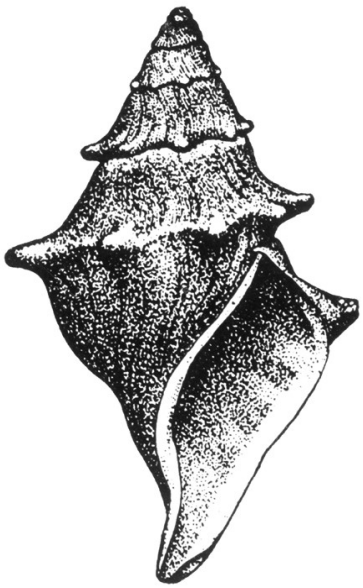
Program and Abstracts

American Malacological Society
83rd Annual Meeting
Newark, DE



July 17-21, 2017

Compiled and edited by Colleen Winters,
Justin Guider, Jennifer Acord, and Elizabeth Shea

Front Cover: Logo is a cross-section of the Delaware state shell,
the channeled whelk, *Busycotypus canaliculatus*.

Inside front cover: *Io fluvialis* from the DMNH collection (DMNH 127238).

Meeting Schedule at a glance

Monday, July 17

Registration begins at noon
AMS Council meeting, 2:30 – 5:00 pm, Room 119
Welcoming Reception, 5:30 pm, Stone Balloon, Main Street

Tuesday, July 18

President's Symposium, 8:45 am, Clayton 128
Group photo, 1:00 pm, Location TBD
Mollusks in Peril, 1:20 pm, Clayton 125
Biodiversity, 1:20 pm, Clayton 120
Auction, 7:00 – 10:00 pm, Clayton Lobby

Wednesday, July 19

Phylogeny & Systematics, 9:20 am, Clayton 125
Mollusk Collections, 9:20 am, Clayton 120
Cephalopod Biodiversity, 10:40 am, Clayton 120
Dispersal, 1:20 pm, Clayton 125
Poster session, 3:00 – 4:30 pm, Clayton 125
Publications Committee meeting, 4:00 – 5:00 pm, Clayton 110
Malacologia Board Meeting, 7:00 – 8:00 pm, Clayton 110

Thursday, July 20

Feeding Strategies, 9:20 am, Clayton 125
Historical Ecology, 9:20 am, Clayton 120
AMS business meeting, 1:30 – 3:00 pm, Clayton 125
Bus to the Delaware Museum of Natural History, 6:00 pm, Clayton Lobby
Bus leaves the Museum at 9:00 & 10:00 pm to return to Clayton Hall

Friday, July 21
Excursions depart at 7:00 am, return by 5:00 pm.

Welcome to AMS 2017!

Dear Friends and Colleagues,

On behalf of the Delaware Museum of Natural History, I'm pleased to welcome you to Newark, DE for the 83rd Annual Meeting of the American Malacological Society! This is the second time the AMS meeting has been held in Clayton Hall and the Museum – the first was 44 years ago in 1973. The attendees at that meeting reads as a who's who of mollusk biologists; I'm hopeful that we will look back on this meeting in 44 years and see similar evidence of productive research and new connections.

The scientific program began with the pre-meeting workshop *Digitizing the 2nd largest Invertebrate Phylum: Mollusks*, organized by Petra Sierwald, Rüdiger Bieler, Gary Rosenberg and Liz Shea and sponsored by an iDigBio Conference Award. The goal of the workshop was to assess digitization progress in Mollusk collections across the country and to develop efficient, Mollusk-specific best practices and workflows to make rigorous data available faster.

The President's Symposium, *Mollusk research in a digital world: creating, integrating and mining large datasets* expands on the workshop to discuss and provide examples of how large, interconnected data sets provide new avenues of research. We'd like to thank Jann Vendetti, Alex Ziegler and Mike Vecchione for tackling this emerging topic from a variety of perspectives. In addition, we are grateful to José H. Leal for organizing the Mollusks in Peril session and to Heather Judkins for organizing the cephalopod biodiversity session.

There are many people at the Museum who helped make this meeting a success. In addition to waiving rental fees for the concluding barbeque and hosting the meeting website, many at the Museum provided administrative support, but especially Jennifer Acord, Alexis Camac, Terri Reed and Judy Julis. The Museum's Society of the Natural History of Delaware Fund provided travel support for Chris Hobbs to conduct research in the collection immediately after the meeting. Finally, thanks to all the wonderful Collections and Research Volunteers who have come to my aid throughout the year as venue consultants, party planners, registration stuffers, taste-testers, and practically professional seamstresses!

Best wishes to all for a productive and fun meeting,

Liz Shea, AMS President 2016-2017 — Halsey Spruance, Executive Director
Jean Woods, Director of Collections — Alex Kittle, Collections Manager

Tuesday ● Clayton 128

Presidential Symposium, *Mollusk research in a digital world: creating, integrating and mining large datasets*

8:45 am Welcoming Remarks, Elizabeth K. Shea, AMS President

9:00 am The North American Mollusk collections – a status report
Bieler R, Rosenberg G, Shea EK and Sierwald P

9:30 am Improving provenance data in natural history collection databases
Rosenberg G and Khoo M

10:00 am A citizen science collaboration focusing on terrestrial malacofauna between the public and the Natural History Museum of Los Angeles County
Vendetti JE, Lee C and Willadsen O

10:30 am Opportunities and challenges for digital morphology
Ziegler A

11:00 am Digital discovery of deepsea diversity
Vecchione M

11:30 am – 12:45 pm Lunch

1:00 pm group photo ● Clayton, TBD

Tuesday pm● Mollusks in Peril ● Clayton 125

1:20 pm Invasive and naturalized slugs of the United States
Paustian ME

1:40 pm Decline of the Tiger Snail *Anguispira alternata* in Northeastern North America
Pearce TA

2:00 pm Risks for Florida's native land snails from the New Guinea flatworm, *Platydemus manokwari*
Collins TM and Warrens A

2:20 pm Society Island *Partula* tree snail survival after a mass extinction: New genomic insights using museum specimens
Haponski AE, Lee TL and Ó Foighil D

2:40 pm Pacific Island Land Snails: Changing perspectives for conservation
Hayes KA and Yeung NW

3:00 – 3:20 Coffee Break

Tuesday pm● Mollusks in Peril ● Clayton 125

3:20 pm Impact of invasive species on Hawaii's land snail diversity and the development of a Pacific Island land snail consortium
Yeung, NW and Hayes KA

3:40 pm Shape variation in the Shining Ramshorn Snail, *Segmentina nitida*, an overview of declining European populations
Hobbs C and Harvey C

4:00 pm Propagation and restoration of freshwater mussels (Bivalvia: Unionidae) to recover the biodiversity of rivers in Virginia and Tennesee
Hua D, McKinney D, Simms D, and Hubbs D

4:20 pm First record of a novel invasive *Corbicula* lineage discovered in the Illinois River, Illinois, USA
Tiemann JS, Haponski AE, Douglass SA, Lee T, Cummings KS, Davis MA and Ó Foighil D

4:40 pm Non-native (and potentially invasive) marine molluscan species in the Florida Keys – the challenge of recognizing what does not belong
Bieler R, Collins TM, Golding R, Healy JM, Granados-Cifuentes C, Mikkelsen PM, Rawlings TA and Sierwald P

5:00 pm Discussion lead by José H. Leal, MIP organizer and Jay Cordeiro, Chair of the AMS Conservation Committee.

7:00 pm AMS Auction ● Clayton Lobby

Tuesday pm ● Biodiversity ● Clayton 120

1:20 pm Sea slugs from French Guiana and the distinctiveness of the Guyanan Ecoregion
Caballer Gutiérrez M and Ortea J

1:40 pm Marine Mollusks of Northwestern Puerto Rico: A taxonomic effort to assist in the preservation of biodiverse beaches and land.
Kostick HL, Willig SA, Villanueva-Cubero L, Jimenez CV

2:00 pm Species diversity of mangrove gastropods and diversification of the Onchidiidae (Gastropoda: Pulmonata)
Goulding TC

2:20 pm Malacology Underground: A Review of Gastropod Diversity in Caves of North America and Their Ecological Significance
Gladstone NS, Slater AG, Carter ET, McKinney ML, Freshour DA and Niemiller ML

3:00 – 3:20 pm Coffee Break

7:00 pm AMS Auction ● Clayton Lobby Pit

Wednesday am ● Phylogeny & Systematics ● Clayton 125

9:20 am Conflict Clade Analysis (CCA) of the freshwater mussels subfamily Unioninae (Bivalvia: Unionoida)
Graf DL

9:40 am Quid est *Clea helena*? Evidence for a previously unrecognized radiation of assassin snails (Gastropoda: Buccinoidea: Nassariidae)
Strong ES, Galindo LA and Kantor YI

10:00 am Use and Limits of Mitochondrial DNA Sequences in the Freshwater Cerithioidean Families Pleuroceridae and Semisulcospiridae
Campbell DC and Lydeard C

10:20 – 10:40 am Coffee Break

Wednesday am ● Phylogeny & Systematics ● Clayton 125

10:40 am Phylogeny and biogeography of helicostyline land snails in the Philippines
Batomalaque G and Rosenberg G

11:00 am Radular malformation in radiations of land snails and its evolutionary-ecological interpretation
Shoobs NF and Rosenberg G

11:20 am The Snail Code: Employing multiple techniques to distinguish two species of *Ventridens*
Winters CM

11:40 am New genetic and morphological data suggests the land snail *Anguispira alternata* (Gastropoda; Stylommatophora; Discidae) is a species complex
Corlett R and Slapcinsky J

12:00 – 1:20 pm Lunch

Wednesday am ● Mollusk Collections ● Clayton 120

9:20 am Shell collecting and the making of modern Japanese science 1830-1925
Callomon, PR

9:40 am The Joseph G. Claud-Mantle collection, and two Sinistral Sacred Chank shells at the Museum of Comparative Zoology (Harvard University).
Nieburger E and Baldinger, AJ

10:00 am RECOLNAT Program: Digitization of mollusc collections at MNHN
Caballer Gutiérrez M, Hennion M, Lozouet P, Héros V, Perez Pimparé E, Pignal M and Bouchet P

10:20 – 10:40 am Coffee Break

Wednesday am ● Cephalopod Biodiversity ● Clayton 120

10:40 am New Bathyteuthid species in the Gulf of Mexico and northwestern Central Atlantic Ocean
Judkins H, K Clark, A Lindgren and M Vecchione

11:00 am Stable isotopes in the eye lenses of *Doryteuthis plei* (Blaineville 1823) reveal natal origins and migratory patterns in the eastern Gulf of Mexico
Meath BM, Peebles EB and Judkins HL

11:20 am The deep sea cephalopod fauna of Wilmington Canyon (Delaware, USA).
Shea EK, Ginzberg R, Poti M, and Nizinski MS

11:40 am Comprehensive morphological and molecular analysis of deep sea cephalopods collected in the North Pacific
Sagorny CL, Nagelmann N, Pracht ED and Ziegler A

12:00 – 1:20 pm Lunch

Wednesday pm ● Dispersal ● Clayton 125

1:20 pm Multiple paternity in *Pomacea canaliculata* (Caenogastropoda: Ampullariidae) in the La Plata Basin of Uruguay
Owens C, Burks RL and Hayes KA

1:40 pm Effects of short-term exposure to the gestagens progesterone and levonorgestrel on the development of juvenile apple snails (*Pomacea canaliculata*)
Frankel TE, Owens C and Hayes KA

2:00 pm Gastropod-killing worms: Discovery of the parasite, *Phasmarhabditis hermaphrodita* (Nematoda), in the US and its lethality to pest slugs, snails and non-target organisms
Mc Donnell RJ, Tandingan De Ley I, Denver DR and Paine TD

2:20 pm Slow crawlers, fast invaders: the dispersal of the exotic slugs *Arion subfuscus*/*fuscus* in northeastern North America
L'Heureux É and Angers B

2:40 pm The conundrum of dams and dam removal to freshwater mussels in small rivers
Krebs RA

3:00 pm Coffee Break and Poster Session

4:00 pm Publications Committee Meeting, Clayton 110

Wednesday pm ● Mollusks in Peril ● Clayton 120

2:00 pm Additional discussion time for Mollusks in Peril, if needed.

