate research experiences.

## Comparing Freshwater Mollusks from Big Lake, Indiana Across 94 Years (1926 and 2020)

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Faunal change happens, but rarely do we have the opportunity to document them. Historical specimens in museums can provide the means to examine these changes. In the 1920s, Herman Wright, as a PhD candidate, sampled mollusks in the Tippecanoe River watershed in Indiana. Big Lake is one of the highest lakes in the watershed, so one might expect it to be relatively pristine, but factors such as increase in human habitations and other land use changes, invasive species, or other circumstances, might have affected mollusk populations. In 2020, Warren Pryor kindly provided us with a modern-day sample from Big Lake to compare with the 1926 samples. After processing the samples, we identified at least 18 taxa, with at least 16 unique taxa, in about 2750 individuals in the 1926 samples, in comparison to 12 unique taxa in about 450 individuals in the 2020 samples. Since 1926, *Promenetus exacuus* and *Armiger crista* dramatically increased their relative abundances by 80 and 40 times, respectively. *Valvata tricarinata* remained about as relatively abundant across the two time periods. In contrast *Pomatiopsis cincinnatiensis* decreased to about an eighth of its original relative abundance, and some other species appear to have declined as well. Unsurprisingly, the highly invasive Asian clam, *Corbicula fluminea*, appeared in the modern sample; it was first documented in the United States in Washington State in 1938, after Herman Wright sampled, so of course it was absent in the 1926 samples. Some species that declined or were not found in the modern sample might be due to the modern sample being taken from a single location (beside the boat launch), whereas the 1926 samples were from multiple locations with different habitats; some of these taxa might prefer different environments. We continue to study what factors might have influenced these changes.



## **Benthic Micromolluscs and Juveniles from Arrecife Alacranes National Park**

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The Alacranes Reef National Park (PNAA) is the largest reef system in the Gulf of Mexico, thus it is the area with the greatest richness of species recorded of all the protected areas of the Gulf of Mexico. Very little is known about the mollusks of the sandy bottoms of this reef. To contribute to the knowledge of this group, an exhaustive inventory of micromollusc and juvenile species was constructed for the PNAA, with notes on the spatial distribution patterns and the relation to the granulometric characteristics of the sediment. 39 sediment samples were taken in 13 sites around the PNAA, 4184 specimens were reviewed to estimate the taxonomic composition identifying more than 200 species of mollusks.

## Diversity in Two *Deroceras* Land Slug Species in Southern California

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*Deroceras laeve* (Müller, 1774) and *D. reticulatum* (Müller, 1774) are the most common *Deroceras* species in Southern California, where they can be ubiquitous in anthropogenically altered environments. They are also frequently intercepted in imported horticultural and agricultural goods and are widely distributed in human-altered landscapes worldwide. Despite their pervasiveness, the diversity and provenance of these species in Southern California have not been analyzed. Therefore, we collected data on morphology and sequenced several phylogenetically informative genes (CO1, 16S, 28S, and H3) from *D. laeve* and *D. reticulatum* specimens collected in Los Angeles, Orange, and San Diego counties from urban gardens, parks, horticultural nurseries, and college campuses, as well as specimens intercepted by the USDA during import inspections. Here, we intend to: 1) discuss genetic diversity (based on four genes) in both species, 2) present a phylogeny of sequence data from our collected specimens and those of *D. laeve* and *D. reticulatum* from elsewhere in the world (from the BOLD and GenBank databases), 3) show intra and interspecific variation in jaw, radula, and reproductive anatomy, and 4) discuss the potential provenance, pathways of introduction, and distribution of *D. laeve* and *D. reticulatum* in Southern California.

## **Water Subsidies Enhance Gastropod and Isopod Species Richness in Southern California**

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Urbanization results in environmental disturbances that can reduce native biodiversity and increase susceptibility to invasion by non-native species. However, understanding how environmental factors affect biodiversity at the scale of individual residences in urban areas remains limited. In Southern California, the region's semi-arid climate makes water availability and yard type of residential areas highly variable and dependent on individual landscaping choices. Understanding how water subsidies and yard types influence biodiversity in residential areas is crucial to predicting how species will respond to an increasingly urbanized landscape. To study the effects of water subsidies and yard types on urban biodiversity, we used a community science approach to survey gastropod and isopod richness and composition in residential areas of Southern California. Surveyors were instructed to conduct 30-minute surveys of their residences for gastropods and isopods and to upload their findings via photographs to the community science platform iNaturalist. A total of 26 surveys were conducted between October and March, yielding a total of 14 species which were all non-native to Southern California. Water subsidies enhanced species richness, and initial patterns suggest that residences dominated by non-native shrubs and flowering plants harbor greater species richness than lawns and native gardens. Next steps include increasing sample sizes, particularly for lawns and native gardens, to compare species richness and composition of gastropod and isopod assemblages across differing residences. Current results show that water subsidies facilitate invasion of non-native species by reducing water stress, and conversely, reducing water subsidies may mitigate the spread of invasive species.

## **Effects of Anthropogenic Sounds on the Behaviour and Physiology of the Eastern Oyster (*Crassostrea virginica*)**

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In recent years, noise pollution has been considered a major problem in the marine environment, particularly in coastal areas. However, there is still a paucity of information regarding the effects of sound on most invertebrates and data on bivalves, including economically and ecologically important species such as oysters, are lacking. To fill this knowledge gap, we measured behavioural (valve gaping) and physiological (energetics) responses of the Eastern Oyster (*Crassostrea virginica*) to pre-recorded sound treatments mimicking human activity in the environment under laboratory conditions. We observed a reduction in valve opening in response to sound intensities mimicking pile driving simulated by pile driving noise (i.e., driving an element into the sea floor by dynamic effect of shocks or vibrations). The observed behavioural response to pile driving intensities was accompanied by a lower long-term concentration of adductor muscle glycogen, but not triglyceride. Interestingly, individual glycogen content and valve gaping responses were not correlated, suggested that the observed behavioural response to sound was not directly driven by the observed physiological response. Sounds intensities mimicking drilling and boating had no effect on energetic physiology nor behaviour. Our results suggest that *C. virginica* is sensitive to a periodic sound (pile driving) and less sensitive to continuous sounds (drilling and boat engines) intensities on the organismal scale. Future studies assessing downstream effects on marine growth, reproduction, and survival are needed to better understand the effects of anthropogenic sounds on oyster populations and the biological communities they support.

## **Effects of Petroleum-Based and Biodegradable Microplastics on Tissue Structure in the Eastern Mudsail *Tritia obsoleta***

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Aquatic ecosystems are increasingly contaminated with microplastics, small (<5mm) chemically diverse particles that are hazardous to aquatic life. Biodegradable plastics are often considered a 'safer' alternative, given the long-term environmental persistence of petroleum-based plastics. We tested two hypotheses: that mixed source (MS), petroleum-based microplastics cause tissue level changes in a digestive organ (hepatopancreas) at high risk of exposure in the snail, *Tritia obsoleta*; and that biodegradable plastics (PLA) elicit changes that are similar to those induced by MS microplastics at similar concentrations. *Tritia obsoleta* are at risk of microplastic exposure as they graze biofilm and, as they occupy the sediment-water interface, are exposed to resuspended particles on an on-going basis. Plastics for the MS treatments were collected from local coastal areas (polystyrene, polyethylene, polypropylene, polyvinyl chloride and polyethylene terephthalate, combined) and were tested at three exposures, including one similar to concentrations found locally (2,250 particles kg<sup>-1</sup> sediment). Locally relevant exposures of MS microplastics disrupted tissue structure of the digestive gland while extreme exposures additionally increased the number of immune cells (hemocytes) in the digestive gland and reduced fecundity. Effects of PLA were similar to those of MS microplastics, at the extreme exposure tested here. These results indicate that both petroleum-based and biodegradable microplastics disrupt the structure of the digestive gland, that tissues are responding to contact with microplastics in general rather than to fragments of specific chemical origin, and that environmentally relevant exposures induce 'hidden', tissue-level changes that are invisible without specialized techniques.

## **The Impacts of a Combination of Thermal and Air Stress on the Survival and Respiration of Winter-Acclimated *Crepidula fornicata***

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With climate change increasing temperature variability, it is important to understand how intertidal organisms respond to elevated thermal stress during the winter. This study investigated the impacts of a combination of elevated temperature stress and air exposure on the survival of winter-acclimated intertidal *C. fornicata*, and the impacts of thermal stress on the snails' subsequent respiration rates. For our survival studies, snails acclimated to 6°C were subject to either a single or a double (spaced 24 hr apart) three-hour thermal stress at 35 or 37°C, in seawater or in air at 100% and 75% relative humidity (RH). Large snails (2-4cm) were remarkably tolerant, even when exposed to air during the thermal stress—no individuals died after exposure to 35°C, and 48 hr mortality was only 10% across all groups stressed at 37 °C, independent of RH. Smaller snails (<1.5cm) were more susceptible to a combination of air-exposure and thermal stress than they were to thermal stress alone, regardless of RH. After a double stress, 35% of snails died following exposure to 35°C in air, while none died after exposure to 35°C seawater. For all experiments, most mortality was observed between 24 and 48 hours after stress. Following a three hour 35 or 37°C thermal stress in seawater, *C. fornicata* respiration rates remained depressed by ≈40% over the next 48 hours. Overall, winter-acclimated *C. fornicata* remain impressively tolerant of thermal stress in both air and seawater, which may promote their success as invasive species, though the implications of depressed respiration rates remain unclear. Future studies should investigate the causes of delayed mortality and depressed respiration following thermal stress.

## **Investigating the Interplay of Genetics and Thermal Stress on Energy Metabolism in Invasive Mollusk, the New Zealand Mud Snail *Potamopyrgus antipodarum***

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In today's world, anthropogenic activities are changing the global temperature at unprecedented rates. Various lines of evidence suggest that many invasive species may be "poised to prosper" in a rapidly warming world, particularly in aquatic environments. A mechanistic understanding of the genetic basis of organismal physiology is critically important to forecast how invasive species will respond to rapidly changing environments, which represents an urgent challenge for biologists. At present, we lack an understanding of the potential adaptive value of different genotypes in colonizing different aquatic niches. The New Zealand Mud Snail (NZMS) is an especially good model to study the invasive potential of mollusks in the face of changing climate because 1) it has colonized all continents in the last 150 years, and 2) is a model for co-evolutionary dynamics. The overarching goal of this study is to determine the genetic and metabolic underpinnings of how global warming will change the invasive potential of mollusks, using NZMS as a model system. Here, we quantified genetic variation in whole-organism metabolic rate across temperatures in NZMS using respirometry approaches and a diverse set of wildtype snail clonal lineages. Our data provide important insights into metabolic plasticity, ecophysiology, and fitness in natural populations of this invasive mollusk. This information is essential not only for a fundamental bridging of the genome-to-phenome gap but also to provide solutions to real-world problems of conservation and management.

