



# The American Malacological Society

**86<sup>th</sup> Annual Meeting**

**July, 13<sup>th</sup> 14<sup>th</sup>**

**Meeting Virtually on Zoom**

**Program and Abstracts**

**Monday July 13th, 2020**

11:00 AM to 11:15 AM	Introduction and Welcome to AMS 2020 Virtual: Tim Collins
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**Monday, July 13<sup>th</sup> 2020, Concurrent Session 1**

	<p><b>Biodiversity &amp; Conservation</b> Session Chairs: Kathryn Perez and Tim Pearce</p>
11:15 AM to 11:30 AM	<p>Quantifying Neglect of Research for Non-commercial Marine Species and the Potential Dangers of Generalizing from Limited Ecological Data Anderson, Brendan M.* ; Lamsdell, J. C. ; Falk, A. R. ; Congreve, C. R.</p>
11:30 AM to 11:45 AM	<p>Exploring the Diversity of Coral-Boring Bivalves in the Florida Keys National Marine Sanctuary MacLean, Sarah K.*; Rawlings, T. A.; Bieler, R.</p>
11:45 AM to 12:00 PM	<p>Native Molluscan Diversity Collapse in the Eastern Mediterranean Albano, Paolo G.*</p>
12:00 PM to 12:15: PM	<p>Using Citizen Science to Understand the Origins of Left-coiling Garden Snails <i>Cornu aspersum</i> Davison, Angus*.; Thomas, P.; 'Jeremy the snail' citizen scientists</p>
12:15 PM to 12:30 PM	<p>Changes in Gastropod Diversity Based on Land Use: A Case Study From Anderson County, Kansas Davis-Berg, Elizabeth C.* , Wilson, B. A., Arnold, C. J. and Almario-Kopp, D.</p>
12:30 PM to 12:45 PM	<p>Poorly Vetted Conservation Ranks Can be More Wrong Than Right: Lessons From Texas Land Snails. Perez, Kathryn E.*; Hutchins, B. T.; Nekola, J. C.</p>
12:45 PM to 1:00 PM	<p><b>Break</b></p>
1:00 PM to 1:15 PM	<p>Is Acid Precipitation a Factor in the Decline of the Terrestrial Tiger Snail, <i>Anguispira alternata</i>, in Northeastern North America (Gastropoda: Discidae)? Pearce, Tim A.*; Brouwer, N. L.; Hulton VanTassel, H.</p>
1:15 PM to 1:30 PM	<p>Biogeographic Regions within Jamaica Defined by Land Snails <a href="#">Kostick, Heather L.*</a></p>
1:30 PM to 1:45 PM	<p>Plans for Ensuring the Survival of South Florida's Tree snails Collins, Timothy M.*; Warren, A.; Held, A.</p>

1:45 PM to 2:00 PM	The Last of the Endodonta Yeung, N. W.; Slapcinsky, John*; Kim, J. R.; Sischo, D. R.; Hayes, K. A.
2:00 PM to 2:15 PM	A 100-year Journey From Discovery to Description: A Hawaiian Land Snail Finally Gets Its Name Yeung, Norine W.*; Slapcinsky, J.; Strong, E. E.; Kim, J. R.; Hayes, K. A.
2:15 PM to 2:30 PM	Species delineation in highly threatened Hawaiian land snails, (Achatinellidae: <i>Auriculella</i> ) using geometric morphometrics Hobbs, Christopher S.*; Yeung, N. W.; Hayes, K. A.
2:30 PM to 2:45 PM	Hawaii's Freshwater Snails: Understudied and Unprotected Hayes, Ken*
2:45 PM to 3:00 PM	MD 55 results- A perspective from bivalve diversity. Valentas-Romera, Bárbara L.*; Simone, L. R. L.
3:00 PM on	<b>Posters on Google Drive</b> <a href="https://drive.google.com/drive/folders/1nCOqmkpiY1yD97YNg_VnLrHvsaxs-Ofk">https://drive.google.com/drive/folders/1nCOqmkpiY1yD97YNg_VnLrHvsaxs-Ofk</a> See page 6 for individual poster chat rooms from 3:00 to 4:00 PM

### Monday, July 13th 2020, Concurrent Session 2

	<b>Systematics &amp; Phylogenetics</b> Session Chairs: Rüdiger Bieler and Gary Rosenberg
11:15 AM to 11:30 AM	Systematics and Geographic Distribution of <i>Galba</i> , a Group of Cryptic and Worldwide Species of Freshwater Snails Alda, Pilar* Lounnas, M.; Vázquez, A. A.; Ayaqui, R.; Calvopiña, M.; Celi-Erazo, M.; Dillon, R.T. Jr. ; González Ramírez L. C.; Loker, E. S.; Muzzio-Aroca, J.; Orlando Nárvaez, A.; Noya, O.; Pereira, A. E.; Martini Robles, L. ; Rodríguez-Hidalgo, R.; Uribe, N.; David, P.; Jarne, P.; Pointier, J.-P.; Hurtrez-Boussès, S.
11:30 AM to 11:45 AM	The Grass Squid <i>Pickfordiateuthis pulchella</i> is a Paedomorphic Loliginid Anderson, F (Andy).E.*; Marian, J. E. A. R.
11:45 AM to 12:00 PM	Setting Molecular Clocks: Cautionary Observations Campbell, David C.*
12:00 PM to 12:15: PM	A Biodiversity Informatics Approach to Family-group Level Classification of Freshwater Mussels (Bivalvia: Unionoida) Graf, Dan. L.*
12:15 PM to 12:30 PM	MolluscaBase – The Evolution of a Community Resource, Part 1 Bieler, Rüdiger *; Rosenberg, G.

12:30 PM to 12:45 PM	MolluscaBase – The Evolution of a Community Resource, Part 2 Bieler, R.; Rosenberg, Gary*
12:45 PM to 1:00 PM	<b>Break</b>
1:00 PM to 1:15 PM	Neogastropods of the lower Waccamaw Formation Campbell, T .D.*
1:15 PM to 1:30 PM	Bivalves of the lower Waccamaw Formation Campbell, T .D.*
1:30 PM to 1:45 PM	Molecular and Morphological Analysis of Ozark Pigtoes ( <i>Fusconaia</i> and <i>Pleurobema</i> spp.) Phelps, Logan T.*; Hayes, D. M.; Harris, J. L.
1:45 PM to 2:00 PM	Ancestral or inverted? An inexpensive PCR-based test effectively contrasts alternative mitochondrial gene orders within chitons Eernisse, Doug J.*, Manh, K. and Sirovy, K.
2:00 PM to 2:15 PM	A Dirty Dorid Disaster: The First Molecular Phylogeny of the Nudibranch Family Discodorididae Bergh, 1891 Donohoo, Samantha A.*; Gosliner, T.M.
2:15 PM to 2:30 PM	Can you do the can-can?: An analysis of the lifters of <i>Goniobranchus nudibranchs</i> Bonomo, Lynn J.*; Gosliner, T. M.
2:30 on	<b>Posters on Google Drive</b> <a href="https://drive.google.com/drive/folders/1nCOqmkpiY1yD97YNg_VnLrHvsaxs-Ofk">https://drive.google.com/drive/folders/1nCOqmkpiY1yD97YNg_VnLrHvsaxs-Ofk</a> See page 6 for individual poster chat rooms from 3:00 to 4:00 PM

### Tuesday July 14<sup>th</sup>, 2020, Concurrent Session 1

	<b>Land Snails and Slugs as Species of Concern in Agricultural, Health, or Other Areas</b> Session Chairs: Amy Roda and Francisco Borrero
11:00 AM to 11:15 AM	The Recipe for Destruction: Pesticides Alone are Not the Only Key to Giant African Snail ( <i>Lissachatina fulica</i> ) Eradication Roda, Amy*; Nachman, G.; Weihman, S.; Yong Cong, M.; and Zimmerman, F.
11:15 AM to 11:30 AM	Giant African Land Sails ( <i>Lissachatina fulica</i> Bowdich, 1822): Florida Eradication Program and Its Effectiveness to Date. Yong Cong, Mary*; Noah, R. H.; Emery, T. ; Smith, T. R.; Roda, A. L.; Wilds, A. R.

11:30 AM to 11:45 AM	<i>Bulimulus</i> Land Snails (Bulimulidae) as Species of Concern in Native and Introduced Ranges – An Issue for the Southern USA Borrero, Francisco J.*
11:45 AM to 12:00 PM	Management of <i>Bulimulus sporadicus</i> (d'Orbigny, 1835) in the Panhandle, FL Dickens, Katrina L.*; Yong Cong, M.; Talamas, E.; Baker, S. M.
12:00 PM to 12:15: PM	Citizen Science: Documenting the Spread of the Black Velvet Leatherleaf Slug in the United States Robinson, David G.*
12:15 PM to 12:30 PM	<b>Break</b>
12:30 PM to 12:45 PM	Spatiotemporal Patterns of Terrestrial Snails and Slugs in the Contiguous United States Gladstone, Nicholas S.*; Bordeau, T. A.; Leppanen, C.; McKinney, M. L.
12:45 PM to 1:00 PM	USDA Terrestrial Mollusk Program: Using Science Based Regulatory Tools to Protect US Agricultural Production Systems from Invasive Slugs and Snails Wilds, Andrew R.*
1:00 PM to 1:15 PM	The Potential Invasiveness of the Eastern Heath Snail in Montana Birdsall, J. L.; Littlefield, Jeffrey L.*; deMeij, A. E.
1:15 PM to 1:30 PM	Distributions of Non-native Terrestrial Molluscs Within and Among Hawaiian Islands: Implications for Statewide Management Meyer III, Wallace M.*; Hayes, K. A.; Yeung, N. M.; Kim, J. R.; Cowie, R. H.
1:30 PM to 3:00 PM	<b>Break until student paper awards at 3:00 PM</b>

### Tuesday July 14<sup>th</sup>, 2020, Concurrent Session 2

	<b>Ecology, Environment, Morphology</b> Session Chairs: Jessica Goodheart and Trevor Hewitt
11:00 AM to 11:15 AM	Chloroplast Identification and Feeding Specificity of the Photosynthetic Sea Slug <i>Elysia papillosa</i> Barber, K*; Middlebrooks, M.; Bell, S.; Pierce, S.
11:15 AM to 11:30 AM	Evolution of Diverse Host Infection Mechanisms Delineates a Cryptic Adaptive Radiation of Freshwater Mussels Hewitt, Trevor*; Haponski, A.; Ó Foighil, D.

11:30 AM to 11:45 AM	Differential Parental Investment in Two Reproductive Life History Adaptations Utilized Within a Poecilogonous species, <i>Alderia willowi</i> (Gastropoda: Sacoglossa: Limapontiidae) Scott, Mariah*; Krug, P.; Bieler, R.
11:45 AM to 12:00 PM	The Effects of Hurricane Irma on a Long-Standing Population of Photosynthetic Sacoglossan Sea Slugs Middlebrooks Michael L.*; Curtis N. E.; Pierce S. K.
12:00 PM to 12:15 PM	Twenty-five Year Trends in the Soft Sediment Molluscan Communities of Tampa Bay, Florida, USA Karlen, David J.*; Dix, T. L.; Goetting, B. K.; Chacour, A.; Markham, S. E.; Campbell, K. W.; Christian, J.; Jernigan, J. M.; Martinez, K.
12:15 PM to 12:30 PM	<b>Break</b>
12:30 PM to 12:45 PM	Seasonal Sea Surface Temperature Variability in the Middle Ages: New Insights from <i>Patella vulgata</i> $\delta^{18}O$ Morgan, Reed J.*; Barrett, J.
12:45 PM to 1:00 PM	Atlantidae Mollusks as Indicators of Environmental Change in the Southern California Current Moreno-Alcántara, Maria*; Aceves-Medina, G.; Lavaniegos-Espejo, B. E.
1:00 PM to 1:15 PM	Stinger Thieves: Nematocyst Diversity and Sequestration in Aeolid Nudibranchs Paggeot, Lisa X.* and Gosliner, T. M.
1:15 PM to 1:30 PM	The Nudibranch <i>Berghia stephanieae</i> is a New Experimental System for Studying the Sequestration of External Cells and Structures Goodheart, Jessica A.*; Masterson, P.; Johnston, H.; Lyons, D.
1:30 PM to 1:45 PM	First Histochemical and Ultrastructural Characterization of the Esophageal Pouch Cells in Chitons (Mollusca, Polyplacophora) Lobo-da-Cunha, A*; Oliveira, E.; Alves, A.; Calado, G.
1:45 PM to 2:00 PM	Organic to Mineral Shell Components Through Molluscan Growth Stages Richard, Stephanie R.*; Prezant, R. S.
2:00 PM to 2:15 PM	Quantitative Measures and 3D Shell Models Reveal Interactions Between Bands and Their Position on Growing <i>Cepaea</i> Shells Jackson, Hannah J.*; Larsson, J.; Davison, A.
2:15 PM to 2:30 PM	Landmark-based Snail Size Measurement Improves Precision and Repeatability of Shell Volume Estimation Over Conventional Shell Size Measures Osborne, Teresa R.*

2:30 PM to 3:15 PM	<b>Break until student paper awards at 3:15 PM</b>
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**Tuesday July 14<sup>th</sup>, 2020, Student Presentation Awards**

3:15 PM to 3:30 PM	<b>Presentation of Student Awards</b>
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**Tuesday July 14<sup>th</sup>, 2020, AMS Members meeting**

3:30 PM to 4:30 PM	<b>AMS Member's Meeting</b>
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**Individual Poster Chat Rooms**

