

ABSTRACT VOLUME



World Congress
of Malacology

2019

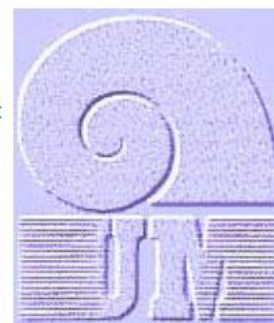
Pacific Grove,
California, USA

August 11-16, 2019

ACKNOWLEDGMENTS

This meeting was made possible due to generous contributions from the following individuals and organizations:

Unitas Malacologica	The program committee:
The American Malacological Society	Lynn Bonomo, Samantha Donohoo,
The Western Society of Malacologists	Kelly Larkin, Emily Otstott, Lisa Paggeot
David and Dixie Lindberg	
California Academy of Sciences	Andrew Jepson, Nick Colin
The Company of Biologists.	Robert Sussman, Allan Tina
The American Genetics Association.	Meg Burke, Katherine Piatek
The Malacological Society of London	



The organizing committee: Pat Krug, David Lindberg, Julia Sigwart and Ellen Strong



The American
Malacological Society

Western Society of Malacologists



THE MALACOLOGICAL
SOCIETY OF LONDON



Table of Contents	Pages
Acknowledgements.....	1
Abstracts	
Symposia and Contributed talks.....	3-226
Poster Presentations.....	227-292

Venom Evolution of West African Cone Snails (Gastropoda: Conidae)

Samuel Abalde*¹, Manuel J. Tenorio², Carlos M. L. Afonso³, and Rafael Zardoya¹

¹Museo Nacional de Ciencias Naturales (MNCN-CSIC), Departamento de Biodiversidad y Biología Evolutiva

²Universidad de Cadiz, Departamento CMIM y Química Inorgánica – Instituto de Biomoléculas (INBIO)

³Universidade do Algarve, Centre of Marine Sciences (CCMAR)

Cone snails form one of the most diverse families of marine animals, including more than 900 species classified into almost ninety different (sub)genera. Conids are well known for being active predators on worms, fishes, and even other snails. Cones are venomous gastropods, meaning that they use a sophisticated cocktail of hundreds of toxins, named conotoxins, to subdue their prey. Although this venom has been studied for decades, most of the effort has been focused on Indo-Pacific species. Thus far, Atlantic species have received little attention despite recent radiations have led to a hotspot of diversity in West Africa, with high levels of endemic species. In fact, the Atlantic *Chelyconus ermineus* is thought to represent an adaptation to piscivory independent from the Indo-Pacific species and is, therefore, key to understanding the basis of this diet specialization. We studied the transcriptomes of the venom gland of three individuals of *C. ermineus*. The venom repertoire of this species included more than 300 conotoxin precursors, which could be ascribed to 33 known and 22 new (unassigned) protein superfamilies, respectively. Most abundant superfamilies were T, W, O1, M, O2, and Z, accounting for 57% of all detected diversity. The different cysteine pattern of mature A conotoxins in Indo-Pacific versus Atlantic cones suggest that piscivory in the cones from both oceans evolved through convergence. In addition, we are studying the evolution of conotoxin venoms in the radiations of vermivorous cones endemic to Senegal and Cabo Verde.

Setting The Foundations and Developing Tools for Studying the Regeneration of Complex Eyes in the Emerging Research Organism, *Pomacea canaliculata* (Gastropoda, Ampullariidae)

Alice Accorsi*¹, Eric Ross¹, Melainia McClain², Timothy Corbin², and Alejandro Sánchez Alvarado¹

¹Howard Hughes Medical Institute, Stowers Institute for Medical Research, Kansas City, MO, USA

²Stowers Institute for Medical Research, Kansas City, MO, USA

The freshwater snail *Pomacea canaliculata* is an emerging research organism in the field of developmental and regeneration biology. This mollusk has a direct embryonic development and possesses complex camera-type eyes, composed of a cornea, lens, retina and optic neuron, which can fully regenerate upon amputation. The adult *P. canaliculata* eye, therefore provides a unique opportunity to understand how a sensory organ is regenerated and functionally integrated with pre-existing adult tissues and to compare it to embryonic eye development. To introduce and develop the necessary molecular, cellular and genetic tools to mechanistically dissect the regeneration of a complex organ that is irreplaceable in all current model organisms, we have developed methods to keep this organism in captivity, to efficiently collect embryos at any developmental stage and culture them ex ovo to facilitate manipulations and live imaging. At present, genomic manipulations of embryos still require optimization, but we found that they can be successfully microinjected with exogenous mRNA. At the same time, we have also generated extensive embryonic development and regeneration transcriptomes and optimized in situ hybridization protocols to validate these molecular databases, to find markers for the various cell types present in the *P. canaliculata* eyes and to localize the expression of molecules driving the regeneration process. Altogether, these data represent the first few steps towards transforming *P. canaliculata* into a genetically tractable research organism for the study of animal regeneration that may eventually be adopted by others to study aspects of animal biology not readily accessible in current model systems.

Influence of Vitamin E on Shell Repair, Haemolymph Biochemical Parameters, Haemagglutination Potential and Ovo-testis Activity of Giant African Land Snail (*Archachatina marginata*) After Shell Damage

John Adesanya Abiona*¹, Abiola Blessing Okunlola¹, Nneka Sandra Obanya¹, and Muhammed Okanlawon Onagbesan¹

¹P.M.B 2240, Alabata Road, Abeokuta. Department of Animal Physiology, Federal University of Agriculture, Abeokuta

A study was conducted on the effect of Vitamin A on shell repair, haemolymph biochemical parameters, haemagglutination potential and ovo-testis activity after shell damage. Forty (40) snails weighing between 150-200 g were randomly divided into four (4) treatments (with ten (10) replicate per treatment). At the commencement of the experiment, shells were damaged (length 3.5 cm and breadth 1.5 cm). The four treatments used in this study were: T1 (1g of vitamin A/kg of concentrate), T2, (2.5g of vitamin A/kg of concentrate) T3 (5g of vitamin A/kg of concentrate) and T4 (0g of vitamin A control). Parameters monitored were new shell growth, haemolymph biochemical parameter (Total protein, albumin, globulin and albumin globulin ratio), haemagglutination titre and ovo-testis activity. Result showed that rate of shell regrowth was not significantly different ($P>0.05$) between the control and those administered with various levels of Vitamin A after shell damage. Similarly, total protein, albumin, globulin and albumin-globulin ratio were not significantly affected by Vitamin A inclusion into the diet of snails. However, inclusion of Vitamin A into snail diet significantly ($P<0.001$) increased haemagglutination titre better than the control. Also, both Oogenic and spermatogenic activities were also positively influenced well than the control. However, the highest levels of activity were recorded at inclusion level of 5 and 2.5 g/kg of concentrate given. It can be concluded from this study that Vitamin A aid in the shell repair process, improve both immune status and reproductive function during period of shell injury in Giant African Land snail (*A. marginata*).

The Vanishing Mediterranean and the Assembly of A Novel Molluscan Fauna in the Levantine Basin

Paolo G. Albano*¹

¹University of Vienna, Department of Palaeontology

The Levantine basin in the easternmost Mediterranean Sea is well known for hosting hundreds of non-indigenous species introduced after the opening of the Suez Canal in 1869. An insufficiently recognized but even more dramatic phenomenon is the disappearance of native species. We here quantify this demise based on samples collected on intertidal and subtidal soft and hard substrates along the Israeli coast. We sampled during two seasons to capture any intra-annual variability and deployed a diverse array of techniques including grabbing, airlift sampling, scraping and handpicking. We used a fine sieve (0.5 mm) to retain small sized and juvenile individuals, deployed an intense identification effort including tracing the morphology of early ontogenetic stages, and considered the empty shells to reconstruct the baseline. The rocky intertidal was dominated by native species (61% and 73% in terms of richness and abundance, respectively) with limited seasonal variation and high spatial heterogeneity. The soft-substrate subtidal (10-40 m depth) showed a marked depth gradient, with assemblages down to 20 m with only 15-19% of native abundance which increased to 73-82% in deeper water, and a strong seasonality with spring dominated by native and autumn by non-indigenous species. Native species richness was below 50% year-around. The preliminary results for the rocky subtidal (10-25 m depth) suggest a similar pattern. Moreover, entire taxa such as Neogastropoda have become very rare (on rocky substrates they were just 4% of the diversity vs 18% in the death assemblage) while ectoparasites such as Pyramidellidae were 28% vs 16%, pointing at a complete reassembly of the local fauna.

Limited Growth and Hindered Reproduction Cause the Demise of Native Mollusks on the Israeli Mediterranean Shallow Shelf

Paolo G. Albano*¹, Jan Steger¹, Zara Guifarro¹, Bella S. Galil², and Martin Zuschin¹

¹University of Vienna, Department of Palaeontology

²The Steinhardt Museum of Natural History, Israel National Center for Biodiversity Studies

We here inspect the causes of the decline of native mollusks on the Israeli Mediterranean soft-substrate shallow shelf based on sampling along two transects off northern and southern Israel in autumn 2016 and spring 2017. We compared the living assemblages with a comprehensive literature-based checklist of Israeli mollusks filtered by appropriate substrate and depth, and the composition of the death assemblage collected with the living organisms. Our sampling intercepted only 24% of the historically recorded species. At individual sites, the living assemblage native richness is between 2.9% and 18.5% of the death assemblage native richness. The abundance of native species peaks in spring (80%, 934 individuals) but drops in autumn to only 15% (279 individuals, notwithstanding two additional replicates were collected) suggesting a mass mortality during summer. Abundant native species like *Abra alba* and *Corbula gibba*, present in the hundreds in spring, collapse although they are reported to be pluriennial species. The comparison of size-frequency distributions from living and death assemblages showed that most native species have small living individuals and do not reach the large sizes of the past, suggesting that while recruitment does occur, death occurs prematurely, for some species possibly before maturity. In contrast, for most non-indigenous species the size range of living individuals overlaps with the dead ones. These two results combined suggest that current environmental conditions (likely including climate warming) disproportionately favor non-indigenous species and that native species reproduction may be hindered, with recruitment potentially coming from deeper waters or other sectors of the basin.

Gene Family Expansions in the Evolution Of Cephalopod Innovations

C. B. Albertin*¹, T. Mitros², H. Schmidbaur³, E. Garcia¹, Z. Y.Wan⁴, O. Simakov³, C. W. Ragsdale⁴,
and D.S. Rokhsar²

¹Eugene Bell Center, Marine Biological Laboratory, Woods Hole, MA 02543

²Department of Molecular and Cell Biology, University of California, Berkeley, California 94720

³Department for Molecular Evolution and Development, University of Vienna, Austria

⁴Department of Neurobiology, University of Chicago, Chicago, IL 60615

Coleoid cephalopods (octopuses, squid, and cuttlefish) have a suite of evolutionary innovations, including their complex centralized nervous system, camera-like eyes, and closed circulatory system, which are classic examples of convergent evolution with vertebrates. Coleoids also present a number of true novelties that have no obvious correlates in other animals, such as their adaptive coloration system and sucker-lined arm crown. To study the genetic bases underlying these morphological innovations, we sequenced the genome of the longfin inshore squid *Doryteuthis pealeii*. We find that the *D. pealeii* genome is substantially larger than that of *Octopus bimaculoides*. The expansions of protocadherins, a family of cell adhesion molecules important for wiring vertebrate brains, and of C2H2 zinc-finger transcription factors described in octopus appears to be even larger in squid. Most importantly, our chromosome-scale assembly also identifies many local expansions of genes expressed in novel cephalopod structures. Some of these gene clusters are cephalopod-, or even squid-specific, while others appear to be local expansions of genes found in distantly related animals. These data serve to highlight a major role for the tandem expansion of both known and novel genes families in the evolution of cephalopod morphological innovations.

Integrated Taxonomy of Cone Snails (Conidae, Gastropoda) Giving New Insight Into the Role of Ecosystem in Speciation

S. Ameri*¹, P. Laxmilatha¹, K. A. Labeeb¹, L. Ranjith¹, and A. Kathirvelpandian²

¹ICAR Central Marine Fisheries Research Institute, Kochi

²PMFGRC of National Bureau of Fish Genetic Resource, Kochi

Integrative taxonomy of cone snails (Conidae, Gastropoda) giving a new insight into the evolutionary process hidden in ecological speciation Cone snails are evolutionary significant molluscs because of its extraordinary taxonomic and ecological diversity. Morphological parameters were recorded for the *Conus catus* species collected from different ecosystems such as rocky intertidal beds, lagoons, and inner reef platforms of Lakshadweep (Arabian Sea) and Andaman Nicobar (Bay of Bengal) archipelagos of Indian Ocean. Specific differences were observed for shell coloration of specimen collected from varying ecosystem and maximum likelihood clustering approach were done based on mitochondrial genes, COI, 16srRNA, 12srRNA and Nuclear Histone3 genes The rocky shore *C. catus* from both Arabian sea and bay of Bengal have the same morphological and genetic character even they are from different seas and the coral reef habituated specimens also following the same pattern of morphogenetic similarity. Multiple molecular markers based analysis revealed that ecological niche depended divergent evolutionary selective pressure is acting on both mitochondrial and nuclear markers are characterized by the ecosystem apart from the physical geographic distance and giving the new insight into the evolutionary genetic process hidden in allopathic speciation. We also observed that *C. striolatus* a morphologically closely related species to rocky shore *C. catus* is the outcome of sympatric speciation through the selection pressures exerting on each other in rocky intertidal ecosystems. The two morph types of *C. catus* are in the way of ecological speciation and the present study also reminds that basic unit of biodiversity conservation should be the ecosystem not the species.

Phylogeny and evolution of Genus *Cremnoconchus* (Gastropoda: Littorinidae) from the Western Ghats, India

Aravind Neelavar Ananthram and Sudeshna Chakraborty¹

¹Suri Sehgal Center for Biodiversity and Conservation, Ashoka Trust for Research in Ecology and the Environment (ATREE, Royal Enclave, Srirampura, Jakkur PO, Bangalore 560064, India)

Genus *Cremnoconchus* is an iconic taxon belonging to the freshwater ecosystem of the Western Ghats, India. It is the lone freshwater representative of an otherwise marine family Littorinidae. Despite its uniqueness, only a few studies that did bring it to the spotlight, addressed questions based on its taxonomy and some aspects of conservation. However, this genus remains to be viewed from the lens of phylogeny. Extensive sampling of waterfalls throughout the Western Ghats have revealed an astonishingly high endemic radiation restricted within 13° - 21°N on the western slope. Phylogenetic analyses show distinct clading of *Cremnoconchus* with respect to the rest of the members of the family. Moreover, a total of 21 species have been identified including 12 undescribed ones. Various species delimitation methods also reiterate these numbers lending strong support to the result. A fossil-calibrated Bayesian inference of the phylogeny depicts the split of this freshwater genus from its marine counterparts around 121 mya. Receding sea level and spatial isolation could have driven the diversification leading to colonozation of freshwater habitats by *Cremnoconchus*. Additionally, species belonging to the northern and central Western Ghats have separated from each other around 82 mya and show deep divergence among themselves. Strong support to the monophyly of *Cremnoconchus* and the consistency of this pattern suggests a need to elevate this genus to sub-family Cremnoconchinae. Strict niche requirements, limited distribution, and high anthropogenic pressure render this taxon vulnerable to extinction demanding immediate action. In addition, reduced dispersal capabilities and its unusual evolutionary history makes its journey an extremely interesting one to unravel.

Tangled Tentacles: How Useful are Currently Available Genome-Scale Data for Resolving Relationships Among the Decapodiform Cephalopods?

Frank E. Anderson*¹ and Annie R. Lindgren²

¹Department of Zoology, Southern Illinois University

²Department of Biology, Portland State University

Relationships among the extant lineages of Decapodiformes -- Idiosepiida (pygmy squids), Myopsida (lolliginid squids), Oegopsida (open-eyed squids), Sepiida (cuttlefishes), Sepiolida (bobtail and bottletail squids) and Spirulida (the ram's horn squid) -- have puzzled cephalopod biologists for over a century. Genome-scale data have great potential to resolve challenging phylogenetic problems like this one, but recent studies of mitochondrial proteome and nuclear genome/transcriptome data have supported conflicting patterns of decapodiform relationships. The standard response to this dilemma has been that broader taxon sampling and even more data will be needed to clarify relationships, but can we do better than that? To squeeze as much phylogenetic insight as possible from currently available genome-scale data, we inferred relationships using all publicly available decapodiform transcriptome and genome data and evaluated the impact of factors known to influence phylogenetic inference, including taxon/data sampling, outgroup choice, missing data, conflicting signals among loci and compositional and substitution rate heterogeneity among lineages. Our findings provide provisional support for a "megadecapodiform" clade comprising Myopsida, Oegopsida and Sepiida, with Idiosepiida the most likely sister group to this clade. However, relationships between Idiosepiida and Sepiolida and within Megadecapodiformes, as well as the phylogenetic position of Spirulida, remain open questions that may require higher-order genomic data (e.g., conserved synteny, rare genomic changes, etc.) to resolve.

Evolution of Mantle Sensory Organs in Bivalves: What Pteriomorphians Tell Us About Convergence and Adaptive Innovations

Jorge A. Audino*¹, Jeanne M. Serb², and José Eduardo A. R. Marian¹

¹University of São Paulo, Department of Zoology

²Iowa State University, Department of Ecology, Evolution, and Organismal Biology

Bivalves exhibit a wide range of mantle structures that are considered key attributes in their ecological diversification. Pteriomorphia (e.g. oysters, scallops, and mussels) show remarkable diversity of mantle sensory structures, including tentacles and photoreceptor organ, and are suitable non-vertebrate models to understand form-function relationships across multiple biological levels. Nevertheless, it remains unknown how many times these sensory organs have evolved and if their evolution is associated with lifestyle transitions. The present study investigated the evolution of mantle tentacles and eyes in Pteriomorphia under a molecular phylogenetic framework for 185 species across 19 pteriomorphian families. Morphological data were acquired for 220 species from museum collections, and ecological data were compiled from the literature. Ancestral state reconstruction indicates that the pteriomorphian ancestor was likely epifaunal., bearing neither tentacles nor photoreceptor organs. Subsequently, eyes have exclusively arisen in epifaunal lineages, at least 6 times independently. In addition, transitions to crevice-dwelling habit are associated with convergent gains of eyespots in some families. Once photoreceptor organs have arisen, secondary losses were frequent when the habit shifted to infaunal. Mantle tentacles were convergently gained in distinct clades of Pteriomorphia. Detailed anatomical evidence corroborates this hypothesis, suggesting also mechano- and chemoreception roles. Interestingly, the shift of the sagittal body plane relative to substrate, from perpendicular to parallel, shows the same historical pattern as tentacle origin. Therefore, change in epifaunal position might have been associated with gains of tentacles as evolutionary novelties.

Diving In The Cold South: The Challenging Biology and Ecology of Antarctic Heterobranchs

Conxita Avila*¹ and Manuel A.E. Malaquias²

¹Dept. of Evolutionary Biology, Ecology and Environmental Sciences, and IrBIO, Faculty of Biology, University of Barcelona

²Dept. of Natural History, Section of Taxonomy and Evolution, University Museum of Bergen

The diversity of Antarctic heterobranchs has been considered low for more than a century. However, many wide areas and deep basins remain underexplored and some groups are understudied. Up to 2015, there were about 80 species of heterobranchs described to live in Antarctica, with Nudibranchia (~35) and Cephalaspidea (~25) as the most speciose groups. Among them, several families and genera are endemic, often being essential for understanding the evolution of heterobranch lineages. Here, we report the most interesting biological and ecological findings over the last years, including reproductive and defensive strategies. We also review the results on the taxonomy and systematics of several Antarctic heterobranchs, in the light of the recent studies from our group. We recently provided integrative taxonomic evidence for the establishment of a new Cephalaspidea family (Newnesiidae), with eurybathic and circumpolar distribution, and the description of a new genus and two new species, namely *Newnesia abyssalis* and *Hocius joani*. This discovery traced the origin of the cephalaspideans, which are worldwide distributed, to Antarctica. Furthermore, our data support the hypothesis that herbivory is the plesiomorphic feeding condition in Cephalaspidea. Detailed morpho-anatomical studies and molecular data of several Philinoidea suggest major changes in the systematics of the group, including a new family, two new genera, and three new species to embrace most of the species described in the Southern Ocean so far. Overall, our results highlight both the need and the importance of multidisciplinary approaches to estimate biodiversity in heterobranch molluscs from Antarctica, one of the still poorly studied areas of the planet.

Exploring Species Delimitation Methods in the *Albinaria cretensis* Complex on Crete Based on RADseq Data

Sonja Bamberger*¹ and Bernhard Hausdorf¹

¹Center of Natural History, Zoological Museum, University of Hamburg

Delimiting species in radiations is notoriously difficult because of incomplete lineage sorting and introgression between incipient species. Next generation sequencing of genome-wide markers may help to overcome these problems. The door snail genus *Albinaria* from the Eastern Mediterranean is one of the most species rich land snail genera. We studied the radiation of the *Albinaria cretensis* complex on Crete. Within this complex, species delimitation was based exclusively on shell characters so far. Competing classifications list 5-9 species with up to 18 additional subspecies. Several of the morphologically delimited species proved to be polyphyletic in a mitochondrial gene tree. We generated double digest Restriction Associated DNA sequencing (ddRADseq) data for 56 *Albinaria* populations. We reconstructed the phylogeny of the complex based on these data and compared the results of several approaches for delimiting species (Structure, Gaussian clustering, etc.) with the classifications based on morphological data. In addition, we evaluated whether the differentiation between allopatric taxa can be explained by isolation by distance using a novel test.

Are Bacteria Important in Chalk Formation in Oysters?

Roxanne Marie Wolfe Banker*¹

¹University of California Davis

Microbially-induced mineralization occurs when microbial consortia within a shell-secreting organism play a central role in nucleation, growth, and morphology of mineral formation. One untested case of microbially-induced mineralization among bivalves are the chalky deposits found in certain oyster species. Chalk is a form of porous, friable calcite that is irregularly interspersed throughout the shells of species that display this feature. Chalk has been hypothesized to be the result of sulfate-reducing bacteria (SRB) activity within the oyster calcifying space. SRB are of particular interest because of their role in calcium carbonate formation in microbial mat systems and other carbonate secreting organisms. The goal of the present study was to manipulate populations of SRB in oysters to determine whether there was an associated effect on chalk expression. Individuals of the Pacific oyster, *Magallana gigas*, were grown in Bodega Bay, CA for approximately 7 months, and were exposed periodically to treatments designed to alter SRB populations and activity within oysters. At the end of the experimental period, oysters were sacrificed and chalk expression was assessed by measuring bulk shell density and the percentage of cross-sectional area occupied by chalk. The amount of SRB in oysters was also quantified to determine whether there was a relationship between populations SRB and chalk formation. Data presented here show treatment groups produced varying amounts of chalk, though increased chalk formation is not associated with enhanced populations of SRB. Results indicate that SRB are not the primary cause of chalk formation, but microbiota within oysters likely play a role in the healthy functioning of organismal processes, including shell formation.

Land Malacofaunal Surveys in Northern Luzon, Philippines: Status and Challenges

Zenaida G. Baoanan*¹ and Roscinto Lumbres²

¹Department of Biology, College of Science University of the Philippines Baguio, Baguio City

²College of Forestry, Benguet State University, La Trinidad, Benguet

Island snail diversity is truly amazing for archipelagic country such as Philippines with the prospect of high level of endemism. The Northern Luzon alone encompasses the two largest mountain chains with different geologic origins, the Central Cordillera and the Sierra Madre. The mountains are mostly made up of mixture of limestone and volcanic materials. To gauge as to how many of the land snails have been reported in Northern Luzon, we surveyed accessible secondary sources. The most comprehensive listing of Philippine land snails was reported by Faustino in 1930 comprising of 1,294 species of which 709 (or more than 50%) are recorded from Luzon. Other relevant sources of information include the work of Springsteen and Leobrero in 1986 on Shells of the Philippines and Gray's Collection of the Cyclophoridae from the British Museum in 1850. We compared these listings with the collections that we have accumulated from several opportunistic field surveys. We then generated a spatial distribution map based on the available geographic references. We suspect that the collated data is an underrepresentation of the actual land snail diversity in the island. Some of the challenges that we have identified based on our actual field experience in Northern Luzon are as follows: 1) security concerns related to insurgency; 2) bureaucracy in obtaining required permits; 3) rugged terrains and unsafe trails going to the forests; 4) lack of taxonomic experts and field based researchers, 5) few funding opportunities for taxonomic researches; 6) issues on the publishability of taxonomic work; and, 7) lack of computer databases, inventories, and information networks for the collection and collation of information. It takes a lot of courage, passion, and determination to do malacology in the most remote regions where silent snails are awaiting to be discovered.

***Pomacea sordida*, Species Complex or Single Species from Rio de Janeiro State, Brazil?**

Kevin Portilho Barbosa*¹, Kenneth A Hayes³, Robert H Cowie², Aline Carvalho Mattos¹, Monica Ammon Fernandez¹, and Silvana Carvalho Thiengo¹

¹Laboratório de Malacologia, Instituto Oswaldo Cruz, Fundação Oswaldo Cruz, Av. Brasil 4365, Manguinhos, CEP21040-900, Rio de Janeiro, RJ, Brasil.

²Pacific Biosciences Research Center, University of Hawaii, 3050 Maile Way, Honolulu, Hawaii 97822, USA.

³Bishop Museum, Honolulu, Hawaii 97822, USA

Despite the ecological and economic significance of Ampullariidae, the taxonomy of many members of this family is still in need of revision. This work, part of a broader Neotropical ampullariid taxonomic revision, aims to examine the species limits and biogeography of *Pomacea sordida*, a potentially threatened apple snail endemic to Rio de Janeiro state. The Mollusc Collection of the Oswaldo Cruz Institute (CMIOC) contains 89 lots of *P. sordida* that were examined morphologically (conchology and soft anatomy), and DNA sequence data were obtained from the 11 lots containing ethanol preserved material. The main diagnostic anatomical features were found in the male reproductive system and specimens from different municipalities exhibited differences in penis sheath shape and the location of its glands in comparison with the previous descriptions. Mitochondrial COI sequences from eight individuals produced five new haplotypes, when compared to two previously published sequences for this species. Analysis of all haplotypes indicated K2P distances of 0.7- 4.3%, values consistent with population structure recorded in other species of *Pomacea*. Such structure is consistent with populations that have disjunct distributions across a heterogenous landscape, resulting in reduced gene flow among populations. Information from newly collected samples in 12 municipalities will help to clarify the taxonomy of *P. sordida*. Additional surveys in Rio de Janeiro will help clarify the biogeography, evolution, and systematics of *P. sordida*, as will additional morphological and molecular analyses. These data will allow us to address the question of species limits in *P. sordida* and the closely related *P. intermedia* which has been confused historically with *P. sordida*.

Neogene Diversification of the Crown Helicostyline Land Snails (Gastropoda: Stylommatophora: Camaenidae) in the Philippines

Gizelle A. Batomalaque^{*1,2,3}, Adnan Moussalli⁴, and Gary Rosenberg^{1,2}

¹Department of Biodiversity, Earth and Environmental Science, College of Arts and Sciences, Drexel University, Philadelphia, USA

²Malacology Department, Academy of Natural Sciences of Philadelphia, Philadelphia, USA

³Institute of Biology, College of Science, University of the Philippines Diliman, Quezon City, Philippines

⁴Department of Science, Museum Victoria, Melbourne, Australia

The Philippines' dynamic geological history and rich fauna provides a setting for understanding island biogeography and evolution. We generated the most complete phylogeny of the Helicostyline derived from 1,990 exons, and estimated the divergence times of clades. Ancestral ranges and biogeographical events were inferred using BioGeoBEARS. The subfamily was not recovered as monophyletic and was divided into three distinct clades. A majority of the species comprised the crown helicostyline, which originated in Luzon during the late Oligocene, and subsequently expanded its range as the islands of the proto-Philippines grew and moved closer to one another. Clades in Mindanao and the west-Central Visayas region represent long-distance dispersals during the mid-Miocene. No vicariance events were inferred as divergence times at the shallow nodes predate the Pleistocene when sea levels oscillated to form mega-islands.

Surviving a Mass Extinction: The Ecology of Persistence in Society Islands Partulids

Cindy Bick*¹, In Hee Lee², David Blaauw², Trevor Coote³, and Diarmaid Ó Foighil¹

¹University of Michigan Department of Ecology & Evolutionary Biology and Museum of Zoology

²University of Michigan Department of Electrical Engineering and Computer Science

³Partulid Global Species Management Programme

Partulid tree snails are endemic to Pacific high oceanic islands and they have experienced extraordinary rates of extinction in recent decades following the introduction of continental predators, most notably *Euglandina rosea*. Most of the loss has involved the Society Islands endemic *Partula* species radiation and we are particularly interested in the small number of surviving Society Islands species. What factors have enabled them to differentially survive almost 50 years of *E. rosea* predation? Demographic analyses of historical wild and captive populations found that higher wild clutch sizes and higher captive reproductive rates were correlated with survival on Tahiti, but not on Moorea. Survival in altitudinal refuges where the predator is relatively ineffective is especially important on Tahiti, but only marginally so on Moorea and on Raiatea. Survival in Tahitian and Moorean valleys requires the presence of specialized microhabitats that are inaccessible to (mangrove fen habitat) or avoided by (sunlit forest edges) the predator. In Tahitian valleys, we tested the role of forest edge solar refuges in the survival of *Partula hyalina*. Using custom-designed and manufactured smart, millimeter size solar sensors, we characterized the solar ecologies of predator populations and of surviving *P. hyalina* populations in the field. Our results indicate that their solar ecologies are significantly different but that any protective effect is intermittent, being attenuated or absent on overcast days. Long-term survival of this species in Tahitian valleys may require proactive conservation of its forest edge solar refuges.

Mobilizing the World's Mollusk Collections

Rüdiger Bieler*¹

¹Integrative Research Center, Field Museum of Natural History, 1400 Lake Shore Drive, Chicago, Illinois 60605, U.S.A.

Management and use of collections have changed rapidly with increasing digitization and on-line accessibility of occurrence data. A comparison of surveys of U.S. and Canadian mollusk collections in 1975 and 2017 shows massive growth (with these 86 collections now holding about 100 million specimens). Where do we go from here – how do we mobilize our worldwide collections to unlock Mollusca's potential for exploring the Earth's biota? An increasing number of collections provide their institution-maintained data via communal portals (e.g., iDigBio, InvertEBase) and/or deliver such data directly to global efforts such as GBIF. How do we align/improve/incorporate regional efforts with other worldwide initiatives? What kind of data aggregation do we need and want to support? A recent workshop on digitizing mollusk specimen data in the U.S. and Canada identified imaging of primary types, expanding taxonomic authority files (MolluscaBase), and initiating collaborative georeferencing as primary near-term goals. What are the next steps? Some needs can be solved entirely in the IT realm (e.g., use tracking), some can be developed at the authority file level (e.g., species attributes), and yet others remain at the collection level (e.g., specimen attributes) but could in part be community-sourced (e.g., communal georeferencing). At the level of all U.S. biodiversity collections, the Biodiversity Collections Network (BCoN) proposed an Extended Specimen Network (ESN) to fill gaps in biodiversity data and provide linkages with associated (genetic, phenotypic, behavioral, environmental) data. How do we as a global mollusk community prepare ourselves to build and grow such a virtual collection that can be accessed in meaningful and novel ways by our users?

Replacing Mechanical Protection With Colorful Faces – Twice: Parallel Evolution of Non-operculate Marine Worm-Snail Genera (Caenogastropoda: Vermetidae)

Rüdiger Bieler*¹, Camila Granados-Cifuentes², Timothy M. Collins², Rosemary Golding^{1,3}, John M. Healy⁴, and Timothy Rawlings⁵

¹Integrative Research Center, Field Museum of Natural History, 1400 Lake Shore Drive, Chicago, Illinois 60605, U.S.A.

²Department of Biological Sciences, Florida International University, 11200 SW 8th St., Miami, Florida 33199, U.S.A.

³Malacology, Australian Museum, 6 College Street, Sydney, NSW 2010, Australia

⁴Biodiversity and Geosciences Program, Queensland Museum, PO Box 3300 South Bank, Queensland, Australia, 4101

⁵Department of Biology, Cape Breton University, 1250 Grand Lake Road, Sydney, Nova Scotia, B1P 6L2, Canada

Vermetidae, a family of sessile and irregularly coiled marine gastropods, has been difficult to resolve, with much hidden diversity, a propensity to raft on floating objects (making them prime candidates for marine invasions), and few adult shell characters suitable for identification. Some vermetid groupings (e.g., *Vermetus sensu lato*) clearly are wastebasket taxa while others long thought to be monophyletic (e.g., species sharing dome-shaped opercula) are now known to have more than one origin in the vermetid tree. Here we demonstrate that another grouping based on a “readily recognizable synapomorphy” – the lack of operculum and concomitant large muscular pedal disk – is also non-monophyletic. One clade, *Thylacodes* (= *Serpulorbis*), consists of comparatively large-bodied and often polychromatic species, clustering with some operculate “*Vermetus*” species. A second new clade with four new species includes smaller-bodied forms and aligns with a different set of operculate species. The new genus is known only from western Atlantic reefs of the Florida Keys, the Bahamas, and Belize. It differs from *Thylacodes* in morphology (protoconch wider than tall), behavior (deep shell entrenchment into substratum), reproductive biology (fewer eggs and capsules per female; obliquely attached capsule stalk), and in some species, a luminous, “neon-like”, quality of the head-foot coloration. Additionally, eusperm and parasperm ultrastructure has revealed distinguishing characters, with a laterally flattened eusperm acrosome observed in two investigated species of the new genus and a spiral keel on the eusperm nucleus in one of those species, the latter feature currently unique within the family. Aspects of predator avoidance/deterrence in non-operculate vermetids apparently involve warning coloration, aggressive behavior, and mucus nets.