## **Validation of Environmental DNA (eDNA) Protocols for Conservation of Freshwater Mussels *Alasmidonta varicosa*, *Margaritifera margaritifera*, and *Lampsilis cariosa***

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Environmental DNA (eDNA) is an emerging tool that uses extracellular DNA or cellular debris collected from environmental samples (soil, water) to detect the presence of a target species without the need for direct visual confirmation. This method is particularly useful in aquatic habitats, where the presence of rare or low-density taxa can be confirmed using small volumes of water and with minimal disturbance to sensitive environments. At Cape Breton University, we have become interested in using eDNA to assist in monitoring the presence and distribution of two freshwater mussel species in Atlantic Canada, *Alasmidonta varicosa* (Brook Floater; SARA-listed), a cryptic, low density species with a limited distribution in mainland Nova Scotia and New Brunswick, and *Lampsilis cariosa* (Yellow Lampermussel; SARA-listed), known only from three populations near Sydney, Cape Breton Island. Here, we report on our efforts to validate existing eDNA protocols for *Alasmidonta varicosa* and *Margaritifera margaritifera* (Eastern Pearlshell), a more common freshwater mussel species in Nova Scotia, and to develop an assay to expand the application of eDNA to *Lampsilis cariosa*. Analysis of DNA from aquatic environments involved environmental water collection and filtration, extraction of eDNA, and use of quantitative PCR to amplify the target DNA to determine species presence/absence. Our results confirmed the utility of species-specific primer/probes for *Alasmidonta varicosa* and *Margaritifera margaritifera*, and demonstrated the first application of custom primer/probes for *Lampsilis cariosa*. We also successfully validated eDNA protocols for all three species based on environmental water samples from sites known to be positive and negative for each target species; however, further work is needed to explore inconsistent eDNA amplifications based on water samples from sites positive for Brook Floater. In the future, we plan to incorporate eDNA techniques into our standard monitoring program for local unionids, and to use eDNA to sample unexplored aquatic environments in Cape Breton Island and mainland Nova Scotia in an effort to find new populations of freshwater mussel species.



## **A Tale of Two Mussels: DNA Barcoding of Unionids from Guanacaste, Costa Rica**

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Two groups of morphologically distinct freshwater mussels (Family: Unionidae) were observed in the vicinity of an aquaculture facility near Cañas, Guanacaste, Costa Rica. Twelve individual DNA samples were DNA barcoded using *cox1*. The first species – collected within the aquaculture ponds – was determined to be *Sinanodonta woodiana*, an invasive species. Specifically, these Costa Rican *S. woodiana* mussels belong to the so-called “tropical invasive lineage” of Chinese Pond Mussels, previously known for extensive spread throughout Southeast Asia. Based on a BLASTn search of GenBank, the second species – collected from a small stream feeding into the aquaculture facility – was closely related to native Mesoamerican species *Psorula profunda*. Based on morphology, this species appears to be in the genus *Nephronaias*. A recent study of Mesoamerican unionid phylogenetics suggested that *Nephronaias* (not yet described on molecular databases such as GenBank) belongs to the tribe Popenaiadini, which is both reflected in our phylogenetic analysis of the putative *Nephronaias* species, and consistent with the recent predictions by Pfeiffer and colleagues. We hypothesize that this species is *Nephronaias tempisqueensis*, which occurs in the same Rio Tempisque watershed where the aquaculture facility is located. Comparisons with physical specimens from various museum and university collections throughout Mesoamerica will be required to confirm whether this species is *N. tempisqueensis*. We also sequenced a portion of the *cox2* gene that is characteristic to the paternally transmitted M-type genome in bivalves exhibiting the unusual doubly uniparental inheritance (DUI) system of mtDNA, suggesting that *Nephronaias* also exhibits DUI.

## **Science Atlantic and the Science Undergraduate Research Experience in Atlantic Canada**

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Undergraduate research in the Atlantic Provinces of Canada has been stimulated over the past 59 years through Science Atlantic (SA), a remarkable organization that connects science education and research across 18 post-secondary institutions within the disciplines of Biology, Chemistry, Computer Science, Earth Science, Environment, Mathematics & Statistics, Nutrition, Physics, and Psychology. For Biology programs, SA facilitates an annual conference where senior students from member institutions meet, share results of their independent/honours research with peers, compete for research and communication awards, and interact with faculty and potential graduate supervisors. SA also provides a focal point for students in their research progression as each student has to compete internally for a limited number of judged presentations allocated to each institution. For students early in their programs who attend the annual conference, SA also has the benefit of increasing their awareness of and accessibility to research opportunities at home institutions. For university faculty, SA provides a place to meet and network with other faculty, discuss issues of shared concern in focal workshops, and above all marvel at the amazing research that can be undertaken at the undergraduate level. Such annual meetings also provide the opportunity to recharge one's batteries and return energized with ideas and enthusiasm for a new cohort of students and research projects. Over the past 16 years, Science Atlantic has provided a venue for my undergraduate students to present research focused on various molluscan-based projects ranging from the feeding ecology of the naticid moon snail, *Euspira heros*, to the development of sustainable fishery for the waved whelk, *Buccinum undatum*, to the role of freshwater snails as intermediate hosts of digenean trematodes. Amazingly, SA has remained a constant in the science undergraduate experience in Atlantic Canada from 1962 onwards, and continues to demonstrate tremendous resiliency in the face of changing funding, Canadian winters, and now Covid-19.

## **Using Digital Natural History Collections in Course-Based Undergraduate Research Experiences (CUREs)**

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Digital natural history collections are a large and growing primary data source that is useful to a wide variety of audiences. This talk will introduce the Biological Collections in Ecology and Evolution Network (BCEENET) and how it has developed, grown, and adapted since its inception in 2019. The network was born out of an undergraduate teaching collaboration between Widener University and the Delaware Museum of Natural History with the intent of bringing together natural history collections professionals, undergraduate educators, data experts, and researchers to support the development and implementation of Course-based Undergraduate Research Experiences (CUREs) using digitized natural history collections (dNHC) data. During the summer 2020, BCEENET led the development of four ecologically based dNHC CUREs that were implemented in Fall 2020 and Spring 2021 ecology classes across the country. Resources created during the CUREs will be available on QUBES for use and customization.

## **Session 7(A-D) Contributed Talks**

### **7A: Shell Biomineralization, Shell Colour, and Scallop Visual Systems**

#### **Evolution of Shell Colour**

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Molluscan shell colours and patterns are not only beautiful, they also serve essential functions for survival. The number of studies published about shell colour have burgeoned over the last few years as interest grows in understanding the fundamental role colour plays in evolution, and because of the desire to control colour in farmed animals. The goal of many of these studies is to identify critical genes and molecular pathways involved in pigment synthesis, however the same colours can be produced by different pigments, and pigments may be synthesized de novo by the animal or come from their diet. The most compelling genetic studies, therefore, are those that have been based on a prior knowledge of the pigments responsible for shell colour. In this talk I will review the functions of colour in Mollusca and the pigments that contribute to shell colour, and share the results of three projects that use molluscan collections from the NHM to explore colour in seashells.

## Shell Pigmentation in the Eastern Oyster (*Crassostrea virginica*)

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Little is known about shell color in the eastern oyster, *Crassostrea virginica*, or of the evolution of color in related species. To better understand the basis of pigmentation, four shell color morphs were described and crossed amongst each other in breeding experiments undertaken in an aquaculture facility. Proportions of color morphs in the progeny show color and pattern are under genetic control. A comparative transcriptome study was then conducted to identify differentially expressed genes between dark and light regions of mantle tissue. Several transcripts were found to be differentially expressed in common across replicate comparisons, including three transcripts coding for enzymes involved in the heme pathway. Raman spectroscopy data do not provide evidence for carotenoid-type pigments, but do show evidence of melanins. Other pigment peaks are consistent with tetrapyrroles. UV/visible spectroscopy results indicate that both black and brown shell colors contain at least two pigments. The absence of characteristic banding patterns indicates that neither pigment is a porphyrin, however the spectra may be affected by the presence of melanins. To further analyze melanins, demineralized shells were subjected to Soluene-350 solubilization, H<sub>2</sub>O<sub>2</sub> oxidation, and hydriodic acid (HI) hydrolysis. Soluene-350 solubilization yielded A500/g and A650/g values, which were similar and therefore did not show evidence for relatively eumelanin- or pheomelanin-rich pigments. H<sub>2</sub>O<sub>2</sub> oxidation afforded low levels of both pyrrole-2,3,5-tricarboxylic acid (PTCA) and thiazole-2,4,5-tricarboxylic acid (TTCA) levels, markers for eumelanin and pheomelanin, respectively. However, the levels of dopa in the HI hydrolysates were extremely high and high levels of 4-amino-3-hydroxyphenylalanine (4-AHP) and 3-amino-4-hydroxyphenylalanine (3-AHP), markers for pheomelanin, were also found, which suggests that pheomelanin also plays a major role in both black and brown pigmentation.

## **Oyster Biomineralisation in Acidifying Oceans: From Genes to Shells**

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Oysters like several other marine calcifiers are well known to be negatively affected by human induced environmental stressors such as ocean acidification (OA). Particularly, the key process affected in oysters is biomineralisation or the shell fabrication which depends on the parameters affected under OA - calcium carbonate state and pH of the ocean. Estuarine oyster species often experience fluctuations in the pH and hence expected to survive wide fluctuations in pH. In this talk, we will present the mechanisms of adaptations of an estuarine oyster species from Hong Kong - *Crassostrea hongkongensis* to OA. The study covers changes in DNA methylation and gene expression of this species under OA which helps these oysters in making error free shells without changes in shell mechanical properties (micro-structure, crystal orientation and micro hardness). This study provides insights about biomineralisation mechanisms of early juvenile and eyespot larval stages of Hong Kong oysters under normal and projected OA scenarios.