<p>Freshwater snails in the Mediterranean Island of Corse (France): distribution and ecology of the family Lymnaeidae, vectors of fasciolosis Alba, A.*; Blin, Q.; Lemonnier, L.; Vázquez, A.A.; Foata, J.; Quilichini, Y.</p>
<p>Size structure and morphometry of the Chinese snail <i>Hexaplex nigritus</i> (Gastropods: Muricidae) in the Ohuira lagoon, Ahome, Sinaloa. Diarte-Plata, G.<sup>1*</sup>; Escamilla-Montes, R.<sup>1</sup>; Granados-Alcantar, S.<sup>2</sup>; Luna-González, A.<sup>1</sup></p>
<p>Choice of refuges of the pygmy octopus <i>Paroctopus digueti</i> in the Ohuira lagoon, Ahome, Sinaloa Escamilla-Montes, R.<sup>1</sup>; Diarte-Plata, G.<sup>1*</sup>; Granados-Alcantar, S.<sup>2</sup>; Luna-González A.<sup>1</sup></p>
<p>Growth of <i>Leukoma asperrima</i> as a possible fishing resource in Sinaloa. Escamilla-Montes, R.<sup>1</sup>; Diarte-Plata, G.<sup>1*</sup>; Granados-Alcantar, S.<sup>2</sup>; Luna-González A.<sup>1</sup></p>
<p>Selective Predation on Native Mussels in Middens Along Great Lakes Inland Rivers Frankila, A.*; Woolnough, D. A.</p>
<p>Growth aspects of the catarina clam <i>Argopecten ventricosus</i> in the wild population in Guasave, Sinaloa. Granados-Alcantar, S.<sup>2*</sup>; Diarte-Plata, G.<sup>1</sup>; Escamilla-Montes, R.<sup>1</sup>; Luna-González, A.<sup>1</sup></p>
<p>Chromodorid Nudibranch <i>Felimare ruthae</i> expands diet and range on Florida's Gulf Coast Gutierrez-Andrade, D.* ; Middlebrooks, M. L.; Cuccinello, S. E.</p>

<p>Composition and community structure of soft-bottom mollusks on the sand bar El Mogote, Bahía de La Paz, Mexico.</p> <p>Herrera-Uria, J.*; Tripp-Quezada, A.</p>
<p>De novo assembly and annotation of the Pacific calico scallop (<i>Argopecten ventricosus</i>) transcriptome for the discovery of immune-related genes</p> <p>Luna-González A.*; Diarte-Plata G.; Escamilla-Montes R.</p>
<p>A morphometric hypothesis of species diversity in the freshwater snail genus <i>Gyrotoma</i> (Pleuroceridae)</p> <p>Minton, R. L.*</p>
<p>Diversity and predicted function of gut microbes from two species of viviparid snails.</p> <p>North, E.<sup>1</sup> ; Minton, R. L.*<sup>2</sup></p>
<p>Mechanical Shell Properties of Eight Species of Cohabiting Unionid Bivalves</p> <p>Prezant, R. S.; Dickinson, G. H.; Chapman, E. J.; Rosen, M. N.; Cadmus, M. B.</p>
<p>Dismantling the Punctoidea: new molecular phylogeny and establishment of Discoidea</p> <p>Salvador, R. B.*<sup>1</sup>; Brook, F. J.*<sup>2</sup>; Shepherd, L. D.*<sup>3</sup>; Kennedy, M.*<sup>4</sup></p>
<p>Krakens and flail snails: the role of fantasy and sci-fi mollusks in science communication</p> <p>Salvador, R. B.*<sup>1</sup>; Cavallari, D. C.*<sup>2</sup>; Carnall, M. A.*<sup>3</sup></p>
<p>Mobilizing data on Pacific Island land snails from collections at Florida Museum of Natural History</p> <p>Slapcinsky, J.*<sup>1,2</sup>; Ibanez, E.*<sup>1,2</sup>; Smith, A.*<sup>1,2</sup>; Noto, D.*<sup>1,2</sup>; Yeung, N.*<sup>3</sup></p>
<p>Genetic Diversity Maintained in Comparison of Wild and Propagated Populations of Imperiled Freshwater Mussels</p> <p>VanTassel, N. V.* ; Zanatta, D. T.</p>
<p>The invasion of the giant African land snail in Cuba: a threat to biodiversity and public health</p> <p>Vázquez, A. A.*<sup>1,2</sup>; Alba, A.*<sup>2</sup>; Sánchez, J.*<sup>2</sup>; Yong, M.*<sup>3</sup>; Coupland, J. B.*<sup>4</sup></p>

Do You Know Your Pigtoes? DNA Barcoding and Geometric Morphometric Analyses Distinguish Between Common Wabash Pigtoe (*Fusconaia flava*) and Imperiled Round Pigtoe (*Pleurobema sintoxia*) in the Laurentian Great Lakes Region  
Willsie, J. A. \*<sup>1</sup>; Morris, T.J.<sup>2</sup>; Zanatta, Z.T<sup>1</sup>.

Recordings of sessions on Google Drive at

<https://drive.google.com/drive/folders/1EZFrSZESC0vU2JooDJUPSjoCCVUbo0je>

for 1 month after meeting.

## **ABSTRACTS**

## **Freshwater snails in the Mediterranean Island of Corse (France): distribution and ecology of the family Lymnaeidae, vectors of fasciolosis**

Alba, A.\*; Blin, Q.; Lemonnier, L.; Vázquez, A.A.; Foata, J.; Quilichini, Y.

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Corsica is a small landmass but it is the wettest of all Mediterranean islands where green forests, woodlands and shrubs and a large mountain range predominate in the island, determining different microclimates (Mediterranean, temperate and alpine) and vast hydrological network. In these conditions, freshwater snails can thrive and as many serves as intermediate host of significant trematode for public and veterinary health, the study of their distribution and ecology is essential to prevent risks and to understand transmission. Here, we present an updated sampling of freshwater snails in Corsica with emphasis on the family Lymnaeidae where the intermediate hosts of the reemergent zoonotic parasite *Fasciola hepatica* are grouped. Lymnaeid snails were frequent in natural environments as well as in farms and pastures lands and were found positively associated to stagnant/low-flow waters. In addition to the five lymnaeid species described in the island, we report, for the first time in Corsica, the presence of the invasive lymnaeid snail *Pseudosuccinea columella* in the wild which could undoubtedly complicate the scenario of fasciolosis transmission in the French island.

**Poster**

## **Native molluscan diversity collapse in the Eastern Mediterranean**

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University of Vienna

We quantified a large-scale extirpation of native mollusks from the Israeli shelf in the Eastern Mediterranean, a region strongly affected by rapidly changing environmental conditions and the introduction of non-indigenous species, based on an extensive sampling programme of mollusks in intertidal, subtidal and mesophotic habitats. We reconstructed historical species richness from shelly death assemblages, quantified the time range they cover with radiocarbon dating, and compared their richness with today's living assemblage diversity. Today's median native richness is 50% of the historical richness in the intertidal, but only 5-12% for the subtidal down to 40 m. Samples from the mesophotic zone show a much higher median of 42%, which is likely an underestimation due to sampling constraints. In contrast, non-indigenous species show assemblages matching the historical richness. Additionally, a comparison between today's and historical native species maximum size shows that shallow subtidal native populations are mostly non-reproductive. In contrast, non-indigenous populations reach reproductive size. These results suggest that a recent large-scale change in environmental conditions is strongly favoring non-indigenous mollusks and is the main cause behind the shallow subtidal native mollusks' decline. As climate continues to warm, the native biodiversity collapse described here will intensify and affect a broader area, counteracted in terms of net diversity only by Red Sea species. Our results call for a quick shift to a low-carbon society, better protection of the mesophotic zone, which still hosts diverse native molluscan assemblages, and the acceptance of this novel ecosystem where non-indigenous species are the only ones able to maintain some degree of ecosystem functioning under such degraded conditions.

## Systematics and Geographic Distribution of *Galba*, a Group of Cryptic and Worldwide Species of Freshwater Snails

Alda, P.<sup>1\*</sup>; Lounnas, M.<sup>2</sup>; Vázquez, A. A.<sup>2,3</sup>; Ayaqui, R.<sup>4</sup>; Calvopiña, M.<sup>5</sup>; Celi-Erazo, M.<sup>6</sup>; Dillon, R.T. Jr.<sup>7</sup>; González Ramírez L. C.<sup>8</sup>; Loker, E. S.<sup>9</sup>; Muzzio-Aroca, J.<sup>10</sup>; Orlando Nárvaez, A.<sup>10,11</sup>; Noya, O.<sup>12</sup>; Pereira, A. E.<sup>13</sup>; Martini Robles, L.<sup>14</sup>; Rodríguez-Hidalgo, R.<sup>6,15</sup>; Uribe, N.<sup>13</sup>; David, P.<sup>16</sup>; P. Jarne, P.<sup>16</sup>; Pointier, J.-P.<sup>17</sup>; Hurtrez-Boussès, S.<sup>2,18</sup>

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Cryptic species are a problem in systematics and biogeography, especially if they are invasive or transmit parasites or pathogens. In this work we study a group of cryptic species of freshwater snails of the family Lymnaeidae that inhabit almost all continents and transmit *Fasciola* to humans and livestock. Our goal is to elucidate the systematics, distribution, and phylogenetic relationships of *Galba* group species based on a robust and integrative approach that includes GenBank morphology, molecular markers, large-scale sampling (all from America), and DNA sequences (including samples from America and the rest of the world). We conclude that the genus *Galba* comprises five species or complexes of species. *Galba cousini* is the only species that can be identified using the shell morphology and internal anatomy (a derived trait) and has the most restricted distribution within the group. The other four species — *G. truncatula*, *G. cubensis* / *viator*, *G. humilis*, and *G. schirazensis* — are cryptic and constitute clades that vary in their genetic diversity, geographic distribution, and invasive potential. We conclude and emphasize that no *Galba* species should be identified without molecular markers. We also discussed how morphological stasis could explain crypticity in *Galba*.

## **Quantifying neglect of research for non-commercial marine species and the potential dangers of generalizing from limited ecological data**

Anderson, B. M.\*<sup>1</sup>; Lamsdell, J. C.<sup>1</sup>; Falk, A. R.<sup>2</sup>; Congreve, C. R.<sup>3</sup>

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Large datasets have allowed biologists and paleontologists to investigate a multitude of ecological processes and have yielded important insights relevant to combating our current biodiversity crisis, but have frequently obfuscated the ways in which our limited understanding of ecology can influence our models. Our patchy understanding of organismal life history impacts our perspective of ecological and evolutionary processes across multiple temporal and hierarchical scales. Problems can arise from generalizing ecological niche parameters across clades, employing inappropriate uniformitarian assumptions, and from taxonomic biases in the organisms chosen for detailed study. Natural history information from benthic marine mollusks can illustrate issues of mis-match between the general trends/responses exhibited within a higher taxon and specific constituent species' ecologies or responses to environmental change. To quantify how research effort varies among study organisms we constructed a dataset of over 1000 species based on random drawing of aquatic organisms from the World Register of Marine Species. The total number of English-language publications for each of these species was evaluated through a Google Scholar search (inclusive of legacy names). Over 80% of species were found to have fewer than 10 papers attributed to them. As expected, taxa which are sourced for fisheries, are congeneric with fished species, or are parasites to fished species have a proportionally higher rate of study when compared to taxa which are not associated with fisheries.

Future conservation work would benefit from more detailed studies of the life history of organisms, as we lack information for many modern groups. The development of "big-picture" datasets should not preclude important smaller studies focusing on one or a few taxa. These smaller scale life history studies represent the raw data from which these datasets can be constructed; therefore, these types of studies should remain a priority investment.

## The grass squid *Pickfordiateuthis pulchella* is a paedomorphic loliginid

Anderson, F.E.\*; Marian, J. E. A. R.

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The wide disparity in adult body size observed both within and among animal taxa has long attracted widespread interest, with several general rules having been proposed to explain trends in body size evolution. Adult body size disparity among the cephalopod mollusks is remarkable, with adult body sizes ranging from a few centimeters to several meters. Some of the smallest cephalopods are found within *Pickfordiateuthis*, a group comprising three described species of squid found in the western Atlantic and tropical eastern Pacific. *Pickfordiateuthis pulchella*, the type species of the genus, was initially proposed to be closely related to the loliginid squids (Loliginidae), with subsequent descriptions of additional species supporting a placement within Loliginidae. *Pickfordiateuthis* is remarkable in that all species reach sexual maturity at about one-fifth to one-tenth the size seen in most loliginid species. To date, no phylogenetic analyses have included representatives of *Pickfordiateuthis*. To infer the phylogenetic position of *Pickfordiateuthis* and explore its implications for body size evolution, we collected specimens of *Pickfordiateuthis pulchella* from Brazilian waters and sequenced regions of two loci -- the mitochondrial large ribosomal subunit (rrnL a.k.a. 16S) gene and the nuclear gene rhodopsin. Maximum likelihood and Bayesian analyses of these sequences support a placement of *Pickfordiateuthis pulchella* as sister to a clade comprising the Western Hemisphere loliginid genera *Doryteuthis* and *Lolliguncula*. Analyses of body size evolution within Loliginidae suggest that a shift to a smaller body size optimum occurred along the lineage leading to *P. pulchella*, with some evidence of shifts toward larger sizes in the ancestors of *Loligo* and *Sepioteuthis*; these inferences seem to be robust to phylogenetic uncertainty and incomplete taxon sampling. The small size and juvenile-like morphological traits seen in adult *Pickfordiateuthis* (e.g., sepiolid-like fins and biserial sucker arrangement in the tentacles) may be due to paedomorphosis.

