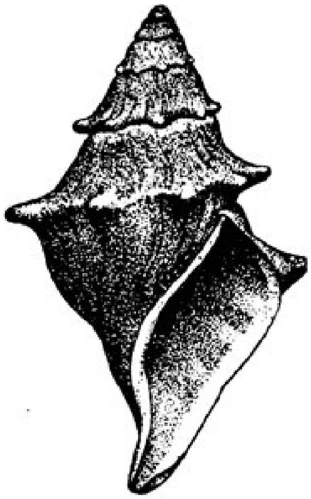
2023 Annual Meeting

American Malacological Society

Program and Abstracts

(last updated 7/31/2023)

Program and Abstracts



AMS 2023

89TH Annual Meeting

Tuscaloosa, Alabama

AUGUST 1-5, 2023

UNIVERSITY OF ALABAMA &
ALABAMA MUSEUM OF NATURAL HISTORY

Compiled and edited by:

M. Carmen Cobo, Meghan Yap-Chiongco, Nickellaus Roberts, & Kevin Kocot

Welcome to the 89th annual meeting of the American Malacological Society!

We're thrilled to be hosting the 89th annual meeting of the American Malacological Society (#AMS2023) at the University of Alabama and the Alabama Museum of Natural History in Tuscaloosa, Alabama. We hope that you will find this to be a stimulating meeting with many interesting talks and posters balanced with ample opportunities to meet with colleagues, share ideas and information, strengthen existing collaborations, and form new ones.

AMS 2023 has 78 registered in-person attendees (plus several remote participants) and 77 presentations. Given the incredible diversity of freshwater molluscs in Alabama, the topic of the President's Symposium (August 2nd) will be “Freshwater Mollusk Diversity in a Biodiversity Hotspot” organized by Dr. Carla Atkinson. In addition to the President's Symposium, two contributed oral presentations – the ‘president's picks' – will be that afternoon. The remaining contributed oral presentations (August 3rd-4th) and posters (August 2nd) have been divided into five broad themes:

1. Ecology and Diversity of Freshwater Mollusks
2. Natural History Collections
3. Ecological Interactions and Adaptations
4. Biodiversity, Taxonomy, and Phylogenetics
5. Physiology and Molecular Biology

Reading the abstracts and preparing the schedule for this meeting was an exciting experience for the organizing committee that highlighted the breadth and interdisciplinary nature of modern malacology research (and made it difficult to place many interdisciplinary talks in the ‘right' session!). In addition to the wide array of research areas represented at AMS 2023, we are particularly pleased that every class of Mollusca is the focus of at least one presentation!

We aimed to make this meeting as student friendly as possible by keeping costs low for students. Student-centered events will include a student (and postdoc!) mixer at Black Warrior Brewing Company (after the poster session on August 3rd) and a student-mentor networking program for in-person attendees (during lunch on August 4th).

Thanks to the leadership of AMS's Justice Equity Diversity and Inclusion (JEDI) committee by Rose Osborne and the efforts of this committee, AMS 2023 will include a panel discussion on inclusive fieldwork and field courses hosted by the Society's Justice, Equity, Diversity, and Inclusion (JEDI) Committee (during lunch on August 3rd). The inclusive fieldwork panel will take place during the lunch hour on in the Bryant Conference Center in Rast B. Time will be split between panelist introductions/main topic presentations and Q&A. During the intros/main topics phase, panelists will highlight 1-3 topics or key points related to their fieldwork and workplace inclusivity experiences. Audience questions will be collected anonymously and addressed by the panel. Attendance to this event is strongly encouraged! Attendees will be invited to join the panelists for an informal continuation of the discussion over dinner (meeting at Hotel Capstone at 7:30 pm). The committee also asks that everyone considers participating in an anonymous survey to help AMS better understand barriers to participation (see next page).

We will be holding the annual AMS Auction (on August 3rd), which wouldn't be the same without with auctioneer Paul Callomon! This is a favorite of many AMS attendees and the funds raised help to support travel and research awards for AMS student members! Donations for the auction will be accepted right up until the last minute and can include non-tangible items like volunteering your time.

The formal meeting program will conclude with the AMS business meeting (on August 4th) followed by the AMS Banquet (free for students!). There will be an optional field trip (on August 5th) to visit to the Alabama Aquatic Biodiversity Center and diverse site on the Cahaba River. Attendees will meet in front of Hotel Capstone at 8 AM (sharp!). You will get wet on this ride! The HaptoNet workshop to develop an NSF TCN proposal focused on digitizing adherent marine organisms (haptobionts) organized by Paul Callomon will also take place on August 5th starting at 8:30 AM (not 11 as previously indicated!) in Mary Harmon Bryant Hall room 328.

Finally, I would like to extend my sincere thanks to our sponsors and everyone who helped make this meeting possible: the organizing committee – especially Carmen Cobo, Carla Atkinson, and Meghan Yap-Chiongco, the AMS Council – especially Amanda Lawless and Liz Shea, our keynote and symposium speakers, the JEDI panel participants, participants joining the meeting remotely, and everyone who braved the Alabama heat to attend AMS 2023 in person!

Roll Tide!

Kevin Kocot on behalf of the AMS 2023 organizing committee.

Justice, Equity, Diversity, and Inclusion Statement

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.

Please consider participating in a voluntary anonymous survey to gather information about the barriers that may be preventing malacologists from fully participating in the AMS, including joining the Society, renewing membership, and attending annual meetings. We also want to understand how these barriers intersect with factors like career stage, identity axes, and other Justice, Equity, Diversity, & Inclusion (JEDI) areas of interest.

https://tinyurl.com/5744r9rp

Contents

- The AMS Council meeting on August 1st is for AMS Council members only. It will be at 3 pm in 328 Mary Harmon Bryant Hall.
- The welcome reception will take place in the Grand Gallery (second floor) of the Alabama Museum of Natural History (Smith Hall) on 8/1 starting at 6 PM. You will be able to get your name badge and 'swag bag' at the registration table there.
- Most AMS 2023 events (oral presentations, poster session, auction, JEDI panel) will take place at the Bryant Conference Center (BCC) located just next door to Hotel Capstone. The registration table will also be staffed in the mornings and during breaks.
- A map of the University of Alabama Camus is available at: https://www.ua.edu/map/
- The AMS 2023 group photo will take place at 4:15 on 8/3 before the auction. Please meet in the BCC near the registration table!
- The AMS business meeting on August 4th is open to all AMS members. It will be at 4 pm on 8/4 in the Bryant Conference Center Rast B room.
- The Banquet will take place immediately following the AMS Business Meeting (6-10 PM on August 4th) in the Grand Gallery (second floor) of the Alabama Museum of Natural History (Smith Hall). Winners of the student presentation award competition will be announced at this time. The banquet is free for students but if you are a non-student and didn't purchase a ticket but want to go, talk to Kevin Kocot.
- Refreshments at the welcome reception and banquet (including beer and wine) are complimentary. There will be a cash bar available at the poster session and auction.
- If you signed up for the field trip, please meet the organizers in front of Hotel Capstone promptly at 8:00 AM on 8/5.
- In the abstracts, presenters of presentations with multiple co-authors are denoted with an asterisk.
- Files associated with oral presentations should be copied to the computer in your session room prior to the session. Helpers should be available to assist during breaks but please try to do this well in advance.

	Tuesday August 1st		**Wednesday August 2nd**		**Thursday August 3rd**		**Friday August 4th**		**Saturday August 5th**
	Alabama Museum of Natural History		**Bryant Conference Center (BCC) – talks, poster session, JEDI panel, auction**						Field Trip (meet in front of Hotel Capstone at 8:00; will return by 5 :00) HaptoNet Meeting (starts at 8:30 in 328 Mary Harmon Bryant Hall)
			Rast A+B		Rast A	Rast B	Rast A	Rast B	
		9:00	**Welcome**	9:00	1. Ecology & Diversity of Freshwater Mollusks	3. Biodiversity, Taxonomy, & Phylogenetics	1. Ecology & Diversity of Freshwater Mollusks	5. Ecological Interactions & Adaptations	
		9:15	**President's symposium**						
		10:30	Coffee break	10:20	Coffee break				
		11:00	**President's symposium**	10:40	1. Ecology & Diversity of Freshwater Mollusks	3. Biodiversity, Taxonomy, & Phylogenetics	1. Ecology & Diversity of Freshwater Mollusks	5. Ecological Interactions & Adaptations	
		12:00	Lunch	12:00	Lunch + **JEDI Panel**		Lunch + **Mentoring Program**		
		1:30	**President's symposium**	2:00	2. Physiology & Molecular Biology	3. Biodiversity, Taxonomy, & Phylogenetics	4. Natural History Collections		
3:00	**AMS Council Meeting** (MHBH 328)	3:00	Coffee break						
		3:20	**Selected Contributed Talks**	3:20	Coffee break				
				3:40	2. Physiology & Molecular Biology				
		4:00	**Poster session**	4:00			**Society-wide business meeting** (Rast B; starts at 4:00 pm)		
				5:00	**Auction** (BCC Birmingham/Central room)				
6:00	**Reception** (Smith Hall)	6:00		6:00			**Banquet** (ALMNH Grand Gallery)		
		6:30	**Student & postdoc mixer** (Black Warrior)	6:30					

Tuesday, August 1

Alabama Museum of Natural History (Mary Harmon Bryant Hall (MHBH) and Smith Hall)

3:00	**AMS Council Meeting** (AMS Council members only)	**(328 Mary Harmon Bryant Hall)**
6:00	**Reception**	**(Grand Gallery, Alabama Museum of Natural History / Smith Hall)**

Wednesday, August 2

Bryant Conference Center (BCC) **Rast A**

9:00	**Welcome**	Kevin Kocot	

President's Symposium: Freshwater Mollusk Diversity in a Biodiversity Hotspot

Moderator: Carla Atkinson

9:15	**President's Symposium opening**	Carla Atkinson	
9:30	**Keynote** (PS-1)	Dave Strayer	Hard problems for freshwater mussel conservation: lagged effects and effective monitoring
10:30	**Coffee break (30 min)**		**(adjacent to Rast A+B)**
11:00	PS-2	Nathan Whelan	Conservation genetics research is critical for freshwater mollusk conservation: recent applications and surprising data
11:30	PS-3	Arthur Bogan	50 years of freshwater bivalves: Shells to DNA
12:00	**Lunch (1.5 hr)**		**(Food trucks outside of BCC or elsewhere)**
1:30	PS-4	Caryn Vaughn	Spatial variation in mussel community composition and richness results in distinct stoichiometric hotspots in rivers across a biogeographic region
2:00	PS-5	Alexa Maine	Freshwater Mussels as a First Food: Cultural and Ecological Significance to the Confederated Tribes of the Umatilla Indian Reservation
2:30	PS-6	Ellen Strong	New insights into the relationships of freshwater gastropods with a new universal probe set for the Caenogastropoda
3:00	**Coffee break (20 min)**		**(BCC Registration Lobby)**

Selected Contributed Talks *Moderator: Kevin Kocot*

3:20	CT-1	Daniel Graf	Unionoid cladomics: a novel biodiversity informatics approach to the new freshwater mussel taxonomy
3:40	CT-2	Elizabeth Davis-Berg	Anderson County Kansas, diversity differences in the Tallgrass Prairie
4:00	**Poster session**		**(BCC Registration Lobby)**
6:30	**Student & postdoc mixer**		**(Black Warrior Brewing Company)**

Thursday, August 3

Bryant Conference Center (BCC) **Rast A**

1. Ecology and Diversity of Freshwater Mollusks *Moderator: Jonathan Lopez*			
9:00	1-1	Matthew Lodato	Linking morphology to resource assimilation: An evaluation of the trophic niche, morphology, and their relationship in functionally similar aquatic species.
9:20	1-2	Russel Minton	Diversity in the desert: Conservation and microbiomics of endemic freshwater snails in West Texas
9:40	1-3	Sabrina Robinson	Mollusk Populations in Loon Lake, Whitley County, Indiana, from 1926 and 2022
10:00	1-4	Yu Kai Tan	Cost of Living: Morphometry Reveals Patterns of Clinal Variations in US Freshwater Mussels (Family Unionidae)
10:20	**Coffee break (20 min)**		**(adjacent to Rast A+B)**
1. Ecology and Diversity of Freshwater Mollusks *Moderator: Matthew Lodato*			
10:40	1-5	Hannah Adkins	Linking Physiology, Behavior, and Thermal Tolerance in Freshwater Mussels.
11:00	1-6	Hannah Collins	Determination of the upper size limit of microplastic particles that can be ingested by the Quagga mussel, *Dreissena bugensis*
11:20	1-7	Irene Sánchez-González	Phenotypic responses to environmental gradients: a three-dimensional quantitative approach to assess mussel shell plasticity
11:40	1-8	Jonathan Lopez	High and low flows place hydrodynamic constraints on freshwater mussel communities
12:00	**Lunch + JEDI panel** *Moderator: Rose Osborne*		**(Rast B; panel starts at 12:30 pm)**
2. Physiology and Molecular Biology *Moderator: Nickellaus Roberts*			
2:00	2-1	Jingchun Li	Comparative transcriptomics revealed molecular mechanisms in bivalve photosymbiosis
2:20	2-2	Matthew McDonald	The Development of Amino Acid Racemization Age Models Based on New and Historically Collected Terrestrial Snails from Jamaica.
2:40	2-3	Giovanna Omura	Evolutionary Adaptations and sensory differentiation: Exploring olfactory receptors in the Phylum Mollusca
3:00	2-4	Andy Tan	Complete Mitogenomes of Photosymbiotic Bivalves Reveal Elaborate Repeats within Non-Coding Regions
3:20	**Coffee break (20 min)**		**(adjacent to Rast A+B)**
3:40	2-5	Meghan Yap-Chiongco	Tracing the Evolutionary Origins of Biomineralization: Insights from Two Aplacophoran Genomes
4:15	**Group photo**		**(meet by registration table)**
5:00	**Auction**		**(BCC Birmingham / Central room)**

Thursday, August 3

Bryant Conference Center (BCC) **Rast B**

3. Biodiversity, Taxonomy, and Phylogenetics *Moderator: Meghan Yap-Chiongco*

9:00	3-1	Megan Smith	Inferring phylogenetic relationships and testing for introgression in taildropper slugs
9:20	3-2	Kevin Kocot	Scaphopoda is the sister taxon to Bivalvia: evidence of ancient incomplete lineage sorting
9:40	3-3	Nickellaus Roberts	Phylogenetic Placement of Mollusca and its Evolutionary Implications
10:00	3-4	Alexandra Tew	A Resolved Phylogeny of Cephalopoda Yields New Insights into This Ancient Invertebrate Lineage
10:20	**Coffee break (20 min)**		**(adjacent to Rast A+B)**

3. Biodiversity, Taxonomy, and Phylogenetics *Moderator: Chandler Olson*

10:40	3-5	David Campbell	What good is a broken barcode: *cox1* in pleurocerids and semisulcospirids
11:00	3-6	Jesús Martínez Sanjuán	Morphoanatomic study and molecular systematics of the family Pruvotinidae (Mollusca, Solenogastres)
11:20	3-7	Timothy Campbell	Molecular Phylogeny and Resulting Classification of Caenogastropoda, Utilizing 28S and *cox1*
11:40	3-8	William Farris	A striking new species of *Dondersia* (Mollusca, Aplacophora) from the Gulf of Mexico and new data from other species of the genus
12:00	**Lunch + JEDI Panel** *Moderator: Rose Osborne*		**(Rast B; panel starts at 12:30 pm)**

3. Biodiversity, Taxonomy, and Phylogenetics *Moderator: Carmen Cobo*

2:00	3-9	Chandler Olson	Icelandic Aplacophora: Remarkable undescribed diversity in the deep sea
2:20	3-10	Adam Frankiewicz	Using Geometric Morphometric Analysis to Differentiate Two Species of Sphaeriidae (*Sphaerium simile* and *Sphaerium striatinum*)
2:40	3-11	Emily McLaughlin	A monograph of Antarctic Solenogastres
3:00	3-12	Nancy Treneman	We're not just in the shallows: shipworm diversity and distribution in marine habitats
3:20	**Coffee break (20 min)**		**(adjacent to Rast A+B)**
4:15	**Group photo**		**(meet by registration table)**
5:00	**Auction (~2 h)**		**(BCC Birmingham / Central room)**