3:00 pm Coffee Break and Poster Session

4:00 pm Publications Committee Meeting, Clayton 110

Wednesday pm ● Clayton Lobby ● Poster Session
3:00 – 4:30 pm

The Mollusk Collection at the Delaware Museum of Natural History
Shea EK, Kittle BA, and Van Stone LJ

Mollusks in the Steel City: The Collection in Carnegie Museum, Pittsburgh, PA
Pearce TA and Sturm CF

Molluscan collections at Florida Museum of Natural History
Slapcinsky J, Bemis A and Paulay G

Digitization of the University of Michigan Museum of Zoology Mollusk (UMMZ) Division Collections
Lee T, Duda TF Jr and Ó Foighil D

New kid on the block: the collection at the Bailey-Matthews National Shell Museum
Leal JH and Godwin, J

The mollusk collection of the Field Museum of Natural History, Chicago
Gerber J, Bieler R and Jones J

The Illinois Natural History Survey (INHS) Mollusk Collection: Data basing and Digitization
Cummings KS and Vinsel RM

Sorting Shells: Finding Efficient Methods for Putting Collection Objects in Order
Woods JL, Van Stone L and Kittle A

Housing, Databasing, Digitizing and Accessibility Upgrades to the Largest Pacific Island Land Snail Collection (Bishop Museum, Honolulu, Hawaii)
Yeung NW, Kim JR and Hayes KA

Egg deposition by *Rossia palpebrosa* (Cephalopoda: Rossiinae) in deep-sea sponges, in temperate Northwest Atlantic and fringes of polar Canadian Arctic
Wareham Hayes VE, Fuller SD and Shea EK

Bioaccumulation of fluoxetine by the invasive freshwater bivalve, *Corbicula fluminea*
Burket SR and Brooks BW

Wednesday pm ● Clayton Lobby ● Poster Session
3:00 – 4:30 pm

Giant clam mantle color is correlated to the reef environment
Rehm L, McCourt RM, Gannon M and Sweeney AM

ASAP ADVANCE: Networking women STEM faculty at undergraduate institutions
Voltzow J, Cronin C, Lacueva G, Sabin RE, Smieja J and Zhong X

Feeding Habits and Prey Selection of Tritons (Gastropoda: Ranellidae), focusing on *Gutturnium muricinum* and *Monoplex nicobaricus*
Stahlberg A and deMaintenon MJ

Life history of *Deroceras reticulatum* in annual ryegrass (*Lolium multiflorum*) fields in Oregon and implications for pest management
Mc Donnell RJ, Cordoba M, Klein ML, Colton A, Dreves A and Sullivan C

Preliminary analyses of the genetic variation of the hooked mussel *Ischadium recurvum*, along the Florida coast
Fontanella FM, Starnes J, Whitaker M and Garner Y

Sexual dimorphism in *Brachioteuthis beanii* (Cephalopoda: Brachioteuthidae) in the northwest Atlantic.
Shea EK and Stadler J

Thursday am ● Feeding Strategies ● Clayton 125

9:20 am A veliconcha unveiled: observations on the larva of *Conus spurius*, with implications for the origin of molluscivory in *Conus*
Leal JH, Kohn AJ and Mensch, RA

9:40 am A hypothesis for the origin of molluscivory in *Conus*
Kohn AJ, Leal JH and Mensch RA

10:00 am Prey preference follows phylogeny: evolutionary dietary patterns within the nudibranch group Cladobranchia.
Goodheart JA, Bazinet AL, Valdés A, Collins AG and Cummings MP

10:20 – 10:40 pm Coffee Break

10:40 am Location, location, location: Position of the epibiont *Crepidula adunca* on its host *Calliostoma ligatum*
Voltzow J, Fetcher N and Iyengar EV

11:00 am Photosymbiosis in subfamily Fraginae
Yamaguchi A, Gentry M, Gannon M, Rosenberg G, Remo A, Kopala D and Horwitz R

11:20 am Maximizing solar energy: Giant clam image analysis and pattern recognition
Cai J, Holt AL, Rehm L, Scarsdale NA, and Sweeney AM

12:00 – 1:20 pm Lunch

1:30 – 2:30 pm AMS business meeting ● Clayton 125

6:00 pm buses depart for concluding barbeque at DMNH
9:00 & 10:00 pm buses return to Clayton Hall

Thursday am ● Historical Ecology ● Clayton 120

9:20 am Stable Carbonate Isotopes in Giant Clam Shells
Gannon M

9:40 am Using Live, Dead, and Fossil Mollusks to Reconstruct the Historical Ecology of Florida's Freshwater Springs
Kusnerik KM, Means GH, Portell RW and Kowalewski M

10:00 am Reassessment of the role of ocean gateway events in molluscan faunal change
Hickman CS

10:20 – 10:40 Coffee Break

10:40 am From North America to South American and back again: the post-Cretaceous peregrinations of the family Cerionidae
Harasewych MG

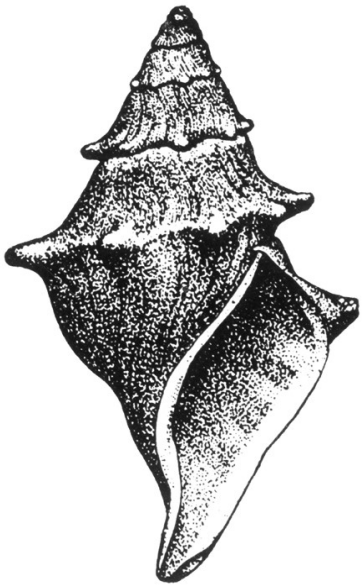
11:00 am Using historical museum collections to determine Amino Acid Racemization (AAR) profiles of Jamaican land snails
McDonald MT

12:00 – 1:20 Lunch

1:30 – 3:00 pm AMS business meeting ● Clayton 125

6:00 pm buses depart for concluding barbeque at DMNH
9:00 & 10:00 pm buses return to Clayton Hall

Abstracts
Alphabetical by author's last name



Phylogeny and biogeography of helicostyline land snails in the Philippines

G. Batomalaque[1,2] & G. Rosenberg[1,3]

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[3]Academy of Natural Sciences of Philadelphia, Drexel University, 1990 Benjamin Franklin Parkway, Philadelphia, PA; gr347@drexel.edu

The Helicostylinae comprise a radiation of 300 species of land snails, 98% of which are endemic to the Philippines. We reconstructed the phylogeny of the group using genomic data from exon capture, aiming to determine if Helicostylinae and its constituent genera are monophyletic, and to reconstruct the timing and routes of colonization of the Philippines and the biogeographic patterns of diversification. Our results support previous suggestions that Bradybaenidae and Camaenidae are confamilial, and suggest two separate colonizations of the Philippines by species currently classified as helicostylines. Some genera prove not to be monophyletic, with clades more closely reflecting geography than current taxonomy.

Mollusks in Peril

Non-native (and potentially invasive) marine molluscan species in the Florida Keys–the challenge of recognizing what does not belong

R. Bieler[1], T.M. Collins[2], R. Golding[3], J.M. Healy[4,] C. Granados-Cifuentes[2,] P.M. Mikkelsen[1], T.A. Rawlings[5], & P. Sierwald[1]

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[4] Queensland Museum, PO Box 3300, South Bank, Queensland, Australia, 4101; john.healy@qm.qld.gov.au
[5] Department of Biology, Cape Breton University, Sydney, Nova Scotia, Canada; Timothy_Rawlings@cbu.ca

Reports of marine invasive species in Florida have focused on large-bodied and conspicuous taxa such as lionfish (*Pterois volitans* and *P. miles*) and the orange tube coral (*Tubastraea coccinea*). However, the majority of marine molluscan species are comparatively small-bodied, under-researched (and often taxonomically confused), and have few published occurrence records in time and space.

How do we decide whether a newly discovered species in Florida is a new arrival or a previously overlooked native species? What kinds of data help in determining that a species is "native"? How do we deal with species that are exclusively known from artificial substrata? When is a non-native species "invasive enough" to warrant attempting local eradication?

Based on extensive field work, a survey of literature data, comprehensive museum collection studies, and anatomical, ultrastructural, and molecular data, we are exploring such questions using examples from marine gastropods and bivalves. Special focus is placed on members of Vermetidae and Gryphaeidae, in view of our recent discoveries of non-native members of both families on the artificial reefs (deliberately scuttled vessels) of the Florida Keys National Marine Sanctuary.

The North American Mollusk collections – a status report

R. Bieler[1], G. Rosenberg[2], E.K. Shea[3], & P. Sierwald[1]

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Research collections of molluscan specimens are held by many different institutions in North America. Collectively, these institutions are the stewards of much of the biodiversity information for the North American continent and many other regions of the world. The individual collections differ in many ways (e.g., in their size, topical specialization, institutional management, staffing, primary user groups, digitization status, electronic access, archival conditions). To address the ever-increasing need for solid baseline data to inform biodiversity research and management, communal data portals and third-party data aggregators make use of available museum data in various ways. Because of limited institutional on-line availability and a large backlog of to-be-databased collections, currently accessible resources are a subset of what is available in North American collections-holding institutions. Digitization of label data and specimen images, with associated georeferencing and mapping, will have to be broadened and accelerated in a community-wide effort. While developments such as dedicated database systems, digital imaging approaches, and communal authority files (e.g., MolluscaBase.org) have provided much-needed tools, other technological advances have riggered new collection needs not foreseen by earlier generations (e.g., molecular sampling, cryogenic storage).

Based on newly collected data from more than 50 North American collections via extensive questionnaires and subsequent discussions held at the (pre-AMS-2017) *Workshop on Mollusk Digitization*, we are presenting an analysis of the current status and needs of the mollusk collections in the United States and Canada.

Bioaccumulation of fluoxetine by the invasive freshwater bivalve, *Corbicula fluminea*

S.R. Burket & B.W. Brooks

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Though identification of contaminants of emerging concern (CECs) in aquatic life has increased over the last decade, most reported observations are from fish. Few articles investigate pharmaceutical exposure, bioaccumulation, and effects in freshwater bivalves. This represents an important gap because adverse outcomes in bivalves have been observed for select pharmaceuticals, including selective serotonin-reuptake inhibitors (SSRI). Though SSRIs and their active metabolites were originally observed in fish residing in urban water bodies, bivalves accumulate some of the highest levels of antidepressants. For example, fish from an effluent dependent river accumulated up to 14±4.6 μg/kg of the antidepressant sertraline compared to unionid mussels that accumulated sertraline to an order of magnitude higher levels (140±21 μg/kg). Such observations deserve study because freshwater bivalves, which are of high ecological and societal importance for sustainable ecosystem services and biodiversity, are increasingly threatened from urbanization. Unfortunately, factors influencing bivalve bioaccumulation of most CECs have not been studied and potentially result from different routes of exposure. Bivalve tissue bioaccumulation patterns of SSRIs suggest that dietary exposure from suspended particulate matter (SPM) is important for exposure of CECs. The SSRI fluoxetine exhibits greater than 50% particulate binding, which may explain why freshwater bivalves accumulate relatively high levels of certain CECs. Therefore, we performed a batch sorption isotherm experiment to determine fluoxetine binding affinity to suspended clays and a 72-hour uptake study with an invasive freshwater bivalve, *Corbicula fluminea*. Water, suspended clay, and tissue concentrations were measured via isotope-dilution LC-MS/MS. Results inform decisions about particulate-bound CECs and exposure modeling.

RECOLNAT Program: Digitization of mollusk collections at MNHN

M. Caballer-Gutiérrez[1], M. Hennion[1], P. Lozouet[2], V. Héros[3], E. Perez Pimparé[4], M. Pignal[4], & P. Bouchet[3]

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The Museum National d'Histoire Naturelle (MNHN), founded in 1793 by the French Revolution, was the first public institution specifically established to conserve natural history specimens, and Lamarck was among its first appointed professors. Although little of the pre-Revolution royal specimens remain, the collections go back to pre-Linnean author Michel Adanson and his *Histoire naturelle du Sénégal* (1757). Other collections with considerable historical and cultural heritage value include the specimens from Napoleon's Egyptian Expedition, and the collections made during the early voyages of exploration on board the ships *Astrolabe* and *Zélée*. From the mid-19th to the mid-20th century the growth of the collections was pulled by colonial expansion in Africa, Madagascar, Indochina and Oceania - but also included the landmark *Mission scientifique au Mexique* or de Morgan's explorations in the Kingdom of Perak and in Persia. Current growth is driven by the *Tropical Deep-Sea Benthos* and *Our Planet Reviewed* programs, and has fully embraced the molecular revolution.

The RECOLNAT Program (ANR-11-INBS-0004) is a country-wide project to digitize all the natural collections in France and make them publicly available on the internet. As a result of this effort, 7.7 million specimens of all phyla have been digitized to date, and 6.7 million images created (https://explore.recolnat.org/).

Within RECOLNAT, the digitization of the molluscan type collection at MNHN has been in progress since 2014, with images of roughly half of the ca 15,000 primary types currently available online (https://science.mnhn.fr/institution/mnhn/collection/im/item/search) and linked to the World Register of Marine Species (WoRMS). The second area of focused digitization efforts is the molecular collection, which initially benefited from kick-off funding by the Sloan Foundation under the Marine Barcoding of Life (MarBOL) initiative. Online access to images of molluscan types in MNHN has considerably diminished the number of requests for actual loans. When historical and modern specimens are considered together, the collections are the source of ~100 research publications every year.

Sea slugs from French Guiana and the distinctiveness of the Guyanan ecoregion

M. Caballer Gutiérrez[1] & J. Ortea[2]

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[2] Departamento BOS, Universidad de Oviedo, Asturias, Spain; jortea@uniovi.es

The fresh water plumes of the Orinoco and Amazon rivers constitute a barrier separating the Caribbean and the Brazilian biogeographic (sub)provinces in the Western Atlantic. The Guyanas is the longest muddy coastline in the world, with desalinated and turbid waters, and is ranked as a distinct Ecoregion, the Guyanan.

In 2014, a biodiversity expedition to French Guiana was conducted as part of the *Our Planet Reviewed* program. The expedition included both a middle-shelf / deep sea component and a shore-based party at Îles du Salut, and 165 stations were sampled from the shore to a depth of 650 m.

To date, 15 species of sea slugs only (including cephalaspids) had been recorded from French Guiana. During the 2014 expedition, 710 specimens belonging to 33 species were collected from 40 stations, at depths between 0 to 307 m. The order Cephalaspidea is best represented, with 19 species. Two species, *Pyrunculus caelatus* (149) and *Pleurobranchaea inconspicua* (119), make up nearly 40% of the catch; 16 species (48.5%) were represented by 5 or fewer specimens, and 11 (33%) are singletons or doubletons. Six species are new or possibly new to science.