## Chloroplast Identification and Feeding Specificity of the Photosynthetic Sea Slug *Elysia papillosa*

Barber, K\* <sup>1</sup>; Middlebrooks, M.<sup>2</sup>; Bell, S. <sup>1</sup>; Pierce, S <sup>1,3</sup>.  
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The sacoglossan sea slug *Elysia papillosa* is associated with two species of the siphonaceous green alga, *Penicillus capitatus*, and less frequently, with *P. lamourouxii*, which frequently co-occur in mixed macrophyte beds. The slug is able to sequester chloroplasts from these algae inside of its own cells for short term use in photosynthesis. However, it is unclear if *E. papillosa* is choosing to consume and/or utilize both algal resources. In order to determine which algal species *E. papillosa* was consuming at the field site Sunset Beach, Tarpons Springs, FL, total DNA was extracted from individual slugs and the algal species matching the gene sequence of the chloroplast genomic gene, *rbcl* (large subunit of ribulose biphosphate carboxylase) was determined. The molecular data indicated that *E. papillosa* were consuming the same algal species from which they were collected. To determine if algal resource had any impact on mean body length of juvenile slugs when feeding on *P. capitatus* compared to *P. lamourouxii*, a laboratory feeding experiment was conducted. Over a three week period, *E. papillosa* fed *P. lamourouxii* achieved a mean body length that was significantly longer than recorded for slugs fed *P. capitatus*. It is surprising that *E. papillosa* grows more quickly while eating *P. lamourouxii* as previous studies indicate that they are significantly more likely to be found on *P. capitatus*. The reasons for this discrepancy are unclear, but may be related to preference or an improved survival while inhabiting *P. capitatus*.

## **MolluscaBase – the evolution of a community resource**

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MolluscaBase, a taxonomically oriented database that aims to provide an authoritative and continuously updated account of all molluscan species, is part of the family of expert databases embodied in WoRMS, the World Register of Marine Species. With its taxonomic content built and maintained by a team of international volunteer editors and its database maintained by a professional data management team at the Flanders Marine Institute (VLIZ) in Oostende/Belgium, MolluscaBase has been rapidly evolving since its inception in 2014. Addressing the needs of the malacological community, MolluscaBase grew beyond the traditional WoRMS focus and is currently adding terrestrial, freshwater, and extinct molluscan taxa. Coverage of synonyms, old combinations and fossil taxa still lags, but is growing quickly. While initially conceived mainly as a one-stop data source for species-level nomenclature and the associated taxonomic literature, the system is rapidly adding resources such as images, ecological attributes, and other context data. Presently, the database contains information on about 273,000 molluscan names at all ranks, of which more than 93,000 are currently accepted at the species level. Of these, more than 77,000 are recent species and more than 16,000 are fossil only. The presentation by two current editors will highlight capabilities, latest developments, and ongoing challenges of MolluscaBase and then open the floor to a Q & A session.

## **The potential invasiveness of the eastern heath snail in Montana**

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The eastern heath snail, *Xerolenta obvia* (Fam.: Hygromiidae), is a dryland massing snail centered in southeastern Europe but which occurs across Europe. In 2012, the snail was reported in Cascade County, Montana, USA and a large population was subsequently located over an estimated 30,000 ha area. Little is known about the eastern heath snail, either in its native range or in introduced areas of North America. This presentation reviews continuing studies on the life history, reproduction, and food habits of *X. obvia* in Montana. This information is essential to assess potential risks and to develop management strategies for this introduced snail.

## Can you do the can-can?: An analysis of the lifters of *Goniobranthus* nudibranchs

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In the last several years, the family tree of Chromodorididae has been undergoing refinement due to molecular work, indicating new relationships between taxa. The genus *Goniobranthus* is one clade of the Chromodorididae and used to be included within *Chromodoris*. This genus was determined to be non-monophyletic and *Goniobranthus* was separated in order to recognize well-defined clades. Molecular work to resolve the internal relationships in *Goniobranthus* has been limited and only recently has been undertaken. Through genetic sequencing, I have sequenced 182 new *Goniobranthus* specimens and added additional species from GenBank. I used two mitochondrial (COI and 16S) genes and one nuclear gene (H3) to begin to resolve the genetic relationships between *Goniobranthus* species. Through my phylogenetic analyses, I have discovered an interesting monophyletic group of *Goniobranthus* lifters, a species complex of *G. roboi* that consists of at least five species, and a species complex of *G. vibratus* and *G. conchyliatus*. Details of this newly documented group are presented here with discussion of the species complexes discovered and morphological differences that reflect the genetic differences will be discussed.

## ***Bulimulus* land snails (Bulimulidae) as species of concern in native and introduced ranges – an issue for the southern USA**

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*Bulimulus* spp. are land snails native mainly to Central and South America, and the West Indies, and do not include species native to the continental USA. Although their taxonomy and biology are not well studied, *Bulimulus* snails have not been considered species of agricultural concern in the USA, since available information suggested feeding habits centered not on crop plants, but on biofilms growing on surfaces. Three species of *Bulimulus* have become established in the continental USA in the last decades, and one species has also been reported from Hawaii. One of these species, a native of South America, has established permanent and increasing populations, and is expanding its distributional range, in urban and suburban residential and agricultural areas in Florida and other southern states. Pending confirmation by molecular studies, this species has been referred to as '*Bulimulus sporadicus*', and may be conspecific with *B. bonariensis sporadicus* (D'Orbigny 1835) from parts of Argentina, Bolivia, Brazil, and Uruguay. Property owners in several southern states have expressed concern about these snails as new arrivals, and as potential agricultural and/or health pests. Crop plant consumption or crop damage have not been directly linked to the snails to date, but effects of their presence on routine maintenance of fields and on harvesting activities have been reported. Meanwhile, several species of *Bulimulus*, including species similar to those established in the USA have been recognized as negatively affecting agricultural practices in South America, and one species has been shown to be a natural carrier of nematodes, a serious health and veterinary concern. These developments prompt the need for resolving taxonomic uncertainty, re-assessing risks represented by these snails to USA agriculture and health, including their current non-quarantine pest status, and elucidating aspects of their population dynamics that can be used in their control and containment.

## Setting Molecular Clocks: Cautionary Observations

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Although molecular clock analyses have been very popular for nearly a quarter century, the reliability of the analyses has received limited attention. Paleogeographic calibrations require a thorough examination of the geological literature. Events such as the formation of the Appalachians, the opening of the North Atlantic, and the formation of the Isthmus of Panama have been used as reference dates in studies on mollusks, but not necessarily in accord with the latest geology. Such calibration is also necessarily imprecise, due to the impossibility of determining exactly what stage of the geological process produced the key split. Many mollusks have a good fossil record, but this does not always lead to good fossil-based calibration of molecular clocks. Fossil-based calibration requires verification that the fossils accurately represent the clade in question, rather than uncritical acceptance of ages from a database. Paraphyly, wastebasket names, and homonyms (including misspellings) all can lead to highly inaccurate calibration points. Even if a calibration date is sound, it needs to be applied to the right point in the phylogenetic tree. Both biogeographic and fossil-based calibrations for mollusks have not always been suitably placed. Applying rates calculated in a previous study to another taxon often involves undue extrapolation, particularly when there are large life-history differences or phylogenetic distances between the previously-studied taxa and the current study. Rates of molecular evolution vary significantly within Mollusca, making interpolations risky as well. Some studies have errors in the use of statistics. Overall, molecular clocks need more alarms and less snoozing.

## **Neogastropods of the lower Waccamaw Formation**

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The lower Waccamaw Formation contains a rich basal Pleistocene fauna with an extreme abundance of mollusks. This diverse subtropical fauna is found in southeastern North Carolina and eastern South Carolina. Roughly 60% of the taxa is extant, and roughly 50% overlap with the Upper Pliocene Duplin Formation of the Carolinas. This study has collected and identified 525 species. In this presentation, I discuss the 139 species in my most speciose order, Neogastropoda; I will be focusing on the notable and the unknown species. 85 of these are in two superfamilies: 45 in Conoidea and 40 in Buccinoidea. Out of the 139, 26 are unidentified to species level, at least 12 are undescribed, and roughly 40 are additions to the known fauna. Half of these species are 9.5 mm or less in maximum size.

## **Bivalves of the lower Waccamaw Formation**

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The lower Waccamaw Formation contains a rich basal Pleistocene fauna with an extreme abundance of mollusks. Roughly 60% of the taxa is extant, and roughly 50% overlap with the Upper Pliocene Duplin Formation of the Carolinas. This diverse subtropical fauna is found in southeastern North Carolina and eastern South Carolina. This study has collected and identified 526 species. In this presentation, I discuss the 176 species of bivalves found; I will be focusing on the notable and the unknown species. Out of the 176, 24 are unidentified to species level, at least one is undescribed, and roughly 50 are additions to the known fauna. Half of the species are 1 cm or less in maximum size.

## Plans for Ensuring the Survival of South Florida's Tree snails

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Populations of Florida's native tree snails in the genera *Liguus*, *Orthalicus*, and *Drymaeus* have been subjected to a variety of pressures, habitat fragmentation and loss, development, overcollection, and, most recently, the introduction of the non-native predatory flatworm *Platydemus manokwari*, the New Guinea Flatworm (NGF). We explore and document the interaction of some of these effects in one location in South Florida and consider options for ensuring the survival of these species.

## **Changes in gastropod diversity based on land use, a case study from Anderson County Kansas**

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Tallgrass prairies are plant and animal communities which once covered much of the United States. The Nature Conservancy acquired 1450 acres of prairie land located near Welda, KS with goal of maintaining and enhancing native biodiversity within the imperiled tallgrass prairie ecosystem. These prairies have very deep soils and higher rainfall than other prairies found further west in the state. It has populations of the threatened plant, Mead's Milkweed and prairie chickens. Here we present results of our periodic surveys since 2004 at the Anderson County Prairies. The preserve contains both native tallgrass prairies as well as areas currently being used as cattle pastures. We have consistently found differences in gastropod diversity over the 15 years samples have been collected by land use with higher counts and different species at the non-pastured versus the pastured land. Differences in soils (pH, conductivity and NPK levels) between the two site types may account for the differences we find in the gastropod data.

## **Using citizen science to understand the origins of left-coiling garden snails *Cornu aspersum***

Davison, A\*.; Thomas, P.; 'Jeremy the snail' citizen scientists  
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Although some species of snail are naturally variable in their chirality, sinistral individuals occur very rarely in most species. The developmental and genetic basis of these rare mirror-imaged individuals remains mysterious. To resolve this issue, the finding of a sinistral garden snail called 'Jeremy' was used to recruit citizen scientists to find further sinistral snails. These snails were then bred together to understand whether their occurrence is due an inherited condition. The combined evidence shows that rare sinistral garden snails are not usually produced due to a major effect maternal Mendelian locus. Instead, they are likely mainly produced by a developmental accident. This finding has relevance to understanding the common factors that define cellular and organismal LR asymmetry, and the origin of rare reversed individuals in other animal groups that exhibit nearly invariant LR asymmetry.

## Size structure and morphometry of the Chinese snail *Hexaplex nigritus* (Gastropods: Muricidae) in the Ohuira lagoon, Ahome, Sinaloa.

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The Chinese snail, *Hexaplex nigritus*, is an endemic species in the Gulf of California. It is part of the marine resources of commercial, fishing, and ecological importance in the state of Sinaloa. There are few studies of aspects of the population dynamics of the species. So the objective of this work was to evaluate the size structure and morphometric relationships in the Ohuira lagoon, Ahome, Sinaloa. Monthly collections were made by free diving from May 2017 to June 2018. The height (from the operculum to the previous part), the width (widest part of the shell), and the length (siphonal channel) were measured from each organism. to the posterior margin of the shell) and the total weight. Histograms of length frequencies by climatic season were made. For the morphometric relationships between height (A) and length (L), they were fitted to a linear model, while height and total weight (PT) at a potential. A one-way ANOVA was performed to compare lengths and weights by climatic season. Also,  $t$  tests were applied to assess the significance of the value of  $b$  in the potential morphometry model. A total of 477 organisms were collected. The maximum length was presented in summer (150 mm) and the minimum in winter (80 mm). In total weight, the highest value was recorded in autumn (600 g) and the lowest in winter (400 g). For the A-LT relationship, the value of the highest determination coefficient was in spring ( $R^2 = 0.7936$ ) and the lowest in winter ( $R^2 = 0.6802$ ). For the PT-A, in all the climatic stations presenting a negative allometric growth, which indicates that the snail is less heavy concerning height. With the information obtained, the guidelines can be given to establishing a sustainable use of the species in the bay of Ohuira, Ahome, Sinaloa.

Poster

## Management of *Bulimulus sporadicus* (d'Orbigny, 1835) in the Panhandle, FL

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*Bulimulus sporadicus* (d'Orbigny, 1835) is a non-native tree snail from the West Indies that was first reported in Florida in 2009, but has spread to counties near Orlando, Tampa, and Tallahassee. Thought to be a detritivore, *B. sporadicus* was not considered an agricultural pest until around 2015 when peanut growers in the Florida Panhandle started seeing the snail "in large numbers." The infestations do not seem to be causing significant crop damage, but current peanut-sorting systems cannot sort peanuts from these snails.

Preliminary surveys were conducted in the Florida Panhandle to investigate snails affecting peanut crops in Santa Rosa and Okaloosa Counties. Peanuts are grown in rotation with cotton, and thus cotton fields were also surveyed. In one cotton field in Baker, Florida, the number of live snails were counted in 14 plots of 1-meter row of cotton. Snail surveys were conducted in early July when plants were full-grown and again in early October during harvesting. Snails seemed to be aggregating and eating detritus, but growers report snails covering and eating young cotton plants, spring weeds, and their winter cover crop. Snails also often aestivate in large numbers on tractors and other equipment, making it easy to spread the snail throughout and between fields.

The scientific literature for *B. sporadicus* is limited. Our preliminary laboratory studies show that metaldehyde may not be as effective for the species as iron-phosphate. Other preliminary observations show that this snail prefers detritus but eats fresh dandelion leaves, romaine lettuce, and carrots. Our future research will test *B. sporadicus* diet preferences and compare laboratory and field results regarding molluscicide efficacy and life history of the snail, i.e. age to maturity. We also plan to utilize our Division's 3D print lab to develop traps for this species.