## **Who Has More Eyes? Life Habits and Allometry Explain Variation in Eye Abundance Among Scallop Species (Pectinidae)**

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Scallops are bivalves with tens to hundreds of eyes along with their bodies, forming a remarkable distributed visual system. Variation in optical units, such as eye abundance, might cause great impacts on visual ecology and associated behaviors. However, how eye abundance varies among scallop species and associated factors still represent a critical gap in knowledge. To understand variation among scallop species, we tested whether eye abundance scales with body size (allometry) and whether it varies with life habits (i.e., cementing, recessing, byssal-attaching, free-living, and gliding). Our hypotheses predicts that larger and more mobile species will have more eyes. We collected data on eye count and shell height (as a proxy of body size) for 31 scallop species with different life habits. Means per species were used for subsequent analysis, and a phylogenetic tree was estimated based on available sequences. We performed a phylogenetic ANCOVA via generalized least squares and pairwise comparisons, using residual permutation procedures to assess statistical significance and size effects. Our results show that both variables, i.e., body size and life habits, contribute to explaining variation in eye abundance. More interesting, gliding scallops (long-distance swimming) and free-living scallops, which represent the most mobile life habits, have significantly more eyes than species with low mobility (recess) or no mobility at all (cement). These results suggest that mobility and occupation of the substrate are important variables shaping distributed visual systems. For example, increased mobility frequently requires greater visual capabilities, which is supported by our data. Overall, we provide evidence to support how allometric and ecomorphological factors affect the scallop visual system, raising new opportunities to investigate visual adaptations and their evolutionary associations.

**7B: Cephalopods: Species Discrimination, Ecology, and Phylogenetic Relationships****Finding a Home for the Ram's Horn Squid (*Spirula spirula*)  
Using Phylogenomics**Pratt, Abigail M.\*<sup>1</sup>; Anderson, Frank E.<sup>1</sup>; Lindgren, Annie R.<sup>2</sup>

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The ram's horn squid, *Spirula spirula*, is the only living cephalopod with an internal, spiral-shaped chambered shell and the sole extant species in the order Spirulida. While long recognized as a member of Decapodiformes (the clade comprising all squids and cuttlefishes), the relationship between Spirulida and the remaining decapodiforms—Oegopsida (oceanic squid), Myopsida (inshore squid), Sepiolida (bobtail squid), Idiosepiida (pygmy squid), Bathyteuthoidea and Sepiida (cuttlefish)—remains unclear. Early morphological studies grouped Spirulida with Sepiida due to the shared presence of a calcified internal shell, but this relationship was questioned in subsequent work due to the unusual combination of characters seen in Spirulida (e.g., *Spirula* has an open, oegopsid-like eye). The few molecular phylogenetic studies to date that have included spirulid data have grouped Spirulida with Oegopsida and/or Bathyteuthoidea, though these studies utilized either mitochondrial genomes (a single linkage group) or a small number of mitochondrial and/or nuclear loci. In this study, we generated a transcriptome from a recently caught specimen of *Spirula spirula* and analyzed these data in combination with previously published transcriptomic and genomic data to help resolve the placement of Spirulida within Decapodiformes, taking into account several potentially confounding factors (e.g., orthology inference, contamination, missing data, conflicting signals among loci and compositional and substitution rate heterogeneity among lineages). We will discuss the results of our phylogenomic analyses and their implications for the phylogenetic position and evolutionary history of Spirulida.



## **Statolith Shape of Loliginid squids: Discriminant Power and Ancestral State**

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Loliginid squids from the northeastern Pacific are partially sympatric, and their identification is difficult as their diagnostic characters often overlap. Statoliths are hard structures with taxonomic value related to the phylogeny of loliginid squids. However, the latter aspect should be properly inferred using more robust methods. Geometric morphometrics was employed to evaluate the discriminant power of the statolith shape of loliginids caught in Mexican waters and to acquire knowledge on its evolution through a comparative phylogenetic method. The loliginid species showed a specific statolith morphology, allowing the species identification. The significant and high phylogenetic signal in statolith shape confirmed that this hard structure is related to the phylogeny of loliginid squids. The ancestral statolith morphologies are not very different from extant forms, probably due to the relatively recent formation of the two genera evaluated and their low evolutionary rate. In addition, the evolutionary rates of statolith shape of species of the genus *Lolliguncula* are faster than those of the genus *Doryteuthis*, especially in *Lolliguncula panamensis*, which could be related to differential habitats within the neritic coastal environment inhabited by loliginid squids.

## **Identification of Loliginid Squids Based on Beak Shape Obtained by Geometric Morphometrics**

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The Loliginidae family (Lesueur 1821) has historically been recognized for having taxonomic problems due to the lack of robust descriptors, thus, we aimed at evaluating beak shape as a taxonomic character for *Doryteuthis opalescens* (Berry 1911), *Lolliguncula diomedea* (Hoyle 1904), and *Lolliguncula panamensis* (Berry 1911) via geometric morphometrics. The chitinous structure of cephalopod beaks was utilized for species recognition, and a thorough morphological description and an identification key were developed for upper and lower beaks of the three loliginid squid species. The results indicated strong taxon differentiation based on beak shape, especially upper beaks, although both (upper and lower beaks) structures exhibited a strong discriminant power at the species level. Differences in both feeding habits and habitat could explain the species-specific beak shape, possibly since the origin of the species due to the higher beak shape similarity between congeners. The taxonomic key and beak shape description developed are a reliable identification source for the three loliginid squid species and could be of use for those interested in determining the feeding ecology of predators when whole squid individuals are not available.

## Seasonal and Interannual Variation of Atlantidae (Pterotracheoidea) in the Pacific Coast of Baja California, México

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Atlantids are holoplanktonic gastropods that bear an aragonitic shell and live in the first 250 m of the water column. It has been suggested that in the long term, they might be affected by ocean acidification. Recently, hypoxic and aragonite undersaturated waters have been observed near surface in the northern California Current System (CCS). However, little is known about how the distribution and abundance of atlantids vary regarding changes in the environmental conditions worldwide. The strongest seasonal changes in plankton species composition and environmental conditions, occur between winter and spring, mainly related to upwelling and water masses distribution. Other important changes in the environment happen in the inter-annual scale related to ENSO (La Niña 2010-2012, El Niño 2015-2016) and marine heat waves (2013-2015). The aim was to determine the species composition and the environmental factors that affect the seasonal and interannual variation of the distribution and abundance of Atlantidae species in the Pacific coast off Baja California between 2012-2016, based in four oceanographic cruises carried out in winter and three in spring, with 284 zooplankton samples analyzed. We found 14 species, where winters were more diverse than springs, with the most species recorded during the warm anomalies observed on the winters of 2014 and 2016. Overall, *Atlanta californiensis* was the most abundant mainly in spring and its relative abundance decreased during the warm anomalous winters, when *A. lesueurii* increased, and *A. turriculata* and *Atlanta* sp 1 were exclusively present. Through canonic correspondence analyses, we determined that atlantids distribution in winters was mainly correlated to physical factors (temperature, salinity, and water masses in the area) while in spring, their distribution was mainly correlated with chemical factors (hypoxic conditions and the aragonite saturation horizon depth).

## 7C: Digitalizing Natural History Collections

### **Telescopes for Malacology**

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In recent years, the U.S. National Science Foundation has funded dozens of Thematic Collection Networks (TCNs) to digitize natural history collections and make their contents searchable online. These collections are an archive of the history of life. They increase verifiability of research and, when networked, make it possible to address formerly intractable questions. These networks allow focus from present to past to detect biotic changes and make projections. Like a network of telescopes, more installations and more observations increase resolving power.

As more collections come online and more specimens are digitized, resolving power increases. But we also need to improve the focus of our telescope. Several problems can affect focus. Marine shells can persist for centuries or millennia. Their presence on beaches doesn't mean a species still lives in the area. Misidentifications affect the signal-to-noise ratio. And many specimens are missing data, such as date collected, which prevents using them to extend baselines to detect biotic change.

The Eastern Seaboard TCN seeks solutions to these problems. Scoring live- versus dead-collected allows informative records to be identified, but doing so for millions of samples is labor intensive. A bioinformatics approach can identify some records as likely based on live collected specimens. This will allow some species to be targeted for direct scoring based on anomalies or gaps in distribution. Bounding boxes for geographic and bathymetric range will be sourced from the Malacolog database. Out-of-range records are those most in need to verification, because if correct, they might signal expanding ranges. When the collecting date is missing, proxy data can be used to constrain it—date of donation, date of cataloguing, dates of birth, death and activity of collectors and donors. A database of agents across institutions would accelerate this work, possibly linked to genealogical databases.

**7D: Marine Bivalves – Living, Boring, and Taxonomically Confusing****Boring Bivalves: Using Molecular Phylogenetics to Resolve Species Identities in *Botula* (Mytilidae)**MacLean, Sarah K.\*<sup>1</sup>; Rawlings, Timothy A.<sup>1</sup>; Bieler, Rüdiger<sup>2</sup>

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Based on morphological examination of coral-boring bivalves in the genus *Botula*, Wilson and Tait (1984) concluded that the genus comprised a single species, *Botula fusca*, with a pan-tropical distribution spanning the Western Atlantic, Pacific and Indian Oceans. Variation in shell colour, habitat (boring into living or dead coral, calcareous rocks, or shells of other molluscs; from intertidal zones to depths of 347-532 metres), and anatomy (digitation on the siphonal membrane), were determined to reflect variation within this one species. In a subsequent review of Recent and fossil *Botula*, Kleemann (2007) expressed doubts about a monotypic *Botula* given “striking morphological differences” between several described species, advocating for the study of soft tissues and application of molecular tools to help resolve species identities. Here, for the first time, we have undertaken a molecular approach to explore species-level relationships within the genus *Botula*. Our taxon sampling was based on freshly collected samples from the Florida Keys National Marine Sanctuary in the context of ongoing research into bioeroding bivalves at reef restoration sites, in addition to previous collections available in the Genetic Resources Repository at the Florida Museum of Natural History and the Santa Barbara Museum of Natural History. Based on preliminary analyses of mitochondrial (COI and 16S rRNA) and nuclear (H3 and 28S rRNA) genes, the genus *Botula* appears to be monophyletic, with the contentious species currently classified as *Leiosolenus kleemanni* (Valentich-Scott, 2008) falling within *Botula* rather than *Leiosolenus*. High levels of sequence differentiation among samples in this study, including ones previously identified as *Botula silicula*, *Botula cinnamomea*, “*Leiosolenus*” *kleemanni*, and *Botula fusca*, supported these as distinct species. Our phylogenetic analyses also identified several cryptic species within Western Atlantic *Botula fusca*. Increased knowledge of diversity within the genus *Botula* should lead to a more accurate understanding of the role of these bioeroding species in reef ecosystems.