In this presentation, we review the composition of the sea slug fauna of French Guiana, and discuss the reality of the Guyanan Ecoregion.

Maximizing solar energy: Giant clam image analysis and pattern recognition

J. Cai[1], A.L. Holt[1], L. Rehm[2], N.A. Scarsdale[1], & A.M. Sweeney[1]

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Tridacnid giant clams are famous for their colorful siphonal mantle patterns. These colors result from the backscatter from the clams' iridescent cells, superimposed on the highly absorbing, near-black symbiotic algae underneath. These iridocytes function to distribute incoming solar flux to algae within the mantle tissue, such that every alga receives a flux that can be utilized efficiently by photosystem II. However, given the apparent utility of this scattering system to the clam, it has remained mysterious why iridocyte patterns are apparently so variable both within and between species of Tridacnids.

Here, we study variations in iridocyte patterning via a set of color-standardized 50-m photographic belt transects from several habitats containing wild giant clams on Palauan reefs. The original set contains 1644 images, and after post-processing and quality control, the final dataset analyzed contains 501 clams. We analyzed the data for correlations in clam iridocyte patterns within and between species and habitat type using the hue of the constituent pixels as a proxy for absorbance of visible wavelengths. After incorporating color standards to the images, we demonstrate that the clam color patterns are composed of two constituent iridocyte types (blue and yellow) and that clams that visually appear to have few to no iridocytes in fact are typically covered with a monolayer of iridocyte cells. We used machine learning methods to probe the environmental dependence of iridocyte hue and spatial density fluctuation. The second-order details of iridocyte density effects may provide insights to optimizing growth in industrial photobioreactor systems.

Shell collecting and the making of modern Japanese science 1830-1925

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Amateur natural scientists in the Meiji period (1868-1912) played an important role in developing a scientific outlook among the Japanese public that has been largely overlooked by historians. Many conventional studies of Japan's development during that time focus on industry, communications and political reforms, but do not assess the effect that the availability to ordinary people of increasingly sophisticated scientific media had on the public perception of natural science.

This talk looks at the history of shell collecting before, during and after the Meiji period. It traces the development of various modes of knowledge-making, the transformation in the basis of scientific knowledge and the technological enhancement of existing standards of objectivity and credibility. Examples are given of Samurai scholars and merchant collectors who used shell collecting as a form of socialized or "citizen" science in harmony with the Japanese public's growing enthusiasm for Western technology.

Finally, there is an introduction to the life and work of Yoichiro Hirase, the most influential figure in the development of Japanese Malacology. His extensive social networks spanned a vast range of people, from rural poultry breeders to the Imperial Household, and extended to shell collectors worldwide, making him a key actor in and ambassador of modern Japanese natural science.

Use and limits of mitochondrial DNA sequences in the freshwater Cerithioidean families Pleuroceridae and Semisulcospiridae

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Many studies have examined molecular phylogenetics within the families Pleuroceridae and Semisulcospiridae using COI and 16S sequence data. However, some sequences are highly divergent, leading to uncertainty about the interpretation of the results. Moreover, taxonomic coverage has remained uneven. Here, we add new DNA sequences to a synthesis of existing data to examine the utility of these genes in more detail to assess the phylogenetic utility of these markers for assessing phylogenetic relationships. For COI, divergence in the protein sequence provides a useful way to identify and exclude problematic, divergent sequences, whereas for 16S we simply determined which sequences were extremely apomorphic.

Exclusion of problematic sequences produces a plausible phylogeny of the two families with a strong biogeographic signal. In Semisulcospiridae, North American *Juga* show convergence on smooth shells in multiple lineages, but genetically match well with major river divides. In Asia, species from Pearl River system of southern China south to Vietnam are very distinct from those of Taiwan, Japan and mainland areas from the lower Yangtze north to Russia. Among the pleurocerids, Mobile, Mississippi, and Appalachicola drainages have distinctive species groups. Distinctive clades also occur in the Atlantic drainages. The results suggest that considerable revision to current genus-level taxonomy is needed, although some key type species remain undocumented. Despite the difficulties, COI and 16S sequences can provide useful phylogenetic data for these families when examined appropriately.

Mollusks in Peril

Risks for Florida's native land snails from the New Guinea flatworm, *Platydemus manokwari*

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The invasive, non-native, terrestrial New Guinea flatworm (*Platydemus manokwari*) was recently discovered in Florida (Justine *et al*., 2015). In other regions where it has been introduced, it has been considered the cause of extinction and/or dramatic decline of native species, particularly land snails, and for this reason is considered one of the World's 100 worst invasive species. Because of this history and given that we observed a large-scale predation event on native Florida tree snails by *Platydemus manokwari* flatworms in August/September of 2015 in Castellow Hammock Complex Preserve, concern is acute for the iconic land snails of south Florida, including *Liguus* and *Orthalicus* spp. The distribution and abundance of *Platydemus* in Florida is, however, unknown at present, particularly near populations of native snails. The mechanisms by which *Platydemus* may be spreading through the state are also unknown. This basic information is required in order to determine the possible impacts of this species in Florida, and to mitigate its further spread in Florida and more broadly through the United States.

As a first step in clarifying the possible impacts of *Platydemus* in Florida, we are working to: 1) document the extent and genetic identity of populations of *Platydemus* flatworms in Florida, particularly near populations of imperiled species such as *Liguus* and *Orthalicus* spp.; 2) given that *Platydemus* flatworms are reported to have limited natural dispersal, clarify the mechanisms by which they are spreading through the state; 3) determine the presence/prevalence of *Angiostrongylus* species, parasitic nematodes responsible for several human central nervous system and gastrointestinal diseases, in selected *Platydemus* flatworm populations; and 4) determine predation effects of *Platydemus* flatworms on *Liguus* and *Orthalicus* spp. tree snail populations in Castellow Hammock Complex Preserve as a test case of *Platydemus manokwari* effects on native south Florida tree snail populations. (PeerJ https://peerj.com/articles/1037/.)

New genetic and morphological data suggests that land snail *Anguispira alternata* (Gastropoda: Stylommatophora: Discidae) is a species complex

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The North American endemic land snail genus *Anguispira* is distributed east of the Great Plains with two additional species in the Columbia River Basin of the Pacific Northwest. Most *Anguispira* species are restricted to hardwood forests where they live under bark and on decaying logs and stumps, although a few species occur in leaf litter and at least one clade with lens shaped shells inhabit cracks in limestone outcroppings. *Anguispira alternata* tolerates the broadest range of habitats of any *Anguispira* species, occurring in both hardwood forests and anthropogenic habitats. The species also has the largest geographic range of any *Anguispira* species occurring east of the Great Plains from southern Canada to at least as far south as northern Georgia. Traditional classifications recognize only five species of *Anguispira*, two with several subspecies, the majority of these were subspecies of *Anguispira alternata.* Recent classifications have treated nearly all former subspecies of *Anguispira alternata* as distinct species but have in most cases not provided a rationale for these decisions. The anatomy of most *Anguispira* species is unknown and species continue to be described based only on shell characters. As a result, species limits within *Anguispira* have remained unclear and in most cases untested. New data based on morphological characters of the shell, and reproductive system combined with DNA sequence data from three mitochondrial (COI, 16S, CytB), and one nuclear gene (LSU) supports prior elevation of several subspecies of *Anguispira alternata* to species level and suggest there are additional undescribed species in the complex.

The Illinois Natural History Survey (INHS) Mollusk Collection: Databasing and Digitization

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The INHS Mollusk Collection (including the former University of Illinois Museum of Natural History (UIMNH) collection) is one of the 15 largest in North America. The collection contains over 485,000 cataloged specimens in over 87,000 lots: (57% bivalves, 41% gastropods, 2% other) (67% freshwater; 20% marine or brackish; 13% terrestrial). Over 99% have been identified to species and the names referenced to a literature source. All of the catalogued lots have been data based and 90% have been geo-referenced. There are about 400 type lots: 200 freshwater gastropods, 150 terrestrial gastropods, and 50 freshwater bivalves. The collection is strong in Unionoida (43,000 lots), freshwater and terrestrial gastropods from the Midwestern U.S. and Conoidea (6,000 lots). We also have strong holdings of freshwater bivalves and gastropods from the Southeastern U.S., Central and South America. About 12,000 lots were collected from 1850-1950 and 46,500 from 1950-present. Just over 73,000 lots are dry and 14,000 stored in ethanol (some were fixed in formalin). We have a backlog of about 5,000 lots. Our greatest needs are new space (we are currently in 5 rooms), new cabinets, and hourly help with our backlog. More than 21,000 soft parts of over 150 species have been preserved and are available for study. The data are stored and managed in Filemaker Pro 14Ⓣ. The Data are served on the web via a Symbiota Portal. We have nearly 3,000 lots with images served on the Great Lakes Invasives TCN Portal and over 800 on the Mussel Project (MUSSELp) website.

Fontanella, F.M., Starnes, J.,
Whitaker, M., & Garner, Y.

Preliminary analyses of the genetic variation of the hooked mussel *Ischadium recurvum*, along the Florida coast

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Although the colonization of new habitats is sometimes a natural process, the number of invasive species has accelerated dramatically in recent years as a result of human activities. Invasive species often outcompete or prey upon native species and have been ranked as the second greatest problem facing global conservation today, exceeded only by habitat loss. A recent survey identified more than 1600 invasives along the coast of Florida, most of which have been shown to have a negative impact on the health and abundance of the native biodiversity and ecosystems. Recent genetic studies of species distributed along both coasts of Florida have uncovered extensive cryptic diversity associated with the Atlantic/Gulf divide, with the genetic break occurring at various points along the southern Florida peninsula. The hooked mussel *Ischadium recurvum* is considered a common indigenous mussel along both coasts of Florida inhabiting hard substrates including wood, rocks and boat dock pilings and has been shown to play an important role in coastal ecosystems. The overreaching goal of this study is to utilize molecular data from two mitochondrial genes to assess the species diversity, conservational status and population genetic structure within the hooked mussel *Ischadium recurvum* along the coast of Florida.

Effects of short term exposure to the gestagens progesterone and levonorgestrel on the development of juvenile apple snails (*Pomacea canaliculata*)

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Intensifying anthropogenic development has led to an increase of endocrine disrupting chemical (EDC) pollution in aquatic environments. Gestagens, which include the steroid hormone progesterone (P4) and the synthetic progestin levonorgestrel (LNG), have been measured in runoff from agricultural fields and in wastewater treatment plant effluent. While both these EDCs have been shown to alter fecundity, morphology, and reproductive behavior in fish, their effects on invertebrates are poorly understood.

Pomacea canaliculata (Ampullariidae), a highly invasive freshwater snail, has previously been used to examine the impacts of tributyltin and testosterone on reproduction (Sternberg *et al.* 2010). *Pomacea canaliculata* are sexually dimorphic and often inhabit environments that are anthropogenically impacted, making them a suitable indicator species for EDC contamination. To examine the impacts of EDCs on *P. canaliculata* growth and motility, juvenile snails were exposed to environmentally relevant concentrations of P4 and LNG.

Juvenile snails (n=15) were exposed for 25 days to either ethanol (control), 30 ng/L P4, 300 ng/L P4, 10 ng/L LNG, or 100 ng/L LNG using static replacement. Snails were fed *ad libitum* and maintained at standard photothermal conditions. To assess growth, shell height was measured on days 14 and 25, and locomotion for each population was assessed using behavioral analysis software on day 14. Snails exposed to both P4 and LNG differed significantly from the control group ($p<0.05$) in both growth rate and activity level, suggesting that P4, LNG, and other related EDCs may be impacting the behavior and possibly the viability of wild populations.

Stable carbonate isotopes in giant clam shells

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Bivalves are useful bioarchives of their surrounding habitat. They are relatively sedentary and incorporate stable isotopes reflecting their local environment as they mineralize their shells. Giant clams (Cardiidae: Tridacninae) provide a vast and continuous environmental record because they: i) have longevity, ii) mineralize their shells rapidly and constantly and, iii) occur in the low latitude tropics, for which paleoclimate is under studied. A thorough literature review of published stable isotope profiles of *Tridacna* was completed to compare species, localities, and time. The most prominent result suggests $\delta^{13}C$ values have become depleted in giant clam shells at a comparable rate to atmospheric CO_2 since the early 1960's. This trend is supported by $\delta^{13}C$ of a *Tridacna derasa* collected from Palau in 2016 and analyzed at the Academy of Natural Sciences. Depletion of ^{13}C in atmospheric CO_2 is thought to be due to the burning of fossil fuels of isotopically light, C_3 plant origin. As fossil fuels burn, they are mixing with contemporary CO_2, of C_3 and C_4 (isotopically heavy) plant origin. Although there are other influences on carbon including diet, atmospheric CO_2 is incorporated into seawater. This is utilized in photosynthesis by algae that live symbiotically with *Tridacna*. Thus, a global change in CO_2 should be apparent in mineralizing organisms. This presentation will review and compare the previous applications of stable carbon isotope analyses in giant clam shells, as well as present a new modern set of profiles for *T. derasa*, particularly highlighting the utility in long term monitoring of $\delta^{13}C$.

The mollusk collection of the Field Museum of Natural History, Chicago

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The Field Museum of Natural History (FMNH) in Chicago was founded in 1893 as the permanent repository for natural history objects displayed at the World's Columbian Exposition. It is a private, non-profit organization.