Friday, August 4

Bryant Conference Center (BCC) **Rast A**

1. Ecology and Diversity of Freshwater Mollusks *Moderator: Carla Atkinson*

9:00	1-9	W.A.N.U. Abeyrathna	Unusually high levels of connectivity in the invasive gastropod, Callinina georgiana (Caenogastropoda: Viviparidae) across a fragmented aquatic landscape: a mitonuclear perspective
9:20	1-10	Jamie Bucholz	Hierarchical structuring of genomic differentiation and beta diversity within freshwater mussel communities
9:40	1-11	Steven George	A comparison of freshwater mussel populations in the Boeuf River, Northeast Louisiana: 550 A.D. to recent times
10:00	1-12	Jay Cordeiro	Integrating the Museum Voucher Specimen into Academic Curricula: A Case Study with Freshwater Mollusks
10:20	**Coffee break (20 min)**		**(adjacent to Rast A+B)**

1. Ecology and Diversity of Freshwater Mollusks *Moderator: Irene Sánchez*

10:40	1-13	Paul Johnson	Recovery of the pale lilliput, Toxolasma cylindrellus: a federally endangered freshwater mussel in Alabama and Tennessee.
11:00	1-14	Monika Bohm	Saving Mussels from Extinction: strengthening the role of zoos and aquariums
11:20	1-15	Daya Hall-Stratton	Species Confirmation and Population Genetics of the Non-native Mystery Snails *Heterogen japonica* and *Cipangopaludina chinensis* Within the Eastern United States
11:40	1-16	Carla Atkinson	Interspecific and intraspecific variation in freshwater mussel tissue stoichiometry
12:00	**Lunch (2 hr) + Mentoring program**		**(Food trucks outside of BCC or elsewhere)**

4. Natural History Collections *Moderator: Emily McLaughlin*

2:00	4-1	Paul Callomon	HaptoNet: digitizing adherent organisms in museum collections
2:20	4-2	Meghan Yap-Chiongco	AplacBase: A Digital Database to Make Aplacophora Less Obscure and Difficult
2:40	4-3	Gary Rosenberg	Determining live- versus dead-collected status of mollusks
3:00	4-4	Carmen Cobo	Uncovering marine biodiversity through Natural History Collections: Solenogastres (Mollusca, Aplacophora) from New Zealand as a case study
3:20	**Coffee break**		**(adjacent to Rast A+B)**
4:00	**Society-wide business meeting**		**(Rast B)**
6:00	**Banquet**		**(Grand Gallery, Alabama Museum of Natural History / Smith Hall)**

Friday, August 4

Bryant Conference Center (BCC) **Rast B**

5. Ecological Interactions and Adaptations *Moderator: Carmen Cobo*

9:00	5-1	John Wares	The Genomic Ghosts of *Geukensia granosissima*
9:20	5-2	Casey Richart	*Phasmarhabditis hermaphrodita*, a biocontrol nematode species, infects and increases mortality of *Monadenia fidelis*, a non-target terrestrial gastropod species endemic to the Pacific Northwest of North
9:40	5-3	Thomas Duda	Effect of habitat type on size-frequency distributions of *Conus* species from seaward and lagoon reefs of Rangiroa (Tuamotu Archipelago, French Polynesia)
10:00	5-4	Tyler Griffin	A multi-study analysis of gut microbiome data from the blue mussel (*Mytilus edulis*) emphasizes the methodological impact of gut voidance on biological interpretation
10:20	**Coffee break (20 min)**		**(BCC Registration Lobby)**

5. Ecological Interactions and Adaptations *Moderator: Kevin Kocot*

10:40	5-5	Meagan Haubner	Using microbiomics to determine why some snails become pests and others are in peril
11:00	5-6	Timothy Pearce	Land slugs and snails eaten by juvenile salmonid fish in two Seattle creeks.
12:00	**Lunch (2 hr) + Mentoring program**		**(Food trucks outside of BCC or elsewhere)**
3:20	**Coffee break (20 min)**		**(BCC Registration Lobby)**
4:00	**Society-wide business meeting**		**(Rast B)**
6:00	**Banquet**		**(Grand Gallery, Alabama Museum of Natural History / Smith Hall)**

Saturday, August 5

Field Trip

8:00 Meet in front of Hotel Capstone

HaptoNet Workshop

8:30 (Mary Harmon Bryant Hall room 328)

President's Symposium:

Freshwater Mollusk Diversity in a Biodiversity Hotspot

PS-1

Hard problems for freshwater mussel conservation: lagged effects and effective monitoring

David L. Strayer

Cary Institute of Ecosystem Studies, Millbrook, NY 12545

The next few decades will likely be a time of change for the already-imperiled freshwater mussel populations in eastern North America, with both serious threats (e.g., climate change, biological invasions, emerging and existing pollutants, fragmentation) and opportunities (e.g., mussel propagation and reintroductions, habitat restoration). Several recent papers have sought to identify the most important threats and needs for mussel conservation and management. Rather than repeating these long lists, I will explore two difficult areas in which the development and application of better scientific understanding can aid mussel conservation in eastern North America. First, the effects of many threats (e.g., fragmentation) and conservation actions (e.g., conservation tillage) are substantially lagged, as are the demographic responses of mussel populations (especially long-lived species). Consequently, mussel populations may be far out of equilibrium with current conditions, and the full effects of both threats and conservation actions may not be apparent for decades, which can lead to both large extinction debts and colonization credits. Better approaches to analyze and understand these lagged effects would benefit both mussel conservation and conservation ecology in general. The second topic that I will discuss is mussel population monitoring, which has greatly improved over the past few decades. Nevertheless, monitoring can be made more effective by making existing data sets more widely available, better coordinating multiple monitoring programs, tuning monitoring programs to be more sensitive to the effects of anticipated drivers, and better integrating monitoring programs into broader programs of research and management.

PS-2

Conservation genetics research is critical for freshwater mollusk conservation: recent applications and surprising data

Nathan V. Whelan[1,2]

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[2]School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University, 203 Swingle Hall, Auburn, AL 36849, USA

Freshwater mollusks are among the most imperiled organisms in the world. Therefore, conservation efforts are urgently needed to prevent declines and extinctions. Such urgency necessitates that management actions, when taken, are effective so limited resources are not wasted. Modern genetics data play an outsized role in ensuring effectiveness of freshwater mollusk conservation. Here, I review recent studies and present novel research that used population genomics data to provide insights that improved conservation of freshwater mollusks. Most freshwater mollusks, particular snails, display high levels of genetic structure. Furthermore, genomic research has revealed that many, possibly all, female freshwater mussels mate with multiple males each reproductive season. Both of these insights from genomic data have considerable utility captive propagation and reintroduction programs. Recent research has also revealed some exceptions to common landscape genomic patterns seen in freshwater mollusks. For example, *Cumberlandia monodonta* displays virtually no genetic structure across is range, which extends from the upper Clinch River in Tennessee to the upper Mississippi River in Minnesota. Genomic data has also uncovered a surprisingly large amount of genetic diversity in narrow-range endemic pleurocerid gastropods, including in three species that were formerly thought to be extinct. Such data, combined with coalescent-based demographic modeling, indicate that pleurocerid populations experience an "all-or-nothing" response to habitat degradation. In other words, when pleurocerid populations experience decline, they will rapidly become extirpated, but populations that do not suffer from decline maintain genetic diversity. Broadly, conservation genomics research is improving management efforts for freshwater mollusks. Such research should be a priority to ensure future conservation of freshwater mollusks accomplishes management objectives.

PS-3

50 years of freshwater bivalves: Shells to DNA

Arthur E. Bogan[1,2,3,4]

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[2]Adjunct Professor, Department of Applied Ecology, North Carolina State University, Raleigh, NC, U.S.A.
[3]Research Associate, Malacology Carnegie Museum of Natural History, Pittsburgh, PA 15213, U.S.A.
[4]Research Associate, Dept. Invertebrates Zoology, Smithsonian Institution, Washington, DC 20560, U.S.A.

It came as a surprise to me when I realized I have been working on freshwater bivalves for 50 years. This work has spanned the transition from work focused initially on shells, both modern and archaeological, to collaboration using an integrative approach. These 50 years have been broken into 4 separate periods, each focused on different aspects of freshwater bivalves: graduate school, University of Tennessee, Knoxville [1973-1980]; Academy of Natural Sciences of Philadelphia [1980-1992]; Consultant [1992-1996]; and North Carolina Museum of Natural Sciences [1996-present]. Trying to use the historical literature forced me to pay closer attention to basic taxonomy of the families Unionidae and Margaritiferidae. When I began, freshwater bivalve research was focused primarily on the shells and with time more comparative anatomy was added to form an integrative picture along with host fish and behavior. The next major shift was the use of starch gel electrophoresis, followed by Sanger sequencing of mitochondrial and nuclear DNA. Finally, the introduction of anchored hybrid enrichment using nuclear DNA with an integrative approach is the latest major step forward in the understanding of unionoid evolution. Intensive fieldwork, applying modern techniques in Asia and Southeast Asia has allowed the development of a more robust phylogenetic understanding of the Unionida. This is a tour of my development and the changing technology applied to these questions, data management, museum collections, and tools to understand this very imperiled group of animals.

PS-4

Spatial variation in mussel community composition and richness results in distinct stoichiometric hotspots in rivers across a biogeographic region

Caryn C. Vaughn[1]* and Carla L. Atkinson[2]
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[2]Department Biological Sciences University of Alabama, Tuscaloosa, AL, 35487, U.S.A.
*Presenting author

Freshwater mussels make important contributions to nutrient cycling and storage in rivers, but the overall magnitude of these contributions varies with mussel abundance, community composition, and species traits. We used an extensive dataset on mussel communities, their life history traits, and functional effect traits across eight rivers from a single biogeographic region, the Ouachita Mountains of the US Interior Highlands, to examine how differences in mussel communities and their functional traits affected overall functional diversity and dispersion and nutrient storage (carbon [C], nitrogen [N] and phosphorus [P]) and nutrient excretion rates (N and P). Our preliminary analyses indicate that there is high variation in richness, biomass, and consequentially excretion rates, nutrient storage, and overall stoichiometry. In general, larger stream reaches tended to harbor mussel beds with more species, greater community biomass, and subsequently higher excretion rates and overall storage. Most striking was how assemblage composition impacted overall excretion and nutrient storage stoichiometry. In particular storage N:P was negatively related to excretion N:P by the mussel communities. This general pattern was related to assemblage composition where communities with a greater proportion of lampsilines had higher excretion N:P and lower storage N:P. Our work highlights the diversity of traits within a single family of aquatic organisms and how that can result in high spatial variation in nutrient storage and cycling.

PS-5

Freshwater Mussels as a First Food: Cultural and Ecological Significance to the Confederated Tribes of the Umatilla Indian Reservation

Alexa Maine[1]

[1] Confederated Tribes of the Umatilla Indian Reservation, Department of Natural Resources, Fisheries Program, Freshwater Mussel Research and Restoration Project, Walla Walla, WA, 99362, U.S.A.

Freshwater mussels in the western United States are in decline, including in the Umatilla River system in eastern Oregon. In 2005 a survey of the Umatilla River, which runs through the Confederated Tribes of the Umatilla Indian Reservation (CTUIR), indicated much of the historic mussel population had been eradicated. Because sustainable harvest of freshwater mussels remains a treaty right, and tribal members recognize the ecological importance of mussels in their river systems, CTUIR is committed to restoring freshwater mussels in the Umatilla River and surrounding basins, as part of their "First Foods" approach to natural resource management and conservation. Restoration efforts have included distribution surveys and monitoring of existing populations, translocations of adult mussels to supplement existing populations, and, more recently, the propagation of juvenile mussels to test the feasibility of reintroduction methods. Until recently little was known about the life history of freshwater mussels in the Pacific Northwest, including information on local host fishes and habitat requirements. Because freshwater mussels require a host fish to complete their life cycle, conservation and restoration efforts are hampered by this lack of host fish knowledge. Current research efforts include testing propagation and rearing methods for transformed juvenile mussels, as well as continuing to develop a broader understanding of host fish associations for all western mussel species.

PS-6

New insights into the relationships of freshwater gastropods with a new universal probe set for the Caenogastropoda

Ellen E. Strong[1]*, Tricia C. Goulding[1], and Philippe Bouchet[2]

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The Subclass Caenogastropoda is the most diverse group of living gastropods, comprising over 160 Recent families and 60% of all gastropod species. Given their great diversity, robustly resolving phylogenetic relationships within the group has remained elusive at higher taxonomic levels. We designed and tested the first universal probe set to capture ultraconserved elements (UCEs) and exon loci with the aim of producing the most comprehensively sampled phylogeny for the group to date. The probe set consists of ~30,000 probes designed to target 1,142 UCE loci and 1,933 exon loci (3,075 total). Phylogenetic analyses of the loci extracted from transcriptomes produced well-supported trees very similar to those published based on transcriptomic analyses. Although there are few caenogastropod genomes, phylogenetic relationships estimated from the analysis of loci extracted from genomes recovered similar phylogenetic relationships. We used this probe set to produce a robust phylogeny for almost 200 caenogastropod terminals representing roughly 30 superfamilies, with special emphasis on the non-neogastropods. We also used the probe set to estimate a phylogeny of the Cerithioidea, with roughly 160 terminals representing almost all currently recognized families. In both phylogenies, almost all interior nodes (inter-familial, inter-superfamilial relationships) were robustly resolved with bootstrap values of 95 or higher; occasional lower support values were seen for relationships between species and occasionally between genera. This new phylogenetic framework provides novel insights into the number and relationships of freshwater clades and demonstrates the utility for resolving phylogenetic relationships across taxonomic levels and evolutionary time scales in this highly diverse subclass.

Selected Contributed Talks

CT-1

Unionoid cladomics: a novel biodiversity informatics approach to the new freshwater mussel taxonomy

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The MUSSEL Project Database (MUSSELpdb; www.mussel-project.net/) was developed to document the accumulated taxonomic and specimen-based data on freshwater mussel species, genera, and families (Bivalvia: Unionoida). Over the past two decades, there has been a community-wide shift in the philosophy, methods, and pace of revisionary work, as evidenced by the proliferation of publications, cladograms, and applicable nucleotide sequences. Before 2001, there were 20 publications with 33 freshwater mussel cladograms, and these were based on fewer than 150 phylogenetically useful DNA sequences (i.e., mtGenomes, COI, ND1, 16S, 18S, 28S, ITS, H3) or morphology. Today, there are more than 470 such cladograms (14x increase) and Genbank has more than 30,000 such DNA sequences (up 200x). As expected, there has been a major impact on freshwater mussel systematics. In 2007, the MUSSELpdb reported the Recent richness of freshwater mussels as 840 species in 161 genera. Today, there are 990 species in 201 genera.Phylogenetic data in the form of trees depicting evolutionary relationships among DNA sequences representing taxa based on cladistic methodology have superseded traditional revisionary work (e.g., synonymies, cresonymies). Freshwater mussel taxonomy today follows *post hoc* from phylogenetic analyses and fluctuates with analyses and results. The MUSSELpdb has adapted to accommodate these new types of data that form the basis of freshwater mussel taxonomy.

The MUSSELpdb includes resources to document and analyze freshwater mussel cladomics — that is, the sets of phylogenetic topologies (i.e., clades) relevant to supra-specific taxa (https://mussel-project.uwsp.edu/db/cladomics_farq.html). The MUSSELpdb cladomic summary for each genus, tribe, family, etc. ranks cladograms according to their usefulness for testing monophyly and sister-relationships, describes statistics of cladogram quality, and depicts relevant species-tree topologies for comparison. My talk will describe some recent innovations to an already innovative dataset and summarize some of the lessons learned to-date.