## **Taxonomic Teredinidae Turmoil and the Effort to Resolve Shipworm Relationships in the Pacific**

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Teredinidae, the enigmatic bivalves known as ‘shipworms’, have been considered a scourge by sailors for as long as there have been wooden ships and other marine structures in which they make their home. Although much maligned because of the damage they cause, they contribute to marine ecosystems, acting as a conduit for terrestrial nutrients into marine systems. More comprehensive knowledge of their taxonomy and distribution across oceans is necessary to understand their biogeography, evolution, and ecology. Despite a long history of study, shipworm taxonomy remains poorly resolved, and many species may await discovery and description, particularly in the Pacific, whose shipworms are not yet as well studied as those of the Atlantic and other oceans. Taxonomy of teredinids has historically relied on morphology, particularly the hard pallets they use to seal their burrows and their reproductive strategies. The addition of DNA sequences to the suite of taxonomic tools for shipworms has revealed synonymies and inconsistencies in species identifications. Integrative studies that include data from anatomy, biogeography, ecology, and genetics have begun to resolve some of the taxonomic confusion, especially for species that are currently considered cosmopolitan. To provide a robust systematic framework for interpreting and revising Hawaiian shipworm taxonomy and to elucidate biogeographic patterns, we have begun a multi-locus phylogenetic study on shipworms from the Hawaiian Islands. Using newly generated mitochondrial and nuclear sequences from 61 shipworms representing 23 species combined with publicly available sequences, we have produced a preliminary phylogeny of Hawaiian shipworms revealing cryptic species and potential regional endemism that was unexpected prior to this study. As we continue this research, the addition of specimens from other parts of the Pacific should provide context for interpreting origins of species in Hawaii and their relationships within Hawaii and beyond.

## **Brooding on Dispersal: Shipworms in the Hawaiian Islands**

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The Hawaiian archipelago's marine ecosystems were colonized by trans-Pacific travelers, arriving on their own or via anthropogenic assistance. Adult shipworms inhabit their wood tunnels for life; where the wood goes, they go, and many teredinid species are considered cosmopolitan. Shipworms bore into and digest wood, therefore the size of their wood residence influences their lifespan. This ephemeral and unpredictable habitat produced a diversity of teredinid adaptations, particularly in reproductive strategies. Several cryptic species pairs in the family differ in reproductive mode, with long- or short-term brooders lacking any obvious morphological differences. The Hawaiian Teredinidae project, launched in 2015, combines morphological, genetic, distributional, and ecological data on shipworms from around the islands and elsewhere to inform our understanding of shipworm dispersal, diversity, phylogenetics, biogeography, and ecology. Phylogenetic analyses of 23 species revealed two cryptic species pairs, with long- and short-term brooding, as distinct species, supporting the independent evolution of different brooding strategies multiple times. While few shipworm species found in Hawaii have been previously sequenced, three non-Hawaiian species from GenBank were available for comparisons to the newly generated sequences. One Hawaiian species is identical to a sequence from a Japanese population and one to an introduced species in the Pacific Northwest. The third comparison revealed a new species, genetically distinct from the others in its species complex. Although two-thirds of the approximately 80 species in the Teredinidae are broadcasters, the Hawaiian shipworm fauna is dominated by brooders; a pattern evident in Guam, the Galapagos and Azores as well. However, most of the species in foreign driftwood on Hawaiian beaches are oviparous, indicating brooders may be more amenable to ship-mediated transport and, once present, are dominate in isolated island marine ecosystems.

## **Distribution and Zoogeography of the Bivalvia of the Eastern Pacific Ocean – 40 Years Later**

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In the early 1980's, Frank R. Bernard published the first comprehensive check-list of marine bivalve mollusks from the Bering Strait (66°N) to the Cape Horn (60°S). Based on that information, the author subsequently revised the distribution and zoogeography of the Bivalvia of the eastern Pacific Ocean. As part of that study, he recognized four main biogeographic provinces. The aim of this study is to reunite the information on bivalves from the eastern Pacific published after Bernard's contributions and, on the light of this new information: 1) to determine the diversity currently known from this area, 2) to update the distributional range for each species, and 3) to re-evaluate the biogeographic scenario previously proposed by Bernard.

The main sources of information for this study arise from the three monographs on the bivalve seashells of the western Americas published by the Santa Barbara Museum of Natural History. These contributions provide accurate information on the species occurring from the Beaufort Sea (71°N) to Isla Chiloé (43°S). These monographs were updated with subsequently published literature from this area. Information on the bivalves from Isla Chiloé to Cape Horn comes from another monograph (in progress), which includes extensive personal sampling in the region.

As part of the present study, a total of 1,234 bivalve species are recognized from the eastern Pacific Ocean. The numerous papers published after Bernard's contribution resulted in hundreds of changes in the distributional ranges of the species, as well as numerous taxonomic changes. In fact, almost 150 new species were described in the last 40 years from the eastern Pacific Ocean. The biogeographic analysis reveals several similarities to the divisions recognized by Bernard, with the exception of South America. These results reflect the great recent advances in the knowledge of the Pacific marine bivalve fauna.



## Will the Real *Mytilus incrassatus* Please Stand Up?

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Like many early-named genera, *Mytilus* Linnaeus, 1758 accumulated a number of species by the early 1800's, using many of the obvious common Latin terms. Linnaeus included edentulous freshwater mussels (modern *Anodonta* and *Margaritifera*) as well as marine pteriomorphs, particularly the marine mussels (modern Mytilidae), so a wide range of possible "*Mytilus*" exist. Several authors perceived their species as thick and named it *Mytilus incrassatus*. In 1849-1852, d'Orbigny published his *Prodrome de Paléontologie Stratigraphique Universelle...* which included replacement names for many homonyms. He noted that *Mytilus incrassatus* Conrad, 1841 and *M. incrassatus* d'Orbigny, 1845 were preoccupied by Deshayes, 1832 [usually cited as 1830]. However, he overlooked *M. incrassatus* Sheppard, 1821 and *M. incrassatus* Eichwald, 1840. Sheppard's species is a form of the extant *Anodonta cygnea* (Linnaeus, 1758), whereas the subsequent uses are all pteriomorphs. Deshayes proposed two names for the same species description in different publications. *Admytilus acutangulus* (Deshayes, 1830) is available for his Eocene Paris Basin mytilid. As further confusion, this name has been incorrectly credited to Lamarck in various sources. Eichwald's species is by far the oldest geologically, from the Ordovician of Estonia. Because Eichwald's species has not been considered congeneric with the others since the mid-1800's, the epithet can be retained as *Ambonychia incrassata* (Eichwald, 1840). Conrad's species, renamed *Mytiloconcha conradiana* (d'Orbigny, 1852) is a mytilid from the Pliocene and Pleistocene of the eastern U.S. The name has been used for a similar Miocene form which in its own turn has an overlooked name, published in a neglected paper on Silurian fossils. *Modiolula subincrassata* (d'Orbigny, 1852) is widespread in the European Miocene but may be a subjective synonym of *Modiolula volhynica* (Eichwald, 1829). Confusion between the homonyms continues into some modern sources.

**POSTER SESSION I**  
**Special symposium: Mollusc-Microbe Interactions**

**Comparison of Microbial Communities in the Olympia Oyster Gut Across the Puget Sound to Define Resident Bacteria and Explore Potential Dysbiosis**

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Oysters, just like many other animals, host a suite of bacteria and other microbes within their digestive system. Considering that oysters are filter feeders, their internal bacterial community at any given moment could be a combination of resident and transient bacteria. The differentiation between these communities can be difficult to define but various strategies have been put to use. In oysters from the Puget Sound, Washington, *Mycoplasma* species and an unidentified bacterial group tend to be present and in relatively high abundance in all oysters. However, the ratio of other bacteria to these core members varies significantly between certain sites. While the true behavior of all bacterial taxa identified in this study cannot be determined through 16S rRNA amplicon sequencing alone, differential abundance analysis reveals trends in bacterial community composition that correlate to survival of implanted oysters. Bacterial sequence data from the gut tissue of Olympia oysters placed in four sites throughout the Puget Sound is used here to identify resident bacterial communities and explore the differences in bacterial taxa which, when correlated to oyster survival, may show signs of dysbiosis. Oysters provide important ecological services to the Puget Sound, and it is therefore important to assess biotic factors, in addition to environmental fluctuations, that may contribute to their health and survival.

## Are Lucinid Bivalves Strictly Dependent on their Chemotrophic Endosymbionts for their Carbon and Nitrogen Requirements?

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Lucinid bivalves are well known for their successful association with endosymbiotic bacteria providing them with a chemoautotrophic regime<sup>1</sup>. However, they still possess the capacity for filter-feeding and are therefore potentially mixotrophs. Histological studies indicate that a seasonal shift between autotrophy and heterotrophy may occur<sup>2</sup>. Moreover, recent findings indicate that their symbionts are diazotrophic and contribute to the nitrogen requirements of their host<sup>3,4</sup>.

In the sediment around *Zostera marina* seagrass meadows near Roscoff (Brittany, France), two sympatric species occur: *Loripes orbiculatus* Poli 1795 (aka *L. lacteus* or *L. lucinalis*) and *Lucinoma borealis* (Linnaeus, 1767). We have analyzed the <sup>13</sup>C and <sup>15</sup>N isotopic signatures from their gills and bodies at different seasons alongside the abundance of bacterial symbionts in their gills and the expression of a set of genes from the symbiont and the host. Preliminary results seem to point out a fundamentally chemotrophic regime for both species although the gill  $\delta^{13}\text{C}$  values differ slightly between *L. orbiculatus* and *L. borealis*. Their  $\delta^{15}\text{N}$  though are similar but vary between seasons, possibly due to a larger abundance of bioavailable inorganic nitrogen sources in winter. Experimental approaches have been designed and are on their way to test these hypotheses in detail.