Margaritiferidae Revisited

Arthur E. Bogan*¹, Ivan N. Bolotov^{2,3}, Van Tu Do⁴, David C. Aldridge⁵, Miguel M. Fonseca⁶, Han Ming Gan⁷, Mikhail Y. Gofarov^{2,3}, Alexander V. Kondakov^{2,3}, Vincent Prié⁸, Ronaldo Sousa^{6,9}, Simone Varandas¹⁰, Ilya V. Vikhrev^{2,3}, Amílcar Teixeira¹¹, Rui-Wen Wu¹², Xiaoping Wu¹², Alexandra Zieritz¹³, Elsa Froufe⁶, and Manuel Lopes-Lima^{6,14,15}

¹North Carolina Museum of Natural Sciences, 11 West Jones St., Raleigh, NC 27601, United States

²BIGER – Institute of Biogeography and Genetic Resources, Federal Center for Integrated Arctic Research, Russian Academy of Sciences, Severnaya Dvina Emb. 23, 163000 Arkhangelsk, Russian Federation

³Northern Arctic Federal University, Severnaya Dvina Emb. 17, 163000 Arkhangelsk, Russian Federation

⁴Department of Aquatic Ecology and Water Environment, Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, 18 Hoang Quoc Viet, Cau Giay, Ha Noi, Viet Nam

⁵Department of Zoology, University of Cambridge, The David Attenborough Building, Pembroke Street, Cambridge CB2 3QY, United Kingdom

⁶CIIMAR/CIMAR – Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, Avenida General Norton de Matos, S/N, P 4450-208 Matosinhos, Portugal

⁷Centre for Integrative Ecology, School of Life and Environmental Sciences, Deakin University, Geelong, 3220 Victoria, Australia

⁸Institut de Systématique, Évolution, Biodiversité ISYEB – UMR 7205 – CNRS, MNHN, UPMC, EPHE, Muséum national d'Histoire naturelle, Sorbonne Universités, 57 rue Cuvier, CP26, F-75005 Paris, France

⁹CBMA – Centre of Molecular and Environmental Biology, Department of Biology, University of Minho, Campus Gualtar, 4710-057 Braga, Portugal

¹⁰CITAB/UTAD – Centre for Research and Technology of Agro-Environment and Biological Sciences, University of Trás-os-Montes and Alto Douro, Forestry Department, 5000-801 Vila Real, Portugal

¹¹CIMO-ESA-IPB – Mountain Research Centre, School of Agriculture, Polytechnic Institute of Bragança, Campus de Santa Apolónia, 5301-854 Bragança, Portugal

¹²School of Life Sciences, Center for Watershed Ecology, Institute of Life Science, Nanchang University, Nanchang 330031, People's Republic of China

¹³School of Environmental and Geographical Sciences, University of Nottingham Malaysia Campus, Jalan Broga, 43500 Semenyih, Malaysia

¹⁴CIBIO/InBIO – Research Center in Biodiversity and Genetic Resources, University of Porto, Campus Agrário de Vairão, Vairão, Portugal

¹⁵SSC/IUCN – Mollusc Specialist Group, Species Survival Commission, International Union for Conservation of Nature, c/o The David Attenborough Building, Pembroke Street, CB2 3QZ Cambridge, United Kingdom

Species assigned to the family Margaritiferidae are restricted to the northern hemisphere and represent the most imperiled family in the Unionida. Recent molecular work has been interpreted as supporting all of the species in this family belong to a single genus, *Margaritifera*. The recent expansion of the Margaritiferidae began with the publication of the complete mitochondrial genome that placed *Lamprotula rochechouartii* (Heude, 1875) from China in the Margaritiferidae. New samples of *Gibbosula crassa* (Wood, 1815) from northern Vietnam were sequenced and also found to belong in the Margaritiferidae. Three other “*Lamprotula*” species were also found to belong to the Margaritiferidae based on mantle attachment scars. Our analyses used five molecular markers in developing a robust phylogeny of the Margaritiferidae. Margaritiferidae was split into two major clades treated as subfamilies, Margaritiferinae and Gibbosulinae. These two major clades were divided into three clades in Margaritiferinae and one in Gibbosulinae. Molecular data, morphology, biogeography and ecological characteristics supported the division of the Margaritiferidae into two subfamilies and the recognition of four genera. Available species have had the complete mitochondrial genome sequenced. The gene order of these taxa supports the phylogeny and the family level separation from the Unionidae. Fossil and calibrated genetic change support the divergence of the Unionidae and Margaritiferidae in the Late Triassic. Separation of the

two Margaritiferid subfamilies is estimated as having occurred in the Mid Jurassic. The genera appear to have arisen during the Cretaceous.

A Squadron of Species: An Analysis of the *Goniobranchnus roboi* Species Complex

Lynn J. Bonomo*^{1,2} and Terrence M. Gosliner¹

¹California Academy of Sciences, Department of Invertebrate Zoology and Geology

²San Francisco State University, Department of Biology

In the last several years, the family tree of Chromodorididae has been undergoing refinement due to molecular work, indicating new relationships between taxa. The genus *Goniobranchnus* is one clade of the Chromodorididae and used to be included within *Chromodoris*. This genus was determined to be non-monophyletic and *Goniobranchnus* was separated out. Molecular work to resolve the internal relationships in *Goniobranchnus* has not been undertaken previously. Only 41 of the 89 potential species have been described formally. Through genetic sequencing, I have added 185 (183 new) *Goniobranchnus* specimens and added an additional 43 species from GenBank. I used two mitochondrial (COI and 16s) genes and one nuclear gene (H3) to begin to resolve the genetic relationships between *Goniobranchnus* species. Through my phylogenetic analyses, I have discovered a species complex of *G. roboi* that consists of at least four species. Details of this newly documented diversity are presented here and morphological differences that reflect the genetic differences will be discussed.

Museums at the Frontline in Archiving the Undocumented Species Diversity of the World

Philippe Bouchet*¹

¹Muséum National d'Histoire Naturelle, Paris, France

Perhaps half of the 150-200,000 species of Recent molluscs are still unknown. However, most of the unknowns live in habitats/environments that are not easily sampled - e.g., the mesophotic zone, the deep sea - or that are fast disappearing - rainforests, fresh water. To these barriers, add permitting constraints, such as the Nagoya Protocol, that de facto restrict exploration and discovery. It is unrealistic to expect that every taxonomist tackling unknown biodiversity has the technical/logistical know-how and political/funding resources to mount ad hoc exploring and sampling expeditions. We must change our attitude to collections. Collections are not the last step of a conveyor belt going from sampling to study and description to archiving. They should be the first step of the chain that goes from bulk sampling to storage to study and description, and then back to archiving. We have to accept sometimes long shelf lives for orphaned taxa without active experts. Unstudied material in museum collections should not be an indicator of failure of a curator's ability; instead, they should be a measure of success of an institution to overcome technical, logistical, political, and funding barriers to build collections with a rich potential for new species discovery. Museums should also change their attitude to citizen taxonomists, who are already responsible for 57% of the new species descriptions, but are often seen by academics as second-class systematists. Proactively giving citizen scientists access to expedition material is part of promoting a new role for museum collections: more integrated and more tuned to the political and social realities of the 21st century.

First 3D-microanatomy of Rissoellid Microsnails Within a Lower Euthyneuran Framework (Heterobranchia, Rissoelloidea)

Bastian Brenzinger*¹, Sebastian Thal¹, Gerhard Haszprunar², Michael Schrödl^{1,2}, Yasunori Kano³

¹BioCenter of LMU Munich, Department Biology II, Großhadernerstr. 2-4, 82152 Planegg-Martinsried, Germany

²SNSB – Bavarian State Collection of Zoology, Münchhausenstr. 21, 81247 Munich, Germany

³Department of Marine Ecosystem Dynamics, Atmosphere and Ocean Research Institute, The University of Tokyo, 5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8564, Japan

Microanatomical studies in combination with molecular phylogenetic trees are invaluable for a combined and integrative understanding of molluscan evolution. The family Rissoellidae, a worldwide clade of microsnails living in marine algal turf, is a perfect target for such integrative studies: rissoellids are diverse, possess complex organs in their minute bodies that are difficult to examine without specialized methods, and their phylogenetic position has been a matter of debate. Molecular phylogenetic studies of the last years surprisingly supported a close relationship with larger-bodied, benthic heterobranchs, the bubble-shelled Acteonoidea that were previously assumed to closely resemble the common ancestor of the entire crown-group Euthyneura. We examined several species of *Rissoella* from Europe, Japan and Australia by creating series of histological sections and reconstructed all organ systems in light-microscopical detail using the 3D software Amira. Focusing on one Japanese species we considerably correct and expand previous histological datasets, and we compare microanatomy and variability (reproductive and digestive tracts, mantle complex) among further species. We also briefly compare Rissoelloidea and Acteonoidea to critically evaluate their putative close relationship and to see if morphological data are consistent with a hypothesis that Rissoellidae originated from larger-bodied, bubble-shelled heterobranchs through paedomorphosis.

Phylogeny of the Lower Heterobranchia Through an Expanded Taxon Sampling and Sanger Sequencing

Bastian Brenzinger*^{1,2,3}, Tsuyoshi Takano^{2,4}, Michael Schrödl^{1,3}, and Yasunori Kano²

¹BioCenter of LMU Munich, Department Biology II, Großhadernerstr. 2-4, 82152 Planegg-Martinsried, Germany

²Department of Marine Ecosystem Dynamics, Atmosphere and Ocean Research Institute, The University of Tokyo, 5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8564, Japan

³SNSB – Bavarian State Collection of Zoology, Münchhausenstr. 21, 81247 Munich, Germany

⁴Meguro Parasitological Museum, 4-1-1 Shimomeguro, Meguro, Tokyo 153-0064, Japan

Heterobranchia is one of the major gastropod clades with such well-known euthyneuran taxa as nudibranch sea slugs, pteropod sea butterflies and panpulmonate land snails. It remains poorly understood, however, how so-called “lower” heterobranchs – mostly minute, marine and still shell-bearing snails originating as early as the Devonian – have evolved to these highly specialized forms. To illuminate the early evolutionary history of the Heterobranchia, we studied lower heterobranchs collected mainly from waters of Europe, Japan, and various other Indo-Pacific localities. Our present dataset contains novel COI sequences (~658 bp for almost 100 species) for two thirds of all extant genera in the lower Heterobranchia and novel 18s rRNA sequences (~1800 bp, 34 species) for all of the 14 extant families. Analysis of the COI gene already resolves many generic and family-level relationships that were unclear or not suggested in previous studies, largely congruent with 18s data. Three major clades have been identified, namely: 1) re-defined Valvatoidea (Valvatidae, Cornirostridae, Hyalogyrinidae) including at least two further marine lineages; 2) Architectonicoidea sensu lato with Architectonicidae, Mathildidae and *Ammonicera*; and 3) a clade of somewhat euthyneuran-like animals, including Rhodopidae and Murchisonellidae, that is sister to Euthyneura. A fourth group of microscopic snails (Orbitestelloidea) shows low evolutionary rates on both genetic markers and may represent the basalmost heterobranch grade or clade. We also give an outlook for future comparative 3D-microanatomical studies and evolutionary reconstruction, altogether expecting considerable progress within understanding of the heterobranch tree backbone in the near future.

The One World Collection Project and its Potential for the Mollusk Collections Community

Carol Roetzel Butler*¹

¹National Museum of Natural History, Smithsonian Institution

The One World Collection project, initiated in 2016, began with the idea of using a simple, high level construct to describe the breadth and diversity of world's natural history collections, indicating their regions of origin and the institutions where they currently are distributed and maintained. The project was quickly expanded to associate staff expertise with each major collection group, including staff's years of experience. The data set now contains information from 79 of the world's largest institutions, and indicates that the global natural history collection comprises at least 1.1 billion specimens, curated by more than 7,800 experts. This high level data allows participating institutions to put their data into both regional and global contexts, identify gaps in planned collection representation, illustrate collections strengths, and forecast staffing needs based on staff demographics. It offers great potential for identifying potential collaborations. These opportunities are illustrated using data from the Smithsonian Natural History Museum, and global data on mollusk collections.

John Thomas Gulick in Japan

Paul Callomon*¹

¹ Academy of Natural Sciences of Drexel University

Though best known in the international scientific community for his pioneering work on the evolution of land snails, J. T. Gulick also played a major role in introducing amateur science to Japan during the fourteen years of his second stay there (1875-1899). Yoichiro Hirase's Conchological Museum and Magazine and the long scientific career of James Tokubei Kuroda – not to mention the description of more than a thousand Japanese mollusk species by H. A. Pilsbry and others between 1899 and 1920 – all stemmed from the influence of Gulick and his contemporaries in the Christian community in Kyoto during the key years 1894-7. This talk compares and contrasts Gulick's encouragement of amateur natural science with the formal model taught by E. S. Morse and his successors at the Imperial University and considers the influence on natural science of social networks across continents and oceans.

How Many Micro-mollusks Are There? A Case Study on Species Richness From Hawai'i

Bianca Campagnari*¹ and Daniel L. Geiger²

¹Santa Barbara Museum of Natural History Quasars to Sea Stars teen program

²Santa Barbara Museum of Natural History Invertebrate Zoology

This study used the statistical metrics Chao1, Chao2, ACE, and rarefaction to estimate and model the total number of species of shelled micro-mollusks in an area from the amount and composition of nine samples collected from the area. The micro-mollusks were collected from the sublittoral zone off Wailea, Maui, and the Chao2, Chao1, and ACE methods of estimating species richness were used. There were 250 species in all the samples, and the estimated total number of species of shelled micro mollusks in this area is 317–375 species.

Placing Peculiar Planorbids of the Pacific Northwest

David C. Campbell*¹ and Charles Lydeard²

¹Gardner-Webb University, Dept. Natural Sciences, 110 S. Main St., Box 7270, Boiling Springs NC 28017

²Morehead State University, Department of Biology & Chemistry, 103 Lappin Hall, Morehead, KY 40351

Morphologically anomalous species have been difficult to place phylogenetically. The hyperstrophic planorbids *Carinifex* and *Vorticifex* from northwestern North America were recognized as lymnaeoidean since their discovery, but the exact affinities have been more problematic. Various hyperstrophic planorbids have been historically associated with these genera. Anatomical data point towards an affinity with *Helisoma*, *Biomphalaria*, and other primarily New World genera, currently assigned to *Helisomatini*. This affects the nomenclature of the tribe, as the widely-used *Helisomatini* is junior to the awkward and obscure Pompholycodeinae, based on a subjective synonym of *Vorticifex* and also a replacement for two older, invalid family-level names. *Carinifex* is currently widely treated as a subgenus of *Helisoma*, reflecting the anatomical similarities. Conversely, the more normal-looking western *Menetus* is treated as the genus for the eastern North American subgenus “*Micromenetus*” (actually a junior synonym of *Dilatata*). Molecular data (28S, COI, and 16S) confirm that *Carinifex*, *Vorticifex*, and *Menetus* are related to *Helisomatini*, but do not support genus-level synonymy with genera from other regions. Within *Vorticifex*, variation in the calmodulin intron suggests that the morphological variability is mostly intraspecific, with perhaps a single extant species.

What's (Dug) up (at Old) Dock II

Timothy Campbell*¹, Lyle Campbell², and David Campbell³

¹Private address

²University of South Carolina Upstate

³Gardner-Webb University

The Waccamaw Formation contains a rich basal Pleistocene (early Gelasian) fauna with an extreme abundance of mollusks (>90% of the fossils) in addition to various echinoderms, arthropods, annelids, corals, bryozoans, and vertebrates. Based upon the ranges of the extant species, the climate seems to have been somewhat warmer than today. This diverse subtropical fauna is found in southeastern North Carolina and eastern South Carolina. Although fossils have been reported since the mid-1800s, no single monograph exists. Through landowner permission to the North Carolina Fossil Club, in four collecting trips to the Old Dock quarry, I have collected and identified 148 species out of approximately 500 known from the lower Waccamaw. So far I have found 75 species of gastropods, 71 species of bivalves and 2 species of scaphopods. These fall respectively into 54, 57 and 2 genera, and 32, 26 and 2 families. Notable species include *Caloosarca rustica* (Tuomey & Holmes, 1857); an aberrant *Conus oniscus* W. P. Woodring, 1928; *Erycina cf. kurtzii* (Dall, 1898); *Pterorytis fluviana* (Dall, 1903); and *Aligena striata* H. C. Lea, 1843. All reasonably complete specimens are being photographed to document the fauna. The overall extinction rate of my specimens is 60% (which would correspond to late Miocene under Lyell's definitions). The species derive from multiple habitats, including 30-40 m deep sandy-bottom shelf, cementing bivalve reef, 10-20 m sandy-bottom shelf, surf, saltmarsh, and freshwater.

Update of Aeolidiidae Systematics with Particular Reference to the Genus *Aeolidiella* Bergh, 1867 (Gastropoda, Nudibranchia)

Leila Carmona*¹, Marta Pola², Terrence M. Gosliner³, and Juan Lucas Cervera^{1,4}

¹Campus Río San Pedro s/n, Marine Research Institute (INMAR), 11510 Puerto Real, Cadiz, Spain.

²Departamento de Biología, Facultad de Ciencias del Mar y Ambientales, Campus de Excelencia Internacional del Mar (CEI-MAR), Universidad de Cádiz, Polígono Río San Pedro, s/n, Ap.40, 11510 Puerto Real, Cádiz, Spain

³Department of Invertebrate Zoology, California Academy of Sciences, 55 Music Concourse Drive, Golden Gate Park, San Francisco, CA 94118, USA

⁴Departamento de Biología, Edificio de Biología, Campus de Excelencia Internacional UAM-CSIC, Universidad Autónoma de Madrid, C/Darwin, 2, 28049 Madrid, Spain

Traditionally, *Aeolidiella* Bergh, 1867 is the aeolidiid genus to which most nominal species have been ascribed. *Aeolidiella alderi* (Cocks, 1852), *Aeolidiella occidentalis* Bergh 1874, *Aeolidiella sanguinea* (Norman, 1877), *Aeolidiella drusilla* Bergh, 1900, *Aeolidiella alba* Risebec, 1928, *Aeolidiella lurana* Marcus and Marcus, 1967 and *Aeolidiella stephanieae* Valdés, 2005 are some examples of species ascribed or transferred to *Aeolidiella* at least once. However, recent studies redefined *Aeolidiella*, in order to recover its monophyly, as a small genus constituted by *A. alderi* (the type species), *A. glauca* (Alder and Hancock, 1845) and *A. sanguinea*. This contribution aims to improve the systematics of this genus by incorporating into the molecular and morphological study specimens of *A. drusilla*. Our molecular phylogeny based on H3, COI and 16S, as well as the species-delimitation analyses reveal the existence of an undescribed genus and a new species of *Aeolidiella*.

“Slugs Count” Mapping Slug Diversity in UK Gardens

Imogen C N Cavadino*^{1,2}, Gerard R G Clover¹, Hayley B C Jones¹, Gordon Port², Helen E Roy³

¹Royal Horticultural Society

²Newcastle University

³Centre for Ecology & Hydrology

Slugs and snails are notorious horticultural pests, widely detested by gardeners and are frequently the most common pest enquiry to the RHS Gardening Advice service. However, not all species of slug and snail found in the UK are considered plant pests, with many species playing important roles in breaking down decaying material and recycling nutrients into the soil. In domestic gardens the presence of these pests is usually recognized by feeding damage, with the culprit species not identified, and little is known about which slug and snail species are present in UK gardens. Using citizen science, this project seeks to engage with gardeners in the UK and empower them to identify species of slug found in their garden. This is achieved through standardized survey methods using refuge traps and torchlight searches. Data verification methods include the traditional and novel, including the use of non-invasive body swabs to identify slugs to species level. By identifying what species occur in UK gardens, we can map the spread of invasive species and the suspected decline of other slug species. The data provided by citizen scientists will be used to feedback information on locally abundant pest and non-pest species, allowing control methods to be targeted to problem species, reducing negative impacts on other wildlife.

Gut Microbiome Analysis of Museum *Oreohelix strigosa* Collections

Bridget Chalifour*¹ and Jingchun Li¹

¹Department of Ecology and Evolutionary Biology, University of Colorado Boulder

Ethanol preserved museum mollusk specimens provide unique opportunities for studying the invertebrate gut microbiome. In order to utilize these samples, we must ensure that gut microbiome degradation is minimal after ethanol preservation. While microbiome compositions are not affected by short-term preservation, the effects of decades-long preservation have yet to be studied. *Oreohelix strigosa* (Rocky Mountain snail) is a land snail found in the talus slopes of the Rocky Mountains, and is an ideal study system. The University of Colorado Museum of Natural History has densely sampled *O. strigosa* for the past century; many are preserved in ethanol. The primary goal of this study was to create a comprehensive assessment of long-term ethanol preservation effects on museum specimen microbiome compositions. The second goal was to quantify any present microbial associations within the gut of *O. strigosa*. Gut DNA was extracted from museum samples ranging in preservation time from 14 to roughly 100 years, coupled with fresh samples from 2018 collected and preserved for fixed periods. Gut microbiome abundance and diversity were assessed using 16S rRNA amplicon high-throughput sequencing. Results showed that *O. strigosa* gut microbiome compositions were consistent among specimens of all ages. The dominant microbial families proposed to make up the snails' core gut microbiome are Enterobacteriaceae, Enterococcaceae and Streptococcaceae. These findings are consistent with *O. strigosa*'s inferred detritus-based diet, which necessitates use of lignocellulosic gut microbes like those mentioned above. This research demonstrated that ethanol effectively preserves gastropod gut microbiomes and that older museum specimens are suitable for microbiome analyses.

Snail of Many Parts – Anatomical Diversity and Ecological Disparity Among Deep-sea Abyssochrysoid Gastropods

Chong Chen*¹, Katsuyuki Uematsu², Hiromi K. Watanabe¹, and Shannon B. Johnson³

¹X-STAR, Japan Agency for Marine-Earth Science and Technology (JAMSTEC), 2-15 Natsushima-cho, Yokosuka, Kanagawa 237-0061, Japan

²Marine Works Japan Ltd., 3-54-1 Oppamahigashi, Yokosuka, Kanagawa 237-0063, Japan

³Monterey Bay Aquarium Research Institute (MBARI), Moss Landing, California 95039, U.S.A.

Discovered just four decades ago, deep-sea chemosynthetic ecosystems are now known to include rich oases formed around a variety of environments such as hydrothermal vents, hydrocarbon seeps, and organic falls (e.g., whale and wood). Although molluscs are a major component of these ecosystems with hundreds of endemic species worldwide, few groups have achieved endosymbiosis, the singular constrained evolutionary pathway to successful exploitation of chemosynthetic energy. Among these, abyssochrysoid gastropods are especially intriguing, as abyssochrysoid genera restricted to chemosynthetic ecosystems have extremely diverse ways of life – for example *Provanna* include deposit feeders and grazers, *Ifremeria* relies on endosymbionts, and *Rubyspira* feeds on whale bones. In the present study, we quantitatively explore the anatomical modifications of abyssochrysoid snails with different ecology using 3D reconstruction based on cutting-edge synchrotron CT data, with a focus on the three abovementioned genera. The emphasis is on the digestive and respiratory systems which are highly modified in each genus, for example the extremely hypertrophied digestive system in *Rubyspira* associated with bone digestion and similarly hypertrophied gill in *Ifremeria* associated with its holobiont condition. Finally, we apply serial block-face scanning electron microscopy (SBF-SEM) to reconstruct the anatomy of *Ifremeria*'s unique Warén's larva, giving some insights to its evolution and adaptation.

Molluscan Receptors and Neuropeptides to Control the Gray Garden Slug, *Deroceras reticulatum*

Man-Yeon Choi*¹ and Seung-Joon Ahn¹

¹USDA-ARS, Corvallis, OR

Neuropeptides that are produced from central nervous system (CNS) are involved in a variety of physiological events including detection of light, odorants, peptides, lipids, neurotransmitters, hormones, etc. PRXamide peptides are one of major neuropeptide families in insects, and play a role in pheromone production, diapause, muscle contraction, water balance, feeding behavior, pigmentation, and ecdysis in insects. The family peptides include pheromone biosynthesis activating neuropeptide (PBAN), diapause hormone (DH), pyrokinin (PK), CAPA, and ecdysis triggering hormone (ETH), etc. PRXamide peptides have been identified from a broad range of animal groups from Arthropod to Mammal, and characterized with a conserved PRXamide sequence in C-terminal ends that is a crucial motif to activate corresponding G protein-coupled receptors (GPCRs). The family peptides have been well documented with specific hormonal signal transductions in insects, but it has not been demonstrated in Mollusca to date. We

identified and characterized the first molluscan PRXamide peptides and GPCRs from the gray garden slug, *Deroceras reticulatum* (Gastropoda) which is a serious pest slug in the Pacific Northwest. The receptors were heterologously expressed in Sf9 cells, tested with various PRXamide peptides, and measured their binding activities. Our research results provide an insight in the evolutionary process with the PRXamide peptides and their receptors in the animal system.

The Status of *Tryonia porrecta* (Mighels, 1845) in the Hawaiian Islands (Gastropoda: Cochliopidae)

Carl C. Christensen*¹

¹Bernice P. Bishop Museum

The species described as *Paludina porrecta* Mighels, 1845 is a freshwater snail first reported from the island of O'ahu in the Hawaiian Islands. Its affinities were unclear for more than a century until Robert Hershler showed it to be conspecific with *Tryonia protea* (Gould, 1855), an inhabitant of desert springs and other aquatic environments in the southwestern United States. The species' status in the Hawaiian Islands remained uncertain, however, as it was unknown whether *T. porrecta* was indigenous to the Islands or was an alien species recently introduced by human commerce. Recent archaeological and other paleoenvironmental studies have since demonstrated its presence on the islands of O'ahu and Hawai'i prior to initial European contact (1778 AD) and on the island of Kaua'i prior to initial Polynesian settlement (ca. 1000 AD). Accordingly, *T. porrecta* must be regarded as indigenous to the Hawaiian Islands, presumably having arrived as a result of long-distance over-water dispersal by waterfowl migrating from western North America. Although often extremely abundant in older sediments from cultivated taro ponds and fishponds, its numbers are now much reduced as urbanization from the early 1900s onward has caused the widespread destruction of lowland wetlands throughout the Hawaiian Islands, especially on O'ahu. There are only a handful of observations of living *T. porrecta* in Hawai'i during the last one hundred years, although the species remains widespread within its North American range.

Snails on the Menu? Using Long-term Ecological Data to Contextualize Performance of a California Kelp Forest Predator and Emerging Fishery Species, *K. Kelletii*

Xochitl S. Clare*¹ and Gretchen E. Hofmann¹

¹University of California, Santa Barbara, Department of Ecology, Evolution, and Marine Biology

Climate change (e.g. ocean warming and acidification) threatens marine ecosystems that support millions of livelihoods. More global change biology research is necessary to address challenges in managing natural resources. For example, California's kelp forests are one of our planet's most productive and dynamic ecosystems, supporting private industry in the form of large- and small-scale fisheries. However, there is limited understanding on how environmental variability will affect molluscan shellfish populations in the kelp forest. Few studies have addressed behavioral impacts of climate change on molluscan kelp forest scavengers, which play a critical role in balancing trophic integrity. To ensure sustainable shellfish populations in the face of a changing climate, we must pair behavioral studies with large-scale population analyses in response to environmental dynamics over time. I will discuss an emerging fishery species and prominent kelp forest carnivorous scavenger sea snail, the Kellet's whelk (*Kelletia kelletii*). I will also discuss my laboratory assessments on feeding and growth in adult *K. kelletii*. Additionally, as part of the Santa Barbara Coastal Long Term Ecological Research (SBC-LTER) project, I will combine SBC-LTER data with data from the California Department of Fish and Wildlife and the Marine Biodiversity Observation Network to examine trends in whelk populations from 2001-2018. My analysis will consider significant upwelling events and warming events that may influence whelk behavior and population dynamics. My work represents an example of how mollusk-focused experimental biologists and data scientists can work together to solve natural resource challenges in our future.

Molluscan Collections in South Africa

Dr. Mary Louise Cole*¹

¹Malacology Department, East London Museum, East London, South Africa

There are three major molluscan collections in South Africa. The KwaZulu-Natal Museum (KZNM) holds one of the largest in the southern hemisphere. Its strengths are marine molluscs of southern Africa and the south-western Indian Ocean, and terrestrial molluscs of South Africa. The Iziko South African Museum contains the most comprehensive collections of Cephalopoda and Polyplacophora for southern Africa. Both collections date to about 1900. The East London Museum (ELM) began to specialize in marine molluscs of the Eastern Cape province in the late 1960's when the first malacology curator was appointed. Recent research focuses on terrestrial molluscs and the collection is growing rapidly. The national freshwater mollusc collection is at the Unit for Environmental Sciences and Management at North-West University. Research on marine molluscs at KZNM led to revisionary papers across a wide range of gastropod families and African marine malacofauna are regularly included in global studies. In the past two decades work on terrestrial molluscs at the KZNM and ELM has produced several revisions and descriptions of over 50 new species. Collections find themselves more secure than twenty years ago. The South African National Biodiversity Institute is encouraging discovery and documentation to address gaps in knowledge, particularly of invertebrates. Museums are supported with grants for surveys, systematic studies and data mobilization. data is currently in demand to inform decision-making for sustainable development and conservation planning. The Department of Science and Technology is investing in collections as irreplaceable research infrastructure through the Natural Science Collections Facility whereby 14 institutions are assisted with achieving common targets.

Reproductive Phenology in the Tropics: What Can Molluscs Tell Us?

Rachel Collin*¹

¹Smithsonian Tropical Research Institute, Panama

Phenology, the timing of reproduction, is a basic feature of organismal life-histories. Understanding the timing of reproduction is increasingly important, as global change alters phenology and surprising knock-on effects of these changes begin to be detected. In the tropics, which are largely viewed as aseasonal, reproduction is often assumed to be continuous. However, studies of gastropods in the Bay of Panama show that this is not the case. Taking advantage of the environmental changes associated with seasonal upwelling has allowed us to test the 2 main hypotheses that have been put forward to explain seasonal timing of invertebrate reproduction: that reproductive timing is a response to variation in temperature or to variation in phytoplankton abundance. Long tropical reproductive seasons also allow for studies of fine scale variation in reproduction, showing how tidal amplitude cycles shape reproductive cycles. Knowledge gained from studying molluscan reproduction complements that gained from other invertebrates, often offering novel insights or conflicting with paradigms developed based on data from other taxa.

Biv3d: Capturing Multiple Dimensions of Biodiversity By Ct-scanning the Shallow-Marine Bivalves of the World

Katie S. Collins*¹, Stewart M. Edie¹, and David Jablonski¹

¹Department of Geophysical Sciences, University of Chicago

We are entering an exciting new era of high-throughput analytical techniques that allow us to gather a wider variety of data from organisms than ever before, permitting integrated analysis of multiple dimensions of biodiversity. Museum holdings are not just the only way to get access to large numbers of specimens for analysis by these new methods, but hugely valuable in their own right as repositories of valuable metadata and historical information on morphology and geographic distributions of mollusc species. Using micro-CT, we are 3D scanning the Recent and fossil shallow-marine Bivalvia held in collections around the world to quantify form and ask questions about biodiversity gradients, biomechanics, and autecology and niche conservatism. This talk will present methodologies and research highlights from the first two years of the biv3d project, from latitudinal trends in shell shape and ornamentation to convergent evolution of borers and razor clams. The power of new analytical techniques is maximised when applied to the wealth of specimens held in collections worldwide.

Apple Snails as a Weed Biocontrol Using Antifeedants

James Coupland*², Fatima Haider¹, Myron Smith¹

¹Carleton University, Dept. of Biology, 1125 Colonel By Drive, Ottawa, ON K1S 5B6

²FarmForest Research Inc, Box 910, Almonte, Ontario, Canada

Apple Snails, are freshwater molluscs originating in South America. These snails (both *Pomacea canaliculata* and *P. maculata*) have been introduced intentionally across several regions around the world as potential food source and have escaped to become one of the top 100 invasive species of aquatic ecosystems. Known for their voracious appetite, these snails pose a significant threat to economically important crops such as rice and taro. Currently, these mollusc invasions are present in the US and rice bowl countries such as Taiwan, S.E. China, Japan, Malaysia, Vietnam and the Philippines. Currently, methods to control invasions include hand-picking, or the use of chemical molluscicides such as niclosamide and metaldehyde. However, since the molluscs prefer seedlings and young crop plants, protecting this stage of the crops is paramount since once the crop has grown sufficiently it is no longer susceptible to attack. Indeed, once the crop is in this phase of production the snails show beneficial properties by reducing competing broadleaf weeds and also fertilizing the crop. Therefore, the goal of this research is to identify natural products capable of “suppressing” the golden apple snails’ feeding long enough to allow the crop seedlings to mature to the unsusceptible crop phase. Once the suppression has ended, the snails can be used as a natural biocontrol system to remove competing weeds. Natural products harvested from 10 different fungal isolates were tested along with commercial products such as Tea Tree Oil (Stockton Inc.), Arcadia (not sure), Venerate (Maronne Bio Inc), and Grandevo (Marrone Bio Inc) to determine their efficacy in suppressing feeding in *P. maculata*.

Why Are There So Few Molluscs in the Polar Oceans?

J. Alistair Crame*¹

¹British Antarctic Survey

Marine molluscs have played a key role in defining some of the largest-scale patterns of life on Earth, with both bivalves and gastropods exhibiting latitudinal diversity gradients (LDGs) in shallow and deep seas. At first sight, it would seem obvious that temperature plays a defining role in the formation of these patterns, and a Metabolic Theory of Biodiversity, based on enzyme kinetics, may have widespread applicability. Equally, it is likely that the rapid transition of the Earth from greenhouse to icehouse states some 34 Myr ago played an important role in differentiating polar faunas. Nevertheless, we now know that modern LDGs extend back in time to the immediate aftermath of the K/Pg. Various bivalve and gastropod clades radiated extensively through the Early Cenozoic, but at a much faster net rate in the tropics than at the poles. It is also apparent that tropical – polar gradients in species richness may be matched with similar gradients in species evenness. Whereas polar molluscan faunas tend to be dominated by one or a small number of taxa, their tropical counterparts show much more even distributions. Dominant molluscan taxa in modern polar assemblages are ecological generalists with particularly broad trophic niches; this is a phenomenon linked to the marked seasonality of primary production at the base of the marine food chain. Prolific Middle Eocene gastropod faunas from Antarctica also show this pattern of strong dominance, long before the Earth cooled. The phenomenon of seasonality may equal that of temperature in defining polar molluscan assemblages.

Subcritical Forces Fatigue and Fracture California Mussel Shells

R.L. Crane*¹ and M.W. Denny¹

¹Hopkins Marine Station of Stanford University

Bivalve shells provide protection from a variety of potentially lethal predatory and environmental threats, ranging in frequency and magnitude from a single powerful predator strike to repeated insults from waves and tightly-packed neighbors. Shells' effectiveness at defending from such forces is traditionally quantified with a simple test of strength in which a shell is compressed until it breaks. However, this technique cannot test the alternative possibility that low magnitude, repeated stresses can break a shell through the process of mechanical fatigue. I explored the threat of fatigue by quantifying and contextualizing the strength and fatigue resistance of the California mussel (*Mytilus californianus*). I repeated the classic strength test by applying an increasing compressive force until fracture. Additionally, I used two distinct tests of fatigue resistance, applying a subcritical load either constantly or cyclically until fracture. Both fatigue tests considered a broad range of subcritical forces to mimic the forces mussels experience in the field. Shells fatigued and broke under both loading conditions - lower forces required more cycles or longer loading periods before fracture. Within ecologically relevant timescales, California mussels would not break under the low forces of jostling neighbors and moderate waves. However, certain predators and environmental threats like impacts from large waves could ultimately generate lethal damage. The potential threat of fatigue raises the question of whether animals can sense and repair accumulating damage. These findings highlight how a range of sublethal threats might underlie variation in shell morphology and microstructure, and provide inspiration for future considerations of the evolution of shell form.