CT-2

Anderson County Kansas, diversity differences in the Tallgrass Prairie

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The northcentral plains region of the United States is classified as a Tallgrass Prairie ecosystem. The Nature Conservancy land (1450 acres) near Welda, Kansas, is protected with the goal of maintaining and enhancing native biodiversity within this imperiled ecosystem. These prairies are characterized as having deep soils and higher rainfall than those found further west in the state. Beginning in 2004, we have periodically sampled the conservancy lands to provide a comprehensive species list for the Kansas Biological Survey. The surveys provide additional information regarding the changing ecological factors that may affect Mollusca and other threatened species such as Mead's Milkweed and prairie chickens. The preserve contains native tallgrass prairies as well as cattle pastures. With over 15 years of sampling data, we have consistently found higher abundance and increased species diversity at the non-pastured land when compared to the pastured land. Differences in soils (pH, conductivity, and NPK levels) between the two site types may account for the differences in gastropod diversity. To better understand the role of ecological factors on diversity and abundance we compared the Anderson County samples to samples collected from other regions throughout the Midwest.

1. Ecology and Diversity of Freshwater Mollusks

1-1

Linking morphology to resource assimilation in functionally similar aquatic species

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Niche partitioning is an important mechanism promoting species coexistence in ecological communities. Yet, how morphological trait variation influences the trophic niches of closely related, co-occurring aquatic species that share common feeding modes is still unclear. We evaluated the relationship between feeding morphology and trophic assimilation using a diverse assemblage of filter-feeders, freshwater mussels (Family: Unionidae), as a model system. To feed, mussels siphon and intercept food particles using latero-frontal cirri on their gills, or fused pairs of cilia that function like a sieve. We used stable isotopic analysis ($\delta^{13}C$ and $\delta^{15}N$) to estimate the trophic niche areas of 11 species. Then, we used scanning electron microscopy to measure the density of latero-frontal cirri for a subset of these same individuals. We found that the trophic niche area overlap among co-occurring species was low (3-22%), indicating resource partitioning. Further, latero-frontal cirri density (CD) varied both within and among species across sites, with average density levels generally increasing from upstream to downstream with the exception of our most upstream site. Across sites and species, trophic niche area was negatively related to CD, with *Lampsilis ornata* having the largest average niche area and lowest CD levels. Our results demonstrate that morphological variation can affect trophic assimilation even among closely related species that share common feeding modes. Specifically, interspecific variation in CD among co-occurring species may promote resource partitioning, whereas intraspecific differences in density levels across populations may represent a phenotypic response to potential spatial variation in food resource variability. Overall, we suggest that intraguild variation in feeding structure morphology is likely a key functional trait underlying species coexistence in these dense and species-rich communities.

1-2

Diversity in the desert: Conservation and microbiomics of endemic freshwater snails in West Texas

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The Chihuahuan Desert in the United States and Mexico is an imperiled freshwater diversity hotspot. Waterbodies in the Chihuahuan Desert are often widely separated with poor hydrological connections between them, leading to unique assemblages within each waterbody. Freshwater habitats and the species they support are highly imperiled in the Chihuahuan Desert; urbanization, groundwater withdrawal, and other anthropogenic activities have led to habitat modification and loss. Concurrent with these changes is declining biodiversity, with many endemic species and those with limited distributions becoming extirpated and extinct. Conservation efforts for desert freshwater endemics require integrated approaches that account for not only the species' specific environmental and life history needs but also those of taxa interacting with or living in and on the species. We sought an exemplar system that encompassed endemism and conservation in the context of desert freshwater springsnails and snail–bacteria interactions. We utilized populations of five endemic *Pyrgulopsis* and three endemic *Tryonia* species collected from springs in West Texas. We used taxonomic and OTU-based analyses of near-complete 16S rRNA sequences to describe the bacterial communities associated with each species. Cyanobacteria, Firmicutes, and Proteobacteria were the three most abundant bacterial phyla across all snail species. Most species possessed significantly different bacterial communities in terms of both composition and relative abundance. We also utilized distance matrix multivariate regression to model three effects on snail bacterial community structure. Our model explained a significant amount of the variation in the bacterial community data, with genetic distance between snail species and water chemistry at each site correlating significantly. Our data suggest that each snail species lives in association with a unique bacterial assemblage. Conservation efforts to protect both desert water and organismal resources should include a microbial context, as bacterial communities are likely the result of environmental and host-genetic factors.

1-3

Mollusk Populations in Loon Lake, Whitley County, Indiana, from 1926 and 2022

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Historical museum collections coupled with modern sampling provide a good opportunity for longitudinal faunal studies. In 1926 and 1927, Herman Wright sampled the mollusks of Loon Lake in the Tippecanoe watershed of Indiana; these, as well as a large collection of samples from the entire watershed, were given to the Carnegie Museum of Natural History Section of Mollusks, with incomplete data. Modern samples collected from the Whitley County Loon Lake allow for the comparison of species and their occurrence over time: Wright's samples revealed 17 taxa and 1792 individuals. So far, modern samples have contained 12 taxa and 326 individuals (though there are many more to count), including some not recorded by Wright: *Laevapex fuscus* (C.B. Adams, 1840), a species of *Menetus* (H. Adams & A. Adams, 1855), and *Dreissena bugensis* (Andrusov, 1897). Wright's interest in the lake and the Tippecanoe system at large lay in studying post-glacial migration of mollusk species up the watershed, in particular their routes and time taken to repopulate the watershed northwards. We will analyze changes in Loon Lake's mollusk populations in relation to this and other considerations that might have influenced populations over the past 97 years, including human-driven habitat change.

1-4

Cost of Living: Morphometry Reveals Patterns of Clinal Variations in US Freshwater Mussels (Family Unionidae)

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Freshwater mussels show high levels of intraspecific shell variation. According to Ortmann's Law of Stream Position, some of this variation may be driven by habitat conditions in which individuals of species in large rivers produce more inflated shells than those in smaller tributaries as an anchoring mechanism. Examination of 1101 specimens (10 species; three tribes) supports Ortmann's Law, however, smooth-shelled and sculptured species responded differently in degree of clinal inflation. Smooth-shell species show strongly positive inflation responses, exhibiting a significant increase in inflation from small tributaries to large rivers, in contrast to constitutively sculptured species, which show weakly positive (*Cyprogenia stegaria*) to negative (*Plethobasus cooperianus*) clinal inflation responses. In addition, facultatively sculptured species (*Cyclonaias pustulosa*) shows a moderately positive clinal inflation response while exhibiting more intense sculpturing in large rivers, suggesting an overlap between the advantage provided by development of sculptures and inflation, which leads to a potential allocational trade-off. To investigate the interactions between these two anchoring traits and environmental conditions, we calculated ratios of volumes of shell to soft-tissue using structured light 3D-scanning and measured how resource allocation varies as a function of flow regime. We found that smooth-shelled and sculptured species displayed distinct patterns of shell/soft-tissue allocation. Smooth-shelled *Fusconaia subrotunda* develops more inflated, thickened shells in large rivers, yielding higher shell/soft-tissue ratios than sculptured *C. pustulosa*. Both anchoring traits are hypothesized adaptations for large rivers, though our results suggest that producing highly inflated shells requires higher resource allocation for shell-building, at the expense of soft tissue growth. Sculpture thus may be a more economical anchoring trait than inflation, which may explain higher abundance of sculptured individuals in large rivers.

1-5

Linking Physiology, Behavior, and Thermal Tolerance in Freshwater Mussels

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As climate change and anthropogenic activities alter surface water temperatures, knowledge of thermal tolerances and a framework for describing thermal guilds are essential for conservating unionid diversity. However, estimates of thermal tolerance in adult unionids exist for <10% of North American species. We evaluated a combination of sublethal physiological (respiration), behavioral (foot extension, gaping), and lethal (mantle retraction, lack of response) endpoints to acute thermal stress (+2℃/h starting at 25℃) to better understand the sequential relationships among endpoints, differences in sublethal endpoints within sympatric and/or among allopatric populations, and whether these endpoints were predictive of differences in lethal endpoints among populations and species. We examined three sympatric species (*Elliptio pullata*, *Leaunio lienosus* and *Lampsilis straminea*), three allopatric species (*Pleurobema riddelli*, *Popenaias popeii*, and *Pyganodon grandis*) and two allopatric subpopulations within the same species (*L. straminea*). Species showed some variation in the relative order of response to acute thermal stress: foot extension could occur either before or after a sudden decrease in metabolic rate (RMR_{peak}), which was always followed by gaping, then mantle retraction and lack of response to probing (CTM). Significant variation in RMR_{peak} occurred among sympatric species. Furthermore, some species showed evidence of adaptive temperature-insensitive metabolism, a thermal response known to occur in some littoral and intertidal marine mollusks, but not previously described for freshwater unionids. Behavioral endpoints did not differ among sympatric species, nor did the lethal endpoint. *L. straminea* from a pond population showed a higher CTM compared to those from a spring-fed river. Increased understanding of linkages between sublethal and lethal thermal endpoints, and variance among species and populations will be of great use in further identifying thermal guilds of freshwater unionids.

1-6

Determination of the upper size limit of microplastic particles that can be ingested by the Quagga mussel, *Dreissena bugensis*

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Quagga mussels (*Dreissena bugensis*) are a freshwater mussel species invasive to the United States. While their presence can cause ecosystem-wide effects in rivers and lakes, their ability to process large volumes of water (up to 8 L/hr/g-dry weight) may have applications for water clarification in freshwater systems. In particular, dreissenid mussels have been proposed to remove microplastics (MP) from wastewater treatment plants. Existing literature on particle feeding by dreissenid mussels focuses on the capture and ingestion of microalgae and bacteria. There are a lack of data on MP particle capture and whether large microfibers and microfragments are ingested or rejected. The type of biodeposit MP will be sequestered in (feces or pseudofeces) has implications for the design of removal and settling systems. To examine this issue quagga mussels were isolated in 250ml beakers and exposed to a known number of MP of the same size and shape. For each type of particle 15-20 mussels were allowed to filter and process particles for 3.5 hours. Biodeposits were collected 1, 24, and 28 hours post exposure period, and digested using KOH to remove organics and isolate MP. MP rejected in pseudofeces and egested in feces were quantified to determine the proportion of MP of each type that are rejected vs. ingested. These data will determine the approximate largest size of MP that can be ingested and therefore egested as feces by *D. bugensis* and inform future work regarding the efficiency and limits of MP removal from engineered systems by this freshwater mussel.

1-7

Phenotypic responses to environmental gradients: A three-dimensional quantative approach to assess mussel shell plasticity

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Phenotypic variability is an important response of organisms to environments. Although shell variation is a well-known phenomenon among freshwater mussel populations, studies examining these differences across several rivers and drainages are uncommon and the degree and factors causing variation are not always well quantified. We combined a novel three-dimensional (3D) geometric morphometric approach and ordination techniques to identify spatial patterns of natural shape variation across four rivers in the Mobile and Tennessee River basins. We scanned individuals from seven species spanning four phylogenetic tribes to understand if phenotypic responses were specific to species, tribe or morphological structure. Our methodology involves 3D surface scanning both valves jointly to quantify variation in inflation and depth of the shell. These scans provide a high-resolution image which creates a mesh with over 500 points per individual that allows for accurate intraspecific comparisons. Our preliminary findings suggest a strong relationship between distance from headwaters and shell variation, especially in sculptured species where downstream populations were significantly more inflated. We plan to continue examining the specific environmental variables related to these differences. Phenotypic responses along the river longitudinal gradient were also substantially stronger in the tribe Quadrulini in comparison to Lampsilini, however, more work to increase our sample size and species representation from these and other tribes is needed to fully reach a conclusion. Exploring shape variability and uncovering the underlying causes is essential to understanding diversity and further explore the ecological relationships between form and function.

1-8

High and low flows place hydrodynamic constraints on freshwater mussel communities

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Riverine mollusk species are governed by the physical (i.e., hydrodynamic) forces generated by flowing water. Sedentary species such as freshwater mussels (Bivalvia: Unionoida) are especially vulnerable because they are unable to move quickly in response to novel flow patterns created by impoundments and water withdrawals. We evaluated the effects of hydrodynamic variables on mussel communities. We reviewed the literature to synthesize the relationships between three categories of hydrodynamic variables (hydrologic, simple hydraulic, and complex hydraulic) and mussel community parameters. We evaluated which variables are most useful in predicting mussel presence, abundance, and species richness, provided recommendations to help standardize their use in characterizing mussel habitat and reviewed the reciprocal influence of mussels on hydraulic forces at the sediment-water interface. Hydrologic variables such as stream size and anthropogenic flow alteration were useful in predicting basin- and landscape-scale changes in mussel communities. At finer scales, complex hydraulic variables—mainly shear stress and Reynolds number—were more useful at predicting mussel community responses. Simple hydraulic variables (flow velocity, depth, discharge) had mixed success as predictors of mussel community parameters and are likely to be indirectly correlated to mussel responses because they are used to calculate more complex variables. Mussels also alter near-bed hydraulic characteristics, resulting in feedbacks between mussel community parameters and local hydraulic variables.

1-9

Unusually high levels of connectivity in the invasive gastropod, *Callinina georgiana* (Caenogastropoda: Viviparidae) across a fragmented aquatic landscape: a mitonuclear perspective

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Aquatic invasions are a threat to global biodiversity because they can disrupt biological communities through competition with native species. The extent of this threat is unclear when there is a lack of information on the species' distributional patterns and dispersal capacity. The banded mystery snail, *Callinina georgiana* is an introduced species in the northeastern United States with a well-documented introduction from the southern US in the 1800s. In parts of its introduced range, the species can reach extremely high densities and is a known egg-predator of native fish such as largemouth bass. In this study we assessed the connectivity patterns of *C. georgiana* for the first time in its invasive range using a combination of mitochondrial (COI) and nuclear (H3) genetic markers. Our study area encompassed the region known as the New York Great Lakes Basin which includes the Raquette River; one of the most fragmented river systems in the eastern United States. Results showed high levels of genetic connectivity across all populations sampled, and while some structuring was observed, it could not be linked to geographic distance. Genetic diversity and demographic results were indicative of population expansion and haplotype diversification, which is likely being driven by multiple human-mediated introductory events such as boat traffic. Such a highly connected metapopulation of *C. georgiana* makes it difficult to develop management strategies for the species in New York State. Our recommendations include tightening current biosecurity protocols in addition to developing high resolution genetic markers which may elucidate more fine scale dispersal patterns.

1-10

Hierarchical structuring of genomic differentiation and beta diversity within freshwater mussel communities

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Elucidating patterns in species and genomic differentiation between and among communities can unveil the drivers of diversity across scales. Freshwater mussels often exist in species-rich assemblages in stream systems and can enhance ecological function. More diverse, species-rich communities may provide a greater suite of ecosystem services than species-poor communities, therefore understanding the patterns and potential drivers of diversity within mussel communities is pertinent to their conservation. Using quantitative surveys and genomic sequencing, we examined taxonomic and genetic differentiation in mussel communities from seven rivers in the Mobile and Tennessee River Basins of the Southeastern USA. We sequenced 17 species from 5 phylogenetic Tribes, including 361 pairwise population comparisons (743 individuals). Preliminary patterns suggest that patterns of taxonomic beta diversity and genetic differentiation (F_{ST}) largely mirror each other, with low genetic structure observed within rivers, weak to moderate genetic structure observed within basin between rivers, and strong genetic structure observed between rivers in different basins. Mantel tests reveal strong patterns of isolation by distance for most species. These data suggest that the same processes may govern patterns of differentiation at both the taxonomic and genomic scale.