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## Hawaiian Land Snails Gut Microbiome Sequencing: A Review and Proposed Methodology

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Animal microbiomics is a rapidly growing field aimed at assessing the genetic diversity of microbes to inform our understanding of biodiversity and the factors that shape it. Similarly, it can increase our understanding of how microbiome composition effects overall species health, thus enhancing our ability to save endangered species. The majority of animal microbiome research has focused on vertebrates, leaving substantial gaps in our understanding of most animals - invertebrates, the neglected majority. Although molluscs are the second most species-rich animal phylum, there are few malacological gut microbiome studies, with most focusing heavily on a few species across ecosystems such as the highly invasive *Lissachatina fulica*. These studies indicate that the diverse gut microbial communities include cellulolytic symbionts that aid plant digestion, and that microbiome diversity varies with host community species-richness and diet. The highly endangered *Achatinella* (Achatinellidae) species have been raised in captivity as part of a long-term program (30+ years) aimed at preventing their extinction. Of the 41 species, only nine species remain in captive propagation; five are extinct in the wild. Populations of these nine species continue to be in decline as questions of their dietary requirements remain unanswered, as does how captive rearing may impact snail microbiome communities and overall fitness. To begin filling knowledge gaps about snail microbiomes, particularly in captivity, we are using a metabarcoding approach to characterize the gut microbiome of preserved specimens from captively reared achatinelline snails deposited at the Bishop Museum, which spans the last 20 years. To our knowledge, this is the first study evaluating the gut microbial communities of Hawaiian land snails. The results from this study will provide baseline data for gut microbial diversity and host-microbe interactions within captive reared populations to improve captive propagation protocols and conservation for this highly threatened group.

## Genetic and Functional Diversity of Clade A Lucinid Endosymbionts from the Bahamas and Florida

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Lucinidae clams are known to harbor environmentally acquired endosymbionts within their gills. Although there has been recent work on the genomic and functional diversity of lucinid endosymbionts, there are uncertainties regarding the extent of this diversity and metabolisms in various environmental conditions. In this study, the genetic and functional differences in endosymbionts was examined for six lucinid species collected in eight total sites from Florida, USA and the Bahamas. There were 42 Metagenome assembled genomes (MAGs) that were generated and they clustered into three species and six subspecies. MAGs were closely related to clade A endosymbionts "*Candidatus Thiodiazotropha endolucinida*" from *Codakia orbicularis* or "*Ca. Thiodiazotropha endoloripes*" from *Loripes orbiculatus* based on phylogenetics and average nucleotide identity (ANI) and average amino acid identity (AAI). The two species that were related to *C. orbicularis* were similar genetically and functionally to each other, but the species that was related to *L. orbiculatus* was genetically and functionally diverse from *the C. orbicularis* species. All subspecies had several genes related to the systems of sulfate, nitrogen, and amino acid metabolism, defense, vitamins and structure/motility. Most of the variability between the species were found in KEGG metabolic categories involved in carbohydrate metabolism and membrane transport whereas the most abundant accessory genes were in energy metabolism and signaling/cellular processes. Location influenced the prophage components present while subspecies did not show much of an effect on the prophages present. Genes were mostly horizontally transferred within the same species regardless of the location. This study suggests that lucinid endosymbiont samples were more genetically and potential functionally similar based on taxonomic specificity, but environment could influence gene expression and activity which should be addressed in future studies.

## Effects of Hydrothermal Vent Chemistry on Reproductive Allocation in Symbiotic Punk-Rock Snails

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Hydrothermal vents occur across geologically distinct settings resulting in hydrothermal fluid chemistries that can vary spatially and temporally. Even vents in close proximity can present different fluid profiles and thus different environments for invertebrate communities. Many species that span across multiple vents and fluid profiles host nutritional bacterial symbionts that depend upon the reduced chemicals in vent fluids. Thus, vent systems provide an opportunity to understand how hydrothermal fluid chemistry can determine host-endosymbiont dynamics. The energetic inputs from the symbiont to the host are constrained by the fluid chemistry, which dictates both the productivity of the symbiosis and the energetic costs to the host living in a highly variable and often hostile environment. Therefore, species that occur across vents which vary markedly in fluid chemistry may exhibit different fitness outcomes. To investigate this, we focused on *Alviniconcha hessleri sensu stricto*, Hessler's Punk-rock Snail, a species restricted to hydrothermal vent fields located along the Mariana Back-arc. This back-arc experiences differences in spreading rate across its length, resulting in hydrothermal vents with effluents that range widely in temperature, pH and metal concentrations. *Alviniconcha hessleri s.s.* relies on the energy provided by chemoautotrophic endosymbionts, which inhabit their enlarged gill tissues. We predict a relationship between vent fluid chemistry, population characteristics and reproductive allocation based on energetic trade-offs. To assess spatial variation in energy allocation to reproduction, we examined population size structure, gonad morphology and gametogenesis in *A. hessleri s.s.* collected from five hydrothermal vents along the Mariana Back-arc. Overall, histological sections and size-structure data indicate that *A. hessleri s.s.* exhibits hermaphroditism with continuous reproduction despite apparent periodic recruitment. Our initial findings suggest that the energetic cost of living in more stressful vent fluids may limit the productivity of the symbiosis and allocation to reproduction by imposing high physiological or maintenance costs.

**Differences in Gut Microbiome Composition and Function  
Between Two Polygyrid Land Snails, *Polygyra cereolus*  
(Muhlfeld, 1816) and *Praticolella mexicana* (Perez, 2011)  
(Gastropoda: Polygyridae)**

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Snail gut bacteria play crucial roles in organic material digestion and nutrient production and have been implicated in aspects of reproduction. Gut microbes are known to differ between snail species, and between anatomical compartments of the digestive tract; dietary changes are also known to alter snail gut flora. To better understand their diversity and function, we studied the gut microbial communities from two polygyrid land snails from Texas, *Polygyra cereolus* and *Praticolella mexicana*. We were interested in whether significant differences in bacterial community composition existed between the two species, and whether differences in microbial diversity corresponded to differences in community function. Using next-generation sequencing of the bacterial 16S V4 region, we discovered significant differences in bacterial community structure between the two snail species. Bacteria ingested from the environment explained many of the significant differences, including higher numbers of Chromatiaceae in *Po. cereolus* and Sphingobacteriaceae in *Pr. mexicana*. Enteric bacteria also differed significantly between snail species; Clostridiaceae and Mycoplasmataceae were more abundant in *Po. cereolus* while Beutenbergiaceae, Flavobacteriaceae, and Nocardioideaceae were more abundant in *Pr. mexicana*. Forty-six functional pathways differed significantly between the two snail species, potentially correlated with differences in bacterial community composition and snail life history. Our data describe the first examination of gut flora diversity in Polygyridae, and we present future opportunities for understanding the microbial differences between polygyrid species.

**Special symposium: Showcasing Molluscan Research at the Undergraduate Level****An Evaluation of Muskrat Middens as Tools for Monitoring Freshwater Mussel Populations**

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One of the main predators of freshwater mussels in North America is the muskrat, *Ondatra zibethicus*. Muskrats eat mussels on lake shores and discard the shells in piles known as “middens”. Monitoring mussel shells within middens may provide valuable information about adjacent living mussel populations and the potential impact that muskrats are having on them. The objective of this study was to evaluate the utility of muskrat shell middens as tools for monitoring freshwater mussel populations. We collected shells from five muskrat shell midden sites on two lakes within Cape Breton, Nova Scotia (Pottle Lake and Forrester's Lake). The shells were measured for length, identified to species, and in the case of sexual dimorphic species, identified to sex. In total we measured 5,636 shells. Living populations adjacent to middens were sampled using quadrats and compared to the midden samples. Living populations in areas without an adjacent midden site were also sampled and compared to sites adjacent to middens in order to examine the potential impact muskrat predation is having on mussel populations. Relative species abundance differed significantly ( $p < 0.05$ ) between midden sites and adjacent live populations with *Lampsilis cariosa* over-represented and *Elliptio complanta* and *Utterbackiana implicata* underrepresented in middens. We found significantly larger shells in midden samples compared to live samples ( $p < 0.05$ ) suggesting that muskrats prefer larger mussels. A male bias sex ratio ( $\approx 2:1$ ) was found within both middens and live populations. Lower mussel densities in areas adjacent to midden sites compared to sites not adjacent to midden sites suggest that muskrat foraging is having a negative impact on mussels. While muskrats do not appear to sample living populations of freshwater mussels randomly in relation to size and species, middens may still be useful in locating and collecting preliminary data on mussel populations.



## **Ecological Thresholds of the Chinese Mystery Snail (*Cipangopaludina chinensis*) in Relation to Nova Scotia Environments**

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The Chinese mystery snail, *Cipangopaludina chinensis*, is a non-indigenous, potentially invasive aquatic species located in North America. To better understand the potential spread of *C. chinensis* in Nova Scotia, the ecological thresholds of the species need to be established. Adult and juvenile *C. chinensis* were tested for salinity tolerance [(0, 5, 10, 15, and 20) ppt], and pH tolerance (initial pH range between 4 and 8) in a 2-week and 4-week laboratory experiment, respectively. The migration patterns of adult *C. chinensis* were monitored bi-weekly at three Halifax Regional Municipality lakes. Migration monitoring was done in spring and summer, noting the depths at which the snails are living when water levels and temperatures change. In the salinity experiments, *C. chinensis* did not survive in salinity concentrations 10 ppt or higher, but did survive in 0 ppt and 5 ppt. This suggests *C. chinensis* could inhabit brackish water with low salinity. At low pH (<5.5), there was some mortality with juvenile *C. chinensis*, but a longer experimental period is needed to establish the pH threshold for both adult and juvenile snails. The lake snail migration surveys show the snails are typically found in shallow water when the water temperature is warm ( $\geq 20^{\circ}\text{C}$ ), and found in deeper water when the temperature is cool ( $\leq 20^{\circ}\text{C}$ ). This research suggests the ecological tolerances of *C. chinensis* may allow for the species to spread into vulnerable freshwater ecosystems across Nova Scotia not previously considered as a suitable habitat, including brackish ecosystems along the coast.