A Congruent Topology for Deep Gastropod Relationships

Tauana Junqueira Cunha*¹ and Gonzalo Giribet¹

¹Harvard University

Phylogenetic efforts to resolve gastropod relationships have historically generated numerous conflicting hypotheses. Here, we use phylogenomics to address deep relationships between the five major gastropod lineages—Caenogastropoda, Heterobranchia, Neritimorpha, Patellogastropoda and Vetigastropoda—and provide one congruent and well-supported topology. We substantially expand taxon sampling for outgroups and for previously underrepresented gastropod lineages, presenting new transcriptomes for neritimorphs and patellogastropods. We conduct analyses under maximum-likelihood, Bayesian inference and a coalescent-based approach, accounting for the most pervasive sources of systematic errors in large datasets: compositional heterogeneity, site heterogeneity, heterotachy, variation in evolutionary rates among genes, matrix completeness, outgroup choice and gene tree conflict. We find that vetigastropods and patellogastropods are sister taxa, and that neritimorphs are the sister group to caenogastropods and heterobranchs. We name these two major unranked clades respectively Psilogastropoda and Angiogastropoda, based on features of their reproductive strategies and early life history. We additionally provide the first genomic-scale data for internal relationships of neritimorphs and patellogastropods. Our results highlight the need for reinterpreting the evolution of morphological and developmental characters in gastropods, especially for inferring their ancestral states.

The Complete Mitochondrial Genome of the Endemic Philippine Land Snail *Ryssota otaheitana* Ferrusac, 1821 (Pulmonata: Chronidae)

Amor M. Damatac II*¹ and Ian Kendrick C. Fontanilla¹

¹Institute of Biology, University of the Philippines Diliman, Quezon City, Philippines

Whole mitochondrial genomes have been increasingly used as markers for phylogenetic inferences. In the Philippines, a marine snail of the Conidae family has been the only species to date whose mitochondrial genome has been fully sequenced despite the country's rich malacofaunal diversity particularly in the terrestrial environment. In this study, we sequenced the complete mitochondrial genome of the land snail *Ryssota otaheitana* (Chronidae), a Philippine endemic pulmonate species. The genome is 13,888 bp in length and encodes the typical 37 genes, including 13 protein-coding, 22 tRNA and 2 rRNA genes. Short intergenic spacers were found, including a reduced 44 bp putative control region. Although the gene content is conserved, *R. otaheitana* showed a novel genome organization involving a change in the relative position of tRNA^{Serine} and NADH dehydrogenase subunit 4 gene segment. Combined with available stylommatophoran mitochondrial genomes, different sets from concatenated sequences of protein-coding and rRNA genes were used for phylogenetic reconstruction. Bayesian Inference and Maximum Likelihood trees congruently supported the monophyly of the Stylommatophora. *R. otaheitana* is grouped with *Deroceras reticulatum* at the base of the group and supposedly forms a monophyletic "limacoid clade". This is consistent with previous studies in which their corresponding families are both members of the informal group based on other morphological and molecular datasets. This study reports the first complete mitochondrial genome from the Chronidae family, which can be used for the classification of Philippine snails and molluscs in general.

The Colour Polymorphism of the Snail *Cepaea nemoralis* ss Indiscrete

Angus Davison*¹, Hannah J. Jackson¹, Ellis W. Murphy¹, Tom Reader¹

¹School of Life Sciences, University Park, University of Nottingham NG7 2RD, UK.

One explanation for the exuberant shell colour polymorphism of the land snail *Cepaea nemoralis* is negative frequency dependent selection, imposed by avian predators. To further understand the evolution of the polymorphism, we applied psychophysical models of avian vision to shell reflectance measures. Traditionally, the view is that the ground colour of the shell is one of a few major colour classes, either yellow, pink or brown. The reality is that sometimes difficult to distinguish the colours. We found that both achromatic and chromatic variation are wholly indiscrete in *Cepaea nemoralis*, being continuously distributed over many perceptual units. Nonetheless, clustering analysis based on the density of the distribution did reveal three groups, roughly corresponding to human-perceived yellow, pink and brown shells. The findings thus have significance for understanding the evolution of the *Cepaea* colour polymorphism, and the nature of the selection that acts upon it, as well as more generally highlighting the need to measure colour objectively in other systems.

***Phasmarhabditis* spp and Invasive Gastropods in the Us: Where Are We in the Battle?**

Irma Tandingan De Ley*¹, Rory Mc Donnell², and Timothy Paine³

¹Department of Nematology, University of California Riverside, California, 92521 USA

²Department of Crop and Soil Science, Oregon State University, Corvallis, OR 97331, USA

³Department of Entomology, University of California Riverside, California, 92521 USA

The nematode *Phasmarhabditis* was found associated with earthworms (New York and Illinois) almost 30 years ago, and around the same time, intensive studies in the UK demonstrated the biocontrol potential of *P. hermaphrodita* from Bristol, leading to its commercialization as a biopesticide (Nemaslug[®]) to manage slugs in horticulture, agriculture and home gardens in Europe. Despite its success, and in spite of the recent discovery of multiple slug-killing *Phasmarhabditis* species in California and Oregon, as well as the increasing market demand for safer control strategies, the product is yet to be introduced in the US. However, its discovery in California sparked renewed research interests in the US and elsewhere, with more new species and records in Europe, Australasia and Asia. A series of laboratory assays demonstrated that *P. hermaphrodita* US isolate is lethal to a number of invasive gastropod pests including giant African land snail (*Lissachatina fulica*), but not to non-target species like banana slug (*Ariolimax californicus*) and four earthworm species (*Amyntas gracilis*, *Eisenia fetida*, *Eisenia hortensis* and *Lumbricus terrestris*). Comparative efficacy of these three *Phasmarhabditis* species together with promising bacterial associates will be determined not only on established pest gastropods but also on emerging ones. Additional information on geographic distribution, nature of parasitism and host range will undoubtedly be critical for this nematode to be used in a multi-faceted approach to mitigate invasive gastropods.

The Complete Mitochondrial Genome of the Pygmy Octopus "*Octopus*" *fitchi* (Cephalopoda: Octopodidae) From the Gulf of California, Mexico Reveals Its Phylogenetic Position Within Octopoda

Ericka Magallón-Gayón¹, Irene A. Barriga-Sosa¹, and Miguel A. Del Río-Portilla*¹

¹Departamento de Hidrobiología, Universidad Autónoma Metropolitana-Iztapalapa. San Rafael Atlixco #186. Leyes de Reforma, Mexico City, Mexico. 09340

"*Octopus*" *fitchi* (Berry, 1953) is the smallest octopus occurring in the coasts of the Panamic province, inhabiting shallow waters (0-20 m) from the Gulf of California, Mexico to Ecuador. Total genomic DNA was obtained and purified from an arm tissue sample, and sequenced by next-generation sequencing. In this study, we report the complete mitochondrial genome sequence of this pigmy octopus species and its phylogenetic relationships with other members of the family Octopodidae. The mitogenome of "*O*". *fitchi* was 15,780 base pairs (bp) in length and a A + T composition bias (75.8%) was detected, as it has been observed in other octopod species. This genome contains 13 protein-coding genes, 22 tRNA genes, and two rRNA genes, as well as a control region. Gene order is maintained as reported for other species of the genus *Octopus*. The results of the phylogenetic analysis and the overall genetic distances reveals that "*O*". *fitchi* does not belong within the *Octopus* genus, nor within other groups as *Cistopus* or *Amphioctopus*, but it suggests that in fact, this species might represent a different genus.

Presence of *Argonauta hians* in Mexican waters?

Miguel A. del Río Portilla*¹, Carmen E. Vargas-Peralta¹, and Carmen Alejo Plata²

¹Departamento de Acuicultura, CICESE

²Instituto de Recursos, Universidad del Mar

Argonauts are small holoepipelagic octopuses, known as “paper nautilus”. They belong to the family Argonautidae, which has a single genus and four species. *Argonauta argo* is a tropical-subtropical cosmopolitan species with a circumglobal distribution in both hemispheres. *Argonauta nodosa* is found in the Southern Hemisphere. *Argonauta hians* also inhabits tropical-subtropical waters, but it is considered absent from eastern Pacific Ocean. *Argonauta nouryi* is a species restricted to the equatorial eastern Pacific Ocean. However, some argonauts have been found in commercial artisanal in Oaxaca, Mexico, which do not correspond to the *A. nouryi* description. Thus, morphological and genetic analysis were used to determine the species of those argonauts. A total of 49 whole and undigested female argonauts were extracted from the stomach contents of five species of large predatory fishes obtained from commercial artisanal catches at different localities along the coast of Oaxaca from January 2016 to June 2018. Total DNA was extracted from arms of three organisms. A pair of primers (16SAR and 16SBR) was used to amplified a 551 bp fragment and comparison with the nucleotide database to determine species. According to the morphological analysis 29 specimens correspond to *A. hians* females (6.2-41.1 mm ML) and 20 to *A. nouryi* females (13.9-50.8 mm ML). Data from the molecular analysis will be presented to corroborate morphological findings.

Redefining *Pila scutata*: A Pathway for Improving the Conservation of a Disappearing Species

K. L. DeLeon*¹, E. E. Strong², and K. A. Hayes¹

¹Bernice Pauahi Bishop Museum, 1525 Bernice Street, Honolulu, Hawai'i 96817

²Smithsonian Institution, National Museum of Natural History, P.O. 37012, MRC 163, Washington, D.C. 20013

Ampullariidae are freshwater snails and basal members of the Caenogastropoda, the largest, and most diverse group of primarily marine snails. While several members of the ampullariid genus *Pomacea* have spread far outside their native range and become major agricultural and environmental pests, some species of the Old World genus *Pila* are thought to have suffered substantial range contractions and population extirpation. Unfortunately, taxonomic confusion and the scarcity of verified biogeographic data make evaluating claims of such reductions difficult. Populations of *Pila scutata*, formerly *Pila conica*, reportedly have substantially decreased in size and number within its native range on the Malay Peninsula due to habitat destruction and possibly direct competition with the invasive ampullariids, *Pomacea canaliculata* and *Pomacea maculata*. Conservation assessments hinge on accurate and updated taxonomy, but confusion over the identity and distribution of *P. scutata* continues to hamper a deeper understanding of its conservation status and relationship to congeners. To begin to alleviate this confusion, we are undertaking a comprehensive re-description of *P. scutata*, including data on conchology, internal anatomy, and a multi-locus phylogenetic analysis. Preliminary genetic data corroborate previous work showing the distinctiveness of *P. scutata* and low genetic diversity across populations in Asia and in Hawaii. Information from reproductive, excretory, nervous and alimentary system anatomy provides distinctive characteristics that may be informative for differentiating it from closely related congeners. Interpreting these data within a broader phylogenetic framework with other *Pila* spp. will provide clear insights into the evolution, biogeography, and conservation of this species.

So What is *Mitrella* Anyway?

Marta J. deMaintenon¹

¹University of Hawaii at Hilo

The neogastropod family Columbellidae is a diverse group of relatively small epibenthic marine snails distributed in temperate to tropical waters worldwide. They are often abundant nearshore, and so are frequently encountered by researchers and collectors. Due to their small size, high diversity and variable morphology however, they are not well known and are often difficult to identify. Consequently, of the roughly 840 nominal living columbellid species, about 25% of them, mostly poorly known taxa, are placed in the genus *Mitrella*. *Mitrella* Risso, 1826 is currently recognized for having a simple, unsculptured biconic shell. Recent molecular phylogenetic analysis of columbellid gastropods was carried out to assess the monophyly and relationships of Columbellidae and some of its constituent genera. Results of these analyses support the monophyly of Columbellidae and of several of the included genera, but *Mitrella* is polyphyletic, suggesting that this simple shell morphology has evolved convergently in several unrelated clades. The objective of this study is to investigate morphological character sets in clades containing nominal *Mitrella* species, including the type species *Mitrella scripta* Linnaeus from the Mediterranean, to assess what characters *Mitrella* actually has and what might be useful to discriminate similar species in other taxa.

3d Printed Traps, Detector Dogs and Bees as Tools For Invasive Snail Detection in Florida

Katrina L. Dickens*¹, Ariane McCorquodale¹

¹Florida Department of Agriculture and Consumer Services, Division of Plant Industry

Mollusks, particularly terrestrial gastropods, are commonly overlooked when surveying for and controlling invasive species. Unlike many insect pests, there is no lure or mass capture trap to help survey for new mollusk infestations. Instead, novel approaches must be utilized to monitor and manage invasive mollusks. The Florida Department of Agriculture and Consumer Services, Division of Plant Industry has been using 3D printing technology to design traps for the giant African land snail, *Lissachatina fulica* (Bowdich, 1822), a pest throughout the worldwide tropics. Traps or trap components are designed using computer software and printed using a 3D printer by depositing successive layers of heated plastic until the object is created. With 3D printing technology, objects are completely customizable and can be designed, produced, and quickly redesigned according to observed snail behavior. To test trap efficacy, laboratory trials were conducted in 56 x 59 x 61 cm mesh cages containing 20 snails and baited with a combination of carrots, snails, and hydrated cat food. The most successful prototype thus far has trapped an average of 71% of snails. Prototype development continues in the effort to improve trapping rates. A second giant African land snail survey tool is a team of detector dogs trained to conduct field survey for snails. Beginning this year, 2019, the program is also collaborating with chemists and an apiary to research the use of bees to detect snails. These tools can be used to ensure the full eradication of the giant African land snail from Florida, as well as to survey for new invasive mollusks.

Dirty Dorid Disaster: An Analysis of the Biodiversity of Discodorididae Nudibranchs

Samantha A. Donohoo^{*1,2} and Terrence M. Gosliner¹

¹California Academy of Sciences, Department of Invertebrate Zoology and Geology

²San Francisco State University, Department of Biology

Due to increases in ocean temperature, the overall biodiversity of coral reefs will continue to change, and key predators such as nudibranch sea slugs may be decimated by the lack of prey. One sponge-eating nudibranch family nicknamed the “Dirty Dorids”, also known as the Discodorididae, are generally small cryptic nudibranchs with retractable gills, and are found in almost every marine ecosystem around the world. The diversity and systematics of the Discodorididae is not well understood due to the high number of diverse species and genera, few curated specimens maintained in ethanol, and major confusion on the evolution of several basal genera. My goal is to determine the diversity and evolutionary history of Discodorididae by utilizing specimens representing around 50+ genera of previously known and unknown species. Using sanger sequencing, I will generate a molecular phylogeny of the cytochrome oxidase I (COI) and 16s mitochondrial genes and 18S, 28S, and histone 3 (H3) nuclear genes, which will then be supported with morphological features used for identification. Within Discodorididae, we expect to find two major subgroups: one composed of genera with extra sensory outgrowths known as caryophyllidia and a second group of genera without caryophyllidia. We anticipate that caryophyllidia evolved later in the evolutionary history of the family because they are only found within the Discodorididae.

New Species of *Uncancylus* Pilsbry, 1913 (Gastropoda: Hygrophila: Planoboidea: Ancyliinae) from South America

Sonia Barbosa dos Santos*¹, Ximena Maria Constanza Ovando¹, Luiz Eduardo Macedo de Lacerda¹, and Dayse Aparecida da Silva ²

¹Universidade do Estado do Rio de Janeiro, Departamento de Zoologia

²Universidade do Estado do Rio de Janeiro, Departamento de Ecologia

Uncancylus Pilsbry, 1913 is a Neotropical freshwater limpet snail, recognized by the protoconch with acute apex like a hook, flexed to the right, well-marked radial lines all over the shell and the presence of periostracal hairs arranged on the teleoconch surface. It includes four species: *Uncancylus concentricus* (d'Orbigny, 1835), widely distributed in South America; *U. crequi* (Bavay, 1904) from Bolivia, Chile and Peru; *U. foncki* (Philippi, 1866) and *U. patagonicus* (Biese, 1948) from South Chile, and one "variety" *U. concentricus bonariensis* established by Strobel (1874) to Argentina, based on shell size and absent of radial sculpture on anterior side. Some authors did not consider *U. concentricus bonariensis* as a valid subspecies; it would be only a result of intra specific variability of *U. concentricus*. Our objective was to clarify that question, by integrated morphological and molecular studies. Morphological studies focused on shell, radula and muscle system. Molecular analysis was based on a dataset consisted of a 660 bp COI matrix. Neighbor-Joining as well as Maximum Likelihood analyzes, using MEGA 7.0.26 software showed the same topology with high support values. These studies allowed us to raise *U. concentricus bonariensis* to the species level discriminating *U. concentricus* from *U. bonariensis* and pointed out a new species of *Uncancylus* to Southwest Brazil. Thus, we increase the number of known *Uncancylus* species from four to six. This result points to new perspectives for a better understanding of the phylogeny and biogeography of Ancyliinae in South America.

Grants: CNPq, Capes

Are All Happy Families Alike? Trajectories of Phylogenetic, Functional, and Morphological Diversity in Marine Bivalve Lineages Following the End-Cretaceous Extinction

Stewart M. Edie*¹, Katie S. Collins¹, David Jablonski¹

¹The University of Chicago; Department of the Geophysical Sciences

Mass extinction events cause extreme crashes in taxonomic and morphologic diversity. Unrelated and morphologically dissimilar clades can suffer similar bottlenecks, but recovery patterns can differ strongly. The Late Cretaceous-to-Recent fossil record of the marine Bivalvia provides an ideal case-study of a major extinction and its impact on long-term diversity dynamics. Using a taxonomically standardized database of marine bivalve genera from the latest Cretaceous to the Recent, we estimated the end-Cretaceous (K/Pg) event removed ~65% of marine bivalve genera. Extinction severity within families was proportional to pre-extinction standing richness, but had limited family-level phylogenetic signal. The taxonomic recoveries of families, however, are not predicted by the size of their respective bottlenecks, and recovery trajectories are also not phylogenetically partitioned—a mixture of families in each major branch of the bivalve tree crash, remain steady, or increase in genus diversity to today. For example, the Veneroidea suffered 76% genus-level extinction but rebounded to become the most diverse bivalve clade today (~130 genera, ~750 species), whereas their sister group, Arcticoidea, lost 67% of its genera but only 6 genera and 13 species exist today. Bottlenecks and recovery dynamics appear to be inversely related for feeding modes that are unrelated to phylogeny. Suspension-feeders experienced much tighter bottlenecks than chemosymbiotics, carnivores, and deposit-feeders, but rebounded with more vigor to become the dominant feeding group today. Comparison of victims and survivors of the K/Pg event along both phylogenetic and functional axes furthers our insight into the evolutionary and ecological consequences of post-extinction recovery.

Looks can be Deceiving: Galápagos Endemic Species of *Chiton* are Sisters, not Different Clades

Douglas J. Eernisse*¹ and Margarita Brandt^{2,3}

¹Department of Biological Science, California State University Fullerton

²Colegio de Ciencias Biológicas y Ambientales, Universidad San Francisco de Quito, Ecuador

³Galápagos Science Center, Ecuador

The authors of separate recent monographs of Chitoninae (Polyplacophora) each used valve characters to assign two impressively large-bodied species of *Chiton* Linnaeus, 1758, both endemic to Galápagos shores, to different New World species groupings. Their classifications had little else in common. In his 1988 monograph, Bullock assigned the first Galápagos species, the heavily-sculpted *Chiton sulcatus* Wood, 1815, to *Chiton* s.s. along with its Caribbean type species, *C. tuberculatus* Linnaeus, 1758, plus two Eastern Pacific species. He placed the smooth-valved Galápagos species, *Chiton goodallii* Broderip, 1832, in subgenus *Diochiton* Thiele, 1893, with its Eastern Pacific type species, *C. (D.) albolineatus* Broderip & Sowerby, 1829, and also including the Caribbean *C. (D.) squamosus* Linnaeus, 1764 and *C. (D.) marquesanus* Pilsbry, 1893, endemic to the French Polynesian Marquesas Islands. In 2006, Kaas, Van Belle, and Strack mostly followed Van Belle's 1983 classification in grouping both *C. sulcatus* and *C. goodallii* into subgenus *Radsia* Gray, 1847, with its Chilean type species, *C. (R.) barnesii*. Bullock had also recognized *Radsia* but elevated to full genus and including only a South African species besides the type species. Our own DNA-based analysis, based on new material from the Galápagos (MB) and ongoing analysis of the family (DE), supports neither conflicting view. Instead, the Galápagos species are resolved as sister species, nested within a group of three tropical Eastern Pacific species, and even closer to the Polynesian, *C. marquesanus*. The phylogenetic position of *C. marquesanus* implies a long-distance rafting event from the Galápagos to the Marquesas Islands, representing an exception to the New World distribution of *Chiton*.

Toward a Fully Resolved Phylogeny of the Neogastropoda: A Phylogenomic Approach Helps Dissecting Backbone Relationships

Alexander E. Fedosov¹, Paul Zaharias², Mark Phuong³, Delphine Gey⁴, Maria Vittoria Modica⁵,
Mandë Holford⁶, Yuri I. Kantor¹, Marco Oliverio⁷, Philippe Bouchet², Nicolas Puillandre²

¹ A.N. Severtzov Institute of Ecology and Evolution, Russian Academy of Sciences, Leninski prospect 33, 119071 Moscow, Russian Federation.

² Institut Systématique Evolution Biodiversité (ISYEB), Muséum National d'Histoire Naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, 57 rue Cuvier, CP 26, 75005 Paris, France.

³ Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA 90095, USA.

⁴ Acquisition et Analyses de Données pour l'histoire naturelle (2AD) UMS 2700, Muséum National d'Histoire Naturelle, Paris, France.

⁵ Stazione Zoologica Anton Dohrn, Naples, Italy.

⁶ Department of Chemistry, Hunter College Belfer Research Center, New York, NY 10021, USA.

⁷ Dept. Biology and Biotechnologies "Charles Darwin". Zoology, Viale dell'Università 32, I-00185 Roma, Italy.

The largest order of marine Mollusca, the Neogastropoda, encompasses over 15,000 described living species that occur from pole to pole and from intertidal zone to abyssal trenches. Seven currently recognized main lineages of the Neogastropoda have originated almost simultaneously in late Cretaceous, which poses a significant challenge to the recovery of a resolved backbone phylogeny. Previous attempts were hampered by limited taxonomic sampling and insufficient amount of nucleotide data, leaving deep relationships of the group unresolved. Here, we report preliminary results of a phylogenomic analysis of the Neogastropoda based on an unprecedented dataset, comprising over 1,700 exons and spanning all recognized main lineages. We recovered a phylogenetic tree that shows an almost fully resolved Neogastropoda backbone. The core Neogastropoda forms a fully supported group that includes all currently recognized superfamilies, but excludes the cancellariids. Tonnoidea + Ficidae form a sister group, and the nematoglossan lineages branch off before the divergence of Tonnoidea + Ficidae and core Neogastropoda. The presented phylogenetic tree suggests the contents of Neogastropoda need to be revised to account for these and other newly demonstrated affinities, some never proposed in the past. In particular, notable rearrangements in the neogastropod classification are necessary to resolve emerging para- and/or polyphyly in the traditional families Cancellariidae, Fascioliidae, Nassariidae and Buccinidae. This new phylogenetic framework allows reevaluation of the evolution of anatomical features that underpin uniquely diversified feeding strategies of the neogastropods, thus shedding light on the routes that have led to the evolutionary success of these predators.

A Phylogenetic Analysis of the Superfamily Acteonoidea (Gastropoda:Heterobranchia)

Kendall Feliciano*¹ and Ángel Valdés¹

¹Department of Biological Sciences, California State Polytechnic University of California, Pomona

Acteonoidea is a superfamily of shelled sea slugs that includes the families Acteonidae and Aplustridae. Bullinidae is another potential family in this group with unclear status, currently being included within Aplustridae. Within each family, the relationships between genera are largely unknown. Members of Acteonoidea are distributed worldwide. This clade has been historically classified as a member of Cephalaspidea due to the presence of a headshield. However, recent molecular analyses have reclassified Acteonoidea into an unofficial group termed Lower Heterobranchia. Although members of Acteonoidea have been traditionally classified based on morphological features, recent studies have indicated that these characters may be homoplastic. The goal of this analysis is to reconcile molecular and morphological data and determine the relationships among members of Acteonoidea. This study will create a molecular phylogeny based on a number of specimens from localities around the globe using two mitochondrial genes (16S and CO1) and one nuclear gene (H3).

Cryptic Coral Connoisseurs: Exploring the Hidden Diversity of Corallivorous Nudibranchs

Allison L. Fritts-Penniman*¹, Paul H. Barber², and Terrence M. Gosliner¹

¹California Academy of Sciences

²University of California Los Angeles

While geographic speciation processes have historically dominated the literature, there is growing interest in ecological speciation, where reproductive isolation evolves as a result of divergent natural selection. Ecological speciation may be an important source of biodiversity on coral reefs, where sister taxa often share ranges with little evidence for divergence via vicariance. A common driver of ecological speciation is host shifting, where species that are adapted to live and feed on a specific host evolve a preference for a novel host, resulting in isolation and diversification. Host shifting has been suggested as a key mechanism for speciation in corallivorous nudibranchs. In this study we integrate ecological, morphological, geographic, and genomic data to evaluate the evolutionary history of corallivorous nudibranchs with respect to their coral hosts. We custom-designed a new targeted bait set to capture 2,018 ultraconserved elements and exons, which can be broadly applied across all heterobranchs. We successfully sequenced 1,951 of the targeted loci and constructed new phylogenetic trees for the coral-feeding *Tenellia* and *Phyllodesmium*. We will present these new, robust trees, along with comparative analyses of the relative roles of hard and soft coral in generating Aeolid biodiversity. We find that the number of coral-feeding nudibranch species, and the number of ecological niches potentially available to nudibranchs, is much higher than previously thought.

Integrative Approach to the Systematics of the Genus *Dondice* Marcus, 1958 (Heterobranchia: Nudibranchia) From the Western Atlantic

Kimberly García-Méndez*¹ and Ángel Valdés*¹

¹Department of Biological Sciences, California State Polytechnic University, Pomona, California, USA

Dondice Marcus, 1958 is a small genus of facelinids nudibranchs that includes four valid species occurring in the Atlantic Ocean, the Mediterranean Sea and the Pacific coast of Mexico. *Dondice occidentalis* (Engel, 1925) and *Dondice parquerensis* Brandon & Cutress, 1985 are sympatric along the Western Atlantic, inhabiting coral reefs and shallow mangroves areas. Historically, the systematics of these species has been based mainly on external morphology, resulting in taxonomic uncertainty. Previous phylogenetic analysis did not find reciprocal monophyly between *D. occidentalis* and *D. parquerensis*, questioning the validity of these species and suggesting the possibility of them being a species complex. Molecular and morphological data from newly collected specimens, and review of literature and type material indicated that *Dondice* from the Western Atlantic contains so far nine different species. In addition, *D. occidentalis* is a species complex of eight genetically distinct taxa. Our results suggested highly genetic differentiation between *Dondice* populations analyzed. Furthermore, anatomical and morphological examinations revealed that coloration is one of the main diagnostic characters for all species. *Dondice parquerensis* from the Caribbean was confirmed as a valid species, whereas the name *Dondice occidentalis* was redescribed and retained for Jamaica populations. The remaining seven new species were distributed across the Tropical Western Atlantic, four were restricted to Florida, one was identified from Bahamas, another from Panama, and the remaining from Brazil. This study evidences how the use of a single approach to delimit species has led to an underestimation of diversity in heterobranchs, and emphasizes the necessity for integrating different lines of evidence in species delimitation studies.

First Restocking Attempt of the Striped Venus (*Chamelea gallina*) Off Portimão (Southern Portugal)

Miguel B. Gaspar*¹, Sandra Joaquim², Ana M. Matias², Cláudia Roque², Paulo Vasconcelos¹, Fábio Pereira¹, Paula Moura¹, Marta Rufino³, and Domitília Matias²

¹Portuguese Institute for the Sea and Atmosphere, Research Centre of Olhão

²Portuguese Institute for the Sea and Atmosphere, Research Centre of Tavira

³Marine and Environmental Sciences Centre, University of Lisbon

The striped venus (*Chamelea gallina*) is an infaunal bivalve species that occurs in the infralittoral zone and supports an important artisanal dredge fishery along southern Portugal. Recently, intensive harvesting coupled with recruitment failure has resulted in large inter-annual fluctuations in stock abundance, threatening the biological and the economic sustainability of this fishery. The implementation of management strategies such as stock-enhancement programmes based on hatchery production of juveniles could promote the rebuilding of bivalve beds. The present study describes the biology (growth and reproductive cycle) and distribution of *C. gallina*. This species shows a high growth rate and short lifespan, a prolonged spawning period (between April and August), matures within its second year of life and occurs preferentially on sandy bottoms between 5 and 11m depth. Overall, this information was used to collect the wild broodstock and to establish the time of the year to assess the potential of *C. gallina* for hatchery production. Several spawning techniques were tested (thermal stimulation, scarification and flow through), and growth and survival of larvae and juveniles were compared by using different nutritional regimes (larvae: *Isochrysis aff. galbana* (T-iso), *Chaetoceros calcitrans* (C. cal) and unfed; juveniles: T-iso + C. cal, T-iso and C. cal) and rearing temperatures (larvae: 20 and 23°C). Based on the results obtained, a production protocol for this species was designed, which allowed the production of millions of juveniles that were used to perform the first restocking attempt with this species, in an area off Portimão (southern Portugal).

Are We There Yet? The Impact of NGS in Molluscan Phylogenetics

Gonzalo Giribet*¹, Tauana Cunha¹, Vanessa L. González², Vanessa L. Knutson¹, Sarah Lemer³,
and Juan Moles¹

¹Museum of Comparative Zoology, Harvard University 26 Oxford St., Cambridge, MA 02138

²Global Genome Initiative, Smithsonian National Museum of Natural History

³University of Guam Marine Laboratory

Molluscan phylogeny—both their position in the animal tree of life, and the interrelationships among the molluscan classes—has been a matter of heated debate for decades, or even centuries. However, major progress in DNA sequencing technologies has allowed us to tackle many of these questions with large data sets, both in terms of loci and taxa. These have, for example, resolved the reciprocal monophyly of Aculifera and Conchifera, have resolved the deep interrelationships of large clades, such as Gastropoda, Bivalvia and Cephalopoda, and NGS techniques are now being applied to many major molluscan subclades, especially within gastropods and bivalves. As we enter a new era in sequencing technologies, we would like to discuss current progress and future areas of inquiry to resolve further questions in molluscan phylogenetics. Examples of recent resolution and future inquiry are drawn from ongoing research in our laboratories, as well as from emerging technologies in genome sequencing, and in utilization of museum specimens previously considered unusable for genomics.

Empirical Test of Crab-clam Predator-prey Model Predictions: Storm-Driven Phase Shift to a Low-density Steady State

Cassandra N. Glaspie*¹, Rochelle D. Seitz², Romuald N. Lipcius³

¹Louisiana State University, Department of Oceanography and Coastal Sciences

²Virginia Institute of Marine Science, College of William and Mary, Department of Biological Sciences

³Virginia Institute of Marine Science, College of William and Mary, Department of Fisheries Science

A dynamic systems approach can predict steady states in predator-prey interactions, but there are very few empirical tests of predictions from predator-prey models. Here, we examine the empirical evidence for the low-density steady state predicted by a Lotka-Volterra model of a crab-clam predator-prey system using data from long-term monitoring, a field survey, and a field experiment. We show that Tropical Storm Agnes in 1972 likely resulted in a phase shift to a low-density state for the soft-shell clam *Mya arenaria*, which was once a biomass dominant in Chesapeake Bay. This storm altered predator-prey dynamics between *M. arenaria* and the blue crab *Callinectes sapidus*, shifting from a system controlled from the bottom-up by prey resources, to a system controlled from the top-down by predation pressure on bivalves. Predator-prey models with these two species alone were capable of reproducing observations of clam densities and mortality rates, consistent with the idea that *C. sapidus* are a major driver of *M. arenaria* population dynamics. Over 40 y post-storm, *M. arenaria* densities hover near a low-density steady state predicted from the predator-prey model. Predation rates observed in the field were similar to modeled mortality rates. Predator-prey models can be used to predict dynamics of natural populations, including phase shifts and densities at steady states. The preponderance of multispecies interactions exhibiting nonlinear dynamics indicates that this may be a general phenomenon.

Do Emergent Technologies (10x Genomics, Pacbio, and Hi-c) Help Molluscan Genome Reconstruction?: Assembling a Reference-quality Genome For *Solemya velum* (Bivalvia: Protobranchia)

Vanessa L. González*¹, Shelbi L. Russell², Rebecca B. Dikow³, Gonzalo Giribet⁴, and Ellen Strong⁵

¹Global Genome Initiative, Smithsonian Institution, National Museum of Natural History, 10th and Constitution Ave NW, Washington DC 20560, USA

²Department of Molecular Cellular and Developmental Biology, University of California Santa Cruz, Santa Cruz, CA, USA

³Data Science Lab, Office of the Chief Information Officer, Smithsonian Institution, Washington, DC 20008 USA

⁴Department of Invertebrate Zoology, Smithsonian Institution, National Museum of Natural History, 10th and Constitution Ave NW, Washington DC 20560, USA

⁵Museum of Comparative Zoology, Department of Organismic and Evolutionary Biology, Harvard University, 26 Oxford Street, Cambridge, MA 02138, USA.

In order to facilitate *Solemya velum* (Bivalvia: Protobranchia) as an emerging model system to study symbiosis and adaptation, we generated a reference-quality genome. We tested emergent technologies for molluscan genome assembly by leveraging 10X Genomics, PacBio Long-reads (Sequel), and Hi-C (Phase Genomics) data. *Solemya velum* is a member of the subclass Protobranchia, one of the poorest known molluscan groups. Protobranchia has diversified and colonized the deepest oceans, with numerous cosmopolitan species at abyssal depths. Of the ca. 750 protobranch species, most are deposit feeders in soft sediments, but two lineages host chemoautotrophic, sulfide-oxidizing bacteria, with concomitant reductions of the hosts' alimentary system, including *Solemya velum*. Previous research has characterized and sequenced the symbiotic bacterial genomes associated and identified in *Solemya velum* (Russell et al. 2017) but genomic resources are still lacking for their host. Iterations and combinations of each data type have resulted in a 2.4GB reference genome with a contig N50 of 210 KB, scaffold N50 of 215 MB and a BUSCO completeness score of 93%. This first reference-quality Protobranch genome will enable us to test hypotheses about mollusc genome evolution and the evolution of symbiotic interactions in marine molluscs.