1-11

A comparison of freshwater mussel populations in the Boeuf River, Northeast Louisiana: 550 A.D. to recent times

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In 1996, the Department of Geosciences at the University of Louisiana at Monroe conducted an archeological dig in the middens of Landerneau Mounds (16CA87) on the Boeuf River to determine the food resource of Native Americans. Many species of fishes and mammals were excavated along with freshwater mussels. Eighteen species of freshwater mussels were identified. Dominant species from 2,504 mussel valves were threeridge (*Amblema plicata*) 33%, pyramid pigtoe (*Pleurobema rubrum*) 20% and wabash pigtoe (*Fusconaia flava*) 14%. Numerically less abundant mussels included: washboard (*Megalonaias nervosa*) 7.9%, pimpleback (*Cyclonaias pustulosa*) 5.3%, southern hickory nut (*Obovaria arkansasensis*) 4.9%, bankclimber (*Plectomerus dombeyanus*) 4.7%, mapleleaf (*Quadrula quadrula*) 4.6%, spike (*Eurynia dilatata*) 2.6%, and Louisiana fatmucket (*Lampsilis hydiana*) 1.2%. Rare mussel species represented by < 1% were: threehorn wartyback (*Obliquaria reflexa*), wartyback (*Cyclonaias nodulata*), lilliput (*Toxolasma parvum*), yellow sandshell (*Lampilis teres*), bleufer (*Potamilus purpuratus*), pistolgrip (*Tritogonia verrucosa*), black sandshell (*Ligumia recta*) and round pearlyshell (*Glebula rotundata*). Recent mollusk surveys in the Boeuf River at five stations yielded twenty-one species of native mussels and the exotic Asiatic clam*, Corbicula fluminea*. Threeridge (*Amblema plicata*) was the dominant mussel at one of the stations sampled and appeared to show no changes in its relative abundance since 550 A.D. Preliminary comparisons of long-term changes in all the other mollusks were apparent. Five species of mussels found at Landerneau Mounds were absent from the recent survey. Changes in the mollusk assemblage are likely due to anthropogenic impacts to streams which included: channelization, weirs and deforestation resulting in increased sedimentation. As a result, several of these species are likely extirpated from the Boeuf River. The use of freshwater mussels discarded by Native Americans not only provides records of their diet but gives insight of the prehistoric mollusk assemblages.

1-12

Integrating the Museum Voucher Specimen into Academic Curricula: A Case Study with Freshwater Mollusks

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College-level curricula in natural sciences underutilize collected specimens as tools for educating students. Courses may involve observation and collection in the field but emphasize survey methodology and data analysis; making little use of collected specimens beyond identification. I encourage the collection of permanent voucher specimens in academia so students can recognize their value in a time of unprecedented environmental degradation and biodiversity loss. Vouchers provide historical documentation of a species in place and time—a biodiversity baseline to track geographic and temporal changes in species and communities. Examples of their utility include: discovering new species and modifying phylogenies, documenting changes in biodiversity, genetic study (e.g. frozen tissue collections), tracking infectious disease, determining invasive species impacts, monitoring change in marine resources, monitoring climate change, and influencing legislative actions. I teach a 9-week intense course on freshwater mollusks at Bridgewater State University in Massachusetts. The course includes three field collecting trips and assembly of a regional specimen collection, emphasizing the value of preservation, good data and record-keeping, accuracy, and precision. Where does this information go? What do students take away? How can we eliminate a wasteful disregard for disposable specimens? Each class donates its collections to the Harvard Museum of Comparative Zoology (MCZ), thereby increasing its collection holdings and scope. Collections document regional distribution, habitat information, and population viability. Massachusetts has 11 species of state or federally protected freshwater mollusks, and students typically find at least two of them. Collection information is shared with the Massachusetts Natural Heritage and Endangered Species Program for use in wildlife conservation. Information is made available beyond the classroom to scientists, educators, students, and the global community of scholars, wildlife managers, naturalists, artists, historians, and indigenous peoples. What's more, each student's name is included on specimen labels as collector and identifier, preserving their legacy in the museum's collections in perpetuity. MCZ accessions are databased online (MCZBase), and student response to to donation process has been very positive. Incorporating voucher specimens into academic curricula is easy and straightforward, and I highlight how best to do this including collections field trips, specimen donation, visiting local museum exhibits and collections and utilization of museum loan material.

1-13

Recovery of the pale lilliput, *Toxolasma cylindrellus*: a federally endangered freshwater mussel in Alabama and Tennessee

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Toxolasma cylindrellus (Pale Lilliput) has been listed as Endangered under the ESA since 1976. Its range was restricted to Estill Fork of Paint Rock River and Hurricane Creek in northeast Alabama until a few specimens were discovered in Lick Creek (Duck River basin) in 2015. Multi-state recovery efforts have focused on establishing new populations with hatchery-reared juveniles. *Toxolasma cylindrellus* have relatively low fecundity ($\bar{x}$ = 11,663 glochidia / ♀), yet juveniles have been repeatedly produced by traditional and, recently, *in vitro* culture techniques. Regional recovery planning identified the Duck River as a priority reintroduction stream for *T. cylindrellus* and ADCNR donated 802 juveniles to TWRA for the first stocking in September 2014. Seventeen subsequent stockings at seven Duck River basin localities have released an additional 3,402 mussels in the basin. Ten ADCNR stockings in the Paint Rock River have introduced 4,413 individuals at two sites. Three ADCNR stockings at a single site in Bear Creek have released 1,160 additional animals. Finally, TWRA has stocked 563 juveniles into the Elk River at a single site for a total of 11,323 *T. cylindrellus* released back into their historic range. Monitoring efforts in Alabama and Tennessee repeatedly recovered tagged adults indicating good growth and survivorship. Additionally, TWRA has located young untagged *T. cylindrellus* near three Duck River Basin stocking localities, and ADCNR verified multiple new recruits at both Paint Rock River reintroduction localities. Targeted survey efforts by ADCNR in 2021 in the upper Paint Rock watershed identified another 12 *T. cylindrellus* occurrences, including the first live individuals observed in the Larkin and Lick Forks since 1964. Expansion of upper Paint Rock populations and successful reintroduction efforts demonstrates the value of the many habitat improvement projects implemented by TVA and TNC across the species range. In combination, these efforts are meeting stated species recovery goals under the Endangered Species Act and could eventually lead to downlisting.

1-14

Saving Mussels from Extinction: strengthening the role of zoos and aquariums

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On a global scale, North America is the major hotspot for freshwater mussel diversity, yet freshwater mussels – as elsewhere – are under threat. Of the around 300 species native to the US and Canada, 74 and 14 species respectively are federally listed as endangered and threatened in the US. The IUCN Red List of Threatened Species currently lists 93 North American freshwater mussel species in threatened categories (44 Critically Endangered, 32 Endangered, 17 Vulnerable) and a further 32 species as Near Threatened. Several Association of Zoos and Aquariums (AZA) organizations are actively involved in freshwater mussel conservation, from advocacy to propagation and field conservation and on to communication and outreach to the millions of visitors these institutions draw annually. AZA's Saving Animals From Extinction (SAFE) programs focus the collective expertise within AZA institutions and leverages their massive audiences to save species. We are in the process of proposing a North American Freshwater Mussel SAFE program within AZA, to focus on advocacy, research, restoration and recovery, and education and outreach about these imperiled yet vitally important freshwater organisms. Here, we introduce our vision for the program, in the hope to connect the program to partners outside of AZA. Such partnerships and networks are vital in increasing capacity for freshwater mussel conservation across all sectors, for improving the messaging around freshwater mussels in zoos and aquariums and increase advocacy for these often overlooked species.

1-15

Species Confirmation and Population Genetics of the Non-native Mystery Snails Heterogen japonica and Cipangopaludina chinensis Within the Eastern United States

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Invasive species are an increasing concern worldwide as they disrupt native ecosystems and species. The Japanese mystery snail (Heterogen japonica) and the Chinese mystery snail (C. chinensis), were intentionally transported from Japan and China to North America in ~1911 and ~1892, respectively, to be cultivated for human consumption. Mystery snails are now found throughout the United States with C.chinensis being the most widely and abundantly reported of the two species. However, the two appear near identical morphologically, with overlapping features making identification difficult. Genetic sequencing is a more reliable method of species identification but has yet to be widely used in their invasive range. For this research, mystery snails have been collected and genetically confirmed from five states (Virginia, Maryland, North Carolina, Pennsylvania, and Maine) with an additional four states (Alabama, New York, New Jersey, and Connecticut) planned for the summer of 2023. Demographic data (snail size, sex ratio, and embryo number) have or will be collected for all populations and will be analyzed for patterns that can be further explored. Data collected so far has revealed a single COI mitochondrial haplotype, confirmed to be H.japonica, from more than 200 snails sequenced. Genetic diversity is especially low and shows evidence of a genetic bottleneck. The lack of C.chinensis found from this wide distribution also suggests that H.japonica is likely more widespread and abundant than has previously been reported. The true range of either species then, also becomes unclear. This uncertainty in species identity and inaccurate reporting can confuse ecological and biological differences between the two, as studies conducted on one species may have been of the other. Additional genetic data can also reveal patterns of species introduction and spread, with our data so far suggesting a single introduction and consequent spread within Eastern United States populations.

1-16

Interspecific and intraspecific variation in freshwater mussel tissue stoichiometry

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Ecological stoichiometry has been proposed as a mechanistic framework that can facilitate the integration of evolutionary biology with ecosystem science. By condensing organisms and their environment into elemental components (e.g., carbon, nitrogen, and phosphorus), ecological stoichiometry provides a powerful framework to make predictions about how changes at one level affects the other, such as how elemental availability in resources can shape consumer phenotypes or how organismal composition can alter nutrient recycling. Organismal stoichiometry can therefore act as a proxy for elemental demand of the organism and can help identify potential agents of selection through the characterization of elemental mismatches between consumers and their resources. Here we characterized interspecific and intraspecific variation in organismal stoichiometry within a family of freshwater bivalve mussels (Unionidae) across seven river systems and 21 sites. We found that interspecific variation in species life-history and body size traits were correlated to body tissue stoichiometry. Specifically, average growth rates positively were correlated with tissue percent phosphorus content. We also observed intraspecific variation in body stoichiometry among sites and in that genetic distances among sites (F_{st}) were correlated to stoichiometric distances. Our results shed light on some of the characteristic determinants of body stoichiometry. We propose that future research should better assess the mechanistic underpinnings of the complex relationships between life-history characteristics, phenotypic variation, and stoichiometric requirements of organisms so we can better predict responses to ongoing changes in nutrient supplies and further isolation and reduced gene flow due to changes in aquatic systems.

2. Physiology and Molecular Biology

2-1

Comparative transcriptomics revealed molecular mechanisms in bivalve photosymbiosis

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Photosymbioses between heterotrophic hosts and autotrophic symbionts are evolutionarily prevalent and ecologically significant, but molecular mechanisms behind such symbioses remain less understood, especially in mollusks. This study compared gene expression patterns in a photosymbiotic bivalve (*Fragum sueziense*) and a closely related non-symbiotic species (*Trigoniocardia granifera*) to detect potential molecular pathways involved in mollusk photosymbiosis. Both species were kept under three different light intensities (normal, reduced, and dark), and transcriptomes were obtained from the mantle (symbiont containing in *F. sueziense*) and foot (no symbionts in both bivalves) tissues through RNAseq. We discovered that *F. sueziense* mantle gene expression differed significantly among the three light conditions, but such differences were not detected in *F. sueziense* foot tissue or in *T. granifera* mantle and foot. This indicated that the presence of algal symbionts greatly impacted host gene expression, presumably because symbiont photosynthesis was regulated by light levels, which in turn affected host molecular responses. Many immune-related genes in *F. sueziense* mantle were significantly down-regulated in the normal light condition and enriched in the dark. This could mean that the host treated symbionts as pathogenic in prolonged darkness and/or the symbionts had mechanisms to suppress host immune functions under normal light. In addition, genes related to host cilia and microtubule generation and movements were highly up-regulated in normal light, suggesting that cilia in the symbiont-containing tissues play important roles in symbiont regulation or photoreception. Other significant pathways that contributed to the symbiotic relationship included ones responsible for regulating antioxidant or other metabolites. Overall, we found both novel and known molecular mechanisms involved in animal-algal photosymbiosis within bivalves. Given that some of the pathways are shared among distantly related host lineages, such as mollusks and cnidarians, it is possible that they are results of convergent or parallel evolution.

2-2

The Development of Amino Acid Racemization Age Models Based on New and Historically Collected Terrestrial Snails from Jamaica

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In the forests of Jamaica assemblages of dead terrestrial snail shells can be found in crevices and other collection points. In these assemblages are a variety of terrestrial snail shells with some of these shells representing species that can no longer be found living in the area. These shell collections are time-averaged death assemblages, the dead organic remains that are still mostly unburied, temporally coarse accumulations in which noncontemporaneous individuals can be found. The time-averaged death assemblages of terrestrial snails found in Jamaica can provide a look into regional diversity and long-term baselines in an era and region under increasing anthropogenic disturbances. If the ages of these dead shells can be determined, then we can see how populations changed over time, with distinct species appearing and disappearing at separate times. To make paleoecological inferences from Quaternary land snail deposits it is important to show a reliable chronological context for the shells found at a specific site. To do this, the ages of individual snail shells need to be determined. Amino acid racemization (AAR) is a widely accepted method for age dating Quaternary mollusk shells and can be used to create age models based on AAR ratios from museum collections. Live-collected historical specimens from the Academy of Natural Sciences of Drexel University malacology collection and recently collected specimens will be used to establish racemization ratios for several Jamaican species. A reverse phase HPLC procedure for stereoisomeric separations of amino acids will be used on these specimens with a known age. The data will be used to generate racemization age models that can be used to estimate the age of field collected shells. Field collected shells from death assemblages with unknown ages will then be analyzed and placed within the age models to determine an approximate date of death for each shell.

2-3

Evolutionary Adaptations and sensory differentiation: Exploring olfactory receptors in the Phylum Mollusca

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Researchers have long been intrigued by the molecular basis of olfaction and the evolutionary adaptations of sensory systems in organisms. Unraveling the molecular basis of olfaction is crucial for understanding the biology, adaptation, and evolutionary history to uncover the mechanisms behind the perception of their environment. There are still gaps to be completed in relation to studies of sensory systems and genes in the phylum, therefore this study focuses on the phylum Mollusca which encompasses a wide range of species with diverse ecological adaptations and intricate sensory capabilities in their organs, such as tentacles, osphradia, and photoreceptors. In this study, we propose that marine mollusks may exhibit a higher abundance of olfactory receptors than freshwater due to greater chemical complexity and variability in marine environments. To investigate the ecology and evolution of G-protein coupled receptors (GPCRs), particularly olfactory receptors, within mollusks, we performed a comprehensive search for potential candidates in the literature of 250 candidates using TBLASTN of 30 complete mollusk genomes available at NCBI with sensitive settings. The sequences were aligned and trimmed, and trees were informed using IQTree. UPhO was used to detect orthologs with and without paralogs from input gene family trees. Our initial findings reveal the presence of numerous putative olfactory receptor candidates across different molluscan genomes. By analyzing the diversity of GPCRs, we aim to explore the potential ecological implications, such as the role of olfaction in adaptation to various habitats and lifestyles in molluscan species. Preliminary stages have provided valuable insights into the presence and distribution of olfactory receptor candidates in mollusks. This investigation will contribute to a deeper understanding of the evolutionary processes underlying the diversity and functional adaptations of GPCRs in mollusks. Moreover, it will serve as a foundation for further studies on the sensory biology of these remarkable organisms.

2-4

Complete Mitogenomes of Photosymbiotic Bivalves Reveal Elaborate Repeats within Non-Coding Regions

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Assembly of plastid genomes is often considered an easy venture today under modern sequencing technology. However, many published bivalve mitogenomes are partial, primarily with protein-coding genes only. Therefore, comprehensive assessment of mitogenome structure from diverse bivalve species is needed to understand molluscan mitochondria evolution and its role in bivalve ecological adaptations. Here, we compared mitogenomes from PacBio long-read assemblies to *de novo* reference-guided assemblies of Illumina short reads for several species in the family Cardiidae, including photosymbiotic species. We observed an inability to assemble complete mitogenomes from short reads alone due to elaborate repetitive sequences in the non-coding “control” region (NCR). In particular, NCRs varied drastically in photosymbiotic bivalves from the genera *Fragum*, *Tridacna*, and *Hippopus*. The mitogenomes ranged from 22 to 30 kbps in all three genera, exceeding those of non-photosymbiotic *cardiids*. These mitogenome expansions arose from species-specific tandem repeats within the NCR, with NCR sizes averaging at 8.3 kbp. We found 10-12 copies of repeats in *F. fragum* and *F. whitleyi* that exceed 500-bp in length, which were three-fold longer than Illumina short reads, and are punctuated by ~100bp of random sequences. Fast evolutionary rate and polymorphic nature of the NCR hinders alignment across different species, making functional roles of the NCR largely unresolved. However, we were able annotate 11 copies of tRNA-R/S interspersed in the NCR of *F. fragum* on top of 24 tRNAs outside its NCR. We postulate that high levels of NCR expansion through long repeats in these photosymbiotic species may be associated with elevated levels of reactive oxidative species in their mantle due to photosymbiotic activities. Our results showed that complete mitogenome assembly might not be achieved by short-reads alone. With potentially important roles in ecological adaptation and evolution of bivalve, NCR and its structures should be further explored.

