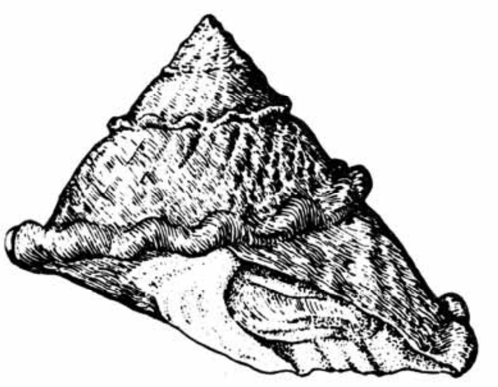

THE WESTERN SOCIETY OF MALACOLOGISTS

Annual Report
For 2024

Volume 57
August 2025

Abstracts and papers from the 57th annual meeting of the
Western Society of Malacologists meeting jointly with the American
Malacological Society 90th annual meeting and the 7th International
Heterobranch Workshop

Pasadena, California - USA
August 4 – 7, 2024

In Memoriam: Carole M. Hertz (17 August 1932–3 September 2024)

Hans Bertsch[1] and Robert Dees[2]

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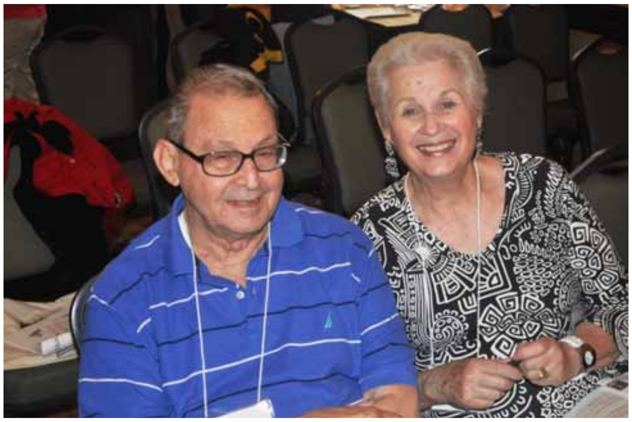
Carole Meisner Hertz was born in Brooklyn, New York, on 17 August 1932. She passed away 3 September 2024 in Escondido, leaving behind her daughters Suzanne Hertz Parlett and Ruth (husband John) Weber, four grandchildren, and one great-grandson. She was predeceased by her beloved husband Jules Hertz on 16 February 2018. She met Jules Hertz on an all-girls vacation trip to the Catskills in the summer of 1954, and they married in 1956, remaining happily together until Jules' death in 2018.

Following a move with Jules to California in 1957, Carole became interested in shell collecting after finding the shell of a *Megastraea undosa* (Wood, 1828) at Point Loma, near her home in San Diego. She and Jules joined the San Diego Shell Club (SDSC) in 1965 and spent the next four decades as energetic members and leaders of the Club.

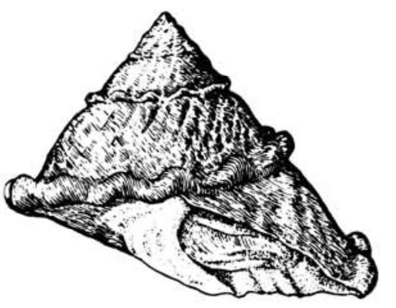
In addition to serving at various times as librarian, treasurer, secretary, or president, Carole served from 1970-2014 as editor of *The Festivus*, the SDSC's monthly peer-reviewed and highly respected publication. Under her leadership *The Festivus* published significant papers on malacological and conchological subjects by expert amateur club members and numerous recognized malacological authorities. She participated in various SDSC events, SCUM (Southern California Union of Malacologists) and WSM (Western Society of Malacologists) meetings. She served as President of the WSM in 1987.

Carole published over 200 papers and notes in *The Festivus*, *The Nautilus*, *Venus*, and other malacological journals. Five species of mollusks have been named in Carole Hertz's honor. She had a broad expertise in malacology and was always enthusiastic, outgoing, and genial, truly interested in others and supportive of what they were doing.

[See also Bertsch & Dees, 2025, "In Memoriam," *The Festivus* 57(1): 50-60, and Bertsch, Groves & Dees, 2025, "Invertebrate Eponyms Honoring Women Members of the Western Society of Malacologists," *WSM Occasional Paper* No. 4: 270 pp.]



Left: Jules and Carole Hertz, 2013 WSM meeting; photo by Paul Valentich-Scott. **Right:** WSM Presidents Carole Hertz (1987), Carol Skoglund (1981), and Kirstie Kaiser (1994); photo San Diego, 1998, courtesy of Kirstie Kaiser.



CONTENTS

The Annual Report of the Western Society of Malacologists is based on its yearly meeting. Distribution of the Annual Report is free to regular and student members who are, at the time of issue, in good standing. Membership dues are $20.00 for regular and institutional members and $8.00 for student members. Forms and payment information can be found at www.westernsocietymalacology.org.

Correspondence regarding membership and orders for additional or back issues of the **Annual Report** should be addressed to the current WSM Treasurer, Kelvin Barwick, 16391 Del Oro Circle, Huntington Beach, CA 92649 USA; rictaxis@gmail.com.

Western Society of Malacologists

Executive Board 2023-2024

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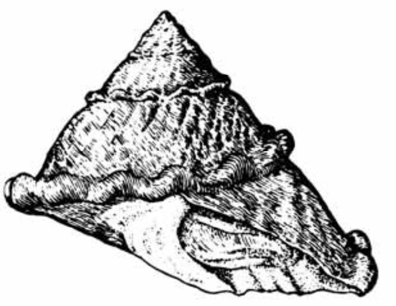


Meeting Program

Sunday, August 4		
9:00	Meeting registration	outside San Gabriel
10:00	Kleptobiology & photosymbiosis workshop	Pasadena Ballroom
3:00	Welcome reception starts	San Gabriel room
4:30	**AMS Council Meeting**	Pasadena Ballroom *(council members only)*
6:00	Welcome reception ends	*registration resumes Monday 8 AM*

Monday, August 5

California Ballroom

8:30 **Welcome address** - Patrick Krug

AMS President's Symposium - Molluscs, symbiosis & specialization: routes to diversity

8:45	Keynote AMS-1	Baldomero Olivera	Using the biology of fish-hunting cone snails to facilitate biomedical discovery
9:30	AMS-2	Ruiqi Li	Molecular insights into bivalve photosymbiosis
10:00	AMS-3	Sónia Cruz	Integrative studies of kleptoplasty in Sacoglossa sea slugs
10:30	**Coffee break (30 min)**		
11:00	AMS-4	Viridiana Avila-Magaña	Bacterial small RNAs promote molecular and cellular dialogue in the symbiotic system of the Hawaiian bobtail squid *Euprymna scolopes*
11:30	AMS-5	Jessica A. Goodheart	Insights into the mechanism and evolution of kleptobiology using the cnidae- stealing nudibranch *Berghia stephanieae*
12:00	**Lunch break (90 min)**		
1:30	AMS-6	Philippe Bouchet	Molluscs as associates, commensals and parasites.:A journey through success stories and bizarre symbioses

JEDI Symposium - Molluscs in education and outreach to underserved, local & indigenous communities

(sponsored by CSU COAST)

2:00	**Introduction**	Teresa Rose Osborne (AMS-JEDI) & Krista Kamer (CSU-COAST)	
	JEDI-1	Ariel Sherman	Incorporating molluscs into educational activities and programs for underserved K-12 students
	JEDI-2	Brant G. Miller	Reciprocity and field expeditions in the Galapagos: Snails as a vehicle for inquiry and cultivating relationships
	JEDI-3	Amira F. Ainis	Archaeomalacology: how mollusk shells inform our understanding of cultural lifeways in the past and serve as proxies for paleoenvironmental reconstructions
	JEDI-4	Jann E. Vendetti	Strategies for engaging diverse Southern California communities in snail science
	JEDI-5	Newton Z. Hood	Using paid internships to increase participation in science from underrepresented groups
3:00	**JEDI panel discussion** *(moderator: Teresa Rose Osborne)*		
3:30	**Coffee break (30 min)**		
4:00	JEDI symposium break-out discussion groups		*San Gabriel*
4:30	Galapagos short documentary screening & wrap-up outreach discussion *(moderators: Christine Parent & Brant Miller)*		*California Ballroom*
5:00 to 7:30	**Poster session & reception**		*International Ballroom*

Tuesday, August 6

California Ballroom

7th Int. Heterobranch Workshop Symposium 1: Marine heterobranchs – ecology, evolution & diversity

8:45	Keynote IHW-1	Ángel A. Valdés	Opening Pandora's Box: Unprecedented levels of sea slug diversity discovered in the fringes of the Coral Triangle
9:10	IHW-2	Kara K. S. Layton	Revisiting phylogenetic uncertainty and mimicry hypotheses in aposematic sea slugs with genome-wide data
9:30	IHW-3	Douglas J. Eernisse	Move over, honeycreepers: Hawaiian siphon limpets include a rival spectacular endemic radiation
9:50	IHW-4	Eric W. Schmidt	How molluscs make their defensive pyrones
10:10	IHW-5	Patrick J. Krug	Defensive polyketides produced by abundant sea slugs (*Alderia* spp.) may be keystone molecules altering estuarine food webs and communities
10:30	**Coffee break (30 min)**		
11:00	IHW-6	Vesa Havurinne	Chloroplast sphericity as means to long-term photosynthesis in solar-powered sea slugs
11:20	IHW-7	Felisa Rey	Habitat conditions and available resources shape the lipidome of the tropical photosynthetic sea slug *Elysia crispata*
11:40	IHW-8	Kathe R. Jensen	Sacoglossa and siphonalean green algae: Co-evolution or co-incident diversification? A literature review.
12:00	**Lunch break (90 min)**		

California Ballroom

7th Int. Heterobranch Workshop Symposium 2: Non-marine gastropods – ecology, evolution & conservation

1:30	Keynote IHW-9	Kenneth A. Hayes	Two decades of Hawaiian land snail research: What we have learned about what we do not know
2:00	IHW-10	Adrienne Antonsen	Characterizing plant community structure in native Hawaiian land snail habitat
2:15	IHW-11	Samantha Shizuru	Plant preferences of Hawaiian arboreal snails and their conservation implications
2:30	IHW-12	Neilia Perry	Identifying food resources for threatened Hawaiian land snails
2:45	IHW-13	Tonatiuh Trejo-Cantwell	Detecting species in snail feces: What the microbiome can tell us about captivity and conservation
3:00	IHW-14	Mandi Hill	Manning the conservation lifeboats for native Hawaiian land snails
3:30	IHW-15	Norine W. Yeung	Ameliorating the Ostromian shortfall inhibiting effective Hawaiian land snail conservation: enacting policies and changing public perceptions
3:30	**Coffee break (30 min)**		
4:00	IHW-16	Jesse E Czekanski-Moir	Beta diversity patterns in Palau Hungerfordia (Caenogastropoda: Cyclophoroidea: Diplommatinidae)
4:15	IHW-17	Meagan L. Haubner	A revised Ampullariidae mitochondrial genome (mtGenome) phylogeny with six new mtGenomes
4:30	IHW-18	Timothy A. Pearce	Land snails on Gull Island, Michigan: Influenced by glacial history?
4:45	IHW-19	Jann E. Vendetti	*Oxychilus* spp. land snail presence and distribution in Southern California
5:00	IHW-20	Robbie M. Snyder	An update on invasive non-marine molluscs and their spread in Hawaiʻi
5:15	IHW-21	Ian M. Oiler	Evolution of Galapagos land snail-associated microbial communities
5:30	IHW-22	Madeleine M. Dieringer	Using community science observations to generate robust species accounts of terrestrial gastropods
5:45	IHW-23	Emily R. Taylor	The biocontrol nematode *Phasmarhabditis hermaphrodita* infects and increases mortality of two life-stages of *Ariolimax columbianus*, the Pacific Banana Slug, in
6:00 to 8:00	**Auction & reception**		*International Ballroom*

Tuesday, August 6

San Gabriel

Contributed talks A - Reproduction & Development

1:30	A-1	Taro Maeda	TBD
1:45	A-2	Serena Caplins	A life-history polyphenism along temporally and geographically shifting environmental factors in the sea slug Alderia willowi.
2:00	A-3	Melanie Medina	It's the way your mucus smells: conspecific recognition in a simultaneous hermaphroditic sea slug
2:15	A-4	Elysse Ornelas-Gatdula	Drug discovery in molluscs – A brief review of current literature
2:30	A-5	Liz Shea	Cephalopod ontogeny and life cycle patterns
2:45	A-6	Gustavo Ramirez	Hydrothermal venting, microbiomes, and the complex egg brooding behavior of *Muusoctopus* sp. in Costa Rican deep-sea seamounts
3:00	A-7	Nancy Treneman	Listening to Velveteen Ears: Velutinidae of Southern Oregon
3:15	A-8	Nathan Shoobs	On the frequency and correlates of sinistrality in *Campeloma*
3:30	**Coffee break (30 min)**		

Contributed talks B - Ecology & Biodiversity

4:00	B-1	Thomas Duda	Variation in body size of *Conus* species (family Conidae) from seaward and lagoon reefs of atolls in the Tuamotu Archipelago (French Polynesia)
4:15	B-2	Gary Rosenberg	Live-dead distinctions and why they are important
4:30	B-3	Maria Moreno-Alcántara	Holoplanktonic gastropod diversity in the Isabel Island Marine Zone National Park, Nayarit, Mexico
4:45	B-4	Omar Ojeda	Taxonomy of the family Eulimidae Philippi, 1853 (Mollusca: Gastropoda) in the Tropical Eastern Pacific
5:00	B-5	M. Carmen Cobo	New Insights into Solenogaster-Coral Dynamics with focus on the Gulf of Mexico
5:15	B-6	Paul Valentich-Scott	Life between spines: Galeommatoidean bivalves of western South Africa

6:00 to 8:00	**Auction & reception**	*International Ballroom*

Wednesday, August 7

California Ballroom

Contributed talks C - Marine Heterobranch Workshop

8:45	C-0	Tori Bolin	Variation in nudibranch density across regions and habitats of Southern California
9:00	C-1	Michael Middlebrooks	Discovery of a population of the temperate sacoglossan sea slug *Elysia chlorotica* in a sub-tropical habitat
9:15	C-2	Xochitl Vital	Temporal and spatial patterns of sea slug diversity in Mexican coral reefs: insights from Autonomous Reef Monitoring Structures
9:30	C-3	Maria Rosario Martín-Hervás	Origin and biogeography of the colourful sap-sucking sea slugs genus *Thuridilla* Bergh, 1872 (Mollusca, Gastropoda, Heterobranchia)
9:45	C-4	Anahy Garza	Snot you it's me: Gastropods are less deterred by sea slug chemical and mucus defense than other consumer taxa
10:00	C-5	Diana Castillo	Investigating the slimy slug: *Hypselodoris* sea slugs from New Caledonia
10:15	C-6	Andres Camacho	Biodiversity and phylogeny of the genus *Halgerda* in New Caledonia
10:30	**Coffee Break (30 min)**		
11:00	C-7	Michelle Millan	*Cerberilla* sea slugs: Mapping diversity and phylogeny
11:15	C-8	Katrina Lam	The genus *Trapania* in New Caledonia: morphological and molecular analysis reveals un-described species
11:30	C-9	Katrina Go Garcia	Mammal or mollusc? Investigating the biodiversity and phylogenetics of bat-winged sea slugs (Mollusca: Gastropoda: Gastropteridae)
11:45	C-10	Hans Bertsch	Historical study comparing the density and diversity of intertidal Nudipleura (Gastropoda: Heterobranchia) communities on the Caribbean and Pacific coasts of Panama
12:00	**Lunch break (90 min)**		

Wednesday, August 7

San Gabriel

Contributed talks D - Conservation & Natural Resources

9:00	D-1	Daya Hall-Stratton	Species confirmation and population genetics of the non-native Mystery snails *Heterogen japonica* and *Cipangopaludina chinensis* within the Eastern United States
9:15	D-2	Itzel S. Pérez-Bustamante	The Pacific oyster *Magallana gigas* cultured in Bahia San Quintín, Baja California, afected by a new poyldorid species *Bocardiella vicentina* .
9:30	D-3	Casey H. Richart	Detrimental non-target effects of the biocontrol candidates in the genus *Phasmarhabditis* (Nematoda, Rhabditida) on the Reticulate Taildropper (*Prophysaon andersonii* ;
9:45	D-4	Bryson Y. Torgovitsky	Scoping review of superfamily Octopodoidea in waters surrounding Japan using legacy data
10:00	D-5	Kesler Randall	A dry collection talk: Revitalizing the San Diego Natural History Museum Marine Invertebrate Collection
10:15	D-6	Meri Arzumanyan	Diversity and phylogeny of terrestrial mollusks of Armenia

10:30 **Coffee break (30 min)**

Contributed talks E - Ecophysiology

11:00	E-1	J. Roberto Oyervides-Figueroa	How does Ocean Acidification impact the biomineralization of abalone species: from a transcriptomic and physical shell analysis approaches?
11:15	E-2	Mason Linscott	Rocks and Spray: Mineral supply constraints on shell form in *Oreohelix* and *Cerion*
11:30	E-3	Jordan James Bond	The energetic demand of acute thermal stress inducing anticipatory response
11:45	E-4	Newton Hood	From a full gut to a full gonad; Using GnRH to examine the link between reproductive

12:00 **Lunch break (90 min)**

California Ballroom

Contributed talks F - Gene Flow & Evolution

1:30	F-1	Samantha A. Donohoo	Systematics of the critically imperiled pleurocerid genus *Lithasia*
1:45	F-2	Nathan Whelan	The unsolved case of the Black Mudalia, *Elimia melanoides* (Gastropoda: Cerithioidea: Pleuroceridae)
2:00	F-3	Annamarie Steed	Population genomics of the Tennessee River drainage endemic Smooth Rocksnail, *Leptoxis virgata* (Gastropoda: Cerithioidea: Pleuroceridae)
2:15	F-4	Ellen Strong	Steppingstones across the arctic: historical biogeography and evolutionary history of the amphi-Pacific mangrove snail *Cerithideopsis*
2:30	F-5	Yu Kai Tan	Within and among species variation reveal if carrier snails (Family: Xenophoridae) are specialist collectors
2:45	F-6	Andy Tan	Evolution of vision-guided defenses in file clams (Limidae)
3:00	F-7	Raquel Hernandez	Phylogeography of a chiton under a temperature gradient
3:15	F-8	Lauren Kallen	The genetic characterization of the corallivore *Drupella fragum* outbreaks on Guam
3:30	F-9	Miranda Dennis	RADSeq coalescent inference reveals Pleistocene divergence but distinct population

3:45 **AMS *In Memoriam***

4:05 **AMS *Business Meeting*** *(California Ballroom)*

4:05 **WSM *Business Meeting*** *(San Gabriel)*

6:00 **Banquet & awards announcements** *(International Ballroom)*

Message from the Presidents

Welcome everyone to the 90th AMS and 57th WSM annual meetings!

We are delighted to welcome members, colleagues and guests to what we know will be a stimulating and productive conference, filled with opportunities to present findings, learn, network and forge new and stronger collaborations. Thank you for coming to Los Angeles!

AMS/WSM 2024 has **130** registered attendees. Our program features four symposia, six sessions of contributed talks, and 32 poster presentations. It’s mollusc time, folks.

This year also marks the 25th anniversary of the inaugural International Workshop of Opisthobranchs in Menfi, Italy (1999). This meeting was followed by conferences dedicated to sea slugs held in Bonn, Germany (2006); Vigo, Spain (2010); Santa Cruz, USA (2012); and Porto, Portugal (2015). The last meeting, in Perth, Australia, was expanded to include all heterobranchs including non-marine snails and slugs (in the spirit of phylogenetic accuracy and community inclusivity!) We continue this tradition by hosting the 7th International Heterobranch Workshop, which includes the Sunday workshop on kleptobiology; two symposia; a session of contributed talks; and many posters. If you like snails and slugs, we’ve got you covered.

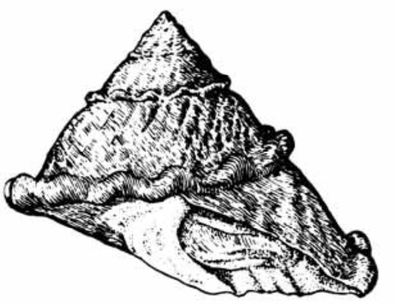
Patrick Krug - President AMS

Christine Parent - President WSM

4–8 AUG 2024

AMS & WSM

LOS ANGELES, CA



Oral Presentations

Alphabetical by First Author

Presenting author <u>underlined</u>
Student presentations marked by an asterisk *

Archaeomalacology: how mollusk shells inform our understanding of cultural lifeways in the past and serve as proxies for paleoenvironmental reconstructions.

Amira F. Ainis

Department of Anthropology; California State University, Los Angeles

As a subfield or archaeology, archaeomalacology is focused on the study of the remains of marine, freshwater, and terrestrial mollusks in archaeological contexts. Mollusk shells are recognized as significant zooarchaeological materials that contribute to our understanding of foodways and subsistence strategies, and a variety of aspects of material culture including art and ornamentation, and they also serve as paleoenvironmental indicators. Shells in archaeological sites represent food remains and raw materials that were used to manufacture a diverse array of utilitarian implements, tools, ornaments, musical instruments, and even currency with the earliest documented use by hominids dating as far back as ~500,000 years to *Homo erectus* in southeast Asia, and widespread use clearly documented by our species during the Middle Paleolithic. Sites with dense accumulations of shell are often referred to as "shell mounds," "shell middens," or "shell-bearing sites" and are common along coastlines and on islands around the world sometimes measuring several meters high and spanning hundreds to thousands of years. Additionally, isotopic analyses and other analytical methods (i.e., sclerochronology) are increasingly being used to reconstruct and interpret paleoenvironmental records and reconstruct the season of harvest and site occupation. In this talk, I will describe some of these archaeological studies of shells and present case studies from my own work as examples of how data derived from marine mollusks is used in archaeological interpretations.