## **A Dirty Dorid Disaster: The First Molecular Phylogeny of the Nudibranch Family Discodorididae Bergh, 1891**

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Due to increases in ocean temperature, the overall biodiversity of coral reefs will continue to change, and key predators such as nudibranch sea slugs may be decimated by the lack of prey. One sponge-eating nudibranch family nicknamed the "Dirty Dorids", also known as the Discodorididae, are generally medium to large cryptic nudibranchs with retractable gills. Discodorids are found in almost every marine ecosystem around the world, making it one of the most diverse families within Nudibranchia. The diversity and systematics of the Discodorididae is not well understood due to the high number of diverse species and genera, few curated specimens maintained in ethanol, and major confusion on the evolution of several basal genera. My goal is to determine the biodiversity and evolutionary history of Discodorididae by utilizing specimens representing 25+ genera composed of numerous described and undescribed species. Using Sanger sequencing, I generated a molecular phylogeny of the mitochondrial genes cytochrome oxidase I (COI) and 16S and the nuclear genes 18S, 28S, and histone 3 (H3), which will then be supported with morphological features used for identification. Within Discodorididae, we mapped the evolutionary history of several unique morphological traits including the presence of extra sensory outgrowths known as caryophyllidia. In regard to caryophyllidia, we expect to find two major subgroups: one composed of genera with caryophyllidia and a second group of genera without caryophyllidia. We know that caryophyllidia evolved only once in the evolutionary history of Nudibranchia; however, our results have shown that caryophyllidia has evolved multiple within the Discodorididae family, potentially due to the complex nature and varied organization of the caryophyllidia.

## Ancestral or inverted? An inexpensive PCR-based test effectively contrasts alternative mitochondrial gene orders within chitons

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The phylogeny of chitons within Mopalioidae Dall, 1889 (Polyplacophora: Acanthochitonina) is still unresolved and competing classifications are in use, with some (e.g., Mollusca-Base) using priority to prefer Tonicellidae Simroth, 1894 to Lepidochitonidae Iredale, 1914 for a similar but not identical assortment of genera. The problem with assigning *Lepidochitona* Gray, 1821 to Tonicellidae is that sequence analyses have instead shown that *Tonicella* Carpenter, 1873 and *Mopalia* Gray, 1847 have close affinities, relative to *Lepidochitona* and related genera (e.g., *Cyanoplax* Pilsbry, 1892, and *Nuttallina* Dall, 1871). In fact, Tonicellidae should be considered a junior synonym of Mopaliidae, restricting Lepidochitonidae to *Lepidochitona* and related genera. Previous sequencing of complete mitochondrial genomes revealed that *Cyanoplax* and *Nuttallina* share an inverted cluster of tRNA genes, relative to the ancestral gene order of this tRNA cluster found in other chitons and even other molluscan classes. We used PCR with custom pairs of primers to test selected genera and species within Mopalioidae, in order to reveal which have either the ancestral or inverted versions of what is presumed to be a rare change in mitochondrial gene order. Species with this derived inversion were inferred to have shared a common ancestor that already had this inversion. Our results agreed with separate phylogenetic estimates previously obtained by one of us (DJE) for mitochondrial 16S and COI gene sequences. We have discovered that some species of "*Lepidochitona*" but not its type species, *L. cinerea* (Linnaeus, 1767), belong to a monophyletic (mostly New World) subgrouping of Lepidochitonidae with the derived inverted mitochondrial gene order. Our sequence results further strongly support the monophyly of a *Mopalia* + *Tonicella* grouping apart from Lepidochitonidae, which is tentatively supported as monophyletic. Within Lepidochitonidae, both sequence analysis and the phylogenetic distribution of an inverted tRNA cluster confirm a Lepidochitonidae subclade that renders "*Lepidochitona*" as polyphyletic.

## Choice of refuges of the pygmy octopus *Paroctopus digueti* in the Ohuira lagoon, Ahome, Sinaloa

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Octopuses are an important resource in the fisheries of many coastal regions of the world, accounting for up to 10% of world production. In the Mexican Pacific for the octopus *Paroctopus digueti*, studies are limited. The objective of the present study is to present an evaluation on the choice of *P. digueti* shelters in the Ohuira lagoon, Ahome, Sinaloa. Seasonal samplings were carried out from autumn 2016 to autumn 2017. Octopuses were collected with and without refuges diving with snorkels at a depth of 4 m in the bay of Ohuira. The organisms were placed individually inside labeled plastic bags, each label containing the information for each individual. Refuges chosen by pygmy octopuses consisting of valves and shells, as well as other types of objects were identified. To create frequency histograms, the characteristics of each refuge were considered, as well as those with hatching eggs (OF- Ovigerous Females) and the hatching of paralarvae (PH). Of the total number of organisms that were captured, 193 were found in shelters. Regarding the presence of *P. digueti* in the shelters, a greater preference for them was observed in the females, which were found during the hatching phase (Ovigerous) and paralarvae, with a greater presence in the valves of the clam *Megapitaria squalida* (36.84%), and the clam *Laevicardium elatum* (31.58%) and to a lesser extent inside a glass bottle (5.26%), sharing this refuge with the oviposition phase of the snail *Hexaplex (Muricanthus) nigritus* (CHMn). The males showed a greater affinity with the Panamanian clam *Trachicardium* (10.53%). In this current study, female pygmy octopuses from *P. digueti* preferred the bivalve shells of species such as the clam *Megapitaria squalida* and the clam *Laevicardium elatum*.

Poster

## **Growth of *Leukoma asperrima* as a possible fishing resource in Sinaloa.**

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Marine mollusk studies establish benchmarks that guide fisheries management. The bivalve *Leukoma asperrima* represents a source of economic income for some populations in Central and South America since these products are highly prized for being an important source of protein, however, in Mexico there is no information on the biology and ecology of these species. Therefore, it is intended to evaluate growth patterns based on the size structure of *L. asperrima* on 6 islands of Laguna de Ohuira, Ahome, Sinaloa. Monthly collections were carried out in the, from October 2016 to October 2017 with six quadrants (1m<sup>2</sup>) for each island. Length frequency histograms were performed. For the calculation of the growth parameters of the von Bertalanffy equation, the FISAT II program was used, using the ELEFAN I routine. A total of 3,225 organisms were captured. The height presented similar patterns, with 30 mm on Isla Bledos, Mazocahui I, and Mazocahui II, while on Isla Bleditos and Tunosa it was 25 mm and 20 mm respectively. For *L. asperrima*, the asymptotic length was set at 42 mm, with a growth coefficient ranging from  $K = 0.84$  on Patos Island to  $K = 1.5$  on Bleditos and Tunosa Island. With growth ranging from 26 mm in height on Isla Patos to 35 mm on Isla Bleditos and Tunosa in its first year of life.

Poster

## Selective Predation on Native Mussels in Middens Along Great Lakes Inland Rivers

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Predators are organisms that gain nutrients from killing and eating other organisms and are an integral aspect of our ecosystems throughout the world. Predators may have a negative impact on rare species if they select for rare species as prey. It is important to understand what prey predators select for and whether predators are preferentially selecting endangered species as it is key for conservation efforts. The purpose of this study was to determine if predators select for a certain species of native freshwater mussels as well as a certain sized mussels (i.e., length, thickness, and weight). Sizes of freshwater mussels were compared from two middens on the Grand (n = 1) and the Flat (n = 1) rivers; the Flat River is a tributary to the Grand River within the Lake Michigan Drainage, Michigan, USA. This study found that longer, therefore assumed to be older, mussels are found in the river when compared to the midden sites. Freshwater mussels found most commonly in the Grand River midden sites were *Epioblasma truquetra* (24.3%), *Amblema plicata* (24.3%) *Lampsilis cardium* (15.1%) while the most common mussel species in the Flat River midden was *Ventustaconcha ellipsiformis* (51.3%) . Rare species were also found in the midden, including the federally endangered *Epioblasma triquetra* (GR = 24.3%, FR = 10.3%). Unique to this study was the measurements taken of the weight and shell thickness as well as if the mussel was scratched or not because midden sites are possible depositional zones if shells do not have scratch marks on them. This study presents data on mussel predation and predator selection of mussel prey in the Great Lakes region. This study shows information about the impacts that predators have on an ecosystem, as well as more understanding about predators.

Poster

## **Spatiotemporal Patterns of Non-native Terrestrial Snails and Slugs in the Contiguous United States**

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The contiguous United States (CONUS) harbor a significant non-native species diversity. However, spatiotemporal trends of some groups such as terrestrial gastropods (i.e., land snails and slugs) have not been comprehensively considered, and therefore management has been hindered. Here, our aims were to 1.) compile a dataset of all non-native terrestrial gastropod species with CONUS occurrence records, 2.) assess overarching spatiotemporal patterns associated with these records, 3.) describe the continental origin of each species, and 4.) compare climatic associations of each species in their indigenous and introduced CONUS ranges. We compiled a georeferenced dataset of 10,097 records for 22 families, 48 genera, and 69 species, with > 70% of records sourced from the citizen science database iNaturalist. The species *Cornu aspersum* Müller, 1774 was most prevalent with 3,672 records. The majority (> 92%) of records exhibit an indigenous Western European and Mediterranean distribution, with overlap in broad-scale climatic associations between indigenous and CONUS ranges. Records are most dense in urban metropolitan areas, with the highest proportion of records and species richness in the state of California. We show increased prevalence of non-native species through time, largely associated with urbanized areas with high human population density. Moreover, we show strong evidence for a role for analogous climates in dictating geographic fate and pervasiveness between indigenous and CONUS ranges for non-native species.

## **The nudibranch *Berghia stephanieae* is a new experimental system for studying the sequestration of external cells and structures**

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The sequestration of functional structures or cells from one organism inside the cells of another is fundamental to the origin of eukaryotes. Interestingly, multiple metazoan lineages have secondarily evolved to sequester dietary cells and organelles (e.g., dinoflagellates, chloroplasts, nematocysts), independent from the original eukaryotic endosymbioses. One example is the ability to sequester exogenously generated cnidarian nematocysts (small venom-filled capsules). This ability is found in several divergent animal lineages, including ctenophores, nudibranchs (Mollusca), flatworms (Platyhelminthes), and acoels. In nudibranchs, which are shell-less gastropod molluscs, we know that nematocysts are harbored in specialized organs called cnidosacs in the tips of dorsal projections called cerata, but little is known about how this structure develops, or about the specific cellular processes involved in nematocyst uptake. Here, we present the nudibranch species *Berghia stephanieae* as an emerging experimental system for studying both pre- and post-metamorphic developmental processes, including the ability to sequester cnidarian nematocysts. Following early development via a stereotyped spiral cleavage program, *B. stephanieae* embryos make a lecithitrophic veliger larva, and eventually hatch out of their egg cases as juveniles, hunting for the sea anemone *Exaiptasia pallida*. Within two days after juveniles begin to feed, the cnidosacs develop at the tips of the first digestive diverticula (branches). This step occurs prior to cerata bud formation, thus rows of cerata only begin to emerge after the first cnidosacs develop. Nematocysts can already be seen within the cnidosacs at this stage. Subsequent development involves the elongation and growth of cerata, as well as the addition of further rows of cerata. For further functional work on the cellular processes involved in nematocyst uptake, we are also developing genome and transcriptome resources for *B. stephanieae*. This research begins to provide a framework in which to begin comparative analyses of convergent sequestration and symbiosis across various metazoan lineages.

## **A biodiversity informatics approach to family-group level classification of freshwater mussels (Bivalvia: Unionoida)**

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The MUSSEL Project Database (Graf & Cummings, <http://mussel-project.net/>) was developed as a resource for studying freshwater bivalve systematics. The MUSSELpdb is distinguished from similar biodiversity informatics initiatives and rendered awesome by the inclusion of "taxonomic opinions." A taxonomic opinion relates three items: 1) a taxonomic work, 2) a named taxon, and 3) a valid taxon that circumscribes the nominal taxon in that publication. For the 958 valid freshwater mussel species and their >4000 synonyms, the MUSSELpdb reports more than 65,000 taxonomic opinions, providing the history of classification that underpins current usage.

Taxonomic opinions regarding genera and species are relatively easy to manage. At minimum, any reference to a binomial species also refers to a genus. But, traditionally, supra-generic taxonomy has been restricted to works that dealt explicitly with family-group level classification. Nowadays, the basis for taxonomy is found in cladograms that result from phylogenetic analyses. However, branching diagrams do not align easily with the data structure of taxonomic opinions the way that synonymies do.

To solve this problem, I am developing a database structure in FileMaker Pro, with analysis resources coded in Python. I have captured cladogram topologies from each of the 213 publications (from 1989 to 2020) with phylogenetic information on freshwater mussels. These works account for 369 cladograms and 6488 clades (i.e., nodes with descendant terminal species-group lineages). Half of these freshwater mussel phylogenetic studies have been published since 2015, and this period coincides with a new phase of vigorous post hoc revisions and clade-naming based on phylogenetic results. My talk will explore how these informatics tools can facilitate comparisons among cladograms to identify conflicting phylogenetic signals and to highlight opportunities for fruitful research.