2-5

Tracing the Evolutionary Origins of Biomineralization: Insights from Two Aplacophoran Genomes

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Although it is believed the ancestor of Mollusca had the ability to biomineralize, the state of mineralized structure the base of the tree remains uncertain. Mollusca is divided into two major groups: Conchifera, or "shelled molluscs," and Aculifera including chitons (Polyplacophora) and the shell-less Aplacophora. Aculiferans produce mineralized structures in the form of shell valves and sclerites. Chitons produce eight aragonitic valves that are not considered homologous to the conchiferan shell due to differing embryonic origin and structural development. Sclerites are spines and scales found along the girdle of chitons and covering the body of the worm-like aplacophorans. While aculiferan sclerites are composed of aragonite, similar to what is present in some conchiferan shells, little is known about the genetic underpinnings of their formation. Transcriptomic and proteomic studies in bivalves and gastropods have shed light on the genes and proteins responsible for shell patterning in conchiferan molluscs. These studies revealed a combination of highly conserved genes and rapidly-evolving genes in mantle transcriptomes across distantly related species. However, our current knowledge of the genetic basis of biomineralization in aculiferan molluscs impedes our ability to identify overarching evolutionary patterns within broad molluscan toolkit. Here we present the progress of an ongoing project aimed at uncovering the genetic toolkit underpinning mineralization within the genomes of the aplacophoran molluscs *Neomenia megatrapezata* and *Epimenia babai*. Using these genomes, we investigated gain and loss of genes identified from studies of biomineralization within Conchifera. Genomic phylostratigraphy was used to compare gene models from our new aplacophoran genomes with publicly available molluscan genomes representing all major groups (excluding Monoplacophora). Supplemented with functional annotation of these genes, this exploration into retention and loss of genes over evolutionary time will aid in untangling the genetic basis of biomineralization and other innovations within this incredibly morphologically disparate phylum.

3. Biodiversity, Taxonomy, and Phylogenetics

3-1

Inferring phylogenetic relationships and testing for introgression in taildropper slugs

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Taildropper slugs (Genus *Prophysaon*) are endemic to the temperate rainforests of the Pacific Northwest of North America. There are nine described species of *Prophysaon*, but species relationships remain poorly understood. We collected 52 specimens from the six most common species of *Prophysaon* from across the Pacific Northwest. We sequenced mRNA libraries on an Illumina NextSeq and assembled transcriptomes using Trinity. Then, we assembled several phylogenomic datasets, ranging from a dataset of single-copy orthologs to a dataset including orthologs and paralogs. We inferred species trees using concatenated Maximum Likelihood and coalescent-based approaches. Regardless of the dataset or species tree inference method used, we consistently inferred a single species tree topology with high support. We also found support for several instances of introgression. Finally, we focused on the sister species *P. foliolatum* and *P. andersoni* and two phenotypically distinct populations that appear to be affiliated with these taxa based on morphology and genetic data. We examined population structure and tested for introgression amongst this subset of taxa. Our results depend on the method applied, but suggest a potential role of hybridization in generating diversity within this subgroup of *Prophysaon*.

3-2

Scaphopoda is the sister taxon to Bivalvia: evidence of ancient incomplete lineage sorting

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The almost simultaneous emergence of major animal phyla during the early Cambrian shaped modern animal biodiversity. Reconstructing evolutionary relationships among such closely-spaced branches in the animal tree of life has proven to be a major challenge, hindering understanding of early animal evolution and the fossil record. This is particularly true in the species-rich and highly varied Mollusca where dramatic inconsistency among paleontological, morphological, and molecular evidence have led to a long-standing debate about the group's phylogeny and the nature of dozens of enigmatic fossil taxa. A critical step needed to overcome this issue is to supplement available genomic data, which is plentiful for well-studied lineages, with genomes from less well-studied but important lineages, such as Scaphopoda. Here, by presenting first chromosome-level genomes from both extant scaphopod orders and leveraging complete genomes spanning Mollusca, we provide strong support for Scaphopoda as the sister taxon of Bivalvia, consistent with the morphology-based Diasoma hypothesis originally proposed 50 years ago. Our molecular clock analysis confidently dates the split between Bivalvia and Scaphopoda at ~520 Ma, prompting a re-interpretation of controversial laterally compressed Early Cambrian fossils, including *Anabarella*, *Watsonella* and *Mellopegma,* as stem diasomes. Moreover, we show that incongruence in the phylogenetic placement of Scaphopoda in previous phylogenomic studies was likely due to ancient incomplete lineage sorting (ILS) that occurred during the rapid radiation of Conchifera. Our findings highlight the need to consider ILS as a potential source of error in deep phylogeny reconstruction, especially in the context of the unique nature of the Cambrian Explosion.

3-3

Phylogenetic Placement of Mollusca and its Evolutionary Implications

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Mollusca is the second most species-rich animal phylum comprising >85,000 species. Since their early and rapid diversification in the late Cambrian (~540 MYA), molluscs can be found globally from terrestrial habitats to extreme environments such as hydrothermal vents. The ecological success of molluscs can largely be attributed to their morphological innovations allowing varied adaptability into diverse ecologic niches. Although the phylum is one of the most well documented and studied, its placement within the larger superphylum Lophotrochozoa is not firmly resolved. Multiple different phylogenetic positions of Mollusca have been recovered across multiple studies within the last decade, often with strong support, implying a mixture of systemic artifacts influencing placement of Mollusca in a larger phylogenomic context. Here we examine the phylogenetic position of Mollusca within Lophotrochozoa based on a new dataset with genomes and transcriptomes from 223 lophotrochozoans broadly spanning the diversity of the group. Considering our results and other recent phylogenomic studies, we consider the evolutionary implications of competing hypotheses for molluscan placement, highlight incongruencies in gene histories recovering these relationships, and propose avenues that may help confidently resolve the phylogenetic position of Mollusca. Firm resolution of the placement of Mollusca within Lophotrochozoa will allow closer investigation of ancestral character states of the phylum. Moreso, resolution of Mollusca's phylogenetic placement will shed light on the evolution of homologous traits between molluscs and members of other closely related phyla, leading to an increased understanding of the gain and loss of diverse traits. Broder understanding of the placement of Mollusks within the tree of life will bring a greater understanding of not only morphology but all aspects of malacology as its diverse and impactful science is only strengthened in the light of well-resolved phylogeny.

3-4

A Resolved Phylogeny of Cephalopoda Yields New Insights into This Ancient Invertebrate Lineage

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Recent studies of cephalopod genomes have revealed these to be highly informative for understanding the Mollusca development of intelligence, color perception, and nuanced methods of communication. Critical to such insights is a well-resolved phylogeny of this unusual mollusc radiation. Historically, morphological data and the fossil record have been utilized to infer the evolution and relatedness of taxa within this class of organisms that are incongruent with emerging sequence based analysis. However, these sequences based phylogenies have been based on limited sequence and taxon sampling, and the relationships between major clades of cephalopods remain unclear. Here we resolve these relationships using targeted sampling of ultra-conserved elements (UCE) from taxa that span all cephalopod orders. Using 44 cephalopod taxa, we analyzed 455 UCE loci under maximum likelihood using IQtree yielding the first well-supported phylogeny of all Cephalopoda. The resulting phylogeny provides critically needed resolution for the earliest divergences in the cephalopod tree of life, and a necessary framework for understanding the evolution of this emblematic clade of invertebrates.

3-5

What good is a broken barcode: cox1 in pleurocerids and semisulcospirids

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Although *cox1* has been widely promoted as a universal molecular barcode for animals, it does poorly in some taxa. Pleurocerid and semisulcospirid gastropods have high species diversity but also high levels of variation in commonly-sequenced genes. This variation includes both extremely divergent sequences and apparently normal but variable sequences. The low-level variation makes delineation of species difficult. However, once the extreme sequences are removed, higher clades largely agree with the results of recent genomic studies. Unsurprisingly, the relationships strongly correlate with drainage divides, with clades associated with the Appalachicola, Mobile, Ohio, and Atlantic Coastal Plain systems. Thus, the variation has not eliminated all phylogenetic signal, but it has obscured it.

3-6

Morphoanatomic study and molecular systematics of the family Pruvotinidae (Mollusca, Solenogastres)

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Solenogastres is a class of marine molluscs characterized by an aculiferous mantle, a longitudinal ventral pedal groove and a terminal or subterminal pallial cavity. Their classification is based in part on the type of mantle sclerites, but further identification past the family level generally requires the study of internal anatomical characters. Taxonomically, the most important characters include the radular structure, the type of ventrolateral foregut glands and the reproductive system. The classical reconstruction method consists of serial histological sectioning of specimens, from which the internal structure can be reconstructed manually in 2D. More recently, it has been demonstrated that microcomputed tomography (Micro-CT) is very useful to determine some characters that are not clear in classical histology and visualize internal anatomy in 3D. Thus, in this study, I have combined both techniques useful in the study of internal anatomy of Solenogastres (histology and Micro-CT) to make the first complete description of some species belonging to family Pruvotinidae from Icelandic waters, collected during the IceAGE campaign. In addition, 16S and COI have been sequenced in order to clarify the systematics of the family Pruvotinidae and attempt to establish a relationship between their internal morphoanatomical characters and their position in the phylogenetic tree.

3-7

Molecular Phylogeny and Resulting Classification of Caenogastropoda, Utilizing 28S and cox1

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Caenogastropoda is one of the most speciose subclasses of Gastropoda, with an estimated 80,000 recent species. It contains most of the large and many small marine gastropods, ~7000 freshwater, and ~6000 terrestrial species. No comprehensive molecular phylogeny of Caenogastropoda exists, though Fedosov *et al.*, 2019 surveyed most of the Neogastropoda. Bayesian and parsimony analyses of 28S data provided the best resolution overall. Published data was supplemented by a few unpublished sequences. 18S changed too slowly to resolve most caenogastropod groupings below orders, and *cox1* reached mutation saturation beyond orders. *Cox1* was used for smaller-breadth analyses resolving groups which were unstable on 28S. Almost all accepted superfamilies were monophyletic or unresolved. Rissooidea *s. l.* appears to be paraphyletic to Vanikoroidea, and should have Barleeiidae, Rissoinidae, and Zebinidae separated as Barleeioidea. Turbinelloidea was supported as polyphyletic, as found by Fedosov *et al.* Truncatelloidea and Cerithioidea have internal divergences in this analysis more than double that of any other superfamilies, and should be elevated to orders; about 5 superfamilies can reasonably be recognized within each. Heterobranchia was confirmed as sister to Caenogastropoda. Viviparoidea + Ampullarioidea (order "Viviparida") was recovered as basal, followed by Cerithiida + *Campanile* (cohort Cerithiimorpha). Cyclophoroidea was weakly supported as a sister to either "Viviparida" or Cerithiimoirpha. Within cohort Hypsogastropoda, Littorinimorpha *s.s.* forms a superorder sister to Latrogastropoda. Within Littorinimorpha, four orders appear to be recognizable: Epitoniida (Epitonioidea, Vermetoidea, and Lyocycloidea sister to Triphoroidea + Abyssochrysoidea), "Littorinida" (Littorinoidea, Naticidae within it + Pterotracheoidea), "Rissoida" (Rissooidea, Barleeoidea, Cingulopsoidea, Hipponicoidea, and Vanikoroidea), and "Truncatellida" (Truncatelloidea *s.l.*). Branches within Latrogastropoda formed a near-polytomy, beyond Calyptraeoidea (including Capulidae) being basal. Harpidae and Babyloniidae place as aberrant members of Olivoidea. Belomitridae, Dolicholatiridae, and Turrilatiridae may deserve their own superfamily Belomitroidea. Other internal groupings of Latrogastropoda supported the results of Fedosov *et al.*, or resolved poorly.

3-8

A striking new species of Dondersia (Mollusca, Aplacophora) from the Gulf of Mexico and new data from other species of the genus

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Aplacophora is a clade of benthic marine mollusks that are worm-like in appearance and covered with small scale- or spine-like protrusions, called sclerites, in place of a shell. Aplacophora contains two clades: Solenogastres and Caudofoveata, which are distinguishable by the presence or absence of the foot, respectively. Unfortunately, due to their small size and the fact that many species live in the deep sea, aplacophorans are an understudied group with very few experts researching them. Meanwhile, there are many open questions on their diversity, morphology, and evolutionary history. In this project, we sought to improve understanding of the solenogaster genus *Dondersia*, a group including several charismatic species with beautiful and bright coloration in life. Notably, *Dondersia* is the type genus of the family Dondersiidae, although the monophyly of the family has been called into question. Through the use of histology, scanning electron microscopy, compound microscopy, and DNA sequencing, we are describing a striking new species of *Dondersia* with purple and yellow coloration and a series of middorsal keels that was collected from an autonomous reef monitoring structure (ARMS) in the Gulf of Mexico while also adding new data to existing species descriptions. Results will further our knowledge of the species-level diversity and morphological disparity of *Dondersia*. There are many unknowns surrounding the evolutionary history and diversity of Aplacophora and the community of malacologists currently studying them is small. With our integrative taxonomic approach applied to a particularly charismatic new species of *Dondersia*, we hope to improve understanding of this group while also working to increase awareness and interest in Aplacophora.

3-9

Icelandic Aplacophora: Remarkable undescribed diversity in the deep sea

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The complex hydrology and bathymetry of the waters surrounding Iceland, combined with the high latitude of the region, make it particularly vulnerable to the effects of climate change. For this reason, it is particularly important to establish baseline knowledge on the biodiversity of this region. To this end, the IceAGE (Icelandic Animals: Genetics and Ecology) project is sampling diverse habitats around Iceland to enable modern biodiversity research around this sensitive area. For part of my dissertation research, I am evaluating the biodiversity of Apalcophora found in this region. Aplacophora includes the molluscan classes Solenogastres and Caudofoveata, which remain a remarkably understudied group of mollusks whose true diversity is estimated to be tenfold higher than the number of described species. Extensive sampling from the IceAGE expeditions to date has generated a huge collection of >3,000 specimens of Aplacophora from 104 unique stations at depths from 117 m to 5,484 m. Work on this collection focusing on stations at depths >1000 m has already revealed an astonishing amount of diversity including over 60 unique species, many of which are new to science. A combination of classical taxonomic techniques like histological sectioning and modern techniques like DNA barcoding will be employed in the description of the many new species represented in this collection. The specimens will then be used to explore the environmental factors that impact the distribution of species. I am particularly interested in seeing if bathymetry and sediment type are correlated to the distribution of higher-level taxonomic groups, like families, in the deep sea. This work will ultimately result in a monograph of Icelandic Aplacophora.

3-10

Using Geometric Morphometric Analysis to Differentiate Two Species of Sphaeriidae (Sphaerium simile and Sphaerium striatinum)

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Sphaeriidae (fingernail or pill clams) are small freshwater bivalves found throughout North America across a wide range of aquatic habitats. The majority of North American sphaeriid species are found in the Great Lakes region (35 species). Although sphaeriids are common and diverse, their biology, ecological roles, and species distributions are poorly studied because they are difficult to identify even to genus. This is because their high phenotypic shell plasticity is not easily encompassed by standard dichotomous keys. The inability to correctly identify sphaeriids leaves them largely undocumented and unmonitored, resulting in inaccuracies in biological and ecological studies and the potential to miss invasive and at-risk species. Geometric morphometric analysis (GMA) used in paleontology has shown promise in separating cryptic species of freshwater mussels (Unionidae). We are testing whether 2D landmark-based GMA of sphaeriid shell shape could be used to separate two similar species of sphaeriids (*Sphaerium simile* and *Sphaerium striatinum).* We collected 278 specimens from 45 locations, mostly in the central and western Great Lakes region. All specimens were initially identified using standard dichotomous keys and selected 121 for genetic ID verification. Each sphaeriid was photographed and 24 2D landmarks were digitized along the right valve shell margin to evaluate each shell's shape. Our results show that the GMA was able to distinguish the two species with an 83% success rate. Moreover, we were able to quantitatively show how and where the shell shapes differed between the species; these differences matched descriptions from Herrington (1962). Although the genetic results are still pending, it appears that the 2D landmark-based method has the potential to separate similarly shaped species of sphaeriids and allow graphical visualization of the differences between the shells of cryptic species. This, in turn, will allow improvement of key couplets used to identify these ecologically important freshwater bivalves.