## **Mantle-flap Lure Morphology and Behavior of *Lampsilis cariosa* (Bivalvia: Unionidae)**

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The glochidia of most species of Unionidae spend time as ecto-parasites on the gills or fins of fishes to complete their metamorphosis to juveniles. Most *Lampsilis* species display highly developed mantle lures which mimic small fishes and attract fish hosts, increasing chances of successful infestation. We examined the mantle lures of yellow lampmussel (*Lampsilis cariosa*) in tank studies and lake habitats in Nova Scotia. The species is listed as “Special Concern” under the Canadian Species at Risk Act and is considered “Threatened” within the province of Nova Scotia. Detailed study of mantle lure morphology and behavior are important to gain a better understanding of this critical stage in the life history of this species. We found yellow lampmussel lure morphology and behavior was similar to *L. cardium*, and *L. ovata*. Variations in yellow lampmussel eyespot size and color patterns were observed among individuals and correlated with the age of yellow lampmussel. We also found variation in lure display behavior in response to light, with more active “full” displays being observed in low light conditions in lab and *in situ* lake environments. This may be related to twilight foraging activity of white perch, the only known fish host for yellow lampmussel in Nova Scotia. Chain pickerel (*Esox niger*) are displacing white perch within Nova Scotia lakes. Other research has suggested that yellow lampmussel may be able use chain pickerel as a fish host. A better understanding of chain pickerel foraging patterns in relation to yellow lampmussel lure behavior is needed to assess the likelihood of this host shift.

## **The Impact of the Freshwater Mussel *Elliptio complanata* on Water Quality**

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Pottle Lake is the drinking water source for the community of North Sydney and surrounding area having the highest raw water quality within the Cape Breton Regional Municipality (CBRM). It also serves as a refuge for an estimated 5.5 million freshwater mussels. These mussels may be contributing to the increased water quality in Pottle Lake. Each mussel filters  $\approx 0.5$ -1L of water every hour, potentially “cleaning” the freshwater in the lake. The goal of this study was to examine the impact the freshwater mussel *Elliptio complanata* (the most common mussel species in Pottle Lake) has on water quality. To address this goal, I did a series of tank experiments examining how freshwater mussel filtration impacts algae, suspended inorganic sediment (silt), metals and dissolved organic carbon (DOC) concentrations in water. It was observed that mussels significantly ( $p < 0.05$ ) reduced concentrations of the metals Al, Si and Mn. Mussels led to significant increases in calcium, magnesium, strontium, and silicon. Mussels significantly reduced silt and algal concentrations over time. And a significant increase in N and P concentrations were also seen in Mussel tanks over time. No significant impact was observed for DOC. My results support the idea that the freshwater mussels are contributing to the high water quality of Pottle Lake and suggest that freshwater mussels like *E. complanata* provide valuable ecological services to surface drinking water supplies.

## Contributed Posters

**Building a DNA Barcoding Library of Western Texas Spring Snails (Gastropoda: Caenogastropoda: Cochliopidae & Hydrobiidae)**

Perez, Kathryn E.\*<sup>1</sup>; Hutchins, Benjamin T.<sup>2</sup>; Schwartz, Benjamin F.<sup>2</sup>; Chastain, Rebecca<sup>1</sup>; Ortega, Christina<sup>1</sup>; Glover, Houston<sup>1</sup>; Spor Leal, Manuel<sup>1</sup>

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The Trans-Pecos (Western) region of Texas has an endemic groundwater-dependent snail fauna, including five species that are federally listed as endangered. These snail populations are usually restricted to one or a few nearby springs and are highly susceptible to extinction due to reduced groundwater discharge, modification of springs by humans, and trampling of springs by livestock and feral, exotic species. Most of the permanent springs where these snails occur are very small, <10 m<sup>2</sup> and several spring snail species have gone extinct between the time they were collected and named. We are working towards establishing a DNA barcoding library for the extant Trans-Pecos spring snails to enable rapid identification of newly encountered spring snail populations. To date, we have collected invertebrate samples using a variety of methods at 46 spring and spring run sites. During these surveys we have confirmed the continued presence of *Assiminea pecos*, *Pseudotryonia adamantina*, 3 of 5 *Tryonia* species, 3 of 4 *Pyrgulopsis* species, and discovered 3 new populations of *Pyrgulopsis*.

## POSTER SESSION II

Special symposium: Showcasing Molluscan Research at the Undergraduate Level

### **Tubercle Construction in *Graneledone boreopacifica* (Octopoda: Megaleledonidae)**

Morrison, Anastasia\*; and Penney, Brian K.

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Two closely related deep sea octopuses, *Graneledone boreopacifica* and *G. verrucosa*, are similar except for their pattern of surface tubercles. However, little is known about the construction or function of these tubercles. Unlike the tubercles of surface octopuses, these tubercles do not appear to change shape. We refined a protocol to stain paraffin embedded sections with Gomori's trichrome in order to compare distribution of muscle, connective tissue and other elements in *Graneledone* mantle versus those of surface octopuses.

## **Evaluating the Putative Role of Exosomal Pathways in the Process of Shell Formation in *Crassostrea gigas***

Muñoz Schuler, Camilo\*; Torres, Viviana; Aguilera, Felipe

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Most mollusks produce external calcified shells, which are fabricated by specialized epithelial cells on the dorsal mantle. This tissue is underneath the shell and expresses a suite of genes encoding secreted proteins that are delivered into the extrapallial space to finally be embedded into the shell. Recent shell proteomic analyses have revealed that secreted proteins, but also proteins lacking a signal peptide, form part of the shell, raising the question of how these non-secreted proteins reach the mineralization front. Some authors have postulated the hemocytes as possible protein carriers; however, there is not a full understanding of how this could be happening. By performing tough bioinformatics analyses on the genomic resources available for the bivalve *Crassostrea gigas*, we found the majority of components concerning the biogenesis and secretion of exosomes, suggesting that this species has the molecular repertoire required to produce exosomes. We further evaluated the expression patterns of those exosomal components in different tissues of this oyster and found that hemocytes seems to be the main exosome-producing tissue, followed by the mantle. Indeed, gene expression of exosome-related proteins, which have also been reported as embedded in the shell, display high expression in mantle, followed by hemocytes, digestive gland, and adductor muscle. Furthermore, shell-forming genes are expressed in a similar fashion, with a dominant expression in the mantle tissue, followed by digestive gland, adductor muscle and hemocytes. Our results indicate that genes encoding components of the shell matrix are not only generated in the mantle but also in other tissues, proposing the participation of non-classical biomineralization pathways in shell formation. Altogether, we suggest that molluscan shell formation is probably aided by diverse tissues, with hemocytes, given their high capacity to produce exosomes and infiltrate into different tissues, being the second most important shell-forming tissue.

## **Tyrosine Hydroxylase-Like Immunoreactivity in the Nervous System of *Tritonia exsulans***

Larade, Donica E.<sup>\*1,3</sup>; Kehoe, Emily F.<sup>1,2</sup>; Croll, Roger P.<sup>3</sup>; Cain, Shaun D.<sup>4</sup>; Wyeth, Russell C.<sup>1,2</sup>

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The sea slug *Tritonia exsulans* (prev. *Tritonia diomedea*) is a model organism for neuroethology, as both sensory responses and the motor control of various behaviors have been studied. Previous research on the gastropod nervous system has supported the importance of catecholamines (i.e., dopamine) in behavioural processes. Tyrosine hydroxylase (TH) is a key enzyme in the catecholamine synthesis pathway that converts tyrosine into the precursor of dopamine, L-DOPA. TH-immunoreactive (TH-IR) cells were found in the central (buccal, gastroesophageal, rhinophore, cerebral-pleural, and pedal ganglia) and peripheral (rhinophore and oral veil) nervous systems. Distributions of central TH-IR neurons varied numerously (37-60) between paired ganglia. Very few TH-IR cells were found in the buccal ganglia; 2 large cells and 2-4 smaller ones were labelled toward the middle of each ganglion. Large axons were labelled across the buccal commissure, where a prominent tract of small axons interconnected the buccal and gastroesophageal ganglia, where cell labelling was inconsistent. Large TH-IR cells were found in the cerebral-pleural ganglia, especially anterior-medially, with a similar number (28-68) of smaller cells in the pedal ganglia. Traceable axons were seen in all commissures and nerves except the pedal posterolateral and anterior buccal nerves, and a central neuropil was labelled throughout all of the central ganglia. Peripheral TH-IR labelling revealed deeper branching innervation, along with thousands of putative sensory cells concentrated subepithelially. Dozens of TH-IR cells and axons were also present in the rhinophore ganglia and surroundings. The overall distributions described here are similar to those found in other gastropods, consistent with a highly conserved presence of TH in peripheral sensory cells and individual central cells across species.

## Flashback Through ARMS: A Study of Mollusk Assemblages in Sisal Reef, Mexico

Villamonte-Cab, Gabriela\*<sup>1</sup>; Suárez-Mozo, Nancy Y.<sup>2,3</sup>;  
Palomino-Alvarez, Lilian A.<sup>2,3</sup>; León-Deniz, Lorena V.<sup>4</sup>; Simões, Nuno<sup>3,5,6</sup>

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Marine communities are always changing due to a variety of factors, such as climate change, overfishing, resource availability, biological interactions like invasive species, or predators. We used the Autonomous Reef Monitoring Structure (ARMS) to assess changes in mollusk fauna (Gastropoda and Bivalvia) through species diversity and the ecological succession changes in one reef (Bajo de 10 Reef) from the southern Gulf of México. Fourteen ARMS units were deployed by scuba divers and withdrawn through quarterly sampling (January, April, July, and October) in 2019. In each month, an ARMS was extracted and processed with its three replicates. Mollusks were assigned a catalog number and deposited at the “Colección de Moluscos de la Península de Yucatán” (CMPY), Unidad Multidisciplinaria de Docencia e Investigación Campus Sisal, Universidad Nacional Autónoma de México. We narrowed the samples to living specimens only and used identification guides to reach the lowest taxonomic level possible. We identified 275 specimens, 46 species, 29 families, and seven orders. *Musculus lateralis* and *Rissoella edbayeri* were the most abundant species. The ecological succession has made itself clear in the present study, in which we found an evident replacement of species in the community composition, with statistically significant differences between ARMS and in the species in each month. We concluded species replacement contributed to shaping the dissimilarity of mollusks assemblages, contributed to a better understanding of the complex ecological temporal patterns in the Gulf of Mexico. Our data are limited to mobile organisms, it is necessary to continue studying to understand how the community behaves in a time interval greater than one year.