## **Growth aspects of the catarina clam *Argopecten ventricosus* in the wild population in Guasave, Sinaloa.**

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The commercial exploitation of the catarina clam *Argopecten ventricosus* is carried out mainly by the fishing activity of cooperatives and permit holders in Mexico, which is increasing and represents an alternative to supply the demand for products at the national and international level. It is important to consider that every species that can be exploited needs to increase its knowledge of its biology and its fishing potential. Therefore, the objective of this work was to evaluate the size structures, morphometric relationships, and growth of the catarina clam *Argopecten ventricosus* in a wild population in Guasave, Sinaloa. The organisms were collected by free diving in the San Ignacio-Navachiste-Macapule lagoon complex in 2018, 2019, and 2020. The maximum distance between the anterior and posterior parts of the valve was recorded from each clam (Anteroposterior length = L), the distance between the apex and the commissure or lower margin of the leaflet (back-ventral width = A) and the maximum distance of the external part between closed right and left leaflets (thickness = E) and the total weight. For the calculation of the growth parameters of the von Bertalanffy equation, the FISAT II program was used, using the ELEFAN I routine. A total of 460 organisms were captured. The size range ranged from 2 to 9 cm in height ( $5.34 \pm 0.67$  cm), length from 4 to 8 ( $5.87 \pm 0.52$  cm), and a total weight of 30 to 110 g ( $55.32 \pm 12.48$  g). For the AL relation, the value of the coefficient of determination highest in 2019 ( $R^2 = 0.8414$ ) and lowest in 2020 ( $R^2 = 0.7724$ ), in the PT-A the maximum was in 2018 and the minimum in 2019. The asymptotic length was fixed in 8.4 cm (2020) to 8.8 cm (2018), with a growth coefficient that varies from  $K = 0.750$  (2020) to  $K = 0.998$  (2018).

Poster

## **Chromodorid Nudibranch *Felimare ruthae* expands diet and range on Florida's Gulf Coast**

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Range expansions of nudibranchs have been recently reported across different habitats. This includes chromodorid nudibranchs, which are carnivorous sea slugs with highly specialized diets that typically feed on only 1-2 sponge species. *Felimare ruthae* is a chromodorid nudibranch that is found in the Caribbean and southern Gulf of Mexico, but has not been previously reported on Florida's Gulf Coast. In 2019, a population of *F. ruthae* appeared on the limestone ledges off of Clearwater, Florida. Diving surveys were conducted to determine the abundance of the nudibranch and the substrate on which it was found. The slug was primarily found crawling and feeding on a large species of sponge that did not look like *Dysidea*, its documented food source. Morphological analysis and DNA barcoding of sponge samples confirmed that the sponge was in genus *Spongia*, indicating that this population of *F. ruthae* also underwent a diet expansion. The defensive secondary metabolites found in *Spongia* are not the same in *Dysidea* and this suggests that the nudibranch had to develop mechanisms that allow it to ingest the chemicals in its new food source. Causes for slug range expansions are diverse and include both natural and anthropogenic reasons, however, the processes that caused the range and diet expansion of *F. ruthae* remain unknown. In this instance, the dietary expansion may have facilitated the range expansion, but that relationship remains unclear.

Poster

## Hawaii's Freshwater Snails: Understudied and Unprotected

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Freshwater ecosystems and their associated fauna, including gastropods, are among the most critically imperiled systems in the world. Accurate data regarding species identities, distributions, abundances, and range contractions are all critical for developing best practices to manage land and aquatic resources. Freshwater snails native to Hawaii belong to two families, Neritidae with two species and Lymnaeidae with four species. While the currently recognized number of freshwater snail species in Hawaii is considerably lower than that for terrestrial snails in the islands, the potential for extinctions may be higher. Hubendick was the last to publish on the taxonomy of Hawaiian Lymnaeidae, but no conservation assessments of lymnaeids in Hawaii have been done in the last century, with the exception of *Erinna newcombi*, which is protected under the US Endangered Species Act. Hubendick recognized five species of native lymnaeids in a single genus *Lymnaea*, and all were considered widespread on multiple islands, except for *L. (Erinna) newcombi*. Others subsequently recognized only two species in the genus *Erinna* and two in *Lymnaea*. A fifth species was recognized, but with uncertain affinities for either genus. No updated taxonomic framework is available for developing effective conservation assessments, yet preliminary surveys and phylogenetic analyses of lymnaeids indicate that there are at least six, and possibly up to eight endemic species, including the only two species of sinistral lymnaeids in the world, *Lymnaea producta* and *L. reticulata*; previously synonymized and treated as a single species, *L. reticulata*. Less than 50 individuals of these sinistral species have been recorded in the last 20 years and are associated with 'vertical wetlands' that are highly ephemeral. Endemic freshwater lymnaeids are adapted, and in many cases, restricted to these habitats. Any impacts to water supply or the spread of invasive species is likely to extirpate these populations, possibly resulting in extinction.

## **Composition and community structure of soft-bottom mollusks on the sand bar El Mogote, Bahía de La Paz, Mexico.**

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It is important to carry out research that deepens the knowledge of the malacological community structure and contributes to proposals of management methods and alternatives for the sustainable use of insular marine resources. We analyzed the composition and community structure of soft-bottom mollusks of sand bar El Mogote and its possible relationship to some environmental variables. During February and September 2003, 192 samples were collected: 96 were biological samples and 96 were sediment samples. The temperature, depth, sediment type, and organic matter were used as environmental indicators. The composition, abundance, and diversity of the malacological community were analyzed using ecological indexes. 3318 organisms were recorded and grouped in two classes: Bivalvia with 2372 individuals (9 orders, 17 families, and 43 species); the most abundant species was *Chione californiensis* (23%); the class Gastropoda included 946 organisms (6 orders, 18 families, and 52 species); the most abundant species was *Crassispira cerithoidea* (17%). In the warm season a total of 67 species were listed, predominating the bivalves, while in the cold season 62 taxa were collected and majority were gastropods. The highest values of richness and abundance were found south of the sand bar in sediments of slime and coarse sand, respectively. At this site, the specific richness (95 taxa) was higher compared to other sites from different latitudes of the western Gulf of California.

Poster

## Evolution of diverse host infection mechanisms delineates a cryptic adaptive radiation of freshwater mussels

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North American watersheds contain the world's highest diversity of freshwater mussels (Unionoida). They collectively exhibit little evidence for ecological differentiation during the adult phase of their life cycle. In contrast, their brief parasitic larval phase involves the infection of a wide diversity of fish hosts. Gravid female mussels have evolved multiple methods for increasing the probability of infecting a host. Many species have a proactive strategy that entails the use of lures to change the behavior of the hosts, e.g., eliciting a feeding response. In this study, we used a genomic approach (ddRAD-seq) to place the diversity of infection strategies used by 54 lampsiline mussels into an evolutionary context. Ancestral state reconstruction recovered evidence for early evolution of mantle lures in this clade, with conglutinates and broadcast infection strategies both being independently derived twice. The most common infection strategy is a mixed one in which mantle lures are clearly the predominant infection mechanism, but gravid females may also release "fragile" conglutinates at the end of the season. This mixed infection strategy clade shows some evidence of an increase in diversification rate. Broad linkage between infection strategies and predominant host genera is also seen in other lampsiline clades: worm-like mantle lures of *Toxolasma* with sunfish (*Lepomis*); complex conglutinates (*Ptychobranthus*), small mantle lures (*Medionidus*, *Obivaria*), or host capture (*Epioblasma*) with darters, and tethered brood lures (*Hamiota*) with bass. Our results confirm that lampsiline mussel clades exhibit specialization in the primary fish host clades their larvae parasitize, and in the host infection strategies they employ to do so. They also support the hypothesis that partitioning of fish hosts may be an important factor in maintaining species diversity in mussel assemblages. We conclude that, taking their larval ecology and host-infection mechanisms into account, lampsiline mussels may be viewed as a cryptic adaptive radiation.

## **Species delineation in highly threatened Hawaiian land snails, (Achatinellidae: *Auriculella*) using geometric morphometrics**

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Hawaii supports a spectacular land snail radiation with >750 species plus numerous undescribed taxa. The Achatinellidae are diverse land snails inhabiting Pacific Islands, with the majority of species endemic to Hawaii. Their distributions, shell morphology and diversification have contributed substantially to our understanding of evolution and island biogeography. Historically, taxonomists have relied on shell morphology for distinguishing among mollusc species, and achatinellids are no exception. However, shell characteristics may vary substantially intraspecifically, with such variation overlapping interspecifically, resulting in taxonomic ambiguity. Delineating morphologically similar species often requires taxonomic expertise, examination of numerous specimens, and the time to develop both. Unfortunately, there is often scarce material available to study rare species, hampering taxonomic studies and further limiting critical research for conservation. Natural history museums house large numbers of specimens, usually shells for molluscs, and sometimes may be the only source material for some taxa. We are applying geometric morphometrics to better understand shell characteristics of two pairs of morphologically similar species within the genus *Auriculella* (*A. uniplicata* and *A. crassula*; *A. pulchra* and *A. ambusta*). These species are not sympatric, although populations have been recorded from the same mountains. Phylogenetics indicate that the species in each of these pairs are not sister taxa, yet species in each pair are similar enough that they are difficult to reliably distinguish conchologically. Using specimens from which we have genetic data and toptotypical material from museum collections, we quantitatively explore the evolution of shell shape in these species using geometric morphometrics. This will potentially enable rapid and objective delimitation of morphologically similar species and facilitate the identification of historical museum specimens. These data will not only inform our understanding shell shape evolution, and changes in shell morphology over time, but also provide critical information for developing conservation management strategies for remaining populations.

## **Quantitative measures and 3D shell models reveal interactions between bands and their position on growing *Cepaea* shells**

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Although historic studies on the snail *Cepaea* were crucial in establishing the role of selection in understanding polymorphism, the qualitative scoring of inherited shell characters has led to a lack of knowledge regarding the mechanisms that control fine variation. We have combined empirical measures of quantitative variation and 3D modelling of shells to understand how bands are placed and interact. By comparing fully banded individuals against shells lacking individual bands, we determine the impact of their absence on the position of the remaining bands. We also use 3D models of shell shape and banding pattern, inferred from 2D photos using ShellShaper software to understand whether differences in band widths are simply a product of greater shell growth on the underside. These findings together provide a general method that may be used for comparative studies of quantitative banding variation in snail shells, the extraction of growth parameters, and morphometrics.

## **Twenty-five Year Trends in the Soft Sediment Molluscan Communities of Tampa Bay, Florida, USA**

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Molluscan species data were compiled from the Environmental Protection Commission of Hillsborough County's benthic monitoring database. The database comprised 1,791 sediment grab samples collected over a 25-year period (1993-2017) as part of the Tampa Bay Estuary Program's Bay-wide Benthic Monitoring Program. A total of 1,180 benthic macrofaunal taxa were identified with the mollusks being represented by 361 taxa or approximately 30.6% of the total taxa. Mollusks ranked as the second most species rich and second most abundant phylum behind the annelids. The mollusk species were represented by 214 gastropods, 134 bivalves, 6 chitons, 6 scaphopods and a single aplacophoran. The bivalve *Mysella planulata* was the most abundant mollusk in Tampa Bay, accounting for 16% of the molluscan abundance and was present in 41% of the samples followed by the gastropod *Caecum strigosum* which accounted for 10% of the molluscan abundance and was present in 17% of the samples. This presentation will examine the distribution and 25-year population trends of some of the dominant soft sediment molluscan species in Tampa Bay as well as for the overall molluscan community. Increases in species richness and abundance were observed over the 25-year monitoring period and reflect improvements in Tampa Bay's water quality.

## **Biogeographic regions within Jamaica defined by land snails**

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A biogeographic region is an area defined by its unique flora and fauna. Most research on biogeographic regions has been done on global, continental or oceanic scales, often based on vertebrate or floral taxa. Terrestrial mollusks have lower vagility so biogeographic regions defined based on vertebrates will miss many areas of endemism for snails. Jamaica has more than 500 endemic species of land snails, but no previous study has used quantitative methods to determine biogeographic regions within Jamaica based on snails or any other taxon. Rosenberg & Muratov (2006) recognized 6 regions on a qualitative basis. Hierarchical cluster analyses using UPGMA were used to delineate biogeographic regions based on species diversity from Jamaican Biotic Survey (JBS) sites. JBS surveyed more than 600 sites around Jamaica between 1999-2002. Presence-only data was used to delineate regions in two different ways: based on raw site data and with groups of 2 or more sites in the same 2 km<sup>2</sup> grid square combined. For both datasets, the first division of the dendrogram occurred in the far eastern portion of Jamaica, corresponding with the Blue Mountain Block of Jamaican geology, and the second division occurred in the western portion of Jamaica with boundaries similar to but not exactly aligned with the Hanover Block. The remaining central area corresponds with the Clarendon block. These blocks may have emerged separately from the ocean and each area shows 20% or greater endemism. Further divisions shown on the dendrograms do not reflect obvious geographic patterns and also have little to no endemism. Further study is needed to see if these biogeographic areas are reflected in phylogenies of Jamaica snails.

## First histochemical and ultrastructural characterization of the esophageal pouch cells in chitons (Mollusca, Polyplacophora)

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The digestive system of polyplacophorans is still poorly investigated and electron microscopy studies are lacking. The digestive system of chitons includes a pair of pouches connected to the posterior region of the esophagus, which are the second largest glands of their digestive system, after the digestive gland. These esophageal pouches, known as sugar glands because they contain a fluid rich in polysaccharide digesting enzymes, were investigated in *Chaetopleura angulata* and *Acanthochitona fascicularis* using light and electron microscopy techniques. In both species, the pouches contain a dense array of finger-shaped villi. The villi epithelium includes absorptive cells, basophilic secretory cells, mucus-secreting cells and basal cells. Some absorptive cells have a dense cover of long microvilli, whereas other absorptive cells have a border of short and sparse microvilli. Both types of absorptive cells contain several lysosomes, mitochondria, peroxisomes with crystalline inclusions, some lipid droplets and large amounts of glycogen. Detection of arylsulphatase activity was used to confirm the identification of lysosomes. The Golgi apparatus is not particularly developed in these cells. The basophilic secretory cells are characterized by the presence of many highly electron-dense vesicles, with a glycoprotein content, a large number of rough endoplasmic reticulum cisternae and a highly developed Golgi apparatus. Mucus-secreting cells are characterized by very large vesicles containing acid polysaccharides. These cells also have a highly developed Golgi apparatus. Basal cells containing oval electron-dense vesicles less than 1  $\mu\text{m}$  in length are found at the base of the epithelium in contact with the basal lamina. Cytoplasmic extensions with the electron-dense vesicles spread out from the cell body that contained the nucleus, some mitochondria and other organelles. In some ultrathin sections, connections between basal cells and nerve terminals were observed. It can be concluded that these glandular pouches are involved in extracellular and intracellular digestion, and accumulate reserves.