3-11

A monograph of Solenogastres (Mollusca, Aplacophora) from the Southern Ocean

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Though Solenogasters (Mollusca, Aplacophora) are present in all oceans and depths, they remain one of the least studied groups of molluscs, with most of the diversity still yet to be described. Moreover, knowledge of their distribution is biased with most species known from two particularly well-studied regions: the North Atlantic and the Southern Ocean. Thiele (1913) wrote the first monograph on solenogasters from the Southern Ocean, describing 13 new species. This later was later extended by Salvini-Plawen (1978). This second monograph, besides dramatically incrementing the known species in this area (from 19 to 74 species), is important as it established the higher-level classification of Solenogastres used today. Since 1978, 16 new solenogaster species have been described from this region, and there are still more 'known' unknowns awaiting formal description. Additionally, many species originally described from the Southern Ocean were based on a single specimen or specimens from a single sampling event, meaning that the distribution of these species has largely been unknown. Lastly, both monographs were written in German, which limits their accessibility. So, despite Southern Ocean Solenogastres being relatively well-documented compared to other regions, an updated document synthesizing known information and describing additional new species is needed. Here we present preliminary data from a project that aims to provide a significantly updated monograph on Southern Ocean Solenogastres with new data from around 800 specimens from five cruises (NBP-12-10, LMG-13-12, PS96, NBP-20-10, and NBP-23-03). This work will synthesize all known Solenogastres species in this area, with updated descriptions and distribution data, including descriptions of new species by means of an integrative taxonomy approach. To date, we have tentatively identified over 100 morphospecies, many of which are new to science.

3-12

We’re not just in the shallows: shipworm diversity and distribution in marine habitats

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Shipworms (Teredinidae, Bivalvia) have a voracious appetite for wood. Their ability to bore into and digest wood transfers terrestrially-derived energy to marine ecosystems. Research in the last few decades has turned from trying to eliminate them to understanding their biology, ecological importance, and utilizing them as a resource for human consumption, industry, and health. Wherever there is wood in the ocean, shipworms are there; only limited by cold (the poles), extreme depths, and low salinity. Hidden from view in their wooden tunnels, they often go undetected, are difficult to access and identify. Consequently, many questions about their biology, unique evolutionary history, and importance are yet to be addressed. Generally, teredines are known as residents of shallow coastal waters, yet they live in a variety of habitats, including the deep ocean, the open ocean, anchialine pools, fresh water rivers and lakes, mud, sea grass rhizomes, limestone, and the living roots of mangroves. Natural dispersal of adults via driftwood occurs across ocean basins, a process enhanced by tsunamis. Ports and harbors abound with introduced shipworms, brought from around the world by wooden vessels and in ballast water, the same ship calling at multiple locations. However, within these introduced species, some have genetic connectivity between the continents and Hawaii, others are composed of cryptic species. What shipworms are tough enough to live in extreme salinities? What species are found in the deep ocean? What habitats are dominated by long-term brooders, short-term brooders, and/or oviparous species and why? I will present discoveries based on research in museum collections, in Hawai’i, the open ocean, and the northeast Pacific, focusing on species diversity and characteristics in different habitats. Shipworms, a common, ubiquitous member of the marine community, offer opportunities to answer important questions in a variety of ecological fields.

4. Natural History Collections

4-1

HaptoNet: digitizing adherent organisms in museum collections

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HaptoNet is a new project that aims to digitize marine invertebrates such as barnacles, tubeworms, corals, algae, and bryozoans that are already in museum collections but to date uncataloged.

“Epibionts” are conventionally defined as having a living “host,” whereas “haptobiont” is more broadly defined as any organism that whose adult stage lives permanently attached to a surface. Such organisms may by chance be attached to a living base without necessarily having a biotic relationship with it.

Museum collections are a vital resource for the study of bioinvasions and climate change, as they can provide broad and long-term spatiotemporal data for many haptobiont species whose biogeographic history is unclear. Preliminary surveys suggest that haptobionts are ubiquitous in marine collections, and this project will greatly increase each institution’s digital presence without expanding its physical space.

The project will also link the fossil record to present-day biota, with particular emphasis on the many well-preserved Plio-Pleistocene haptobionts in museum collections.

HaptoNet participants will use a new online image-based collaborative platform to distinguish, identify and tag haptobionts on museum specimens. By cloning the existing metadata to them, entire new records can be created with no additional input. These will be shared with aggregators such as GBIF and iDigBio, greatly expanding their coverage.

Sixteen institutions are currently taking part in the development process, including non-museum collections. Broader impacts include training students and non-professionals in imaging, visual detection and identification of organisms, biogeography and bioinformatics.

4-2

AplacBase: A Digital Database to Make Aplacophora Less Obscure and Difficult

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As small, shell-less, and worm-shaped molluscs members of Aplacophora (Solenogastres + Caudofoveata) have challenged malacologists since their discovery 150 years ago. Despite their key role in the understanding of mollusc evolution, Aplacophora is one of the lesser known groups among Mollusca. Though common in the global benthic malacofauna, aplacophorans often go unnoticed, are left unidentified, or are simply discarded for research as their identification requires a combination of complex and time-consuming methods and is inaccessible for the untrained. As a consequence, less than 500 species have been described from the two major groups, though the true number is estimated to be ten times higher. Most Aplacophora from remote locations constitute new taxa, but even from well-studied areas new species are still being routinely discovered. Here, we present AplacBase: a freely accessible online database about Aplacophora. Our aims are: to provide 1) an up-to-date species list of Solenogastres and Caudofoveata including their known distribution ranges; 2) a compilation of 150 years' worth of aplacophoran literature; and 3) a photo database and keys for fast and efficient identification of animals to at least higher taxonomic levels. AplacBase is aimed at both experts and non-experts and will include additional information about the animals and their ecology. We hope AplacBase will not just support and facilitate future aplacophoran biodiversity research, but also contribute to make scientific progress (especially taxonomy and biodiversity research) more accessible to the general public, as a resource to raise awareness and public participation in biodiversity and nature conservation.

4-3

Determining live- versus dead-collected status of mollusks

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Aggregated data from museum collections, especially when associated with detailed collecting event information, play an increasingly important role in providing baseline data for, and highlighting changes in, species distributions. However, mollusks are often dead-collected, so their presence does not mean that a species currently occurs at a site. Shells on beaches, for example, can be thousands of years old, representing former occurrences. To address this issue, a “vitality” status has been proposed for addition to the Darwin Core; it will allow for standardized piping of this information to data aggregators, such as InverteBase, iDigBio, and GBIF. Participants in the Eastern Seaboard Thematic Collection Network (ESB TCN, funded by NSF) capture this information in their collection databases. The minimum recommendation uses “live” (at least one specimen was alive when collected), “dead” (no specimen was alive when collected), or “cannot be determined” as statuses.

Other allowed values are “Iive and dead” (lot contains both live- and dead-collected specimens); “fresh dead“ (no specimen was live collected, but at least one was fresh dead), and “possibly live” (at least one specimen might have been live-collected). These map to the minimum coding as “live”, “dead”, and “cannot be determined”, respectively. Another field documents means of inferences of the status, e.g., fluid preserved, behavior observed, dried tissue present, statement by collector, worn, faded, bore hole, single valve). Only one is needed in ESB TCN; if multiple inferences are provided, they can be separated by pipes (“|”).

Live/dead status often can be assigned informatically through queries. For example, if the sample is fluid-preserved or behavior was recorded, the specimens can be inferred to have been live-collected. In addition to understanding changes in distribution, flagging the vitality of samples can help in finding genetic material for DNA studies or in identifying appropriate specimens for color measurements, etc.

4-4

Uncovering marine biodiversity through Natural History Collections: Solenogastres (Mollusca, Aplacophora) from New Zealand as a case study

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Natural history collections contain valuable primary specimen-based data of known taxa, which may have been collected last week or 100 years ago. As such, they are fundamental for taxonomic and phylogenetic studies and for understanding species distributions. Ensuring global access to this information is one of the main challenges for natural history museums today, with efforts focused on digitization of specimens and integration of this information into existing databases. In addition, many collections hold unidentified lots, which often contain undescribed species, that constitute valuable resources for biodiversity studies. The lack of taxonomic expertise and limited resources for taxonomic studies hinder the identification and/or description of these specimens, this being another of the challenges to which natural history museums are currently confronted. We show here the preliminary results of a study of about 200 Solenogastres (Mollusca, Aplacophora) representing roughly 50 species from the Museum of New Zealand Te Papa Tongarewa and the National Institution for Water and Atmospheric Research (NIWA). The results of this study, in which we followed an integrative taxonomic approach, contribute to our knowledge of solenogaster diversity (with the discovery of new species) and distribution (with new data on known species). Thus, this is a good example to demonstrate the value of natural history collections for advancing on our knowledge of marine biodiversity.

5. Ecological Interactions and Adaptations

5-1

The Genomic Ghosts of *Geukensia granosissima*

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Observations that biodiversity - particularly marine species - is redistributing itself as the environment changes has been a key indicator of the climate change era. Historical surveys help us identify such patterns in taxa that might not be typically monitored for distribution or abundance. As recently as 1992, the southern ribbed mussel *Geukensia granosissima* was considered to be relatively abundant in northeastern Florida. Climate velocity predictions might suggest that these mussels would now have cryptically invaded the marshes of Georgia, which has historically only had the congener *G. demissa*, with possible ecosystem consequences. I re-surveyed *Geukensia* from both coasts of Florida and sites in Georgia for mitochondrial and nuclear genomic diversity. As of this report, *G. granosissima* is all but gone from the Atlantic coast of Florida, though some signature of its history remains in these data. The reason for this rapid fluctuation in distribution is not known but is important for clarification of regional biogeographic patterns.

5-2

Phasmarhabditis hermaphrodita, a biocontrol nematode species, infects and increases mortality of *Monadenia fidelis*, a non-target terrestrial gastropod species endemic to the Pacific Northwest of North America

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Biocontrol efforts in pest management lead to the commercialized mass production and distribution of biocontrol species. Although many ‘biocontrol gone awry’ examples have resulted in disastrous ecosystem impacts, this strategy persists in many agricultural applications. The nematode *Phasmarhabditis hermaphrodita* is sold as a biocontrol agent on three continents and targets pest gastropod species such as *Deroceras reticulatum*. *Phasmarhabditis hermaphrodita* is not presently approved for use in the United States. Investigations into the potential for *P. hermaphrodita* to infect non-target gastropod species of conservation relevance, however, are lacking. We examined the effects of three strains of *P. hermaphrodita* on mortality in the snail *Monadenia fidelis*, which is endemic to the Pacific Northwest of North America. Using laboratory infectivity assays, we observed higher mortality in snails exposed to nematodes as compared to water-treated controls. Across the 71-day study, snails exposed to each of the three nematode strains, each analyzed at two different doses, experienced a mean 50% mortality by days 20-42. All nematode-treated snails were dead by the end of the study. By contrast, control snails experienced no mortality. *P. hermaphrodita* killed smaller juvenile-stage snails at rates significantly faster than larger snails. Our results provide direct evidence that *P. hermaphrodita*, a commercialized biocontrol nematode species not approved for use in the U.S., infects and kills the non-target gastropod species *Monadenia fidelis*. Our findings suggest that introduction of *P. hermaphrodita* to new ecosystems might negatively affect endemic gastropod biodiversity. Further, for an accurate and unbiased assessment of host susceptibility in infectivity trials, multiple host development stages should be examined. This study advocates for further investigation of biocontrol nematode impacts on additional non-target gastropod species, and extreme caution in commercial efforts to expand the use of *P. hermaphrodita* and other biocontrol nematodes to new countries.

5-3

Effect of habitat type on size-frequency distributions of *Conus* species from seaward and lagoon reefs of Rangiroa (Tuamotu Archipelago, French Polynesia)

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Intertidal marine benches and subtidal reefs represent distinct habitats that contrast in their topographical complexity, exposure to wave energy, and substrate types, features that may affect characteristics of the organisms and communities that inhabit them. For example, while *Conus* species exhibit higher population densities on intertidal benches, subtidal reefs harbor a greater diversity of species, including more large-sized species than benches. These observations have been attributed to higher wave energy at benches, which may limit the sizes of species that occur in this habitat, and presence of a greater number of microhabitat types at subtidal reefs, which may support greater species diversity. If high wave energy constrains the sizes of species that occur at benches, it should also affect the size-frequency distributions of species in this habitat. Nonetheless, size-frequency distributions should not be affected if the lower diversity of microhabitats at benches limits the diversity of species that occur in this habitat. To evaluate these hypotheses, we surveyed cone snail communities at seaward and lagoon sites of Rangiroa, a very large, open atoll in French Polynesia, and determined if individuals of species from intertidal benches at seaward sites differ in size from those from subtidal reefs within the lagoon. As anticipated, although subtidal reefs had greater species diversity and generally more individuals of large-sized species, population densities were higher at intertidal benches. Nine species occurred in both habitat types, including eight with sufficient sample sizes for further analyses. These eight species showed different size-frequency distributions between the two habitats. On average, individuals were 1.2 to 2.4 times larger at subtidal reefs in the lagoon than at intertidal benches of seaward sites. Hence, the relatively high wave energy of intertidal marine benches may not only limit the presence of large-sized *Conus* species, but also affect the size frequency distributions of species in this habitat type compared to subtidal reefs.

5-4

A multi-study analysis of gut microbiome data from the blue mussel (*Mytilus edulis*) emphasizes the methodological impact of gut voidance on biological interpretation

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The blue mussel (*Mytilus edulis*) is a model organism used in several gut-microbiome surveys. Although raw sequence data are often publicly available, unifying secondary analyses are lacking. The present work analyzed raw data from seven projects conducted by one group over seven years. Although each project had different motivations, experimental designs and conclusions, all selected samples were from the guts of *M. edulis* collected from one location in Long Island Sound. The goal of this analysis was to determine which independent factors (e.g., collection date, depuration status) were responsible for governing composition and diversity in the gut microbiomes. The primary trend in the results was a clear differentiation between microbial communities from mussels that had been allowed to void their gut during a no-food period prior to dissection and those from mussels that had not. This finding supports the developing paradigm about the difference between transient microbes ingested with food and then voided shortly afterward and resident microbes that reside permanently in the digestive tissues. Ultimately this effort highlights the importance of performing secondary multi-study analyses of raw microbiome sequence data, and of tailoring experimental designs and sampling schemes to match the specific experimental questions being addressed in future work.

5-5

Using microbiomics to determine why some snails become pests and others are in peril

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Microbiomics is an expanding field that aims to characterize the microbial symbionts of an organism and determine how microbial communities coevolve with their hosts. To date, we know that the microbiome assists with host metabolic functioning, diet preference, can alter host gene expression, and contribute to many other physiological processes that impact host fitness. Despite the dramatic increase of microbiomics research in the past decade, our knowledge of how microbiome communities impact organismal fitness and the role microbiomes play in the successful establishment of invasive species remains biased towards vertebrate taxa. Molluscs are the second most diverse animal phylum but are severely underrepresented in microbiomics research in proportion. Many gastropod taxa range from highly invasive pests to critically endangered species, making them excellent candidates for exploring the link between microbiome symbionts and other ecological processes. The Hawaiian Islands are home to an amazing radiation of land snails, most of which are endemic. Unfortunately, native snails have declined precipitously in the last century. To better understand better understand the role microbiomes play in the ecology, evolution, conservation of snails, we are assessing the differences among microbiome communities associated with various snail species, including native and non-native species in Hawaii. Expanding our understanding of how symbiotic communities differ among diverse snail groups is crucial for determining what microbiome-mediated mechanisms play a role in species fitness. The results from this work will be used to inform conservation management practices for both the control of invasive snails and the preservation of native snail communities within the Hawaiian Islands.