Utility of Molluscan Collections in Answering Ecological Questions and Climate Change

Terrence M. Gosliner*¹, Kelly Larkin¹ and Vanessa Knutson²

¹Department of Invertebrate Zoology and Geology, California Academy of Sciences, 55 Music Concourse Drive, San Francisco, CA 94118, USA

²Museum of Comparative Zoology, Harvard University

Scientific collections have been utilized primarily for systematic studies, but have also a wide range of utility in answering fundamental questions in comparative biology, medical sciences, and a wide array of other applications. In studying tropic specialization, museum collections provide additional opportunities to examine predator/prey interactions. Traditionally, stomach contents of specimens in museum collections have been utilized to identify potential prey of species of interest and examples of this methodology are illustrated with the heterobranchs with the Polyceridae and Arminidae. With the advent of molecular techniques and barcoding genes we have also been able to expand our knowledge of trophic relationships by sequencing stomach contents. This has even resulted in the discovery of novel taxa. Museum specimens also provide a window into historical distributions of species and permit us to ascertain when range expansions have begun to expand as a response to climate phenomena such as El Niño events and longer-term distributional shifts in response to climate change. Museum collections also provide clues to examining sympatry and allopatry of cryptic and pseudocryptic species. Historical collections provide critical baseline data for detecting natural and anthropogenic change and are critical to understanding of historical distributional changes.

Evolution of Yoyo Clams: Within-Host Ecological Shifts Lead to Dramatic Morphological Changes

Ryutaro Goto*¹, Teal A. Harrison², and Diarmaid Ó Foighil²

¹Seto Marine Biological Laboratory, Field Science Education and Research Center, Kyoto University

²Department of Ecology and Evolutionary Biology and Museum of Zoology, University of Michigan

Colonization of a novel host (host shift) and subsequent adaptation has been well recognized as a main driver of morphological diversification in symbiotic and parasitic organisms. However, how within-host ecological shifts affect their morphological evolution remains not well investigated. The Vasconiellinae (Galeommatidae) (usually called “yoyo clams”) are a clade of tiny bivalves commensal with burrowing mantis shrimp hosts. In the sand flats of eastern Florida, six vasconielline species, including five *Divariscintilla* species and one *Parabornia* species, sympatrically share a single stomatopod host: *Lysiosquilla scabricauda*. The two genera occupy distinct microhabitats within the host burrow: *Divariscintilla* species attach to the burrow wall using a highly specialized hanging foot structure, whereas *Parabornia squillina* is an ectocommensal that directly attaches to the host body surface. In this study, we performed molecular phylogenetic analyses of Vasconiellinae based on two nuclear and three mitochondrial genes to test for evidence of within-host speciation events. Our analyses identified two such events, one involving a cryptic sister *Divariscintilla* species pair that retained the ancestral burrow wall microhabitat and exhibited very modest levels of morphological differentiation. In contrast, the other within-host sister species pair, *D. octotentaculata* and *P. squillina*, have distinct morphologies and microhabitats. Our data imply that the ectocommensal *P. squillina* evolved from a burrow-wall-commensal ancestor and that, associated with this within-host ecological shift, it underwent reductive loss of many distinctive *Divariscintilla* morphological characteristics (e.g., hanging foot structure, highly-developed tentacles, and internalized shells). Our results indicate that within-host speciation can lead to pronounced morphological change if it involves a shift in microhabitat, even on very small spatial scales.

Investigating Species Diversity and Endemism in Hawaiian Microsnails (Stylommatophora: Achatinellidae: Pacificellinae)

Tricia C. Goulding*¹, Norine W. Yeung¹, and Kenneth A. Hayes¹

¹Bernice P. Bishop Museum, Malacology Center, 1525 Bernice St., Honolulu, Hawaii, 96817, USA

Hawaiian land snails are exceptionally diverse but highly threatened by habitat loss, introduced species, and climate change. The diversity of these land snails is rapidly declining, and their taxonomy needs to be revised to inform conservation efforts. There are thirteen nomenclaturally valid specific and subspecific names for the Pacificellinae in Hawaii. In order to evaluate species diversity with modern phylogenetic methods, 130 specimens were sequenced for COI, and representatives were selected for additional sequencing (16S, ITS2, 28S, and H3). Phylogenetic analyses show that the monophyly of *Lamellidea* Pilsbry, 1910 and *Pacificella* Odhner, 1922 is well-supported, and indicates that there are at least ten Pacificellinae taxa in Hawaii. Pairwise genetic distances between COI sequences of two ecologically and morphologically distinct species, *Lamellidea oblonga* (Hawaii) and *Lamellidea micropleura* (Moorea) are approximately 4.8%, while genetic distances between Hawaiian taxa are between 3.2% and 6.6%. Unlike many Hawaiian land snails that are endemic to a single island, many *Lamellidea* species are found on multiple islands. Two species of Pacificellinae are shown to be broadly distributed in the Pacific, one of which appears to be a modern introduction to Hawaii. *Lamellidea oblonga* is more closely related to species in the South Pacific than to those in Hawaii, consistent with the hypothesis that *L. oblonga* represents a second colonization. Due to the geographic isolation of Hawaii, it has been expected that colonization of the islands by land snails was rare, yet this phylogenetic data shows that the Pacificellinae in Hawaii are the result of at least four successful colonizations and one recent introduction.

Unravelling the Rainbow – Attempts to Understand the Evolution of Shell Colour in Molluscs

Heather E. Grant*¹, Heather E. Grant², and Jessica Wade³

¹Natural History Museum, Department of Life Sciences

²University of Edinburgh, Institute of Evolutionary Biology

³Imperial College London & Centre for Plastic Electronics, Blackett Laboratory

Understanding how new biological colours originate and why they are maintained is fundamental to our understanding of evolutionary ecology and developmental biology, but despite over a century of interest, this question has never been fully addressed. In this talk I will discuss the results of studies that begin to tackle this failing from a number of different angles. Of particular interest is the observation based on analyses of >44,000 lots of bivalves in the NHMUK collection, supplemented with literature searches, that shell colour is distributed in a phylogenetically significant manner. Although similar colours can arise from different pigments or from structural elements, the broad scale phylogenetic distribution of colour in Bivalvia, along with the co-occurrence of ‘sets’ of colours, likely reflects in part the distribution of classes of pigments. This confirms the idea that the major classes of pigments found in molluscan shells are evolutionarily ancient and continue to contribute to shell colouration, despite recent genomic evidence that suggests that protein moieties associated with pigments may be evolutionarily diverse. However, preliminary Raman spectroscopy studies confirm that green bivalve shell pigments are markedly dissimilar to the most common shell pigments, which are otherwise capable of producing a rainbow of colours. Finally, mapping colour and pattern onto a phylogenetic framework for deep-sea gastropods shows that colour is lost in deep-sea clades as might be expected if the production and/or incorporation of pigments into shell is energetically costly.

Slugs, Slugs, and More Slugs: New Aeolid Nudibranch Species from Western North America

Brenna Green*¹ and Terrence M Gosliner¹

¹Department of Invertebrate Zoology and Geology, California Academy of Sciences

Molecular analysis of nudibranchs from the temperate northeastern Pacific historically assigned to the family Flabellinidae has revealed a more complex taxonomic picture than previously recognized. Our molecular studies using the COI, 16s, and H3 markers, combined with morphological study, have uncovered multiple new species from the west coast of North America within Flabellinidae sensu lato. Many of these new species form north-south sister pairs with overlapping ranges, following a pattern found in several other recent studies of cryptic diversity among northeastern Pacific mollusks.

Evolution, Revolution, or Neither? Uses of Digitized Molluscan Specimen Records

Robert Guralnick*¹

¹Department of Natural History and the Department of Natural History, University of Florida, Dickinson Hall, Gainesville, FL 32611

Museum collections digitization has accelerated dramatically in the last two decades, catalyzed by national and international investments and with the goal of enabling new research outcomes and societal benefits. Here I will provide an overview based on a bibliometrics analysis of how digitized collections data are being used in research activities, with a focus on molluscan cases. In particular, I will examine the trends in published research uses of molluscan digitized data in comparison to other metazoan groups, growth of data papers, and trends in data citation. I also provide comparisons of collections digitization rates based on data available in GBIF and iDigBio and touch on some complexities with publishing systems and full use of molluscan collections in particular. Next, I compare growth trajectories in digitization of molluscan collections data with growth of molluscan data resources developing in the arena of citizen science, and the potential and challenge with integrating data resources towards being able to better map and monitor molluscan diversity trends. Finally, I discuss new opportunities for large-scale imaging, auto-extraction of trait data, and trait-based cyberinfrastructure to support a new generation of research on ecometrics of shell shape. An overall assessment is that molluscan digitization is primed for a revolution if the right approaches, funding mechanisms, and collective efforts of the community coalesce. This revolution is much needed given current state, especially in comparison to overall remarkable gains made in the larger collections community in terms of novel, enabled research around collections digitization.

Molluscan Fauna in Bhutan

Choki Gyeltshen*¹, Edmund Gittenberger², Pema Leda¹, Sangay Dema¹

¹National Biodiversity Centre, Ministry of Agriculture and Forests, Serbithang, Thimphu, PO. Box.875, Bhutan, +975-2-351417

²Naturalis Biodiversity Centre, Postbus 9517, 2300 RA Leiden Bezoekadres: Vondellaan 55, Leiden, +31-0-622555670

The molluscan fauna of Bhutan probably consists of ca. 200 species. Endemism is expected to be high, but cannot be judged in detail because the adjoining areas, like Arunachal Pradesh, India, are insufficiently known. A characteristic, Palaearctic, terrestrial malacofauna is known from western Bhutan, above 2000 m a.s.l. The limited data on aquatic molluscs also support the distinction between the northern, Palaearctic and the southern, Indo-Malayan parts of the country. Additionally, there are striking differences between the various main valleys. Some species that are not known from Nepal occur both in Bhutan and south of the Brahmaputra River in parts of India. Apparently, this river cannot be considered to be an important biogeographical boundary. Several genera are represented from Bhutan southeastwards, sometimes as far as Vietnam and Indonesia. Preliminary checklist of molluscs in Bhutan will be represented.

Dynamic colorful skin and colorblind camouflage by cephalopods

Roger T. Hanlon*¹

¹Marine Biological Laboratory

Rapid neural polyphenism is a unique feature of cephalopods that sets them apart from other molluscs. The so-called “chromatophore system” is a complex collection of pigmentary and structural coloration elements that can produce a wide diversity of patterns, colors and contrasts for both signaling and camouflage. Recent research has unraveled some unexpected mechanisms of how chromatophore organs and iridophore cells are controlled and how they interact to manipulate available light for visual diversity. For example, iridescence (structural coloration) has been discovered in chromatophore organs (previously thought to be solely pigmentary) indicating more complex light interactions than previously realized. Opsin molecules – identical to those in the retina - have been found in the skin and, in octopus, patches of skin express chromatophore colors when shone with light, suggesting that the opsins are light-sensitive and perhaps influencing color patterns peripherally with little or no central brain control. Cuttlefish control their camouflage patterning visually and many experiments in the past decade have revealed the mechanisms of how they achieve this in a fraction of a second. All experiments and analyses thus far support the prospect that cephalopods are color blind. But many of their predators have color vision, and it appears (to human vision) that their camouflage is color coordinated to their surrounds. We are measuring this with RGB cameras as well as hyper-spectral imagers to determine whether cephalopod camouflage patterns are color coordinated to background colors in the color space of different predators.

Phylogenomic Analyses Confirm a Novel Invasive North American *Corbicula* (Bivalvia: Cyrenidae) Lineage

Amanda E. Haponski*¹ and Diarmaid O' Foighil¹

¹University of Michigan, Department of Ecology and Evolutionary Biology and Museum of Zoology

The genus *Corbicula* consists of estuarine or freshwater clams native to temperate/tropical regions of Asia, Africa, and Australia that collectively encompass both sexual species and clonal (androgenetic) lineages. The latter have become globally invasive in freshwater systems and represent some of the most successful aquatic invasive lineages. In the New World, three invasive clonal morphotypes have been recognized—Forms A and B in North and South America, and C (South America). A putative fourth North American invasive morph, Form D, was recently described in the Great Lakes watershed, where it occurs in sympatry with Forms A and B. An initial study showed Form D to be conchologically distinct, however, its genetic distinctiveness using standard molecular markers was ambiguous. To resolve this issue, we analyzed 1,699-30,027 nuclear genomic loci and confirmed Form D to be a distinct invasive New World lineage with a population genomic profile consistent with clonality. A majority of the phylogenomic analyses recovered the New World invasive Forms A, B, C, and D as members of a clonal clade, sister to the non-clonal Lake Biwa (Japan) endemic, *C. sandai*. The age of the clonal clade was estimated at 1.49 million years (my) whereas estimated ages of the four invasive lineage crown clades ranged from 0.27-0.44 my. We recovered no evidence of nuclear genomic admixture among the four invasive lineages in our study populations. In contrast, 2/6 *C. sandai* individuals displayed partial nuclear genomic assignments with multiple invasive clonal lineages. These results provide new insights into the origin and maintenance of clonality in this complex system.

Conservation Genomics of the Partulidae

Amanda E. Haponski*¹, Cindy Bick¹, Taehwan Lee¹, and Diarmaid Ó Foighil¹

¹University of Michigan, Department of Ecology and Evolutionary Biology and Museum of Zoology, Ann Arbor, MI 48109

Partulid tree snails are endemic to the Pacific high islands and represent one of the most infamous examples of oceanic island mass extinctions. Although they collectively range across ~10,000 km of Oceania, half of their species diversity is endemic to a single Eastern Pacific hot spot archipelago, the Society Islands. Using a combination of museum, captive, and remnant wild snails, we obtained the first high-resolution nuclear genomic perspective of the evolutionary relationships of all five genera comprising 43 of the 104 recognized species, including many extinct or extirpated taxa, from 14 archipelagoes. We present range wide phylogenomic relationships among the five genera and a more detailed perspective of the evolutionary relationships within the genus *Partula*, highlighting the survival and extinction of endemic Society Island *Partula* from the well-studied islands of Moorea and Tahiti.

Gain and Losses of the Operculum in Gastropod Evolution

Gerhard Haszprunar*^{1, 2}

¹SNSB-Zoologische Staatssammlung München, Münchhausenstrasse 21, D-81247 München, Germany.

²Department Biology II and GeoBio-Center, Ludwig-Maximilians-University of Munich, Germany

In order to infer evolutionary origin and loss of the operculum in the gastropod life-cycle literature data were browsed and analyzed. Evolutionary gain of the operculum, which is a genuine gastropod novelty, is probably directly correlated with torsion suggesting benefit for the larval phase rather than for adult conditions. Loss of the operculum in postlarval gastropods has happened multiple times in evolution, mostly due to large modifications (limpets, slit-like apertures; tube-like shell) or reduction of the shell. Notable exceptions are helicoid shells of (in part) terrestrial Neritimorpha, and of Hygrophila and Eupulmonata. In particular the pulmonate groups remain enigmatic in this respect, since in particular stylommatophoran groups with secondary closure structures (e.g. Clausiliidae) are very successful subclades. Loss of operculum in planktonic larvae is restricted to very few clades (caenogastropod Lamellarioidea, opisthobranch Pteropoda), all with highly deviated conditions of larval shells. Whereas all planktonic larvae of remaining clades (with regular protoconchs) show an operculum, direct or intracapsular developers often have lost it. These correlations suggest that a larval operculum has been and still is essential for planktonic larvae throughout gastropod evolution.

Biocontrol of Land Snails: Unlearned Lessons and Non-Target Impacts

Kenneth A. Hayes*¹, Carl C. Christensen², Norine W. Yeung²

¹Bernice Pauahi Bishop Museum, Pacific Center for Molecular Biodiversity

²Bernice Pauahi Bishop Museum, Malacology

The use of non-host specific agents for the biological control of land snail pests has a long and disastrous history. This is most strikingly exemplified with the purposeful introduction of predatory land snails (e.g. *Euglandina* and *Gonaxis spp.*) and other agents (e.g. *Platydemus manokwari*) to control the Giant African Snail, *Lissachatina fulica*, in its non-native ranges in Hawaii and other islands throughout the tropics and subtropics in the Pacific, Indian and Atlantic Ocean. More than sixty years ago, Mead and other malacologists warned of the hazards of applying practices developed in the field of insect biological control, where biocontrol agents may be highly host-specific, to the use of generalist predators or parasites against nonmarine molluscan pests. Unfortunately, many of the lessons that should have been learned from these failed biocontrol programs have not been widely learned or applied to contemporary efforts, and initiatives to develop non-host specific control agents continue without careful evaluation of the potentially innumerable non-target impacts. Here we briefly review the failures of past biocontrol efforts of nonmarine snail pests and the impacts that continue to reverberate across ecosystems and highlight recent control initiatives that illustrate a clear failure to learn from the past. In doing so, we hope to emphasize the need to do better if biocontrol efforts are to be effective and do no harm to the one of the most threatened faunas in the world. We also review claims of successful biocontrol of terrestrial molluscs and offer suggestions for how the safety and true effectiveness of such initiatives may be evaluated.

Poisonous Eggs From *Pomacea* snails Have Evolved a Defensive Protein that Damage Cell Membranes with a pore-forming Toxin Delivered by a Lectin

M.L. Giglio¹, S. Ituarte¹, V. Milesi², E. Prieto³, MS Dreon¹, S. Mate¹, J. Ip⁴, J-W. Qiu⁴, and H. Heras*¹

¹Instituto de Investigaciones Bioquímicas de La Plata “Prof. Dr. Rodolfo R. Brenner”, INIBIOLP. CONICET - Universidad Nacional de La Plata

²Instituto de Estudios Inmunológicos y Fisiopatológicos, IIFP. CONICET- UNLP

³Instituto de Investigaciones Físicoquímicas Teóricas y Aplicadas, INIFTA. CONICET – UNLP –

⁴Hong Kong Baptist University, Hong Kong, China

Poisonous eggs from *Pomacea* snails have evolved a defensive protein that damage cell membranes with a pore-forming toxin delivered by a lectin We found that the eggs from the invasive freshwater snail *Pomacea* maculata have evolved a defensive strategy against predation involving a neurotoxin, PmPV2. PmPV2 is a dimeric pore-forming toxin which combines two immune proteins: a lectin and a membrane attack complex/perforin (MACPF) module. The aim of this study was to investigate PmPV2 interaction with membranes using enterocytes as a model of the first cells that the toxin would encounter when ingested by a predator. The toxin withstands digestive proteases in vitro and can attach to mice enterocyte glycocalyx in vivo, suggesting it reaches the intestinal tract in an active form. At the cellular level, PmPV2 specifically interacts with membrane cholesterol (MACPF) and its lectin module interacts with glycoproteins. It has affinity to negatively charged glycans as revealed by a glycan array and hemagglutination assays. Though Atomic Force Microscopy we observed that PmPV2 inserts into phospholipid/cholesterol lipid bilayers and oligomerizes into pore-like structures. Additionally, PmPV2 binds to the plasma membrane of intestinal Caco-2 cells recognizing specific glycoproteins, alters their surface morphology and eventually leads to cell death. Intestinal cells exposed to the toxin changed their membrane permeability in patch-clamp experiments in a fashion compatible with the formation of ~14nm pores. This effect is inhibited by aminated monosaccharides, highlighting the importance of the lectin module. The study provides the first evidence to our knowledge of the molecular mechanism of pore formation for an animal defensive toxin containing a MACPF/CDC domain.

The Gulick effect: How Malacological Collecting, Observation, and a Prepared Mind Changed Evolutionary Theory

Carole S. Hickman*¹

¹University of California, Berkeley, Department of Integrative Biology

John Thomas Gulick's research on land snails in Hawaii was both innovative and influential in the late nineteenth and early twentieth century development of modern evolutionary theory. Although there is a recent revival of interest in and appreciation of Gulick as a theorist, there is little commensurate effort to understand his considerable academic preparation in science and the recognition he received during his lifetime. It is easy to dismiss the Rev. Gulick as a missionary whose paid vocation was not science. Likewise, it is difficult to devote the requisite attention to his scholarly precise writing, wordsmithing, and attention to detail in a modern age that is quick to dismiss such writing as verbose. Perhaps the strongest objections to Gulick have arisen from the shifting baseline in museum collection philosophy in the Anthropocene age of human-caused extinction. This baseline effect is most acutely felt on oceanic islands and in the small, geographically isolated populations and environments in which he collected. The breakthroughs of avocational science are overdue for celebration. They are of increasing public interest as historians popularize lives of the "hidden figures" of women, the contributions of outstandingly well-educated clergy and missionaries, and the achievements of high school dropouts. Where does Gulick fit in this picture? His formally prepared mind (academic training in biology and graduate degree from Williams College) exceeded that of Charles Darwin. So did his publication record in what are today prestigious journals with high impact factors. And his achievements in evolutionary biology were recognized late in his life by receipt of two honorary doctoral degrees.

Population Genetics of European Populations of the Shining Ramshorn Snail, *Segmentina nitida* - Or Are They?

C.S. Hobbs*^{1,2}, R. Vega¹, D.A. Dawson², G.J. Horsburgh², C.D. Harvey¹

¹Ecology Research Group, Section of Life Sciences, Canterbury Christ Church University

²NERC Biomolecular Analysis Facility, Department of Animal and Plant Sciences, University of Sheffield

The Shining Ramshorn Snail, *Segmentina nitida*, a rare freshwater snail found predominantly in drainage ditches and marshland, has seen a marked decrease in population (~80%) over the last 100 years in the UK. This has mainly been attributed to over-dredging of drainage ditches as part of land management, land conversion from grazing to arable farmland, as well as eutrophication caused by run-off of fertiliser from agricultural land. *Segmentina nitida* is a priority species for the UK Biodiversity Action Plan, with further research recommended in the plan to inform reintroduction and translocation for the conservation of *S. nitida*. This paper will present population genetics analyses of microsatellite, nuclear (ITS2) and mitochondrial (COI) markers for *S. nitida* individuals from Poland, Germany, Sweden, and the UK, to identify genetic patterns and differences within and between populations. Two distinct genetic lineages of *Segmentina nitida* were identified, one present in eastern Europe (Poland, Sweden), and one in western Europe (UK, Germany), with both lineages present in Germany. No genetic admixture was observed in German populations containing both lineages. Inferences as to these patterns are explored, focusing on the existence of a potential separate species or sub-species, *Segmentina clessini*. These findings have implications for the conservation of *S. nitida* in the UK and beyond, especially in relation to potential translocation and reintroduction plans. This work is part of a larger PhD project looking at various aspects of *S. nitida* including 2D geometric morphometrics, breeding, and improved sampling for *S. nitida*.

Trans-Atlantic Rafting – American Bivalves on British Shores

Anna M. Holmes*¹

¹Department of Natural Sciences, National Museum Wales

Trans-Atlantic rafting – American bivalves on British shores The Gulf Stream allows the British Isles to sit on the same latitude as Newfoundland (Canada) and Moscow (Russia) but keeps our average land and sea temperatures at least 6 degrees warmer. However, this warm current brings with it an abundance of debris including anthropogenic waste in the form of plastics which, especially during high winds, are thrown onto land. Violent storms pounded the shores of the UK and Ireland in 2013-2014 resulting in a record amount of anthropogenic waste to be churned up and cast ashore. Bait pots, fishing spools, buoys and other items were discovered on beaches in western Ireland and southwestern England. Attached to these 'rafts' were numerous invertebrate species that were later identified as originating from the southeast coast of the United States. The majority of molluscs were byssally attached bivalves that are able to hang on to objects and hence make excellent rafters. Since this initial onslaught further new records of west Atlantic bivalves attached to buckets, ropes and buoys have continued most with natural ranges of Caribbean through to North Carolina. These rafting species of bivalve have not yet been recorded as reproducing here – it is likely that in our relatively chilly British waters they are unable to do so. However, recent accounts indicate rising sea temperatures in parts of Britain, particularly in the southwest where the majority of the non-natives have been discovered. Are these rafting species potential invasives?

Clash of the Chitons: How Morphology, DNA, and Distribution Differ in Three *Nuttallina* Species

Newton Z. Hood*¹ and Douglas J. Eernisse¹

¹Department of Biological Science, California State University Fullerton

The chiton genus *Nuttallina* (Mollusca: Polyplacophora: Lepidochitonidae) is extremely common along the California coast, but while WoRMS and some earlier authorities have recognized only *Nuttallina californica* (Reeve, 1847) as valid in California, newer evidence has confirmed that three species are present with only subtle morphological distinctions and substantial genetic divergence. Differences in their geographic and microhabitat distributions have been poorly understood, but *N. californica* was known to dominate north of Point Conception, whereas *N. fluxa* (Carpenter, 1864) is dominant in southern California, extending south to the Pacific coast of Baja California Sur, Mexico. However, we have found that *N. californica* can occasionally be common at cool exposed sites south of Point Conception, and a third species, *N. sp. A*, is known from few localities in both southern and central California. We tested for differences in the morphology, microhabitat, or latitudinal distribution of each of the three species of *Nuttallina*. We sampled *Nuttallina* from central and southern California, and subsampled both high and low microhabitats at selected localities. Randomly selected individuals were identified with a PCR-based DNA assay, taking advantage of known sequence differences and using species-specific 16S and COI primers. Morphology was compared with a morphometric analysis of the fifth of eight disarticulated valves and comparisons of the girdle and gills. Our general conclusion is that the species can be surprisingly patchy, reflecting environmental differences in habitat. These *Nuttallina* species provide a useful system for investigating competitive interactions and range shifts between these ecologically important intertidal grazers.

Signatures of Divergence, Invasiveness and Terrestrialization Revealed by Four Apple Snail Genomes

Jack C.H. Ip*¹ and Jian-Wen Qiu¹

¹Department of Biology, Hong Kong Baptist University

The family Ampullariidae includes both aquatic and amphibious apple snails. They are an emerging model for evolutionary studies due to the high diversity, ancient history and wide geographical distribution. Insight into drivers of ampullariid evolution is hampered, however, by the lack of genomic resources. Here we report the genomes of four ampullariids spanning the Old World (*Lanistes nyassanus*) and New World (*Pomacea canaliculata*, *Pomacea maculata* and *Marisa cornuarietis*) clades. The ampullariid genomes have conserved ancient bilateral karyotype features and a novel Hox gene cluster rearrangement, making them valuable in comparative genomic studies. They have expanded gene families related to environmental sensing and cellulose digestion, which may have facilitated some ampullarids to become notorious invasive pests. In the amphibious *Pomacea*, novel acquisition of an egg neurotoxin and a protein for making the calcareous eggshell may have been key adaptations enabling their transition from underwater to terrestrial egg deposition.

The Evolution and Diversification of Eyes in Strombid Gastropods

Alison Irwin*¹, Ellen Strong², Nicholas Roberts³, Elizabeth Harper⁴, and Suzanne Williams¹

¹Department of Life Sciences, London Natural History Museum

²Department of Invertebrate Zoology, Smithsonian Institution's National Museum of Natural History

³School of Biological Sciences, University of Bristol

⁴Department of Earth Sciences, University of Cambridge

Strombidae is a family of charismatic marine snails with many bizarre and beautiful shell morphologies. The family can be recognised by the presence of a 'stromboid notch' – a fluting of the outer lip that allows the second of its two long eyestalks to peer out from under the shell. These large camera eyes are thought to provide surprisingly good visual acuity, second only in Mollusca to the predatory Cephalopoda and Pterotracheoidea, which use vision for prey pursuit. It is extraordinary that such sophisticated eyes are found within the slow-moving, herbivorous strombids. These complex eyes likely contributed to the success of the lineage, yet vary enormously in size and structure across the family Strombidae and more so within the superfamily Stromboidea. However, the diversity and evolution of strombid eyes have not yet been investigated. This project will address this lack by integrating morphological, molecular and behavioural approaches within a phylogenetic framework. We will use mitogenomics and Sanger sequencing to recover a robust phylogenetic history of the family Strombidae, and test for monophyly of Stromboidea, key families and genera. We will then investigate the evolution of camera-type eyes by building a database of morphological traits from key taxa, obtained by computed tomography and histological methods, and map these traits onto the phylogeny. This approach will show how morphology of eye components varies across families in Stromboidea, and within Strombidae. Our data will enhance the current understanding of strombid visual capabilities, giving a new perspective on how strombids see their surroundings, and add to our knowledge of the evolution of vision in Mollusca.

Biodiversity Hotspots and the Dynamics of Diversity Gradients: Marine Bivalves in Time and Space

David Jablonski*¹, Stewart M. Edie¹, Katie S. Collins¹, Kaustuv Roy², and James W. Valentine³

¹Department of Geophysical Sciences, University of Chicago

²Section of Ecology, Behavior & Evolution, Division of Biological Sciences, University of California San Diego

³Department of Integrative Biology, University of California, Berkeley

The rich fossil record of marine bivalves provides an evolutionary and biogeographic laboratory for analyzing the origin and maintenance of diversity patterns in time and space. Like many marine groups, modern shelf-depth bivalves show a strong latitudinal diversity gradient, with a dramatic increase in species richness, ecological variety, and morphological disparity from poles to equator, and a distinct longitudinal structure of diversity hotspots. Defining hotspots by taxonomic richness (number of co-occurring species or higher taxa), they lie in the tropics with the West Pacific “Coral Triangle” towering above all other regions; if defined as concentrations of narrow geographic range sizes (see Igea & Tanentzap 2019 for birds and mammals), hotspots shift to the eastern boundaries of tropical seas (which are confined on the north by equatorward-flowing ocean currents and on the south by cold upwelling waters), and to the south-temperate regions: New Zealand, southeast Australia, southern South America, South Africa – a striking contrast to mammals and birds, where hotspot types mostly coincide. The late Cenozoic fossil record shows that the latitudinal gradient is underlain by an Out-of-the-Tropics dynamic, with genera tending to originate in the tropics and expanding to higher latitudes; global analyses of geologic ages of genera suggest that this dynamic operates in all tropical richness-hotspots. Narrow-range hotspots in the temperate zone are composed of significantly older genera than are tropical faunas, suggesting extratropical range-hotspots are mainly diversity accumulators or sinks (albeit with some local origination). Combining modern and fossil data gives a richer picture of the dynamics underlying present-day biogeography

One or Two Black Species of *Cyerce*? Bergh's Footnotes and What Pease Did Not Mention

Kathe R. Jensen*¹

¹Natural History Museum of Denmark, Zoology section, Universitetsparken 15, DK-2100 Copenhagen Ø, Denmark

For many years *Cyerce nigra* Bergh, 1870 was considered a junior synonym of *C. nigricans* (Pease, 1866). However, consistent differences in color pattern, *C. nigra* having yellow stripes on one side of cerata and *C. nigricans* having spots on both sides, led to separation of the two species. Bergh (1871) described radular teeth and penis of *C. nigra* based on drawings by Semper, and Gascoigne's (1974) description of the penial stylet of *C. nigricans* seemed to be identical to this. Pease did not mention spots on both sides of cerata in his original description of *Lobifera nigricans*, and no anatomical information was included. My recent examination of *C. nigra* specimens from Western Australia showed that the penial stylet was completely different from that described by Bergh and Gascoigne. Re-examination of Bergh's description revealed a footnote in which he explains that the specimen from which Semper had drawn radula teeth and penis had a different color pattern, namely spots on both sides of cerata. Dissection of a specimen of *C. nigricans* from New Caledonia confirmed the straight penial stylet of this species. Morphological and anatomical descriptions of the two species, confirming that they are different species, will be presented, and this will be compared with other species of the genus.

Understanding Phylogenetic Relationships in Cladobranchia (Nudibranchia, Heterobranchia, Gastropoda) using NGS Data

Dario Karmeinski*¹, Jessica Goodheart², Tatiana Korshunova³, Alexander Martynov⁴,
Michael Schrödl⁵, Heike Wägele¹, and Alexander Donath¹

¹Zoological Research Museum Alexander Koenig, Bonn, Germany

²Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, USA

³Koltzov Institute of Developmental Biology, Moscow, Russia

⁴Zoological Museum of the Moscow State University, Moscow, Russia

⁵NSB-Bavarian State Collection of Zoology

The species-rich taxon Cladobranchia (Nudibranchia, Heterobranchia) currently comprises approximately 98 genera from 22 families of exclusively marine gastropods. Despite attempts to shed light on the evolution of the group, the phylogenetic position of most of its families is still subject to debate. While past efforts of gaining a better understanding of the relationships within Cladobranchia using barcoding gene approaches did not result in phylogenies with satisfactory resolution, the first phylogenies using transcriptomic multi-gene approaches only covered a limited number of species omitting many families with uncertain position. To overcome this problem, we sequenced the transcriptomes of 21 species of heterobranch sea slugs and combined our data with raw reads from 40 species of Heterobranchia available from public databases. In order to obtain a high number of genes suitable for phylogenetic analyses, we assembled the raw reads using six different transcriptome assembly tools. For each species, we identified the best assembly using a variety of descriptive parameters. We then searched the assemblies for orthologous genes that are presumed to be single-copy in molluscs and combined them in a phylogenetic supermatrix. Here we show our first results from the broadened dataset.

Phylogenetic Variability of Neural Circuitry in Nudipleura

Paul S. Katz*¹, Akira Sakurai², Arianna N. Tamvacakis², and Joshua L. Lillvis³

¹University of Massachusetts Amherst

²Georgia State University

³Janelia HHMI Research Campus

Swimming evolved independently several times among the Nudipleura (Nudibranchia and Pleurobranchomorphs). Neural circuit evolution appears to have involved the use and reuse of a core set of homologous contralaterally-projecting interneurons. However, the synaptic connectivity of these neurons and the genes that they express differs, leading to differences in the functions of homologous neurons. We found that independently-evolved dorsal-ventral flexion swimming in *Tritonia* and *Pleurobranchaea* involves convergence on the expression of orthologous serotonin receptors in a particular homologous interneuron. These receptors are not expressed in that neuron in *Hermisenda*, which does not produce the behavior despite the presence of orthologous receptors in its brain transcriptome. We also found that two species with homologous left-right flexion swimming behaviors, *Dendronotus* and *Melibe* have homologous neurons in their swim circuits but that these neurons exhibit different synaptic connectivity. Thus, the neural basis for the production of a homologous swimming behavior is different despite the use of homologous neurons. Together, these results show that the presence of identified neurons and their core properties of neurotransmitter phenotype, soma location, and axon morphology are more constrained than the properties that lead to the production of behavior such as neurotransmitter receptor expression. This can be used to predict which features of neurons are more likely to be conserved, which will vary, and which will have functional consequences.