Characterizing plant community structure in native Hawaiian land snail habitat

Adrienne K. Antonsen[1], Wallace M. Meyer, III[2], Samantha H. Shizuru[1], Meagan L. Haubner[1,3], Nelia S. Perry[4], André R. O. Cavalcanti[2], David R. Sischo[5], Norine W. Yeung[6], and Kenneth A. Hayes[1,3,6]

[1]Pacific Center for Molecular Biodiversity, Bernice Pauahi Bishop Museum, 1525 Bernice St., Honolulu, HI, 96817
[2]Biology Department, Pomona College, 175 W. Sixth St., Claremont, CA 91711
[3]Plant and Environmental Protection Sciences, University of Hawaiʻi at Mānoa, Honolulu, HI, 96822
[4]Molecular Biology Program, Pomona College, 175 W. Sixth St., Claremont, CA 91711
[5]Snail Extinction Prevention Program, Department of Land and Natural Resources, 1151 Punchbowl Street, Honolulu, HI 96813
[6]Malacology, Bernice Pauahi Bishop Museum, 1525 Bernice St., Honolulu, HI, 96817

Native Hawaiian land snails represent one of the most spectacular evolutionary radiations among terrestrial gastropods. Unfortunately, over 40% of the more than 759 species that once existed in Hawaiʻi are thought extinct. To protect the remaining species, we have initiated a large-scale study to identify ecological factors that support snail populations across the Hawaiian archipelago. To better understand snail plant preferences, plant diversity, and community structure we surveyed 1600 square meters of snail habitat from nine sites spanning both mountain ranges on Oʻahu, six in the Waiʻanae mountains and three in the Koʻolau mountains. Sites ranged from mesic to wet cloud forest and included 152 plant species. Plant communities significantly differed among sites, confirming that results from the previous study restricted to Mount Kaʻala, the highest point on Oʻahu, may not be applicable across other sites on Oʻahu. Nonetheless, many sites shared certain characteristics, such as high cover of *Metrosideros polymorpha* (*ōhiʻa lehua*) and *Cibotium* spp. (*hāpuʻu*). Despite previous findings that these species are not preferred host plants for snails, it could be that the presence of these overstory and mid- story species create conducive conditions for snails. Continued research stemming from this baseline characterization of plant community structure has high potential to inform restoration recommendations regarding plant community components that may be most influential on snail presence, diversity, and abundance. Deepening our understanding of diverse habitats across the range of Hawaiian land snails is a critical step toward assessing, protecting, and restoring this distinctive malacofauna, which holds substantial ecological and cultural value.

Diversity and phylogeny of terrestrial mollusks of Armenia

Meri Arzumanyan, Arevik Ghrmajyan, Gohar Zhamakochyan and Marine Arakelyan

Department of Zoology, Faculty of Biology, Yerevan State University, Alex Manoogian 1, 0025, Yerevan, Armenia

Armenia, located in the south part of the Caucasus, stands as a biodiversity hotspot, boasting a rich ecosystem and species. Among its treasures are the terrestrial mollusks, a diverse and often overlooked group of organisms. This study attempts to shed light on the current diversity and phylogeny of terrestrial mollusks in Armenia, focusing on the largely distributed terrestrial mollusks found in Armenia: such as *Helix lucorum, Xeropicta derbentina, Fruticocampylaea narzanensis, Chondrula tridens, Merdigera obscura*, etc., and some rare species such as: *Helix buchii, Levantina escheriana*, etc.

Through a combination of field surveys, morphological analyses, and molecular techniques, this study reveals the evolutionary relationships among Armenia's terrestrial mollusks. By constructing phylogenetic trees and investigating the genetic signatures of these organisms, to gain insight into their evolutionary history and biogeographic patterns. In this study we also present the updates on distribution of some rare and endangered species of Armenia. In conclusion, this study serves as a comprehensive overview of the diversity and phylogeny of terrestrial mollusks in Armenia. It underscores the importance of preserving Armenia's natural heritage and highlights the need for continued research to unravel the mysteries of its unique ecosystems.

Bacterial small RNAs promote molecular and cellular dialogue in the symbiotic system of the Hawaiian bobtail squid *Euprymna scolopes*

Viridiana Avila-Magaña[1], Margaret McFall-Ngai[1,2], Edward Ruby[1,2]

[1]Division of Biosphere Sciences and Engineering, Carnegie Institution for Science
[2]Division of Biology and Biological Engineering, California Institute of Technology

Host-associated microbes coexisting in symbiosis employ diverse mechanisms to initiate and promote molecular and cellular crosstalk that results in mutual benefit. Small RNAs (sRNAs) carried in bacterial outer membrane vesicles (OMVs) have proven to play a key role in the conversation between the Hawaiian bobtail squid and its bioluminescent bacterial symbiont, *Vibrio fischeri*. These sRNAs function as signaling molecules within host epithelium in the organ housing the symbionts, the light organ, modulating the immune response and promoting host homeostasis. Using distinct approaches such as Hybridization Chain-Reaction fluorescence *in situ* hybridization (HCR), and high-throughput sequencing techniques such as RNA Antisense Purification (RAP), sRNA and total RNA sequencing, we have identified several bacterial sRNAs inducing profound changes in squid cellular physiology, particularly relevant in modulating host's immune response. Moreover, we have been able to uncover a diel rhythmicity underlying this dialog.

Further, gene expression profiling revealed some potential pathways related to host epigenetics, enabling us to uncover transcriptional patterns of host genes resulting from symbiotically induced modulation of the light organ. Taken together these results demonstrate the potential for sRNA-signaling during initial colonization and throughout symbiosis. Finally, we speculate that analogous mechanisms using bacterial sRNAs and rewiring regulatory networks by inducing host epigenetic modifications may be common among a wide range of beneficial host-microbe associations.

An historical study comparing the density and diversity of intertidal Nudipleura (Gastropoda: Heterobranchia) communities on the Caribbean and Pacific coasts of Panama, with additional inter- provincial density data

Hans Bertsch

Research Associate in Malacology, Natural History Museum of Los Angeles County; 192 Imperial Beach Blvd., #A, Imperial Beach, CA 91932

During 7 August to 18 September 1974, I conducted a comparative intertidal survey measuring the density per area searched of the Nudipleura fauna on both coasts of Panama. A total of 1,350 rocks were turned over, measured, and examined; 60 specimens of 20 Nudipleura species were found. The density of Nudipleura at the Pacific sites was 7.5 times greater than at the Atlantic sites. The Shannon-Weaver Index of diversity was slightly higher on the Pacific coast (H’ = 0.84365) than on the Atlantic coast (H’ = 0.79867). Additional density data based on per time searched further confirmed this relation. Although the Caribbean faunal province has long been considered to have a very low density of nudipleura, these are the first data presented in support of this idea.

Variation in nudibranch density across regions and habitats of Southern California

Tori L. Bolin, Christine H. Jackson, and George D. Jackson

Department of Earth and Biological Sciences, Loma Linda University, Loma Linda, CA 92354, USA

As climate change and other anthropogenic factors continue to stress marine environments, a deeper understanding of nudibranch distribution and population dynamics is essential for the monitoring and conservation of these species. Research on nudibranch populations in Southern California is currently limited. The aim of this study was to improve understanding of local nudibranch populations by investigating their spatial and habitat preferences, as well as species-specific densities. Timed count surveys were conducted at intertidal and subtidal sites in Cabrillo Beach, Shaw’s Cove, and La Jolla.

Density values from these surveys revealed that subtidal habitats had higher species and individual densities compared to intertidal habitats. Furthermore, Cabrillo Beach exhibited greater species and individual densities than the other regions. Statistical analysis identified an interaction between region and habitat type that significantly influenced species density, suggesting that both factors play a role in shaping nudibranch communities. These findings reveal important patterns in nudibranch community structure in Southern California and highlight the need for baseline survey data in less-studied regions to inform effective conservation strategies.

The energetic demand of acute thermal stress inducing anticipatory response

Jordan James Bond[1], Beck A. Wehrle[2], and Kwasi M. Connor[1]

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Anthropogenic activities have induced unprecedented environmental fluctuations in our coastal systems. Byproducts of this unmitigated change are elevated air and water temperatures, increased ocean acidity, and decreased dissolved oxygen, all of which induce stress responses on biological systems. The sessile mussel *Mytilus californianus* must cope with elevated air temperatures and acute heat shocks during low-tide. The response to heat shock is energetically demanding on cellular systems prompting anticipatory responses in model systems. This means an upregulation of mechanisms that are implemented to maintain biological systems, while reassigning energy allocation away from growth. As a proxy for energy acquisition, we measured amylase activity (starch digestion) in mussels acclimated to simulated tides in laboratory conditions to isolate the effects of aerial heat on digestion. Previous evidence showed negative effects of elevated aerial temperature on amylase activity, as a byproduct of acclimation to thermal cycles. In the current study, we predicted that increased feeding and digestion would mitigate this effect. We subjected mussels to a two-week tidal acclimation period (one daily low- tide) of two air temperature conditions. Control conditions were a fixed isothermic (15 C) temperature, while treatment was 25 C⍰ applied at low tide. The specimens were then subdivided into groups of fed and fasted. This acclimation period preceded extreme acute heat shocks (32 C⍰) at low tide with subsequent feeding cycles at high tide for all groups. The results showed robust activity in fed (cool and hot) and fasted cold groups during low-tide. Suggestive of preparing to feed and digest starch during oncoming high-tide. Alternatively, the least energetically optimal state, starved and hot, showed reduced enzyme activity during low-tide. The acute heat stress following the acclimation also proved to be detrimental. Hence, rising temperatures due to Global Climate Change increase the risk of local extinction or poleward migration of mussels.

Molluscs as associates, commensals and parasites: A journey through success stories and bizarre symbioses

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A symbiotic way of life is the rule – not the exception – for a great number of species of marine molluscs. Most species are small to minute, with adult sizes in the range of 2-10 mm, and many live in close relationship with other invertebrates, as commensals, associates, and parasites. This means that a scientific inventory of marine molluscs only remotely resembles the shell collecting of hobbyists, and differs also fundamentally from the environmental surveys of ecologists and conservationists. Many families, including the very speciose ones, have species with highly specialized diets, and a number of these are semi-sessile or sessile on their hosts. The existence of such species is revealed only if the hosts are appropriately sampled and scrutinized. In parasitic species with infestation prevalence usually on the order of 1–20%, this requires examination, and sometimes even dissection, of large suites of specimens of the hosts. Such a specialized approach is never carried out in routine faunal surveys, which consequently miss the majority of commensals, associates and parasites. In this journey through the world of symbiotic molluscs, I will review classic symbiotic radiations such as in the families Eulimidae, Ovulidae and Pyramidellidae, and I will also show lesser known – and sometimes bizarre - symbioses involving e.g., Galeommatoidea, Solenogastres, and Caledoniellidae.

Biodiversity and phylogeny of the genus *Halgerda* in New Caledonia.

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The genus *Halgerda* is a member of the family Discodorididae, endemic to the Indo-Pacific region, and the most diverse genus in the family. Several studies have been conducted over the years to revise the classification of *Halgerda*, expand molecular data, and explore its diversity. Although the use of molecular data in recent studies has led to a better understanding of the taxonomy of this genus, there are cryptic/undescribed species from the Indo-Pacific region that have yet to be described. This study will be centered on the study of potentially undescribed species of *Halgerda*, collected from New Caledonia. The goal is to provide a full description of these undescribed species by analyzing 83 specimens morphologically and genetically. We hypothesize that differences between the specimens examined, justify the introduction of new species names.

A life-history polyphenism along temporally and geographically shifting environmental factors in the sea slug *Alderia willowi*.

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Across a species range, selection imposed by environmental conditions leads to shifts in optimal life- history strategies, in some cases leading to plasticity or local adaptation. Yet, how local adaptation and plasticity interact is less well known. Larval type in *A. willowi* is modulated by seasonally and latitudinally varying environmental conditions, primarily temperature and salinity. We explore the trade-offs among life-history traits and how those traits attune local adaptation and plasticity in response to salinity and temperature between three populations spanning the range of *A. willowi*. We contrast acclimation to temperature and salinity with local adaptation in an experiment that exposes each population to low salinity (12 ppt, 16℃), high temperature (32 ppt, 24℃), and “benign” conditions (32 ppt, 16℃). Warm- adapted southern populations had higher growth rates and higher reproduction in high temperatures than the northern population. Southern populations exhibit a live-fast die-young strategy in high temperatures, while northern populations showed local adaptation to low salinity. Southern and central populations shifted the proportion of larval type in high temperature, but there was no shift in larval type in response to low salinity, relative to benign, suggesting that local adaptation fine tunes life- histories to the dominant environmental stressor along a species range.

New Insights into Solenogaster-Coral Dynamics with focus on the Gulf of Mexico

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Coral reefs and banks are iconic biodiversity hotspots that provide crucial habitat and food resources for numerous marine metazoans, largely composed of understudied invertebrates. Within Mollusca, thousands of species are associated with corals, yet many of these relationships remain poorly understood, with some associations involving Bivalvia and Gastropoda relatively well-characterized. Solenogastres (superclass Aplacophora) exhibit a prevalent association with cnidarians, with at least half of the ~300 described species dependent on them (mostly Octocorallia and Hexacorallia). However, our understanding of these relationships remains poorly known, hindered by significant knowledge gaps within this molluscan group. Solenogastres have been documented across all oceans and depths, with species described from diverse marine habitats. Due to sampling biases and taxonomic challenges, certain regions still lack comprehensive species descriptions. The Gulf of Mexico is one of these areas. In 2010 an explosion on the Deepwater Horizon oil rig in the Gulf of Mexico led to the largest marine oil spill in U.S. history, and work is ongoing to assess and restore impacted Gulf seafloor organisms and ecosystems, particularly coral ecosystems. The Mesophotic and Deep Benthic Communities portfolio, led by NOAA, is working with a multidisciplinary group of partners including the NMNH to plan and implement the restoration efforts. One of the goals is to fill biodiversity knowledge gaps and identify defining characteristics of deep-sea communities. Here we present a review of the existing data of the complex relationship between solenogasters and cnidarians globally but with special focus on these dynamics in the Gulf of Mexico and including the description of three new species of Solenogastres associated with octocorals.

Investigating the slimy slug: *Hypselodoris* sea slugs from New Caledonia

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The genus *Hypselodoris* is a member of the family Chromodorididae, endemic to the Indo-Pacific region. Species of *Hypselodoris* exhibit a wide range of vibrant colors and an elongated body. The present research aims to explore the

characteristics of over 150 *Hypselodoris* sea slug specimens collected from New Caledonia by utilizing a combination of molecular and morphological analyses, to discover and classify new species and provide insights of their phylogenetic relationships. This study will allow us to obtain a better understanding of the genus and explore its diversity.

Integrative studies of kleptoplasty in Sacoglossa sea slugs

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Sacoglossa sea slugs show, for some species, a remarkable intracellular retention of functional chloroplasts, “stolen” from macroalgae. Such chloroplasts can stay functional for some days to several months. Functional kleptoplasty occurs despite the presumably absence of algal nucleus genetic material with an important role in chloroplast regulation, as these genes have been transferred to the algal nucleus over the evolution of endosymbiosis. The mechanism for chloroplasts retention and the biological relevance of this remarkable association between a metazoan and an algal-derived organelle remains controversial and will be addressed.

Particular attention will be given to the host benefits in Sacoglossa kleptoplasty. While some works claim that retained chloroplasts are slowly digestible ‘snacks’, others advocate that they enhance the overall fitness of sea slugs much more profoundly. Time dependent incorporation of ^{13}C and ^{15}N in sea slugs’ tissues will be shown, as the time frame of the process indicates that photosynthesis-derived metabolites were made available to the host through functional chloroplasts. The presence of specific ^{13}C-labelled long-chain fatty acids, absent from the algal food, further indicate animal based-elongation using chloroplasts-derived precursors. Different experimental approaches, advantages and lacunes, and “what’s next?” will be discussed.

Beta diversity patterns in Palau *Hungerfordia* (Caenogastropoda: Cyclophoroidea: Diplommatinidae)

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The archipelago of Palau includes more than 500 limestone karst outcrops and islands. The endemic diplommatinid genus *Hungerfordia* occurs exclusively in these limestone habitats. We discuss the beta diversity patterns of this genus, and the implications of these patterns for understanding community assembly processes and problems in conservation biology. The more northern limestone groups tend to have stronger assemblage turnover over relatively short distances, whereas the more southern islands tend to have more similar assemblages. This could be consistent with different ages of the northern and southern terrestrial limestone habitats (the rocks themselves were formed underwater, and then upthrust at later dates we don’t currently have the geology to estimate). The relatively high species turnover from island to island also has implications for the “SLoSS” (Single Large or Several Small) problem: in Palau it is relatively easy to find combinations of four or more small islands that support greater combined species counts of *Hungerfordia* than the largest limestone island—on a smaller total area. We briefly touch upon the generalizability of this finding for terrestrial gastropods, which often have very small geographic ranges. The upshot for land snail conservation biology may be that we need to advocate for the conservation of small patches of habitat, in addition to the larger habitat patches that conservation biologists who work on megafauna are already working to conserve, i.e., Single Large *and* Several Small habitats may be necessary to conserve terrestrial biodiversity.

RADSeq coalescent inference reveals Pleistocene divergence but distinct population histories in the pseudocryptic Pacific nudibranch genus *Hermissenda*

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The Pacific nudibranch *Hermissenda crassicornis* (sensu lato) is a well-known model organism in neuroscience. This species was recently split into three pseudocryptic species based on differences in genetics, morphology, and behaviour. We used ddRADSeq data from 33 individuals (2354 loci) and coalescent isolation-with-migration models to estimate the demographic history of the clade. We inferred (1) a novel phylogenetic tree topology, (2) relatively old divergence times (0.55 and 1.29 mya), (3) a much larger population size in the southern species *H. opalescens*, and (4) no gene flow between the sympatric species *H. crassicornis* and *H. opalescens*. Overall, our results support the need to reassess previous studies that used *H. crassicornis* (sensu lato) as a model organism.

Using community science observations to generate robust species accounts of terrestrial gastropods

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Very little is known about native terrestrial gastropod natural history and life history compared to other imperiled fauna in the ongoing mass extinction. With terrestrial gastropods playing a vital role in nutrient cycling and other ecological processes, this lack of knowledge poses a critical problem. A literature review of the Pacific Sideband (*Monadenia fidelis)* revealed little is known about this species, even though it is the largest land snail native to the Pacific Northwest. This project aims to fill gaps in knowledge of the Pacific Sideband using community science. We curated observations of the Pacific Sideband which were identified by expert malacologists on the community science platform iNaturalist, a network which allows individuals to share and identify biological occurrences. We annotated observations (n=3961) of the Pacific Sideband from Oregon, Washington, and British Columbia to quantify its natural history and life history characteristics including the snail's life stage (adult or juvenile), number of juvenile shell whorls, food items, microhabitat, and aestivation. For the first time, we identified the Pacific Sideband as an important consumer of lichens. iNaturalist observations of the Pacific Banana Slug (*Ariolimax columbianus*) were also curated and annotated to create species accounts for both terrestrial gastropod species. The Pacific Banana Slug data were subsampled to determine the number of observations needed to develop statistically significant life history and natural history characteristics. This study demonstrates that the community science platform iNaturalist can assist in developing a better ecological understanding of under researched, imperiled species.

Systematics of the critically imperiled pleurocerid genus *Lithasia*

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Widespread anthropogenic stress in the southeastern United States, particularly in the Tennessee and Mobile River drainages, has led to a severe decline in aquatic species diversity. This decline coincides with an increased need to conserve remaining diversity. However, for many freshwater groups, modern systematic reviews have not been done, which often hinders effective conservation planning because species boundaries are poorly defined. The genus *Lithasia* is an imperiled freshwater pleurocerid snail genus composed of 15 currently recognized species that are distributed throughout the Ohio, Mississippi, Cumberland, and Tennessee River drainages. Taxonomic classifications of *Lithasia* have been predominantly based on shell morphology, which originally resulted in 30 nominal species. However, current species-level classification in the genus is based on vague shell characteristics and past research has indicated that at least two unrecognized species exist within *Lithasia*. Moreover, relationships among species are unclear. Our goal was to generate a robust phylogenetic framework for the genus *Lithasia* that can be used for taxonomic revisions and to re-evaluate the conversation status of each *Lithasia* species. Using the 3RAD restriction-site associated DNA sequencing approach, we generated genome-scale data and a molecular phylogeny of *Lithasia* with representatives of each currently recognized species of *Lithasia* and spanning the distribution of each species. Samples from populations historically considered subspecies and potentially undescribed species were also collected to evaluate their taxonomic status. We inferred relationships among species using maximum likelihood, species tree inference, and network-based approaches. Our results show that species-level taxonomic revisions are needed as multiple unrecognized lineages exist. Historical and current ranges of numerous species will be more restricted as a result of taxonomic revisions, which will require new conservation assessments for most *Lithasia* species.

Variation in body size of *Conus* species (family Conidae) from seaward and lagoon reefs of atolls in the Tuamotu Archipelago (French Polynesia)

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Characteristics of cone snail (family Conidae) populations and communities are predicted to differ depending on habitat type. In particular, high wave energy and greater exposure at low tides are posited to restrict body sizes of cones at intertidal marine benches in comparison to subtidal reefs. Here we tested this prediction by comparing shell sizes of cone snail species that occur at both seaward and lagoon sites at two atolls in the Tuamotu Archipelago: Makemo and Rangiroa. At Makemo, we also compared sizes of individuals from a seaward site, sites within a small channel or “hoa” that allows water exchange between the sea and lagoon, and sites at increasing distances from the hoa for species that occurred at these sites. While eight species with adequate sample sizes for analyses occur at both seaward and lagoon sites at Rangiroa, we only observed sufficient sample sizes of two species at both seaward and lagoon sites at Makemo. All of these species exhibited significantly larger body sizes at lagoon sites that are largely comprised of subtidal reefs than at seaward sites that represent intertidal marine benches. These results support the prediction that habitat type influences the body size of cone snails. We also found that body sizes of cone snails steadily increase from the seaward site, through the hoa, and with increasing distance from the hoa in the lagoon. These results as well as our infrequent observations of small-sized individuals at lagoon sites suggest that cone snail larvae settle at seaward sites and individual snails migrate through hoas and contribute to recruitment of lagoon populations.

Move over, honeycreepers: Hawaiian siphon limpets include a rival spectacular endemic radiation

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Hawaiʻi is famous for its endemic radiations but mostly for the fauna and flora found above its beaches. In contrast, most of its marine species have long-lived planktonic larvae and are widely distributed across the Pacific. Endemic species are known, but rarely large radiations. High on rocky shores are small panpulmonate siphon limpets, *Siphonaria* spp., avoided by native Hawaiians as opihi ʻawa. For decades they were lumped as *S. normalis* Gould, 1846, also considered to be widespread across the Indo-Pacific. We integrated shell morphology and combined gene DNA analysis sampling of five Hawaiian islands, finding evidence for four separate species. Two are indeed broadly distributed across the tropical Central Pacific. A third, *S. chirura* Pilsbry, 1921, is revived as a valid species with a distinct shell morphology, currently known only from Hawaiʻi but probably having planktonic larvae. We provisionally restrict *S. normalis* to our fourth species (or species complex) because it is often similar to Gould’s illustrated holotype. In our experience, it is the most commonly encountered siphon limpet in Hawaiʻi*,* and is an endemic with dramatic variation in shell morphology across our sampled localities. Most surprisingly, we observed extreme mitochondrial *cox1* divergence between localities (mean 22.6 percent sequence difference); the minimum was 6.5 percent between two localities a mere 5 km apart. Our sparse sampling of this

diversity implies that *S. normalis* should be evaluated carefully for its conservation status. The extent of *cox1* sequence divergence observed among Hawaiian populations is much greater than is known for any other species of *Siphonaria*. Amy Moran (pers. comm. in lit., June 6, 2024) and her students recently found juvenile siphon limpets at multiple O'ahu localities crawling away from benthic egg masses. It is likely that this striking genetic divergence is related to partitioning of populations in which direct development limits dispersal.