The mollusk collection is part of the "Invertebrates" collection unit which encompasses all invertebrate groups except insects, arachnids, and myriapods. The collection has a world-wide scope and includes marine, freshwater and terrestrial forms. It comprises currently ca. 382,000 cataloged molluscan lots, of which ca. 84% are gastropods, 15% bivalves, and 1% cephalopods, chitons, scaphopods, Solenogastres, and Caudofoveata. Approximately 35,000 to 40,000 molluscan (sub)species are represented.

Collection strengths are terrestrial gastropods of North America, Australia, the Pacific Islands, South America, and the Caribbean; marine mollusks of southern Florida and adjacent areas; mollusks (along with other invertebrates) from deep-sea habitats, such as hydrothermal vents, cold seeps and wood falls. The many notable institutional and private collections absorbed include: University of Utah, Cleveland Museum of Natural History, P.P. Carpenter, J. Ferriss, L. Hubricht, A.J. Kohn, and W. Weyrauch.

Several thousand type lots, including ca. 450 primary types, are present. High-resolution images of primary types are available on-line.

So far, 76% of the molluscan collection has been databased and the information is (with few exceptions) available to the public on-line (http://collections-zoology.fieldmuseum.org/list?f%5B0%5D=ss_CatCatalog%3A%22Invertebrate%20Zoology%22). Currently, 15% of these databased records are georeferenced. Digitization efforts are ongoing, currently supported under the TCN InvertEBase grant (NSF EF 14-02667).

Malacology underground: A review of gastropod diversity in caves of North American and their ecological significance

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A diverse snail fauna exists within the caves of central and eastern North America, represented by over 95 genera and 260 terrestrial and aquatic species. In most freshwater and surface environments, gastropods play significant roles in many food webs and provide a diverse array of ecosystem services, including: accelerating decomposition of leaf litter and woody debris, detoxification of soils by means of calcium sequestration, control of algae growth, maintenance of water quality, and nutrient cycling to larger vertebrate fauna. In subterranean environments, the diversity and ecology of gastropod species have not been well studied. Although direct evidence is lacking, it is likely that aquatic and terrestrial snails facultatively or obligately living in subterranean habitats provide similar services.

Here, we review the biodiversity of facultative and obligate cave-dwelling snails of central and eastern North America based upon historical observation records and recent bioinventory efforts. Our preliminary dataset shows that aquatic snail diversity is approximately ¼ that of terrestrial diversity in subterranean environments. Of the terrestrial and aquatic genera observed, *Helicodiscus* and *Fontigens* have the highest number of records, respectively. Further, although there was far greater terrestrial snail diversity, there are nearly six times as many known aquatic cave obligates than terrestrial cave obligates. While this pattern could represent sampling biases between groups, it may represent a natural phenomenon whereby aquatics are more prone to cave obligate adaptations. Lastly, we briefly discuss the potential roles these gastropods may play within cave systems.

Prey preference follows phylogeny: Evolutionary dietary patterns within the nudibranch group Cladobranchia

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Nudibranch sea slugs within Cladobranchia occupy a diverse array of marine environments and feed on a variety of prey items, but most specialize on cnidarians. This likely played a role in the evolution of nematocyst sequestration, a well-known diet-related innovation within this clade. The broad range of prey preferences present in two major taxa within Cladobranchia suggest that prey preference is relatively labile over evolutionary timescales, but there exist many well-documented cases where cladobranch species are tightly associated with specific prey. This raises questions about the roles that dietary specialization and prey preference shifts have played in the evolution of this group. The prevalence of prey preference shifts in large clades of marine taxa such as Cladobranchia is poorly known, partly because the well-supported phylogenetic hypotheses required for studying this phenomenon have been lacking. In this work, we identify and resolve the major lineages within Cladobranchia using RNA-Seq data, and use ancestral state reconstruction analyses to better understand the evolution of prey preference within this group of organisms. These analyses answer several questions regarding the evolutionary relationships within Cladobranchia, including support for the monophyly of Arminida as sister to Tritoniidae (which both preferentially prey on Octocorallia) and multiple origins of nematocyst sequestration within Cladobranchia. Ancestral state reconstruction analyses support a cladobranchian ancestor with a preference for prey within Hydrozoa. There is strong phylogenetic correlation to prey preference within Cladobranchia, suggesting prey specialization within this group is evolutionarily important. Shifts between different prey types have occurred rarely throughout the evolution of Cladobranchia, indicating that this may not have been an important driver of the diversity within this group.

Species diversity of mangrove gastropods and diversification of the Onchidiidae (Gastropoda: Pulmonata)

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A diverse assemblage of molluscs are specialized to mangroves, but are threatened by continued habitat loss. With the help of collaborators, our lab has undertaken extensive fieldwork across the Indo-West Pacific to collect new material which can be used for molecular and morphological analyses. Gastropods have been sampled from over 250 stations, focusing on type localities, and COI sequences obtained from over 5,000 specimens representing more than 200 species. Species are strongly supported, reciprocally monophyletic units separated by a clear barcode gap (which can slightly differ between genera). Biogeographic patterns of species diversity are discussed.

The Onchidiidae are one of the most poorly known groups of mangrove gastropods and the taxonomy of the onchidiids has long remained in confusion. However, thanks to extensive sampling, sixty-five species of onchidiids are now known from the tropical Indo-West Pacific. Many onchidiid species and several genera are undescribed. Every genus is being taxonomically revised (papers published, in press, or in progress). A multi-locus phylogeny is presented, as well as geographic patterns of diversification across the family.

Conflict Clade Analysis (CCA) of the freshwater mussels subfamily Unioninae (Bivalvia: Unionoida)

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Conflict Clade Analysis (CCA) is intended to minimize the need to illustrate the multiple trees that might result from exploration of data partitions or phylogeny reconstruction methods based on the view that mere resolution of an alternative topology without branch support need not always merit concern. CCA compares the branch support of all the clades among alternative topologies to a reference tree and results in a list of clades that are 1) well-supported among alternative trees (e.g., bootstrap ≥70, posterior probability ≥95), but 2) not well supported in the reference tree. CCA highlights where individual analyses differ, and the results can be presented as a concise table rather than multiple tree figures.

CCA is implemented as a Python script using PAUP, RAxML, and Mr. Bayes text files as input. The previous version of CCA did not allow for missing taxa. That is, all taxa needed to be represented among the topologies to be compared. The current version allows for comparisons among clades even if taxa are missing by joining pruned alternative topologies with either the largest or smallest consistent reference clades.

As a demonstration of the utility of CCA (as well as potential shortcomings), the phylogeny of the freshwater mussel subfamily Unioninae was analyzed using four separate gene fragments obtained from Genbank: COI, 16S, ND1, and 28S. Only COI was shared among all included terminals, and individual and combined partitions were analyzed under parsimony, likelihood, and Bayesian criteria. Results will be used to discuss the phylogeny/classification of the Unioninae.

Mollusks in Peril

Society Island *Partula* tree snail survival after a mass extinction: New genomic insights using museum specimens

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The tree snail family Partulidae is endemic to Oceania and represents one of the most infamous recent examples of oceanic island mass extinctions. Deliberate introduction of the predatory rosy wolf snail *Euglandina rosea* in the late 20th century led to the extinction/extirpation of ~55/61 Society Island partulid species. A small number of species from the genus *Partula* still survive in the wild either in montane cloud forest >1,000m in elevation (*P. otaheitana* on Tahiti), where the predator is relatively ineffective, or in Tahitian (*P. clara* and *P. hyalina*) or Moorean (*P. taeniata*) valleys. This begs the question, why are these populations surviving, especially when models predicted their extinction within three years of coming into contact with *E. rosea.* A previous mitochondrial (mt) phylogeny based on museum, captive, and remnant wild specimens recovered a close genealogical linkage among the three valley survivors on both islands. However, Society Island partulid evolutionary studies to date have been characterized by a lack of congruence among different molecular markers (e.g., allozymes, mt genotypes, or nuclear ribosomal DNA) so it is unclear how accurate the mt phylogeny is. For this special session on endangered mollusks "Mollusks in Peril 2017," we present a high-resolution nuclear data set using next generation sequencing methods to phylogenomically assess the differential survival of Society Island Partulidae. We ask 1) What can phylogenomic data tell us about the radiation of this clade across this archipelago? and 2) Are the valley survivors genealogically linked?

From North America to South America and back again: The post-Cretaceous peregrinations of the family Cerionidae

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Human-mediated impacts are altering the planet, so much so, that scientists have now designated this period a new geological epoch, the Anthropocene. One of the hallmarks of this new epoch is the mass extinction of plants and animals globally. While all groups are being impacted, the headlines most often feature stories of mammal and bird extinctions, or other charismatic vertebrate megafauna. Yet, recorded molluscs extinctions outnumber mammal and bird extinctions combined. Nowhere is this more evident than on Pacific Islands, which have seen the estimated 6000+ species, mostly single island endemics, reduced dramatically. The Hawaiian Islands support one of the world's most spectacular radiations of land snails, with 10 families containing 750+ recognized species, and at least 300 more remaining to be described. Unfortunately, like most of the fauna throughout the Pacific islands, Hawaiian land snails are mostly extinct, with some estimates as high as 95% for some families, and rates as high as 10% per decade. Although most of this spectacular diversity has been irretrievably lost, there remain many species, including several undescribed taxa, that may be possible to save. However, this will require dramatic changes to the perspectives of snails, by both the conservation community and the public, and revised approaches to conservation. Here, we offer some insights into the perspective problem and offer suggestions for the direction conservation must take if we are to have any hope to save what remains of this spectacular fauna, and what has been called the jewels of the Pacific.

Mollusks in Peril

Pacific Island land snails: Changing perspectives for conservation

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Human-mediated impacts are altering the planet, so much so, that scientists have now designated this period a new geological epoch, the Anthropocene. One of the hallmarks of this new epoch is the mass extinction of plants and animals globally. While all groups are being impacted, the headlines most often feature stories of mammal and bird extinctions, or other charismatic vertebrate megafauna. Yet, recorded molluscs extinctions outnumber mammal and bird extinctions combined. Nowhere is this more evident than on Pacific Islands, which have seen the estimated 6000+ species, mostly single island endemics, reduced dramatically. The Hawaiian Islands support one of the world's most spectacular radiations of land snails, with 10 families containing 750+ recognized species, and at least 300 more remaining to be described. Unfortunately, like most of the fauna throughout the Pacific islands, Hawaiian land snails are mostly extinct, with some estimates as high as 95% for some families, and rates as high as 10% per decade. Although most of this spectacular diversity has been irretrievably lost, there remain many species, including several undescribed taxa, that may be possible to save. However, this will require dramatic changes to the perspectives of snails, by both the conservation community and the public, and revised approaches to conservation. Here, we offer some insights into the perspective problem and offer suggestions for the direction conservation must take if we are to have any hope to save what remains of this spectacular fauna, and what has been called the jewels of the Pacific.

Reassessment of the role of ocean gateway events in molluscan faunal change

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Molluscan biogeographers have long invoked opening and closure of ocean gateways to explain faunal change. However many classic stories fall apart with increased sampling, data on directions of gene flow, connectivity patterns, better dating, detailed reconstruction of global tectonic events, paleooceanographic data, and climate modeling. Current interest in gateways is driven by their prominent role in global climate change and heat transfer. This is a good time to reinterpret molluscan patterns with new data. Examples developed here are (1) asymmetric exchange of high-latitude marine mollusks coincident with opening of the Beringian Gateway and (2) anomalous and incongruent low latitude patterns in shallow and deep Wallacea relative to the Southeast Asian Gateway.

Beringian Gateway. A field expedition to the Tjörnes Seacliff Fossil Shellbeds in Iceland provides new data on the taphonomic and stratigraphic setting of the *Serripes* Zone appearance at 3.6 Ma of North Pacific mollusks that is consistent with geologic data for a much earlier opening of the Beringian gateway connection between the North Pacific and Arctic/Atlantic.

Southeast Asian Gateway. Documentation of new relict and narrowly endemic deep-water trochoidean and seguenzioidean gastropods in Wallacean Indonesia must be explained by a longer geologic history of changing relationships between land and sea during collisions and suturing of plates and microplates, subduction, volcanic arc formation, extensional tectonics, disappearances of landmasses and seaways and a longer list of oceanographic and atmospheric variables, seafloor topography, and enigmatic disjunction between living fossil taxa (e.g. abyssochrisid gastropods, coelacanth fish) currently restricted to deep Wallacea and southern Africa.

Mollusks in Peril

Shape variation in the Shining Ramshorn Snail, *Segmentina nitida*, an overview of declining European populations

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The Shining Ramshorn Snail, *Segmentina nitida,* is a rare freshwater snail found predominantly in drainage ditches and marshland that is experiencing marked declines in distribution in the United Kingdom (UK) and mainland Europe. The species was included in the IUCN Red Data Book for Invertebrates before guidelines changed in 1994 and is included on the UK Biodiversity Action Plan as a priority species for conservation.

To assess and compare morphological diversity of *Segmentina nitida* populations in the UK and Europe, we collected and photographed the shells of 590 individuals from 28 populations across Poland, the Czech Republic, Germany, Sweden, the Netherlands and the UK. The photographs were digitized using landmark-based analysis software (TPS Suite). Analysis of centroid size showed significant differences between populations, as did relative warp scores, with similarities between Germany, the UK, and the Netherlands. Discriminant Analysis and Canonical Variant Analysis (CVA) also show distinct groupings of populations by country of origin. Differences in shell aperture shape and size may result from adaptation of populations to local habitat, vegetation and water chemistry.
We discuss how these data will be combined with population genetics work and habitat characterization to link *S. nitida* phenotypes to genotypes and habitat types, helping conservation efforts and possible local reintroduction of the species in the UK.