## **De novo assembly and annotation of the Pacific calico scallop (*Argopecten ventricosus*) transcriptome for the discovery of immune-related genes**

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De novo assembly and annotation of the Pacific calico scallop (*Argopecten ventricosus*) transcriptome were performed to get immune and immune-related genes. Scallops were challenged with inactivated *Vibrio parahaemolyticus* IPNGS16. RNA from gill, adductor muscle, digestive gland, hemocytes, and gonad was pooled for the construction of a single cDNA library that was sequenced by NextSeq 500 platform 2 × 75 paired-end chemistry. Before assembling with Trinity, reads were analyzed with FastQC, Trimmomatic, and Prinseq. Assembled sequences were analysed by CD-HIT-EST and TransDecoder. An annotation was performed against NCBI-nr and RefSeq protein databases and KAAS (KEGG). RT-qPCR was performed to get expression of immune and immune-related genes in scallops treated with probiotic bacilli added to culture water. The assembly yielded 107,516 contigs. TransDecoder yielded 25,285 sequences of which, 20,398 were annotated against the NCBI-nr protein, most of them scored with *Crassostrea gigas*. Sequences mapped to gene ontology (15,262) were distributed in molecular functions (~13,000), cellular components (~11,000), and biological processes (~13,000). The KAAS analysis showed biological categories for metabolism (13%), cellular processes (12%), processing of genetic information (10%), organismal systems (19%), environmental information (13%), and human diseases (33%). Within the organismal systems, 467 immune and immune-related genes (KO) were identified. Sixty-four immune and immune-related genes were annotated/blasted against the NCBI-nr and RefSeq protein databases. Bacilli significantly increased the expression of the HSP70 and PRP. The analysis of gene transcripts involved in the immune response of *A. ventricosus* will lead to a better understanding of its immune response against pathogens in culture systems.

Poster

## Exploring the Diversity of Coral-Boring Bivalves in the Florida Keys National Marine Sanctuary

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Coral reefs are diverse ecosystems and provide critical habitat for many species. The health of coral reefs depends on a network of complex interactions between organisms living within and on the reef, yet many of these interactions are not well understood. Common, yet poorly studied, constituents of coral reefs include the “coral-boring bivalves” - a polyphyletic assemblage of molluscs that use mechanical and/or chemical mechanisms to bury into living or dead corals. The aim of this study was to support ongoing conservation efforts in the Florida Keys National Marine Sanctuary (FKNMS) by using a molecular approach to determine the identities and species richness of the coral-boring bivalve community. An additional goal was to explore relationships between these species and those on other reefs worldwide to determine if some species are truly cosmopolitan, as has been hypothesized. Our examination used a variety of molecular markers (mtDNA: COI, 16S rRNA, 12S rRNA; nuclear DNA: H3, 28S rRNA, 18S rRNA) and was based on freshly collected samples from the FKNMS, in addition to previous collections available in the Genetic Resources Repository at the Florida Museum of Natural History. Our results supported the presence of at least eight species of coral-boring bivalves in the FKNMS, spanning three bivalve families. Also, due to high levels of sequence variation found in *Leiosolenus bisulcatus*, *Lithophaga antillarum*, and *Petricola lapicida*, there is the suspected presence of three additional cryptic species. Increased knowledge of boring bivalve species identities/diversity in the FKNMS should lead to a better understanding of their interactions with corals and the health of reef ecosystems.

## **Distributions of non-native terrestrial molluscs within and among Hawaiian Islands: implications for statewide management**

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Human-mediated transport has led to the introduction of many non-native terrestrial molluscs to the Hawaiian Islands. However, we lack an archipelago-wide framework for understanding how human-mediated transport and other ecological factors influence distributions of non-native terrestrial molluscs within and among islands in the archipelago. To understand non-native terrestrial mollusk distributions across the archipelago better, we surveyed 519 sites on Kauai (71 sites), Oahu (102), Maui (128), Hawaii (120), Lanai (19), and Molokai (80). In addition to exploring how richness and assemblage structure differed among islands, we also analyzed whether non-native terrestrial mollusk assemblages differed between low (< 500 m) and high (> 500 m) elevation areas. Higher species richness on Oahu support the hub-spoke model that asserts that species first become established on Oahu (main port for import of goods) and then colonize the other islands. However, we found that once a species is established in the archipelago, few barriers limit its ability to colonize other islands. Within island differences in assemblage structure between low and high elevations, with high elevation areas dominated by species from temperate regions and low elevation areas dominated by tropical species, are larger than those among islands; this finding highlights that within island ecological factors are currently more important than between island dispersal barriers in structuring land snail assemblages. Although more effort is certainly needed to prevent initial introductions to the archipelago, more attention to inter-island transport of non-native molluscs is warranted. Focus on species from temperate regions is particularly critical if conservation managers are going to mitigate the deleterious impacts non-natives are having on native flora and fauna, as high elevation areas are often the last refuges of native species in the Hawaiian Islands.

## The Effects of Hurricane Irma on a Long-Standing Population of Photosynthetic Sacoglossan Sea Slugs

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The ability to photosynthesize by stealing chloroplast from food algae, known as kleptoplasty, has made sacoglossan sea slugs the subject of numerous studies. The ability to maintain active chloroplast varies widely between sacoglossan species, but some are able to photosynthesize for many months after feeding. *Elysia crispata* is a large Caribbean sacoglossan which can feed on and sequester chloroplasts from multiple species of algae and maintaining functional photosynthesis for 3-4 months post feeding. In the Florida Keys there is an ecotype of *E. crispata* which lives in mangrove swamps and adjacent habitats, known as the clarki ecotype. A large population of clarki ecotype *E. crispata* in a borrow pit on Crawl Key has been the basis for many studies dating back to the 1960's and continuing through the 2010's. In 2017 Hurricane Irma caused widespread devastation to the Florida Keys and removed any trace of the slugs from this location. A series of detailed searches on numerous dates throughout 2018 and 2019 failed to locate a single *E. crispata*. A detailed survey in 2019 found that the algal population, including important food sources utilized by *E. crispata*, had completely rebounded following the hurricane although the slugs have not returned. The reason the slug population has failed to repopulate is not clear but may be due in part to their very short larval dispersal stage. Although the clarki ecotype can be found in other locations in the Florida Keys, the loss of this population is a setback as it represented one of the best studied populations of photosynthetic sea slugs.

## **A morphometric hypothesis of species diversity in the freshwater snail genus *Gyrotoma* (Pleuroceridae)**

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Alabama has long been recognized as an aquatic biodiversity hotspot, and the Coosa River, in particular, was home to over 80 endemic freshwater snail species. Due to human activity, over 40% of the snails have been extirpated including the pleurocerid genus *Gyrotoma*. *Gyrotoma* species varied in terms of shell shape and sculpture, and were restricted to certain reaches of the Coosa. Diversity estimates based on shell morphology have ranged from 44 nominal taxa to the modernly recognized six *Gyrotoma* species. However, basing pleurocerid species boundaries on qualitative morphological features poses many taxonomic and systematic issues. In an effort to better estimate species diversity, geometric morphometrics and Gaussian mixture models were used to assign individual *Gyrotoma* shells to one of three clusters. Individuals in each cluster had significantly different shapes along with different combinations of quantifiable shell traits. No specific distributional patterns were observed between clusters. Though separable statistically, each cluster cannot be assigned to its own species. However, the clusters represent testable hypotheses of possible *Gyrotoma* diversity for when additional data is available.

Poster

## Atlantidae mollusks as indicators of environmental change in the Southern California Current

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The holoplanktonic gastropods of the family Atlantidae (Pterotracheoidea) have a short life cycle, and even though they respond rapidly to environmental changes, it is unknown how their distribution and abundance vary regarding the intra and inter-annual changes in the environmental conditions. In the California Current System (CCS) the most intense intra-annual changes in the environmental conditions and in the planktonic species composition happen between winter and spring. Other important changes in the environment happen in the inter-annual scale; in this study mainly related to the Blob 2013-2015 and El Niño 2015-2016. We determined the intra and inter-annual variation of the distribution and abundance of Atlantidae species in the Pacific coast off Baja California between 2012-2016. Four oceanographic cruises were carried out in winter and three in spring with 284 zooplankton samples analyzed. Overall, 14 species were found where *Atlanta californiensis* was the most abundant, mainly in spring. During winter 2014 and 2016, warm anomalies occurred and the relative abundance of *A. californiensis* decreased, while *A. lesueurii* increased, as well as the exclusive presence of *A. turriculata* and *Atlanta* sp 1 was observed. Winter surveys had more richness (S), diversity (H'), and evenness (J) compared to spring, and in both seasons the greater values were found in the oceanic region. The differences in the community structure shows that atlantids are good indicators of intra and inter-annual environmental changes in southern CCS.

## **Seasonal Sea Surface Temperature Variability in the Middle Ages: New Insights from *Patella vulgata* $\delta^{18}O$**

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In light of ongoing climate change, it is increasingly imperative to construct highly resolved long-term climate models to understand the historical dimensions of climatic variability. It is especially desirable that these models be interpreted alongside archaeological data, in order to examine the human dynamics of climate change and the ways that past societies have adapted to changing conditions. Most proxy records for historical temperature variability are annual in resolution and only reflect a single season—to understand the full complexity of climate systems, it is thereby necessary to supplement these records with records that can capture intra-annual seasonal variability, with both summer and winter maxima. This paper will present the analysis of over 1,150 isotopic samples from 35 shells of *Patella vulgata* to reconstruct seasonal sea surface temperature (SST) during the Late Antique Little Ice Age, Medieval Climate Anomaly, and modern period on sites of archaeological significance from Orkney in northern Scotland. The results illustrate the seasonal variability of these periods, and show Late Antique cooling and Medieval warming. They also highlight the need for further attention to the influence of microenvironmental factors such as a shell's tidal zone in making use of intertidal paleoclimate proxies.

## Diversity and predicted function of gut microbes from two species of viviparid snails.

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Animal gut bacteria are involved in critical functions of their hosts, including nutrition, behavior, immune responses, and development. In snails, gut bacteria play crucial roles in organic material digestion and nutrient production, and have been implicated in aspects of reproduction. Snail gut microbes are known to differ between species, and between anatomical compartments of the digestive tract. Dietary changes are also known to alter snail gut flora. In an effort to better understand their diversity and function, we studied the gut microbial communities from two viviparid snails, *Campeloma decisum* and *Cipangopaludina japonica*. We were interested in addressing two central themes: whether significant differences in bacterial community composition existed between the two species; and whether differences in microbial diversity corresponded to differences in community function. Using next-generation sequencing of the bacterial 16S V4 region, we found no significant differences in alpha and beta diversity between *C. decisum* and *C. japonica*. Firmicutes and Proteobacteria were the most abundant bacterial phyla in both species, while Bacteroidetes had a mean abundance 100x higher in *C. japonica*; nine taxonomic groups were significantly different between the snail species. Pseudomonads and Enterobacteriaceae were notably more abundant in *C. decisum*, while Proteobacteria and Chitinophagaceae were more abundant in *C. japonica*. Peptidoglycan synthesis, pyruvate fermentation, and aerobic respiration by cytochrome c were the three most abundant microbial pathways represented in the viviparid gut. Fourteen functional pathways differed significantly between *C. decisum* and *C. japonica*, potentially correlated with differences in bacterial community composition and snail life history. Our data fill in data gaps regarding gut microbes in Viviparidae, and highlight future research paths examining the prevalence of Firmicutes and unidentified diversity in both snail species.

Poster

## **Landmark-based snail size measurement improves precision and repeatability of shell volume estimation over conventional shell size measures**

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Body size is intimately tied with nutritional needs and scales at which animals interact with their environments. Snail body size is understudied, despite hundreds of years of conchological interest in gastropod functional morphology. Perhaps, drawbacks of traditional shell size measurements such as shell height and maximum diameter, which are not directly comparable across morphologically disparate taxa, have hampered taxonomically broad body size studies. I propose a transition from traditional morphometric size analyses to a size measurement robust to shape differences: centroid of shell landmark configurations. Precision and repeatability of centroid size was compared to traditional size measurements by repeatedly imaging specimens from six populations of Pacific Island micromolluscs (family Diplommatinidae). Centroid size; maximum, mean, and geometric mean of shell height and width; and conical volume (volume of a cone of similar height and width to specimen) were measured from landmark configurations. Precision was assessed as strength of correlation with external shell volume, measured from microCT scans. Repeatability was assessed by comparing methodologically introduced size variance to real biological differences in size between specimens. Additionally, scaled landmark configurations were explored as a means to differentiate morphologically similar species. Centroid most closely correlated with external shell volume, and only maximum dimension had a lower percent measurement error than centroid. Hierarchical cluster analysis successfully grouped images by population based on scaled landmark configurations, but internal and stability validation measures were uninformative for selecting the best agglomeration method or number of clusters. These findings demonstrate that centroid size outperforms traditional size measurements in both precision and repeatability and that data used to calculate centroid (i.e. landmark configurations) can be useful in morphospecies identification. These methods could be used to measure body size from taxonomically diverse shell images widely available in publications and digital collections, facilitating macroecological and biogeographic studies on gastropod body size.