Snot you it's me: Gastropods are less deterred by sea slug chemical and mucus defense than other consumer taxa

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Sea slugs in genus *Alderia* are highly abundant (up to 9,000/m^2) in temperate estuaries of the Northern Hemisphere and could be an important food resource in ecologically sensitive nursery habitats. However, recent work found that *Alderia* spp. biosynthesize defensive polypropionate metabolites that deter feeding on live and dead slugs by co-occurring fish, crab and worm predators. How slug biomass enters benthic food webs thus remains unclear. Observations of feeding behavior suggested that both mucus and chemistry played a role in repelling predation attempts on live slugs. Here, we extended prior work by investigating whether gastropod predators and scavengers were more likely to feed on sea slugs compared to consumers from other taxa. We hypothesized that gastropod consumers would be less deterred by slug defenses either because they also produce slime and/or polypropionates, or are specialists adapted to heterobranch defenses. We also scored the feeding responses of three non- molluscan scavengers feeders (anemone, ophiuroid and holothurian). Live slugs deterred nearly all feeding attempts by 5 of 6 non-molluscan species, but the three scavengers consumed dead slug tissue. In contrast, 3 of 4 gastropods consumed all live *Alderia*, although slugs repelled 50% of predation attempts by Kellet's whelks; 3 of 4 gastropods also consumed dead slugs, except the sea slug-eating sea slug *Navanax*, which only fed on live prey. Thus, most tested gastropods were broadly tolerant of slug defenses, providing one pathway for energy to flow from algae mats through sea slugs to higher trophic levels. However, most gastropods had longer prey handling times to consume slugs versus controls, suggesting polypropionate-laden mucus still acts as a partial defense against gastropods, while also deterring scavengers willing to ingest dead slug tissue (another pathway for chemically defended biomass to enter food webs).

Mammal or mollusc? Investigating the biodiversity and phylogenetics of bat-winged sea slugs (Mollusca: Gastropoda: Gastropteridae)

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Bat-winged sea slugs (family Gastropteridae) have "wing-like" parapodia, which makes them rather distinctive organisms. Their ability to actively swim under distress is shared with only a few other heterobranch sea slug groups. They are found in a variety of marine habitats and have a widespread distribution. Despite mapped occurrences of Gastropteridae throughout all major oceans, there is very little pre-existing general information about this family. Much of their genetic data, let alone life history traits, remain undetermined. The five genera of the family Gastropteridae include some species that are difficult to distinguish from one another. The objective of the present study is to construct a molecular phylogeny for approximately 100 specimens of Gastropteridae collected from the surrounding waters of New Caledonia, an Indo-Pacific archipelago. Sequencing of CO1, H3, and 16S genes will provide preliminary phylogenetic trees, and examination of internal morphology via dissection will be of further aid in species delineation. Ultimately, the exploration of genetic and morphological traits of Gastropteridae will lead towards a more comprehensive understanding of this group, and furthermore promote future studies that seek to incorporate more complex dynamics in nature.

Insights into the mechanism and evolution of kleptobiology using the cnidae-stealing nudibranch *Berghia stephanieae*

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The intracellular uptake and storage of structures from one organism inside another is fundamental to eukaryotic origins, and multiple lineages have evolved to sequester such structures secondarily from their prey. These are most often types of endosymbiosis, such as in cnidarian-dinoflagellate endosymbiosis, in which cases the genome of the cell or structure is often retained inside the host cell. However, little is known about the mechanism of sequestration and maintenance of function in systems where the structure is stolen independently from its recipient genome, such as with cnidarian nematocysts (a process called kleptocnidy). We use the nudibranch gastropod species *Berghia stephanieae* to investigate the molecular and developmental mechanisms that underlie kleptocnidy.

Berghia is well known for its predation on the anemone *Exaiptasia diaphana*. During digestion in *Berghia*, *Exaiptasia* nematocysts move into a structure called the cnidosac in the *Berghia* ceras, where they are phagocytosed and stored by cells called cnidophages. My collaborators and I have shown that *Berghia* selectively sequesters nematocysts over other *Exaiptasia* tissues, and we document that nematocyst theft developmentally begins shortly after feeding, prior to the formation of appendages (cerata) where the organ responsible for kleptocnidy (the cnidosac) resides. We have also constructed a genome for *Berghia,* and used RNA-seq and spatial transcriptomics to begin identifying genes that may be involved in kleptocnidy in nudibranchs. These putative markers include phagocytosis genes like c- type lectins, which are known to function in other types of endosymbiosis. The long-term goal of this project is to uncover how phagocytosis was modified for kleptocnidy in nudibranchs in order to better understand how evolution uses structures made outside of a given organism to generate diversity.

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 six states (Virginia, Maryland, North Carolina, Pennsylvania, New York, and Maine) with an additional seven states (Alabama, New Jersey, Massachusetts, Rhode Island, Connecticut, West Virginia, and Ohio) collected and to be sequenced. Demographic data (snail size, sex ratio, and embryo number) have been collected for all populations and will be analyzed for patterns that can be further explored. Data so far has revealed two COI mitochondrial haplotypes, 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 few introductions and consequent spread within Eastern United States populations.

Chloroplast sphericity as means to long-term photosynthesis in solar-powered sea slugs

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Some sea slugs in the superorder Sacoglossa can take chloroplasts from their prey algae and retain them photosynthetically functional inside their own cells, a phenomenon known as kleptoplasty. Despite over a century of research on the topic, the molecular mechanisms enabling kleptoplasty are still largely unknown. However, it is known that the chloroplasts involved in kleptoplasty are natively tolerant to osmotic shocks, and only very specific sacoglossan species can incorporate the chloroplasts as functional kleptoplasts. We characterized the existence of state transitions, a common light acclimation mechanism of green algae, in several prey algae of Sacoglossa and in the respective kleptoplastic sea slug species. Our data show that even if an alga has fully functional state transitions, they are immediately lost during the chloroplast-to-kleptoplast transition in the animals. Interestingly, an immediate loss of state transitions was also noticed in the algae themselves when shocked with high and low salinity environments. The salinity shocks were concomitant with changes in chloroplast ultrastructure, particularly under low salinity, as determined by confocal microscope imaging of thousands of chloroplasts. Confocal imaging of the sea slugs revealed that kleptoplasts originating from different algal sources are nearly perfect spheres inside sacoglossans capable of functional kleptoplasty, whereas their shape in the algae or in freshly fed *Placida dendritica*, a sacoglossan not capable of functional kleptoplasty, was highly unordered and non-spherical. We hypothesize that even if the forced sphericity comes with a trade-off of losing state transitions, it offers long-term structural integrity to the kleptoplasts, and is a fundamental component of functional kleptoplasty in sacoglossan sea slugs.

A revised Ampullariidae mitochondrial genome (mtGenome) phylogeny with six new mtGenomes

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The Ampullariidae, commonly known as apple snails, are a diverse family of globally distributed amphibious snails. Some apple snail species are among the most invasive agricultural pests worldwide and it is likely that the development of amphibiousness has facilitated their dispersal, as well as their success in becoming major ecosystem engineers within their native ranges. The study the evolution of amphibiousness within the Ampullariidae may yield insights into adaptive trait evolution and the underlying mechanisms facilitating the transition across novel habitats (e.g. aquatic to terrestrial). However, phylogenetic relationships within the family and to the sister taxon require resolution before hypotheses about the role of amphibiousness in their evolution. Previous multi-locus phylogenetic analyses provided substantial resolution at the species level, but some deeper relationships and affinities among some of the major clades remain poorly supported. To help further resolve some of these relationships we produced twelve mitochondrial genomes (mtGenomes) from species representing each ampullariid clade concurrently with representatives from families Campanilidae, Cyclophoridae, and Viviparidae as potential sister taxa. Although these initial twelve mtGenomes provided some deeper resolution and supported a sister relationship with Campanilidae, a lack of genomic material for the genus *Marisa* left one clade poorly supported. We have increased taxon sampling by generating six additional mtGenomes via Oxford Nanopore Technologies long read sequencing approach, ensuring that all clades are better represented in this updated phylogeny. Here, we present the most complete and up to date phylogeny of Ampullariidae providing deeper node resolution and support for the sister taxon. These data will provide the foundation for assessing evolution across the family and to test hypotheses about how amphibiousness and other traits may have contributed to their diversification.

Two decades of Hawaiian land snail research: What we have learned about what we do not know

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Hawaiian land snails serve as an exemplar of the current biodiversity crisis threatening society, with nearly 40% of the species lost to extinction in the last century, and some families having seen declines of 97% (e.g., Amastridae) among their ranks. Nearly one-third of the remaining species will likely go extinct in the next decade without immediate and effective intervention. As with biodiversity broadly, the conservation of land snails in Hawaii, and across the Pacific, is hampered by a dearth of understanding of nearly all aspects of their biology, including taxonomy, biogeography, and ecology. For nearly two decades we have attempted to address the first two knowledge gaps that have made it difficult to know what remains, where they are, and what their relationships are to one another or to species outside of Hawaii. Having addressed large portions of the Linnean and Wallacean shortfalls for land snails in Hawaii, our team has turned its attention to other major knowledge gaps for lands snails, the most pressing of which includes dietary ecology, life history influences, and public perception. To this end, we have been engaged in a long-term research, training, capacity building, and public perception campaign aimed at filling shortfalls in hopes of developing effective conservation actions that will insure the long- term sustainability of native land snails and their ecosystems. Here, we present several aspects of this conservation research program and how Hawaiian land snails may move from being an exemplar of extinction to a model system for moving conservation beyond a species centric focus that has dominated conservation for decades. Expanding conservation to the broader ecosystem level understanding will allow for more effective management of the structure and function of ecosystems on which all of life rely.

Phylogeography of a chiton under a temperature gradient

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Genomic tools provide a powerful means for quantifying marine connectivity, particularly in benthic and sessile species. Chitons are benthic in adulthood and have a short larval stage, so their dispersion is limited. *Stenoplax limaciformis* is a chiton species distributed in rocky shores along the northwest Pacific. We analyzed populations of that species from three marine ecoregions with variable oceanographic factors. DNA of 144 chitons samples were sequenced using ddRAD-seq method. We applied MAF 0.05 and missing data 90% filters, so 5814 SNPs were maintained. Population genetic and demographic analyses were performed to analyze genetic diversity and to describe gene flow among sites. Admixture resolves three genetic groups which coincide with marine ecoregions. The Northern ecoregion has a $HE = 0.101$ and $FIS = 0.026$, the lowest when compared with other ecoregions. A redundancy analysis identified candidate loci involved in local adaptation related to Chlorophyll-a in localities where sea surface temperature is lower. Chitons from the three marine ecoregions have a signal of population expansion, which also coincides with the direction of sea currents.

Manning the conservation lifeboats for native Hawaiian land snails

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Since the year 1500, more than 40% of documented animal extinctions have been molluscs, with Pacific Island land snails accounting for most of these extinctions. Of the 759+ land snail species recognized (99.9% endemic) in Hawai'i, it is estimated that ~100 of the approximately 300 remaining species will go extinct in the next decade without immediate and effective intervention. Biogeography, captive rearing, and educational outreach are critical tools in the conservation arsenal for battling extinction. To help in the battle, the Disney Conservation Fund provided a two-year award to support six students at the Bishop Museum (BPBM) to: 1) develop maps of historical and updated distributions for 100 species 2) care for captive-reared snails at the BPBM Pūpū Ola: Kāhuli Captive Rearing Research Center; 3) develop and participate in community outreach and educational events aimed at increasing awareness and appreciation of snails; and 4) assisting in the maintenance (e.g. weeding, predator monitoring) of predator-proof snail enclosures with Hawaii State Department of Land and Natural Resources Snail Extinction Prevention Program (SEPP). To date, six students participated in the captive rearing of over 2,300 individuals from 9 critically imperiled species and 1,641 snails have been reintroduced into protected snail enclosures on Oʻahu. Interns also assisted SEPP with predator sweeps and site maintenance of a snail enclosure. Outreach efforts engaged at least 8,000 people via science festivals, collections tours, social media, and workshops for the public and conservationists. With the project's end in September 2024, we will provide conservation managers with 171 species distribution maps, allowing natural resource managers state-wide to more effectively plan conservation actions aimed at preserving Hawaiian land snails facing imminent extinction. Additionally, new educational outreach activities are currently being developed, including K-12 curriculum, science festival demonstrations, and public engagement events.

Using paid internships to increase participation in science from underrepresented groups

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There is still a huge issue in academia with recruiting and retaining Black students, with Black people only 5% of STEM PhDs awarded in 2021. A good way to help improve that number is through the use of paid internships. Paid internships are a great way to increase participation from underrepresented groups in science and I have benefited greatly from them. Dating back to my years as an undergraduate, I participated in the IBIO Summer program at the University of Illinois at Urbana-Champaign where I was able to get paid to conduct research over the summer leading to my first presentation later that summer. During my PhD program, I have benefited from the Ridge2Reef (R2R) Program at UCI which enabled me to form a collaboration with the White Abalone Team at the Bodega Marine Lab, which has been foundational to my dissertation research. Being an Aquarium of the Pacific Fellow exposed me to a lot of networking and career building opportunities that I will lean on as I explore careers outside of academia, along with the opportunity to get a behind the scenes view of how the Aquarium of the Pacific operates. Paid internships, such as the Aquarium's CELP scholar program and African American Scholar program, enables participation in marine science and malacology by students who cannot afford to work for free.

From a full gut to a full gonad; Using GnRH to examine the link between reproductive and nutritional physiology

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Historic over-fishing reduced white abalone (*Haliotis sorenseni*) resulting in their listing to the Endangered Species list in 2001. Captive breeding efforts, led by UC Davis Bodega Marine Laboratory, have increased production substantially over the past decade, but still fall short of the target 100,000 animals a year necessary for recovery. This shortfall is largely due

to difficulties inducing gametogenesis and spawning. The diet of the *H. sorenseni* can impact the number of gametes they produce, and lipids have been shown to play an important role in larval development and survival in many marine invertebrates. This led us to explore the effects of a high lipid diet on abalone hormone levels by adding (seeding) a high lipid alga, *Nannochloropsis* sp., to their environment and collecting central nervous tissue (CNS) to measure the reproductive hormone, Gonadotropin-Releasing Hormone (GnRH), which regulates reproductive behavior and gametogenesis, using an ELISA protocol modified for abalone GnRH detection. Here, I am presenting data collected on the relationship between diet and GnRH where we observed that females increased their GnRH production while males decreased their GnRH production. In addition, we saw that the high lipid diet had beneficial impact on body length under heat stress. Examining the environmental factors that stimulate the release of GnRH can prove to be useful for increasing production, as well as aid in future studies focusing on white abalone reproduction.

Sacoglossa and siphonalean green algae: Co-evolution or co-incident diversification? A literature review.

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The association between the Sacoglossa (Gastropoda: Heterobranchia) and the siphonalean green algae (Ulvophyceae *sensu latu*) has been pointed out in many publications since the 1960ies and, based on morphology-based cladistic analyses, it was hypothesized that speciation by host switching and resource-tracking accounted for the diversification of the Sacoglossa (Jensen, 1997: Evol. Ecol. 11: 301- 335). Since this publication, phylogenies of both the Sacoglossa and their prey algae have undergone major changes, especially based on molecular studies. For the present literature review, about 20 papers on phylogenetic relations within the Sacoglossa plus approx. 30 papers on Heterobranchia (or Gastropoda or Mollusca), including at least one sacoglossan species were examined; 10 of these included time-calibrated phylogenies. About 80 papers on evolution of Ulvophyceae were examined; 10 of these included time-calibrated phylogenies. Papers on fossil Heterobranchia and Ulvophyceae were also included. Several additional papers on tectonics and accompanying climate and marine habitat changes during the critical time-periods were likewise included. Time-calibrated phylogenetic analyses of the Sacoglossa indicate a mid- or late-Triassic origin of this group, which would coincide with the formation of the Tethys Ocean. The major diversification took place during late Cretaceous and Paleogene times. For the prey algae, the monophyly of Ulvophyceae is still debated, but their origin goes back to Neoproterozoic times. However, several major groups separated during Triassic and Jurassic times, and major diversification of the groups most utilized by sacoglossans took place during Cretaceous and Paleogene times. This indicates co-incident diversification, but other explanations will be discussed.

The genetic characterization of the corallivore *Drupella fragum* outbreaks on Guam

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In the context of climate change and the naturally increasing sea surface temperatures, it is crucial to understand the dynamics of population outbreaks of *Drupella fragum*, a marine gastropod known for preying on Staghorn corals. These outbreaks have the potential to decimate coral colonies rapidly, but the underlying causes remain poorly understood. My research aims to investigate the factors driving population outbreaks of *D. fragum* in Guam, with a specific focus on population genetics. Employing a genome subsampling approach using Gras-di, we examined the genetic connectivity, diversity, and relatedness of *D. fragum* outbreak populations at two sites on Guam: Agat and Tanguisson. Tanguisson has had no observed outbreaks while Agat has. We found minimal genetic structure indicating high connectivity between the two sites. Both sites demonstrate moderate genetic diversity, with Tanguisson exhibiting slightly higher expected heterozygosity than Agat. Additionally, the inbreeding coefficient for Agat was marginally higher than that of Tanguisson, albeit both values remain relatively low. Samples were collected from the Agat site before, during, and after an outbreak for temporal comparison.

Consistent with the findings outlined above, none of the temporal populations displayed significant genetic differences. Moderate diversity was observed among the temporal populations. Regarding inbreeding, a moderate level was detected, with samples collected after the outbreak showing the highest level. These results collectively suggest substantial gene flow between populations. Furthermore, within Agat, low structure and high connectivity indicate substantial gene flow, suggesting that outbreak and non-outbreak populations are indistinguishable.

Defensive polyketides produced by abundant sea slugs (*Alderia* spp.) may be keystone molecules altering estuarine food webs and communities

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Marine ecology rarely considers heterobranchs as key players, with sea slugs presumed to be highly specialized, rare and of little effect on prey species. These biases are challenged by studies that show the impacts of heterobranchs as invasive species, or cascading effects as climate change alters the distribution and abundance of sea slugs and their kin. The chemical richness of heterobranchs represents another potentially overlooked way in which these taxa may pivotally affect community and ecosystem ecology. Metabolites that deter predators can be bioactive at low concentrations and have off-target effects on other organisms. Such candidate ‘keystone molecules’ may alter community structure and function in unexpected ways with ecosystem-level impacts. Here, we report that five novel polyketides (alderenes A-E) are biosynthesized by sea slugs that reach exceptional densities (up to 9,000 slugs/m^2) in Northern Hemisphere estuaries. Alderenes comprise only 0.1% of slug wet weight, yet rendered live slugs or dead flesh unpalatable to three co-occurring predators, rendering a potential food resource unavailable. In addition to redirecting energy flow in this critical nursery habitat, alderenes also affected the surrounding mudflat community, attracting and repelling species that would not be linked to *Alderia* in any traditional interaction network. In field assays replicated across seasons, slug compounds displaced infauna (crustaceans, molluscs and polychaetes) from the upper sediment of the mudflat, but attracted ovipositing California horn snails. By altering community structure, alderenes may exert surprising effects on processes ranging from bioturbation to reproduction of species not obviously associated with the producing sea slugs. Heterobranchs maintain a rich arsenal of compounds, both sequestered from dietary sources and biosynthesized *de novo*; the off-target effects of gastropod defensive chemicals warrants greater attention by ecologists for their potentially widespread but overlooked ecological roles.

The genus *Trapania* in New Caledonia: morphological and molecular analysis reveals undescribed species

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Historically sea slug species were classified by their morphological characteristics, but molecular analysis has shown that morphology alone is unreliable for classifying sea slug species. Species of the genus *Trapania* display color variation and it is difficult to delineate species based on external morphology alone. Recent molecular studies on *Trapania* biodiversity resulted in categorizing species differently than in past morphological studies. For the present study we focused on specimens of *Trapania* collected from New Caledonia during several expeditions. There were a total of 111 specimens collected. The DNA of each specimen was extracted and three genes (COI, 16S and Histone H3) were amplified via PCR and sequenced. These data were aligned with GenBank sequences from past studies to produce phylogenetic trees using Bayesian and Maximum Likelihood methods. The trees are used to re-examine the classification of existing *Trapania* species as well as to identify potentially undescribed species.

Revisiting phylogenetic uncertainty and mimicry hypotheses in aposematic sea slugs with genome- wide data

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A scarcity of genomic resources in many diverse marine invertebrate groups limits our ability to establish robust phylogenetic frameworks that are fundamental to our understanding of evolution. Here, we use novel sequence capture datasets to address this deficit in chemically defended and aposematic nudibranch molluscs. First, we use 300 genes to resolve the phylogeny of the most diverse family of nudibranch, Chromodorididae. We uncover several non-monophyletic genera in both concatenation and coalescent-based trees, and we uncover conflicting phylogenetic signal in a key query taxon, Cadlinellidae. We then use a hypothesis-testing framework through gene genealogy interrogation to resolve this recalcitrant node. We also use a newly discovered geminate pair to establish the first time-calibrated phylogeny for nudibranchs, indicating a mid-Eocene origin of Chromodorididae. Next, using 1,700 genes, we test hypotheses about regional mimicry in a polychromatic chromodorid genus, *Felimida*. Here, we confirm the amphi-Atlantic distribution of *F. binza* and further demonstrate that discrete morphotypes on either side of the Atlantic are genetically identical mimics of locally abundant congeners. Phylogenetic network analysis indicates extensive hybridization among *Felimida* species, likely contributing to the pattern of mitonuclear discordance recovered in some individuals. In all, the phylogenomic tools applied here significantly improve resolution at both deep and shallow evolutionary scales and provide critical insight into the generation of diversity in this aposematic group.

Molecular insights into bivalve photosymbiosis

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Photosymbioses between heterotrophic hosts and autotrophic symbionts are evolutionarily widespread and ecologically significant. However, the molecular mechanisms underpinning these symbioses remain underexplored, particularly in non-cnidarian organisms such as bivalves. In bivalves, obligate photosymbiosis is confined to two extant lineages: the heart cockles (subfamily Fraginae) and the giant clams (subfamily Tridacninae), both of which form symbiotic relationships with dinoflagellate algae of the family Symbiodiniaceae. In this work, we investigated the molecular evolution of photosymbiosis from the transcriptome and genome perspectives. We first examined gene expression patterns in the photosymbiotic bivalve *Fragum sueziense* under varying light conditions to identify potential molecular pathways involved in molluscan photosymbiosis. We discovered that the presence of algal symbionts significantly influences host gene expression in symbiont-containing tissues, revealing both novel and established molecular mechanisms of animal-algal photosymbiosis. Notably, many of these molecular pathways are shared with distantly related host lineages, such as cnidarians, suggesting that parallel and/or convergent evolution plays a crucial role in shaping host-symbiont interactions across these groups. Further, we investigated the long-term impact of photosymbiosis on bivalve genome evolution using giant clams from the genus *Tridacna*. Comparative genomic analyses highlighted substantial symbiosis-driven genomic features, including the expansion of gene families related to immunity and shell formation, as well as a significant proportion of lineage-specific genes. Remarkably, genomes of several *Tridacna* species include large proportions of repetitive elements, likely a consequence of a symbiosis-adapted immune system. Moving forward, elucidating the molecular mechanisms of photosymbiosis in marine bivalves will advance our understanding of the fundamental processes driving the evolution of photosymbiosis, and the genomic factors contributing to organismal diversification and phenotypic innovation.