Mollusks in Peril

Propagation and restoration of freshwater mussels (Bivalvia: Unionidae) to recover the biodiversity of rivers in Virginia and Tennessee

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The greatest diversity of freshwater mussels (Unionidae) is concentrated in North America with roughly 297 recognized species. However, this fauna has experienced dramatic declines, such that federal recovery plans for endangered species proposed a strategy of propagation of young mussels for release to natal rivers to augment declining populations. A range of cost-effective methods was used to culture 15,000-50,000 juvenile mussels including 12-20 endangered species to tag-able size (>15-20 mm) for annual release in rivers in Virginia and Tennessee. Of those, pale lilliput (*Toxolasma cylindrellus*) is facing extremely high risk of extinction in the wild. In June 2016, 3,878 juvenile mussels of *T. cylindrellus* were successfully propagated at the Cumberland River Aquatic Center, Tennessee Wildlife Resources Agency and 3,876 juveniles of this species are being grown out. The survival rate of this species has remained approximately 100% during the past 11 months.

A mark-recapture monitoring process using Passive Integrated Transponder (PIT) tags was used to assess survival and growth of those released mussels. Evaluation of site suitability based on in-situ survival and growth of juvenile mussels indicated that mussel restoration and recovery varied among release sites. The overall mean detection probability and survival rate of released federally endangered species Cumberlandian combshell (*Epioblasma brevidens*) in the Powell River in TN reached 97.8% to 98.4% and 99.7% to 99.9% (per month), respectively, during 9 successive recapture occasions in the 2-year study period, regardless of seasonality. Propagation, release and monitoring of juveniles represent a viable set of tools to recover endangered mussel species and restore populations damaged by anthropogenic impacts.

Judkins, H., Clark, K., Lindgren, A.,
& Vecchione, M.

Cephalopod Biodiversity

New Bathyteuthid species in the Gulf of Mexico and northwestern Central Atlantic Ocean

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The family Bathyteuthidae currently contains 3 recognized species: *Bathyteuthis abyssicola* (Hoyle 1885), *Bathyteuthis bacidifera* (Roper 1968), and *Bathyteuthis berryi* (Roper 1968). As part of a large-scale molecular-based phylogenetic study of Decapodiformes, Lindgren (2010) incorporated two samples of *Bathyteuthis, B. abyssicola* and *B*. sp. A (MV), which were collected over Bear Seamount in the northwestern Atlantic Ocean. At the time, though found to be genetically distinct from *B. abyssicola*, no formal description of "sp. A" was conducted, leaving its taxonomic status uncertain. Recently two comprehensive deep-sea research initiatives in the Gulf of Mexico (GOM), the Offshore Nekton Sampling and Acoustics Program (ONSAP) and the Deep Pelagic Nekton Dynamics of the Gulf of Mexico program (DEEPEND), collected multiple *Bathyteuthis* sp. specimens for closer examination. Morphological and molecular techniques (COI, 16s) were used to identify and separate species. We report here records of three new *Bathyteuthis* sp. from both the Bear Seamount region in the northwestern Atlantic and the GOM based on both genetic and morphological data. Morphologically, these new species of *Bathyteuthis* lack arm base photophores on arms I-III, a feature present in all three of the currently recognized species. Additionally, both 16S and COI sequence data support a separate distinct clade for each of the new species. This study documents 3 new *Bathyteuthis* species in the Gulf of Mexico and northwestern Central Atlantic Ocean which suggests that there may be additional new records of this genera to be discovered in the world's oceans.

A hypothesis for the origin of molluscivory in *Conus*

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In the hyperdiverse neogastropod genus *Conus*, most of the ~700 extant species whose diets in nature are known are rather specialized predators on marine worms, mainly polychaete annelids, that they paralyze with neurotoxic venoms and then swallow whole. These vermivorous species are scattered throughout recent species-level molecular phylogenetic trees that currently include about half of the known species. This and other phylogenetic evidence indicates that vermivory is likely the primitive feeding mode in the genus. The remaining approximately 20% of species mainly comprise two other feeding guilds, specializing on fishes and on other gastropods as prey. Phylogenetic analyses indicate that piscivory originated several times in the evolutionary history of *Conus*, while molluscivory arose only once. Present molecular genetic data indicate that all known specialist molluscivorous species are more closely related to each other than to any species outside their large clade. The similarities in several life history characteristics of *Conus spurius* described in the previous presentation motivated us to examine its other morphological and phylogenetic attributes for evidence relevant to the hypothesis that it or a close ancestor also gave rise to the modern molluscivorous *Conus* clade. In addition to similarities in veliconcha morphology and developmental mode, the following attributes are also consistent with that hypothesis: egg mass type, adult radular tooth morphometry, phylogenetic position, and age of earliest fossil records. The monophyletic clade of extant molluscivorous *Conus* species may have evolved in the Miocene from a vermivore or mixed vermivorous-molluscivorous ancestor with these attributes, such as *C. spurius*.

Marine mollusks of northwestern Puerto Rico: A taxonomic effort to assist in the preservation of biodiverse beaches and land

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Taxonomic surveys are beneficial for providing information on the biodiversity of a site. These surveys can also provide evidence as to why a site should be protected for further research. Puerto Rico has rich biodiversity throughout the island in a variety of habitats, both terrestrial and aquatic.

In March 2016 and September 2016, surveys of marine mollusk shells were conducted on several beaches throughout Puerto Rico, with a focus on the northwestern part of the island. The purpose of these surveys was to assist with taxonomy and education efforts. Although, there are several excellent resources for marine mollusks in the Caribbean, there are not too many recent (within the last 10 years) or regionally-specific resources for Puerto Rico.

In Aguadilla and Isabela, Puerto Rico, there is a grassroots effort to preserve coastal land that is threatened by development. The diverse species documented in this survey support the need to maintain the beaches and adjacent coastal area in a natural state to provide ecosystem services. Educational brochures highlighting mollusk diversity will inform local residents and visitors of the ecological significance of the area.

The conundrum of dams and dam removal to freshwater mussels in small rivers

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The 90,580 registered dams in the country possess an average age of 56 years and they provide drinking water, irrigation, hydropower, flood control, and recreation to our communities and economy. Each dam also creates areas of impoundment that together compose about 17% of stream reaches. Actual impacts from habitat change are only recently characterized. Beyond the directly affected regions, making lotic streams lentic, dams lead to regulation of stream flow that can be assessed from USGS data, changes in temperature and isolation of fauna between lotic zones. Recent studies in NE Ohio focused on two river systems severely impacted by dams, the Cuyahoga River that famously led to the clean water act, and the nearby Mahoning River, currently considered one of the most degraded systems in the nation. A special emphasis is placed on one stream reach where multiple dams have been removed.

Impoundments devastated the local fauna of freshwater mussels (Unionidae) across these two watersheds even as they partially protected downstream areas from scouring floods, with moderately diverse assemblages (ca. 10 species) remaining only in flowing reaches distant from dams. Headwater dams, however, instilled a more insidious decline long-term, perhaps through lost variation in flows, and they induced dominance of species generalists like *Lampsilis siliquoidea* and *Pyganodon grandis* in areas where water quality has reportedly improved. Removal of dams has only exacerbated species loss in the short term, especially where revitalized habitat is isolated. Single stream studies continue to highlight enigmatic loss, where removal of point source problems fail to lead to improvements in the fauna, and a more meta-approach on flow dynamics, often applied in large rivers, may better explain limits to improvements of small streams across regulated watersheds.

Using live, dead, and fossil mollusks to reconstruct the historical ecology of Florida's freshwater springs

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Aquatic communities of Florida's freshwater ecosystems have been studied by ecologists for over 50 years. In contrast, death and fossil assemblages, which preserve molluscan-components of past communities and can provide a unique historical perspective, have received limited attention.

Three types of samples were collected from Florida's Silver, Ocklawaha and Wakulla rivers: living mollusks (life assemblages), surficial shell accumulations (death assemblages), and river bank sediments (fossil assemblages). A total of 75 bulk samples from 21 localities were processed and all specimens (n=22668) have been counted and identified to species level where possible (20 species total).

Quantitative analyses indicate that diversity is highest in fossil assemblages, intermediate in death assemblages, and lowest in living communities. Many live and dead samples are dominated by recent invasive taxa, such as *Corbicula fluminea* and *Melanoides tuberculata*, while fossil samples include species that are rare or absent in live and death assemblages, suggesting changes in mollusk communities that predate modern ecological research. Nonmetric multidimensional scaling indicates that, for all three rivers, the live assemblages are distinct in faunal composition from the corresponding fossil and death assemblages. Also, live assemblages from different rivers diverge in faunal composition more notably than do fossil assemblages.

The results tentatively indicate that, when compared to past ecosystems, present-day mollusk associations shifted notably in faunal composition, display depressed diversity, and are regionally more heterogeneous in faunal composition. Comparisons of live, dead, and fossil mollusks may be used to quantify recent shifts in biodiversity, composition, and spatial structuring of freshwater communities impacted by anthropogenic changes.

New kid on the block: The collection at the Bailey-Matthews National Shell Museum

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The Bailey-Matthews National Shell Museum collection (BMSM) was established with the Museum opening in 1995. BMSM currently encompasses about 122,000 catalogued lots and includes private donations, collections originally in other institutions, and Museum-collected material. It consists of Recent mollusks, with a focus on the Gulf of Mexico, Florida, and the Caribbean. Fossils represent only 5.5% of the collection lots. In 2011, BMSM incorporated circa 11,000 lots from the local Florida Gulf Coast University. The 10,000-lots Redfern Collection, donated in 2014, includes material illustrated in Colin Redfern's "Bahamian Seashells" books. Regional relevance of the collection is exemplified by circa 8,000 lots of marine mollusks from Sanibel and Captiva islands and neighboring areas. In 2012, to assist with data-entry efforts, BMSM received the first of two grants from the Institute of Museum and Library Services (IMLS). Only 29,000 lots had been catalogued between the Museum opening and 2012. Since 2012, an additional 83,000 lots have been catalogued. Cataloguing of the entire collection backlog was completed in 2017. In 2016–17, funding from one IMLS grant has allowed staff to update the taxonomy and species-level nomenclature of more than 3,500 marine taxa, using WoRMS as the baseline reference. The Museum is now re-organizing the collection to accommodate these changes. Metadata are available from the Shell Museum web site at http://shellmuseum.emc2webs.com/collection/ and iDigBio/Global Biodiversity Information Facility (GBIF) at http://ipt.idigbio.org/resource?r=bmnsm-shell. About 9,300 lots are georeferenced through GBIF. Future needs include funding for linking/posting selected images and improving georeferencing capabilities of the collection.

A veliconcha unveiled: Observations on the larva of *Conus spurius*, with implications for the origin of molluscivory in *Conus*

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The veliconcha larva of the predatory gastropod *Conus spurius* Gmelin, 1791 is described and for the first time illustrated based on material from Sanibel Island, Florida. Hatchling veliconchas were 1470–1570 µm (mean = 1530) long, with first protoconch whorl maximum diameter 670–740 µm (mean = 710), and estimated egg diameter 570 µm. Veliconchas can swim for a few minutes to a few hours before settling. They have well-developed paired velar lobes each 600–700 µm in length, an extensible foot with a distinct metapodium separated from the remainder of the foot by a transverse fold, and operculum. Several early life history traits of *C. spurius*, particularly hatching as large veliconcha larvae with predominantly lecithotrophic, nearly non-planktonic development, closely resemble those of a well-defined clade of *Conus* species that prey on other gastropods. They contrast with the majority of species in this hyperdiverse genus, which hatch as much smaller planktonic, obligatory planktotrophic veliger larvae. Recent molecular phylogenetic trees suggest that the characters “pelagic development” and “non-pelagic development” (or nearly so: <1 day) are distributed independently of phylogeny in the larger clade that includes *C. spurius* and the molluscivorous species.

Digitization of the University of Michigan Museum of Zoology Mollusk (UMMZ) Division Collections

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The University of Michigan established a collection of mollusks during the first half of the 19th century. With current holdings of approximately five million specimens, the Mollusk Division collections have long ranked as one of the most important freshwater and land snail collections in North America. The collections are most notable for their breadth of taxonomic and geographic coverage, type collection and relative age. Significant sub-collections include the Bryant Walker Collection, Royal Ontario Museum Collection, F.C. Baker Wisconsin Freshwater Collection, Stelfox Sphaeriid Collection and J.B. Burch Lyophilized Tahitian Land Snails. In 2009, ethanol-preserved collections were relocated to a newly renovated Research Museums Center (RMC) to address storage limitations and safety issues. Additional renovations at the RMC have recently been completed and include installation of new archival specimen cabinets, environmentally-controlled collection space, research laboratories and libraries, and a demonstration room for teaching and public programs. Mollusk dry collections are currently moving to the RMC with an expected completion date of March, 2018. Computerization of records of the UMMZ Mollusk Division's collection began in 2005 with implementation of the *Specify* database with support from a NSF's Biological Research Collections (BRC) grant. Digitizing has considerably advanced recently through the support by two NSF awards, 'InvertEBase' and 'Great Lakes Invasives' Thematic Collections Networks (TCN). Since 2014 more than 100,000 specimen records have been uploaded to portals (i.e., Symbiota and iDigBio), more than 7000 lots have been imaged, and 37 graduate/undergraduate students have been hired and trained for data entry, taxonomy, geo-referencing and specimen curation.