## **Developing an Alternative, Lab-Based Diet for Hawaiian Ground Snails – Food Preference Research and Nutrient Analyses**

Thomey, Lilly K.\*; Sischo, David R.

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Many rare and endangered species rely on captive propagation to prevent extinction. Understanding an organism's natural diet and associated foraging behavior is critical to diet replication in a lab environment. Terrestrial snail species of the Hawaiian Islands face many threats, including invasive predators, habitat loss, and climate change. Ex situ captive rearing programs, like Hawai'i's Snail Extinction Prevention Program (SEPP), are essential for keeping these native snail species from the brink of extinction. Amastridae is an endemic family of imperiled ground and semi-arboreal snail species that feed on decaying leaves of native plants including, but not limited to, māmakī (*Pipturus albidus*), ūpuhe (*Urera glabra*), and 'ie'ie (*Freycinetia arborea*). Currently, rearing amastrid species is restricted to the islands due to their reliance on wild-collected native plant material for food. The objective of this research is to develop an alternative, lab-based diet that will meet the nutritional needs of amastrid species. We performed buffet style feeding trials with *Amastra intermedia* individuals to quantify the type and proportion of preferred food items. Next, we sent preferred food material off for nutrient analyses. Using the results of the nutrient analyses, we identified commercially available ingredients to compose alternative manufactured diets. Results of our feeding trials and nutrient analyses will be presented, as well as suggestions for future diet research. An effective manufactured diet for Amastridae would enable the expansion of captive rearing efforts to participating partners outside of the state, significantly increasing the potential for conservation.

## **Quantification of Connective Tissue Versus Spicule Content in *Dorid nudibranch* Mantle Networks**

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*Dorid nudibranchs* typically possess innumerable calcareous spicules arranged in complex networks, but we know little about how these networks function. Species appear to have different amounts and arrangements of connective tissue relative to the spicule network: connective tissue may be limited to areas surrounding the spicule network cords, or it may occupy most of the space in the mantle. These arrangements likely affect the mechanical properties of the mantle tissue. Previous work in our lab developed protocols for generating models of nudibranch histology from CT scans using the program, 3D Slicer. From these models we can extract the volumetric ratios of connective tissue and spicules in comparison to each other, and to the total tissue volume in several species of nudibranch. These data will be used to create models of spicule/connective tissue networks to test functional hypotheses.

## Holey Shell: Quantifying Bioerosion in *Tridacna derasa* Shells

Allen, Victoria\*<sup>1</sup>; Gannon, Michelle<sup>2</sup>; Velinsky, David<sup>2</sup>

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Giant clams (Tridacninae) are an essential part of the ocean ecosystem as they filter water, prevent eutrophication, and serve as shelter for many different species of ocean life. As ocean acidification increases, giant clams face an ever-growing challenge to build as well as maintain their calcium carbonate shells. The structural integrity of their shells is further threatened by bioeroding organisms that bore holes into these structures. Bioerosion by green algae (*Ostreobium*) and sponges (*Cliona*) affects giant clam shells throughout the Indo-Pacific and Pacific oceans. The aim of this study is to determine the predominant type of bioerosion experienced by *Tridacna derasa* living in three habitat types in Palau. Qualitative differences were visually observed and quantitatively measured across sections in three shells, each from a different habitat in Palau. Bioerosion by boring sponges, aided by photosymbiotic *Symbiodinium*, yields a smaller number of large, scalloped holes while bioerosion by green algae leads to a larger number of 10x smaller holes with rough edges scattered throughout the shell. Additionally, analysis of variance in the number and size of holes between shells reaffirmed observed similarities and differences between the shell's predominant method of bioerosion. The data also suggests that the clams were infected at the mariculture facility negating intended conservation efforts of the Palau Mariculture Demonstration Center. Researchers considering use of giant clam shells for trace metal, stable isotope, or genetic analyses should be especially aware of the potential contamination left by bioeroders in the shell's matrix.

## Contributed Posters

## Genetic Differentiation Between Populations of *Tridacna maxima* (Bivalvia: Cardiidae: Tridacninae) Across the Saudi Arabian Coast: Phylogeographical Approach

Othmen, Abdelwaheb Ben<sup>1</sup>; Deli, Temim<sup>1</sup>; Ouanes, Zouhour<sup>2</sup>; Mansour, Lamjed<sup>3</sup>

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The present investigation focuses on population genetic structure analysis of the endangered giant clam species *Tridacna maxima* across part of the Red Sea, with the main aim of assessing the influence of postulated potential barriers to gene flow (i.e., particular oceanographic features and marked environmental heterogeneity) on genetic connectivity among populations of this poorly dispersive bivalve species. For this purpose, 44 specimens of *T. maxima* were collected from five sampling locations along the Saudi Arabian coast and examined for genetic variability at the considerably variable mitochondrial gene cytochrome c oxidase I (COI). Our results revealed lack of population subdivision and phylogeographic structure across the surveyed geographic spectrum, suggesting that neither the short pelagic larval dispersal nor the various postulated barriers to gene flow in the Red Sea can trigger the onset of marked genetic differentiation in *T. maxima*. Furthermore, the discerned shallow COI haplotype genealogy (exhibiting high haplotype diversity and low nucleotide diversity), associated with recent demographic and spatial expansion events, can be considered as residual effect of a recent evolutionary history of the species in the Red Sea.

## **New Data on Abyssal Solenogastres (Mollusca, Aplacophora) with the Study of a Collection from the Clarion-Clipperton Fracture Zone**

Cobo, M. Carmen\*; McLaughlin, Emily L.; Kocot, Kevin

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Solenogastres (Mollusca, Aplacophora) are one of the least known molluscs, despite being diverse and essential to the understanding of the evolution of the phylum. Although many of the recently described Solenogastres come from abyssal locations, most have been described from the continental shelf and slope with just 31 of the 296 formally described species known from depths below 3500 m. Here we present preliminary results of an integrative taxonomic study on a collection of abyssal Solenogastres (38 specimens) from the Clarion-Clipperton Fracture Zone (CCZ) collected during the SO 205 MANGAN cruise. Specimens were first classified into morphospecies based on their habitus and mantle sclerites. At least one specimen of each morphospecies was selected for detailed study. These were sectioned in three parts with the middle region imaged under a low-vacuum, low-accelerating voltage SEM, to obtain ultrastructure-level data on the mantle sclerites and high-quality DNA (16S and COI barcodes). The anterior and posterior regions were preserved for further analysis (histology for complete species identification). The obtained data show that that this relatively small collection is surprisingly diverse: with roughly seventeen distinct species, most of them apparently new to science, representing six different families. Thus, this work reveals the importance of the study of deep-sea areas to better understand the real solenogasters diversity. Moreover, the nature and extent of potential impacts related with mining in polymetallic nodule areas are poorly known, but of great concern. Therefore, before the impacts of deep-sea mining can be assessed, determining the biodiversity in these habitats becomes crucial.

Acknowledgments: The authors are grateful to Pedro Martínez-Abizu for providing this material. This work was funded by SO 205 Projekt MANGAN and NSF award 1846174.

## Brazilian Troglobitic and Troglophilic Snails

Silva, Fernanda S.\*<sup>1</sup>; Cavallari, Daniel C.<sup>2</sup>; Salvador, Rodrigo B.<sup>3</sup>;  
Cunha, Carlo M.<sup>4</sup>; Bichuette, Maria E.<sup>5</sup>

1. Museu de Zoologia da Universidade de São Paulo, São Paulo, SP, Brazil; 2. Departamento de Biologia, Faculdade de Filosofia, Ciências e Letras de Ribeirão Preto, Universidade de São Paulo, Ribeirão Preto, SP, Brazil; 3. Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand; 4. Universidade Federal de São Paulo, Campus Baixada Santista, Santos, SP, Brazil; 5. Laboratório de Estudos Subterrâneos, Universidade Federal de São Carlos, São Carlos, SP, Brazil

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The Brazilian territory is very extensive and harbors circa 20,000 caves, most of which are calcareous. Only a small fraction of the approximately 1,000 terrestrial and freshwater gastropod species reported from Brazil inhabit cave environments exclusively. Most descriptions of troglobitic gastropod species have been carried out in recent works, however; the first one being *Potamolithus troglobius* (Simone & Moracchioli, 1994). Caves are among the least explored habitats in Brazilian malacology, so the recent discovery of endemics shows the importance of a better exploration of those habitats. Given this scenario, as a first step we are preparing a complete checklist of troglobitic (exclusively cavern-dwellers) and troglophilic (also found in the epigeal areas in the vicinities) gastropods from Brazil. It includes both terrestrial and freshwater species, with information on current taxonomy, geographical distribution, the threats they are exposed to, and prospects for conservation and follow-up studies. To produce the present list, we carried out a bibliographic survey of the main checklists and catalogs of Brazilian mollusks as well as descriptions of more recent species and regional checklists. Our preliminary list counts with 22 species distributed in 15 genera and 11 families, with a geographic distribution that goes from Piauí state in the north to São Paulo state in the southeast. Despite the number of caverns in Brazil, there are relatively few troglobitic species in the country.

## **New Record of *Zoogenetes harpa* (Say, 1824) in Utah, USA**

Detlor, Jordon D.\*<sup>1</sup>; Holcomb, Kate<sup>1</sup>; Wagner, Eric<sup>2</sup>

1. Utah Division of Wildlife Resources, Salt Lake City, UT, USA; 2. 280 W. Center, Logan, UT, USA

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The Boreal Top (*Zoogenetes harpa*) is a minute terrestrial snail with a reddish-brown, conical shell consisting of four whorls, the first two being nearly smooth and the last two having widely spaced cuticular ribs in the direction of the growth lines. Although widely distributed in the Northern Hemisphere, distribution records are sparse for this species. Records include Japan, Scandinavia, Swiss Alps, Northern Russia, Canada, and Northern U.S. (Acad. Nat. Sci. Phila.; U.S. Nat. Mus.; Illinois Nat. Hist. Survey). *Zoogenetes harpa* was found in Utah for the first time in April 2021. To date, eight live individuals (four of them juveniles) have been found from two distinct locations in the Uinta Mountains near Vernal, Utah (approximately 40°N latitude). All individuals were found under fallen logs at or near the bottom of canyons in mountain forests (2,260 - 2,500 m elevation) dominated by fir trees. The authors identified this species based on shell morphology, but hope to validate the identification genetically. The Utah Division of Wildlife Resources plans to continue surveys for this species to better understand its distribution, habitat use, and threats in Utah.