## **Stinger Thieves: Nematocyst Diversity and Sequestration in Aeolid Nudibranchs**

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Nudibranchs encompass over three thousand species around the world, with much remaining diversity to describe. One subgroup of nudibranchs is commonly called aeolids: a specialized group of nudibranchs that have a remarkable adaptation of being able to sequester nematocysts from their prey and use them as part of their own defensive mechanism. Nematocysts are also known as “explosive cells”, a variety of special organelles that are present in cnidarians. This project focuses on the specificity of nematocyst sequestration in multiple aeolids and cnidarians along the central California coast. This study samples a wider geographical area and encompasses more species representing several distinct lineages of aeolid nudibranchs compared with previous research on nematocysts sequestered by nudibranchs. Nudibranchs and their cnidarian prey were collected via tide-pooling, observed with Differential Interference Contrast (DIC) microscopy, where nematocyst identification was observed. The nematocyst diversity in aeolid nudibranchs is different across taxa as well as within one taxon. Several aeolid nudibranchs had the highest nematocyst diversity, whereas a handful of aeolid nudibranchs only sequestered a couple nematocysts from its cnidarian prey. We also see that aeolid nudibranchs tend to predate upon a wide variety of prey species and that they keep different nematocysts from different cnidarian species. This work increases the understanding of how this unique adaptation of sequestering nematocysts has evolved in Nudibranchia.

## **Is acid precipitation a factor in the decline of the terrestrial tiger snail, *Anguispira alternata*, in northeastern North America (Gastropoda: Discidae)?**

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We used museum and other records to document a 51% decline in county occurrences of the land snail *Anguispira alternata* in 26 states in northeastern North America, from 705 counties before versus 347 counties after the year 1960. This decline appears to have begun about the middle of the 1900s. The decline appears to be real (rather than an artifact of search effort) as evidenced by a decline in the proportion of *A. alternata* among all land snails documented before and after 1960. Because acid precipitation increased in the mid-1900s and it has known negative effects on other biota, we consider it a possible factor in the decline of *A. alternata*. If acid precipitation played a role, we predict that *A. alternata* would be more likely to disappear from counties that experienced more severe acid precipitation. Preliminary analyses found a trend consistent with that prediction, but lacked strong statistical support. Here we account for two factors that could influence apparent persistence or disappearance of *A. alternata*: (1) collector effort (insufficient collector effort in some counties after 1960 could yield false negatives) and (2) calcium availability (limestone bedrock or calcium-rich soil could buffer affect of acid precipitation). We consider these two factors along with an estimate of acid rain severity for each county in testing whether acid precipitation played a role in the decline of *A. alternata*, using 4835 records of *A. alternata* and 128,099 additional records of all land snail species from 26 states in northeastern USA.

## **Poorly vetted conservation ranks can be more wrong than right: lessons from Texas land snails.**

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Setting priorities for scarce conservation dollars requires an accurate accounting of the most vulnerable species. For many invertebrates, lack of taxonomic expertise, low detectability and funding limitations are impediments to this goal, with conservation ranks usually based on expert opinion, the published literature, and museum records. Because of biases and inaccuracies in these data, they may not provide an accurate basis for conservation ranks, especially when compared to de novo field surveys. We assessed this issue by comparative examination of these data sources in re-ranking the conservation status of all 254 land snail taxa reported from Texas, USA. We confirmed 198 land snail taxa, including 34 new state records. Our assessment of the entire land snail fauna of Texas resulted in 1) a near doubling of recommended Species of Greatest Conservation Need (SGCN) and 2) a 79% turnover in the makeup of SGCN taxa. Field sampling strongly outperformed museum and literature data in the encounter rate of both the entire fauna and all SGCN species, with the latter two demonstrating bias towards larger-bodied species. As a result, conservation priorities based solely on expert opinion, museum and literature records may be more wrong than right, with taxon-appropriate, targeted sampling required to generate accurate rankings.

## **Molecular and Morphological Analysis of Ozark Pigtoes (*Fusconaia* and *Pleurobema* spp.)**

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Pigtoe mussels (Unionidae: Pleurobemini: *Fusconaia* and *Pleurobema* spp.) are a group that have caused taxonomic confusion. Recent molecular work has revealed cases of cryptic diversity and convergent evolution within the group. One such case is the presence of a genetically distinct lineage formerly recognized as *Fusconaia flava* within the Ozark Highlands. This lineage has so far been identified from the Missouri and Arkansas river drainages. There are also uncertainties regarding the taxonomic status of *Pleurobema rubrum* and *P. sintoxia* across the species' geographic ranges. We used the CO1 mitochondrial gene to explore genetic variation and geometric morphometric techniques to analyze morphological variation in 92 specimens of *Fusconaia* and *Pleurobema* from the northern Ozarks. Analysis of the CO1 region revealed that most specimens morphologically identified as *F. flava* collected from the Ozarks region represent the genetically distinct lineage, and that locally, *F. flava* may be more restricted in range than previously thought. It also revealed that Ozark Highlands specimens of *Pleurobema rubrum* and *P. sintoxia* are genetically indistinguishable at the CO1 region, consistent with previous research from other geographical areas. Geometric morphometric analysis revealed overlap in the shells from 3 *Fusconaia* species as well as the *P. rubrum/sintoxia* group.

## **Mechanical Shell Properties of Eight Species of Cohabiting Unionid Bivalves**

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Bivalve shell is a good barometer of environmental conditions. The relatively simple prismatic-nacreous shell is considered the most primitive exoskeletal structure among the recent bivalves. This shell type is found in all members of the unionid mussels. Because a changing environment can impact biomineralization and thus shell structure at both the macro and micro levels, it could be difficult to separate the roles that habitat and environment plays versus genetics in shell strength. Variation in shell mechanics across unionid taxa remained unexamined, either within habitat or across taxa. Here we confirm the highly conservative nature of the prismatic-nacreous shell through a study of the prismatic: nacre thickness, relative shell microhardness (a measure of resistance to deformation that aligns with strength), and resistance to fracture in eight species of unionids cohabiting a small portion of the Allegheny River in Pennsylvania.

Poster

## Organic to Mineral Shell Components Through Molluscan Growth Stages

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The organic component of the molluscan shell allows for orderly biomineralization and ensures structural integrity that is crucial to survival. This organic component typically is found to compose 2-5 % of the total shell. Because macro- and microstructure of shell is known to vary with environment, ontogeny, and across taxa, we ask the question if the ratio of organic to mineral in shell also varies with growth across taxa. The organic to mineral shell ratio of three marine and one freshwater species of mollusc was examined for possible changes in organic proportions during growth. Specimens of the marine gastropods *Crepidula fornicata*, *Littorina littorea*, and *Littorina saxatilis* and the freshwater bivalve *Corbicula fluminea*, were separated into small, medium, and large size classes and shell organic proportion was measured. In each species, the average organic proportion of the small size class was found to be significantly larger than the average organic proportions of the medium and large size classes. It is possible that the greater relative amount of organics in the shell of juveniles is related to the structural value of the organic matrix in small, thinner shells and the association of these matrix with the growth and integrity of the calcified shell. As the organic matrix is known to be energetically more expensive to produce than the calcified shell portion, we suggest that energy expended in these smaller stages of growth allows for a more rapid production of a shell and that this "expense" is a valuable trade-off for the protection the shell offers the young mollusc.

## **Citizen Science: Documenting the spread of the Black velvet leatherleaf slug in the United States**

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USDA APHIS PPQ

The Black velvet leatherleaf slug *Belocaulus angustipes* (Heynemann, 1885) is native to northeastern Argentina and southernmost Brazil. It was first detected in 1960 in Mobile, Alabama and then New Orleans, Louisiana. Since then it spread to all the Gulf Coast states. It differs from the Black African slug *Laevicaulis alte* (Férussac, 1821), which is currently restricted to Hidalgo County, Texas, by its smaller size, narrow body and a distinctive black velvet appearance of its dorsum. In 2015, with the cooperation of the Texas Invasive Species Council, the USDA posted a flyer requesting the general public report the presence of *B. angustipes* and to submit samples for molecular analysis. Numerous citizen scientists have responded since then, and it has been possible to track the spread of the invasive slug, most recently reaching South Carolina and North Carolina. Most of the county records are thanks to participating citizen scientists. The molecular evidence indicates at least two distinct introductions to the United States.

## **The Recipe for Destruction: Pesticides Alone are Not the Only Key to Giant African Snail (*Lissachatina fulica*) Eradication**

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Globally, giant African snail (*Lissachatina fulica*) (Bowdich, 1822) is considered one of the most important invasive snails. Once introduced, extensive and costly eradication efforts are often undertaken. However, more often, the eradication effort is abandoned due to the rapid expansion of the pest range and the cost limitations of controlling the populations. We studied the reproductive capacity and population dynamics of south Florida snails for two years to evaluate the likely success of the eradication program. A total of 23,890 snails, ranging from 25-131 mm, were measured, dissected and the number of eggs in each snail counted. Only 5% of snails had eggs, which were found year round. We evaluated the effect of control measures on six populations having >1000 adult snails and used data from the two largest populations to investigate how environmental factors interacted with population dynamics and control measures. The addition of metaldehyde pesticides produced the largest reductions in snail numbers. Interestingly, populations with fewer snails were already declining before the use of metaldehyde, although metaldehyde treatment accelerated the process. A recent evaluation of the eradication program in Trinidad and Tobago highlighted that the use of pesticides alone will not achieve eradication. Intensive pesticide treatments with metaldehyde and thiodicarb have not reduced snail populations. Snails persisted in protected areas such as on inaccessible private properties, in elevated areas, or in thick brush or debris. Alternative strategies, which include continuous outreach, debris removal, access to control populations, surveys when snails are active, and a rapid response to new detections, are essential to help achieve eradication.

## **Dismantling the Punctoidea: new molecular phylogeny and establishment of Discoidea**

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The superfamily Punctoidea is a group of stylommatophoran land snails typically of small to minute size. Its classification has been historically unstable, with its family-level composition differing markedly from author to author. To complicate matters even further, the families Charopidae and Punctidae had an unsettling number of subfamily-level taxa proposed and almost immediately put into synonymy. Presently, Punctoidea is thought to contain seven families: Charopidae, Cystopeltidae, Discidae, Endodontidae, Helicodiscidae, Oreohelicidae and Punctidae. We conducted a phylogenetic analysis of 56 terminal taxa, representing all punctoid families, using a combination of mitochondrial (COI, 16S) and nuclear (ITS2, 28S) markers and both Bayesian Inference and Maximum Likelihood. Our results indicated that Punctoidea, as previously interpreted, is widely polyphyletic, comprised of three unrelated groups: (1) the Laurasian family Helicodiscidae, whose phylogenetic relationships were not fully resolved but seems closely related to Arionoidea and Limacoidei. (2) The newly-recognized superfamily Discoidea, also Laurasian and containing the families Discidae and Oreohelicidae. (3) The Punctoidea sensu stricto, a predominantly Gondwanan clade containing monophyletic Punctidae, Cystopeltidae and Endodontidae, and a paraphyletic Charopidae. Endodontidae is the most basal branch, followed by Cystopeltidae. Our results also showed that Cystopeltidae, rather than being restricted to Australian semi-slugs, is actually a more diverse clade, also containing a South American branch of snails previously assigned to Charopidae. Further research should focus on defining diagnostic morphoanatomical features for this family and on whether any South African or New Zealand genera also belong to it. Charopidae is paraphyletic without the inclusion of Punctidae (which has nomenclatural priority); however, since its internal relationships were not well-resolved in our study, we retain the usage of the family until further investigations are conducted.

Poster

## **Krakens and flail snails: the role of fantasy and sci-fi mollusks in science communication**

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Works of fiction inspire science, facilitate science communication and environmental education. Pop culture from films, art, anime, literature, comics, video games to tabletop games can kickstart science communication. Surprisingly perhaps, mollusks of all kinds are extremely pervasive across pop culture, from the legendary Kraken to Lord Helix and flail snails. For the past few years we have been using the platform offered by the Journal of Geek Studies (<https://jgeekstudies.org/>) to discuss mollusks from science fiction and fantasy, using them as a starting point to delve deeper into the scientific information that inspires authors and creators. In many cases fandom communities have made these connections themselves. Discussions about Pokémon, Lord of the Rings, Splatoon, Magic: The Gathering, and others have led to topics such as systematics, evolution, paleontology, biomechanics, ecology and conservation. References in pop culture, which are consumed by huge audiences, can be an entry point for people to become curious about related science. For instance, the article about molluscan Pokémon is one of the most accessed on the website (around 6,000 reads in the past year). While nature documentaries (from Cousteau to Attenborough) have increased interest in nature and even resulted in conservation efforts, their results have proven to be short-lived and focused on a narrow cast of animals. With beloved molluscan elements of pop culture as a hook, it's easier to raise awareness and passion about the real animals and secure a longer-lasting effect, ultimately making people care a little more about these typically-ignored creatures who are unfortunate enough to share the planet with us.

Poster

**Differential parental investment in two reproductive life history adaptations utilized within a poecilogonous species, *Alderia willowi* (Gastropoda: Sacoglossa: Limapontiidae)**

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Species are usually adapted to produce only one form of larvae. A species able to make multiple forms of larvae presents an opportunity to better understand the comparative parental investment in differing life-history strategies, which remains largely unexplored. Poecilogonous species have adults that appear the same, but create different forms of larvae, an adaptation that occurs in several gastropod families. Using a poecilogonous species that produces planktotrophic ("self-feeding") and lecithotrophic ("yolk-fed") larvae, we compare within-species energy expenditure and parental growth rates between these common types of marine invertebrate larvae. *Alderia willowi* is a hermaphroditic sea slug with seasonal poecilogony. Most individuals produce large, lecithotrophic larvae in the summer and a variable percentage of adults instead lay small, planktotrophic larvae in the winter. Here, we present preliminary results of a study that raised *A. willowi* under common garden conditions to measure parental growth rates and egg production, controlling for confounding variables relating to species-level differences or environmental conditions. Adult *A. willowi* specimens were field-collected and acclimated to lab conditions, before measuring growth (length and area) as well as egg output and type of eggs produced. The goal is to determine if total parental investment is significantly costlier for slugs producing planktotrophic versus lecithotrophic larvae; while the per-offspring difference in these strategies is well known, the extended or lifetime costs remain unexplored. If so, we plan to determine which egg type per clutch is more energetically expensive to produce and which has higher egg viability. Overall, the project is intended to contribute to our understanding of reproductive adaptations and the evolution of life-history trade-offs, examining unrecognized costs of alternative offspring provisioning strategies.