Slow crawlers, fast invaders: The dispersal of the exotic slugs *Arion subfuscus/fuscus* in northeastern North America

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The invasion success of an exotic species relies partly on its ability to expand its geographic distribution. Just such species are found within the European slug species of the *Arion subfuscus/fuscus* complex, which have experienced an explosive expansion of their distribution in Québec in only fifty years. Such a rapid increase of distribution seems unusual for species for which moving actively is so slow. This project thus aims to assess the dispersal mode responsible for the expansion of the distribution of these slugs. Genetic analyses revealed the disjunct distribution of some mitochondrial haplotypes, suggesting the importance of passive dispersal. Furthermore, the identity and origin of slugs in Québec are completely different from those previously reported in regions of the United States adjacent to Québec. This distribution, coinciding with the presence of the Canada-USA border, supports the importance of passive transportation for these species. Altogether, these results suggest the important role of humans in the transport of these slugs and their invasion success.

Using historical museum collections to determine Amino Acid Racemization (AAR) profiles of Jamaican land snails

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Patterns of racemization of amino acids in the shells of Jamaican land snails may offer useful insights into population dynamics during the late Holocene. Live-collected specimens from the Academy of Natural Sciences of Drexel University malacology collection will be used to establish historical racemization rates. A reverse phase HPLC procedure for simple and precise stereoisomeric separations of amino acids will be used on samples with a known age. The data will be used to determine standard racemization rates to determine the age of dead-collected and subfossil shells. From the data we should also be able to determine if the racemization rates are species specific or can serve as a general AAR profile for genera or species groups. AAR profiles for Jamaican land snails would be very useful when looking into population changes over time. Once enough field data can be collected historical population changes can be compared to climate and environmental changes both natural and induced.

Life history of *Deroceras reticulatum* in annual ryegrass (*Lolium multiflorum*) fields in Oregon and implications for pest management

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Deroceras reticulatum (Agriolimacidae) is the most damaging gastropod pest in the Pacific Northwest region of the United States. A diverse range of crops are damaged particularly in the agriculture-rich Willamette Valley including seed crops, vegetables, fruits, legumes, grains, forage crops, and ornamentals. The grass seed industry is most heavily impacted and in recent years, slug damage has accounted for nearly $100 million in losses to this $500 million industry.

To elucidate the life history of *Deroceras reticulatum* in annual ryegrass (*Lolium multiflorum*), which is a particularly vulnerable crop, slugs were collected weekly (Fall and Spring) or fortnightly (Winter and Summer) from underneath 16 slug blanket traps (DeSangosse) at six annual ryegrass fields in the South Willamette Valley. All specimens were returned to the laboratory where they were identified, counted, weighed and assigned to different life history stages i.e. neonate, juvenile or adult.

Our results show that populations of *D. reticulatum* peaked in annual ryegrass fields in western Oregon in early November. Juvenile slugs dominated in early Fall (October) but as the season progressed, adult slugs became more and more common. In fact, adult slugs were the dominant life history stage collected through late Fall, Winter and Spring. The bulk of egg laying occurred in Spring. These results are discussed in the context of optimizing slug management strategies in grass seed crops in Oregon.

Gastropod-killing worms: Discovery of the parasite, *Phasmarhabditis hermaphrodita* (Nematoda), in the US and its lethality to pest slugs, snails and non-target organisms

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Phasmarhabditis hermaphrodita (Nematoda: Rhabditidae) is a nematode parasite that is lethal to many pest species of terrestrial gastropods. It is currently used as a commercially available biological control agent (Nemaslug®) in Europe to protect a wide range of crops from slug and snail damage.

Multiple past attempts at recovering *Phasmarhabditis* from slugs and snails in the US have been unsuccessful but we recently discovered *P. hermaphrodita* from a range of slug species in both California and Oregon. Infectivity trials with this US strain caused significant mortality to the pest slugs, *Deroceras reticulatum* (Agriolimacidae) and *Lehmannia valentiana* (Limacidae), and the pest snails, *Cornu aspersum* (Helicidae) and *Lissachatina fulica* (Achatinidae) at rates equivalent to or higher than the Nemaslug®'s recommendation of 30 infective juveniles/square cm. It did not cause mortality to three earthworm species *Amynthas gracilis* (Megascolecidae), *Eisenia fetida*, and *Eisenia hortensis* (Lumbricidae).

The implications of the discovery of *Phasmarhabditis hermaphrodita* in North America and its potential role as a biological control agent of pest gastropods in the US will be discussed in this presentation.

Cephalopod Biodiversity

Stable isotopes in the eye lenses of *Doryteuthis plei* (Blaineville 1823) reveal natal origins and migratory patterns in the eastern Gulf of Mexico

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Stable isotope analysis is an emerging tool to examine trophic pathways and migratory patterns of marine organisms. Squid play important roles as both predator and prey in marine ecosystems. Stable isotope ratios of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) found within cephalopod tissues provide information on both trophic level and habitat of their basal resources. Studies have documented ontogenetic changes in stable isotope ratios within squid eye lenses. Concentric layers of crystallin proteins are added to the lens as the squid ages; the center of the lens contains the oldest layer and the youngest layers are on the outermost surface. The crystallin proteins are rich in carbon and nitrogen, providing suitable sources for isotopic analysis of both $\delta^{15}N$ and $\delta^{13}C$. *Doryteuthis plei* is a common inshore squid in coastal waters of the western Atlantic region. This study identified patterns of geographic movements of *D. plei* in the eastern Gulf of Mexico using changes in isotope ratios in eye-lens layers. This study also identified natal origins by comparing the trends in the core layers to previously mapped isoscapes in the region. Isotopic analyses suggest that these squid begin their lives in the deep chlorophyll maximum of the outer shelf.

The Joseph G. Claud Mantle collection, and two sinistral Sacred Chank shells at the Museum of Comparative Zoology (Harvard University)

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One premier shell collection of the early 20th century is the Joseph George Claud-Mantle collection that consists of over 4,300 species totaling 4,950 specimen lots. His collection was donated to the Museum of Comparative Zoology, Harvard University in June 2011. Among the rarities in the Claud-Mantle collection is the sinistral Chank Shell, *Turbinella pyrum*, from the Indian Ocean; this specimen was recently valued at $45,000, not just for its rarity in nature, but also for its religious significance to the Hindus, as the place where Vishnu, God of the Sea, had historically hidden sacred scrolls. The Claud-Mantle specimen doubled the holdings of sinistral Chank shells at the MCZ. The first was acquired from the Duchess of Portland collection from the 1700's. These two rare, religiously important, and economically valuable shells, how they arrived at the MCZ, along with other treasures found within the Claud-Mantle collection are discussed.

Multiple paternity in *Pomacea canaliculata* (Caenogastropoda: Ampullariidae)

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Fertilization of a single female's eggs by multiple males (i.e. multiple paternity - MP) can increase genetic diversity, thereby improving the success of small, founding populations. *Pomacea canaliculata*, native to South America, is also an extremely successful invader worldwide. Its success both as an invasive and in its native range may, in part, be facilitated by a reproductive strategy that includes MP.

To better understand the role of MP in the population dynamics of *P. canaliculata*, ten egg clutches were collected from Maldonado, Uruguay in December 2014. After hatching, snails were preserved in 95% ethanol prior to DNA extraction and genotyping. For each clutch, species identity was confirmed with mitochondrial COI gene sequences of four individuals and the frequency of MP was estimated by genotyping a random subset of hatchlings at five microsatellite loci.

Nine of the ten clutches were *Pomacea canaliculata* and the tenth was deposited by *Pomacea* sp., a previously undescribed species. Preliminary microsatellite analyses recovered 5-8 alleles at four of the loci, confirming the presence of MP in *P. canaliculata*. One locus had only two alleles and exhibited a significant heterozygote deficiency. Additional analyses of hatchlings from the remaining clutches will confirm this pattern and allow the estimation of the frequency of MP in this native population. These data will then be compared to results from non-native populations in Hawaii and China to better understand the role of MP in the invasive success of *P. canaliculata*, and possibly closely related congenerics.

Mollusks in Peril

Invasive and naturalized slugs of the United States

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Populations of slugs have become naturalized worldwide through international trade. Many of these slug species can be invasive, and many are pests of significant economic and ecological concern. A major influx of mainly European species has entered the United States over the past two centuries, and the accidental import and spread of slugs continues.

I will review the taxonomy, biogeography (original and nonnative ranges), and ecology (habitats, food, disease transmission) of the nonnative slugs that occur in the US. In addition, I will discuss the agricultural and ecological effects of our most serious pest species. The invasion biology and origins of most naturalized slug species are poorly known, because researchers have inconsistently collected slugs, and identifications often have been tentative or incorrect. Some major pest slugs abroad, such as *Arion vulgaris* and some veronicellids, have not yet been introduced to the US and remain of quarantine significance.

Mollusks in Peril

Decline of the Tiger Snail *Anguispira alternata* in Northeastern North America

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A recent publication demonstrated that *Anguispira alternata* populations declined in Pennsylvania starting around the 1960s. The publication suggested that acid precipitation, which increased markedly about the time the snail decline began, could be responsible for the decline. This study examines occurrences of *A. alternata* more broadly geographically in northeastern USA to address two questions. (1) Is the population decline of this species peculiar just to Pennsylvania, or is it more widespread geographically? (2) Did areas with more severe historic acid precipitation also experienced greater declines of *A. alternata* populations? Preliminary results confirm a widespread decline in northeastern USA, although less decline in West Virginia and Virginia. This talk further explores the role of acid precipitation and other hypotheses regarding this snail's decline.

Mollusks in the Steel City: The Collection in Carnegie Museum, Pittsburgh, PA

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Carnegie Museum was founded in 1895 with a generous donation from the industrialist Andrew Carnegie. From its inception, malacology has been a fundamental area of study at Carnegie Museum. From the nascent collection comprising mollusks from F Holland, G Clapp, and HH Smith, it has grown to a collection of over 150 000 lots. There are an additional 24 000 uncataloged lots. The bulk of this growth has been due to the work of curators AE Ortman, ST Brooks, GK McMillan, JJ Parodiz, and TA Pearce. Honorary Curator of Conchology G Clapp donated a sizable collection of terrestrial gastropods while V Sterki was the source of many Pupillidae (sl) and Sphaeriidae.

The collection is estimated to contain more than 19 000 species in 2789 genera and 389 families. All extant classes are represented except the Monoplacophora. The collection is strongest in its representations of terrestrial gastropods (52% of the collection) and freshwater mollusks (20% of the collection). The terrestrial gastropods of North America are a particular strength as are the freshwater Unionoida of North and South America. Another group with sizable holdings are the Sphaeriidae; numbering some 16 000 lots. While the marine mollusks make up 28 % of the collection, there are no families of notable depth of coverage. The type collection comprises 2025 lots, 1416 of them being primary types.

The collection at Carnegie Museum is worldwide in distribution. North America represents 74% of the collection. In descending order, the rest of the collection is represented by Australia/South Pacific, Europe, Asia, South America, Africa, and Antarctica.

Giant clam mantle color is correlated to reef environment

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Giant clams (Sub-family Tridacninae) are known for their symbiosis with the photosynthetic dinoflagellate genus *Symbiodinium*. The giant clams have evolved an optimally efficient symbiosis using iridocyte cells that redistribute solar energy such that all light is absorbed while each individual dinoflagellate avoids non-photochemcal quenching. These iridocytes are visible to humans due to the fact that they backscatter at low intensities but with relatively high contrast to the highly absorbing, black layer of algae deeper in the tissue. The apparently high intraspecific and interspecific in iridocyte patterns in this system remains unexplained. We investigated correlations between environmental nutrients, habitat type, and iridocyte patterns in this system.

We conducted photographic surveys of three different reef types (i.e. barrier, lagoonal, and fringing reefs) in the Republic of Palau, using the belt transect method. taking photos of giant clams within 1m of each side of a 50m transect tape. Each photo contained a color standard near the clam to allow us to standardize color between images, independent of the illuminant at each site. Preliminary qualitative results show that ~50% of clams located within barrier reefs exhibit long-wavelength reflecting iridocytes while ~50% of clams located in the inner reef (i.e. lagoonal and fringing reefs) have sparser iridocytes that are short-wavelength reflecting. Our nutrient data show that these inner reefs experience higher particulate carbon compared to the outer reefs indicating higher particulate nutrients in the inner reefs.

President's Symposium

Improving provenance data in natural history collection databases

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A growing use of natural history collections is documenting changes in distributions of species during historical times. Until the 20th century, however, collecting dates were not routinely recorded. Various forms of proxy data must therefore be used to constrain when a particular sample might have been collected. The date of cataloguing puts an upper limit on potential collecting dates, as do dates of death of agents such as collectors, donors, and other previous owners. Archival material such as field notes and accession records that help determine more accurate provenance information can also provide constraints. Sources such as "2,400 Years of Malacology" and "Shellers from the Past and Present" are making it increasingly easy to find dates of birth and death. Information in such sources should be captured in standardized biographical databases to allow automated bounds on collecting dates to be applied via agent fields in collection databases. A random sample of about 200 records of more than 200,000 in the ANSP database that lack date of collection shows that for 41%, date of death information improves on date of cataloguing as a constraint on date of collection. If further historical information such as dates of travel, residence, and employment were included in biographical databases, additional improvement on these bounds could be obtained. A model for such a biographical database is presented. Collection databases need a one-to-many structure for provenance information to track the chain of ownership of specimens more rigorously, and to allow cleaner interface with biographical databases.