5-6

Land slugs and snails eaten by juvenile salmonid fish in two Seattle creeks

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Creatures living in different realms, e.g., terrestrial and aquatic habitats, can be expected to encounter each other rarely. For that reason, we were surprised to find land snails and slugs in the diets of juvenile salmonid fish from two creeks in Seattle, Washington. We examined the diets of 186 cutthroat trout, *Oncorhynchus clarkii* (Richardson, 1836), 6 Coho salmon, *O. kisutch* (Walbaum, 1792), and 2 Chinook salmon, *O. tshawytscha* (Walbaum, 1792) that were caught in Thornton and Taylor Creeks in Seattle in the summer of 2019. Stomach contents were removed by flushing, so fish were not harmed. While fish had consumed aquatic and terrestrial arthropods and gastropods, surprisingly, aquatic snails and land slugs were the two prey groups that made up the greatest biomass in the diets of these 194 fish: the freshwater snail *Potamopyrgus antipodarum* made up 12.6% by mass of the diets, while land slugs made up 10.8% by mass of the diets. How did the slugs become available for the fish to eat? We found that slugs were a greater proportion of the fish diets after rainfall, suggesting that rain plays a role in the meeting of these creatures from two different realms. Previous studies found that terrestrial arthropods are knocked into water from overhanging vegetation during rain or wind events, but in our experience, overhanging vegetation is not a common habitat for land slugs. Given that fish are unlikely to venture onto land to consume slugs, we speculate that slugs become available to fish predators during rainstorms when either (1) flowing rainwater washes slugs into creeks or (2) slugs resting near a creek become submerged as creek water levels rise.

1. Ecology & Diversity of Freshwater Mollusks
2. Physiology & Molecular Biology
3. Biodiversity, Taxonomy, & Phylogenetics
4. Natural History Collections
5. Ecological Interactions & Adaptations

P-1

Determining clearance rates of native juvenile *Lampsilis fasciola* and invasive *Corbicula fluminea* at differing algal concentrations

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Freshwater mussels (Unionidae) are a diverse guild of long-lived, filter-feeding benthic bivalves, and are among the most globally threatened group of animals. The non- native invasive bivalve species, *Corbicula fluminea*, co-occurs with native mussels in many waterways, and have the potential to overlap in feeding and potentially out-compete native species. While native mussels and Corbicula have similar functional roles as filter-feeders, previous research has found mixed results regarding how Corbicula influence adult mussels. However, little work to date has been conducted to discern how they impact the more sensitive and fast-growing juvenile life stage of freshwater mussels. To better understand potential interactions between Corbicula and a common juvenile mussel species, *Lampsilis fasciola*, we conducted clearance rate experiments at two algal concentrations (low and high algae availability). Based on previous literature, we expect clearance rates to be similar between species, with Corbicula having a slightly higher per mass clearance rate. It is also likely that clearance rates by both species will be greater in the higher food treatment, as mussels are known to adjust their filtration rates in the presence of additional food. Our work will highlight potential competitive interactions between *C. fluminea* and juvenile *L. fasciola* at differing algal concentrations and will demonstrate the role that food availability plays in freshwater mussel clearance rates. Additionally, it will provide insight into the potential vulnerabilities of juvenile mussels when in the presence of high densities of invasive *C. fluminea.* More attention should be focused on the functional roles invasive species play in aquatic ecosystems in comparison to native species to better understand the implications of their introduction.

P-2

Mississippi Pearls: An overview of current freshwater mussel research in Mississippi

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The State of Mississippi currently holds 85 species of unionid mussel, including 16 species listed by the United States Fish and Wildlife Service as either threatened or endangered. Currently, 9 other species found in Mississippi waters are being considered for listing by the USFWS, with up-to-date distribution data needed for each species. Information is also needed for all species of conservation concern within the state to complete the 2025 State Wildlife Action Plan, with 46 species currently proposed as species of greatest conservation need in the state. Historic sporadic sampling of the mussel fauna of Mississippi through time has left large gaps in the current knowledge of the statuses of some of the state's most imperiled species. Recently, biologists for the Mississippi Department of Wildlife, Fisheries, and Parks (MDWFP) in conjunction with the USFWS have created a full distribution database for all vouchered mussel specimens known from the state of Mississippi. Biologists at MDWFP have also begun conducting system-wide mussel surveys across the state, focused on determining species occurrence, species richness, and CPUE. Herein, we discuss the importance of freshwater mussel conservation in Mississippi, and current MDWFP projects focusing on surveying freshwater mussels in the state.

P-3

SHELD, A trait database for freshwater mussels of the United States of America

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The United States of America harbors a diverse collection of freshwater mussels comprising 301 species distributed among 60 genera and two families (Margaritiferidae and Unionidae), each having a unique suite of traits. Mussels are among the most imperiled animals and are critical components of their ecosystems. Successful management, conservation and research requires a cohesive and accessible source for acquiring information on species' traits. Although trait-based analysis for freshwater mussels has increased, only a proportion of traits representing the diversity of species have been individually collated into separate sources. Decentralized and non-standardized trait information impedes large-scale analysis. Assembling trait data in a synthetic database enables comparison across mussel species and lineages and allows for the identification of data strengths and weaknesses. We collated data from the primary literature, books, government reports, theses and dissertations, and museum collections into a centralized database. Our database includes current taxonomy, morphology, reproductive ecology and life history, fish hosts, habitats, thermal tolerance, geographic distribution, available genetic information, and conservation status. By collating these traits, we aid researchers in assessing variation in mussel traits and modelling ecosystem change.

P-5

Status of Aquatic Snail Research in the State of Mississippi

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The state of Mississippi has among the highest rates of freshwater diversity within the United States. Documentation of fish, mussel, and crayfish distributions have been ongoing since the beginning of the 20th century. In comparison, the study of aquatic snails in Mississippi is severely lacking predominately due to a poor understanding of taxonomy and a lack of available resources needed to determine species identification. The intent of Mississippi state and federal biologists is to initiate surveys for aquatic snail species. The purpose of our efforts is to understand the diversity of aquatic snails in the state and to generate known distributions for each species. Prior to current efforts, only one concentrated survey for aquatic snails had been completed in the state and the majority of aquatic snail collections housed at the Mississippi Museum of Natural Science were collected as by-catch from historical fish surveys. At that time only 235 lots of aquatic snails from Mississippi had been curated, but efforts were made to identify the backlog of aquatic snails from Mississippi. Currently, the collection has grown by 145%, with approximately 10% of lots remain unidentified. A preliminary list of the known aquatic snails within the state of Mississippi is representative of 25 native and 2 non-native species. However, future taxonomic work and survey effort within the state will more than likely contribute to an increase the number of taxa. Preliminary surveys conducted since 2022 have improved our understanding of the aquatic snail diversity within the state and has led to re-discovery of the Big Black Rocksnail (*Lithasia hubrichti*) that was presumed extinct nearly 60 years ago. Future surveys are needed to understand the complete distribution of endemic snails like the Big Black Rocksnail and many other species within the state of Mississippi.

P-6

Freshwater mussels upstream of a manmade waterway: a case study of a tributary to the Tennessee-Tombigbee waterway in the southeastern USA

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The Tennessee-Tombigbee Waterway (Tenn-Tom) is a 234 mile-long shipping channel which was constructed between 1972 and 1984. The waterway connected two major river basins by dredging and creating an extensive lock and dam system between the Tennessee River (Mississippi River Basin) and the Tombigbee River (Mobile River Basin). Although no mussel species in the area were listed at the time of project completion, the decline of mussel richness and subsequent listing of eighteen species in the drainages within Mississippi (Tennessee River: 2 state and 4 federally listed; Tombigbee River: 2 state and 10 federally listed) may be attributed to the alteration of habitats and hydrological function of tributaries which followed construction of the Tenn-Tom. Updating distributional records for mussels in impacted tributaries will inform listing and recovery efforts for threatened and endangered mussels. Luxapalila Creek was the first of several tributaries which will be surveyed in coming years to assess the status of freshwater mussels in tributaries flowing into the Tenn-Tom Waterway.

P-7

Freshwater mussel use of microhabitats in the Colorado River, Texas

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Mussels are not distributed homogenously within a watershed and can occur patchily in relatively high densities throughout a system. However, habitats that are suitable to sustain mussel communities may vary across systems. Within sand-bed lowland rivers, many mussel beds are generally concentrated in areas downstream of features where hydrological effects are minimized in the river. Even within these areas, mussels are not evenly distributed. Therefore, understanding distributional patterns among microhabitats is a critical component in the conservation and recovery of these aquatic organisms. Mussel surveys were conducted on 14-16 June 2022 at three shoreline sites on the Colorado River near Wharton, TX during low water conditions (i.e., wadeable, non-diving conditions). The three sites ranged between 170 m and 180 m in length and were searched using a tactile technique along 15m transects placed perpendicular to the shoreline, spaced 10 m apart and subdivided into three, 5 m segments (i.e., nearshore, middle, outer). A total of 1,028 mussels representing eight species were collected among the three sites. The most abundant mussel species was Threeridge (*Amblema plicata*; 52.2%), followed by Pimpleback (*Cyclonaias pustulosa*; 23.7%) and Yellow Sandshell (*Lampsilis teres*; 18.8%). Sixteen individuals of federally petitioned mussel species were collected during the survey, eleven Texas Pimpleback (*Cyclonaias petrina*) and five Texas Fawnsfoot (*Truncilla macrodon*). The majority of mussels were located between 2 - 5 m from shore, within the nearshore sub-transect in silt and clay substrates, with a few found in the areas that transitioned from silt and clay to coarse sand. Results from this survey effort will help with the identification of suitable habitats within hydrologically stable areas of sand-bed lowland rivers.

P-8

Establishing Modern Tools for Developmental Study of the Brown Garden Snail, *Cornu aspersum* (Muller, 1774) (Mollusca: Gastropoda: Stylommatophora)

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With the rapid increase of available genomic and functional resources for mollusks, the biology of this group is undergoing a renaissance of comparative developmental studies. However, given that there is no established model system for the study of development for air-breathing terrestrial gastropods (Superorder Eupulmonata), there remains a lack of functional genetic toolkits for Eupulmonata. Thus, it is pivotal to establish modern genomic resources for this lineage, in tandem with complete descriptions of embryonic development, with the goal of understanding the genetic mechanisms underlying the development of eupulmonate gastropods. To address this, we propose the brown garden snail, *Cornu aspersum* (Müller, 1774), as a model for developmental study due to its wide distribution, rapid onset of sexual maturity of six months, and a high reproductive capacity (multiple clutches of synchronously developing eggs). We documented a complete embryonic staging system of *C. aspersum* using confocal microscopy, immunohistochemistry, and fluorescent *in situ* hybridization. The genomic resources and protocols developed from these procedures will establish resources for future gene identification and expression of genes involved in developmental processes underlying molluscan adaptations to terrestrialization. Additionally, the availability of a comprehensive staging system with detailed descriptions of embryonic development will aid in comparisons with better-studied aquatic gastropod models, such as the freshwater snails *Lymnaea stagnalis* and *Biomphalaria glabrata*.

P-9

Effect of a neuropeptide on muscle contraction in the meadow slug, *Deroceras laeve*

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Neuropeptide hormone signaling is an important regulatory system in animals. Neuropeptides are small proteins that act as signaling molecules in the nervous system, and they play a key role in regulating a wide variety of physiological processes, including growth, reproduction, and behavior. However, it remains elusive in slugs and snails. Here we report that a neuropeptide affects the muscle contraction, thereby leading to deformed body shapes and unusual movement in the marsh slug. To identify the slug that were collected from the Chadwick Lake in Mississippi. Two diagnostic marker genes, cytochrome c oxidase (COI) and 28S rDNA (ribosomal DNA), were PCR amplified and sequenced, revealing that the slug is *Deroceras laeve*. To understand the activity of a slug neuropeptide, called neuromedin U (heptapeptides), it was administered via injection into the body cavity and its responses were observed for 5 min. The responsiveness of the slug tail and tentacles were measured by touching it with a plastic tip 1 min after injection. As a result, the body shape and movement were affected by the peptide in a dosage-dependent way, where 400 picomole and more showed the detrimental effects, such as the stiffened tail and irresponsive tentacles, suggesting that neuromedin U impacts muscle contraction in the slug. As the amounts increased, the effects went severe, leading to paralysis and eventually death at a dose as high as 1000 picomole. Besides the muscle contraction, the treated slugs secreted significantly large amounts of slime over a couple of minutes, which seems to be also associated with the muscle contraction of the mucous and pedal glands. In conclusion, neuromedin U plays a crucial role in muscle contraction in *Deroceras laeve*. providing an insight on the biorational management of the lawn pest slugs.

P-10

Cryptic Cousins: The *Cernuella* Conundrum

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Cernuella virgata, the vineyard snail, is listed by USDA APHIS as a nationally regulated pest of concern and if established in the U.S. it could threaten multiple agricultural commodities. Three taxa of the geomitrid snail genus *Cernuella* are commonly encountered in Europe; *Cernuella virgata* (da Costa), *C. cisalpina* (Rossmässler) and *C. neglecta* (Draparnaud). The first two species have identical genital morphology, while *C. neglecta* can be distinguished by a single character within the phallus. These three "species" have been traditionally distinguished from shell morphology, however a preliminary molecular analysis suggested there may be several clades present with in the species complex that are not distinguishable by morphology. To further clarify *Cernuella* spp. we conducted species delimitation (ASAP) and phylogenetic analyses (Maximum likelihood and Bayesian) on 141 *Cernuella* spp. specimens from 19 countries using the COI, ITS-1 and ITS-2 genes regions. Results suggest that there are up to 11 clades, which may represent cryptic species. Five of the predicted clades are present in the United States, with clade 3 established along the East Coast since the 1940's. Continued US regulation efforts for the *Cernuella* species complex would benefit by having the ability to discriminate between the established Clade 3 and the remaining more recently introduced clades (5,7,9, and 11) which have very restricted distributions in the US. Further work is ongoing to utilize high throughput sequencing to generate additional nuclear and mitochondrial sequences, to conduct in silico comparisons to previously described exon capture baits, and to design diagnostic primers capable of discerning between different clades.

P-11

First records of Monoplacophora from the Eastern Antarctic

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Dating back to the Paleozoic, Monoplacophora are often referred to as Mollusca's "living fossils". While they resemble limpet-like gastropods at first glance, monoplacophorans constitute their own class. 30 extant species of Monoplacophora have been recorded from the continental shelfs down to abyssal depths during the last 70 years, with still little knowledge about their biology and ecology. Three monoplacophoran species have been described from the Southern Ocean, and in contrast to other localities where records of Monoplacophora are often restricted to one or two individuals or few empty shells, the waters surrounding Western Antarctica host a comparatively high abundance of these molluscs. During the course of the "IcyInverts NBP-03-23" expedition aboard the Nathaniel B. Palmer along the Eastern Antarctic continental shelf in 2023, we used an epibenthic sledge to collect benthic macrofauna. At two stations, in sediments trawled from 412 m and 512 m depth, we found a total of 48 living adult Monoplacophorans. Based on external characters of the shell (e.g. size, shell height, position of apex in relation to the shell margin) and the soft body (e.g. number of ctenidia, oral tentacles) we identified them as two species within the genera *Laevipilina* J. H. McLean, 1979 and *Micropilina* Warén, 1989 (family Neopilinidae Knight & Yochelson, 1958) potentially representing lineages new to science. Notably, individuals of the small-sized and brooding *Micropilina* sp. were exclusively found at one station, potentially suggesting limited dispersal abilities, while *Laevipilina* sp. was collected at both stations. Our findings present the first records of Monoplacophora from these parts of Antarctica, increasing the known distribution ranges of both genera. Further morphological and molecular data is needed for comparison between eastern and western Antarctic Monoplacophora and to evaluate potential distribution patterns.

P-12

A Global DNA Barcode Library for Solenogastres (Mollusca, Aplacophora)

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Solenogastres (Mollusca, Aplacophora) is a clade of shell-less vermiform marine molluscs. Though found worldwide, many regions and depths remain unexplored concerning this group and new taxa continue to be discovered from even relatively well-known areas. Therefore, their true diversity is thought to be tenfold higher than currently described. Identification of solenogasters requires the work of trained specialists and time-consuming histology. With climate change and the current dearth of taxonomists, advancing new tools is essential to speed up identification before the current diversity is lost. DNA barcoding has been demonstrated to be an effective tool to identify most taxa. However, most solenogasters have been described based only on morphological features, and few solenogaster barcodes are currently available. Here we developed a broadly sampled DNA barcode library for solenogasters using the mitochondrial genes cytochrome c oxidase subunit I (COI), 16S rRNA (16S), and cytochrome b (CytB). To connect morphological and molecular data histology and scanning electron microscopy were performed to identify barcoded specimens. This work provides a DNA barcode library consisting of 505 COI, 345 16S, and 136 CytB sequences from more than 180 lineages. The identification of barcoded species has made this library a useful tool to speed up the identification of solenogasters. These data will be useful for non-experts identifying solenogasters using molecular tools and work as a foundation for future solenogaster research.