## **Mobilizing data on Pacific Island land snails from collections at Florida Museum of Natural History**

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Commerce, housing, and agriculture can result in considerable losses in native biodiversity by altering or destroying natural habitats, as well as introducing non-native predators and competitors. Mollusks are particularly susceptible to environmental degradation and introduced predators. As a result, they have experienced the majority of all extinctions since 1500, with most among land snails from Pacific Islands. However, even these extensive losses may be under-estimated because our knowledge of the snail fauna of most islands is based on relatively few surveys and many islands have not been resampled in more than a century. Natural history collections can play a vital role in recording past and current biodiversity patterns that are necessary to document species losses and take action to preserve surviving taxa. However, the information inherent in natural history specimens needs to be digitized to make it readily accessible for conservation efforts, and records need to be georeferenced to allow them to be easily mapped. These needs prompted a consortium of North American natural history collections with extensive holdings of Pacific Island land snails to embark on a project to digitize their Pacific Island land snail collections. These data will ultimately be compiled and served through the Pacific Island Land Snail Biodiversity Repository (PILSBRY). Florida Museum of Natural History houses a unique collection of snails from caves on several Pacific Island archipelagos and collections from several biologists that have lived on different islands. These records and their field notes are being electronically cataloged and georeferenced and are available online through our Specify portal (<http://specifyportal.flmnh.ufl.edu/iz/>), and are regularly harvested by iDigBio, OBIS, GBIF, DiscoverLife, and InvertEBase. These early efforts have already uncovered a new invasive species introduction, as well as native taxa that are not previously reported from islands.

Poster

## **MD 55 results- A perspective from bivalve diversity.**

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The Marion Dufresne (MD55) oceanic expedition travelled between Rio de Janeiro and Espírito Santo coasts, Southeastern Brazil, collecting sediment and biological samples from 67 stations. The area explored during the expedition covers several ecological relevant regions, as the Vitória- Trindade sea mount Chain, off Espírito Santo. Faunal diversity collected from this expedition was preliminary reported, as well as the bivalves, which samples belong to 22 families according to the sampled ecosystem: continental shelf and slope, seamounts, and deep fauna. Here we update this report analyzing 457 dry and alcohol preserved samples from the expedition, deposited at Muséum National d'Histoire Naturelle, France, and Museu de Zoologia of Universidade de São Paulo, Brazil. This preliminary analysis indicates 199 morphotypes that can be attributed to 37 families, being two of those morphotypes identified as *Incertae Sedis*. Some samples showed greater morphotype diversity than the species number registered for the families at the region, such as in *Cuspidariidae*, *Galeommatidae*, *Leptonidae*, *Limidae*, *Limopsidae*, *Nuculanidae*, *Poromyidae*, *Propeamussidae*, *Thyasiridae*, *Tindariidae*, *Trapeziidae*, *Verticordiidae* and *Vesycomiidae*. Also, this result indicates possible new occurrences of the families *Philobryidae* and *Astartidae* for the region. An underwork study on *Lucinidae* collected on this expedition has shown that its samples present two new occurrences and a new *Pleurolucina* Dall, 1901 species. The result of this study (1) serve as an example of the necessity to stimulate and preserve traditional taxonomy training, (2) brings light to the diversity of bivalves species that can be found at the South Western Atlantic, especially at seamounts and deep waters environments, (3) also should encourage new expeditions as well as law reinforcements to protect seamounts and deep sea environments, that has been extensively prospected and explored for oil extraction.

## **Genetic Diversity Maintained in Comparison of Wild and Propagated Populations of Imperiled Freshwater Mussels**

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Knowledge of genetic diversity and structure of wild stock unionid species has advanced extensively, but there has not been similar advancement in our understanding of captive bred unionids in comparison to wild populations. This study provides empirical data critical for effective, responsible propagation efforts. Null hypothesis: wild and captive bred mussel populations have equivalent genetic diversity. Microsatellite generated genotypes from multiple loci were obtained for *Lampsilis fasciola* (Wavy-rayed Lampmussel) and *Ptychobranthus fasciolaris* (Kidneyshell). No significant differences were detected between wild and propagated *L. fasciola* based on genetic diversity metrics (allelic richness, observed and expected heterozygosity, and inbreeding coefficient) using Kruskal-Wallis tests. Pairwise genetic differentiation values were significant, but low temporally and among wild caught adult and hatchery raised *L. fasciola* juveniles. Pairwise genetic differentiation values for *L. fasciola* were significant and higher, suggesting some fixation of alleles and limited differentiation. Pairwise genetic differentiation for *P. fasciolaris* was not significant. These findings, corroborated by STRUCTURE analyses, support a single genetic population. There is no evidence of significantly reduced genetic diversity between wild and propagated individuals. We hypothesize that the contribution of at least 10 females combined with the contribution of multiple males to each glochidial brood help maintain the genetic diversity reflecting the natal population.

Poster

## **The invasion of the giant African land snail in Cuba: a threat to biodiversity and public health**

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The giant African snail *Lissachatina fulica* (Bowdich, 1822) is a well-known invasive species considered one of the most dangerous and widely introduced land mollusk worldwide. This species is of major medical and conservationist concerns due to its capacity of transmitting the rat lungworm *Angiostrongylus cantonensis* that produces meningoencephalitis in humans, and the ability of out competing local species of land snails. Here we present a series of results from its first detection in Cuba with a detailed yearly chronology of invasion throughout the island. Data on the first experimental results concerning demographic parameters of *L. fulica* in Cuba show a type I survival curve, mean life expectancy of 71 weeks, sexual maturity after 22 weeks and a 85% hatching probability. One-year old snails show means of 77.3 mm of shell length and 57.7 g of weight. An ecological multivariate analysis in natural conditions directly relate *L. fulica* with African-rooted religious activities. We found an overall dominance of *L. fulica* over Cuban local and endemic land snails in 36 studied localities in which we observed a mean of 37 individuals/25m<sup>2</sup>. The dynamic of new positive sites with *L. fulica* in Cuba do not match the natural colonization speed for this species, which shows a patchy distribution typical of human-mediated introductions. Parasitological studies from field-collected individuals show an overall prevalence of 65% (range 0 – 100%) of *A. cantonensis* and a mean intensity of 102 larvae. Considering that *A. cantonensis* was first detected in Cuba in 1979, these results suggest that *L. fulica* may be a major actor of a 'parasite spill-back' increasing the risk of human infection. Our results show the need of an outreach program involving health and conservation authorities that work alongside with key religious leaders to tackle the dispersal of *L. fulica*.

Poster

## **USDA Terrestrial Mollusk Program: Using Science Based Regulatory Tools to Protect US Agricultural Production Systems from Invasive Slugs and Snails**

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The United States Department of Agriculture (USDA), Animal and Plant Health Inspection Service (APHIS), Plant Protection and Quarantine (PPQ) leads federal initiatives to protect US agricultural production systems and natural resources from exotic plant pests and disease. As a regulatory agency, USDA is unique in its focus on using science to inform policy development, determine regulatory statutes, and decide response strategies to mitigate damage and loss from invasive exotic terrestrial mollusks. USDA is positioned at international and interstate commerce crossroads where the agency can regulate commodities that could spread injurious pests to new areas of the US. When non-native species of mollusks are detected on commodities, USDA uses validated treatment protocols when available. If no treatment options exist, the infested commodity is either re-exported or destroyed. When exotic species are detected in the landscape, USDA forms technical working groups and response guidelines that provide responders with science based strategies to quickly and effectively eradicate or contain the pest species. Compared to other plant pests, the body of scientific knowledge regarding the potential impacts of exotic mollusks on US agriculture is limited. This lack of information makes it difficult to develop, fund, and establish appropriate preparedness/response programs targeting invasive mollusks. USDA is promoting outreach and collaboration across the academic community to inform scientists about current and future research needs.

## **Do You Know Your Pigtoes? DNA Barcoding and Geometric Morphometric Analyses Distinguish Between Common Wabash Pigtoe (*Fusconaia flava*) and Imperiled Round Pigtoe (*Pleurobema sintoxia*) in the Laurentian Great Lakes Region**

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The Wabash Pigtoe, *Fusconaia flava*, and the related Round Pigtoe, *Pleurobema sintoxia*, are freshwater mussels native to the Great Lakes region with overlapping distributions. *F. flava* are widespread and common while *P. sintoxia* are imperiled in parts of its distribution. These species are similar in shell shape and coloration and have confounded many freshwater malacologists, likely resulting in misidentifications that could have impacts on status assessments and recovery efforts. The main objective of this study was to determine whether geometric morphometric analysis can be used to distinguish between these species. For each specimen collected a preliminary identification was made, shell measurements and foot color were recorded, and photos of the left shell valve were taken. Genetic samples were collected from 133 of 246 specimens; DNA was extracted, COI mtDNA was sequenced, and species identification was confirmed. Landmarks were digitized along the shell outline from photos of the left valves. Landmarks were analyzed and species assigned using canonical variates analysis and assignments were compared to the results of the DNA sequence data. The two species were significantly different in shape. Landmark data correctly assigned 99.2% of specimens to their DNA-confirmed species identity, compared to only 82.0% accuracy of field identifications. Foot color was only 77.0% accurate in identifying species. An identification quiz of a subset of the left valve photos from 50 barcoded specimens was taken by participants with different experience levels; the mean score was 77.0% correct. *P. sintoxia* was often misidentified as *F. flava* indicating that *P. sintoxia* may be more common than previously believed.

Poster

## **A 100-year journey from discovery to description: A Hawaiian land snail finally gets its name**

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Naming species is a requisite for understanding their biology and conservation in the face of the biodiversity crisis. On average, 50 new species are described daily, and it may take 20 more years for some species to be formally described. At the same time, it is estimated that as many as 150 species a day go extinct. The biodiversity crisis is especially acute for Pacific Island land snails and in recent decades new species are often described after their extinction, when it is too late to conserve them. Millions of specimens are housed in natural history collections and among them are numerous species to be described, some waiting more than a century. The Bishop Museum Malacology collections comprises about 6 million specimens, many representing threatened or extinct species, and some undescribed. At least 200 Hawaiian endodontids in the collection are undescribed, and all but one of these is probably extinct. Although extinct Hawaiian land snails have been described recently, no extant species have been described since 1960. Since 2004, >1000 surveys for land snails in Hawaii have recovered nearly 300 endemic species. We estimate that about 10% of these represent undescribed taxa, several of which have been waiting formal description for more than 100 years. One such species, recorded alive in 2013, was first discovered in 1912 by researchers at the Bishop Museum, and only recently has been named – , in honor of long-time champions of Hawaiian biodiversity, Wayne and Betsy Gagne. Like most Pacific Island land snails, this species is threatened with extinction, but in naming it, we have given it the recognition needed to conserve it. With an estimated 7 million species awaiting description, we must address the taxonomic impediments to conserve the remaining biodiversity with one of the first steps of providing a name.

## The Last of the Endodonta

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Endodontidae are endemic to Pacific islands and most species are recorded from Polynesia, Lau Archipelago, and Palau. The genus *Endodonta* contains 11 species - all endemic to the Hawaiian Archipelago. No extant *Endodonta* species has been described for more than 50 years, although new taxa have been described from extinct species more recently. Since 2004 more than 1,000 land snail surveys have been conducted to record the remaining terrestrial gastropods in Hawaii. Although two of the 18 species of *Cookeconcha* have been found alive on Oahu, no live *Endodonta* spp. have been recorded from the main Hawaiian Islands. The only extant *Endodonta* known is an undescribed species on Nihoa, which was first recorded in 1923. In 1980 Carl Christensen collected specimens of this species, and we recorded it last in 2015. Despite nearly 100 years having passed since its discovery, it has remained unnamed. Using an integrative taxonomic approach that includes conchology, reproductive anatomy, radula morphology, and genetics, we are finally describing the last living *Endodonta*. Most member of the family, because of their ground dwelling habits, are vulnerable to extinction and most of the species in Hawaii are already gone. In describing this remaining *Endodonta* species, our hope is to inspire increased awareness and appreciation that spurs on conservation for this highly threatened group. Unless protection of this species is implemented, it may be extinct within the next decade and will lose the last of a lineage that existed for millions of years, and the stories it could tell.

## **Giant African Land Sails (*Lissachatina fulica* Bowdich,1822): Florida eradication program and its effectiveness to date.**

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*Lissachatina fulica* (Bowdich, 1822) is considered among the top 100 most damaging species worldwide. In 1975, Florida became the only location in the world to eradicate *L. fulica*. A second introduction was detected in 2011 in a residential neighborhood of Miami, Florida. A joint State and Federal eradication program was created to eradicate this pest. A strategy was developed based on a new understanding of the biology and ecology of *L. fulica* as well as successes and failures of eradication programs in other parts of the world. A total of 32 core areas have been detected in residential, commercial, and agricultural areas in Miami-Dade and Broward counties. Available molluscicides were laboratory tested to determine the most effective products and concentration to use in the field. Iron phosphate and boric acid were found less effective compared to metaldehyde. As a result, the eradication program incorporated metaldehyde in four concentrations (3.25%, 4%, 7.5, and 25%) into its control methodology. Additional control strategies employed include bi-weekly inspection and plant debris removal of infested and neighboring properties, extensive public outreach in affected communities and the use of detector dogs and night surveys to locate hidden populations. These efforts have resulted in no live snails being detected since December 2017 and declaration of 23 of the 32 cores as snail free. As it stands, the program is positioned to declare eradication of this pest in Florida in the Fall of 2021.