Rocks and spray: Mineral supply constraints on shell form in *Oreohelix* and *Cerion*

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Geographic variation in metabolic resources necessary for functional trait expression can limit the distribution of species. For species that need to produce and maintain biomineralized traits for survival, spatial variation in mineral macronutrients may constrain species distributions by limiting the expression of biomineralized traits. Here, we examine how geographic variation in CaCO3 can limit the expression and distribution of heavily biomineralized shell ornaments in two highly speciose land snail systems: montane *Oreohelix* from Western North American and coastal Bahamian *Cerion*. By integrating isotopic, distributional, and shell measurement data, we show that CaCO3 availability constrains ornamentation expression in both systems but with key discrepancies that are associated with organismal ecology and differences in environmental setting. This trait-environment relationship shared across multiple land snail systems provides a basis for future investigations of CaCO3 macronutrient constraints on shell form and highlights the diverse pathways this resource can follow to influence terrestrial mollusc biomineralization.

Gene expression atlas of a kleptoplastic sacoglossan, *Plakobranchus ocellatus*, over its life history

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Plakobranchus ocellatus (Heterobranchia, Sacoglossa) exhibits kleptoplasty, whereby it sequesters photosynthetically active algal chloroplasts within animal cells. We found no photosynthesis-related algal genes in the molluscan nuclear and mitochondrial DNA through genome sequencing and comprehensive bioinformatics analysis. This result suggests that photosynthetic capabilities can be transferred between species through organelle sequestration without horizontal gene transfer. However, the molluscan factors facilitating kleptoplasty are still under debate. We are using the cost- effective RNA-seq method (Lasy-seq) to identify these factors. In sacoglossans, gene function prediction is primarily based on sequence homology, but temporal information on gene expression can improve the accuracy of functional ortholog prediction. Gene expression profiles of *P. ocellatus* at various life stages will clarify the set of conserved animal genes involved in the development and diurnal cycles and investigate how these genes adapt to the unique physiological process of photosynthesis. Additionally, this gene expression catalog will aid in identifying unknown genes involved in the kleptoplasty phenomenon. Today, we will present our progress on the early life stages and diurnal gene expression of *P. ocellatus* type black.

Origin and biogeography of the colourful sap-sucking sea slugs genus *Thuridilla* Bergh, 1872 (Mollusca, Gastropoda, Heterobranchia)

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Thuridilla Bergh, 1872 is a lineage of colorful, herbivorous sea slugs (Gastropoda: Sacoglossa) distributed worldwide in temperate and tropical waters. Recent work revealed an exceptionally rapid, cryptic radiation of 13 species in the Indo-Pacific, raising questions about mechanisms of speciation in this group. Here, we studied the diversification and historical biogeography of *Thuridilla* using a nearly complete taxon set (28 out of 32 recognized species), and a multi-locus approach combining two mitochondrial (COI and 16S) and one nuclear gene (H3). Species relationships, diversification times, and ancestral geographical ranges were inferred using relaxed-clock methods together with Bayesian discrete p hylogeographic analyses under three calibration scenarios using the oldest fossil known of Sacoglossa, *Berthelinia elegans* Crosse, 1875 and tectonic events. *Thuridilla* is hypothesized to have an Indo-West Pacific origin between 28–18 Mya during the Early Miocene. The highest diversity of the genus is in the Western Pacific (14 spp.) with a peak in the East Indies Triangle (18 spp.), whereas the Atlantic is depauperate with only four species occurring in this ocean basin. In the western Pacific, speciation likely occurred during transient allopatry during Plio-Pleistocene sea-level fluctuations. The limited diversity of the Atlantic Ocean is hypothesized to be derived from Miocene vicariant events associated with the closure of the Tethys Sea, dispersal across southern Africa, or long-distance dispersal across the East Pacific Barrier prior to the uplift of the Isthmus of Panama. *Thuridilla* is absent in the Eastern Pacific, potentially resulting from the extinction of ancestral lineages following the uplift of the Isthmus of Panama.

It's the way your mucus smells: conspecific recognition in a simultaneous hermaphroditic sea slug

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In marine invertebrates such as simultaneous hermaphroditic sea slugs with no secondary sexual traits or specific visual displays, mechanisms to communicate information related to the quality and fecundity status of a potential mate may be crucial for ensuring higher fitness outcomes. We show that the sea slug *Doto chica* is able to recognize conspecifics in absence of adult slugs via mucus trails, and that there are differences in the chemical composition of mucus based on quality of a partner. These results provide evidence of the presence of chemical components in the mucus that may aid in mate finding and choice in these hermaphrodites.

Discovery of a population of the temperate sacoglossan sea slug *Elysia chlorotica* in a subtropical habitat

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Elysia chlorotica is a sacoglossan sea slug found primarily in the Northeastern Coast of the United States and Canada. The slug has been extensively studied for its ability to retain functional chloroplasts sequestered from its algal food for many months post feeding. Although there have been a few isolated reports with limited detail of *E. chlorotica* from Florida and Texas from the 1980's, no large populations have been previously reported like those seen in temperate climates. Here we report on a large population of *E. chlorotica* found within Tampa Bay, Florida in February 2024 and compare them to specimens from Martha's Vineyard Massachusetts. Gross morphology and radular dentition were very similar between the two populations. The Tampa Bay specimens were found living on a mat of the algae *Vaucheria litorea* in a shallow mangrove swamp, the same algae fed upon by the slugs in Martha's Vineyard. Dietary DNA barcoding confirmed that they were also feeding upon this alga. At the time of discovery, the Tampa Bay slugs were laying eggs and beginning to senesce, similar to the life cycle for specimens from Massachusetts. By the end of March 2024 all the slugs had died, and the algae had vanished from the area. Although there are some population level differences, the gross morphology, radula shape, diet, ecology, and genetic sequences all support the fact that both populations are *E. chlorotica*.

Cerberilla sea slugs: Mapping diversity and phylogeny

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Throughout several expeditions to the South Pacific Island of New Caledonia, several specimens of Cerberilla sea slugs have been collected. While these sea slugs have been classified in the family Aeolidiidae, recent genetic analysis has generated some doubt as to whether they should be classified this way. For this project we examined nineteen specimens collected in Nouméa, New Caledonia, each of which have gone through DNA extractions. Three specific genes were amplified and analyzed: mitochondrial CO1 and 16S, and nuclear Histone H3. The resulting sequences were analyzed using phylogenetics (MrBayes) and species delimitation (ABGD) software and compared with other sequences of Cerberilla available in GenBank. Dissections were then performed for further analysis of the specimen's morphology to allow for a full description of the species. This project will lead to further discovery and description of potentially new species and provide valuable data to understand the evolution of these under-researched marine organisms.

Reciprocity and field expeditions in the Galapagos: Snails as a vehicle for inquiry and cultivating relationships

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Scientists frequently conduct research in field locations but too often collect data and leave without significant engagement with local communities. As a result, there are missed opportunities to communicate the broader scientific impacts and why a specific ecosystem is important to research. Reciprocity has emerged as a key component for how we interface with the landscape and communities associated with our field work, in this case, the Galapagos Archipelago. Dr. Miller will discuss specific efforts in the Galapagos that highlight the reciprocal engagement with local communities, students, and teachers, as well as lessons learned from working with Indigenous communities in the US.

Holoplanktonic gastropod diversity in the Isabel Island Marine Zone National Park, Nayarit, Mexico

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Holoplanktonic gastropods are classified into two taxonomic groups: pteropods (Heterobranchia: order Pteropoda, suborders Euthecosomata, Pseudothecosomata, and Gymnosomata) and heteropods (Caenogastropoda: superfamily Pterotracheoidea, families Atlantidae, Carinariidae, and Pterotracheiidae). In recent years, thecosome pteropods and atlantid heteropods have been recognized as 'the canaries in the coal mine,' as their aragonite shells make them prone to being affected by ocean acidification. Despite their importance as indicators of environmental change, their distribution and abundance are still unknown in many areas of the Pacific Ocean. The continental shelf of Nayarit is recognized as an oceanographic transition zone where insular ecosystems are a prominent feature, contributing to biological diversity and productivity. Among them, the Isabel Island Marine Zone National Park is located on the continental shelf of Nayarit. However, until now, there has been no knowledge about the zooplankton diversity inhabiting this area. Therefore, this work represents the first record of holoplanktonic gastropods in the area. The study was based on 10 zooplankton samples obtained during 2020-2022. The samples were collected at three sites in the north and eastern region of the island using horizontal trawls at a depth of 1 m, with a cylindro-conical net measuring 110 cm in length, 40 cm in diameter, and with a mesh size of 300 µm. To obtain the holoplanktonic gastropods, the samples were processed without fractioning. A total of 3,307 organisms belonging to 22 species were found, including 11 heteropods and 11 pteropods.

Evolution of Galapagos land snail-associated microbial communities

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The ecology and evolution of Galapagos land snails in the genus *Naesiotus* have been studied for over two decades, providing insight into island biogeography and patterns of biodiversity. However, little is known about the microbial relationships with the snail hosts and how those relationships may be evolving as the host snails have colonized and diversified into most of the available niches in the Galapagos Islands. There are many ways that members of a microbiome can be hugely important for host health, including controlling diet breath, pathogenic effects, and other symbiotic relationships. My project characterizes, for the first time, the microbial communities living in these snails and their connections with the environmental microbiome and host ecology. We account for many ecological variables that drive community assembly in most of the macro-communities and discover whether those same factors are important for creating differences in the microbial communities of the host snails and the substrates they live on. We are especially interested in whether island ages affect microbial diversity like they do in the snail hosts and what that means for microbial barriers to dispersal. This project allows us to understand some of the environmental factors that are affecting microbiome communities' assembly/composition and will provide clues to their function.

Taxonomy of the family Eulimidae Philippi, 1853 (Mollusca: Gastropoda) in the Tropical Eastern Pacific

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The family Eulimidae Philippi, 1853 comprises marine gastropods parasitic on echinoderms. Eulimids are distributed in all oceans, along large latitudinal and bathymetric ranges. These snails are characteristic for their small size (~5 mm) and lack of sculpture on their shells, which make them seem alike. Since the family is taxonomically complex, it uses to be overlooked in faunistic studies. This means we are missing a large amount of knowledge on molluscan diversity, especially if we consider that eulimids can be one of the richest families in tropical waters. This taxon has been studied in the Tropical Eastern Pacific (TEP), however the identity of many species is not clear and there is evidence that new ones can be found. The main goal of this study is to know how many and which eulimid species inhabit the Tropical Eastern Pacific. We carried out the examination of specimens from different Mollusk and Echinoderm collections in Colombia, Mexico and the United States. Additionally, we collected live specimens with their hosts. The material was compared and photographed, descriptions were made for each species and their records were updated. Our revision resulted in 19 genera with 46 species, 11 of which are considered new. We discuss the relation of the TEP Eulimidae with those from the Western Atlantic and the Western Pacific. This is the first work in more than a century dealing with this family in the TEP in a more comprehensive way.

Using the biology of fish-hunting cone snails to facilitate biomedical discovery

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The superfamily Conoidea are a biodiverse group of venomous neogastropods (>10,000 species). Among the most remarkable are the 100 to 200 species of fish-hunting cone snails. There are eight lineages of piscivorous cone snails; conventionally, each is treated as a subgenus of *Conus*. A number of distinctively different fish-hunting strategies have evolved. Understanding which lineages use these different strategies has accelerated discovery of novel venom components evolved by a specific clade to facilitate prey-capture.

One large group of piscivorous *Conus* (in the subgenus *Phasmoconus*) has evolved venom components that inhibit sensory -motor coordination by rendering proprioceptive circuitry in potential fish prey non- functional. Because some *Phasmoconus* use a highly specialized ambush strategy to capture fish, the role of an inhibitor of proprioception in the venom armamentarium of this group of fish-hunting *Conus* can readily be rationalized. This example illustrates how an individual bioactive *Conus* venom peptide can not only be understood at a molecular level, but can be used to identify the specific cell type and physiological circuit targeted, and the behavioral consequences on the envenomated prey. This information is key to exploring potential biomedical applications.

Drug discovery in molluscs – A brief review of current literature

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Molluscs have played pivotal roles in biomedical research. For example, *Aplysia californica*, the California sea hare, has long been used as a model organism for studying the nervous system due to its atypically large neurons. Molluscs are also rich sources of natural products; these are often secondary metabolites used as chemical defense against predation or produced in response to stressors in the environment. More than a dozen drugs isolated or derived from marine organisms have been approved by the FDA and two notable drugs of molluscan orgin are ω-conotoxin MVIIA ziconotide and brentuximab vedotin. In 2004, ω-conotoxin MVIIA ziconotide, isolated from the cone snail *Conus magus*, was approved as an analgesic and is far more potent than morphine. In 2011, approval was granted to brentuximab vedotin, an antibody-drug conjugate consisting of the chimeric anti-CD30 monocolonal antibody and the drug Monomethyl auristatin E, which was synthesized from dolastatins, originally isolated from the sea hare *Dolabella auricularia*. These two examples highlight the importance of molluscs as a source of biomedically important compounds. Here, we will examine and highlight more recent areas of research that utilize molluscs related to drug discovery, specifically molluscan-derived antiviral and antibacterial compounds produced as a line of defense against pathogens. We will focus on how they are isolated, identified, and validated using *in vitro* models.

How does Ocean Acidification impact the biomineralization of abalone species: from a transcriptomic and physical shell analysis approaches?

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Ocean acidification (OA), derived from the increasing concentration of anthropogenic CO2 and its subsequent changes in seawater carbonate chemistry, threatens marine life, particularly calcifier mollusks like abalone species (*Haliotis* sp.). OA negatively impacts the biomineralization process of shell construction and, which is, therefore, the main defense mechanism against predation and environmental pressures.

This study aimed to evaluate the effect of ocean acidification on the biomineralization process based on transcriptomic and physical shell analyses of two native Mexican abalone species, the red abalone (*Haliotis rufescens*) and green abalone (*H. fulgens*), after three months of exposure to two acidified conditions: pH= 7.8 and pH= 7.5, and control ambient conditions pH≈ 8.0. The pH was controlled by bubbling CO2 into seawater containers of the experimental system using Aquamedic pH computers and solenoid valves. As quality control of the CO2-enrichment experiment, weekly water samples for total alkalinity and dissolved inorganic carbon determination were taken, and complementary *p*CO2 and aragonite saturation state (Ωara) were calculated from the measured parameters of carbonate chemistry. In de-occupied shells, we have determined the weight:shell length ratio, shell thickness, and relative proportion of shell layers. In addition, we have obtained the mineralogical composition of the prismatic layer. We observed a reduction in the shell thickness, a decrease in the relative proportion of the prismatic layer, and alterations in the mineralogical composition under acidified conditions. However, the impact of OA varied between the abalone species, with the shell of *H. fulgens* being more affected. The following steps will be focused on understanding the metabolic process underlying these dissimilar responses through the gene expression evaluation of biomineralization-involved genes, which will be achieved by the constructed RNA-Seq libraries from mantle tissue (44% GC content and 29.2 M reads mean).

Land snails on Gull Island, Michigan: Influenced by glacial history?

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Of more than 565 islands in the upper three U.S. Great Lakes, land snails have previously been reported from only eight islands. To start filling this knowledge gap, we report land snails from Gull Island in NE Lake Michigan, the most far out of the 14 islands in the Beaver Island Archipelago and smaller than the other eight islands from which snail faunas have been reported. Consistent with Island Biogeography theory, this smallest and most distant island has the fewest species of these nine islands. But could glacial history also influence which snails occur on the islands?

Land snail faunas on islands in northern Michigan appear more like faunas farther north on the Upper Peninsula than those on the adjacent northern Lower Peninsula. Glacial history starting about 18,000 years ago had ice covering the area, then the retreating glaciers exposed the land, which would have become populated by cold-adapted snails, then lake levels rose isolating the islands from the mainland, so when warm-adapted snails arrived in the area, they occupied the mainland but had a water obstacle hindering dispersal to the islands. Under this hypothesis, snail species occurring on both islands and mainland are expected to be more cold-adapted, while those on the mainland but absent from islands are expected to be warm-adapted. This pattern holds for 4 larger (dime to quarter sized) species. The pattern is less clear for smaller species, perhaps because smaller species might disperse across water more easily.

The Pacific oyster *Magallana gigas* cultured in Bahia San Quintín, Baja California, affected by a new poyldorid species *Bocardiella vicentina*

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The Magallana gigas oyster or Japanese oyster is one of the most important bivalve molluscs and production worldwide. In Mexico, the largest production of this bivalve is obtained in San Quintín Bay (BSQ), in the state of Baja California, which is around 2,000 tons per year. Bivalve molluscs in general and Pacific oysters are exposed to infestation by borer worms of the Spionidae family that make up the *Polydora-Boccardia* complex. One of its main characteristics is that they can settle on calcareous shells and then drill them, forming tunnels where they establish a shelter to live. Recent studies confirmed the presence of two phenotypes in the Bay, making their correct identification essential. The aim of this study was to characterize both phenotypes morphologically and genetically. For this purpose, cultured oysters were obtained from nine farms in the Bay and the polydorids themselves, which were identified by conventional taxonomy under a microscope and following dichotomous keys, were extracted. Additionally, this identification was complemented with the help of scanning electron microscopy (SEM). For genetic characterization, Sanger sequencing and next generation massive sequencing were performed. The results obtained from the conventional taxonomic analysis indicated that one of the phenotypes corresponds to *Polydora websteri*, which was confirmed with the molecular genetic analysis, which indicated a 99.5% similarity with this species. The conventional taxonomic analysis and by SEM of the second phenotype indicated that it is a polydorid of the genus *Boccardiella* without coinciding with any of the species described for the genus. The analysis of the mitochondrial genome corroborated its belonging to the indicated genus, but with little similarity (79.85%) with one of the described species, *Boccardiella hamata*, corroborating that it is a new species called *Boccardiella vicentina*. Likewise, specific markers were designed to identify this new species, providing a very useful diagnostic tool for monitoring this epibiont.

Identifying food resources for threatened Hawaiian land snails

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Estimates indicate that 35% of the 759 Hawaiian land snail species remain, with 100 more species under threat of imminent extinction. Understanding the diets of critically endangered Hawaiian land snails is foundational for the development of effective conservation plans, but our current understanding of the microbes composing Hawaiian snail diets remain rudimentary. Meyer et al. (2023) proposed a new framework for elucidating which microbes may form the foundation of Hawaiian land snail diets by comparing microbial assemblages on plants that are preferred and avoided by snails. Here, we tested a similar hypothesis that microbial assemblages (bacterial and fungal) differ on plants preferred and avoided by snails and expanded the scope of the research to include three sites in wet (Mount Kaʻala Natural Area Reserve and Puʻu Ohia) and montane mesic forests (Honouliuli Forest Reserve) on Oʻahu. Using Meyer et al.'s (2023) data from Mount Kaʻala, we also investigated how microbial compositions change across years and seasons. We found that: (1) microbial assemblages differed on preferred and avoided plants across sites, and (2) while assemblages differed among years, preference category (preferred and avoided) had a larger influence on microbial assemblages. Our findings illustrate how Meyer et al.'s (2023) approach is a potentially powerful tool for developing hypothesis on key microbes composing Hawaiian land snail diet. We have identified bacterial and fungal OTUs that likely play a role in plant selection and may form the foundation of their diets. These microbes should be further tested in feeding trials to evaluate their influence on snail fitness and fecundity. This work is part of a crucial first step in elucidating land snail diets, ultimately informing: (1) efforts in captive rearing of critically endangered land snails, (2) habitat restoration efforts in native forests, and (3) habitat quality assessments and monitoring practices.

Hydrothermal venting, microbiomes, and the complex egg brooding behavior of *Muusoctopus* sp. in Costa Rican deep-sea seamounts

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Seamounts and deep-sea mounds, rocky edifices scatter across the ocean that together represent a combined global surface area approximating that of the African Continent, are highly underexplored benthic biodiversity hotspots. Over a decade ago, an expedition exploring heat transfer and water movement across sea mounds in the Costa Rican Pacific made a completely serendipitous discovery: hundreds of deep-sea octopus (*Muusoctopus* sp.) brood their egg clutches exclusively at focal sites of relatively warm (10-15°C) hydrothermal venting on rocky outcrops. This was a novel observation at the time highlighting the ecological importance of sea mounds on many species including emblematic deep-sea octopods. To further explore the ecology of sea mounds in general, and potential influence of the venting fluid microbiome on deep-sea octopus nursing behavior, specifically, we set sail on two expeditions in 2023 on the Schmidt Ocean Institute's R/V Falkor (too). We explored *La Pampa Submarina*, a deep-sea region off the Nicoya Peninsula of Costa Rica. We report a fifth site of widespread octopus nurseries correlated with warm hydrothermal venting at La Pulpería Hill, a previously unexplored rocky structure, and showcase strategies aimed to test the following questions in the future: Do octopus brood at hydrothermal venting sites because the fluids ensure a long-term sediment-free surface for their egg clutches? Do octopus brood at hydrothermal venting sites because warmer temperatures speed embryo development? Does the microbiome of the venting fluids provide an advantage to the developing embryo or brooding females?

A dry collection talk: Revitalizing the San Diego Natural History Museum Marine Invertebrate Collection

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In 2021, the San Diego Natural History Museum (SDNHM) received funding from the US Institute of Museum and Library Services to improve the condition, management, and accessibility of our dry Marine Invertebrate Collection. For nearly 25 years, the collection has been unstaffed and nearly inaccessible, but with new staff and funding, this underutilized scientific resource is being revived. The collection is believed to house millions of regionally, temporally, and taxonomically important specimens, but suffers from data inaccessibility and inadequate physical and taxonomic curation. This project is mitigating these weaknesses through specimen digitization, collection analysis, and rehousing. Historically, each specimen lot in the collection was recorded on a paper catalog card. After scanning all 93,000+ cards, we employed Optical Character Recognition (OCR) technology and large-scale data cleaning to produce an initial digital dataset, now available online via InvertEBase. Review by trained volunteers maximized our dataset's quality, culminating in the collection's first comprehensive and publicly accessible digital specimen catalog.