Our New Understanding of Dead-Shell Assemblages: A Powerful Tool for Deciphering Human Impacts

Susan M. Kidwell*¹

¹University of Chicago, Department of Geophysical Sciences

Malacologists have always embraced both empty shells and live-collected individuals but remained skeptical of their reliability, given that some species occurring “dead-only” might be relicts of past conditions (e.g., lower sea level, wet periods) or transported out of their life habitats. Geological analysis of dead-shell assemblages – motivated initially by oil exploration and now by historical ecology – has yielded three important findings for malacology. (1) Post-mortem transport is usually minor, i.e. is small compared to spatial vagaries in larval settlement on inter-annual and -decadal scales (established via ‘live-dead’ comparisons in marine and, increasingly, terrestrial settings). Few dead shells are preserved in life position but their assemblages nonetheless capture the bathymetric, pollution, and other gradients that pattern source living communities. (2) Dead-shell assemblages acquired from marine benthic samples reflect remarkably prolonged time-averaged accumulation (~100 y in estuaries, multi-thousand y on shelves), but shells are heavily weighted toward recent cohorts (last few decades or 20th Century; ¹⁴C-calibrated age-dating of individual shells). (3) The combination of habitat-scale spatial fidelity and a skewed geologic-age structure yields both a bright snapshot of the species that dominated the recent-past and a ~complete historic register of occupation, including rare species. Bias is only against species with especially fragile and/or organic-rich shells (e.g., lyonsiids, pinnids): live-dead mismatch in species abundances signals a recent change in the living community, shifting it off its baseline, rather than poor preservation. Dead-shell assemblages are thus reliable guides to gradients in composition and diversity hot spots, and are an efficient means of detecting, retroactively, a wide array of human impacts.

The Evolution of Mollusks at Deep-sea Hydrothermal Vents and Methane Seeps

Steffen Kiel*¹

¹Swedish Museum of Natural History, Stockholm

Origin and evolution of the faunas inhabiting deep-sea hydrothermal vents and methane seeps have been debated for decades. The dominant animals in these ecosystems – including mollusks – derive their nutrition from symbiotic chemotrophic bacteria, which spawned the hypotheses that the evolutionary history of these faunas is independent from that of photosynthesis-based food chains. Two case studies using fossil mollusks are presented here to assess this hypothesis. (i) A molecular phylogeny of bathymodiolin mussels time-calibrated by fossils indicates that the group originated and acquired sulfur-oxidizing symbionts in the Late Cretaceous, long before its major radiation in the Middle Eocene. Novel types of symbioses (intracellular and methanotrophic symbionts) evolved only after this major radiation. Thus, contrary to expectations, the major radiation may have not been triggered by the evolution of novel types of symbioses. (ii) The fossil record shows that trends in body size, relative abundance, and epifaunal/infaunal ratios among mollusks track estimates of seawater sulfate concentrations through the last 150 million years. Furthermore, the two main faunal turnovers during this time interval coincide with major changes in sulfate concentrations. Because sulfide at seeps originates mostly from seawater sulfate, variations in sulfate concentrations should directly affect the base of the food chain of this ecosystem and are thus the likely driver of the observed macroecologic and evolutionary patterns. The results imply that the methane-seep fauna evolved largely independent from developments and mass extinctions affecting the photosynthesis-based biosphere.

Macro (and Micro!) Molluscs of the Kimberley Marine Region of Western Australia

Lisa Ann Kirkendale*¹, Zoe T. Richards^{1,2}, Andrew Hosie¹, Peter Middelfart¹

¹Western Australian Museum, Aquatic Zoology Department

²Curtin University, Trace and Environmental DNA Laboratory, School of Molecular and Life Sciences

The Kimberley marine region, which occurs within the Australian North West Shelf, is one of the least explored areas of Western Australia given its remote position in the far north as well as sheer size. A diversity of ecological features, such as vast gulfs, myriad islands and large embayments, provide a range of habitat for still little explored marine life. The Kimberley Woodside Collection Project was a multi-year field program focussed on assessing diversity and abundance across marine groups, and we highlight our findings on decapod crustaceans, reef building corals and of course, macromolluscs. Firstly we will examine the similarity of North West Shelf fauna to neighbouring areas, secondly we will consider the latitudinal attenuation in diversity and lastly we will examine inshore and offshore patterns of endemism. Micromolluscs were specifically targeted utilizing specialized sampling protocols in the final two years of the program. This fauna is challenging to collect, sort, image and study and is regularly overlooked in worldwide biodiversity assessments. The results from the Kimberley are impressive with 624 micromollusc species observed from 70 stations based on a total of 1884 identifications. This diversity represents 99 families or superfamilies, 21 of which were not recorded previously with 18 families doubling or more in the number of taxa recorded. This is the first step in characterizing the assets of a faunal component that is more diverse than many other well-known marine groups in the region, underpins food webs but without taxonomic study, remains outside the scope of traditional conservation initiatives.

Non-invasive Audio-video Sampling of Gastropod Activity

Christopher L. Kitting*¹

¹California State University East Bay Department of Biological Sciences

Non-invasive environmental monitoring can quantify animal activities while minimizing risks to environments, often among protected species and habitats. Faint sounds often are overlooked, but can monitor animal activity as individuals or whole assemblages. Video recording offers good (not best) audio capabilities, but audio tracks usually get abandoned (later simulated) for nature videos. In educating broad audiences, multiple senses reinforce human memory and understanding. However, labs usually have audible and electrical interference. Outdoors, wind, waves, other animals, and man-made sounds interfere with audio monitoring. An animal's motion, such as a shell's friction against another surface, also is very audible. But upon rather rare feeding, instructive feeding sounds (if above water) are barely audible with the unaided ear, stethoscope, or simple tubing. Proper remote microphones (above or below water) can monitor and record activity clearly. A video track can help identify sources of sounds. Kitting's historic audio recordings from tape are no worse than modern digital recordings. However, many analog to digital conversions lose much signal. New examples with common *Cornu* (*Helix*) garden snails are convenient practice, by starving a group of individuals, and offering them raw vegetables. Even starved individuals failed to feed frequently on their locally common habitat plant, *Agapanthus* ("Lily of the Nile"). Despite subtle motion of their head, feeding was audible and rhythmic for extended periods when undisturbed, even in light. Such natural micro soundscapes can uncover hidden behaviors, even in darkness or murky water, prevent disturbance to specimens and environments, and provide memorable, instructive evidence for broad audiences.

Modification of the Penial Twin Papillae System Within the Tribe *Otalini* (Stylommatophora, Helicidae)

Jeannette Kneubühler*^{1,2} and Eike Neubert^{1,2}

¹Department of Invertebrate Animals, Naturhistorisches Museum der Burgergemeinde Bern, Bernastrasse 15, CH-3005 Bern, Switzerland

²Institute of Ecology and Evolution, University of Bern, CH-3012 Bern, Switzerland

Phylogenetic relationships within the Helicinae are not yet fully understood. Currently, the subfamily is composed of the clades *Allognathini*, *Helicini*, *Otalini*, and *Thebini*. Although relationships in most clades are well understood, genetic and anatomical data are still lacking in *Otalini*. This study presents a more complete phylogenetic tree based on a larger taxon sampling than so far presented in previous studies. Investigation is based on genetic analysis and a comparative evaluation of anatomical traits of the genital organs. Within the clade *Otalini*, *Eremina* forms a basal lineage opposite to *Rossmuessleria*, *Cornu*, *Cantareus*, and *Ercella*, which form the second major clade. A third clade is formed by *Massylaea*, *Maurohelix*, *Alabastrina*, *Guilia*, *Siretia*, and *Otala*. The genus *Alabastrina* differs from all other known genera by bearing a penial appendix. *Guilia*, which clusters within the lineage *Alabastrina*, bears no such appendix and is thus considered to form a separate generic entity. Within the clade *Otalini*, some genera possess the twin penial papilla system, which is shared with *Allognathini*, *Thebini* and *Helicini*. For this reason, it has to be considered a plesiomorphic trait within the subfamily Helicinae. However, *Otalini* are also characterised by a reduction in functionality of the epiphallial papilla, i.e. the papilla becomes a solid cone, while the opening of the epiphallus into the penial chamber is deviated and consists of a simple pore. This character state can be observed in *Cantareus*, *Cornu*, *Ercella*, *Massylaea*, while in *Alabastrina*; and *Guilia*, the epiphallial papilla is almost completely lost, superficially resembling the anatomical details characteristic of the subfamily Murellinae and Ariantinae.

The More, the Merrier: Expanding Taxon Sampling to Address Heterobranch Phylogeny in a Phylogenomic Context

Vanessa L. Knutson*¹, Bastian Brenzinger², Yasunori Kano³, Michael Schrödl², Nerida Wilson⁴, and Gonzalo Giribet¹

¹Museum of Comparative Zoology, Harvard University

²NSB-Bavarian State Collection of Zoology

³Department of Marine Ecosystem Dynamics, Atmosphere and Ocean Research Institute, The University of Tokyo

⁴Molecular Systematics Unit and Aquatic Zoology, Western Australian Museum

The phylogeny of heterobranchs has been researched extensively, but has been problematic because of the independent or parallel evolution of many morphological features. While our knowledge of heterobranch phylogeny has improved markedly through the use of cladistic methods combined with the traditional Sanger sequencing of genetic markers, relationships remain largely unresolved at the generic and familial levels partly due to a lack of sufficient phylogenetic signal sampled from these traditional loci. Additionally, the placement of some major groups at higher levels of classification remains problematic. Recent studies have applied next-generation sequencing (NGS) technologies to data collection for phylogenomic analysis of molluscan, gastropod and heterobranch relationships, and these have shown promising results thus far. However, this approach has yet to be applied to Heterobranchia on a large scale, and due to limited taxon sampling, many heterobranch relationships remain untested or unresolved. Sampling across Heterobranchia, with a focus on marine heterobranchs, we have generated and assembled de novo more than 120 transcriptomes to use in combination with publicly available data for phylogenetic inference in this charismatic group. For the first time, we include transcriptomes of several “lower heterobranch” or unassigned lineages such as murchisonellids, omalogyrids, as well as meiofaunal taxa such as *Rhodope*, in a huge effort to test and resolve their positions in the heterobranch tree. Here we present our methods and preliminary results. Answering long-standing questions of phylogeny in Heterobranchia will better enable the study of the evolution of fascinating characters and behaviors including shell-loss, gill placement, kleptoplasty, and diet in this diverse and speciose clade of gastropods.

Revolutionizing Biodiversity and Systematics Research on Aplacophora (Mollusca) and Training the Next Generation of Malacologists

Kevin M. Kocot*^{1,2}

¹University of Alabama

²Alabama Museum of Natural History

Aplacophora is an ecologically important and phylogenetically significant clade of worm-shaped marine molluscs. Basic questions about aplacophoran biodiversity and evolution, such as the number of species, evolutionary relationships, and ancestral states of key characters remain unanswered. The number of aplacophoran taxonomists, which has always been small, has declined in recent years. Meanwhile, known but undescribed species and specimens collected in environmental surveys that remain unidentified continue to grow in number. Specimen identification often requires the labor-intensive process of histology, but newer technologies such as micro-CT scanning and DNA barcoding could significantly accelerate this process. I will present on a new project aimed at dramatically accelerating the pace of the study of aplacophoran biodiversity and systematics while training the next generation of malacologists. Specimen identification will employ a novel workflow combining stereo light microscopy, micro-CT, and SEM of whole specimens, DNA barcoding, and compound light microscopy of permanent sclerite mounts - all from the same animal. Goals of this project include identification of thousands of specimens, description of >50 new species, characterization of the faunas of particularly diverse and understudied regions, monographs for select taxa in need of revision, and production of a reference DNA barcode library. Further, the first aplacophoran genomes will be sequenced, enabling target-capture phylogenomics. A well-resolved and broadly sampled phylogenetic framework will make possible a revised classification that accurately reflects the group's evolutionary history as well as ancestral state reconstruction of key traits for Aplacophora, Aculifera, and Mollusca as a whole.

The Tyranny of Remoteness: Contemporary Chances and Challenges for Collection-Based Malacological Research Down Under

Frank Köhler*¹

¹Australian Museum Research Institute, Australian Museum, William St, Sydney, NSW 2010, Australia

Australia is among the ten most biodiverse countries on earth and is especially well known for its highly endemic terrestrial biota, which has evolved in splendid isolation since the late Mesozoic. It has also one of the longest coastlines in the world that, straddled by both the Indian and Pacific Ocean, stretches from the Tropics to the Antarctic and boasts an exceptionally rich marine life. Being comparatively sparsely populated, some of Australia's regions are among the most remote and pristine environments in the world, a circumstance that renders them both incredibly valuable for biodiversity conservation and highly susceptible to threats resulting from human activities. These unique settings create challenges and opportunities to building contemporary collections that meet the increasing demands of research in the 21st century in terms of new, rapidly developing technologies and the aggregation of large biodiversity datasets.

Land Snails (1) : Dinosaurs (0) – Phylogenomics Resolves Late Mesozoic Diversification of Helicoid Land Snails

Frank Köhler*¹, Makiri Sei², Gary Rosenberg³ and Adnan Moussalli⁴

¹Australian Museum Research Institute, Australian Museum, 1 William St, Sydney NSW 2010, Australia

²Smithsonian Institution, National Museum of Natural History, PO Box 37012, MRC 163, Washington, D.C. 20013–7012, USA

³Academy of Natural Sciences of Philadelphia, Drexel University, 1900 Benjamin Franklin Parkway, Philadelphia, PA 19103, USA

⁴Sciences Department, Museum Victoria, GPO Box 666E, Melbourne Vic 3001, Australia

Comprising approximately 4,700 extant species in 16 families, the superfamily Helicoidea has a nearly global distribution and considerable evolutionary antiquity. We have reconstructed a time-calibrated phylogeny using a dataset that included almost 175,000 base pairs from 477 nuclear protein-coding genes of 87 species representing all families but one. Our analysis resulted in a strongly supported phylogeny that sheds new light on the spatiotemporal patterns of helicoid diversification on a global scale. To recapitulate their extraordinary evolutionary journey takes us back into the mid Mesozoic, more than 66 million years ago... Together with their sister group Sagdoidea, Helicoidea are today well represented in Central America by several distinct lineages that have diverged from one another between the mid-Cretaceous and early Paleogene (about 100 to 50 million years ago). Our analyses demonstrate that these lineages have persisted in Central and/or western North America through the Cretaceous-Palaeogene mass extinction, which was triggered by the impact of a massive meteorite near the Yucatan Peninsula. By incorporating plate tectonic models, we have reconstructed potential biogeographic pathways of their global diversification since the K/Pg boundary testing previously suggested hypotheses of helicoid biogeography.

Crypsis and The Jack-of-All-Trades Hypothesis: Are Island or Mainland Snails Better at Camouflage?

Andrew C. Kraemer*¹ and Christine E. Parent²

¹Creighton University

²University of Idaho

Species frequently evolve coloration that matches their background in response to predation pressure (crypsis). Effective crypsis not only requires species to generally match the coloration of local backgrounds, they must do so from the perspective of local predators. Since different predator species often have distinct visual abilities, tradeoffs are thought to drive prey species to either evolve a high degree of crypsis from the perspective of the most dominant predator species or evolve a moderate degree of crypsis from the perspective of several predator species (the jack-of-all-trades hypothesis). Few studies have evaluated whether species tend to evolve specialized crypsis or utilize a 'jack-of-all-trades' approach to crypsis. We compare a group of closely related island and mainland snail species (genus *Naesiotus*) to test the hypothesis that complex predator communities (i.e. Ecuadorian and Peruvian mainland communities) lead to poorer crypsis and simple predator communities (i.e. communities from the Galápagos Archipelago) lead to greater crypsis.

Ecological Insight into the Origins of Photomutualism: How Sea Slugs Benefit from Kleptoplasty

Patrick J. Krug*¹, Andre LaBuda¹, and Holly V. Moeller²

¹California State University, Los Angeles

²University of California, Santa Barbara

Kleptoplasty, the retention of functional chloroplasts within heterotrophic cells, is a form of acquired metabolism that can provide insight into the origins of photosynthetic mutualisms and endosymbiosis. Among animals, only sacoglossan sea slugs maintain photosynthetically active chloroplasts. About half of sacoglossans digest plastids within hours; most remaining species are short-term retainers (STR) with ingested plastids functioning up to two weeks. In five independent origins of long-term retention (LTR), species maintain plastids for over a month. These transitions are a model for studying the evolution of mixotrophic metabolism but recent studies proposed that slugs only benefit from kleptoplasty during starvation, or that photosynthesis kills starving STR species. To explore the ecological context of kleptoplasty, we compared fitness, feeding rate and photosynthetic function over time for five STR and two LTR species with a fed/starved x light/dark design. Photosynthesis and feeding had additive or synergistic benefits for most species; effects varied by chloroplast source more than slug retention type. Growth was consistently highest in light x fed treatments and lowest in light x starved treatments. All species fed at lower rates in the light, yet grew more. These results counter prevailing hypotheses that kleptoplasty evolved as a buffer against starvation. Instead, our findings suggest shifts to partial autotrophy were favored because kleptoplasty maximizes growth while reducing the rate of feeding on chemically defended macroalgae, and reveal a crucial role of photosynthesis by sacoglossans under ecologically relevant conditions.

Arminid Ambiguity : Establishing Significant Genetic and Morphological Markers to Assess Diversity in the Nudibranch Family Arminidae

Kelly Larkin*^{1,2} and Terry Gosliner¹

¹California Academy of Sciences

²San Francisco State University

Arminidae is an underrepresented and understudied family of nudibranchs within Cladobranch research. Originally grouped together by a single shared characteristic of an oral veil, confusion over Arminid relationships has persisted over time. This evolutionarily interesting group of nudibranchs consists of one genus with lateral gills found globally, and a more derived gill-less genus restricted to the Indo-Pacific. Additionally, Arminids represent one of the few groups of specialist predators on octocorals, with the two main *Arminid* genera, *Dermatobranchus* and *Armina*, split between the two lower classifications of Octocorallia, Alcyonacea and Pennatulacea, respectively. My project illuminates issues with previous species descriptions and has doubled the known diversity of *Dermatobranchus*. I will present the current state of Arminid diversity using genetic phylogenies and atypical morphological features, with an assessment of their feeding ecologies and the future direction of mapping *Arminid* species divergence through time.

Exon Capture Resolves a Recent Radiation and Uncovers Mitonuclear Discordance in Nudibranchs

Kara K.S. Layton^{*1,2,3}, Jose I. Carvajal², and Nerida G. Wilson^{1,2}

¹University of Western Australia, School of Biological Sciences

²Western Australian Museum, Aquatic Zoology and Molecular Systematics Unit

³Memorial University of Newfoundland, Department of Ocean Sciences

Recent mitochondrial phylogenetic work on *Chromodoris*, a group of colourful and toxic nudibranchs in the Indo-Pacific, demonstrated poor resolution and short branch lengths that likely reflect a recent radiation. That study also provided the first evidence for mimicry in the genus. Sequence capture is an emerging approach in the field of systematics that has been shown to resolve phylogenies across moderate scales of divergence, although its efficacy has never been tested in recently radiated taxa with high levels of incomplete lineage sorting and introgression. This study presents data for 2,925 exons from 1,630 genes, derived from 15 nudibranch transcriptomes. Here we present four cases of mitonuclear discordance, never reported before in nudibranchs, that likely derive from mitochondrial introgression or capture. We also confirm one putative mimic in this study. Sister-species relationships and species-level entities were recovered with high support in both concatenated Maximum Likelihood (ML) and summary coalescent phylogenies, but the ML topologies were highly variable while the coalescent topologies were consistent across datasets. Our work also demonstrates the broad phylogenetic utility of 149 genes that were previously identified from eupulmonate gastropods. This study is one of the first to demonstrate the efficacy of exon capture for recovering recently radiated taxa and the first to provide evidence for mitochondrial introgression in nudibranchs.

A Mitochondrial Genome Phylogeny of Mytilidae (Bivalvia: Mytilida)

Yucheol Lee*¹, Taeho Kim², and Joong-Ki Park²

¹Department of Biological Sciences, Sungkyunkwan University

²Division of EcoScience, Ewha Womans University

The family Mytilidae is a family of bivalve mussels that are distributed worldwide in diverse marine habitats. Within the family, classification systems and phylogenetic relationships among subfamilies remain not yet fully resolved. In this study, we newly determined 9 mitochondrial genome sequences from 7 subfamilies: *Bathymodiolus thermophilus* (Bathymodiolinae), *Modiolus nipponicus* (Modiolinae), *Lithophaga curta* (the first representative of Lithophaginae), *Brachidontes mutabilis* (Brachidontinae), *Mytilisepta virgata* (Brachidontinae), *Mytilisepta keenae* (Brachidontinae), *Crenomytilus grayanus* (Mytilinae), *Gregariella coralliophaga* (Crenellinae), and *Septifer bilocularis* (the first representative of Septiferinae). Phylogenetic trees using maximum likelihood and Bayesian inference methods for 28 mitochondrial genomes (including 19 previously published sequences) showed two major clades with high support values: Clade 1 ((Bathymodiolinae + Modiolinae) + (Lithophaginae + Limnoperninae)) and Clade 2 (((Mytilinae + Crenellinae) + Septiferinae) + Brachidontinae). The position of the genus *Lithophaga* (representing Lithophaginae) differed from a previously published molecular phylogeny. Divergence time analysis with a molecular clock indicated that lineage splitting among the major subfamilies of Mytilidae (including the habitat transition from marine to freshwater environments by ancestral Limnoperninae) occurred in the Mesozoic period, coinciding with high diversification rates of marine fauna during that time. This is the first mitochondrial genome-based phylogenetic study of the Mytilidae that covers nearly all subfamily members, excluding the subfamily Dacrydiinae.

Genomic Signatures of Evolution in *Nautilus*

Sarah Lemer*¹, David Combosch¹, and Gonzalo Giribet²

¹University of Guam, Marine Laboratory

²Harvard University, OEB

Living fossils are model organisms to study both long-term and ongoing adaptation and speciation processes. However, many aspects of living fossil evolution and their persistence in the modern world remain unclear. Here, we investigate three major aspects of the evolutionary history of living fossils: cryptic speciation, population genetics and effective population sizes, using members of the genera *Nautilus* and *Allonautilus* as classic examples of true living fossils. For this, we analyzed genome wide ddRAD-Seq data for all six currently recognized nautiloid species throughout their distribution range. Our analyses identified three major allopatric *Nautilus* clades: a South Pacific clade, subdivided into three subclades with no signs of admixture between them; a Coral Sea clade, consisting of two genetically distinct populations with significant admixture; and a widespread Indo-Pacific clade, devoid of significant genetic substructure. Within these major clades, we detected five *Nautilus* groups, which likely correspond to five distinct species. With the exception of *Nautilus macromphalus*, all previously described species are at odds with our data, testifying to the prevalence of cryptic species among living fossils. Detailed F_{ST} analyses further revealed significant genome-wide and locus-specific signatures of selection between species and differentiated populations, which is demonstrated here for the first time in a living fossil. Finally, approximate Bayesian computation simulations suggest large effective population sizes, which may explain the low levels of population differentiation commonly observed in living fossils.

Go with the Flow? - Diversity and Speciation in Endemic Freshwater Gastropods in the Kaek River, Thailand

Nora Lentge-Maaß*^{1,2} and Dr. Matthias Glaubrecht¹

¹Centrum für Naturkunde (CeNak) - Center of Natural History, Universität Hamburg - Zoologisches Museum, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany

²Museum für Naturkunde (MfN), Leibniz Institute for Evolution and Biodiversity Science, Invalidenstraße 43, 10115 Berlin, Germany

Due to the discrepancy between taxonomic diversity and morphological disparity, often species names not necessarily reflect distinct evolutionary entities. To create true biological diversity, allopatric speciation is still conceived as an important underlying mechanism. However, an increasing number of studies also find ecologically driven speciation as potential cause. Lacustrine gastropods from several Cerithioidean freshwater families, such as paludomids, thiarids and pachychilids, are well suited to study these distinct mechanisms extensively which are involved in speciation and adaptive radiation. However, lacustrine settings, e.g. in Lake Tanganyika and the Malili lakes on Sulawesi, were often found to be rather complex, while radiations in a riverine environment are both rare and poorly studied. In a unique setting at the Kaek River in Thailand, originally 10 mostly endemic pachychilid species have been described. Following a revision of these *Brotia* snails we found in our evaluation sympatric, parapatric and allopatric occurrences, providing an ideal model to study the various fundamental mechanisms in speciation. In an integrative approach we combine biometrics and geometric morphometrics of the shell, morphological differentiation of the radula, ecological and life history data (i.e. viviparous reproductive strategies) with a genetic dataset on mitochondrial divergence and whole genome data using ddRAD sequencing. We present the first results of our morphological and genetic dataset, which we use to compare and assess ecological vs. geographical factors as drivers of speciation, which led to the diversity in *Brotia* snails at the Kaek River.

Sexual Selection and Reciprocity in Euthyneuran Gastropod Mating Systems

Janet L Leonard*¹, Chantal Stock²

¹Long Marine Laboratory, University of California-Santa Cruz, Santa Cruz CA 95060 USA

²Faculty of Biology, Theoretical Biology, University in Bielefeld, 33619 Bielefeld, Germany

The euthyneuran gastropods (opisthobranchs and pulmonates), are a clade composed almost exclusively of simultaneously hermaphroditic species with some form of internal fertilization. The mating behavior of many taxa is characterized by reciprocity, in which the both members of a pair act as male and as female in a single mating interaction. Reciprocity may take the form of simultaneous reciprocal copulation or alternation of sexual role in a series of copulations. Reciprocal mating has classically been understood as a solution to the problem of sexual conflict created by a preferred sexual role in hermaphrodites. However not all species have reciprocal mating. Moreover, the type of reciprocity may vary even within a genus, as in *Ariolimax*. Some species of pulmonates and opisthobranchs copulate apparently unilaterally or in chains where an individual may act as both male and female but not normally with the same partner. Some of this variation may be related to body shape. Species of pulmonate with a more globose shell usually have unilateral copulation while those that have a more laterally compressed shell typically have reciprocal copulation. The relationship between reciprocal copulation and reciprocal paternity is not clear, given the prevalence of sperm storage in these taxa. In opisthobranchs, species with a greater separation between male and female genital openings tend to have unilateral copulation, chain copulation or alternation of sexual roles between a pair of individuals. Here we will explore the evolutionary implications of explicitly reciprocal copulation vs. other patterns with a view to understanding the effect, if any, on the cost of sex problem.

Generating Molecular Tools to Study Gastropod Development

Maryna Lesoway*¹ and Jonathan Henry¹

¹University of Illinois, Urbana-Champaign, Department of Cell and Developmental Biology

The rapidly decreasing costs of sequencing, coupled with the increasing availability of genome editing tools, have taken developmental biology by storm. Taking advantage of the broad applicability of techniques such as CRISPR/Cas9, we are developing the calyptraeid gastropod, *Crepidula atrasolea*, as a laboratory-based research organism for development. This species offers several advantages, such as direct development, year-round availability of embryos, amenability to experimental manipulation of embryos, and rapid sexual maturity. Further, their robustness to broad environmental parameters facilitates inland laboratory culture. Using currently available genomic and transcriptomic data, we are using plasmid and CRISPR-based approaches to developing transgenic animals. However, appropriate facilities are required for rearing and tracking large numbers of animals, including transgenic lines. We have therefore designed and customized an automated marine rack aquarium system, which measures and maintains physical parameters such as temperature, salinity, and pH. This also includes an in-house built automated feeding system, capable of tracking and adjusting food delivery in response to feeding rates. In parallel, we have developed a database and tracking app, Snail Trail, to link physical aquarium parameters to biological outputs. We are currently measuring growth rates and reproductive output of snails in our aquarium system to optimize system parameters. Using this system to increase the size of our laboratory population of brooding animals provides sufficient embryonic material for genetic and other experimental manipulations, and will make distribution of animals and transgenics to the broader research community possible.

Hemocyanin and Habitat Shifts of Heterobranchia

Bernhard Lieb*¹ and Gabriela Schäfer¹

¹University of Mainz, Institute of Molecular Physiology

Hemocyanin, the respiratory protein of most mollusks is one of the largest proteins described in nature. Hemocyanin-subunits encompass about 3,400 amino acids referring to a cDNA of nearly 11,000 bp and comprises an enormous amount of genetic information. We are using this information to address multiple phylogenetic issues within Mollusca for years. Since hemocyanin is the oxygen transporter of most mollusks, it is directly linking the animals to their specific habitats. Therefore, the evolution of this protein is strongly associated with their living conditions and can be used as a tool to reconstruct the evolution of distinct lineages. Currently, we focus on Heterobranchia, a very diverse gastropod clade that comprises over 30,000 marine, limnic or terrestrial species. The immense variety of habitats within this clade arose from multiple independent habitat shifts within different lineages. These drastic changes in their living conditions affected the respiratory system of these gastropods encompassing morphological and molecular adaptations. In consequence, the reconstruction of phylogenetic trees based on hemocyanin data unraveled some problems when analyzing marine, terrestrial and limnic species in one data set. Within clades which share common habitats phylogenetic analyses are pretty robust and well supported. Additionally, within Tectipleura, we observed several independent hemocyanin gene duplications which correlate to independent habitat shifts, and thus, the hemocyanin of Heterobranchia seems to be very useful in both, phylogenetic and ecological issues. We will present new possibilities, advantages and new challenges but also pitfalls we unraveled so far.

Recognizing and Predicting Global Patterns of Marine Mollusk Ornamentation Expression through Machine Learning

T. Mason Linscott*¹ and Christine E. Parent¹

¹University of Idaho, Biological Sciences; Institute for Bioinformatics and Evolutionary Studies

Compared to their freshwater and terrestrial counterparts, marine mollusks possess the greatest degree of shell biomineralization. The robustness of the exoskeleton of marine species has been attributed, in part, to the high degree of availability of calcium carbonate in marine environments. Individual studies have documented a higher proportion of heavily-biomineralized, ornamented (e.g. possessing ribs, spines, or keel, etc.) species in highly supersaturated aragonite ($\Omega_{\text{aragonite}}$) regions than in less supersaturated regions. As biomineralization and ornamentation expression are highly labile within some marine species, and ornamentation expression is one of the key morphological characters used to delimit extant and fossil taxa, understanding the role of $\Omega_{\text{aragonite}}$ in marine mollusk ornamentation expression at the intra- and interspecific levels is vital to interpreting species diversity in the fossil record and among extant taxa. Further, $\Omega_{\text{aragonite}}$ is predicted to decrease globally due to anthropogenic climate change so there is need to understand the effects of saturation state to predict the future distribution and expression of ornamentation. We developed an object detector that classifies images into ornamented- and smooth-shell taxa and applied it to geo-tagged images of all marine mollusks. This process generated a global dataset to test the association of water chemistry and other environmental variables with ornamentation expression. The dataset was then used for training and validation for a Random-Forest classifier that predicts ornamented species occurrence given local environmental variables. We found that ornamented species occurrence is significantly associated with key environmental variables and that ornamentation expression is predicted to change globally under future scenarios of climate change.

Casting a Wide Net: Capturing Gene Regulatory States That Drive Morphogenesis in Slipper Shell Snails, and What They Can Tell Us About Molluscan Evolution

Deirdre C. Lyons*¹, Kimberly J. Perry², and Jonathan Q. Henry²

¹Scripps Institution of Oceanography, U.C. San Diego, CA, USA.

²Department of Cell and Developmental Biology, University of Illinois, Urbana, IL, USA.

One of the most fascinating enduring questions in biology is how the great diversity of extant organisms came to be. In each generation, an animal first acquires its basic body-plan through the process of development; thus studying development in a comparative context can help explain how animals have different shapes, physiologies, behaviors, and adaptations. In many cases, developmental cell fate specification in animals is well-understood, thanks to the study of gene regulatory networks (GRNs). GRNs describe the steps of cellular differentiation over time, with a focus on regulatory connections between transcription factors and signaling molecules. While GRNs have been constructed for animals that fall into the deuterostome and ecdysozoan clade of metazoans, there are no comprehensive GRNs among the Spiralia. One reason for the paucity of GRN-level analysis in the Spiralia, especially among molluscs, is that the construction of GRNs requires direct gene perturbation. Relatively few molluscan species have been used for this approach. Among those species that have, calyptraeid gastropod slipper shells in the genus *Crepidula* are well-suited for experimentally dissecting the developmental process from a molecular perspective. *Crepidula* species have been used to understand embryonic cell lineages in marine animals since the late 19th century and modern fate-mapping, along with advancements in gene editing capabilities, have made them excellent experimental systems for exploring gene function among marine gastropod molluscs. I will describe our work establishing a framework for GRN analysis of cell fate decisions and morphogenesis in these species, and discuss how such data can be used to understand molluscan embryogenesis in comparison to other metazoan developmental programs.

Empirical Testing of Minimum Sample Size and Marker Number Required For Estimating Population Genomic Parameters Using Ddrad Seq Data from *Webbhelix multilineata* (Mollusca, Gastropoda, Stylommatophora)

Jermaine Mahguib*¹, Kyung Seok Kim¹, and Kevin Roe¹

¹Iowa State University

Population genetic studies sample individuals from populations and sequence molecular markers to estimate genetic diversity, levels of inbreeding, population structure, and genetic connectivity. A variety of markers have been utilized, such as AFLP's and microsatellites, each accompanied by "rule of thumb" ranges of acceptability for numbers of samples and markers appropriate to utilize for different studies. In population genomics, the same is sought but through use of far greater numbers of markers, like single nucleotide polymorphisms (SNPs) which are ubiquitous throughout genomes. While individual SNPs represent little variability, large numbers of them (thousands to tens of thousands) can provide enough genetic variability for inference of population parameters. The transition from traditional genetic markers to genomic markers has occurred remarkably fast with the rapidly increasing availability of next generation sequencing technologies, and guidelines for sampling schemes are less established. A few studies have used simulations to address the question of minimum sample sizes for population genomics, and one has used an empirical data set from a plant system. In the present study, minimum sample size and number of SNP markers required to accurately estimate intra-population (effective number of alleles, expected/observed heterozygosity) and inter-population (F_{ST}) parameters will be investigated for a gastropod system. Knowledge of an informative minimum sample size for population studies is of particular interest in cases involving endangered species where sampling may be restricted, and of general interest as fewer samples reduces overall cost. These findings should serve to additionally support a growing establishment of guiding principles for best practices in population genomics generally, and for gastropods specifically.

Comparison of Biogeography Patterns of Two Freshwater Snails - *Physa acuta* and *Helisoma anceps*

Kelly Martin*¹ and Jingchun Li¹

¹University of Colorado Boulder, Museum and Field Studies Department

Native to North America, Physidae and Planorbidae are long-established, globally-invasive snails and are the most abundant and widespread freshwater gastropod families. Their adaptability to diverse ecosystems makes these snails ideal intermediate hosts for many parasitic trematodes. To date, studies examining each family's genetic diversity focus predominately on their invasive range, with considerably less sampling within their native range. Recent phylogenetic studies of North American *Physa acuta* identify significant east-west genetic structuring, however, the factors leading to the observed patterns remain unclear. The objective of this study is to address the biogeography of two Western United States freshwater snails, *Helisoma anceps* (Gastropoda: Planorbidae) and *P. acuta* (Gastropoda: Physidae), to compare the population genetic patterns between the species and determine if watersheds, geographic distance, or other biotic factors contribute to the observed genetic structuring. While *H. anceps* and *P. acuta* often occur sympatrically, their life history characteristics vary. Specifically, *P. acuta* is known to have higher fecundity, reproductive plasticity and effective passive dispersal abilities. Preliminary results corroborate the east-west genetic structuring of *P. acuta* and improve the resolution of a previously identified distinct clade from west of the Rocky Mountains to the southwest United States. Across the sampling range, *H. anceps* has more pronounced genetic structuring than *P. acuta*. Comparison between the species offers insight into how biogeographical factors in the Western United States impact genetic variation of freshwater gastropods and provides implications for their species-specific role in parasite-host relationships.