## **Conservation Agreement and Strategy for Springsnails in Nevada and Utah**

Crookshanks, Chris<sup>1</sup>; Sjöberg, Jon<sup>1</sup>; Miskow, Eric<sup>2</sup>; Szabo, Kristin<sup>2</sup>;  
Holcomb, Kate<sup>\*3</sup>; Wheeler, Kevin; Jenness, Jeff<sup>4</sup>; Stevens, Larry<sup>4</sup>;  
Mellon, Cassie<sup>5</sup>; Mellison, Chad<sup>5</sup>; Schwemm, Michael<sup>6</sup>; Saito, Laurel<sup>7</sup>;  
Van Horne, Rachel<sup>8</sup>; Phillippi, Matthew<sup>9</sup>; Wullschleger, John<sup>10</sup>

1. Nevada Department of Wildlife, NV, USA; 2. Nevada Division of Natural Heritage, NV, USA; 3. Utah Division of Wildlife Resources, UT, USA; 4. Springs Stewardship Institute, AZ, USA; 5. Bureau of Land Management, UT, USA; 6. U.S. Fish and Wildlife Service, NV, USA; 7. The Nature Conservancy, NV, USA; 8. U.S. Forest Service, UT, USA; 9. USDA Natural Resources Conservation Service, UT, USA; 10. National Park Service, NV, USA

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There is an increasing concern and need for the conservation of springsnails and the unique spring and springbrook habitats on which they depend. Nationwide, several of these species have been listed as endangered or threatened under provisions of the Endangered Species Act; others are undergoing review by the U.S. Fish and Wildlife Service for possible future listing actions. These species can be particularly susceptible to localized threats such as water diversion, invasive species, development, or trampling by ungulates. In 2017, multiple agencies, stakeholders, and other interested parties in Nevada and Utah completed a Conservation Agreement for springsnails. The corresponding conservation Strategy was completed in 2020. The conservation actions described in the Strategy are expected to lead to the protection and enhancement of 103 springsnail species and their associated habitats in Nevada and Utah. Conservation Agreements and Strategies have been an important conservation tool for Nevada and Utah for more than 20 years and, in many cases, have resulted in precluding the need to list at-risk species.



## **Working Towards a Phylogeny of Central Texas Cavesnails (Gastropoda: Caenogastropoda: Cochliopidae)**

Perez, Kathryn E.\*<sup>1</sup>; Diaz, Pete<sup>2</sup>; Gibson, Randy<sup>2</sup>; Villanueva, Taylor<sup>1</sup>;  
Spor Leal, Manuel<sup>1</sup>; Serrano, Mercedes<sup>1</sup>; Hutchins, Benjamin T.<sup>3</sup>;  
Schwartz, Benjamin F.<sup>3</sup>

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There are 13 described species of minute, phreatic (subterranean aquatic) snails; all stygobitic or stygophilic, and endemic to the Edwards-Trinity Aquifer System of Texas and Mexico. Their underground habitat, microscopic size, and difficulty of sampling make them challenging to study. Nine species are in *Phreatodrobia* and several other species are ascribed to monotypic genera including *Stygopyrgus*, *Texapyrgus*, *Phreatoceras*, and *Balconorbis*. These snails have a wide variety of shell morphologies from flat to tall (planispiral and trochoform to conic and elongate-conic) and partially to fully uncoiled. They have been documented in river drift, from wells and springs, and recently in the hyporheic zone of streams. Recent collection efforts at ≈180 sites have extended the known ranges of the phreatic snails of the region and yielded unidentifiable snails, including some with intact tissue suitable for DNA work. A preliminary molecular phylogeny (COI & LSU) finds several distinct clades currently identified as *Phreatodrobia nugax*, *Phreatoceras* (uncoiled shell) nested within *Phreatodrobia*, and perhaps repeated evolution of a flat shell shape among members of *Phreatodrobia*.

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## List of attendees

<b>Allen, Victoria</b>	<i>Drexel University</i>
<b>Anderson, Laurie</b>	<i>South Dakota School of Mines and Technology</i>
<b>Asis, Ann-Geneve</b>	<i>Texas A&amp;M International University</i>
<b>Audino, Jorge</b>	<i>Iowa State University</i>
<b>Ball, Caitlin</b>	<i>Tufts University</i>
<b>Bauer, Will</b>	<i>Acadia University</i>
<b>Beinart, Roxanne</b>	<i>University of Rhode Island</i>
<b>Ben Othmen, Abdelwaheb</b>	<i>University of Monastir</i>
<b>Bennett, Rachael</b>	<i>Cape Breton University</i>
<b>Beresford, Rod</b>	<i>Cape Breton University</i>
<b>Bettters, Melissa</b>	<i>Temple University</i>
<b>Bieler, Rüdiger</b>	<i>Field Museum of Natural History, Chicago</i>
<b>Blaine, F. Matthew</b>	<i>The Florida State Collection of Arthropods</i>
<b>Bradbury, Catlin</b>	<i>Saint Mary's University</i>
<b>Brennin Houston, Ree</b>	<i>Fisheries and Oceans Canada</i>
<b>Bullis, David</b>	<i>State University of New York</i>
<b>Burns, Leah</b>	<i>Cape Breton University</i>
<b>Callomon, Paul</b>	<i>Drexel University</i>
<b>Campbell, Barbara</b>	<i>Clemson University</i>
<b>Campbell, Timothy</b>	<i>TD Campbell High School</i>
<b>Campbell, David</b>	<i>Gardner-Webb University</i>
<b>Cavadino, Imogen</b>	<i>Royal Horticultural Society; Newcastle University</i>
<b>Chalapalli, Shreya</b>	<i>Carnegie Museum of Natural History</i>
<b>Chalifour, Bridget</b>	<i>University of Colorado Boulder</i>
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<b>Cobo, Carmen</b>	<i>The University of Alabama</i>
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<b>Collins, Timothy</b>	<i>Florida International University</i>
<b>Crook, Robyn</b>	<i>San Francisco State University</i>
<b>Davis-Berg, Elizabeth</b>	<i>Columbia College Chicago</i>
<b>DeLeon, Kelli</b>	<i>Bernice Pauahi Bishop Museum</i>
<b>deMaintenon, Marta</b>	<i>University of Hawaii at Hilo</i>
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<b>DiNuzzo, Eleanor</b>	<i>University of Massachusetts Dartmouth</i>
<b>Dodge, Christine</b>	<i>Oregon State University</i>
<b>Douglas, Lauren</b>	<i>Cape Breton University</i>
<b>Dove, Sindy</b>	<i>Memorial University of Newfoundland</i>
<b>Drescher, Brandon</b>	<i>Brown University</i>
<b>Duda, Tom</b>	<i>University of Michigan</i>
<b>Dufour, Suzanne</b>	<i>Memorial University of Newfoundland</i>
<b>Earl, Chandra</b>	<i>Bernice Pauahi Bishop Museum</i>
<b>Field, Victoria</b>	<i>Bremen University</i>
<b>Franzen, Alex</b>	<i>University of Oklahoma</i>
<b>Fraser, Meghan</b>	<i>Mount Allison University</i>
<b>Friesen, Olwyn</b>	<i>Weston Family Northern Scientist/University of Manitoba</i>
<b>Genovese, Gina</b>	<i>Saint Anselm College</i>
<b>Giani, Nichole</b>	<i>Clemson University</i>
<b>Gibson, Glenys</b>	<i>Acadia University</i>
<b>Gosselin, Louis</b>	<i>Thompson Rivers University</i>
<b>Goulding, Tricia</b>	<i>Smithsonian Institution, National Museum of Natural History</i>
<b>Graf, Daniel</b>	<i>University of Wisconsin-Stevens Point</i>
<b>Griffin, Tyler</b>	<i>University of Connecticut</i>
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<b>Gutierrez Andrade, Daniela</b>	<i>The University of Tampa</i>
<b>Halvonik, Adriana</b>	<i>University of Costa Rica</i>
<b>Hanson, Nova</b>	<i>Memorial University of Newfoundland</i>
<b>Haubner, Meagan</b>	<i>Bernice Pauahi Bishop Museum</i>
<b>Hewitt, Trevor</b>	<i>University of Michigan</i>
<b>Holcomb, Kathryn</b>	<i>Utah Division of Wildlife Resources</i>
<b>Huang, Andy</b>	<i>Bernice Pauahi Bishop Museum</i>
<b>Hunter, Kerry</b>	<i>KwaZulu-Natal Museum</i>
<b>Irwin, Alison</b>	<i>Natural History Museum, London</i>
<b>Kawamoto, Regina</b>	<i>University of Hawaii Manoa; Bernice Pauahi Bishop Museum</i>
<b>Kelley, Patricia</b>	<i>University of North Carolina Wilmington</i>
<b>Keretz, Shay</b>	<i>Central Michigan University</i>
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<b>Kocot, Kevin</b>	<i>University of Alabama</i>
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<b>Lallier, François</b>	<i>Sorbonne Université</i>
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<b>Lee, Taehwan</b>	<i>University of Michigan Museum of Zoology</i>
<b>Li, Ruiqi</b>	<i>University of Colorado Boulder</i>
<b>Lim, Jean</b>	<i>University of Miami</i>
<b>Lipae, Harold</b>	<i>University of the Philippines Los Baños</i>
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<b>Manuel, Sofía</b>	<i>Universidad Autónoma de Yucatán</i>
<b>Martel, Andre L.</b>	<i>Canadian Museum of Nature</i>
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<b>Middlebrooks, Michael</b>	<i>University of Tampa</i>
<b>Mikkelsen, Paula</b>	<i>Field Museum of Natural History, Chicago</i>
<b>Millwood, Joshua</b>	<i>University of Alabama</i>
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<b>Slapcinsky, John</b>	<i>Florida Museum of Natural History</i>
<b>Sollows, Mary</b>	<i>New Brunswick Museum</i>
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<b>Steeves, Laura</b>	<i>Dalhousie University</i>
<b>Stewart, Donald</b>	<i>Acadia University</i>
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<b>Wyeth, Russell</b>	<i>St. Francis Xavier University</i>
<b>Yeung, Norine</b>	<i>Bernice Pauahi Bishop Museum</i>
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Thanks for virtually visiting our island –  
we hope to see you in person someday soon

*Ne'multes*

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