Collection analyses yielded interesting findings, including an incredible geographic spread, extreme data quality disparities, and many unlabeled specimens and outdated scientific names. Alongside digital advancements, this project is improving physical storage and expediting specimen retrieval through drawer reorganization, labeling with updated scientific names, modernization of drawers and cabinets, and creation of an efficient specimen inventory locator. This project lays the groundwork for future curatorial and scholarly work in this collection, through enhanced collection accessibility and ease-of- use. A refined triage strategy informed by the digitized collection and aided by organizational improvements of this project will guide upcoming efforts for potential deaccession of irrelevant materials. We are exploring collaborations with other institutions and research initiatives to maximize the scientific impact of the collection. The SDNHM is now positioned to revitalize this collection as a leading, efficient, and lasting resource for the North Pacific region.

Habitat conditions and available resources shape the lipidome of the tropical photosynthetic sea slug *Elysia crispata*

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Sacoglossan sea slugs inhabit the interface between two marine biospheres: fauna and algal flora. Macroalgae serve not only as a food source but also as providers of functional chloroplasts, which integrate into sea slug cells while they digest other cellular components of the algae. These sequestered chloroplasts, known as kleptoplasts, remain functional for variable periods. This strategy enables these mixotrophic animals to acquire energy through both heterotrophic digestion of algal compounds and autotrophic pathway via kleptoplast photosynthesis. Chloroplasts present a unique lipidome profile that is preserved in sea slug tissues. Consequently, photosynthetic sea slugs exhibit a complex lipidome that includes a diverse array of lipids, encompassing unique compounds from both animal and algal tissues.

The objective of this study was to investigate the effect of habitat on the lipidome of the photosynthetic sea slug *Elysia crispata*. Individuals of *E. crispata* were sampled in two habitats in the North-western tropical Atlantic (Sistema Arrecifal Veracruzano and Mahahual) under two feeding conditions: in their wild state and after one week of starvation. The polar lipidome of *E. crispata* was analysed using liquid chromatography and tandem high-resolution mass spectrometry (LC-HR-MS & MS/MS). Significant differences were identified in the abundance of structural and signaling phospholipids (PC, PI, PG, PS, CL), suggesting different nutritional and physiological states between populations. The results suggest that individuals from Veracruz had a better nutritional state, while those from Mahahual seemed to have experienced periods of food scarcity before sampling. The composition of exclusive lipids from sequestered chloroplasts (MGDG, DGDG, SQDG) demonstrated a clear separation by habitat rather than by feeding conditions, validating the nutritional plasticity of *E. crispata* to acquire chloroplasts from different macroalgal sources based on available resources. This study confirms the advantages of using lipidomics as a tool to enhance our understanding of the ecology of marine invertebrates.

Detrimental non-target effects of the biocontrol candidates in the genus *Phasmarhabditis* (Nematoda, Rhabditida) on the Reticulate Taildropper (*Prophysaon andersonii*; Ariolimacidae)

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Many species of terrestrial gastropods are serious agricultural pests. An Integrated Pest Management (IPM) approach is one that seeks to be effective while minimizing hazards to the environment including humans. For terrestrial gastropods, an IPM often uses sensible pesticide use, biorational molluscicides, and where available biological control via the nematode roundworms *Phasmarhabditis*. Two species of *Phasmarhabditis* have been made commercially available as biological control agents in Europe, where it is thought that these roundworm species are native, and there is interest in using these nematodes in North American agricultural systems. Biological control efforts have a tumultuous history, and there can be multiple reasons for failure of biological control; here, we test that the biological control agent might negatively impact non -target native species. Terrestrial gastropods are perhaps the most impacted fauna in the ongoing mass extinction, and North America has a rich terrestrial malacofauna. We must take care to minimize the pressures that this fauna might receive from human impacts. Here, we examined the effects of three species of *Phasmarhabditis* nematodes (*P. papillosa*, *P. hermaphrodita*, and *P. californica*) on the Reticulate Taildropper (*Prophysaon andersonii*), a species of slug native to the Pacific Coast of North America. We subjected 54 *P. andersonii*, in three replicates of three individuals, to two rates (high and low) of the three nematode species. All 54 were dead by Day 23, whereas 15 of 18 (83%) of the slugs in the water control treatment were still alive. These results provide direct evidence that *Phasmarhabditis* nematodes, including two species that are commercialized biological control agents, infects and kills the non-target slug *Prophysaon andersonii*. This research adds to growing evidence that *Phasmarhabditis* nematode species cause significant mortality in a wide range of non- target terrestrial gastropods including native species. We strongly caution against using these species as biological control agents in North America.

Oxychilus spp. land snail presence and distribution in Southern California

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Introductions of non-native terrestrial gastropods into California have occurred since the early 1900's. For some species, determining their identity has been straightforward; with others, it is challenging. The latter is particularly true for members of the European land snail genus *Oxychilus*. Three species of *Oxychilus* are reported to occur in Southern California as non-natives; *O. draparnaudi, O. cellarius,* and *O. alliarius*. *Oxychilus cellarius* and *O. draparnaudi* are so morphologically similar that experienced malacologists struggle to differentiate between them. In this study, we aimed to determine which species of *Oxychilus* are present in Southern California using an integrative taxonomic approach. Approximately 150 *Oxychilus* spp. tissue samples from museum collections and newly collected specimens were sequenced for CO1, ITS2, and 28S genes; dorsal mantle characters (*'phylacites' and longitudinal grooves*) from live-collected snails were drawn and photographed for ~50 specimens; and radulae and jaws from a dozen specimens were imaged by SEM. Herein, we report that *O. draparnaudi* is the most widely distributed *Oxychilus* species in the region, and that its dorsal mantle morphology is more variable than reported in the literature.

Live-dead distinctions and why they are important

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Molluscan shells can persist on beaches for centuries or millenia, so their occurrence in an area does not mean that a species still lives there. This gap in data standards has recently been addressed by the addition of a field for "vitality" in the Darwin Core, which is a standard for data exchange for natural history collections. Adding this field to millions of previously digitized records can be accelerated by bioinformatic approaches. A case study of three species of arcoid bivalves (*Noetia ponderosa*, *Lunarca ovalis* and *Anadara transversa*) found in the northeast US demonstrates the importance of live-dead distinctions. During the previous interglacial period, *Noetia ponderosa* lived as far north as Massachusetts, but it does not currently live north of Chesapeake Bay, as shown by observations on iNaturalist and specimens vouchered in museum collections. Integration of data on portals such as InvertEBase, iDigBio and GBIF can accelerate visualization of data and aid in finding specimens appropriate for addressing particular questions.

How molluscs make their defensive pyrones

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Sacoglossans molluscs make large amounts of pyrone polyketides, which are implicated in chemical defense, preservation of the photosynthetic apparatus, and other properties. These molecules are made by a recently described family of enzymes, the animal fatty acid synthase-like polyketide synthases (AFPKs). Although they belong to a clade including the animal fatty acid synthases that make relatively simple lipids, the AFPKs are responsible for producing diverse and structurally complex polyketides in molluscs, arthropods, and perhaps other taxa. Advances in bioinformatics, protein structure, and biochemical function of AFPKs reveal how enzyme sequences lead to the distinct chemical families underpinning sacoglossan biology. For example, some AFPK families synthesize short pyrones involved in chemical defense, while others make longer polyketides associated with long-term photosynthesis in the molluscs. AFPKs are part of a greater biochemical diversity of lipid metabolizing enzymes found in nearly every molluscan genome, most of which represent totally unknown pathways and molecules.

Incorporating molluscs into educational activities and programs for underserved K-12 students

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I teach grades 9-12 at the Downtown Magnets High School, in the Los Angeles Unified School District (LAUSD), serving a student population that remains heavily under-represented in STEM fields. Before completing my Master of Arts in Teaching (MAT) degree , I did thesis research for my M.S. of Biological Sciences on cryptic species in the Elysia marginata complex, marine heterobranchs that are widely studied for kleptoplasty, extraordinary regeneration abilities, and anticancer drug discovery. I received a Blinks scholarship to study at the Friday Harbor Laboratories as a graduate student, and COAST undergraduate funding. I will describe how this background in malacology informs my teaching and outreach as I develop new activities, lessons and programming for diverse students.

I aim to expose my students to marine and mollusc science and encourage them to consider college and STEM degree pathways, so they have opportunities these fields offer. I developed a field-trip program to bring students to the lab where I did my Master's degree, showing them a college campus and research setting, and engaging students in thinking about systematics and malacology in an accessible manner. I will discuss challenges such as starting a new course in marine biology never offered before at an under- resourced high school, and how to infuse a fixed curriculum with examples drawn from molluscan research. Examples include squid dissection to illustrate adaptation; an ammonite activity to highlight evolutionary concepts; shell classification to address biodiversity; cone snails as examples of predation; and gastropod phylogeny and barcoding to explain mitochondrial versus nuclear genes. Other efforts to expose students to opportunities in STEM that leverage my background in gastropod systematics include bringing students to the LA Science Center, facilitating student participation in a nanotechnology competition at UCLA, and engaging with NSF-funded summer research through RET and RAHSS programs.

Plant preferences of Hawaiian arboreal snails and their conservation implications

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Effective conservation of Hawaiian land snails and other members of the neglected majority (invertebrate animals) remains hampered by a lack of knowledge of foundation ecology. For example, determination of which plants are necessary for snail survival is relatively unknown, and understanding of the reasons for plant preferences is limited. As part of a large-scale investigation of native arboreal snail ecology across the islands, we investigated plant preferences at nine sites on Oʻahu, Hawaiʻi across the islands' two main mountain ranges; the Waiʻanae and Koʻolau ranges. At each site, we set out six to eight 5x5 meter plots, each divided into 4 transects and 36 transect points. We then used a point-intercept method to determine plant survey coverage. After plant data was collected in each plot, surveyors were then assigned a plant species and recorded the number of snail species and total snails on that plant in the plot. Across all nine sites, we collected plant-preference data from 57 plots, 136 plant species, and observed 5512 snails. We found that snails preferred some mid-story tree species, such as *Psychotria mariniana* (*kōpiko*), and *Antidesma platyphyllum* (*hame*), but avoided some of the most abundant plant species in Hawaiʻi's forests, including *Metrosideros polymorpha* (*ʻōhiʻa lehua*) and *Cibotium* spp. (*hāpuʻu*). These data support the hypothesis that protecting and restoring diverse plant assemblages with a focus on key plant species for snails may enhance native Hawaiian arboreal snail conservation. These data also provide opportunities for research needed to develop and evaluate effective snail conservation strategies. Continuing research is exploring if (1) snail fitness is enhanced when feeding on biofilms from preferred plants, and if (2) microbial assemblages on preferred and avoided plants differ across islands. Furthermore, these complex ecological interactions may be applied to gain a broader understanding of invertebrates communities in Hawaiʻi's native forests.

On the Frequency and Correlates of Sinistrality in *Campeloma*

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Shell collectors and biologists alike have long been fascinated by snail shells exhibiting a reversal of normal coiling direction. This fascination is due, at least in part, to the rarity of chiral reversal in most gastropod lineages. The frequency of reversed individuals in populations from which they are known varies substantially – in some groups (e.g. Camaenidae, Partulidae), the relative proportion of sinistrals and dextrals has been shaped by predation and sexual selection. A perplexing example of variation in the rate of chiral reversal is found in the genus *Campeloma* (Viviparidae), a group of ovoviviparous snails endemic to North America east of the Rocky Mountains. These normally dextral snails produce sinistral embryos at rates between 0.5 and 25%, but the observed rate of sinistrality in adults is usually less than half that of the embryonic young, suggesting high associated mortality. Unlike better-studied pulmonate models of chiral dimorphism, many *Campeloma* are asexual parthenogens. While parthenogenetic offspring are ostensibly genetically identical to one another and their parent, broods from both dextral and sinistral *Campeloma* mothers routinely contain both sinistral and dextral individuals.

To better understand the frequency and correlates of chiral reversal in the genus, we examined the *Campeloma* holdings of 7 North American malacological collections, counting the number of dextral and sinistral individuals in over 4000 lots (>50,000 individuals). In approximately half of these lots, we also counted and determined the chirality of all the associated embryonic snails. We present the preliminary results of our range-wide examination in geographic and evolutionary contexts, and discuss the relationships between sinistrality, survivorship, and reproductive mode.

An update on invasive non-marine molluscs and their spread in Hawaiʻi

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Invasive species are a threat to natural resources, agriculture, and human health. In order to create biosecurity plans, critical information regarding invasive species identification and their spread and establishment are needed. In the absence of these key data, resource managers and other stakeholders will find it challenging to reliably assess threats and prioritize resource management activities.

Historically, many invasive non-marine (including freshwater) snail species have been introduced to the Hawaiian Islands via the agricultural and horticultural trade. Once established, they often spread rapidly between nurseries and other related facilities. As part of ongoing efforts to monitor and manage the introduction and establishment of invasive snails in Hawaiʻi, we conducted 45 nursery/agricultural facility surveys in 2023-2024. Surveys consisted of timed searches by 2-3 experienced malacologists based on the size of the facility as well as any identification of previously undetected snail species. In total, we identified 57 invasive snail species and over 2000 individuals were collected. Three new species were recorded on the island of Oʻahu, bringing the total number of established non-native terrestrial molluscs in Hawaiʻi to 81 species. Effective mitigation and eradication strategies for non-native species requires early detection and accurate species identifications, as well as a clear understanding of their dispersal once established in Hawaiʻi. Our data indicate that long term monitoring of nurseries and agricultural facilities is effective in rapidly detecting new invasive species. However, without consistent funding and support for monitoring efforts, future invasive species will likely cause substantial economic and environmental damages before they are detected.

Population genomics of the Tennessee River drainage endemic Smooth Rocksnail, *Leptoxis virgata* (Gastropoda: Cerithioidea: Pleuroceridae)

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The Tennessee River drainage is a hotspot of freshwater diversity. The Smooth Rocksnail, *Leptoxis virgata,* is a freshwater gastropod in the family Pleuroceridae with a historical range that encompasses approximately 700 km of the middle and upper Tennessee River, including multiple tributaries. However, the species has suffered from range decline because of extensive impoundments on the Tennessee River. Currently, *L. virgata* is a candidate for listing under the U.S. Endangered Species Act. However, a robust conservation assessment for *L. virgata* is hindered by a lack of research on the species, including basic surveys and a complete absence of population genetic information. Using a 2b- RAD sequencing approach, we assessed the genetic diversity of remaining populations in tributaries of the Tennessee River. We also examined population structure and connectivity. Despite current habitat fragmentation, populations have high levels of genetic diversity and low inbreeding. Genetic structure analyses indicated that each sampled tributary holds a unique genetic cluster, or genetic population of *L. virgata*. We also observed downstream increases in genetic diversity and isolation by distance, patterns seen in many other riverine species. However, sampled populations are separated by six major dams. Therefore, gene flow inferred from population genomic data must predate dam construction, and population fragmentation could result in genetic drift and a loss of genetic diversity over a long enough time period. Furthermore, severe fragmentation leaves any given remaining *L. virgata* populations vulnerable to anthropogenic activities. Nevertheless, *L. virgata* is one of the most wide-ranging pleurocerids in the Tennessee River drainage, and persisting populations hold high levels of genetic diversity. Given population genomic data, particularly the number of populations with relatively high genetic diversity, *L. virgata* may not warrant listing under the ESA.

Steppingstones across the arctic: historical biogeography and evolutionary history of the amphi-Pacific mangrove snail *Cerithideopsis*

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The gastropod family Potamididae (Cerithioidea) is circum-tropical in distribution and comprised almost exclusively of mangrove specialists, whose earliest undisputed members appeared during the Eocene and are of Tethyan origin. The genus *Cerithideopsis* is one of the oldest living genera of potamidids and is found in mangrove and salt marsh habitats of the New World tropics and the Indo-West Pacific. They are thought to have been widespread throughout Tethys and the Americas by the Middle Eocene and their trans-Pacific distribution the result of climate-driven vicariance; possible explanations include cooling at the end of the Eocene or early Miocene aridity which restricted the distribution of mangroves, or the closure of the Tethyan corridor at the end of the Early Miocene. These scenarios hinge on the tenuous assignment of three fossils to *Cerithideopsis* from the Eocene of Peru and California. There are no other fossils until the Pliocene of the Western Atlantic ~2.4-5.4 MA, leaving a gap in the fossil record of ~30 MA. Our serendipitous discovery of an unrecognized potamidid species presents an alternative scenario. *Tachyrhynchus erosus* is found in the North Atlantic, North Pacific, and Arctic Oceans primarily in sublittoral habitats from 13 - 457 m and is currently classified in the Turritellidae. Analyses of a three- gene dataset (nuclear 18S rRNA and 28S rRNA, mitochondrial COI) reveal the species to be an unrecognized member of *Cerithideopsis* and sister to the Neotropical clade. Fossil calibration indicates that Neotropical *Cerithideopsis* and *Tachyrhynchus erosus* diverged ~29 MA during a time of high productivity under Oligocene Coolhouse climate conditions. The crown age of the Neotropical clade is ~16 MA which is much younger than would be expected under a vicariant hypothesis and indicates that stepping-stone migration via the NA Land Bridge is the most likely explanation for the current amphi- tropical distribution of *Cerithideopsis*.

Evolution of vision-guided defenses in file clams (Limidae)

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Predator-prey interactions promote dramatic innovations, such as complex eyes, through coevolutionary arms races. However, studies of such interactions often focus on the eyesight of predators, overshadowing prey vision as an important contributor to prey-predator dynamics. To date, there is no systematic investigation on the evolutionary connections between defense mechanisms and vision in bivalves. We propose File Clams (Limidae) as a novel marine molluscan system to assess trait covariation between defense and vision; limids exhibit diverse yet unconventional defense strategies, including tentacle autotomy, escape swimming, nesting, chemical defense, and warning signals. Combining their truly cosmopolitan distribution across all depths (from shallow reefs to deep sea >3200 m), Limidae is uniquely suitable for examining multi-trait covariations in relation to predator/prey- induced natural selection. Theoretically, if an organism can visually detect predators before an attack, it is beneficial to have a proactive defense strategy, i.e. preventing the attack from happening, such as warning signals. Otherwise, a reactive strategy, i.e. responding to attacks when they occur, might be less costly. This study established a Limidae molecular phylogeny using six genes to test this hypothesis.

Results show that the monophyly of Limidae is universally supported in our reconstructions; relationships within the family, however, remain unresolved. The genera *Limea* and *Limatula* are non- monophyletic and appear to be nested within *Ctenoides*. Trait correlation test shows that proactive defense is significantly correlated with neritic (high visibility) habitat and rarely occurs in species occupying bathyal (low visibility) habitats, supporting our hypothesis. If proactiveness is cued by visual predator detection, transition to deep waters with limited light might nullify the benefit for vision, thus favoring reactive defense. Future work should identify eye types and complexity in Limidae to directly characterize their visual abilities and further investigate multi-trait evolution in response to predation pressures.

Within and among species variation reveal if carrier snails (Family: Xenophoridae) are specialist collectors

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Carrier snails of the family Xenophoridae are known for their unique “collecting” behavior — agglutinating foreign objects such as other shells, corals, stones and sand grains to their own shell for camouflage, physical defence, or stabilization on soft sediments. Deep-water species purportedly specialize in collecting pointy objects to enarmour their shells against non-visual predators; shallow- water species instead collect various objects for visual camouflage. To explore the evolutionary pattern of these behaviours, we constructed a maximum likelihood phylogeny of xenophorids from nearly 500 specimens. Our phylogeny largely supports the validity of described genera, and revealed more than 10 potentially undescribed species. Intensity of collecting behavior, measured as shell area covered by agglutinants, appears conserved within genera. We further characterized collecting behavior by categorizing and counting agglutinants on museum specimens. We computed pairwise dissimilarity matrices for agglutinant assemblages amongst all 11 sampled species, and among 52 individuals of one wide-ranging shallow-water species (*Xenophora conchyliophora*). Most species including distant relatives showed significantly different collecting behaviours, except two Australian-endemic species that show high agglutinant similarity. However, we noted that by aggregating agglutinant counts across individuals (species trait means) one may overlook high intraspecific variation. The intraspecific variance in agglutinant dissimilarity within *X. conchyliophora* alone is comparable to the variance of 11 other *Xenophora* species combined, suggesting strong influence of local adaptation throughout the species range. In *X. conchyliophora* isolation-by-distance only accounts for a small part of the overall variance based on weak positive correlation between pair-wise geographic distance and shell attachment dissimilarity (R =0.3). Local adaptation can arise due to purifying selection reducing variation within a population. However, multiple adaptive optima throughout a species' range can lead to overall balancing selection on the species level, leading to high levels of intraspecific variation. Our results raise the question whether highly variable collecting behaviour within species is due to selection toward multiple local optima.

The biocontrol nematode *Phasmarhabditis hermaphrodita* infects and increases mortality of two life- stages of *Ariolimax columbianus*, the Pacific Banana Slug, in laboratory infectivity trials

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Maintaining biodiversity is crucial to an ecosystem's health and stability. Gastropods are by far the largest class within the phylum Mollusca, with over 60,000 described species. Despite this tremendous diversity, much scientific focus has historically centered on pest species, with less attention paid to the native fauna that inhabit diverse ecosystems and face threats from human activities. Malacopathogenic nematodes are currently sold as biocontrol products to control crop-damaging pest slugs. *Phasmarhabditis hermaphrodita* is one such nematode, sold as Nemaslug® on three continents. Although some advocate bringing Nemaslug® to US markets, it is currently not permitted in this country due to unknown effects on non-target species. While the lethality of *P. hermaphrodita* in pests is well- studied, there is less knowledge of effects on non-target gastropod species, such as the Pacific Banana Slug, *Ariolimax columbianus*. *A. columbianus* is not only an important decomposer in forest ecosystems, but also serves as a familiar cultural icon of the American Pacific Northwest. In this study, the potential impact of *P. hermaphrodita* on two life-stages of *A. columbianus* was investigated using laboratory infectivity trials. The ability of nematodes to kill both juvenile and adult-stage slugs was analyzed. We found that *P. hermaphrodita* caused 100% mortality in both slug life-stages, with a faster rate of mortality observed in juveniles as compared to adults. By contrast, only 4% of untreated control adults and 16% of control juvenile slugs died during the experiment. These results provide evidence that the biocontrol nematode *P. hermaphrodita* is lethal to a native, non-target species, *A. columbianus* in laboratory infectivity trials, with a differential mortality rate between juvenile and adult life-stages. Our results highlight the need for comprehensive non-target testing in evaluating the potential ecological impacts of biocontrol organisms and suggest that *P. hermaphrodita* might negatively impact terrestrial gastropod biodiversity in North America.