Integrative Systematics of the Genus *Thuridilla* Bergh, 1872 (Mollusca, Gastropoda, Heterobranchia) Reveals a Cryptic Radiation of Polymorphic Sea Slug Species

M. Rosario Martín-Hervás^{*1,2}, Leila Carmona², Manuel António E. Malaquias³, Patrick J. Krug⁴,
Terrence Gosliner⁵ and J. Lucas Cervera^{1,2}

¹Departamento de Biología, Facultad de Ciencias del Mar y Ambientales, Campus de Excelencia Internacional del Mar (CEIMAR), Universidad de Cádiz, Avenida República Saharaui s/n, Apartado 40, 11510 Puerto Real (Cádiz), Spain

²Instituto Universitario de Investigación Marina (INMAR), Campus de Excelencia Internacional del Mar (CEIMAR), Universidad de Cádiz, Avenida República Saharaui s/n, Apartado 40, 11510 Puerto Real (Cádiz), Spain

³Phylogenetic Systematics and Evolution Research Group, Section of Taxonomy and Evolution, Department of Natural History, University Museum of Bergen, University of Bergen, PB 7800, 5020 Bergen, Norway

⁴Department of Biological Sciences, California State University, Los Angeles, CA 90032-8201, USA.

⁵Department of Invertebrate Zoology, California Academy of Sciences, 55 Music Concourse Drive, San Francisco, CA 94118, USA.

A major problem for biodiversity conservation of marine gastropods is that significant species diversity remains 'hidden' as cryptic or pseudocryptic species. Body color pattern is important for identifying species of *Thuridilla* Bergh, but has also led to controversy about the conspecificity of color morphs in the *T. gracilis* (Risbec, 1928) complex of Indo-Pacific species. The most recent hypothesis considers two species within the complex as valid: *Thuridilla gracilis* and *T. splendens* (Baba, 1949), whereas *T. bayeri* (Er. Marcus, 1965) and *T. ratna* (Er. Marcus, 1965) are considered junior synonyms of *T. gracilis*. We inferred a worldwide phylogeny of *Thuridilla* using a multi-locus approach, combining one nuclear (H3) and two mitochondrial (COI and 16S) genes, using both Bayesian and Maximum likelihood criteria. Furthermore, species delimitation analyses (ABGD, GMYC, bPTP) and the comparison of radular teeth were performed to assess the systematics of the genus. Remarkably, the *T. gracilis* complex contained 14 delimited species, all distinguishable by radular characters and external morphology as well as by molecular analyses. The four traditional species plus the 10 new species we identified together comprise a relatively recent yet polymorphic radiation, with each having a diagnostic color pattern. This radiation represents the bulk of the cryptic diversity in the genus: our analyses revealed that *Thuridilla* comprises 33 species, including 11 undescribed taxa, of which 10 are in the *T. gracilis* complex. Our phylogenetic insights provide a novel comparative framework for studying how color patterns drive radiations among diverse heterobranch groups, including these colorful and rapidly diversifying sacoglossans.

Essential Oils as Novel Tools for Managing the Invasive Slug *Deroceras reticulatum* (Agriolimacidae: Gastropoda)

Rory J. Mc Donnell*¹, Matthew L. Klein¹, Thomas G. Chastain¹, and Carol J. Garbacik¹

¹Department of Crop and Soil Science, Oregon State University, Corvallis, OR 97331, USA

Deroceras reticulatum is one of the most damaging gastropod species throughout the world. In the Pacific Northwest region of the U.S. this slug is particularly problematic and causes an estimated \$100 million worth of damage to the grass seed industry annually in Oregon. Despite this economic impact, molluscicidal baits are the mainstay of control throughout the region. However, considerable variation in efficacy is frequently reported by growers. Thus, there is an urgent need to develop alternative approaches for slug management. One such option is essential oils which have been used to control other pests such as aphids, mites and weevils but they have been largely overlooked when it comes to gastropods. In this study, the LC50 of thirteen plant-derived essential oils against adult *D. reticulatum* were determined in a laboratory Petri dish bioassay. Thyme and spearmint oil were most lethal to slugs and in phytotoxicity bioassays they did not have any major adverse effects on two cultivars of perennial ryegrass (*Lolium perenne*) and two cultivars of tall fescue (*Festuca arundinacea*). In microcosm studies with annual ryegrass (*Lolium multiflorum*), the oils performed comparably to the industry standard, Slug-Fest[®], causing 97.5 % mortality of *D. reticulatum*. Although they are more expensive than conventional chemical controls, these essential oils cause rapid mortality, are non-toxic to humans, and are exempt from pesticide registration and residue tolerance requirements under U.S. federal law. Thyme or spearmint oil could also be used on certified organic operations or in rotation with conventional chemicals when other modes of action are needed.

Fresh cucumber as a novel attractant for invasive gastropods

Rory J. Mc Donnell*¹, Maria Cordoba¹, and Jocelyn G. Millar²

¹Department of Crop and Soil Science, Oregon State University, Corvallis OR 97331

²Department of Entomology, University of California, Riverside CA 92521

Terrestrial gastropods cause economic damage to crops in a number of ways, including reducing yield due to consumption of seeds, seedlings, roots and aerial parts of mature plants. Control strategies are focused heavily on molluscicides, which are ineffective under certain conditions. Thus, there is an ongoing need to develop alternative management options. One such approach is the development of novel attractants for use in traps and in attract-and-kill strategies. In contrast to insects, very little work has been done to explore the chemical ecology of gastropods, and what little work has been done has been relatively superficial. However, even these preliminary studies have clearly shown that chemical cues play a major role in a wide range of gastropod behaviors. A primary goal of this study was to develop a generic bioassay that can be used to identify novel attractants for any terrestrial gastropod species by high-throughput screening of attractant sources. The optimized method uses arrays of glass T-tubes with cameras positioned above them to record snail choices. Using the bioassay, >1500 choice and no-choice tests demonstrated that cucumber was consistently the most attractive to *Cornu aspersum* and *Deroceras reticulatum*. Our results also showed that previous feeding influenced subsequent food choice for both species, but this conditioning was not absolute and could be broken. The attractiveness of cucumber was confirmed in field trials in Oregon where both *D. reticulatum* and *C. aspersum* were significantly attracted to traps baited with cucumber. These results demonstrate the potential importance of fresh cucumber as a novel attractant for management and detection of pest gastropods.

Elucidating the Molecular Basis of Pigmentation in the Tropical Abalone, *Haliotis asinina*

Carmel McDougall*¹, Daniel J. Jackson², and Bernard M. Degnan³

¹Australian Rivers Institute, Griffith University

²Department of Geobiology, Georg-August University of Göttingen

³School of Biological Sciences, University of Queensland

Elucidating the molecular basis of pigmentation in the tropical abalone, *Haliotis asinina* The molluscan shell is an ontological record of molecular patterning events over time, and, as a result, has been a favourite subject for the development of mathematical models of biological pattern formation. Despite this historical interest, very little is understood of the molecular pathways involved in the shell patterning process. Previously, we identified a gene, *sometsuke*, which is differentially expressed in the mantle edge and correlates with areas of red pigmentation in the shell. Here, we show that this gene is one member of a larger gene family associated with pigmentation in abalone. Expression studies reveal that these genes have discrete expression patterns and encode proteins that are bound to pigment molecules within the mantle. The secretion of these proteins and incorporation into the extracellular matrix results in external shell pigmentation patterns, which we also show are influenced by the diet of the animal. Evolutionary analysis reveals that the *sometsuke* gene family appears specific to abalone, indicating that intricate molecular shell patterning systems may have evolved independently in different molluscan lineages.

Genomic Analysis of Contagious Cancers of Clams

Michael J. Metzger*¹

¹Pacific Northwest Research Institute

Cancer is normally an evolutionary dead-end—neoplastic cells that arise and evolve within an organism either regress or they kill their host, and the death of the host marks the death of the cancer lineage. However, in some cases, neoplastic cells develop the ability to spread from individual to individual, turning from conventional cancers into clonal contagious cancer lineages. The natural transmission of cancer cells has been observed in two mammals (Tasmanian devils and dogs), and we have found that a leukemia-like disease in soft-shell clams (*Mya arenaria*) is due to the horizontal spread of a clonal cancer lineage. We also analyzed mussels (*Mytilus* sp.), cockles (*Cerastoderma edule*), and carpet shell clams (*Polititapes aureus*) and found that the neoplasias in all three of these species are due to independent transmissible cancer lineages. We have assembled an initial draft reference genome for *M. arenaria* using 10X Chromium methods, and we are generating a new reference genome using PacBio sequencing combined with HiC data. Using these references, we are investigating genomic changes in the evolution of this unique cancer lineage, including SNPs, structural variation, and copy number variation. In particular, we found a retrotransposon, *Steamer*, which is expressed and amplified in genomic DNA of the contagious cancer lineage. Genomic analysis of cancer samples from isolated clam populations in Maine and Prince Edward Island shows that at least 130 sites are found in cancer cells from both populations. These common sites likely integrated early in the evolution of the cancer lineage, and they have been conserved either as passenger or driver mutations.

Envisioning the 21st Century Museum

Christopher Meyer*¹

¹National Museum of Natural History, Dept of Invertebrate Zoology MRC-163, Washington DC 20560

Natural history museums play a critical role in documenting global anthropological, biological and geological diversity. They inspire generations and instill a sense of wonder and appreciation for the world around us. Importantly, museums exist to be used. Given the level of ongoing and predicted global change, museums provide time capsules of diversity and longitudinal breadth to examine temporal patterns in phenology, range shifts, species interactions and diversity loss or gain. The future of natural history museums will pivot from providing inventory-like services to more observatory functions. They should provide strategic windows to the past by partnering with place-based observatories or targeted regions of predicted change. A key to unlocking this potential requires a change in the socialization of data associated with samples. Museums host more than voucher samples for comparative identification purposes. They host a suite of derived products and associated information that cascades from these records of diversity in time and space. Increasingly museums capture whole communities through curation of environmental samples. These stores of information should be rapidly mobilized, using existing standards and ontologies, and served to aggregators such as GBIF, OBIS, NCBI or EMBL. Updates to taxonomies, classifiers or metadata must be enabled. New data release policies can be incentivized by assigning globally unique identifiers early in the data chain to maintain the connections between material samples and assure appropriate attribution. Data aggregators provide tools for tracking usage and attribution that can be used reciprocally to determine priorities in digitization or new collections. Molluscs have and will continue to play an important role in spearheading these developments.

A New Intriguing Species of *Psilodens* (Caudofoveata, Limifossoridae)

Marcel Sabino Miranda*¹, Carmen Regina Parissotto Guimarães², and Flávio Dias Passos^{1,3}

¹Graduate Program in Animal Biology, University of Campinas

²Department of Biology, Center of Biological and Health Sciences, Federal University of Sergipe, São Cristóvão, Brazil

³Department of Animal Biology, Institute of Biology, University of Campinas, Campinas, Brazil

Psilodens is a genus of caudofoveates whose species are generally rare and occur in low abundances, with a distribution restricted to the deep-sea (<1800 m); actually, only 3 species are known. Through collections made off the Brazilian Northeastern coast, a distinct species of *Psilodens* was found, and is here described through the light and scanning electron microscopies. It has a slender body, up to 3 mm long, with an anterior trunk bearing a midventral suture line that was never recorded for any species of *Psilodens*. A bipartite oral disc is present, as well as a radula with 18 transverse rows of paired teeth; there are no median denticles and the tip of each tooth is heavily sclerotized. The adpressed sclerites are in general drop-shaped but slightly elongated, rounded at the base and pointed at the tip, and ornamented with a central longitudinal keel; in the suture line they are lanceolate, keeled and the blade is twisted in 90° relative to the base, a unique character never reported for other caudofoveates. We analyzed 171 specimens obtained from 50 to 3000 m depths, mostly occurring in the upper slope. It appears to be endemic from the Brazilian coast, and so has a more restricted geographical distribution, a pattern also recorded for other species of *Psilodens*. Its high abundance and the occurrence in a wide bathymetric distribution not restricted to the lower slope are but unlike other species of this genus. This finding shows that the Southwestern Atlantic has unique, yet undescribed species of aplacophorans, whose distribution patterns are beginning to be revealed.

Unravelling a Hidden Biodiversity: The Caudofoveata (Aplacophora) from the Southwestern Atlantic Ocean

Marcel Sabino Miranda*¹, Carmen Regina Parissotto Guimarães², and Flávio Dias Passos^{1,3}

¹Graduate Program in Animal Biology, University of Campinas

²Department of Biology, Center of Biological and Health Sciences, Federal University of Sergipe, São Cristóvão, Brazil

³Department of Animal Biology, Institute of Biology, University of Campinas, Campinas, Brazil

In the Atlantic Ocean, caudofoveates are well recorded from its northern part, contrary to the southern, where they are less investigated, suggesting a possible biodiversity break between 8°S and 36°S, including most of the Brazilian coast. This situation started to change by collection efforts in the Southeastern Brazil, resulting in finding some species from this place. However, a main question still remains: does that faunal break really exist? Recently, samples became accessible from the northeast, between Sergipe and Alagoas States, revealing that a great biodiversity of caudofoveates is present along all the Brazilian coast. We analyzed 2,000 individuals from 400 samples collected in this area, and in addition lots from collections of the Museum of Zoology of São Paulo and the Brazilian National Museum. Seven Chaetodermatidae, three Prochaetodermatidae and two Limifossoridae were found. Six species represent new records for the Brazilian coast, and six are probably new and now are under the description process. Eight species are distributed along the southwestern Atlantic, having their northern limit in Brazil, and three were previously recorded from the North Atlantic and are now recorded from the Brazilian coast. Only one species of *Psilodens* appears to be endemic. These findings show that a biodiversity break of caudofoveates in the Southwestern Atlantic does not occur, and that the distribution of most of species appears to be continuous along the eastern coast of Americas. A connection among the faunas from the North and South Atlantic is envisaged.

Phylogenetic Systematics of the Genus, *Cyerce* Bergh 1871 (Sacoglossa, Caliphyllidae) Using Molecular and Morphological Data

Karina Moreno*¹ and Dr. Ángel Valdés¹, Dr. Terrence Gosliner², and Dr. Patrick Krug³

¹California Polytechnic State University, Pomona, Department of Biological Sciences

²California Academy of Sciences, Department of Invertebrate Zoology

³California State University, Los Angeles, Department of Biological Sciences

The genus *Cyerce* Bergh 1871 is a group of sea slugs in the family Caliphyllidae, characterized by having bifid rhinophores, enrolled oral tentacles, multiple flattened, leaf-like cerata, and a transverse groove splitting the foot sole of the animal transversally. *Cyerce* currently includes eleven accepted species distributed throughout tropical and subtropical areas of the Indo-West Pacific, Eastern Pacific, Northern Atlantic, Caribbean, and Mediterranean. Species of *Cyerce* are stenotropic herbivores that possess remarkable adaptations such as aposematic coloration, synthesis of polypropionates, and acquisition of plastids from their algal hosts. The evolution of these traits in *Cyerce* has not been studied, although observed in other lineages within Sacoglossa. Cladistic analyses have been performed on Sacoglossa, but a species level phylogenetic analysis for the genus *Cyerce* are lacking. The objective of this study is to produce a monographic review of the genus *Cyerce* using both molecular and morphological data. In order to resolve the evolutionary relationships among *Cyerce* species, two mitochondrial genes (CO1, 16S) and nuclear gene (H3) were sequenced from 109 specimens borrowed from museums or collected in the field. Bayesian analyses were used to generate phylogenetic trees. The internal anatomy of the *Cyerce* specimens was studied to supplement molecular data. This included dissections of the radula and male reproductive anatomy. A species delimitation analysis with ABGD was performed using CO1 aligned sequences to support phylogenetic analyses. Fifteen genetically distinct species of *Cyerce* were recovered from the analyses with observed differences in size of the buccal mass and radula across species.

Mating Behavior in Aeolids did not Complete so Quickly

Yasuhiro Nakashima*¹ and Keita Yokoi²

¹Nihon University, College of Economics

²Nihon University, College of Bioresource Sciences

Though the average duration of mating in nudibranchs appears several minutes, some mate for very long time (several hours) and others very short. The copulation time of *Hermisenda crassicornis* is reported only about four seconds (Rutowski 1983) and that of *Facelina bilineata* not longer than several seconds (Hirano 2000). Due to difficulties to video record their mating behavior in those days, the behavior was not described precisely. We recorded the mating behavior of several aeolid species and analyzed them. Some species, *Sakuraeolis enosimensis*, *Pteraeolidia ianthina*, and *Abronica purpureoanulata*, copulated in an ordinary manner like many dorid nudibranchs, and others, *Facelina bilineata* and *Cratena lineata*, did not copulate but mated by exchanging spermatophores. Immediately after a jellylike spermatophore was deposited next to the genital orifice, it was sucked in the orifice spontaneously. Though the average time needed for this sequence in *Facelina bilineata* was about 20 seconds, which was close to the description by Hirano, it took about eight and a half minutes in *Cratena lineata*, which was not so short in comparison with copulating species. The position at which a spermatophore was deposited and the way to take in it in *Facelina bilineata* and *Cratena lineata* differed in various points from hitherto reported aeolid species. This suggests that mating with spermatophores in aeolids evolved a few times in parallel. But the present study showed there is no temporal advantage to mate with spermatophores. Further, they were reported to suffer from losing spermatophores during mating. We will examine the advantage to mate with spermatophores.

Molecular Insights into Species Recognition Within Southern Africa's Endemic *Tricolia* Radiation

Tshifhiwa C. Nangammbi*¹, David G. Herbert², and Peter R. Teske³

¹Tshwane University of Technology

²KwaZulu-Natal Museum

³University of Johannesburg

The validity of morphology-based species boundaries between the southern African representatives of the genus *Tricolia* was assessed using mitochondrial COI and 16S rRNA sequence data. Phylogenies obtained from individual and combined genetic datasets recovered eight distinct clades. In addition, two well-supported multi-species clades were recovered, comprising respectively *T. africana* and *T. capensis*, and *T. bicarinata*, *T. insignis* and *T. kraussi*. Within these clades, genetic variation was very limited and there was no differentiation between the nominal species. In both cases the distributions of the nominal taxa coincide with well-known biogeographic disjunctions, and there is evidence of overlapping and intergrading shell characters. We propose that both of these unresolved clades be recognized as single, phenotypically plastic species. Despite the resultant loss of species due to synonymy, the phasianellid fauna of southern Africa remains the most diverse in the world, with 10 endemic species and three Indo-West Pacific species.

Improved Monitoring of Pest Slugs in Australia

Michael Nash*^{1,2}

¹School of Agriculture, Food and Wine, University of Adelaide, Urrbrae, SA 5064, Australia.

²School of Life Science, La Trobe University, Melbourne VIC 3086, Australia.

Infestations of exotic pest snails and slugs in Australian grain crops cause crop damage and yield loss from their feeding and impose significant costs of field control, yet are difficult to quantify. Snails cause additional harvest costs for grain producers and the possibility of losing access to markets. For example, *Ceratomyxa virgata* was included in formal import standards (Feb 2015) for wheat and barley as part of the China-Australia Free Trade Agreement. A typical overall enterprise cost to Australian farms with snails is \$33.10/ha/yr, with \$27/ha spent on bait and \$16.50/t spent on post-harvest cleaning. Where slugs persist, if untreated they cause canola yield loss of 60%-80%, with \$30-\$50/ha cost for bait applied at establishment. \$14-16m is spent on molluscicides in Australia annually. Where snails and slugs are a high risk (SE SA and SW Vic.) growers have shifted away from growing canola. The opportunity cost of not growing canola is estimated up to \$270m annually. In SW Victoria where canola is grown, 95% is sown into burnt and/or cultivated ground. Integrated management of these pests is needed for successful control, yet cultural controls are limited in conservation farming systems commonly adopted in Australia in response to reduced rainfall. IPM in arable systems in Australia is hamstrung by a lack of monitoring to underpin control decisions. Monitoring of slugs is particularly challenging prior to sowing because conditions are dry, hence pest activity is limited. Cameras are being used to uncover pest ecology. The understanding of environmental triggers for activity and feeding are being used to enhance bait efficacy.

A Fresh Look at Melanopsidae (Caenogastropoda: Cerithioidea): Evolutionary Systematics, Biogeography and Conservation Genetics

Marco T. Neiber*¹, Simone Cianfanelli², Fabrizio Bartolini², Thomas von Rintelen³, and Matthias Glaubrecht¹

¹Universität Hamburg, Center for Natural History (CeNak)

²Università degli Studi di Firenze, Museo di Storia Naturale – La Specola

³Museum für Naturkunde Berlin, Leibniz-Institute for Evolution and Biodiversity Science

Melanopsidae occur in subtropical and temperate regions of the Western Palearctic and are also reported from Zealandia, which is an unparalleled disjunction among freshwater animals. Melanopsidae also have a rich fossil record. We sequenced nuclear and mitochondrial markers of a representative sample of species/genera covering the entire geographic range of the group. We compare the timeframe for the evolution of major melanopsid lineages with geologic events and elucidate scenarios that may have shaped distribution patterns. Our phylogenetic analyses suggest that Melanopsidae are not monophyletic. *Holandriana* is more closely related to Pleuroceridae and Semisuclospiridae than to Melanopsidae s.str. The Zealandian taxa (Zemelanopsidae) were recovered as the sister group of a clade including *Melanopsis*, *Microcolpia* and *Esperiana* (Melanopsidae s.str.). *Esperiana* branches off first, while *Microcolpia* represents the sister group of *Melanopsis*, which is comprised of three lineages: 1) western Mediterranean region, 2) eastern Mediterranean region and 3) Italy. While the Italian populations show little shell variability, the eastern and western *Melanopsis* lineages are highly variable. Several geographically coherent groups in *Melanopsis* can be ranked as species. However, in a number of cases morphologically distinct forms were not recovered as monophyletic units. The Italian narrow-range endemic *M. etrusca* was known historically from twelve populations, half of which have already gone extinct. We used AFLP markers to assess the genetic diversity in the remaining populations, which showed that the westernmost populations are genetically distinct from the remaining populations. Recovery plans, which are urgently needed to prevent a further decline of the species, ought to take population structuring into account to preserve the genetic diversity.

Using Comparative Genomics to Reveal the Underpinnings of Bioluminescence Symbioses in Bobtail Squid

Michele K Nishiguchi*¹, Elizabeth Heath-Heckman², and Daravuth Cheam³

¹New Mexico State University, Dept. of Biology

²University of California, Los Angeles, Dept. of Ecology and Evolutionary Biology

³New Mexico State University, Dept. of Biology

Due to their large size (~3.5 Gb) and high repetitive content, cephalopod genomes have long been intractable to study. However, with the recent sequencing and assembly of cephalopod genomes, studies of these molluscs are now possible. Of particular interest are the bobtail squids, many of which develop photophores where bioluminescent bacterial symbionts reside. Intermittent presence of the symbiosis within the group allows us to use comparative genomics to determine regions of the genome that are under selection in symbiotic lineages that could be instrumental in the evolution of these mutualistic associations. We have used high-throughput sequencing to generate reads from five bobtail squid genomes, four of which maintain symbioses with luminescent bacteria (*Euprymna scolopes*, *E. tasmanica*, *Sepiola affinis*, and *Rondeletiola minor*), and one of which does not (*Sepietta neglecta*). Using BWA, we assembled reads from all five species to the published *E. scolopes* genome to generate low-coverage (4-8x) genomes for each species. We then used Platypus to call genome variants based on read coverage and mapping quality. The dS/dN ratio for each squid species was calculated to determine which loci carry hallmarks of positive selection, as well as determining evolutionary rate. As a separate measure of selection, the software package Saguaro was utilized to determine whether squid that are geographically isolated (Pacific vs. Mediterranean) undergo similar genomic accommodations to symbiosis. Our study is, to our knowledge, the first whole-genome comparisons within the cephalopoda, and will greatly add to our knowledge of both genome dynamics within the sepiolid group and the mechanisms in which genomes evolve to accommodate microbial symbioses.

The Effects of Land Subsidence and Uplift on Intertidal Mollusks Including Commercially Important Bivalves Following the 2011 Great East Japan Earthquake

Kenji Okoshi*¹, Masahiro Suzuki¹, and Waka Sato-Okoshi²

¹Department of Environmental Science, Toho University, Japan

²Graduate School of Agricultural Science, Tohoku University, Japan

The Great East Japan Earthquake that occurred on the 11th March 2011 caused a great deal of damage to the organisms that inhabit the coast of the Tohoku district of Japan. In this paper, we mainly focus on the earthquake's impact on bivalves including commercially important Manila clam, *Ruditapes philippinarum* that inhabit the sandy intertidal zone, with specific emphasis on the long-term effects of land subsidence and uplift. As previous studies have not discussed the details of the separate physical events of this type of natural disaster, this study divided it into four main events; (1) the initial earthquake including liquefaction, (2) subsequent tsunamis and following (3) land subsidence and (4) ground uplift. During the liquefaction period, bivalves were brought to the surface with jets of water and were then swept away by the tsunamis. The tsunamis have also contributed to dispersion of benthic organisms. In addition to these events, land subsidence resulted in marked changes to the vertical position of the intertidal zone. These large changes in the physical environment cannot recover in the short term and the re-adjustment of tidal communities is expected to take several decades. However, land subsidence has also formed new intertidal zones, which will ultimately promote the colonization of various organisms including the Manila clam. Oysters have begun to die from the upper intertidal zone due to the effect of subsequent ground uplift. These disturbances to the ecosystem have destabilized these bivalve species resulting in fluctuations in abundance and community structure for at least eight years following the earthquake.

Fish-Hunting Cone Snails: How Correlating Behavior with Venom Peptides Facilitates Biomedical Applications

Baldomero M. Olivera*¹, Shrinivasan Raghuraman¹, and Helena Safavi²

¹University of Utah, Salt Lake City, UT

²University of Copenhagen, Denmark

The fish-hunting lifestyle of some cone snail species was established by the ground-breaking work of Alan Kohn when he was doing his Ph.D. graduate research in Hawaii. In the years since this discovery, it has become clear that there are over 100 species of cone snails that primarily prey on fish. Alan Kohn's thesis established how *Conus striatus* captures fish, a strategy that we now call "taser and tether". However, it has become clear that the different lineages of fish-hunting cone snails have evolved a variety of strategies, some of them quite divergent from that of *Conus striatus*. We will describe these alternative fish-hunting strategies, and show how the bioactive venom peptides evolved by a cone snail species correspond to the behavioral repertoire of that piscivorous *Conus*. An overview of how the discovery and characterization of biomedically-significant peptides can be accelerated by knowing how the fish-hunting cone snail uses its venom peptides to capture fish will be presented for the different strategies for capturing prey evolved by the various lineages of piscivorous *Conus*. The potential applications of venom peptides from fish-hunting cone snail venoms to address the opioid crisis will be summarized.

Pushing Boundaries: Investigating the Disturbance of the Pugnacious Nudibranch *Phidiana hiltoni* in Northern California

Emily Otstott*^{1,2} and Terry Gosliner¹

¹California Academy of Sciences

²San Francisco State University

The northward progression of the pugnacious nudibranch *Phidiana hiltoni* was documented in 2011, with its northern range limit jumping from the Monterey Peninsula to Marin County, CA. The rise of *P. hiltoni* at Duxbury Reef (DR) in Marin County coincided with a decline in several resident nudibranch species, potentially from *P. hiltoni* consuming these species and increasing competition for prey. To determine if vulnerable nudibranchs of DR are still in decline or whether the reef is recovering from the disturbance of *P. hiltoni*, I have conducted monthly to bimonthly timed counts in 2018 and 2019. *Phidiana hiltoni* is still the most abundant nudibranch at DR, more than doubling its abundance since 2011. While some vulnerable species have not been observed at DR since the arrival of *P. hiltoni*, others have made a comeback. Behavioral responses of the southern *Hermisenda opalescens* and northern *H. crassicornis* to the historically southern *P. hiltoni* were observed to investigate whether the northern species would be more vulnerable than the southern. *Phidiana hiltoni* was not more likely to attack one species over the other, but behavioral responses of the *Hermisenda* spp. did differ. Future efforts will aim to investigate the overlap of prey between *P. hiltoni* and other hydroid-eating nudibranchs at DR.

Molecular and morphological studies of *Burnupia* Walker, 1912 (Gastropoda Hygrophila)

Ximena M. C. Ovando*^{1,3}, Dayse A. Silva^{2,3}, L. E. M. Lacerda¹, and Sonia B. Santos.^{1,3}

Universidade do Estado do Rio de Janeiro, Instituto de Biologia Roberto Alcântara Gomes. Rua São Francisco Xavier, 524, Maracanã, Rio de Janeiro, RJ, Brasil. CEP: 20550-900.

¹Laboratório de Malacologia Límnica e Terrestre

²Laboratório de Diagnóstico por DNA.

³Programa de Pós-graduação em Ecologia e Evolução (PPGEE)

Traditionally, *Burnupia* Walker was grouped within "Ancyliidae", but its taxonomic position has always been controversial. Pilsbry suggested a close relationship between *Burnupia* and *Uncancylus* Pilsbry, 1913 based on characters of the radula. According to some authors, spermatozoa of *Burnupia stenochorias* Melvill & Ponsonby, 1903 were similar to *Biomphalaria glabrata* Say, 1818 (Planorbidae). Molecular evidence has suggested that *Burnupia* does not belong of Ancyliinae such as all other representatives of Planorboidea. For a long time, this genus was considered endemic to Africa until *B. ingae* Lanzer, 1991 was described from Brazil. Currently, *Burnupia* has approximately 22 species, probably few of them are valid. Due to the curious distribution and controversial taxonomic position, we propose: 1. To infer the relationship between South African and Brazilian *Burnupia* species based on molecular analysis. 2. Identify diagnostic characters for *Burnupia* by studying shell sculpture, soft parts and radula morphology from populations from South Africa and Brazil. In an attempt to increase the robustness of our phylogenetic analyses, some Ancyliinae species were included. For molecular analysis, the mitochondrial cytochrome oxidase I (COI) and 18S markers were used. The DNA was extracted with phenol-chloroform protocol and subsequently the amplified material was sequenced. For phylogenetic reconstructions the maximum likelihood (ML) and Bayesian inference were chosen. Differences between populations were detected in pigmentation pattern, radula, shell sculpture, shell size and shape of the muscular scars. Molecular analyses support the previous the maintenance of *Burnupia* as a separate clade from Ancyliinae. These are preliminary results and need more representatives of Planorboidea in order to refine the phylogeny of the group.

Slug Thieves: Nematocyst Acquisition Process in Aeolid Nudibranchs

Lisa Xie Paggeot*^{1,2} and Terry Gosliner¹

¹California Academy of Sciences, Department of Invertebrate Zoology and Geology

²San Francisco State University, Department of Biology

Nudibranchs encompass over three thousand species around the world, and still counting. One subgroup of nudibranchs is called aeolids: a specialized group of nudibranchs that are capable of stealing nematocysts from their cnidarian prey and using them as part of their own defensive mechanism. Nematocysts are also known as “explosive cells”, a variety of special organelles that are present in cnidarians. The relationship between the nematocysts in nudibranchs and their cnidarian prey remains unclear due to the variation and diversity within nematocysts. Earlier studies also show a discrepancy in the results, warranting a project looking at different species of aeolid nudibranchs and their cnidarian prey. My project focuses on comparing nematocyst content in multiple aeolids and cnidarians along the Californian coast to examine specificity of nematocyst selection and retention within Nudibranchia. Preliminary results show that different aeolid nudibranchs vary in the diversity of nematocysts they retain, and these only represent a subset of nematocysts found in their prey.

The Role of Ecological Interactions in the Diversification of Galapagos' Land Snails

Christine E. Parent*¹

¹University of Idaho

Islands are ideal systems to track the evolutionary processes of diversification through time. In Galapagos endemic land snails these processes have left a signature in the form of predictable patterns of phenotypic differentiation and community assembly over time. As species accumulate via speciation and colonization on islands, biological communities increase in diversity and complexity, and species niche space becomes increasingly defined by a greater number of biotic dimensions whereas abiotic conditions remain the same across the archipelago. In Galapagos *Naesiotus* snails, phenotypic variation within species is found to be greatest on youngest islands and declines with island age, and this decline is tightly associated with the number of congeneric competitors found on each island. These results strongly suggest a pattern of increasing competition reducing phenotypic variation within species on older islands consistent with stabilizing selection. By reconstructing the evolutionary history of *Naesiotus* snails and characterizing phenotypic variation and environmental and ecological variation where species occur, it becomes possible to determine the effect of selection stemming from increasingly complex communities on the tempo and mode of phenotypic differentiation. Ultimately this work represents a first critical step in understanding the influence of multidimensional selection on the rate and trajectory of phenotypic evolution in natural systems where multidimensional niche space prevails.

***Falcidens* Salvini-Plawen, 1968 (Chaetodermatidae), a Genus of Aplacophora with a Great Taxonomical and Morphological Diversity in Brazilian Marine Deep Waters**

Flávio Dias Passos*^{1,2}, Marcel Sabino Miranda², Paulo Vinicius Ferraz Corrêa², and Paola Visnardi Fassina²

¹Department of Animal Biology, Institute of Biology, University of Campinas, Campinas, Brazil

²Graduate Program in Animal Biology, University of Campinas

The genus *Falcidens* is one of the most speciose among the caudofoveate aplacophorans, with about 40 described species distributed worldwide. These species exhibit a great morphological diversity, and recently, molecular studies have suggested that this genus may not be monophyletic. Obtained from bottom samples collected in Brazilian oil-rich marine areas, many specimens of *Falcidens* have been analyzed, revealing that such morphological diversity is also present in the Southwestern Atlantic. Three species were already identified, *F. targatus*, *F. acutargatus* and *F. australocaudatus*, and at least four other new ones are present in that material. The first two are from the subgenus *Chiastofalcidens*, and so bear sclerites with a criss-cross ornamentation and a moderate tail. *F. australocaudatus* has a long, distinguished tail and is similar to *F. caudatus* and *F. hartmani* from the north Atlantic and north Pacific, respectively. Two of the new ones have homogeneous bodies, but one is very long and the other is short and robust; they are similar to *F. sagittiferus* (North Europe) and *F. limifossorides* (Pacific Central and South America), respectively, also from the north Atlantic. The third new species remembers *F. procerus* (Pacific South America) in its slender tailed body shape. A fourth new species has a body shape similar with individuals of genus *Chaetoderma*, and the sclerites are similar with *F. sterreri* (North Europe). This genus is here recorded as a species-rich and morphologically diverse in Brazilian waters, as in other parts of the world, filling up a gap on the knowledge about these molluscs from the South Atlantic.