Cephalopod Biodiversity

Comprehensive morphological and molecular analysis of deep sea cephalopods collected in the North Pacific

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Several eight-armed cephalopods (Cephalopoda: Octopodiformes) were dredged during the scientific cruise SO-249 BERING conducted in the North Pacific during the summer of 2016. This zoological sample comprises three largely intact adult incirrates, two incirrate egg clutches with multiple specimens each, as well as an almost completely intact adult cirrate. All individuals were measured and photographed on board directly following capture. In addition, tissue samples were obtained for later DNA extraction. Subsequently, all specimens were fixed in formalin for more comprehensive structural analyses.

The incirrate material was collected at around 2,500 m depth near the Alpha Fracture Zone of the western Bering Sea, while the single cirrate specimen was dredged at about 4,200 m depth on Tenji Guyot of the Hawaiian-Emperor seamount chain. In order to preserve the structural integrity of these rare specimens, non-invasive imaging techniques were applied to obtain data on internal organ systems conventionally used for species identification. In addition, DNA barcoding was performed to provide additional information about the taxonomic relationship of these deep sea specimens.

This talk describes how the specimens were captured and summarizes the results obtained using photography, magnetic resonance imaging, contrast-enhanced micro-computed tomography, as well as histology. In addition, we describe the findings of the molecular analysis. This study represents the first comprehensive taxonomical analysis of cephalopod specimens based on

Cephalopod Biodiversity

The deep sea cephalopod fauna of Wilmington Canyon (Delaware, USA)

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The biodiversity and distribution of deep-sea cephalopods is poorly understood, and much of what is known comes from midwater and benthic trawling activities in the Northeast. In this study, we examined approximately 12,000 photographs from 6 transects conducted in Wilmington Canyon, Delaware, USA. Images were collected using the Woods Hole Oceanographic Institution's towed-camera apparatus (TowCam) aboard the NOAA Ship *Henry Bigelow* in August 2014 as part of NOAA's Northeast Deep-Sea Coral Initiative. Although the primary focus of the cruise was documenting biodiversity and distribution of sessile benthic fauna, incidental photographs of cephalopods were common. Image analysis provides a new avenue for understanding the biodiversity, distribution, and habitat of cephalopods in the Atlantic canyons.

Images were color corrected and then examined for the presence of cephalopods and other epibenthic fauna. Images were annotated with keywords, and the subset of images with cephalopods was re-examined and individuals were identified to the lowest taxonomic rank possible. Navigational data were linked to each image via the timestamp, which allowed precise latitude and longitude to be assigned to individual cephalopods encountered along the transect line.

Each transect contained between 2–17 cephalopods, with 46 unique individuals encountered. The incirrate octopod *Graneledone verrucosa*, and the sepiolid *Rossia* sp. were the most commonly encountered species, followed by the incirrate octopod *Muusoctopus johnsoniana* and the cirrate octopod *Stauroteuthis syrtensis*. One mature female of *Rossia* sp. with eggs was documented, supporting the importance of sponges as nursery habitat for sepiolid eggs.

Shea, E.K., Kittle, B.A., & Van Stone, L.J.

The mollusk collection at the Delaware Museum of Natural History

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The Mollusk collection at the Delaware Museum of Natural History (DMNH) was established in 1972 when the Museum was opened, although many of the purchases and collecting expeditions pre-date the physical structure. The collection was the source of many specimen plates in R. Tucker Abbot's seminal work *American Seashells,* 2nd edition. The collection is actively growing via donations and curator research; recent highlights include terrestrial snails from the Delmarva Peninsula and deep sea cephalopods from the Northwest Atlantic. Computerization of collection records started in the 1980s, and approximately 90% of holdings have a digital record. However, collection data are incomplete, inconsistent, not georeferenced, and taxonomically out of date making them difficult to use. The initiation of the InvertEBase digitization grant in 2014 has propelled the collection forward, and importantly moved it on-line for the first time. Digitization activities in the collection are focused on transitioning the terrestrial and freshwater specimens from a legacy Access database into Specify v.6 and then pushing data to the Symbiota and iDigBio data portals. Future digitization efforts will focus on adding georeferenced locality data to all records, and adding images to select records.

Approximately 44% of the DMNH collection is from North America, 2% from South America and 54% from the rest of the world, especially the Indo-West Pacific. Within North America, the collection contains approximately 22% terrestrial gastropods, 7% freshwater bivalves, 5% freshwater gastropods, and 65% marine bivalves and gastropods. The South America holdings include 5,038 lots with 28,700 specimens, most of which come from Brazil, Peru, Ecuador and Venezuela.

The physical specimens in the collection are being minimally conserved by swapping out original boxes for acid free boxes and replacing cotton stoppers with synthetic. All new collections are freeze treated prior to processing. A 2015 preventative conservation assessment of the landsnails estimated that 0.5% of specimens have indicators of early Byne's efflorescence. Future conservation efforts include replacing the 40+ year old cabinets with archival cabinets appropriate for natural history collections.

Cephalopod Biodiversity

Sexual dimorphism in *Brachioteuthis beanii* (Cephalopoda: Brachioteuthidae) in the Northwest Atlantic

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In the northwest Atlantic, two morphotypes of *Brachioteuthis* sp. were collected during exploratory cruises to the Gully Marine Protected Area conducted by Canada's Division of Fishes and Oceans in 2007. CO1 barcoding of fresh tissue indicated that both morphotypes are *Brachioteuthis* cf. *beanii*. Here we examine whether there are consistent external morphological characters that can be attributed to males and females of this species, and trace the development of these features back to their earliest expression.

Over 200 specimens of fixed and vouchered *Brachioteuthis* specimens ranging in size from 22 – 105 mm ML were measured, dissected, and sexed. Eighty-seven males and 68 females were identified based on the presence of the spermatophoric complex or nidamental glands, respectively. The minimum size of a male with a recognizable spermatophoric complex was 39 mm and the minimum size of a female was 39.5 mm. The remaining 48 specimens were not sufficiently developed to assign sex, and are considered juveniles.

Adult males are more fusiform in shape with fewer small photophores on the external mantle, and sculpturing in the form of tubercules on the mantle that develops concurrent with the spermatophoric complex. Adult females have a more flaccid mantle, with larger and denser chromatophores on the mantle and head.

Radular malformation in radiations of land snails and its evolutionary-ecological interpretation

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A striking pattern of radular malformation is reported in the endemic adaptive radiation of the land snail genus *Naesiotus* (Bulimulidae) from the Galapagos Archipelago. This pattern manifests as an abnormally high rate of longitudinal abnormalities in radular teeth. These abnormalities are asymmetric across the radular membrane, which suggests that they represent somatic mutations. A similar set of radular abnormalities has previously been reported in *Albinaria* (Clausiliidae) from the Greek Ionian Islands, a group notable for its non-adaptive radiation.

While a high rate of somatic mutation might be expected in the context of ecological release in the early phase of adaptive radiations, the presence of a high rate of radular abnormalities in a non-adaptive radiation would seem to contradict this hypothesis because lineages do not experience ecological release in non-adaptive radiations. Different interpretations and explanations of these phenomena are explored in the context of evolutionary ecology and recent theoretical advances in the understanding of evolutionary radiation, with the ultimate goal of clarifying the dynamics of evolutionary radiation as a process in land snails.

Slapcinsky, J., Bemis, A., & Paulay, G.

Molluscan collections at Florida Museum of Natural History

J. Slapcinsky, A. Bemis, & G. Paulay

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Florida Museum of Natural History (UF) houses 500,000 specimen lots of at least 2.5 million specimens of mollusks, all of which are databased and accessible online at http://specifyportal.flmnh.ufl.edu/iz. An additional 50,000 lots remain to be cataloged. The collection is among the largest and fastest growing molluscan collections in the United States, with the most online accessible specimen records in the world. It has achieved this rapid growth through field surveys by molluscan specialists as well as the acquisition of relinquished collections from Alabama State Museum, Miami University, Rollins College, and Tulane University, and others. These include important collections by J. Beal, T. McGinty, C. T. Simpson, H. H. Smith, E. and H. Vokes, and J. Weber. The holdings are approximately 40% terrestrial, 40% marine, and 20% freshwater and include more than 1,200 primary types and 7,200 secondary types. Gastropods represent 80%, bivalves 19%, and all other mollusk classes make up 1%. The collection encompasses the largest non-marine snail collections in the world from several regions including Hispaniola, Mexico-Central America, Madagascar, and Pakistan, and especially large holdings from the southeastern US, West Indies, Andean South America, Southeast Asia, and Oceania. Marine holdings are especially strong for Florida and the Caribbean and rapidly growing for the Indo-Pacific. Recent surveys and DNA barcoding efforts have resulted in nearly 10,000 tissue samples stored in liquid nitrogen and approximately 50,000 associated photographs. We are currently investigating ways to rapidly catalog new specimens, retroactively georeference historic data, and cope with rapidly changing molluscan taxonomy.

Feeding habits and prey selection of Tritons (Gastropoda: Ranellidae), focusing on *Gutturnium muricinum* and *Monoplex nicobaricus*

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Ranellids are a family of carnivorous gastropods that have been largely overlooked in the scientific literature. To investigate these relatively understudied species, several individuals from two species, *Gutturnium muricinum* (Röding, 1798) and *Monoplex nicobaricus* (Röding, 1798), were observed over a period of several months. Tritons were kept separated from each other and each was offered a selection of molluscan prey items to observe what and how often each species would eat. It was found, as expected, that *G. muricinum* feeds exclusively on bivalves. This species was also found to prefer *I. californicum* over other prey and individuals of this species were found in intertidal pools where these bivalves were concentrated. *Monoplex nicobaricus* was found, as expected, to prefer gastropods as its main prey. However, unlike previous reports, *M. nicobaricus* was observed to feed on dead and/or partially opened oysters in preference to live prey. This species also would ignore prey that could defend itself or move quickly, and would not actively pursue unless the prey was unable to escape. From these observations, it was concluded that *M. nicobaricus* is mainly an opportunistic feeder with preference for whatever it can reasonably catch with little effort. Individuals also displayed dormancy cycles, wherein they would feed for a few days in succession, then bury themselves in sand for anywhere from a few weeks to a few months. During these times of dormancy some individuals were observed to be building or repairing their shells.

Quid est *Clea Helena*? Evidence for a previously unrecognized radiation of assassin snails (Gastropoda: Buccinoidea: Nassariidae)

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The genus *Clea* from SE Asia is from one of only two unrelated families among the megadiverse predatory marine Neogastropoda to have successfully conquered continental waters. While little is known about their anatomy, life history and ecology, interest has grown exponentially in recent years owing to their increasing popularity as aquarium pets. However, the systematic affinities of the genus and the validity of the included species have not been robustly explored. A five-gene mitochondrial (COI, 16S, 12S) and nuclear (H3, 28S) gene dataset confirms the placement of *Clea* as a somewhat isolated offshoot of the family Nassariidae and sister to the estuarine *Nassodonta*. The assassin snail *Clea helena*, a popular import through the aquarium trade so named for their voracious appetite for other snails, is found to comprise a complex of at least four species. None of these likely represents true *Clea helena* described from Java, including a specimen purchased through the aquarium trade under this name in the US and one that was recently found introduced in Singapore, both of which were supported as conspecific with a species from Thailand. The introduction of *Clea* "*helena*" through the aquarium trade constitutes a significant threat to native aquatic snail faunas which are often already highly imperiled. Comprehensive systematic revision of this previously unrecognized species complex is urgently needed to facilitate communication and manage this emerging threat.

Mollusks in Peril

First record of a novel invasive *Corbicula* lineage discovered in the Illinois River, Illinois, USA

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Over the past century the genus *Corbicula* has become one of the most common and successful invasive species in North America. One confounding factor in understanding this invasion is that these invasive populations appear to exclusively comprise asexual androgenetic clonal lineages. To date two clonal morphotypes have been recognized in North America– Forms A and B. Here, we report on a new North American invasive *Corbicula* morph recently discovered in the Illinois River (Great Lakes watershed) that was found co-occurring with Forms A and B. We performed a preliminary analysis of the distinctiveness of the new morph from sympatric Forms A and B using shell phenotype characteristics and mitochondrial (mt) and nuclear DNA markers. Individuals were unambiguously assigned to one of three discrete shell phenotypes, Form A, B, or the new morph, with the latter specimens characterized by fine rust-colored rays and white nacre with purple teeth. This new morph also was distinguishable from Forms A and B with nuclear 28S ribosomal DNA sequences. However, individuals of the new morph and sympatric Form A shared an identical mtDNA haplotype possibly a result of androgenetic egg capture. In light of these subtle morphological differences and conflicting signal from the mtDNA and nuclear 28S sequences we performed a preliminary phylogenomic analysis using ~2,600 nuclear genomic loci collected via the next generation double digested restriction associated sequencing (ddRADseq) method. These comprehensive new results also reveal this new morph to be distinct from sympatric Forms A and B.