Scoping review of superfamily Octopodoidea in waters surrounding Japan using legacy data

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Museum specimens and databases are historically underutilized in modern ecological reviews, and this is especially true for cryptic marine species. With the advent of digital databases, museum records of specimens collected for past research are a valuable resource that can be used to document species distributions, update common names with accepted taxonomy, and assess historical trends in cataloging natural history. Capitalizing on this, we undertook a scoping review of fishery-targeted octopus species in Japan. Octopuses are famously cryptic animals which are a staple of Japanese culture and cuisine with evidence of human consumption dating back to Japanese prehistory. For this study, data were obtained from publically available, online natural history databases and revealed that fifty distinct species of octopus within the superfamily Octopodoidea have been cataloged from Japanese waters since the 1800s. Taxonomic assignments for each specimen in the compiled database were verified against accepted nomenclature in the World Register of Marine Species (WoRMS) and obsolete taxon assignments were substituted with accepted ones. Of the twelve Japanese octopus fishery targets, only three had publically available species distributions maps available via the Food and Agriculture Organization of the United Nations (FAO)– *Octopus conispadiceus*, *Amphioctopus fangsiao* (as *Octopus fangsiao*), and *Octopus sinensis*

(as *Octopus vulgaris*). Findings from our scoping review of museum data revealed *O. conispadiceus –yanagi-dako* in Japan– was the most archived species in Japanese waters. However, our determined distribution range for *O. conispadiceus* does not align completely with the FAO-reported range suggesting a possible systematic error related to mis-identity and/or taxonomic assignment in the latter database. Furthermore, conflicting reported ranges between museum specimen and FAO data suggests that a broad range review and revision of third-party databases is needed, not only for octopus but potentially for all fisheries species in order to resolve definitive baseline taxonomic and range identification.

Detecting species in snail feces: What the microbiome can tell us about captivity and conservation

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Hawaiian land snails are declining, and the remaining species are in danger of imminent extinction. Conservation efforts face significant challenges for rearing snails in captivity, and programs at the Bishop Museum and Hawaiʻi Department of Land and Natural Resources often suffer from periodic mass mortalities of snails with undetermined causes. Hawaiian arboreal snails feed on microbial biofilms on the surfaces of plants, while ground dwelling species feed on microbes and decaying plant matter. In captivity, both arboreal and ground dwelling species are fed a monoculture of fungus, with arboreal snails supplemented with fresh, wild native plant cuttings, and ground dwelling species offered artificially aged native plant cuttings. One explanation for mass die offs witnessed in captivity is the possible change in dietary microbial diversity over time. While little is known about snail microbiomes, microbiome diversity has been reported to decrease in elephants translocated from the wild to a captive environment. Such decreases in microbial symbiont diversity potentially lead to dysbiosis, a loss of beneficial symbionts and influx of pathogenic microbes. To assess temporal changes in the microbiome of captively reared snail populations, we have sampled species from four species of wild collected snails upon their arrival in the lab, and at three, nine, and eighteen weeks after starting captivity. We sequenced the V1-V9 regions of the 16S from 83 fecal samples using long read amplicon sequencing on the Oxford Nanopore Technologies MinION®. Using these data, we have characterized the microbiome of snail feces over time to better understand changes in bacterial communities for four endemic species (*Amastra intermedia*, *A. micans*, *A. spirizoma*, and *Laminella venusta*) of ground-dwelling snails. Further characterization of microbiome assemblages and diversity will help us better understand dietary changes and possible impacts to fitness in captive reared populations fed on different diets.

Listening to velveteen ears: Velutinidae of southern Oregon

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The Velvet Ear Snails of the family Velutinidae are a tricky bunch, often mistaken for nudibranchs with their fragile shell enclosed by colorful mantles. If you want to find one in the intertidal zone, look for their ascidian prey, and then, look closer, because their mantle coloration and texture often blend perfectly. Ascidians are often acidic, and in response, velutinids secrete copious amount of goo, often, it seems, more than their own body weight. Intertidal surveys from 2006 to the present revealed 2 new species and one possible genetically distinct variety, with a total of 7 species: *Lamellaria diegoensis, Limneria prolongata, Velutina* n.sp. 1, *Velutina* n.sp. 2, *Marsenina rhombica* and its ‘grey’ variety, *M. stearnsii,* and *M. zadei*. Molecular sequencing of CO1, 16S, 28S, and ITS loci placed the two new species in the genus *Velutina. Marsenina rhombica* contained a possible genetic variant, generally recognizable by its large size and mantle coloration. *Marsenia rhombica* was found on nine ascidian species; at the other end of the spectrum, *Velutina* n.sp. 2 and *M. stearnsii* specialize on one. *Velutina* sp. 2 has a restricted distribution, at four sites within 0.07° latitude, and can be found on the same rock year after year. Egg cases (formed in the ascidian tunic) and the larvae they contained were examined. Larvae matured to the echinospira veliger stage inside the egg cases. Egg cases, although found throughout the year, were most

frequently encountered in the fall. Abundance of the entire family and of species from year to year varied from almost absent to abundant. 2023 was a great year for *L. prolongata*, with all size classes observed, yet this species could hardly be found from 2014 to 2017.

Opening Pandora's Box: Unprecedented levels of sea slug diversity discovered in the fringes of the Coral Triangle

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While biodiversity discovery is deemed critical for conservation efforts in a rapidly changing Earth, government support for taxonomic research and systematics is inadequate. The void is sometimes filled by non-traditional sources of funding such as private foundations and citizen science programs. Here we examine an example of how an eclectic but focused effort has resulted in the discovery of an unprecedented level or sea slug diversity.

New Caledonia is an archipelago located in the south Pacific Ocean, just outside the Coral Triangle. Because of its relatively isolated geographic location, New Caledonia has been hypothesized to contain lower levels of biodiversity than comparable land masses within the Coral Triangle. However, several research expeditions and an untiring citizen scientist effort has produced numbers of morphospecies comparable to well-studied areas in the Philippines, often regarded as "the center of the center" of marine biodiversity. Moreover, molecular studies on those morphospecies have revealed even higher numbers of cryptic and pseudocryptic taxa. The questions now are: Where is the end? How many new species remain undiscovered in New Caledonia? How many new species we will discover if we apply the same effort in the Philippines, Papua New Guinea, Indonesia, and beyond? And are we going to be capable to catalogue the diversity of life on Earth within a reasonable timeframe? Like Pandora, we [taxonomists] are unable to tame our curiosity and we have opened the sea slug biodiversity box, but hopefully we have not left hope inside!

Life between spines: Galeommatoidean bivalves of western South Africa

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The Galeommatoidea are a diverse but little-studied group of small bivalves, well known for the symbiotic relationships many species have with a range of invertebrate taxa. We examine and illustrate four species collected from the Western Cape region of South Africa, providing new details on their habitat preferences and depicting the mantle structure of live specimens for the first time. We discuss *Brachiomya* new species, and report the first records of *Monacuta subtriata* (Montagu, 1808) from South Africa. *Brachiomya* new species and *Monacuta subtriata* have obligate symbiotic relationships, living between the spines of different burrowing echinoids, while *Kellia becki* (W.H. Turton, 1932) and *Melliteryx mactroides* (Hanley, 1857) are free-living. DNA data and phylogenetic analyses are provided for three of the species. Videos of *Brachiomya* feeding between urchin spines and the free-living *Melliteryx* in habitat are presented.

Strategies for engaging diverse Southern California communities in snail science

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This presentation will describe outreach activities aimed at engaging underserved communities from Southern California in mollusk-related citizen/participatory science projects managed by the Natural History Museum of Los Angeles County. These include in-person “bio-blitz” events with Museum interns, direct engagement with community members via iNaturalist, and research projects for community college students that use iNaturalist data.

Cephalopod ontogeny and life cycle patterns

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All cephalopods are direct developers and hatch with a similar body plan including a circumoral arm- crown, a head with well-developed eyes and brain, a beak with a radula, a ventral funnel, and a mantle covering the viscera. Unlike in other mollusks, there is no larval phase in the strict sense of the definition, because structural features of post-embryonic stages are directly involved in the morphogenesis of the adults. Cephalopods have two developmental modes: they produce either small planktonic hatchlings as paralarvae, or large hatchlings as juveniles. During early life, developmental processes (ontogeny and growth) have a larger impact on morphology than on ecology and are therefore more useful for discriminating phases and stages of the life cycle. As organisms grow, ecological changes (e.g., lifestyle, habitat) becomes more important.

Here, we re-examine and re-define the main phases of the life cycle (Embryonic, Paralarval, Juvenile, Subadult, Adult, Senescent), as well as several important stages within (e.g., hatchling and settlement). We show that shifts in phases and stages are species-specific and size dependent and often involve changes in lifestyle and/or habitat. Using this new terminology, we examine the patterns of cephalopod life cycles and find that there are four main patterns (Holopelagic, Holobenthic, Merobenthic, Meropelagic) based on the presence of a Paralarval phase and the habitat occupied by each phase. The definitions and terminology proposed here provide a unifying framework for future ecological, evolutionary and life cycles research on cephalopods.

Temporal and spatial patterns of sea slug diversity in Mexican coral reefs: insights from Autonomous Reef Monitoring Structures

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Although sea slugs are characteristic fauna of coral reef ecosystems globally, they are often elusive in the tropical waters of the Western Atlantic. Ecological studies of this group are challenged due to a lack of sampling effort through different seasons and the difficulty of detecting these organisms in biological inventories. Autonomous Reef Monitoring Structures (ARMS) are an excellent tool for studying cryptic species like sea slugs. To improve our understanding of the ecological succession of sea slugs in the Tropical Western Atlantic, we analyzed two different localities on the Mexican coast: Bajos de Sisal Reef (Southern Gulf of Mexico) and Puerto Morelos Reef (Caribbean Sea) at different temporal recruitments in two levels: moments (year 1 and 2) and months (3, 6, 9, 12, 15 and 18) using ARMS as a collection method. In total, 50 ARMS were placed at the mentioned coral reefs between 2018 and 2020. After the experimental time, we recovered them and searched for sea slugs. A total of 220 organisms were found, belonging to 28 species. Bajos de Sisal obtained the greatest species diversity (19 species), while half of this amount was found in Puerto Morelos (10). The two localities have different species richness and recruitment times, with only one shared species: *Elysia velutinus*. Also, we only found one constant species in Bajos de Sisal, *Phydiana lynceus*, frequently recorded in almost all the months. In this work, we found 8.5% of the sea slug diversity recorded in the Caribbean. We report four determined species for the first time in the country, and even one family for the Gulf of Mexico, highlighting the need to increase sea slug inventories in the area. Studies of this type allow us to comprehend the distribution and diversity patterns of this popular group of mollusks in this region of the world.

The unsolved case of the Black Mudalia, *Elimia melanoides* (Gastropoda: Cerithioidea: Pleuroceridae)

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Research on freshwater gastropods lags far behind that of most other mollusk groups. This results in imperiled freshwater gastropods not receiving adequate conservation attention. One such species is the pleurocerid Black Mudalia, *Elimia melanoides* (Conrad, 1834), which is restricted to the upper Black Warrior River drainage in Alabama, USA. In 2016, U.S. Fish and Wildlife Service concluded that *E. melanoides* could not be listed under the U.S. Endangered Species Act because of taxonomic uncertainty. Yet, a high risk of extinction for *E. melanoides* was undisputed. To clarify the taxonomic status of *E. melanoides*, we generated a genome-scale dataset and thoroughly evaluated historical material. Phylogenomic analyses

revealed three distinct lineages of *E. melanoides sensu lato*. Several populations of *E. melanoides* were determined to be upstream clinal variants of a widespread species, *Elimia hydeii* (Conrad, 1834). The two other lineages were determined to be *E. melanoides* and a synonym of *E. melanoides*, *Anculosa* (*Mudalia*) *turgida* Haldeman, 1840. We also determined that another unrecognized, and extinct, species was historically present in the Black Warrior River drainage. Conrad's type of *E. melanoides* is lost, but the original description and an ideotype indicate that the unrecognized, extinct species is what Conrad described as *Anculosa melanoides* in 1834. However, in 2003, a neotype was designated for *E. melanoides*. Thus, the name *E. melanoides* belongs to an extant lineage, and no name is available for the extinct entity that Conrad described in 1834. This glimpse into the taxonomy of Pleuroceridae underscores the amount of work that will be required to adequately address pleurocerid systematics. More broadly, our findings have implications for our understanding of clinal variation, the true level of gastropod extinctions, and the importance of combining genomics and traditional museum work for taxonomy.

Ameliorating the Ostromian shortfall inhibiting effective Hawaiian land snail conservation: enacting policies and changing public perceptions

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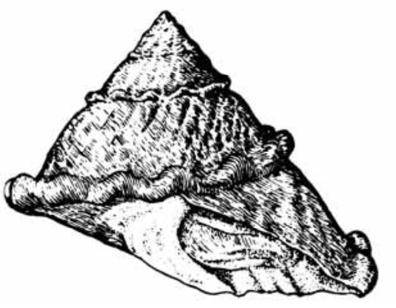
Eight knowledge shortfalls (Linnean, Wallacean, Prestonian, Darwinian, Hutchinsonian, Raunkiaeran, Eltonian, and Ostromian) have been identified as major barriers of effective conservation. The first seven describe knowledge gaps that can be addressed through biological research. The Ostromian, deals directly with conservation effectiveness that is impacted by the lack of clear methods of data collection, species assessments, actions, and ultimately funding and policies. While we have been addressing shortfalls for Hawaiian land snail conservation for the past 15 years, it has become clear that more effort needs to go towards using our understanding and expertise to address the Ostromian shortfall. To do so, we have incorporated research into broad outreach activities, training 200+ interns and volunteers, many from groups underrepresented in conservation. In turn, they have developed educational material (e.g. field guides, trading card games, enlarged 3D printed models of native snail shells; curriculum) to raise awareness about the plight of native snail species and the broader issues of their ecology and evolution. Through engagement with community artists and the broader community, native land snails been used to produce murals, clothing, jewelry, and labels for beverages, showcasing the beauty and cultural value of these native species. 2023 was designated the Year of the Kāhuli (a Hawaiian term for land snails) by the Governor of Hawaii and a bill to designate states snails representing each of the islands or island groups were passed unanimously in 2024 as a direct result of our outreach efforts. These efforts and others have begun to chip away at the Ostromian shortfall for Hawaiian land snails by

1) providing more effective conservation species assessments and management actions by standardizing survey methodologies, providing life history data via captive rearing, and assessing ecological needs; and

2) increasing funding opportunities and community engagement in saving the remaining land snails of Hawaii.



Poster Presentations

Alphabetical by First Author

Presenting author underlined
Student presentations marked by an asterisk *

Building a Citizen Science Portal to Track the Invasive Nudibranch *Doris pseudoargus* in the Northwest Atlantic.

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The northeastern Atlantic nudibranch *Doris pseudoargus* has recently been reported from the shores of Massachusetts, New Hampshire and Maine, USA. The original report included one observation from Nova Scotia, Canada that has since been questioned. No other reports exist from north of Portland, Maine. However, *D. pseudoargus* has recently been found in Long Island Sound. How far has this species actually spread? Fortunately, such a colorful and relatively large mollusc provides a good opportunity for citizen scientists to collect data. To that end, we created an informational website and reporting mechanism using Survey123 and StoryMaps. Early submissions have already somewhat extended the northern boundary of the species. This project may help us quickly delineate the extent of the invasion, allowing us to study unaffected regions before the nudibranch spreads further.

First record of the Asian Clam *Corbicula fluminea* in Ensenada Baja California.

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Ensenada, Baja California is characterized by intermittent runoff occurrences, typically limited to the rainy season, and scarce hot springs, devoid of documented native freshwater clam populations. Notably, the region encompasses the 'Emilio López Zamora' reservoir, vital for water storage and urban supply. However, an unexpected phenomenon unfolded during the dry season of 2021: a substantial accumulation of deceased freshwater clam shells was serendipitously discovered along a stretch of sandy reservoir bed.The goals of this study were to determine the identity of the clam, analyze its possible origin and consider its potential control/use. A sampling of 100 these shells was carried out to perform morphological and molecular identification. Morphological identification was carried out using conventional malacological techniques of taxonomy based on shell morphology. Molecular identification was conducted by extracting DNA from both the shell and periostracum of deceased clams, employing whole-genome amplification (WGA) in conjunction with PCR and sequencing techniques. The integration of classic malacological methods with molecular analysis unequivocally confirmed the lineage of the clam as Corbicula sp. form A/R. This is the first record of this invasive species in the city of Ensenada, Baja California that was confirmed by conventional taxonomy and molecular methods. The WGA method demonstrated its efficacy in identifying deceased mollusks when only the shell remains and nucleic acid availability is constrained. The origin of the clam within the reservoir remains elusive, underscoring the need for future investigations to delve into its potential for biomonitoring, bioremediation, and aquaculture applications.

Filling gaps: resolving the systematics of Facelinidae (Heterobranchia, Nudibranchia)

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Aeolids are the second most specious group within Cladobranchia. Furthermore, during the last ten years, some have been genuinely studied, leading to big systematic changes such as new superfamilies, families, genera and, of course, species. However, the taxonomic status of Facelinidae Bergh, 1889 remains unresolved, even though many authors point out that this family is polyphyletic. This contribution aims to bring some light to the systematics of Facelinidae by including representatives of 22 out of the 30 genera. Additionally, to clarify the relationship between Facelinidae and other aeolids, our molecular phylogeny (based on H3, COI and 16S genes) comprises species of Babakinidae Roller, 1973, Glaucidae Gray, 1827, Myrrhinidae Bergh, 1905, Flabellinidae Bergh, 1889, Flabellinopsidae Korshunova, Martynov, Bakken, Evertsen, Fletcher, Mudianta, Saito, Lundin, Schrödl & Picton, 2017 and Aeolidiidae Gray, 1827. Our results confirm the polyphyletic status of Facelinidae, and because of this, other aeolid families will need to be redefined.

Kleptoplasty in *Elysia diomedea* from the coast of Ecuador: peculiarities and insights from diet and survival experiments

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Kleptoplasty, the adaptation that allows sacoglossan sea slugs to sequester functional plastids from their algal host to utilize photosynthetic products as an alternative energy source has been extensively studied during the past few decades. However, the photosynthetic slug *Elysia diomedea* (Opisthobranchia: Sacoglossa) remains under-researched compared to other congeneric species, leaving many aspects of its ecology and natural history unexplored. This study aimed to elucidate critical factors in the biology and behavior of *E. diomedea*. Specimens were collected from the coast of Ecuador in the southeast Pacific. Laboratory experiments assessed the species' responses to varying diet and light regimes. Four marine algae species—*Codium fragile*, *Ulva lactuca*, *Padina* sp., and *Pterocladia* sp.—were provided to analyze survival times and dietary preferences. Individuals were also subjected to starvation to evaluate their resilience, with morphological changes and reproductive parameters, including egg masses and hatching times, recorded. The findings demonstrated that *E. diomedea* can thrive under artificial fluorescent lighting, surviving up to 61 days without food. Among the tested seaweeds, *Codium fragile* and *Padina* sp. emerged as the preferred diets for sustaining *E. diomedea* in captivity. These results contrast with studies on other sacoglossans, highlighting the unique ecological adaptability of *E. diomedea*. In conclusion, this study provides valuable insights into the survival strategies and diet preferences of *Elysia diomedea*, underscoring its potential for long-term maintenance under controlled conditions. Future research should focus on the molecular mechanisms underlying kleptoplasty in *E. diomedea,* unraveling the peculiar ecological and evolutionary traits found and their implications for understanding energy acquisition, behavior, and resilience in marine environments.

DNA barcoding reveals that a coral reef population of the sea slug *Elysia crispata* feeds mostly on cryptic epilithic algal species

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Elysia crispata is a kleptoplastic sacoglossan sea slug which is found throughout the Caribbean on coral reefs or inshore along mangroves and manmade limestone cuts. Previous PCR based DNA barcoding studies have demonstrated that this species sequesters, maintains, and utilizes chloroplasts from at least 30 ulvophycean algal species throughout the Caribbean. However, few studies have combined DNA barcoding of the sequestered algal chloroplasts with ecological surveys of the animal's habitat. In addition, next generation sequencing (NGS) based DNA barcoding now allows a much more detailed examination of the sequestered chloroplast population. In this study we examined a population of *E. crispata* from Pickles Reef, near Key Largo, FL, USA. Field surveys examining macroalgal coverage on the reef were conducted on June 12, 2019, and December 16, 2019, and animal samples were collected and preserved for DNA extraction during the surveys. Both PCR based and Illumina NovaSeq NGS based DNA barcoding studies targeting chloroplast genes were performed on collected animals. The results showed that the majority sequestered chloroplasts did not match algal species observed during the surveys. Most chloroplasts were from simple cryptic epilithic algal species of the *Pseudochlorodesmis*/ *Siphonogramen* complex, which, if present, were too small and closely associated with coral rocks to be visually identified during the algal surveys.

Changes in molluscan dominant taxa in San Diego soft bottom benthic habitats over time

Wendy Enright

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The City of San Diego (City) began monitoring the soft bottom benthic invertebrate community and various physical and chemical properties of the sediments in the 1960s to document potential impacts of its treated wastewater outfall. Since that time, the length of the wastewater outfall pipe has been extended, technological improvements in treatment, and population increases have taken place. The City's current fixed grid of monitoring stations was put in place in 1991 yet sampling equipment and benthic infauna processing protocols have remained largely unchanged since that time. Data are presented here highlighting changes in numerical abundance, species richness, and dominant taxa over time at three stations along the 98-m contour. This contour corresponds to the depth of treated wastewater discharge for the City and the stations represent nearfield and farfield (north and south) localities. Data are also presented for sediment grainsize. In general, all three stations are numerically dominated by bivalves in the Lucinoidea and Tellinoidea superfamilies, although their relative contributions vary over time. The Nuculanoidea are also common. Gastropods are present, though rarely dominant. Scaphopoda, "Aplacophora", and Polyplacophora are rare. Similarities between communities, as shown by SIMPER analysis in PRIMER, are greater than their dissimilarities when comparing samples with similar grainsize, demonstrating little to no impact of the treated wastewater on communities. Rather, the physical environment is the primary driver of molluscan community composition in this region.

A new *Elysia* species from Florida: Convergent reduction in parapodia in *Halimeda*-eating sea slug lineages from the Atlantic and Pacific

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Convergent evolution among species that share a niche offers insight into how selection and constraint together shape adaptation. We present a new species of *Elysia* from the Atlantic coast of Florida ("*Elysia* sp. 53"). Slugs range

from 3 to 10 mm and are cryptic on their host, *Halimeda tuna* or *H. discoidea*, on which they make distinctive, meandering feeding scars. The species has not been previously documented from this well-explored shoreline, but is readily found to depths of 12 m on most dives by an experienced collector. Phylogenetic analyses of a 5-gene dataset for 412 sacoglossans recovered this elysiid as sister to *E. marcusi* from Florida and the Caribbean. The parapodia of *Elysia* sp. 53 are completely fused, leaving a smooth dorsum with a diagnostic medial groove; fused parapodia in *E. marcusi* left an asymmetric C-shaped groove. *Elysia* sp. 53 produces egg masses with blobs of yellow extra-capsular yolk, like *E. marcusi*, but with planktotrophic development, a distinctive combination of features among Atlantic elysiids. The radula of *Elysia* sp. 53 has just 4 to 6 teeth per limb with a massive ascus; teeth are distinctly scoop-shaped, downward-curving with lateral denticles, different from *E. marcusi* (hosts: *H. opuntia*, *H. goreaui*) and *E. velutinus* (hosts: *H. incrassata*, *H. monile*). Parapodia are partly fused in Indo-Pacific *Halimeda*-eaters including *E. pusilla*, a complex of 12 species, and the *E. stylifera* complex. Convergent reduction in parapodia is likely adaptive for slugs adhering to flat algal surfaces in turbulent water, and highlights the flexible nature of traits under selection. Diagnostic radular differences remain informative for species delineation and description, however. The well-studied coast of Florida continues to reveal cryptic heterobranch species, highlighting the wealth of unrecognized diversity in this lineage, and suggesting isolation by the Gulf Stream current promoted speciation and endemicity along the peninsula.