P-13

First Records of Epimeniidae (Solenogastres, Aplacophora) from the Arabian Sea

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Belonging to the enigmatic group of worm-like molluscs called Aplacophora, Solenogastres Gengenbaur, 1878 includes over 300 species found in marine habitats world-wide. Most knowledge of Solenogastres is from preserved material with limited observations from live animals reported in the literature. The genus Epimenia Nierstrasz, 1908, however, encompasses six species described from the Indo-Pacific of which four have been the subject of published observations of behavior and/or development. During three expeditions exploring diversity within the Arabian Sea off the coast of Oman, 25 specimens of Epimenia were collected from or adjacent to colonies of the soft coral Scleronephthya corymbosa by SCUBA diving. These specimens were assumed to be Epimenia arabica Salvini-Plawen, 1991 given the nearby type locality of this species in the Red Sea. Five individuals were kept alive in a research aquarium with Scleronephthya sp. obtained from a local aquarium shop for five months. Both preserved and live animals were investigated via dissection and histological sectioning to confirm species identity. Currently, we are unable to assign these animals to any known species within Epimenia due to discrepancies in taxonomic characters such as the radula and reproductive anatomy. Disagreement in descriptions of these animals further call into question current accepted classification within this genus and requires taxonomic revision. DNA barcodes will be used along with morphological data in order to clarify species boundaries within this group. Here we present histological sections and lateral dissections that highlight key taxonomic characters of Epimenia sp. from Oman. Further we remark on live observations of these animals, including feeding and mating behaviors, adding to the limited knowledge of solenogaster behavior.

P-14

Using transcriptomics to further understand Polygyridae (Gastropoda, Stylommatophora)

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Polygyridae (Gastropoda, Stylommantophora), a diverse family of land snails found across North America, are an integral part of their ecosystems. While members within this family perform nutrient cycling functions, they can also be problematic invasive species in some contexts. Like most land mollusks of North America, Polygyridae are relatively understudied and thus taxonomic relationships at all levels within the group are unclear. The seven accepted tribes within Polygyridae were originally described based on morphological characteristics of the shell, which are now known to be widely variable within species. With the addition of molecular data via DNA barcoding, only two of the seven tribes were recovered as monophyletic. However, these studies were based on only a few barcodes and may fail to clarify relationships between clades because of low phylogenetic signals due to the low vagility of this group. Here we outline the methodology of an upcoming project to investigate these relationships. In this study, we will generate transcriptomes from representatives of each tribe to produce a comprehensive phylogenetic tree to investigate relationships within Polygyridae. Using the resulting tree, we will perform ancestral state reconstruction of key morphological traits in order to assess taxonomic usefulness of different characters. This study will highlight the most useful characteristics for revisionary taxonomy of this group while expanding our knowledge of the evolutionary history and ecological roles of Polygyridae.

P-15

Unveiling the Molluscan World Through Fashion: Exploring Sea Silk and Crushed Shells to Ignite Undergraduate Interest in Research

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Engaging students in interdisciplinary scientific research, particularly in the field of fashion and molluscan studies, can be a daunting task. We propose an innovative approach to captivate and communicate the allure of molluscan research by intertwining the worlds of fashion and marine biology. By incorporating the unique materials of sea silk and shells into fashion, we aim to create a visually captivating experience that sparks curiosity and cultivates interest in the intricate world of molluscs.

This poster highlights the fascinating use of sea silk and shells shedding light on the ecological significance of molluscs and their pivotal role in marine ecosystems. Sea silk, a rare and exquisite fiber produced by certain molluscs offers a unique avenue for connecting students to the wonders of interdisciplinary research. SeaWool and Oystex are constructed from crushed oyster shells combined with recycled water bottles to create innovative fabrics. The inclusion of mother-of-pearl buttons, derived from the luminous inner layer of molluscs shells, further enriches the fashion elements of this educational approach. With their iridescent beauty, these buttons serve as visual symbols representing the intricate and delicate nature of molluscan ecosystems. by exploring the sustainable use of molluscs in fashion, we can raise awareness about responsible sourcing and environmental conservation among students.

This innovative fusion of fashion and molluscan research aims to ignite a passion for the study of these remarkable creatures. We hope to inspire scientific inquiry of novel approaches to conservation issues around fashion, nature, and biodiversity by bringing light to the effects of fashion on molluscan populations. This poster sets the stage for the possible development of interdisciplinary inquiry, blending elements of marine biology, fashion, and environmental consciousness, to nurture a profound appreciation for the intersection of fashion and molluscan research.

P-16

Seahorse and Co: Engaging thousands in malacology through online resources

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One of the most beautiful aspects of our planet is its incredible biodiversity. It is essential for taxonomists and systematic biologists to nurture the innate human interest in this biodiversity. Arguably, the best way to foster this interest is by making the exploration of biodiversity as easy as possible. However, this information has a long history of inaccessibility to all but a privileged few. Biodiversity information has been guarded by financial, social, and educational barriers. Seahorse and Co is an online platform that strives to address issues of accessibility and foster interests in our planet's biodiversity. Mollusks are uniquely suited for outreach efforts because of the calcium carbonate shells that these animals produce. Almost everyone that's gone to the beach has dabbled as an amateur malacologist collecting shells and wondering about the animals that produced them. This makes mollusks a natural starting point for curiosity about our planet's biodiversity. For this reason, we have focused our efforts on creating approachable and easy to use mollusk identification guides that are freely available online. Our guides currently encompass 18 states of the Eastern Seaboard and Gulf of Mexico and include 600 species from 123 unique families. In symphony with these guides, we have produced educational videos on our YouTube channel explaining shell features among other malacological topics. This platform has received exciting levels of engagement with 15,000 site sessions and over 1875 hours of use on identification guides in the last 6 months and over 20,000 views on our videos in the last year. Ongoing and planned expansion to the scope of this project include providing more detailed species descriptions, the creation of west coast identification guides, and the creation of more educational videos. We are eager to collaborate with other malacologists! Check out this project at: www.SeahorseandCo.com.

P-17

Measuring Millions of Marine Mollusks

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Mollusks are ecologically diverse and have a robust fossil record making them well-suited for research examining faunal change over time and space. There are over 100 million individual mollusk specimens in US natural history collections, with an average of 1,100 specimens per species. Collections are currently digitizing their holdings and sharing data with data portals (e.g., iDigBio, GBIF, Symbiota). As part of the digitization process, localities are being georeferenced, specimens are being photographed, and characters traits are being assessed.

Currently, far fewer specimens are photographed than are available in collections. Finding ways to increase the number of individuals photographed while minimizing the potential for measurement error will make digital natural history collections (dNHCs) more accessible for research and encourage their use in course-based undergraduate research experiences (CUREs) such as those developed by the Biological Collections in Ecology and Evolution Network (BCEENET).

We present a “spilled lot” photography workflow that maximizes the number of specimens photographed while maintaining sufficient image quality for taxonomic identification. We discuss sources of measurement error, how an internally-developed computer program will correct these errors, and explore a short-cut that uses the angle of the spire as a part of the length and width calculations.

P-18

Using digitized Mollusk collections in BCEENET CUREs to expand undergraduate research opportunities

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Digitized natural history collections (dNHCs) are a large and growing primary resource that are widely available for use in research, education, and outreach. Millions of expertly identified vouchered specimens are freely available and easily accessible through web portals such as iDigBio, GBIF, Symbiota, and OBIS. Many of these records are georeferenced or include locality information as well as digital images.

The Biological Collections in Ecology and Evolution Network (BCEENET) is a community of undergraduate educators, collections professionals, and data experts who are using dNHCs to increase the accessibility of undergraduate research opportunities by developing Course-based Undergraduate Research Experiences (CUREs). Four CUREs have been developed that can be implemented online, in-person, or in a hybrid format at a variety of instructional levels. Because these CUREs take place during class time and only require access to a computer and the internet, they broaden participation in undergraduate research experiences.

Here we describe the existing BCEENET CUREs that can be adapted for use with molluscan taxa or to incorporate new research ideas. We highlight resources, training, and funding available to support implementation.

P-19

The tall and the short of it: Abiotic correlates of land snail shell size and shape in the Belau archipelago (Republic of Palau, Oceania)

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Because of their poor vagility and propensity for endemism, Pacific Island land snails may exhibit strong environment-phenotype relationships. Desiccation risk and calcium availability likely place powerful selective pressures on land snails. However, previous single-species studies on relationships between land snail shell size and moisture, temperature, or calcium availability have shown conflicting results. Therefore, we connected fine-scale habitat variation to shell size and shape variation for entire land snail assemblages of the Belau archipelago in the tropical northwestern Pacific (Republic of Palau, Oceania). We measured and compared microclimate and environmental chemistry in sites and microhabitats across Belau. Land snail shell morphology was quantified using geometric morphometrics, and shell size and shape variables were compared between microhabitats. Live vegetation microhabitats were subtly but significantly hotter, drier, and windier than organic litter or rock microhabitats. In most of the archipelago, snails found in live vegetation were significantly larger and had a bimodal spire index distribution, as compared to snails found in organic litter or rock. Land snail assemblages found in some high-calcium areas were also morphologically distinct. Larger size in vegetation may be a mechanism for desiccation resistance through decreased surface area-to-volume ratio. Spire indices for vegetation-dwelling snails may be under selective pressure to maximize stability in a gravitationally challenging environment. However, one of the modal spire indices for vegetation-dwelling snails was similar to a theoretically unstable spire index. Our results show that relationships between microhabitat and shell size and shape were significant even when environmental and morphological variability was subtle. Our data can be used to identify habitat characteristics that correlate with land snail diversity to advance conservation goals.

P-20

On the Snail Trail of an Aquatic Invader: The Global Spread of the New Zealand Mud Snail *Potamopyrgus antipodarum* (Mollusca, Caenogastropoda)

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Invasive species are widely recognized to be one of the biggest threats to aquatic ecosystems. Among the 100 worst invasive species in Europe, the New Zealand mud snail (NZMS) stands out as an important exemplar for aquatic invaders. In this study we reviewed over 400 publications to identify the initial occurrences of the NZMS following its introduction to England in 1859, from which it has rapidly expanded its range across Europe. Although similar patterns were observed in its introductions to Australia (1872) and the US (1987), long-term estimations about the invasion in Japan (2000) and Chile (2011) cannot be made yet due to their relatively recent occurrence. The success of the invading populations can be partially attributed to several factors, including the NZMS's parthenogenic and ovoviviparous nature, its phenotypic plasticity, the absence of natural predators, and the lack of parasitic interactions, particularly trematodes. The invasive trajectory of the NZMS was traced by its first records in Europe, Australia, North American, Japan and Chile. This extensive dataset provides a valuable resource for monitoring and understanding the spread of this invasive species, thereby informing management strategies to mitigate its impact on aquatic ecosystems worldwide. Furthermore, given the NZMS's invasive nature and evidence of its human-induced introductions, this study emphasizes the importance of predicting its future invasive routes in the coming decades, as the species is expected to extend its range further. It also sheds light on the critical role that global shipping plays in facilitating the spread of invasive species, underscoring the urgent need for robust biosecurity measures and enhanced regulation to prevent further ecological disasters

P-21

Characterizing the nature of invasion: A trait-based analysis of extralimital mollusks from the Quaternary to present southern California

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California coastal marine ecosystems are sensitive to climate change; for instance, Big blob and EL Niño events resulted in rapid warming, which caused observable latitudinal shifts of marine species across a range of temporal and spatial scales. Shallow marine invertebrates, particularly mollusks, have been used to develop provincial biogeography and compare with the past latitudinal shift in response to climatic events. Several species' quaternary occurrences have been found outside their present-day limit, which could be critical to interpreting the causes of change in the whole community over time. This research aims to classify the invasibility of these taxa on the basis of their modern biogeography, abundance, and ecological traits. Fundamentally, for a species to be called an invasive has to pass through four stages: arrival, establishment, integration, and spread into a new environment. Our study will help identify whether these anomalous assemblages are "Ephemeral" or "Established" invasives and to understand the mechanisms driving these adaptations to a novel environment. We hypothesize that the fitness and abundance of these faunas vary towards the margins of their geographic range in relation to temperature variations or other environmental variables. Trait-based approaches help to trace the species distribution and the success of their invasion, contraction of range, or potential extinction through deep time, historically and could be a helpful tool to predict the future benthic assemblages of coastal southern California. A comprehensive database of the body size of these taxa over large temporal (Quaternary to present) and spatial scales along the warm and cold-water transition zone of southern California will demonstrate the invasive fitness capability and plasticity compared to natives in a stressful environment.

P-22

Characterization of Unknown Microbial Borings in Late Cretaceous Ammonites

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During the preservation assessment phase of an ongoing stable isotope study of Late Cretaceous ammonites from the Western Interior of North America, unusual microtubules were discovered across a majority of imaged specimens. A common method to determine if molluscan shell material is suitable for geochemical analysis is observation of nacreous layer microstructure using SEM imaging. That study examined structural preservation of nacre tablets among multiple genera including Baculites, and Scaphites and various heteromorph species. The prevalence of microborings among these specimens prompted our morphological study documenting the unknown penetrative features.

We hypothesize that the tubules were either a result of microbial boring, or a naturally occurring feature within ammonite shell material. Algae, fungi, and cyanobacteria have all been documented to form microborings in modern and fossilized calcium carbonate with a diverse array of morphologies. The tubules in our specimens are mostly non-branching and of continuous width, with a preferred orientation relative to the shell microstructure. They have some morphological similarities to cyanobacterial borings, but are much narrower than those previously recorded, and they are not a good match for other reported microboring morphologies.

To characterize these features, we measured the tubule width, length, quantity, and the angle of the tubule relative to the nacre tablet structure. We compared multiple ammonite genera from the same biostratigraphic time period but found no systematic variation in tubule morphology. We did characterize two different size (tubule width) groups within at least one representative of each taxonomic group, but we have not found any systemic pattern to the occurrence of the larger tubule type. Our data suggests that tubule quantity and length increase as the depositional age decreases and nacre quality improves. Ultimately, we intend to determine the palaeoecological significance of these microborings by establishing a correlation between tubule presence, taxonomy, age, and depositional factors.

P-23

First records of parasitic Nematoda in Solenogastres (Mollusca, Aplacophora): findings of the NBP23-03 “IcyInverts” expedition to the Eastern Antarctic

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General knowledge on the biology and ecology of Solenogastres (Mollusca, Aplacophora) is still scarce. They are found from the shallow intertidal, along the continental shelfs, and down to the deep sea, but living of observations of these animals are nearly anecdotal. Known biotic interactions between Solenogastres and other organisms have been restricted to 1) specialized predation of Solenogastres on a range of invertebrates like polychaetes, nemerteans, or cnidarians on which some solenogaster lineages live epizootically; and 2) commensalism(?) between a virtually sessile species of Solenogastres living within rosseliid glass sponges. Among the numerous Solenogastres collected during the NBP23-03 expedition to the Eastern Antarctic in spring 2023, we discovered two cases of Solenogastres with endoparastic nematodes. The solenogastres belong to two different lineages of the non-monophyletic family “Proneomeniidae” Simroth, 1893 collected from two different sampling stations. While unremarkable from the outside, dissection of these solenogasters revealed the presence of nematodes in the midgut and ventral blood sinus. Overall, infestation rate of this species seems to be low, with only two out of the around 500 collected specimens affected. Based on indirect sequencing the parasitized Solenogastres’ gut contents, we propose that infestation most likely occurs via their food source. To our knowledge this is the first report of a parasite found in an aplacophoran mollusc, and to fully under understand the effects of this biotic interaction between the Solenogastres and the nematodes, further anatomical and molecular investigations of both hosts and parasites are needed.

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