President's Symposium

Digital discovery of deepsea diversity

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Biodiversity exploration in the deep sea has become increasingly dependent on digital imagery. This development has been facilitated by growing use of "telepresence-enabled" operations by remotely operated vehicles (ROVs), allowing many more researchers to participate in the operations. Such imagery allows a unique perspective on morphology, behavior, and small-scale distribution. Although a picture may be worth a thousand words, understanding this imagery requires collation with several other sources of digital information, including dive tracks, ancillary data, nearby geological features/fauna and sometimes specimens collected and information derived from them. Systems to bring all of these bits and bytes together are in various stages of development, but most still require digital digging by the researcher. Although I focus here on digital issues, the need to "ground truth" by specimen collection is very important. Furthermore, such visual exploration presents a snapshot of diversity and is often very different from the results of other methods, such as net collection or analyses of the stomach contents of predators.

I will present examples of these issues for unpublished observations of cephalopod natural history from ROVs, including recent dives. These examples include faunal comparisons, clues to reproductive behavior, and vertical distribution of pelagic species.

President's Symposium

A citizen science collaboration focusing on terrestrial malacofauna between the public and the Natural History Museum of Los Angeles County

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The terrestrial malacofauna of Southern California is generally understudied and particularly poorly inventoried in the urban and suburban environments of Los Angeles County. This accounting shortfall (of native and non-native species) is partly due to the jigsaw puzzle of private land (e.g. backyards) that characterizes LA County's urban sprawl. The Natural History Museum of Los Angeles County has sponsored a citizen science initiative called SLIME (Snail and slugs Living In Metropolitan Environments) that uses the iNaturalist web platform to centralize terrestrial gastropod observations from citizen scientists throughout Southern California. Since November, 2015 the SLIME project has revealed 3 species records for the State of California and six new records for Los Angeles County, including the snails— *Cochlicella barabara* and *Lauria cylindracea*, and slug – *Arion hortensis*. The success of the SLIME project has been in its person-to-person and virtual collaborations between the public and Museum systematists, creating a genuine citizen science partnership. The particular success of the "bioblitz" in recovery the diversity of the Southern California malacofauna is particularly relevant, as it required little training, limited resources, and produced a robust inventory of local species.

ASAP ADVANCE: Networking women STEM faculty at undergraduate institutions

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The National Science Foundation's ADVANCE program provides support for the participation and advancement of women in academic science and engineering careers. Our project created a network of 70 women from the STEM fields of biology, chemistry, computer science, engineering, mathematics, and physics. Participants were tenured or tenure-track faculty at 27 undergraduate institutions across the country. The heart of the project was a set of alliances that brought together groups of four to six women in the same or similar STEM field and at the same career level for peer mentoring. Each alliance met virtually for four years approximately once a month. Each year the alliances also met face-to-face, either at an all-participant meeting or simply with their alliance members. All-participant meetings also included workshops on professional development and opportunities for all women at the same career level and for all those in the same discipline to meet and explore issues specific to their careers and disciplines. Of the original cohort, only one member left academia and many successfully achieved tenure and/or promotion. Members appreciated the support of their peers, which helped reduce the feelings of isolation often experienced by women STEM faculty at undergraduate institutions.

Location, location, location: Position of the epibiont *Crepidula adunca* on its host *Calliostoma ligatum*

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Individuals of the sedentary, suspension-feeding slipper limpet *Crepidula adunca* are epibiotic on several species of gastropods. In the San Juan Islands, Washington, USA, they occur almost exclusively on shells of the trochid *Calliostoma ligatum*, which hosts almost no other epibionts. We conducted a census of a population of these hosts over several weeks to determine where on the shell the epibionts were positioned and whether they had moved on the same host shell or from one host to another. Most epibionts occurred on the left side of the dorsal surface of the body whorl of the host, with the second-most common location being in the middle of the posterior, dorsal region of the body whorl. Epibionts on the ventral surface tended to be much smaller in size and were restricted to the left side of the host's shell. Individuals of *Crepidula adunca*, especially small individuals, can move from one site to another on a host as well as between hosts. Images of hosts with and without epibionts taken in a recirculating flow tank indicate that the positions of the epibionts on the dorsal surface most likely cause them to receive an enhanced flow of water up the surface of the host's shell. These results support the hypothesis that the epibionts are benefitting from this association.

Cephalopod Biodiversity

Egg deposition by *Rossia palpebrosa* (Cephalopoda: Rossiinae) in deep-sea sponges, in temperate Northwest Atlantic and fringes of polar Canadian Arctic

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One of the key ecosystem functions of sponges is the provision of habitat. Here we illustrate one association between a deep-water sponge [Porifera: *Mycale* (Mycale) *lingua* (Bowerbank, 1866)] and its functional role to a small cephalopod (Cephalopoda: Rossiinae), in temperate Northwest Atlantic and fringes of the polar Canadian Arctic Oceans. As part of an ongoing Canadian effort to identify Ecologically and Biologically Significant Areas for conservation and protection, sponges have been collected opportunistically in multispecies research surveys to systematically document and identify sponges. *Mycale* (*Mycale*) *lingua*, a common deep-water sponge found from Baffin Island Shelf to the Grand Banks of Newfoundland were observed with clusters of eggs embedded in the sponge body, nestled within the long spicule tracts. Eggs were identified as the sepiolid cuttlefish *Rossia palpebrosa* Owen, 1834, based on examination of the stage of 28 embryos. Eggs showed multiple stages of development, with at least two hatchlings. Additional observations of eggs occurred in *M. loveni* (Fristedt, 1887), *Melonanchora elliptica* Carter, 1874, *Iophon piceum* (Vosmaer, 1882), and several unidentified sponges. Densities ranged from 4-18 eggs/sponge; however majority of sponge samples were retrieved in pieces (<15cm) due to fragility of tissue combined with sampling method |(i.e. research trawl activity), making densities conservative estimates. The ecological importance of *R. palpebrosa* as a global prey species is not well understood in this region but are believed to constitute a significant element in marine food webs.

The Snail Code: Employing multiple techniques to distinguish two species of *Ventridens*

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Land snail identifications based on shell characteristics alone can be problematic due to variation within species and similar characteristics between species. Molecular identification using nuclear and mitochondrial gene sequences has proven to be difficult due to overlap in intraspecific and interspecific sequence differences. Species identification using characterization of the reproductive organs is more reliable due to low intraspecific variation however dissection can be delicate work. In this study we employed all three methods to determine which factors were most helpful in distinguishing between two land snails that can be, by eye alone, difficult to tell apart: *Ventridens ligera* (Say, 1821) and *Ventridens demissus* (A. Binney, 1843). Data for shell morphology, genetic sequence for mitochondrial cytochrome oxidase I and nuclear ribosomal region ITS1-5.8S rDNA-ITS2-28S rDNA, and reproductive characteristics were first analyzed individually and then combined and analyzed by multivariate statistics. Species-specific differences were identified in both genetic sequences. Differences in shell morphologies were more subtle and less informative when analyzed alone. Multivariate analysis uncovered several factors helpful in distinguishing these species. We plan to use the resulting information from this study as a guide for other difficult species identifications.

Sorting Shells: Finding efficient methods for putting collection objects in order

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The Mollusk collection at the Delaware Museum of Natural History contains over 250,000 lots of dry shells. Finding a single cataloged specimen within this large collection is challenging when the specimens are out of numeric order within a species. As part of the routine collections care volunteers have begun to put these large species into numerical order, but progress is slow. To streamline the process, we are testing sorting methods familiar to computer programmers to assess which methods are the fastest. In August 2016, we conducted a preliminary test with museum patrons during a series of 2 consecutive special events days. On the first day, visitors were asked to sort a drawer of forty-four specimen trays containing random three-digit numbers into numerical order using any method they desired (=untutored). The main approach to the task observed, was grouping like numbers (=grouping). On the second day, visitors were taught a sort-merge method for doing the ordering, and we observed no differences in sort time from before. Based on these preliminary results, we began a new trial which simulates real world conditions more closely. In these trials, we increased the number of trays, used similar specimen labels as those used in the collection, and added specimens to the boxes. Volunteers and staff have been doing timed trials for three methods: untutored, grouping, and sort-merge. This poster describes the results of these two experiments, and provides suggestions for how to quickly put large numbers of collections items into order within a physical collection.

Photosymbiosis in subfamily Fraginae

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Photosymbiosis is a mutually beneficial relationship between a host organism and photosynthetic algae that provide food. It has been directly observed in three genera of subfamily Fraginae (Bivalvia: Cardiidae), but not all fragines have symbionts. To maximize the sunlight available for photosynthesis, some cockles gape their valves and expose mantle tissues that house the algae, as observed in some species of *Fragum*. Others have microstructural windows allowing sunlight to pass through the thin shell to algae living within; this has been observed in *Corculum cardissa*. Data for some species are incomplete or contradictory, for example, *Fragum fragum* has been reported to gape, but also to have translucent areas on the shell. To infer what strategies are used in species known to have photosymbionts, we observed microstructures along cross sections of *C. cardissa*, *F. fragum*, *F. unedo*, *Lunulicardia retusa*, and *L. hemicardia*. As expected, we found regions within *C. cardissa* that are consistent with windows and for the first time, imaged a similar structure in *F. fragum*. Windows are composed of fibrous prismatic crystals that are perpendicular or slightly oblique to the outside of the shell, likely directing light through the shell. *F. unedo* is known to gape its shell to allow for algal exposure to sunlight; the shell did not contain windows. *L. retusa*, and *L. hemicardia* also lack windows. Based on these findings, we predict that *L. retusa* and *L. hemicardia* also gape their shells to allow exposure of algae to sunlight. *Americardia media,* used as a control, does not host photosymbionts and does not have windows. Photosymbiosis in Fraginae is not associated exclusively with windows, yet their presence or absence can be a useful tool in assessing the host-algae relationship in species known for their association when no photographic evidence is available.

Mollusks in Peril

Impact of invasive species on Hawaii's land snail diversity and the development of a Pacific Island land snail consortium

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Habitat destruction, climate change, and invasive species are wiping out land snails at an alarming rate and most of these extinctions are from Pacific Islands. There are an estimated 6000 Pacific Island land snail species, with at least 250 already recorded as extinct, and some estimates indicating as much as 75% may have already been lost. The native Hawaiian land snail fauna once had over 750 species (99.9% endemicity), but current extinction estimates vary across families from 40-100%.

Impacts of invasive species is considered the second largest threat to biodiversity. Species such as rats (*Rattus* spp.), Jackson's chameleons (*Trioceros jacksonii*), and carnivorous land snails (e.g. *Euglandina* spp. and *Gonaxis* spp.) have exacted a heavy toll on Hawaiian land snail biodiversity and continue to negatively impact surviving populations; several additional species have recently been recorded as extinct in the wild. With the continued influx of non-native species to Hawaii combined with climate change, extinctions are likely to continue without drastic action to mitigate these impacts.

The development of a Pacific Island land snail consortium has been suggested to foster local, national, and international partnerships to conserve diverse, but highly threatened fauna. Several snail conservation groups are already developing strategies to curb the impacts of invasive species, and these methods need broad input and to be shared widely. Foremost among the priorities for the consortium should be eradicating threats such as *Euglandina* spp., and rats, and developing plans to conserve and grow remaining populations of snails.

Housing, databasing, digitizing and accessibility upgrades to the largest Pacific Island land snail collection (Bishop Museum, Honolulu, Hawaii)

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Biodiversity loss is a hallmark of the Anthropocene, and snails have the highest number of recorded extinctions of any animal group, with most of these losses on Pacific islands. Unlike many soft-bodied ivertebrates, snails often leave a record in the form of their shells that can provide insights into historical and contemporary processes. Such knowledge is necessary to conserve natural resources that play vital roles in maintaining ecosystem integrity. Conservation of this vast diversity requires accurate taxonomy and current understanding of biodiversity. Critical to developing this knowledge and making decisions about biodiversity conservation are museum natural history collections.

The largest Pacific island land snail collection in the world is at the Bishop Museum (BPBM). To protect this collection and improve physical and virtual accessibility to this critical data resource for researchers, natural resource managers, students, and the public, we are: 1) rehousing specimens in environmentally stable and protective containers, 2) digitizing all collection data to make these readily available to the community both in-house and via web-accessible databases, and 3) imaging all specimens on which the original descriptions are based.

To date, we have databased and rehoused >30,000 lots and digitally imaged >300 type specimens. Specimen data and images are being made available through portals such as the National Hub (IDigBio), Global Biodiversity Information Facility (GBIF), and BPBM webpages. Additionally, five student interns produced educational videos of their digitization projects, which will be made available to the public via BPBM social media and newly designed malacology exhibits.

President's Symposium

Opportunities and challenges for digital morphology

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Recent advances in digital data acquisition, analysis, and storage have revolutionized the work in many biological disciplines. While today the digital approach forms the basis of research in disciplines such as genomics, proteomics, or structural biology, it has not yet found widespread acceptance in morphology. This is surprising, given the latest improvements in non-invasive imaging and three-dimensional visualization techniques. In fact, these developments now pave the way towards a digital era in morphology as well.

Using selected mollusk as well as other metazoan taxa as examples, the present talk provides a comprehensive overview of the opportunities offered by the application of digital imaging and visualization techniques in various morphological study areas. In addition to data acquisition and analysis, further advantages of digital morphological techniques such as an increase in data transparency or the possibility for data mining will be outlined. However, the challenges that a more widespread application of these methodologies is presently facing will also be addressed. The talk will conclude by illustrating that the application of digital imaging and visualization techniques in morphology is bound to reduce the present gap between genomic and phenomic research in zoology.

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