The pleasure oyster *Crassostrea corteziensis* related whit an intracellular prokaryote belonging to the order Rickettsiales

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In several species of bivalve mollusks of commercial aquaculture importance, the presence of intracytoplasmic vacuoles (IVS) that could correspond to Rickettsiales like-organisms (RLOs) has been observed. These bacteria have sometimes been associated with tissue damage and mass mortalities. However, the type of symbiotic association they maintain with their host has not been defined. RLOs were observed on the west coast of Mexico in routine health checks of the pleasure oyster, *Crassostrea corteziensis*, over a 10-year period. In this study the RLOs were characterized morphologically and genetically. Additionally, the intensity and prevalence of RLOs were evaluated in relation to the seasonality, height and sex of the host. Morphological characterization of the RLOs was performed by conventional histology in combination with scanning electron microscopy (SEM). Shotgun sequencing and amplicon sequencing of hypervariable regions of the 16S rRNA gene were performed from DNA extracted from tissue samples embedded in paraffin (FFPE). At the histological level, RLOs were observed as basophil inclusions causing hypertrophy to the host cell without apparent changes in the surrounding tissue. At the ultramicroscopic level, the RLOs showed a bacillus-cocoid morphology. Metagenomic analyses associated with *C. corteziensis* detected sequences of the order *Rickettsiales*, families *Anaplasmataceae* and *Rickettsiaceae* with a low relative abundance (<2%). Demonstrating that there is an association between RLOs with bacteria of the order *Rickettsiales*. The prevalence of RLOs in *C. corteziensis* was low (5%). The highest prevalence was in summer (14%) and in females oysters with a size range of 83-103 mm. Eighty- nine percent of organisms showed low intensities (Grade 1). The absence of tissue alterations, the prevalence and low intensity suggest that the RLOs maintain a commensal relationship with the host. However, the monitoring of the RLOs is recommended considering changes in this interaction might occur due to climate change.

Effect of formulated diet pH on the biological performance and enzymatic activity of juvenile blue abalone *Haliotis fulgens*

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The green abalone is a species with significant potential in aquaculture and high market value. However, the industry faces a major challenge in the availability of adequately formulated diets, particularly concerning stability in the water column.

Evidence suggests that diets with an acidic pH improve water stability, increase feeding, and reduce production costs. Despite the known benefits of acidic pH for diet stability, the effects of a lower pH diet on abalone's biological performance. This study aimed to evaluate the impact of dietary pH on the biological performance of green abalone (initial weight: 2.17 ± 0.04 g; initial length: 2.61 ± 0.08 cm). Three isoproteic (15.52%) and isolipidic (1.51%) diets based on a commercial diet, ABKELP®, with three pH levels (5, 7, and 8) were formulated. A fourth treatment using fresh algae Macrocystis pyrifera served as a control. The abalone were fed these diets in triplicate for five and a half months. Results showed no significant differences in growth and survival among the dietary treatments. However, diet water stability increased with decreasing pH, being significantly higher for the pH 5 diet compared to the pH 8 diet. Muscle lipid content was significantly lower in abalone fed the control diet (0.12 ± 0.01%) compared to other treatments, though no significant differences were found in muscle protein, carbohydrates, moisture, and ash content. Digestive enzyme activities (alkaline protease, trypsin, leucine aminopeptidase, and chymotrypsin) were significantly lower in abalone fed the control diet. The highest in vitro protein digestibility was observed with enzyme extracts from abalone fed the pH 5 or control diet (degree of hydrolysis = 8%). Total heterotrophic bacteria counts in the digestive tract were similar among treatments, but Vibrio counts were higher in abalones fed the pH 7 diet. In conclusion, the ABKELP® diet with pH 5 showed higher water stability and slightly better growth and diet digestibility, potentially leading to lower production costs due to higher feed efficiency.

Hawaiian land snail genomics: A preview of the first *Achatinella* whole genome

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The Hawaiian Islands are a biodiversity hotspot and home to half of all species listed under the US Endangered Species Act. Hawaii also holds the unfortunate distinction as an extinction capital of the world. Hawaiian land snails have suffered devastating losses, and an estimated 100 species will go extinct in the next decade if we do not fill the knowledge gaps limiting our understanding of how to save them. Understanding Hawaiian land snail evolution is critical for understanding environmental interactions and developing conservation strategies. Whole genome sequencing (WGS) is vital tool for understanding biodiversity and the evolutionary processes that shape it. Capturing a comprehensive view of an organism's blueprint for life affords us a look into how gene structure, function, and selection have shaped species, and how we might use those insights to stem the tide of extinction. Most genomic studies focus primarily on vertebrates, particularly charismatic mammals and birds, leaving most biodiversity understudied. To date, no complete genome for any Hawaiian land snail species has been published. As part of an integrative study into ecology, evolution, and genomics, this project is generating whole genomes for seven endemic species using Illumina MiSeq short read and Oxford Nanopore Technologies (ONT) long read sequencing. Here, we present the first and most complete genome for endemic Hawaiian tree snail, *Achatinella fuscobasis*. Data from this genome and others combined with ongoing studies on dietary ecology, plant preferences, and captive rearing strategies will provide crucial insights to better inform conservation management practices and fill the knowledge gaps surrounding terrestrial snail evolution in the Hawaiian Islands.

Multiple origins of freshwater invasion and parental care reflecting ancient vicariance events in bivalve family Cyrenidae (Mollusca)

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Habitat transitions in living organisms are key innovations often coupled with species diversification after their successful adaptation to new environment. The Cyrenidae is among the most well-known heterodont bivalve groups that have successfully invaded freshwater systems from brackish water environments and display diverse lineage-specific developmental modes. Phylogenetic and molecular clock-based divergence time analyses using 12 complete mitochondrial genome sequences suggest that Cyrenidae species independently colonized freshwater habitats during three distinct spatial and geological periods, reflecting ancient vicariances associated with plate tectonic events: one from the American continents approximately in the Early Jurassic and the two others from Australasian/East Asian continents in the Early/Middle Cretaceous and the Paleogene-Neogene boundary, respectively. Our ancestral state reconstruction analyses for habitat types, reproduction modes, and biogeographic origins confirm the hypothesis of multiple freshwater invasions and repeated parallel evolution of the parental care system (i.e., direct development with internal incubation of juveniles) during the evolutionary diversification of Cyrenidae species. This research was supported by the National Research Foundation of Korea (NRF) grant funded by the Korean Government (MSIT) (No. 2020R1A2C2005393).

Philinoglossa sp A: What environmental factors drive the boom and bust abundances in San Diego waters?

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Philinoglossa sp A is a relatively uncommon cephalaspid (Gastropoda: Heterobranchia) recorded by the City of San Diego's ocean monitoring program. Despite continued collection and monitoring for almost three decades, generally one or less individuals are recorded annually generally in shallow, sandy habitats (less than 40m). However, a select few of these locations exhibit intermittent spikes in recorded abundance, with greater than ten to twenty individuals collected in a single grab. These instances can be followed by several years of omission from the record, only to reappear again in the same location at high abundances. In this study, we compared trends in recorded abundances of *Philinoglossa* sp A with contemporaneous environmental data (sediment type and grain size distribution, sediment chemistry, overlying water chemistry) and co-occurring infauna abundances to attempt to understand the drivers behind the boom and bust population cycles. Preliminary data indicate that *Philinoglossa* sp A abundances in San Diego waters may be driven by the physical environment and associations with other infauna of similar dietary requirements.

The Effects of Heat Stress and Calorie Restriction on Impaired Memory Retention in the Terrestrial Slug *Deroceras reticulatum* (Mülller, 1744)

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The terrestrial slug *Deroceras reticulatum* (Müller 1744) was used to examine if memory disruption could be restored by 110ermetic interventions. Hormesis is the process by which a potentially harmful stimulus elicits beneficial effects in the correct dosage and duration. From single-trial aversive stimulus conditioning, memory retention factor (Rf) was used to assess the effects of conditioning and oxidative damage via H2O2-injection at one day and seven days. Results from the conditioning showed a significant increase in Rf1 in the experimental group compared to the control (p=0.04) but not Rf7 (p=0.31). The induction of an oxidatively damaged phenotype was supported with significantly decreased Rf1 in H2O2 injected-slugs compared to the saline-injected control (p=0.04). Calorie restriction (CR) and heat stress (HS) have been shown to extend lifespan in model systems, and they are thought to act, in part, through a 110ermetic mechanism. However, to our knowledge, the combination of both CR and HS has yet to be explored in the context of a systems-level assay, such as memory retention. HS and CR administered independently did not confer significant protection/recovery from oxidative damage (p=0.53 and p=0.74, respectively). Co-administration of HS and CR similarly failed to offer significant protection/recovery from oxidative damage (p=0.21). Consequently, it was concluded that wild-caught phenotypically diverse terrestrial slugs used in the current study are susceptible to short-term conditioning (Rf1), but not long-term conditioning (Rf7) and that oxidative damage from H2O2 disrupts memory. However, recovery from oxidative damage in terms of memory via a 110ermetic mechanism through HS, CR, or HS+CR had only a weak directional effect.

Three new species of sacoglossans from Ecuador: integrative analyses of heterobranch diversity in the Eastern Pacific

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Though badly underestimated, heterobranch species richness is increasingly well documented from biodiversity hotspots in the tropical western Pacific, and temperate waters of the North Pacific. In comparison, the fauna of southeastern Pacific coasts remains poorly known. Recent studies found a depauperate fauna in the tropical eastern Pacific, with few geminate species sister to Caribbean taxa, suggesting mass extinction following final closure of the Panamanian Isthmus and recent colonization from the central and western Pacific. However, an improved understanding of southeastern Pacific species, their ecology and evolutionary relationships may clarify global patterns of diversification and mechanisms of speciation. Here, we present data supporting the existence of three taxa provisionally identified as new species from Ecuador. Data on host use, internal and external morphology are reported, with evolutionary relationships based on phylogenetic analyses of a 5-gene dataset for 412 delimited sacoglossan taxa. *Elysia* sp. 52 (also sampled in Panama) was sister to *E. bennettae* from Australia, within a clade from the tropical Indo-Pacific that feeds on *Chlorodesmis* and *Udotea*; although resembling *E. nealae*, data including radular morphology suggest this is a new species. *Elysia* sp. 51, a small grey species, was sister to the Caribbean seagrass-eating *E. serca* (which was not distinct from Northern Atlantic material identified as *E. catulus*). Surprisingly, the Ecuadorean elysiid eats *Ulva*, a non- siphonaceous alga not typically considered a suitable sacoglossan host, but also consumed by the co- occurring *E. diomedea*. Limited algal diversity may have led to unusual host shifts in the temperate southeastern Pacific. Finally, a new *Placida* sp. is documented, found as far north as Baja California, Mexico. This species is distinct from the recently described *P. sudamerica* from the southwestern Atlantic coast of South America. These species may provide new model systems for the study of host shifting and kleptoplasty.

Enumerating and conserving the riparian macroinvertebrate communities of Babeldaob, Palau

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Palau's watersheds are among the largest in Micronesia and are national- and state- level priorities for conservation. Palau's largest island, Babeldaob, is of special interest because it solely contains all of the country's rivers. Community composition of freshwater macroinvertebrates is likely similar across most Pacific islands; however, information is lacking in some regions. Pacific freshwater species numbers tend to be depauperate. Many of these species are amphidromous (i.e., juveniles of a species return to freshwater from the ocean). Geographic ranges of Palau freshwater macroinvertebrates are poorly known. For example, previous studies suggest that morphology-based identifications for many of these species are unreliable. There have also been few recent comprehensive surveys, inconsistent species identification, and little genetic identification. To address this knowledge gap, we conducted freshwater macroinvertebrate surveys in Palau. We identified species using morphology and molecular-based characters (e.g. COI barcodes). Results of the morphological assessment suggest that there are 17 species of freshwater gastropods and eight species of decapods. This study supports maintaining Palau's biodiversity through the inventory and identification of freshwater macroinvertebrates. Molecular- based tools can also help to identify invasive species. Information and identification tools developed in our work is regularly shared with Palau's conservation officers to assist in their conservation efforts.

Three new species of *Sacoproteus*, sea slugs that mimic different species of *Caulerpa* including highly invasive 'killer algae'

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Mimicry is one of the most compelling examples of natural selection in action, often allowing consumers to escape detection by predators while resting or feeding on a host. Large but cryptic sea slugs in the genus *Sacoproteus* Krug, Wong, Medina, Gosliner & Valdés, 2018 are remarkable mimics of chemically defended algae, *Caulerpa* spp., including highly invasive species of global concern. Three new algal mimics (*S. nishae*, *S. yhiae*, and *S. browni*) were separated from *S. smaragdinus* in 2018, having been previously grouped together under one name in the genus *Stiliger*. Notably, each slug taxon appears to mimic a different algal species. The high degree of crypsis afforded by their algal mimicry likely contributed to the taxonomic obscurity of these species, as they hid in plain sight. Here, just a few years later, we report three more new species of *Sacoproteus* from New Caledonia. Each taxon is genetically differentiated by DNA barcoding markers, and supported as distinct by multiple methods of quantitative species delimitation. The species are also distinguishable by external morphological features. Thus, "*Stiliger smaragdinus*" turned out to be at least seven species, a level of cryptic diversity that is not unusual for marine heterobranchs and highlights how true species richness remains underestimated for many groups. We expect more *Sacoproteus* spp. are yet to be found, given the number uncovered in only a few years of work. These crawling salads provide a valuable model system for studying the evolution of mimicry and host specificity in marine systems.

Methodologies for Imaging Mollusk Specimens at the Museum of Comparative Zoology

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Museum collections play a critical role in malacological research by preserving centuries worth of collected specimens and their data for future study. Today, these specimens are becoming more accessible as museums push to digitize their collections. Producing high-quality digital photographs of specimens is an important part of the digitization process. This poster documents the evolution of the digital photography approaches and setup used by the Malacology Department at the Museum of Comparative Zoology (MCZ), to increase image quality and workflow efficiency. It also outlines the protocols used for imaging specimens based on their preservation method (dry- or ethanol-preserved), shell shape, and size. Additionally, this poster charts how the number of MCZ mollusk photographs publicly available online has increased over the past four years due to the following: grant imaging progress, researcher requests, fieldwork imaging of live specimens, and media generated by visiting researchers. For example, two NSF grants – Mobilizing Millions of Marine Mollusks of the Eastern Seaboard (ESB) and Pacific Island Land Snail Biodiversity Repository (PILSBRy) – have funded the generation of hundreds of photographs of type specimens, which are of particular importance to malacological research.

Seek and you will find: micromollusks in the gut content of the sea cucumber *Astichopus multifidus*

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In relation to mollusks, the family Eulimidae is known for its close relationship with members of the class Echinodermata, as it is a parasite of all its classes, including the Class Holothuroidea. Some species of this group, commonly known as sea cucumbers, are an important source of income in the regions. In some cases, their populations have been so diminished that some species can no longer be exploited. To take advantage of the material collected for studies of *Astichopus multifidus* species, the gut contents were reviewed to look for mollusks. Thus, the stomach contents of 137 cucumbers collected off the coast of Sisal, Yucatán in three sites distributed in six trips during March and August 2017 were reviewed. The holothurians were anesthetized, and fixed, and the digestive tracts were dissected.

Subsequently, the gut was examined and the conchological material was separated regardless of whether it was complete, ruptured, or eroded. Material was then separated by morphotype, and incomplete or very worn shells were discarded. A total of 2,348 shells of Bivalvia, Gastropoda, and Scaphopoda were found. From those, 36 species of bivalves and 82 species of gastropods were identified. Due to the lack of complete shells, 26 bivalves, 112 gastropods, and 2 scaphopods were identified as morphotypes at different levels (Class, Family, or Genus). At least one photograph was taken of each species or morphotype recorded. It is worth highlighting that the preservation of some shells suggests that they were ingested alive and subsequently disintegrated in the cucumber's gut. This is not the first study to record shells within the gut of sea cucumbers, but it is the first to identify them beyond the family level. This work shows that collaborations allow us to take advantage of information obtained from the sacrifice of a living being.

Not Blown Away: Over Three-Quarters of Species in a Pacific Atoll Land Snail Assemblage Remain Five Years Post-Typhoon

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Severe storms have the potential to disperse land snails carried by strong winds between islands and archipelagos or to drown endemic fauna in storm surges. We compared land snail assemblages collected from Kayangel atoll (Kayangel State, Republic of Palau, Oceania) before and after the passage of Typhoon Haiyan in 2013. Most land snail species remained present after the storm, including two species endemic to the atoll (*Palaina moussoni* Crosse, 1866 [Diplommatinidae] and an undescribed species of *Palaua* Baker, 1941 [Euconulidae]. Three species were not recovered post-Haiyan, and three species were reported for the first time after the storm. We conclude that the atoll's land snail fauna is fairly resilient to the impacts of severe storms. This finding raises the hope that at least one harbinger of climate change – increased prevalence and severity of storms – may pose minimal risk to certain imperiled and endemic Pacific Island land snails. We also compare our collections to 20th century collections by Ito and Thannum that include additional species not otherwise known from Kayangel atoll.

Developing an experiment to identify food resources critical to land snails in wet Hawaiian cloud forests

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Hawaii is located within a biodiversity hotspot and supports one of the most species rich land snail assemblages with 759 described species, 99% of which are endemic to the archipelago. Estimates suggest that nearly 65% of species have already gone extinct with most of the remaining species being vulnerable to extinction in the next decade. Though there are current conservation efforts focused on protecting these species, foundational ecological knowledge, such as what composes critical components of their diet, is still lacking. Hawaiian land snails feed on the bacteria, fungi, and algae on the surface of plants which is known as the phyllosphere. However, little is known about which microbes form critical components of their diet which can influence their overall fitness and fecundity. Previous research across multiple islands in Hawaii have found that Hawaiian land snails prefer certain understory plants and avoid many widely distributed native plant species. Using plant preference data to ground experiments, recent studies have found that phyllosphere assemblages on preferred and non-preferred plants differ across sites in Oahu. This study will build upon this work and investigate if microbial assemblages between preferred and non-preferred plants differ across different Hawaiian Islands. Sampling will be conducted in the wet forests in west Maui Watershed, Maui. I will replicate the methods and procedures outlined in Meyer et al. (2022, 2023) and incorporate Algal 23S regions, which have not been previously examined. I hypothesize that algal assemblages as well as bacterial and fungal assemblages will differ between preferred and avoided plants. If patterns are concordant across islands, this could help identify important food resources for snails in wet forests critical for Hawaiian land snail conservation.

Picky eaters? Shedding light on trophic specificity across Nudibranchia

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As a taxonomically and ecologically diverse and geographically widespread taxon, nudibranch gastropods provide scientists with a fruitful basis for the study of evolutionary processes, speciation, and ecology. Despite tremendous efforts to gather field observations on nudibranch sea slugs, the sheer number of taxa makes it challenging to obtain and compare detailed information on their ecology. This especially applies to the trophic ecology of nudibranchs, a crucial piece of information for our understanding of their general biology and their role in complex and changing marine ecosystems. A broadly hypothesized high trophic specificity in most species of nudibranch gastropods forms the basis for many ecological and evolutionary studies. However, evidence of dietary specificity is lacking for the majority of nudibranch species. In this study, we aim to shed further light on trophic specificity in nudibranch gastropods using DNA metabarcoding, by establishing a protocol that will allow the identification of prey organisms present in nudibranch gut contents to test for the taxonomic diversity, or lack thereof, in nudibranch diets. To do so, we are using both modern material from field collections in 2023 and 2024 as well as museum specimens from families spanning across Nudibranchia. DNA metabarcoding presents a scalable as well as cost- and time-effective method that will allow us to obtain high amounts of information on the trophic ecology of nudibranch gastropods alongside field observations in an integrative approach. This method holds potential to help us answer a plethora of questions including the role of nudibranch gastropods in trophic networks, their abilities to adapt to changing landscapes, putative drivers of speciation, their population-scale ecology as well as their chemical and visual ecology.

Comparison of ecomorphospaces of land snail communities on islands and nearby mainland

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Oceanic islands are often regarded as test tubes of evolution. Isolated and colonized by relatively few species, islands are home to many of most renowned radiations. Whether and how biodiversity might differ on island systems compared to the nearby mainland has intrigued researchers for decades and remains unresolved. The goal of the present study is to examine the influence of evolutionary constraints and ecological drivers of ecomorphology among land snail species forming assemblages found on an island system (the Galapagos islands) and on a nearby mainland system (the Peruvian Andes). Land snails of the Family Bulimulidae were sampled across the two landscapes. Ecological and shell morphological data will be assembled and curated for all species encountered at each site (i.e., for each snail community sampled). Evolutionary relationship among species will be inferred from genomic markers, and a phylogenetic framework will be used to estimate diversification rates and assess evolutionary constraints for each group. We will then use a multivariate analysis approach to examine the relationships and differences between shell morphology (using geometric morphometric) and ecological data at the species and community levels.

Early-life Stages of Cephalopods – An Identification Handbook

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Thirty years have passed since Sweeney et al. (1992) produced the highly influential "larval handbook", a practical guide to identifying the early life stages of cephalopods. At the CIAC2018 *Paralarval and Juvenile Cephalopods* workshop, attendees recognized the need to produce an updated reference focused on this important but poorly understood phase of life. Consequently, a team of 48 authors from 14 countries and five continents are writing a new, Open Access book that reviews and summarizes 30 years of progress in our understanding of the early life stages of cephalopods. This 600-page book will be a richly-illustrated presentation of the size-based characters needed to identify species in all currently recognized families. The family chapters will be accompanied by approximately 400 illustrations and many high-quality color plates. Introductory chapters will describe and define the early life cycle phases and stages, outline collecting and fixation methodologies, and identify best practices in illustration and photography. A community-vetted key to families and a glossary of early life history terms will be included and augmented with illustrations.
We anticipate the book will be published by Springer in 2025 and hope it will serve as an essential reference in the field and as inspiration for a new generation of early life history researchers.