Community Structure of Intertidal Muricids (Mollusca; Muricidae) Present in Verde Island, Batangas City, Batangas Philippines

Ruthela P. Payawal*¹, Brian B. Valencia¹, Adelyn Escobar¹, Karl Arbie Borrero¹

¹Dept of Biology, College of Science, Polytechnic University of the Philippines

Muricidae, a family of predatory marine snails is the second largest family under the Order Neogastropoda. Their feeding habits and therapeutically useful compounds make them an important family of marine gastropods. Verde Island, located in Batangas City, Philippines, was identified as one of the rich biodiversity areas in the planet. However, there is no existing record on the diversity of Muricidae in the area. This study aimed to provide baseline information about the community structure of family Muricidae in Verde Island. Sampling was conducted during wet and dry season done thru gleaning in seven 20 meter transects with ten 1x1 m² quadrats in the six barangays of the island. Physico-chemical parameters of the sea water (temperature, dissolved oxygen, pH, and conductivity), abundance, frequency and relative values of each species were recorded. A total of thirty-one(31) species belonging to six subfamilies composed the Muricidae community at Verde Island. Analysis of variance (ANOVA) revealed that there is no significant difference between the species diversity of intertidal muricids and seasons ($p=0.736$). However, there is a statistically significant difference between the species diversity of intertidal muricids among the different barangays of Verde Island ($p=0.001$). Canonical Correlation Analysis (CCA) showed that the diversity and abundance of different species were influenced by physicochemical properties of the island.

Missing Gaps in the Family Goniadorididae H. Adams & A. Adams, 1854 (Mollusca: Nudibranchia). Past, Present and Future.

Sofia Paz-Sedano*¹, Terrence M. Gosliner², and Marta Pola^{1,3}

¹Departamento de Biología, Facultad de Ciencias, Universidad Autónoma de Madrid; Campus de Excelencia Internacional UAM + CSIC, C/ Darwin, 2, 28049 Madrid, Spain

²Department of Invertebrate Zoology, California Academy of Sciences, San Francisco

³Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM), Campus de Excelencia Internacional UAM + CSIC, Madrid, Spain

The family Goniadorididae H. Adams & A. Adams, 1854 is a group of Nudibranchs whose species richness, systematic, biogeography and phylogeny is far from known. This family includes eight different genera (*Okenia* Menke, 1830, *Goniadoris* Forbes & Goodsir, 1839, *Ancula*, Lovén, 1846, *Lophodoris* G. O. Sars, 1878, *Spahria* Risbec, 1928, *Trapania* Pruvot-Fol, 1931, *Goniadoridella* Pruvot-Fol, 1933, and *Murphydoris* Sigurdson, 1991) within which around 130 species are currently considered valid. However, the richness of the family is highly underestimated since approximately 100 more species are found in different field guides reported as unidentified. In addition, some of the valid species lack complete anatomical descriptions, several species have been synonymized without consensus among experts and, in the last years, cryptic and pseudocryptic species have been reported, masking not only the exact number of species but also their real distribution range. Molecular data are missing for most of the species and phylogenetics studies have only been carried out for one of the eight genera belonging to this family. Moreover, the latest studies show that the phylogenetic relationship between the species of the different genera are not resolved, and that Goniadorididae is deeply needing a worldwide revision. In summary, the few studies available in the family Goniadorididae keep this group of nudibranchs still very unknown to science, with a wide variety of pending studies involving different fields of research, such as taxonomy, systematics, biogeography and ecology.

Community Structure of Intertidal Muricids (Mollusca; Muricidae) Present in Verde Island, Batangas City, Batangas Philippines

Ruthela Perez*¹, Brian B. Valencia¹, Adelyn Escobar¹, and Karl Arbie Borrero¹

¹Department of Biology, College of Science, Polytechnic University of the Philippines

Muricidae, a family of predatory marine snails is the second largest family under the Order Neogastropoda. Their feeding habits and therapeutically useful compounds make them an important family of marine gastropods. Verde Island, located in Batangas City, Philippines, was identified as one of the rich biodiversity areas in the planet. However, there is no existing record on the diversity of Muricidae in the area. This study aimed to provide baseline information about the community structure of family Muricidae in Verde Island. Sampling was conducted during wet and dry season done through gleaning in seven 20 meter transects with ten 1x1 m² quadrats in the six barangays of the island. Physico-chemical parameters of the sea water (temperature, dissolved oxygen, pH, and conductivity), abundance, frequency and relative values of each species were recorded. A total of thirty-one(31) species belonging to six subfamilies composed the Muricidae community at Verde Island. Analysis of variance (ANOVA) revealed that there is no significant difference between the species diversity of intertidal muricids and seasons ($p=0.736$). However, there is a statistically significant difference between the species diversity of intertidal muricids among the different barangays of Verde Island ($p=0.001$). Canonical Correlation Analysis (CCA) showed that the diversity and abundance of different species were influenced by physicochemical properties of the island.

Micrarionta Land Snails Living on San Clemente Island, California: One Species or Two?

Timothy A. Pearce*¹, Marvin C. Fields¹, and Nathan Brouwer²

¹Carnegie Museum of Natural History, Section of Mollusks

²University of Pittsburgh, Department of Biological Sciences

Nomenclature of the larger *Micrarionta* living on San Clemente Island has shifted from a form in 1939 (*M. gabbi* form *maxima*) to a full species in 1990 and 1996 (*M. maxima*), to a synonym (of *M. gabbi*) since 2003. However, samples of fully grown shells from the island consistently hint at the presence of size bimodality, so this study reopens the question whether *M. maxima* should be considered a distinct species. Multivariate analysis of more than 20 shell characters of more than 700 individual shells could discern two clusters. Larger shells tend to occur on the NE side of the island, which tends to have more mesic habitat. Are the two forms a single species that grows larger in moister habitats, or are they two species with different habitat preferences? This talk addresses whether *M. gabbi* and *M. maxima* are one species or two, by examining shell morphology with respect to the snails' position on the island and their habitat. Molecular analysis could be examined to corroborate the morphological findings.

Phylogenetic Patterns of Dorid Nudibranch Spicule Networks

Brian K. Penney*¹ and J. Mitchell Young¹

¹Biology, Saint Anselm College

Dorid nudibranchs are a key taxon for investigating the evolution of feeding, defense and color patterns. However, a robust phylogeny of the group has proven elusive, partly because their soft bodies make it hard to identify clear morphological characters. Recent molecular phylogenies suggest large rearrangements of traditional groupings based on reproductive, radular and gill characters. Dorid nudibranchs typically contain innumerable calcareous spicules so we used micro-CT scans of species from across the phylogeny to examine the arrangement of spicule networks for new characters. *Cadlina* + *Aldisa* possess networks of small, rodlike spicules embedded in sheaths of connective tissue that reticulate in a trabecular fashion. Both rhinophores and gills are heavily invested with spicules and tubercles are supported by columns of spicules and connective tissue. Dorididae + Discodorididae have dense basal mats of spicules, to which the organized spicule rosettes of the tubercles are connected by branched roots of spicule tracts. Both rhinophores and gills are heavily invested with spicules. *Onchidoris* + *Okenia* possess dense, overlapping sheets of branched spicules, tubercles with spicules that cascade over the mantle surface. Rhinophores have many spicules but gills are aspiculate. Hexabranchus + Chromodorididae + Polyceridae have isolated spicules of varying shapes, which are often absent from regions of the body such as rhinophores, gills, and tubercles. This grouping supports recent molecular phylogenies and the conclusion that the Cryptobranchia and Phanerobranchia are not monophyletic. Histological work suggests connective tissue and muscle connections vary somewhat independently, potentially providing new supporting characters.

Molecular Phylogeny of African Vitrinidae: Unravelling Tertiary Distribution Patterns

Beat Pfarrer*^{1,2}, Bastian Brenzinger², Yasunori Kano³, Michael Schrödl², Nerida Wilson⁴, and Gonzalo Giribet¹

¹Department of Invertebrate Animals, Naturhistorisches Museum Bern, Bernastrasse 15, CH-3005 Bern, Switzerland

²Institute of Ecology and Evolution, University of Bern, Bern, Switzerland

The Vitrinidae represent the life form of semislugs with small translucent shells, belonging to the superfamily Limacoidea. The family consists of approximately 120 species with a few widespread taxa in the Holarctic and a considerable number of small range taxa in the Afrotropis. Furthermore, the family is speciose on the Macaronesian Islands and in Eastern Africa, where it approaches the equator. Little information is available on the phylogeny of the Vitrinidae, due to reduced conchological and anatomical traits. Our investigation comprised vitrinid species from Europe, East Africa and Macaronesia. Here, two mitochondrial markers, CO1 and 16S and a set of nuclear markers, namely H3, ITS2 and 28S were used for the molecular aspect of the study. The molecular and the anatomical data provided an intriguing first insight into the phylogenetic relationships of these major groups. A hitherto unknown East African species revealed to be directly related to the Macaronesian group rather than to the supposed East African congeners. The separation of the East African Vitrinidae into two major clades could be confirmed, i.e. *Arabivitrina* Thiele, 1931 and *Calidivitrina* Pilsbry, 1919. The sister taxon relationship between the Macaronesian and East African Vitrinidae could be proven. On the one hand, this combined clade connects to the European Vitrinidae with *Eucobresia* as sister taxon. On the other hand, our results confirm that this combined clade is part of the well-documented, certainly Tertiary transsaharian biocoenosis. This work presents the first stepping stone to the future exploration of the biogeographical aspects and the evolutionary life history of the Vitrinidae with a new molecular dataset.

Archipelago-Wide Patterns of Diversity and Divergence Among an Endemic Radiation of Galápagos Land Snails

John G. Phillips*^{1,2,3}, T. Mason Linscott^{1,2,3}, Andrew M. Rankin^{1,2,3}, Andrew C. Kraemer^{1,4}, and Christine E. Parent^{1,2,3}

¹Department of Biological Sciences, University of Idaho, 875 Perimeter Dr., Moscow, ID 83843

²Institute for Bioinformatics and Evolutionary Studies (IBEST), University of Idaho

³BEACON Center for Evolution in Action, 567 Wilson Rd., East Lansing, MI 48824

⁴Department of Biology, Creighton University, 2500 California Plaza, Omaha, NE 68178, USA

⁵Department of Malacology, Academy of Natural Sciences of Drexel University

Species diversity on islands is typically initiated by colonization. Newly arrived species on remote islands are likely to encounter less predation and competition, which might facilitate their divergence and speciation within island as they fill previously unoccupied niche space. Thus, establishing patterns and timing of colonization can enhance our understanding of adaptive radiation. Herein, we use *Naesiotus* snails in the Galápagos islands to estimate timing of colonization from mainland South America. We explore inter-island patterns of colonization and within-island radiations to understand their contribution to community assembly. Contradicting previously published topologies, phylogenetic reconstructions using genome-scale data suggest that most *Naesiotus* form island-specific clades, with sympatric speciation dominating cladogenesis. Time-calibrated phylogenetic and ancestral area reconstructions generally align with geologic age of the islands, although colonization from the mainland and a few colonization and speciation events among and within islands predate previously estimated dates of island emergence. Galápagos *Naesiotus* also adhere to the island progression rule, with colonization proceeding from old to young islands and within-island diversification occurring earlier on older islands. Our work provides a framework for evaluating the contribution of colonization and in situ speciation to the diversity of other Galápagos lineages.

Factors influencing microevolutionary processes in taxonomically challenging land snail species of *Trochulus* (Gastropoda: Hygromiidae)

Małgorzata Proćków¹, Joanna R. Pieńkowska², Tomasz Strzała³, Elżbieta Kuźnik-Kowalska⁴,
Jarosław Proćków⁴, Paweł Błazej⁵, Paweł Mackiewicz⁵

¹Museum of Natural History, Faculty of Biological Sciences, University of Wrocław, ul. Sienkiewicza 21, 50-335 Wrocław, Poland

²Department of Cell Biology, Faculty of Biology, Adam Mickiewicz University, ul. Umultowska 89, 61-614 Poznań, Poland

³Department of Genetics, Faculty of Biology and Animal Science, Wrocław University of Environmental and Life Sciences, Koźuchowska 7, 51–631 Wrocław, Poland

⁴Institute of Biology, Faculty of Biology and Animal Science, Wrocław University of Environmental and Life Sciences, ul. Koźuchowska 5b, 51-631 Wrocław, Poland

⁵Department of Bioinformatics and Genomics, Faculty of Biotechnology, University of Wrocław, ul. F. Joliot-Curie 14a, 50-383 Wrocław, Poland

Species of the genus *Trochulus* are ideal organisms to study evolutionary and ecological processes leading to genetic differentiation and reproductive isolation in the absence of morphological differences, or to explain the morphological variability in the absence of genetic divergence. Clear conchological distinction between *T. phorocheatus*, *T. hispidus* and *T. plebeius* did not always agree with the mtDNA sequence analyses: 69% of *T. phorocheatus* sequences are monophyletic and the remaining are grouped with *T. hispidus*. The genetic similarity and the lack of significant differences in the reproductive system may indicate an ability to hybridization. We also revealed: (1) conchological distinction between *T. striolatus* and *T. sericeus*; (2) anatomical, ecological and genetic differentiation of *T. graminicola*; (3) compatibility of morphological traits and monophyly of *T. striolatus*, and (4) intermediate shell phenotypes of *T. coelomphala* and *T. hispidus*, whose genitalia were typical of *T. coelomphala* and their COI gene sequences were grouped with either *T. coelomphala* or *T. hispidus* complex. *T. hispidus* and *T. sericeus* do not represent separate biological species since they can freely interbreed giving fertile offspring and do not form separate phylogenetic lineages. Their morphological divergence results from phenotypic plasticity and selection associated with the habitat. Hairy *T. sericeus* prefers forests and moist shaded places, while mostly hairless *T. hispidus* chooses more dry habitats and open areas, exposed to the sun. This supports the hypothesis that the lack of hairs is associated with the loss of a potential adaptive function due to the change from wet to dry habitats. Research supported by the National Science Centre, Poland (2016/21/B/NZ8/03022).

Sequencing Historical Collections to Unlock Systematic and Nomenclatural Issues

Nicolas Puillandre*¹, Paul Zaharias¹, Jawad Abdelkrim², Yuri Kantor³, and Alexander Fedosov³

¹Institut Systématique Evolution Biodiversité (ISYEB), Muséum National d'Histoire Naturelle

²Acquisition et Analyses de Données pour l'histoire naturelle (2AD) UMS 2700, Muséum National d'Histoire Naturelle

³A.N. Severtzov Institute of Ecology and Evolution, Russian Academy of Sciences

The advent of molecular systematics has brought deep and broad rearrangements for most molluscan taxa. Until now, the sources of the sequences primarily have been newly collected specimens rather than historical museum specimens. However, natural history collections will remain irreplaceable because they host specimens of taxa that are unlikely to be – or, when extinct, will never be, collected again, and are the repositories of name-bearing specimens necessary to link names to molecularly-defined groups. Such museum material usually has not been adequately preserved for sequencing and its use in molecular studies has been problematic. Formalin seems to constitute the worst way of preserving samples for DNA sequencing, as it causes cross linkages within the DNA, base modification, and fragmentation. Although positive results have been reported, the success rate is generally low. Samples preserved in low-grade ethanol also causes DNA fragmentation that are also comparatively inaccessible to PCR-based methods, although here again success stories do exist. Soft parts preserved dried are protected from degrading agents, water in particular, and sequencing success rates are generally good depending on the handling of the tissues post mortem. Finally, mollusk shells have also been successfully sequenced. Second generation sequencing methods offer cost-effective opportunities to sequence short fragments of DNA, e.g. through hybrid-enrichment approaches, and are the most promising for accessing historical DNA in collections. Whatever the solution, historical collections should not be considered as lost for DNA-based studies, but as an incomparable reservoir of material to answer systematics and evolutionary questions, whose potential is only beginning to be realized.

Diversification in a Rainforest Land Snail: The Genus *Corilla* Adams & Adams 1858

Dinarzarde C. Raheem*¹ and Thierry Backeljau²

¹Department of Life Sciences, Natural History Museum, London SW7 5BD, UK

²Royal Belgian Institute of Natural Sciences, Vautierstraat 29, B1000 Brussels, Belgium

The Western Ghats–Sri Lanka biodiversity hotspot has a phylogenetically diverse land-snail fauna, with many taxa being endemic or largely endemic to this region. Among the genera endemic to the hotspot is the pulmonate land snail *Corilla* H. & A. Adams, 1858. Species of *Corilla* inhabit tropical rainforest and moist monsoon forest, where they are usually found on the forest floor, among leaf litter and decaying wood. Taxonomic diversity in *Corilla* is concentrated in Sri Lanka, where ten of the 11 extant species occur, all endemic to the island. The Sri Lankan species constitute two distinct groups, a lowland group and a montane one. The shells of lowland and montane species differ in the overall shape and colour, the form of the lip and the arrangement of the folds inside the mouth of the shell. How have these patterns evolved? A preliminary phylogenetic study based on mt DNA sequence data, while not resolving most deep-level relationships within Sri Lankan *Corilla*, suggests that speciation has involved multiple transitions between montane and lowland habitats, with convergence towards a lowland shell morphology. We are exploring these issues further in an ongoing study on the species diversification and systematics of Sri Lankan *Corilla*. The study is based on extensive recent collections; our analytical approach involves the phylogenetic analysis of genomics (RADseq) data, ancestral state reconstructions, and multivariate analysis of shell morphological and climatic data.

High-Throughput Identification of Homologous Neurons in the Nudibranch *Berghia stephanieae*

M. Desmond Ramirez*¹, A. Tamvacakis², J. Dwyer¹, and J. Bergan¹, P. Katz¹

¹University of Massachusetts Amherst

²Georgia State University

Divergence between homologous neurons across species is thought to be a major source of species-specific variation in neural circuitry and behavior. In nudibranchs, we can individually identify homologous neurons across species using soma location, axonal projection, and neurotransmitter expression. In the case of swimming nudibranchs, homologous neurons are involved in different neural circuits which underlie different types of swimming behavior. For example, the same neuron may be important for the neural circuit for swimming in one species, but not involved in the swim circuit in another. These differences are at least partially determined by receptor expression, which varies between and within species. Despite the tractability of the nudibranch brain, only a handful of neurons have been identified and characterized. To facilitate comparisons of neurons within and between species, we have developed high-throughput methods for identification and characterization of neurons in nudibranch brains based on anatomy and gene expression, creating a brain atlas for the reference species *Berghia stephanieae*. This atlas includes morphological, physiological and molecular information for each neuron from new and emerging methods like CLARITY tissue clearing, lightsheet microscopy, and single cell RNA-seq as well as more traditional immunohistochemistry and in situ hybridization. The *Berghia* brain atlas will provide a foundation for cross-species comparisons of homologous neurons in nudibranchs to better understand constraints that maintain neuron homology as well as differences in gene expression that lead to divergent neuron physiology and neural circuit function in behavior.

Sea Slugs of Southern Norway; An Example of Citizens Contributing to Science

Cessa Rauch*¹ and Manuel António E. Malaquias¹

¹Section of Taxonomy and Evolution, Department of Natural History, University Museum of Bergen University of Bergen, PB7800 5020 Bergen, Norway

Citizen scientist are volunteers that help out scientists by providing them with data as a hobby in their spare time. The concept originated from the United States and United Kingdom during the 1990s in an attempt to open up science to the public. Ever since it became a vastly popular tool for crowdsourcing data. And although Citizen Science also has its pitfalls, it is due to its success that the concept is extensively spread. In Norway: sea slugs of Southern Norway is an example of a Citizen Science project. With a tiny but tight community of around 180 active members. The project focusses on sea slugs that live along the coast between the Bergen area southwards to the Swedish border, as this area had been a scientific void for nearly 80 years. The project goals are to establish an image and genetic library of all collected species, explore the occurrence of cryptic species complexes, and monitor the presence of alien species. Southern Norway alone has a coastline of about 8000 Km, which makes it a particularly challenging task to get a proper overview of the sea slug diversity. But thanks to our established network of Citizen Scientists, the project already registered 100 different species and a total of 1800 new entries in our database. This successful relationship results from the fact that we actively involve Citizen Scientists in the project. Which makes the project a prime example of how citizens can decisively contribute to the success of a scientific endeavour, making the all experience much more challenging, dynamic and rich.

Assessing Aquatic Communities Using *Stagnicola elodes* and its Assemblage of Trematode Parasites

Timothy A. Rawlings*¹, Hanna J. MacLean¹, and Brooke A. McPhail²

¹Department of Biology, Cape Breton University, Sydney, Nova Scotia, B1P 6L2, Canada

²School of Public Health, University of Alberta, Edmonton, Alberta, T6G 1C9, Canada

Freshwater snails play critical roles as intermediate hosts in the life-cycles of many species of digenean trematodes. Over the past seven years, we have periodically sampled trematode cercariae emerging from freshwater snail species (including *Amnicola*, *Gyraulus*, *Helisoma*, *Physa*, *Promenetus*, and *Stagnicola*) in Blacketts Lake, a small (172 ha) suburban freshwater lake in eastern Canada. Our sampling has uncovered 13 morphologically-discrete larval types representing 35 genetically-distinct parasite lineages (putative species), with each parasite typically associated with a single snail species. The large freshwater snail, *Stagnicola elodes*, currently harbours the greatest diversity of trematodes in Blacketts Lake, with 13 parasite species identified to date. This species richness is lower than the 16 species reported for *S. elodes* from Douglas Lake, Michigan, in 1937, but greater than the 8 species reported from the same lake following 50 years of human impact. Inter-lake comparisons of trematode communities associated with host species, such as *S. elodes*, have the potential to reveal interesting and biologically-meaningful measures of the relative health of aquatic communities. Lower parasite richness, for instance, can be indicative of environments unable to support specific parasite lifecycles due to factors associated with pollution, habitat loss, and species introductions. Likewise, different assemblages of parasites within a given host can reflect differences in presence of intermediate and definitive hosts. Given the widespread geographic distribution of *S. elodes* in North America, and its propensity to be exploited as an intermediate host by trematodes, this freshwater snail holds great potential as a bioindicator for assessing the relative integrity of aquatic environments.

Genome Assembly of the Pearl Oyster *Pinctada margaritifera* : a Tool for Environmental and Evolutionary Research

Celine M.O. Reisser*¹, Jeremie Vidal-Dupiol², Jeremy Le Luyer¹, Chin Long Ky¹, and Serge Planes³

¹IFREMER Centre du Pacifique, UMR241 Ecosystemes Insulaires Oceaniens, Labex Corail, BP49, 98725, Vairao, Tahiti, Polynésie Française

²IHPE Université de Montpellier, CNRS, IFREMER, université de Perpignan Via Domitia, Montpellier, France

³PSL Research University, EPHE-UPVD-CNRS, USR3278 CRIOBE, Labex Corail, Université de Perpignan, 52 Av. Paul Alduy, 66860 Perpignan Cedex, France

Pearl farming, through the aquaculture of the pearl oyster *Pinctada margaritifera*, is the second economic resource of French Polynesia, after tourism. However, the industry is facing an economic crisis, partly linked to overproduction and a reduction of pearl quality. In addition, record high temperatures were monitored in the last few years in Polynesian lagoons, which results in higher stress and mortality in the cultivated stocks. Facing global change and a decrease in the economical income of the pearl industry, Ifremer and the French Polynesian government are studying ways to improve this industry and increase pearl quality while decrease oyster aquaculture impact on the lagoon. Today, genomic resources are widely used to study species reaction to their environment, and specific genetic architecture of economically relevant traits (growth, resistance to disease, pearl color). Ifremer thus sequenced and assembled the first genome of the black lip pearl oyster, *P. margaritifera*, using Illumina 120x and PacBio 15x sequencing. *P. margaritifera's* genome is 1.3Gb long and contains 19116 scaffolds (N50= 119126bp, L50=3326) and about 54000 genes. Interestingly, this genome size is bigger than other *Pinctada* species (all under 1Gb). We will present the characteristics of the pearl oyster genome, its peculiarities with regard to probable gene family expansions and contractions during its evolution, and illustrate its current use in various environmental and evolutionary studies, such as pearl color and quality, sex determination, or the reproductive effort of natural versus exploited stock in lagoons.

Molluscan Mycophagy

Casey H. Richart*¹, BJ Stacey, Kathryn Turner, and Liam E. O'Brien

¹Santa Barbara Botanic Garden

Engaging the public in science can be mutually beneficial. A benefit to science includes the documentation of ecological interactions where a researcher may have difficulty compiling a sufficient number of events to make statistical inferences. Here we report on the citizen science project Molluscan Mycophagy (<https://www.inaturalist.org/projects/molluscan-mycophagy>) that collects ecological interactions of terrestrial gastropods consuming fungi including lichens. Currently, 450 observations from 72 species of terrestrial gastropods have been curated to the project. We report on a systematic survey of Arionoidea and Limacoidea observations in order to make general inferences across these species. Molluscan mycophagy is a year-long phenomenon that peaks in the Fall and Spring. Fungal food appears most important to *Prophysaon andersoni*, *P. foliolatum*, and *Hesperarion niger* where ca. 20% of observations show fungus consumption. The primary aim of this project is to identify which terrestrial gastropods consume the most fungus and which fungi are most often consumed by terrestrial gastropods in order to lay the groundwork for future research. Through collaboration between scientists and citizens we have a much better understanding of who the key players are in an ecological interaction that is potentially important to food web, nutrient cycling, and dispersal processes. This project rewards citizen scientists that were motivated to seek out molluscan mycophagous interactions by offering them concrete ownership of their contributions in the form of authorship on a manuscript that summarizes these findings. The hope is to help create a culture of positive reinforcement to other citizen scientists that may desire such recognition.

Distribution Patterns and Genetic Differentiation of the Endangered Thick-Shelled River Mussel *Unio crassus* Philipsson, 1788 in Southwest Germany

Ira Richling*¹ and Cornelia Krause¹

¹Stuttgart State Museum of Natural History, Zoology

The Thick-shelled River Mussel *Unio crassus* (Unionidae) is one of the most threatened species of aquatic molluscs in Central Europe and suffered dramatic population losses in the last decades. At present more or less isolated remnants of a former continuous distribution range remain. Despite its critical conservation status and a boom in research on freshwater mussels basic questions on intraspecific diversity, distribution patterns and the resulting taxonomic concepts still remain unresolved. However, this knowledge is crucial for any conservation activities. The limits of previous attempts trying to master the extremely high variability in shell morphology are clearly reflected in the creation of literally hundreds of names/synonyms and demand the promising inclusion of genetic data. We therefore studied genetic diversity and differentiation by microsatellite analyses and mitochondrial COI sequence data of populations of *Unio crassus* from Southwest Germany. With populations from tributaries of Rhine (North Sea) and Danube (Black Sea) this area covers the two large drainage systems of Central Europe. An additional set of samples included the last remaining population from the Weser drainage (North Sea as well). A total of 17 populations represented by 25 individuals each was studied. The analysis of COI sequences revealed at least two major lineages in the study area: In the catchments of the Rhine both lineages are present and populations have an admixed population structure, whereas the populations of the Weser and the Danube drainage systems showed lower genetic diversity.

Development and Integration of Lures into Southern Florida's Giant African Snail (*Lissachatina fulica*) Eradication Program

Amy L. Roda*¹, Jocelyn G. Millar², Mary Yong Cong³, Chris Jacobsen⁴, and Rory J. McDonnell⁵

¹United States Department of Agriculture

²Department of Entomology, University of California Riverside

³Division of Plant Industry, Florida Department of Agriculture and Consumer Services

⁴Department of Plant and Environmental Protection Services, University of Hawaii

⁵Department of Crop and Soil Science, Oregon State University

Lures are essential tools in eradication programs for invasive species. However, their use in programs aiming to control or eradicate terrestrial gastropods is relatively unexplored. The southern Florida *Lissachatina fulica* eradication program allowed a realistic evaluation of their utility. In field studies, immature and adult *L. fulica* were attracted to banana fruit and a commercially produced bait. Only the commercially produced snail bait did not attract mammals, however the bait was rapidly infested with fly larvae. A distillate made from cat food attracted snails more than the commercial bait and did not attract flies and vermin. However, inconsistency between batches prevented reliable use in the program. A commercially available papaya flavored oil was found to attract more snails than the cat food distillate. Chemical analysis of the oil identified 22 chemicals, which comprised > 98% of the volatile profile emitted. A synthetic blend was made that emitted the same release rates of the papaya oil odors. In laboratory and field bioassays, the synthetic papaya oil, applied to cotton wicks as water and canola oil or water and mineral emulsions, attracted more snails than oil emulsion control wicks. When tested in the southern Florida *L. fulica* eradication program, direct ground application of the synthetic papaya oil emulsion increased the number of snails killed by over 87% when compared to water emulsion controls. The synthetic lure provides a non-toxic, inexpensive and consistent attractant that could aid in *L. fulica* eradication and management programs.

Morphometric Species-Level Discrimination of Fossil Taxa in a Neogene Venerid Species Complex

Peter D. Roopnarine*¹

¹Department of Invertebrate Zoology and Geology, California Academy of Sciences

Species delimitation within fossil molluscan species complexes is problematic. The underestimation of fossil diversity hampers accurate assessments of paleobiogeographic, evolutionary and extinction patterns. Increasingly sophisticated morphometric methods allow greater resolution of distinct evolutionary units, but establishing species boundaries using statistically significant differences alone ignores numerous intraspecific complications. Here I propose a criterion based on interspecific morphometric distances among morphologically-similar, phylogenetically close species that are qualitatively and stratigraphically distinct. Distances form the basis of a metric whereby other units in a complex are recognized as distinct phylogenetic units only if their morphometric distances exceed the metric. *Lirophora* a diverse bivalve venerid genus which originated in the western Atlantic 35 mya. The genus has spread throughout the tropical western Atlantic and eastern Pacific. It is abundant in the fossil record and there are at least 4 extant species, but species are difficult to distinguish. *Lirophora latilirata* is a Miocene species from the Calvert Formation of Maryland; however, a widespread Recent species bears the same name. Because the western Atlantic experienced significant oceanographic changes and high extinction after the Miocene, it is unlikely that the Recent and Miocene species are the same. Geometric morphometric and elliptical Fourier analyses of specimens from the Miocene, Pliocene, Pleistocene, and Recent of the southeastern United States suggest that the Recent group is a distinct, unnamed species. Analysis of Miocene-Recent specimens from this region suggests that the true diversity of the genus is at least four times greater than currently recognized.

A Brief History of Computerization of Mollusk Collections

Gary Rosenberg*¹

¹Academy of Natural Sciences of Philadelphia, Drexel University

Computerization of mollusk collections in the United States started in the 1970s. The original SELGEM standards emphasized rigorous formatting, with several consequences. In some cases information was lost, for example recording only last names and initials for collectors and donors. In other cases information was added, such as administrative divisions and latitudes and longitudes for localities. Verbatim fields were lacking that would have allowed determining what inferences were made as data were standardized, as were metadata fields for documenting how the inferences were made and who made them. Some fields were initially omitted from the standards, for example, ocean, continent and habitat classification (marine, freshwater, terrestrial) and have been added haphazardly at different institutions when they were considered useful. The initial data model did not support one-to-many structures for identifications, provenance, or citations, so they were usually not rigorously treated. Many of these issues are common to other natural history disciplines, and many have been addressed by development of standards like Darwin Core, but there are also issues that affect mollusks in particular. A raw count field can leave it unclear what was counted: e.g., valves or individuals for bivalves. Many mollusks are found as dead shells, but mollusk databases usually do not have fields indicating whether individuals were live or dead-collected. Development of enhanced standards will improve the usefulness of mollusk collections in addressing research questions.

Integrating Population Genetics and Genomics with Shell Shape Analyses on the Brooding Chiton *Onithochiton neglectus* (Polyplacophora:Chitonidae)

Priscila M. Salloum*¹, Anna W. Santure¹, Pierre de Villemereuil², and Shane D. Lavery¹

¹School of Biological Sciences, The University of Auckland, New Zealand

²Centre for Functional and Evolutionary Ecology (CEFE), Montpellier, France

The current state of DNA sequencing technologies has prompted invaluable advances in the field of molecular ecology for non-model species, in which the increasing accessibility to generate Single Nucleotide Polymorphisms (SNPs) using reduced representation sequencing has been playing a major role. These changes have raised concerns about the future of other broadly adopted methodologies, such as mitochondrial DNA (mt-DNA) and morphological analyses. To test the comparability and complementarity of methods involving SNPs, mt-DNA and morphology in non-model species, we used *Onithochiton neglectus*, a chiton endemic to New Zealand with brooding behaviour and low gene flow. *O. neglectus* presents extensive morphological variation and is broadly distributed across a latitudinal gradient, in which isolated populations are potentially subjected to local selective pressures. We generated a large panel of SNPs, sequenced the mitochondrial genes COI and 16S, and analysed variation in shell shape using geometric morphometrics for 16 *O. neglectus* populations collected across New Zealand and its Sub-Antarctic Islands. We identified strong agreement in the SNPs and mt-DNA results of population stratification. A comparison between the mt-DNA and morphological patterns across populations revealed inconsistencies in *O. neglectus* taxonomic classification, highlighting the need for a revision. SNPs give more resolution to the patterns revealed by mt-DNA, and allow for additional tests regarding local adaptation. We conclude that these three approaches were highly complementary for the complex *O. neglectus* system, and combining SNPs with mt-DNA and morphology allows a wider range of questions to be addressed with higher precision in studies of wild species with problematic taxonomy and limited genetic information.

Mollusca Types in Great Britain: A Union Database for the UK

Andreia Salvador*¹, Anna Holmes², and Harriet Wood²

¹Department of Life Sciences, Natural History Museum, London

²Department of Natural Sciences, Amgueddfa Cymru – National Museum Wales

Type specimens are essential to the study of malacology and many are distributed across a wide range of museums in the UK. The aim of the project (2016-2018), funded by the John Ellerman Foundation, was to unify images and information on Mollusca type specimens in several large collections in Great Britain. Malacological curators from Amgueddfa Cymru – National Museum Wales and the Natural History Museum, London worked with staff at seven partner museums in six UK cities (Kelvingrove Art Gallery & Museum, Glasgow; The Hunterian Museum, Glasgow; The Great North Museum: Hancock, Newcastle-upon-Tyne; The Manchester Museum; Leeds City Museum; World Museum, Liverpool; and Royal Albert Memorial Museum, Exeter). Together we developed an online resource connecting these Mollusca collections for the first time. Currently, data on over 1800 type lots are available on the Mollusca Types in Great Britain website (<https://gbmolluscatypes.ac.uk/>).