Quantifying Biomass of *Alderia* Sea Slugs in West Coast Mudflat Estuaries

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Keystone molecules are increasingly being considered as having the potential to structure ecological communities. However, demonstrating that a molecule is a significant structuring mechanism for an ecosystem requires an understanding of both the distribution of those molecules and their biomass in the ecosystem. Sea slugs in the genus *Alderia* produce nontoxic polyketide metabolites that deter predators. Although *Alderia* spp. are small, they can reach high densities (>1,000/m2), suggesting that these polyketides may have the potential to play a significant role as keystone molecules in mudflat estuary ecosystems. To quantify the extent to which these polyketides may prevent energy from primary producers reaching higher trophic levels, we aimed to estimate the total biomass of *Alderia* sea slugs along the

west coast of the United States. We first constructed species distribution models for both *Alderia* species found in this region. Biomass was quantified by integrating average biomass per species with density data from quadrat samples within their known ranges. Combining these models and biomass estimates, we predicted the total biomass for each species. Our findings highlight the potential influence of *Alderia* on trophic structure and energy dynamics in mudflat estuaries, underscoring their ecological importance.

Spectrum of Secrets: species delimitation and cryptic diversity in the genus *Candiella* Gray, 1850 (Nudibranchia: Cladobranchia: Tritoniidae)

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Candiella is considered the most species-rich genus of the family Tritoniidae in the Atlantic Ocean. Taxonomically, *Candiella* species pose a major challenge due to their general body shape and overlapping geographic ranges and colour patterns, which are often associated with cryptic species. In this study, we aim to investigate the systematics of several *Candiella* species and the presence of cryptic species in "*Candiella manicata*" species complex from the northeastern Atlantic. Our integrative approach combines morpho-anatomical characters as well as two mitochondrial (COI and 16S) and one nuclear gene (H3). Species delimitation analyses using ABGD, ASAP, bPTP and mPTP revealed that "*C. manicata*" is an Atlantic-Mediterranean species complex that includes at least four different species. We also provide new morpho-anatomical characters and taxonomic notes for all species studied. Overall, this study provides valuable insights into the continued growth of marine diversity in the northeastern Atlantic Ocean, a region that has been the subject of scientific study for more than 250 years.

Sea-slug Solar Power: Applying insights from kleptoplasty to biophotovoltaics technology

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Global energy demand is projected to increase 32% by 2040, far outpacing renewable energy deployment. Due to the high resource costs and heavy metal consumption of some conventional technologies like photovoltaic solar cells, the pace of renewable energy development cannot keep up with that of energy consumption. New sustainable technologies must be considered, such as biophotovoltaics (BPV) which have the potential to diversify, stabilize, and accelerate the clean energy transition without exploiting rare earth metals and other finite resources. Current limiting factors for this technology relate to the efficiency and useful lifespan of BPV cells. Kleptoplasty may hold some insight as to how we can support photosynthetically active chloroplasts in an artificial BPV cell after isolating them from their host algae.

This study aims to demonstrate the viability and increased efficiency of a BPV cell that uses isolated chloroplasts (instead of the more conventional entire algal cells) as photosynthetic drivers of electricity production. We construct bio-"bottle"-voltaic devices, one using intact algal cells to produce electric current and another using a novel biofilm constructed from isolated chloroplast suspension. Electrical power output will be measured from both devices to compare energy efficiency and organismal longevity. If an isolated suspension of chloroplasts demonstrates higher photoelectric efficiency than intact algal cells, prolonging the useful life of isolated chloroplasts becomes essential to BPV technology. Biochemical, behavioral, and physiological mechanisms contributing to sacoglossan kleptoplasty can provide inspiration and insight for future BPV engineering applications.

Completing the puzzle of Bivalves from the Gulf of Mexico: the crucial contribution of a regional repository

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Over the past century, global biodiversity patterns have changed due to anthropogenic pressures and climate change. Biodiversity inventories in different regions of the world have been essential tools for understanding the distribution of organisms in detail. The Gulf of Mexico (GOM) is bordered by the United States, Mexico, and Cuba and hosts multiple aquatic habitats. Bivalves, an important component of the GOM fauna, are frequently used as bioindicators in ecological studies. Here, we update the bivalve checklist of Turgeon et al. (2009) using recent literature (47 peer-reviewed papers published between 2009 and 2020), the online datasets GBIF and Invert-E-base, and records and photographs of specimens collected as part of the Mexican project Biodiversidad Marina de Yucatán (BDMY). We also describe species distributions across two biogeographical regions. We list 640 species of Bivalvia belonging to 314 genera, 75 families, and 17 orders. Our focus on the Campeche Bank yielded 168 species; 128 of those species were photographed, and 11 genera are illustrated here. Areas bordering the United States dominated bivalve diversity at all taxonomic levels, followed by those in Mexico and Cuba. The list includes 16 newly described species since 2006 for the GOM, which represents an addition of 2.5% of the reported species almost 15 years ago. In this work, we provide for the first time an illustrated catalog with 128 photographs of 20% of the 640 bivalve species in the list, which were collected at the Campeche Bank, GOM. This study expanded our understanding of bivalve diversity in the GOM and we emphasize the importance of biological collections, especially in the region, as sources of information for decision-makers, and the general public; this type of repositories can provide opportunities for collaboration and study from various interdisciplinary approaches.

Biogeographic Affinities of Northeast Pacific *Calliostoma*

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Calliostoma Swainson, 1840 is well known for having beautiful shells, but little is known about its phylogenetic relationships, especially within the North Pacific (NP), one of the most species-rich biogeographic regions. We aim to unveil the biogeographic and phylogenetic relationships of northeastern Pacific (NEP) Calliostomatidae with a combined mitochondrial COI + 16S and nuclear ITS2 analysis, also incorporating publicly available sequence data when available. Our preliminary results agree with and extend earlier findings but with denser taxonomic sampling. Like earlier authors, we resolved at least three geographically-restricted clades within Calliostomatidae: NP, tropical American, and mostly European clades. Within the NP, we could have found support for either separate NEP and northwestern Pacific (NWP) radiations, or perhaps a complete mixture of NEP and NWP species. Instead, we found a monophyletic NEP grouping, and another with mixed NEP and NWP species, implying only rare exchanges across the NP. Our results support a division of NEP species into separate radiations. One is endemic to the NEP and includes most familiar shallow-water species. The other includes a mixture of NEP and NWP species and includes more deep-water species. Although we included only a single nuclear marker, these about 700 bases spanned both conserved coding regions (5.8S and 28S rDNA) and a more variable non-coding internal transcribed

spacer 2 (ITS2) region. Addition of this ITS2 region to our combined result, or analyzed by itself, improved the resolution of deeper affinities for the NEP clade. In either case, the represented NP species versus the tropical New World species were found to be reciprocally monophyletic. The combined gene as well as the separate ITS2/mitochondrial gene trees also supported similar relationships among the NEP *Calliostoma* species. One implication of this phylogenetic estimate is that a great diversity of shell sculpturing has arisen within the NEP geographical region.

Increasing public interest and study of urban land snails and slugs through Atlanta S.L.I.M.E.

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Building on the success of the community science initiative S.L.I.M.E. (Snails and slugs Living in Metropolitan Environments) in southern California, nearly five years ago, “Atlanta S.L.I.M.E.” was launched in Georgia to promote increased public interest and study of urban land snails and slugs across the metropolitan Atlanta region. This effort is based out of Georgia State University (GSU), a large, public minority-serving institution in downtown Atlanta. Since late 2019, multiple undergraduate and graduate students at GSU have participated in data collection and research on terrestrial gastropods including by adding many hundreds of observations to iNaturalist. Projects with students have focused on documenting the diversity of native and non-native land snails and slugs, comparing communities in and beyond Old Growth Forests, and analyzing variation in assemblages impacted by different human-environmental issues. Efforts to engage the public have included an annual ‘Urban Slug Walk’ at parks across the city as part of the Atlanta Science Festival held every March. The number of iNaturalist observations since launching the initiative has increased from under 100 to over 1500 across Atlanta, and with work expanded to the state level through the addition of a “Land Snails and Slugs of Georgia” iNaturalist project instead of only focusing on the city. Our impact increased significantly during the pandemic with a shift in student projects as well as opportunities for families to safely social distance and engage in outdoor learning through community science. Our reach has also extended now to involve faculty and student participation from a nearby HBCU. We are currently writing up new discoveries in having identified multiple species not previously reported in Georgia, and we continue to build new resources for students and the public to contribute to the study of land snails and slugs around Atlanta.

Genetic sex determination of *Kelletia kelletii*

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Kellet's whelk, *Kelletia kelletii*, a kelp forest gastropod, fisheries species, and historical non-model species, is increasingly becoming a subject of research for understanding its ecology and management. A method for determining *Kelletia kelletii* sex non-invasively (e.g., without dissection) is needed to support cross-mating experiments and other research on this species. Genomics and molecular biology techniques were used to sex *Kelletia kelletii* non-invasively using a small sample of foot tissue. Dissection of whelks yielded samples for RNA extractions as well as physiological sexing for validation. Putatively sex-determining genes SOX9, FOXL2, WNT4, SRY, and DMRT1 were found through analysis of a previously assembled transcriptome, then aligned with sequences from model species to design primers for use in RT-qPCR to test for quantitative differential gene expression between males and females. Results found SOX9, WNT4, and DMRT1 showed significant differences in expression between male and female foot tissue. However, expression levels in confirmatory sex organs (i.e. penis (M) or egg capsule gland (F)) tissues showed no relationship of significant gene expression between males and females. These results were not conclusive, as the genes selected may not be direct indicators of sex determination in the foot tissue of marine mollusks. Current directions of this project include replicating the procedure with an increased sample size of foot and gonad tissue to verify results, as well as designing primers for and performing RT-qPCR on genes involved in the whelk endocrine system (estrogen, androgen, and testosterone receptors), as these genes are more likely to be functioning as direct indicators of sex determination in whelk foot tissue.

Investigating microhabitat variation between co-occurring *Nuttallina* (Mollusca: Polyplacophora) species

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Nuttallina sp. A remains undescribed since its 1984 informal introduction by Stephen C. Piper's UCSD PhD dissertation. Piper noted a separation in tidal height where *N*. sp. A co-occurs with the more southern congener, *Nuttallina fluxa* (P.P. Carpenter, 1864), in San Diego County, but we still know little about its northern co-occurrence including any ecological differences or interactions with *Nuttallina californica* (Reeve, 1847). We have investigated how *N.* sp. A coexists when overlapping in range with the extremely common, *N. californica,* along California's Central Coast, in anticipation of its formal separate description. Earlier surveys north of Point Conception revealed all localities but one dominated by *N. californica* with *N*. sp. A. at a single wave-protected locality in Monterey County, unusual for its sandstone substrate. Before our investigation, it was unclear how these species might differ in microhabitat if found together. Our investigation found that *N*. *californica* and *N.* sp. A co-occur at the same small beach near Pismo Beach in San Luis Obispo County but are noticeably separated in their respective microhabitats. We confirmed that morphology can be used to distinguish these species by employing the combination of morphological study and PCR-based assays pioneered by Newton Z. Hood in his 2020 CSUF Master's thesis. Remarkably, we found *N. californica* exclusively in a sea cave, and *N*. sp. A was only found on a rocky intertidal platform exposed to sunlight, separated by 172 meters across a sandy cove beach. *N*. sp. A was found on rocks that vary in hardness, suggesting that substrate could be less important than other factors, such as exposure to sunlight or the amount of wave exposure. Their near co-occurrence, yet divergent utilization of microhabitats over a proximate spatial scale presents an opportunity to examine ecological niche differences between the species.

** MCLEAN MEMORIAL GRANT RECIPIENT STUDENT REPORT **

Success or failure: Assessing the Potential Invasion of Late Pleistocene Mollusks in Southern California.

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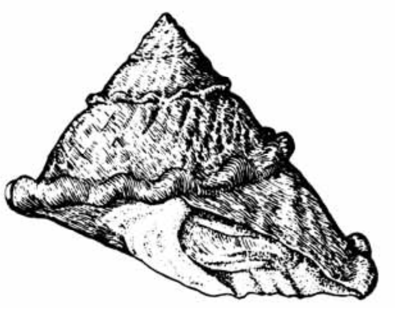
Coastal ecosystems are warming rapidly due to climate change, causing species to migrate and adapt to environmental changes through ecological and evolutionary processes. These shifts in species' distribution alter biodiversity patterns and can have negative ecological effects. The sedimentary record of southern California marine terraces preserves evidence of the profound paleoclimatic shifts of the Quaternary Period. Fossil assemblages from these deposits are often considered to be thermally anomalous, containing species found outside their modern-day biogeographic range. These extralimital species,- or local invasives, showed a dynamic distribution range during glacial-interglacial cycles and can thus be utilized as potential migrators during climate warming conditions. However, it is important to understand if these extralimitals were well established or temporarily lived in novel ranges. In this study, we quantified the invasiveness using a mathematical framework that evaluates the performance of extralimital species in their introduced and native ranges by using inter and intra-specific comparisons. While this method has been used in modern invasion ecology, our goal is to apply it to the fossil record. By doing so, we hope to gain a deeper understanding of a species' potential invasiveness in the past, present as well as future range dynamics. Our results showed only 7.5% of the total invaders from the Late Pleistocene are considered "good invaders" (well established), and 60% are weak performers in the introduced ranges. This framework suggests that not all invaders become well-established due to their eco-evolutionary differences, which might suppress most species from becoming successful invaders. Our next step is to understand the limitations of this method in fossil records and facilitate a more comprehensive performance analysis by incorporating size, density, and other demographic parameters for assessing invasion success.



Meeting Minutes

Minutes, Executive Meeting, Western Society of Malacologists
Fifty-seventh Annual Meeting, 04 August 2024, Pasadena, CA

The meeting was called to order at 6:40pm. Officers present: Christine Parent (president), María Moreno Alcántara (1st vice-president), Kelvin Barwick (treasurer), Wendy Enright (secretary), Jann Vendetti (member-at-large). Past president Hans Bertsch also present.

Governance issues – The question of raising dues was brought up. Kelvin will start tracking financial records to see if we are still covering our costs. Hans was also in favor of charging more for those members requesting a paper copy of our reports.

Student Grants and other awards – Jann had two applicants this year that were both funded.

- $1000 to Andre Arturo Leon for 3D modeling California limpets
- $1000 to Luke Carlo McLean for studies on *Mytilus* species morphological shifts across the Holocene

Discussion on how to promote both the McLean museum-based research grant as well as the more general student grant.

Christine will be judging all students for this meeting's presentation awards. We will give $200 each for the top oral and poster presentations.

Reports – Kelvin's treasurer's report showed that across all WSM funds, we were down about $600. Funds have been fairly stable year to year even going back as far as 2010. Hans moved to accept the report with Maria as second. Motion carried.

Nominations – Finding new officers remains a challenge. Suggestions were made to form a recruiting committee and to address this during the general membership meeting. Right now, the general meeting is at the same time as AMS so we will try to meet during the lunch break on Tuesday or Wednesday.

- Wendy, Kelvin, and Jann agreed to continue in their roles so the search for another member-at-large and more vice presidents continues.

An annual report committee was formed with Wendy, Hans, and Christine as members.

Next year's meeting in Sonora – Maria will give a more detailed presentation at the general meeting. Joint meeting with the Mexican malacological society March 31st-April 5th. Hoping to have Paul Valentich-Scott give a symposium and focus on "malacology without borders". The meeting will be very student-centered.

Miscellaneous business:

The gavel is missing – perhaps it is still with Bill Wright.

The question of whether WSM should try to rejoin AMS was brought up but not resolved. Further discussion revolved around what our society may look like in the future. Issues of cost, relevance, and connectivity remain a challenge. One idea to make meetings easier is to have a virtual meeting every other year or even to only meet every two years.

The meeting concluded with a hope for continued discussion at the general meeting.

Respectfully submitted,

Wendy Enright

Wendy Enright, Secretary

Minutes, General Membership Meeting, Western Society of Malacologists
Fifty-seventh Annual Meeting, 07 August 2024, Pasadena, CA

The meeting was called to order at 1250pm and all were welcomed by the president. Officers present: Christine Parent (president), María Moreno Alcántara (1st vice-president), Kelvin Barwick (treasurer), Wendy Enright (secretary), Jann Vendetti (member-at-large). Ten additional members were also in attendance.

STUDENT AWARDS

- Announcement of McLean grant awards for museum-based research: (Jann Vendetti):
    - ◊ Andre Arturo Leon based in Germany ($1000)
    - ◊ Luke Carlo McLean working on Mytilus ($1000)
  - ∗ General discussion of how to better promote both the student and Mclean grants. Ideas included more social media; Instagram, as well as LinkedIn postings directly on the colleges' funding pages
  - ∗ A student representative may help us out. Kenadee Zernickow from the Doug Eernisse lab volunteered to fill that role. She will link up with Danielle Zacherl to promote the regular student research grant.
  - ∗ Membership as part of the grant (present at next conference as well); conference registration as well? Encourage to send summary or present at next conference so other students can see the benefits of applying for the grant
  - ∗ KB moved to offer membership as part of the grant; HB second – motion carried
  - ∗ Ad hoc to provide conference support as well

- WSM Student Grant – only two applicants, but both are strong so we're funding both
    - ◊ Tiffany Tang – *Calliostoma* species investigations
    - ◊ Nefertiti Wong – integrating proteomic and metabolic response of fat horse mussel and green octopus (in Santa Rosalia, Baja)
  - ∗ Student poster and student talk prizes: $500/each. Woot!!
    - ◊ Judged in collaboration with AMS.

  Winners will be announced at the closing banquet. (beautiful certificate being printed by Tom from the AMS)

REPORTS

- Treasurer's report (Kelvin)
  - ∗ Still having to pay the PayPal fees
  - ∗ We are now the custodians of the McLean student grant but KB keeps the accounting of those moneys separate

  - ∗ KB went through the report line by line and explained what everything means; our society is solvent and stable (last year showed a loss of $659 which is not bad)
  - ∗ Reminder – WSM can’t take in more than $50K a year in order to maintain the nonprofit status
  - ∗ Suggestion to adjust payment amount for PayPal folks or to look into extra fee for paper copy membership by Hans. KB will be looking into that
  - ∗ Paul VS and Angel expressed support;
  - ∗ Ángel moved that we add a $20 surcharge for print copies if we can figure out how to do it online – Coulson volunteered to help if needed ; Hans second; motion carried (as of 2025); print & web updates
  - ∗ HB moved to accept, congratulate KB on a job well done, and DE 2nd
- Secretary’s report followed by motion to accept and voted.
  - ∗ Annual reports up to date; occasional paper on eponyms in progress; apologize for delay; complete and send to reviewers before October; hope to publish by end of year or very early next year
  - ∗ DE asked to get more caught up on BHL; Wendy will reach out to Pat LaFollette to see about that; whatever we can do to make those links more broadly available
  - ∗ PVS moved to accept; CP 2nd

NEW BUSINESS

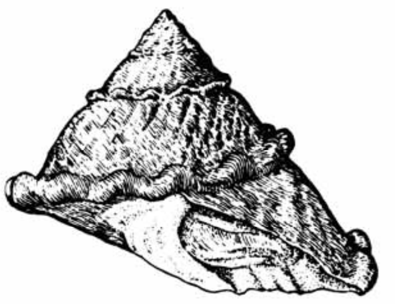
- Nominations for next year’s officers
    - ◊ President (This will be the current First Vice President) Maria Moreno
    - ◊ First and Second Vice Presidents (we do not have a Second VP to move up into the First VP spot) tentative Vanessa Delnavez for 2027; Christine will ask Casey (Kelvin asked him as well); Doug also talked to Alyssa Frederick (White Abalone project)
      - ⇒ Casey Richart accepted and will serve as president in 2026
    - ◊ Secretary Wendy
    - ◊ Treasurer Kelvin
    - ◊ Two Members-at-Large (we only have one, now) Mason & Coulson
  - ∗ Should we create a student rep position? Kennadee (at this point, non-voting) KB moved, Maria second; motion passed
  - ∗ CP moved to accept the slate, Doug second; motion passed
  - ∗ Nomination committee?
  - ∗ Election of nominated officer (show of hands)
- Any miscellaneous items or issues raised by the membership. None
- Formal transfer duties to next president and closing the meeting. (Virtual gavel transfer)

- Report from incoming president about next year's meeting.
  - Joint meeting w/ Mexican Malacological Society
  - RENAMAC
  - Very cool logo with symbolic colors and representative glyphs
  - Plans solidified with the team from MMS
  - Held at the university of Sonora in Hermosillo at the art center; two venues plus outdoor areas
  - University waiving the costs of the venue and the salaries of the folks working there
  - Comcaac nation will be our cultural hosts; chants/arts & crafts/ceremonies/services
  - Pre-Meeting workshops and short courses (virtual)
  - Keynotes and symposia (Deneb Ortigosa, Crisalejandra rivera); Paul VS – Malacology without borders
  - Oral/poster presentations
  - Student awards
  - Photography contest
  - WSM-sponsored mentoring lunch to promote interactions with researchers (speed dating)
  - Already have a great schedule of talks and events; banquet Friday, Field trip to Tiburon Island on Saturday (very special to be able to visit)
  - Registration begins September 1st
  - Abstract submission until Dec 15
  - Early bird reg from 84 to 153 but might vary depending on exchange rate
  - Payment via paypal
  - Hotel Colonial very close to the university
  - Can get flights many diff ways

Meeting was adjourned.

Wendy Enright

Wendy Enright, Secretary



Treasurer's Report

Treasurer's Report August 4, 2024

WSM Cash Flow for June 2, 2023 to July 29, 2024

Outflows[1]

Student Poster/Talk awards	$(100.00)
WSM Student Grant (n=2)	$(2,004.99)
J. H. McLean Student Grant in Collections-Based Research (n=3)	$(4,009.98)
Annual report production and mailing (2022[2] & 2023)	$(912.85)
Office Supplies	$(66.63)
Web page backup (Dreamhost)	$(4.68)
Bank Charges	$(12.00)
2024 Conference Expense (honorary member's registration)	$(375.00)
Total Outflows	$(7,486.13)

Inflows

Individual Memberships (n=57;13-student,41-regular,3-honorary)	$983.49
Institutional Memberships (n=6)	$412.76
Interest	$12.53
WSM Student Grant ($3,956.75 available)	$1,080.00
J. H. McLean Student Grant in Collections-Based Research ($8,046.33 available)	
Initial transfer from SBMNH	$7,056.31
Anonymous donation	$5,000.00
Total Inflows	$14,873.87
Total Net	**$7,387.74**
Total Net sans McLean Student Grant Funds	**($658.69)**

Cash on hand as of July 29, 2024

Account	*Bank Balances*	*Sans McLean Grant Funds*
Operating	$19,404.09	$11,357.76
Savings	$13,218.65	$13,218.65
Credit card	0.00	$0.00
Totals	**$32,622.74**	**$24,576.41**

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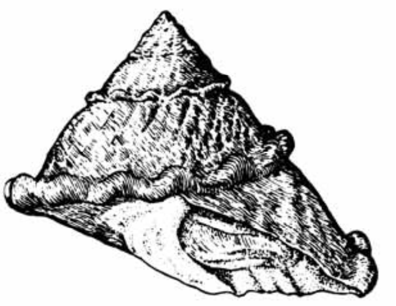
[1] PayPal cost on $640 not realized above, 2.9% plus $0.30 per transaction: $(32.51)

[2] Printing cost paid by Pasadena City College.



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