***Mytella strigata* Emerging as an Invasive Marine Threat in Southeast Asia**

Kitithorn Sanpanich^{*1,2} and Fred E. Wells^{3,4}

¹Institute of Marine Science, Burapha University

²Harry Butler Institute, Murdoch University

³School of Molecular and Life Sciences, Curtin University

⁴Field Museum of Natural History

The Central and South American mytilid mussel *Mytella strigata* was recently reported from the Philippines and Singapore, where its population has expanded exponentially in the last two years. We report the species has recently become widespread in the inner Gulf of Thailand, with densities reaching 40,800m⁻². It is a potential threat to lucrative Asian green mussel (*Perna viridis*) aquaculture and could be introduced to Australia, where it could foul pearl aquaculture farms. The concurrent finding of the invasive false mussel *Mytilopsis sallei* at two new sites in Thailand emphasises the urgent requirement for a detailed invasive marine species survey in the region.

Living in an Alga: A Preliminary Comparison of the Fauna Associated to Shallow-Water Red Algae from Antarctica and the Mediterranean

Júlia Sardà-Avila*¹, Rafael Sardà², and Conxita Avila¹

¹Dept. of Evolutionary Biology, Ecology and Environmental Sciences, and IrBIO, Faculty of Biology, University of Barcelona, Av. Diagonal 643, 08028 Barcelona, Catalonia

²CEAB-CSIC, 17300 Blanes, Girona, Catalonia

Shallow-water marine benthic algal communities usually harbor extremely high densities of organisms that may play essential roles in nutrient and energy flow, as well as in the ecology of the algae. In Antarctica, these communities have been scarcely studied so far, and when they are analyzed, this is done for a few taxonomical groups separately, thus missing the overall perspective of the whole communities. Our study intends to describe the nearshore Antarctic Peninsular benthic community living in the red alga *Gymnogongrus turquetti*, and to compare the results to an ecologically similar alga, *Sphaerococcus coronopifolius* from the Mediterranean; both algae belong to the Class Florideophyceae, Order Gigartinales. Samples of these two species were investigated in order to establish an inventory and determine abundance, species richness, diversity, and size of the organisms. Using SCUBA, the selected algae were gently removed from the substrate and enclosed in a plastic bag during the summer season (at the different localities). Samples were fixed and preserved, and all epibionts were removed later in the laboratory. A total of 4398 specimens from the Mediterranean and 4040 specimens from Antarctica were found in ca. 250 g of algae, within five replicates, respectively.

LiMPETS, a Citizen Science Program, Demonstrates the Effectiveness of California's Marine Protected Areas in Allowing Owl Limpets (*Lottia gigantea*) to Grow Larger and More Abundant.

Hannah Sarver*¹, Rosemary Romero², and John Pearse³

¹Pacific Grove Museum of Natural History

²Greater Farallones Association

³Professor Emeritus, Department of Ecology and Evolutionary Biology University of California, Santa Cruz

LiMPETS (Long-term Monitoring Program and Experiential Training for Students) is a citizen science program for students, educators, and volunteer groups (limpets.org). Citizen scientists monitor the coastal ecosystems of California's national marine sanctuaries, increasing awareness and stewardship of these important areas. This statewide program provides hands-on coastal monitoring experiences that empower teachers, students, and the community to conduct real science and serve as ocean stewards. Through our rocky intertidal program students monitor a variety of marine mollusks including *Lottia gigantea* (Sowerby 1834) at LiMPETS sites, some of which are located inside California Marine Protected Areas (MPA's). LiMPETS has been collecting size measurements and counts of *L. gigantea* since 2006 because they play an important ecological role as their grazing activities maintain biodiversity in rocky intertidal assemblages. Moreover, they are important prey for Black Oystercatchers, and are harvested for food by people. Student-collected data were analyzed to understand the impacts of over-harvesting on population structure of *L. gigantea*. Average individual size and abundances were compared between two pairs of MPA (no-take) and non-MPA LiMPETS sites, one in San Mateo County and one Santa Cruz County, California. *L. gigantea* sizes from MPA sites were larger on average and more abundant in MPA sites than non-MPA sites. These results indicate that long-term citizen science data are useful and when combined with MPA monitoring can be used to better understand the effects of over-harvesting on central coast *L. gigantea* populations.

Updates on Giant Clam Status and Restocking Efforts in the Philippines

Sherry Lyn G. Sayco*¹, Patrick C. Cabaitan¹, Cecilia Conaco¹, Lala Grace Calle¹, Jeremiah Noelle C. Requilme¹, Eymard John P. Sy¹, Roger G. Dolorosa², Elmer G. Villanueva², Niño Jess Mar F. Mecha², Krizia Meryl A. Ecube², Girley S. Gumanao³, Christine Mae A. Edullantes³, Tracy D. Tabalanza³, and Rezelle B. Sobradil³

¹The Marine Science Institute, College of Science, University of the Philippines, Diliman, Quezon City, 1101, Philippines

²Western Philippines University, Puerto Princesa, Palawan, Philippines

³Davao del Norte State College, Panabo, Davao del Norte, Philippines

Giant clam populations have declined because of overharvesting and other disturbances. This has led to their listing in the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES). In the Philippines, it has been 34 years since the last nationwide survey of giant clams was conducted. To provide an updated status of giant clams in the country, selected sites in three major islands; Luzon, Visayas, and Mindanao were surveyed. Giant clam diversity and abundance were assessed along transects at 1-15 m depth in selected coral reef areas at each site. Initial results showed that *Tridacna crocea*, *T. maxima* and *T. squamosa* were common at all sites. *Hippopus hippopus*, *H. porcellanus*, and *T. derasa* were only recorded in few sites in Luzon. *T. noae*, a species previously confused with *T. maxima*, was observed in Luzon and Mindanao. Individuals of the largest species, *T. gigas*, which was deemed virtually extinct in the country since the 1970s, were not observed at any of the surveyed sites except in Palawan, Luzon. However, natural recruits from restocked *T. gigas* were reported in Luzon and Mindanao indicating successful restocking efforts since 1980s. Apo Reef in Luzon had the highest diversity of giant clams with six of eight species present. Calaguas, also in Luzon, had the highest abundance with a clam density of 0.04 individuals/m² compared to the other sites where density was typically ≤ 0.01 individuals/m². Updated information on the local distribution, abundance, and diversity of giant clams is essential for establishing protection and management strategies for this endangered species.

Sexual Differentiation in Somatic Growth Within Two Species of Freshwater Mussels, *Lampsilis cardium* and *Lampsilis siliquoidea*, as a Function of Environmental Impacts

Mariah Scott*¹ and Rüdiger Bieler²

¹University of Chicago: Committee of Evolutionary Biology

²Field Museum of Natural History: Integrative Research Center

Females have to balance their survival and somatic growth with the fitness of their offspring. Somatic growth rate differences between females and males of a given species may provide insight into how costly reproduction is for females, in comparison to their male counterparts. Sexual dimorphism in shell shape is evident in these two species. Are there significant growth rate differences between females and males of *Lampsilis cardium* or *Lampsilis siliquoidea*? If so, does the amount of sexual differentiation in somatic growth differ between habitats? This study compares between female and male *Lampsilis cardium*, as well as female and male *Lampsilis siliquoidea*, from two watersheds for each species to answer these questions. The comparisons of males and females of a single species will be limited to shells taken from a single collection event. Samples from each location will include the right shell valves of up to 30 females and 30 males of the species, utilizing existing museum collections. Optical 3-D scans of the specimens will be combined with cross-sections to determine the amount of external area and shell thickness added annually for a specimen. These measurements will allow specimens to be analyzed morphologically, with simulations of their growth rates over time. The growth of a specimen will be a model of the change in shell volume and shell cavity volume of females, compared to males, over successive years of growth.

Decline and Stabilization of Black Abalone in Monterey Bay, California

J. Selgrath*^{1,2}, J. Carlton³, R. Elahi¹, J. Pearse⁴, T. Thomas⁵, J. Watanabe¹, and F. Micheli¹

¹Stanford University

²Pacific Grove Museum of Natural History

³Williams College

⁴UC Santa Cruz

⁵J.B. Phillips Historical Fisheries Project

Historical ecology seeks to describe the alterations that have occurred in communities and ecosystems over time in response to shifts in natural conditions and human impacts, thus providing us with the tools to predict how ecosystems may respond to future change. However, records are often missing of basic changes that have occurred to biodiversity and the environment. This can be true even for common species in well-studied ecosystems, such as Monterey Bay. When baseline data are missing, the long-term knowledge of scientists, naturalists, and others can provide a powerful opportunity to understand the past. In an ongoing project to reconstruct ecosystem changes in Monterey Bay, CA, we interviewed approximately 50 people who were students or researchers in Monterey Bay from 1938 to 2019. Black abalone (*Haliotis cracherodii*) are an intertidal species of abalone that are now listed as endangered. We report high densities of black abalone in the Monterey Peninsula area in the early- to mid-twentieth century. Following the return of sea otters to the area in the 1960s, black abalone populations gradually declined, and existing populations became spatially restricted to deep crevices. However, since the mid- 1980s, populations of black abalone in the Monterey Peninsula have remained stable.

Astonishing Photochemical Diversity in the Scallop *Argopecten irradians* (Pectinidae) Indicates Sophisticated Visual System

Jeanne M. Serb*¹

¹Iowa State University, Department of Ecology, Evolution and Organismal Biology

Understanding how molluscs perceive their photic environment can be challenging when color learning assays are difficult to employ and interpret. Here we apply a molecular approach to study color vision. Color discrimination is typically considered to arise from antagonism between two or more opsin-based photopigments that are sensitive to different portions of the light spectrum, called color opponency. Alternatively, color opponency can also be mediated through two opsins within a single cell when the opsins have distinct intracellular signal transduction cascades. We tested hypotheses on the visual capabilities of the scallop, *Argopecten irradians*, by first determining the molecular diversity of photopigments with tissue-specific transcriptomic data. We identified twelve complete opsin gene sequences that were phylogenetically placed into five major opsin clades, indicating difference in signal transduction cascades. Then, using a combination of RNA isolated and synthetic genes, we successfully expressed eleven opsins in vitro. Spectral analysis of these opsin proteins demonstrated that all are light sensitive and have different photochemical properties, including chromophore preference and absorbance maxima. Our results provide evidence that color opponency is possible within scallops and the next steps are to test hypotheses on spatial and temporal expression differences. These data provide the foundation to better understand sensory evolution in bivalves, which will require comparative and integrative approaches.

Discovery of New Light-Sensing Proteins in the Scallop: Strategies to Best Utilize Large Datasets

Jeanne M. Serb^{*1}, G. Dalton Smedley¹, and Davide Faggionato¹

¹Iowa State University, Department of Ecology, Evolution and Organismal Biology

The rise of high-throughput RNA sequencing (RNA-seq) and de novo transcriptome assembly has had a transformative impact on how we identify and study genes in the phototransduction cascade of non-model organisms like molluscs. But the advantage provided by the nearly automated annotation of transcriptomes may at the same time hinder the possibility for gene discovery and the discovery of new gene functions. Standard functional annotation based on domain homology to known protein families can only confirm group membership, not identify the emergence of new biochemical function. Here, we show the importance of a strategy that circumvents the limitations of semiautomated annotation, then apply this workflow to photosensitivity as a means to discover non-opsin photoreceptors. We hypothesize that non-opsin G-protein-coupled receptor (GPCR) proteins may have chromophore-binding lysines in locations that differ from opsin. We provide the first case study describing non-opsin light-sensitive GPCRs based on tissue-specific RNA-seq data of the common bay scallop *Argopecten irradians*. Using a combination of sequence analysis and three-dimensional protein modeling, we identified two candidate proteins. We tested their photochemical properties and provide evidence showing that these two proteins incorporate 11-cis and/or all-trans retinal and react to light. photochemically. Based on this case study, we demonstrate that there is potential for the discovery of new light-sensitive GPCRs, and we have developed a work-flow that starts from RNA-seq assemblies to the discovery of new non-opsin, GPCR-based photopigments.

A Rock-boring and Rock-ingesting Freshwater Bivalve (Shipworm) From the Philippines

J. Reuben Shipway*¹, Daniel L. Distel², Gary Rosenberg³, Gisela P. Concepcion⁴, and Margo G. Haygood⁵

¹University of Massachusetts

²Ocean Genome Legacy, Northeastern University

³Academy of Natural Sciences, Drexel University, Philadelphia

⁴Marine Science Institute, University of the Philippines

⁵Department of Medicinal Chemistry, University of Utah

Shipworms are a group of wood-boring and wood-feeding bivalves of extraordinary economic, ecological and historical importance. Known in literature since the fourth century BC, shipworms are both destructive pests and critical providers of ecosystem services. All previously described shipworms are obligate wood-borers, completing all or part of their lifecycle in wood and most are thought to utilize wood as a primary source of nutrition. Here we describe a new anatomically and morphologically divergent species of shipworm, *Lithoredo abatanica*, that bores in carbonate limestone rather than in woody substrates and lacks adaptations associated with wood boring and wood digestion. The species is highly unusual in that it bores by ingesting rock and is among the very few known freshwater rock-boring macrobioeroders. The calcareous burrows and burrow linings of this species resemble fossil borings normally associated with bivalve bioerosion of wood substrates (ichnospecies *Teredolites longissimus*) in marginal marine and marine settings. The occurrence of this newly recognized shipworm in a lithic substrate has implications for teredinid phylogeny and evolution, and interpreting paleoenvironmental conditions based on fossil bioerosion features. Finally, we report the presence of Type-II methantrophic endosymbionts in the gills of *Lithoredo abatanica* – the first known occurrence of this symbiotic association in the Animal Kingdom.

Biodiversity, Evolution, and Extinction in the Imperiled Galápagos-Endemic Land Snail Genus *Naesiotus*

Nathaniel F. Shoobs*^{1,2}, Andy C. Kraemer^{3,4}, John G. Phillips^{4,5}, and Christine E. Parent^{4,5}

¹Department of Malacology, Academy of Natural Sciences of Philadelphia

²Department of Biodiversity, Earth, and Environmental Science, Drexel University

³Department of Biology, Creighton University

⁴Department of Department of Biological Sciences, University of Idaho

⁵BEACON Center for Evolution in Action

Though virtually unknown to the public in comparison to their charismatic vertebrate neighbors, such as Darwin's finches or giant tortoises, the bulimulid land snails of the genus *Naesiotus* (Gastropoda: Stylommatophora: Bulimulidae) form the most species-rich and phenotypically diverse evolutionary radiation endemic to the Galápagos archipelago. The magnitude and evolutionary import of Galápagos bulimulid diversity has largely been veiled by a lack of basic taxonomic work on the group. While the majority of species have been described for over a century, no comprehensive systematic account of the Galápagos bulimulids has ever been completed, despite numerous historical attempts. With 89 available names, 61 validly described species and 10-20 new species in need of description, *Naesiotus* is long overdue for a systematic revision. The necessity of this work is compounded by the fact that, like many other Pacific island land snail faunas, a significant number of *Naesiotus* species have recently been driven extinct. Most species in the genus have suffered dramatic reductions in population and range sizes since the mid 1970s. Insufficient taxonomic knowledge of both the past and present diversity and distributions of *Naesiotus* species precludes an actionable understanding of their evolution or their rapid, ongoing extinction. In this talk, we provide an overview of what is known about the diversity, distribution, and rapid decline of this spectacular, yet poorly known portion of the Galápagos terrestrial fauna drawing from phylogenetic and morphological studies, extensive field surveys, and the examination of all extant museum material.

First Global Phylogeny of the Deep-Sea Gastropod Genus *Scaphander* Reveals Higher Diversity, a Possible Need for Generic Revision and Polyphyly Across Oceans

Justine Siegwald*¹, Trond R. Oskars¹, and Manuel António E. Malaquias¹

¹Department of Natural History, University Museum of Bergen

Scaphander (Gastropoda, Cephalaspidea) is a genus of deep-sea, soft-bottom snails currently comprised of about 17 valid extant species distributed worldwide. The traditional use of shell-based systematics and the difficulties to sample deep-sea species have led to rather confusing systematics of the genus. Valdés (2008; 2015) studied in detail several species of *Scaphander* from the tropical southwest and Eastern Pacific, and Eilertsen and Malaquias (2013) revised the systematics of the Atlantic species, providing the first molecular phylogeny for *Scaphander*. To revise the systematics of the worldwide *Scaphander* and infer species relationships, we extended the taxon sampling including so far about 70% of the recognized diversity plus several other members of the family Scaphandridae and have used an integrative taxonomy approach, combining morphological characters, multi-locus molecular phylogenetics (COI, 16S rRNA, 18S, 28S rRNA), and molecular species delimitation methods (ABGD, GMYC, PTP). We present the first global phylogeny of the genus, which points to greater species diversity and the possible need to reassess the taxonomic status of genera commonly confused with *Scaphander*, such as *Meloscapander* and *Sabatia*. The results suggest that the biogeography and cladogenesis of *Scaphander* do not conform with a pattern of separate radiations in the Indo-West Pacific and the Atlantic + Eastern Pacific.

Weird is the New Normal - How Understanding Adaptations Informs Deep Molluscan Phylogeny

Julia D. Sigwart*¹

¹Queen's University Belfast, Marine Laboratory

Perhaps the most notably unifying feature among all the classes of molluscs is their differentness. The ability of the molluscan body plan to take on new form and new niches is what sets molluscs apart among the animals. Arthropods have greater numbers, but no phylum has greater disparity than Mollusca. The path to our current understanding of molluscan evolution is littered with bizarre creatures that defy the 'typical' boundaries of their clades - bivalved gastropods, chitons with no foot, , vermiform bivalves, cephalopods and snails with dermal sclerites, and the relentless repeated evolution of both shell loss and supplementary armor. While such creatures are usually individually dismissed as one-off weirdoes, in fact they show us the absolute power of molluscs to test the limits of animal evolution. Recently derived living species with mosaic features defy our assumptions about the polarity of key morphological characters. Such innovations and recombinations have been a persistent feature of molluscan evolution for over 540 million years. A comprehensive understanding of molluscan phylogeny must have room not only to accommodate, but also celebrate molluscan weirdness.

Red Listing can Protect Deep Sea Biodiversity

Julia Sigwart*¹, Chong Chen², Elin Thomas¹, Monika Bohm³, and Mary Seddon⁴

¹Queen's University Belfast

²Japan Agency for Marine-Earth Science and Technology

³Zoological Society of London

⁴IUCN

Only forty years ago, we discovered the marvellous deep-sea hot spots that we call hydrothermal vents. Just over 600 of these miniscule, auditorium-sized oases exist in the vast deep expanse of the ocean. The IUCN Red List has been disproportionately used for well-studied species with possible restoration actions, and successfully applied to molluscs from many environments but mainly terrestrial and freshwater groups. During the last year, we have completed Red List assessments for a pilot set of 15 hydrothermal vent endemic molluscs (of around 700 global vent endemic animals). The Scaly-foot Snail or Sea Pangolin, *Chrysomallon squamiferum* occur at three sites-- the total seabed area of the three vent fields is only around 0.02 km² (about two football fields), and two sites are under mining exploration licences granted by the International Seabed Authority. Based on the small number of locations, and the potential for a future threat to suddenly drive the species much closer to extinction, the Scaly-foot Snail is now listed as Vulnerable to extinction, and all Indian Ocean vent endemic molluscs are assessed either as Vulnerable or Endangered. The inclusion of iconic deep-sea species in the Red List is long overdue given their exceptional scientific importance, and it seems an appropriate commemoration for the 40th anniversary of the discovery of the natural wonders at hydrothermal vents, and the 70th anniversary of the IUCN.

Neogastropod Phylogeny: New Insights after a Study on Buccinoideans

Luiz Ricardo L Simone*¹

¹Museu de Zoologia - University of São Paulo, Brazil

A sample representing the superfamily Buccinoidea has been recently studied, based on detailed phenotypy. Samples of the main families were processed in a phylogenetical analysis and have helped to reorganize the phylogeny and taxonomy of the Neogastropoda. One of the results is the suggestion of dividing the order Neogastropoda into two suborders Toxoglossa and Stenoglossa. The former grouping only Conoidea. While Stenoglossa can be subdivided as shows the following cladogram: (Benthobiidae (Muricoidea ((Columbellidae ((Buccinidae (Dorsanidae-Nassariidae)) (Fasciolaridae-Melongenidae))) (Volutoidea-Cancellarioidea)))). Argumentation and explanations for the above suggested arrangement will be given in order to collaborate fulfilling a gap between order and family levels in Neogastropoda.

Is the Flamed Tigersnail, *Anguispira alternata*, a Species Complex or Complex Species?

John Slapcinsky*¹, Reham Fathey², Ryan Corlett¹, Timothy A. Pearce³, and Kenneth H. Hayes⁴

¹Florida Museum of Natural History, 1659 Museum Road, Gainesville, Florida 32611, USA

²Cairo University, El – Gammaa Street, Giza, 12613, Egypt

³Carnegie Museum of Natural History, 4400 Forbes Avenue, Pittsburgh, Pennsylvania 15213, USA

⁴Bishop Museum, 1525 Bernice Street, Honolulu, Hawaii 96817, USA

The land snail genus *Anguispira*, endemic to North America, has a distribution primarily east of the Great Plains with two disjunct species in the Colombia River basin. Most *Anguispira* inhabit rotting wood except for a group that occurs on limestone outcrops, and the subgenus *Zonodiscus*, which lives in leaf litter. One species, *Anguispira alternata*, is arguably the best-studied land snail species in eastern North America. Yet, despite this distinction, the taxonomy of the genus and *A. alternata* in particular remains unsettled. The last systematic treatment of the genus, more than 70 years ago, recognized only five highly variable species with numerous subspecies. Subsequently, several subspecies have been treated as full species without justification. Most of these are one of two groups, taxa treated as forms or subspecies of *A. cumberlandiana* or *A. alternata*. Recent work by others incorporating DNA data demonstrated that the taxa treated as forms or subspecies of *A. cumberlandiana* should be recognized as species. Our recent collecting focused on acquiring topotypic material for all named taxa in addition to material from across each taxon's geographic range is facilitating reanalysis of the taxa treated as subspecies of *A. alternata* using additional genetic and anatomical data. These data indicate that many, but not all, of the named forms of *A. alternata* should be species-level taxa and revealed several cryptic species. These taxa are recovered as distinct lineages in phylogenetic analyses and are congruent with morphologically recognizable clades. Many of the taxa treated as subspecies of *A. alternata* overlap in range without intergradation, supporting their recognition as distinct species.

Molluscan Biomineralisation in the Antarctic – An Integrative Approach

Victoria A. Sleight*¹

¹Department of Zoology, University of Cambridge

Molluscs owe some of their evolutionary success to their ability to biomineralise. Despite centuries of fascination with molluscan shells, we are yet to form a fundamental molecular and cellular understanding of how they develop, grow, remodel and regenerate after damage. The Antarctic clam (*Laternula elliptica*) lives in the Southern Ocean at temperatures almost permanently below 0 °C. Its shell is at risk of damage from both acidifying seawater and scouring icebergs, making it a valuable model to study biomineralisation with particular relevance to cold water biology and environmental protection. In fact, this clam has a remarkable capacity to repair severe shell damage and is a uniquely tractable system to study shell regeneration and remodelling. Here, I will present data from my multidisciplinary research that investigates the development, growth and repair of molluscan shells. I use embryology, histology, immunohistochemistry, electron microscopy, proteomics, gene expression, transcriptomics and gene network analysis to show that the initial developing shell (prodissoconch I and II) is built using a distinct suite of developmental genes, rather than well-characterised biomineralisation candidates known to be involved in adult shell secretion, and that shell repair does not seem to recapitulate shell development. In addition, I explore functional modules of the mantle gene regulatory network in adult animals, discovering that candidate biomineralisation genes fall into two different modules, one responsible for transport of ions and another responsible for the production of extracellular matrix proteins. I will discuss these findings in the context of shell evolution and propose future directions for the field of molluscan biomineralisation.

Miocene California and Caribbean Mollusks Refine Age of the Salada Formation, Southwestern Baja California Sur, México

Judith Terry Smith*¹

¹U.S. National Museum of Natural History

Miocene California and Caribbean Mollusks refine age of the Salada Formation, southwestern Baja California Sur, México For decades yellow marine sandstones were regarded as Pliocene and mapped as the Salada Formation on both sides of the Baja California peninsula. Described by Heim (1922), the type section in Arroyo La Salada was lost to science until the early 1990s when Schwennicke (1998) recovered and measured the 12-m thick section (GPS N24° 30.153', W111° 31.573'). The unit crops out only in the Magdalena embayment as far south as Arroyo La Muela, north of Todos Santos. Some 700 m downstream from the type section Smith (1991) collected a hard gray concretionary layer equivalent to the lower Salada beds and identified the Middle Miocene (15 – 13 Ma) California index species *Amusium lompocensis* (Arnold) and *Amusiopecten vanvlecki* (Arnold), also *Interchlamys aidei* (Harris) described from Falcón, Venezuela, *Clementia dariena* (Conrad), *Cyathodonta gatunensis* (Toula), *Psammotreta (Leporimetis) trinitaria* (Dall), and *Raeta hasletti* (Anderson). A slightly older Caribbean assemblage is found in Arroyo La Muela (GPS N23° 32'49", W110° 14'33"): *Turritella abrupta* (Conrad), *Cymia henekeni* (Maury), *Cymatophos turbacoensis* (Anderson), and *Pyrucilia diadela* (Woodring). The formation has broader importance as one of the northern outliers of the Perrilliat (1981, 1987) Pacífico – Atlántico Province, named for Caribbean mollusks in the La Mira basin, Michoacan, that expanded the Tertiary-Caribbean Province of Woodring (1966). In tectono-stratigraphic terms, the Salada Formation was deposited when the Baja California Peninsula lay against mainland México (Lyle and Ness, 1991), before the ancient Gulf of California began to open at ca 12 Ma (Sutherland et al, 2012, Geosphere).

Considering the Process of Speciation while Investigating Species Limits Suggests Reinforcement as a Driver of Speciation in Taildropper Slugs

Megan L Smith*¹ and Bryan C Carstens¹

¹Ohio State University

By considering the population-level processes that drive speciation, we can estimate species boundaries while gaining insight into the process of speciation. Most approaches to species delimitation have considered divergence-only models, and, while these models are appropriate for allopatric speciation, they fail to capture many of the processes that drive speciation, such as gene flow (e.g. in reinforcement) and population size changes. To enable biologists to consider these processes while inferring species boundaries, we introduce the R-package *delimitR*, which uses machine learning and the Site Frequency Spectrum, and show that it has error rates comparable to traditional approaches to species delimitation. We use *delimitR* to investigate speciation and species limits in taildropper slugs (Genus *Prophyaon*) from the Pacific Northwest of North America, and find evidence that refugial dynamics, population expansion, and secondary contact have led to speciation. Considering the processes that have driven speciation in *Prophyaon*, we make predictions about ecological variation. We then use ecological data, including soil pH and foraging height, to test these predictions. Our results support a complex interplay of selective and neutral forces as having driven speciation in *Prophyaon*. By considering process, we avoid erroneous inferences that can be made when population-level processes like migration drive speciation but only divergence is considered. Further, we take advantage of the proliferation of Next-Generation sequence data to make biologically meaningful inferences about species limits and how these limits arise. Our results show that *delimitR* can serve as an important conceptual bridge uniting investigations into the process of speciation.

Holding Mirrors up to Nature: The Structure and Function of the Eyes of Scallops

Daniel I. Speiser*¹

¹University of South Carolina, Department of Biological Sciences

The eyes of animals come in a variety of forms and some of the most unusual designs are found in molluscs. Scallops, for example, have dozens of eyes arrayed along the edges of their valves. These eyes provide scallops with visual acuity that far exceeds that which is observed in other bivalves. The eyes of scallops are among the only eyes known to use a concave mirror to focus light for image-formation and they are one of the very few types of eyes that contain two separate retinas. In my talk, I will discuss two recent findings regarding the eyes of scallops. First, we found that the eyes of two species of scallop demonstrate light-evoked pupillary responses. Both the bay scallop *Argopecten irradians* and the sea scallop *Placopecten magellanicus* have pupils that constrict to approximately 60% of their fully-dilated areas within several minutes of being exposed to light. At the cost of sensitivity, we predict that narrower pupils improve spatial resolution in the eyes of scallops by decreasing the influence of optical aberrations. Second, we find that tightly-packed, nanoscale spheres are likely responsible for the iridescent blue appearance of the eyes of *A. irradians* and other scallop species. Computational models indicate that the physical properties of these nanospheres are well-suited for scattering short wavelength light. Further, we find that these nanospheres are absent from black-eyed species of scallop such as *P. magellanicus*. We hypothesize that light-scattering nanospheres help prevent off-axis light from degrading image contrast in the eyes of *A. irradians* and other blue-eyed scallops.

Contrasting Phylogeography of Two Limpet Genera in the Southern Ocean

Hamish G. Spencer*¹, Claudio González-Wevar²

¹University of Otago, Department of Zoology

²Universidad Austral de Chile, Instituto de Ciencias Marinas y Limnológicas (ICML)

Molecular techniques are increasingly used to elucidate the phylogenetic relationships among molluscan species and to delineate their various geographical ranges. Such approaches have been particularly useful in groups of cryptic species and those with few or confusing conchological characters. Here we examine the relationships among two groups of limpets that are abundant on rocky coasts of the Southern Ocean. Both groups are associated to a greater or lesser degree with the bull kelp, *Durvillaea antarctica*, which is now recognized as an efficient long-distance rafter that is capable of carrying a host of invertebrate species vast distances across the Southern Ocean. Nevertheless, the two limpet groups show very different phylogeographic patterns. Members of the patellogastropod genus *Nacella* occur on numerous subantarctic islands, with most island groups having endemic species that are closely related to species on islands upstream or downstream in the Antarctic Circumpolar Current. Apparently, colonization by *Nacella* of new island groups shortly after their emergence often leads to speciation. By contrast, two cryptic species in the pulmonate genus *Siphonaria*, *S. lateralis*, and *S. fuegiensis*, are broadly co-distributed across the sub-Antarctic and exhibit low levels of genetic diversity across this range. Understanding the evolutionary history of these groups clearly requires further information, which we suggest comes from an understanding of their ecology and reproductive biology.

Deciphering Shell Color Pigmentation Pathways in the Pearl Oyster *Pinctada margaritifera* (Linnaeus 1758) through Whole Transcriptome Sequencing and Fine Gene Expression Tuning

Pierre-Louis Stenger*¹, Chin-Long Ky¹, Céline Reisser¹, Serge Planes², and Jeremie Vidal-Dupiol³

¹IFREMER, UMR 241 Écosystèmes Insulaires Océaniques, Labex Corail, Centre Ifremer du Pacifique, BP 49, 98725 Tahiti, Polynésie française

²PSL Research University, EPHE-UPVD-CNRS, USR 3278 CRIOBE, Labex Corail, Université de Perpignan, 52 Avenue Paul Alduy, 66860 Perpignan Cedex, France

³IHPE, Univ. Montpellier, CNRS, Ifremer, Univ. Perpignan Via Domitia, Montpellier France

Pearl farming is the 2nd resources of French Polynesia but its intensification in the 2000s has induced non-negligible environmental impacts and an unprecedented economic crisis. In this context, farmers, politicians and scientists are working together to invent the sustainable pearl farming of tomorrow. Among the routes of improvement, intensification and diversification of the pearl color is one of the main. The pearl oyster *Pinctada margaritifera* has the capacity to produce the most varied and colorful pearls in the world. However, the molecular mechanisms governing this phenotype remain misunderstood. In this context our study aims to decipher the molecular mechanisms encoding three important colors phenotype (red, yellow, green) through a transcriptomic study (RNA-Seq and RT-qPCR). Several candidate genes and pathways differently regulated have been identified. The red would results from the down-regulation of the porphobilinogen deaminase (heme pathway). The yellow would be due to four different pigments secreted alone or in combination; bilirubin (heme pathway), pheomelanin (Raper-Manson pathway), sepiapterin and xanthopterin (pterins pathway). The green would arise from the mix of black eumelanin (Raper-Manson pathway) or blue phorcabilin (heme pathway) with one of yellow candidate pigments or directly through the production of the green biliverdin or cobalamins (heme pathway). These results remain to be validated through methods enabling the direct detection of these pigments (e.g HPLC or resonance RAMAN). Our study provides candidate pathways to understand how color is controlled in *P. margaritifera*, and genes that could be studied for implementation of a color marker-assisted selection in this economically important species.

Mollusk Collections – A 50-year Perspective: Where Have We Been and Where Are We Going?

Ellen E. Strong*¹

¹Department of Invertebrate Zoology, Smithsonian Institution, National Museum of Natural History, MRC-163, P.O. Box 37012, Washington, DC 20013-7012, USA

The last 50 years has witnessed remarkable advances in our ability to capture, analyze, aggregate and access collections data. 50 years ago, the computer age was just beginning, and collection digitization was in its infancy. The arrival of desktop computers in the early 1980s allowed the development of databases of specimens held in collections. This period saw SEM become a routine tool in the study of molluscan shells, and witnessed the proliferation of isotopic analyses to track environmental conditions and model niche space. Collections have also become valuable tools in climate research, and for conservation management. The molecular revolution has transformed our approach to recognizing and circumscribing species, but the full power of next generation sequencing as applied to historical mollusk collections is yet to be fully realized. A renaissance is underway in comparative morphological and anatomical studies using 3D reconstruction techniques, including microCT. Pressing issues on the horizon include repatriation of natural history objects and an increasing regulatory burden. Digitization and 3D printing offer unprecedented opportunities for sharing information, but threaten to usher in an era of specimen-free biology. With dwindling staff and support for museums, now more than ever we need to think strategically about what and where to collect, and what aren't we collecting that we should. Building collaborative networks are an important way to leverage existing expertise and collections resources. Far from being static objects, integrated with new knowledge and with other objects across space and time, collections provide a dynamic framework from which to understand the changing natural world and our place in it.

Targeted Sequencing and Phylogenomics of the Critically Imperiled Pleuroceridae

Ellen E Strong*¹, Nathan V Whelan^{2,3}, Nicole Garrison³, Paul D Johnson⁴, and Jeffrey T Garner⁵

¹Department of Invertebrate Zoology, Smithsonian Institution, National Museum of Natural History, Washington, DC 20013-7012, USA

²United States Fish and Wildlife Service, Southeast Conservation Genetics Lab, Warm Springs Fish Technology Center, Auburn, AL 36849, USA

³School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University, Auburn, AL 36849, USA

⁴Alabama Aquatic Biodiversity Center, Alabama Department of Conservation and Natural Resources, Marion, AL 36756, USA

⁵Alabama Division of Wildlife and Freshwater Fisheries, Florence, AL 35633, USA

The Pleuroceridae is the second most diverse family of North American freshwater gastropods and one of the most imperiled; 79% of pleurocerid species (i.e. ~128) are considered vulnerable, threatened, or endangered, and at least 33 species and 1 genus have already gone extinct. The greatest challenge facing pleurocerids is lack of an accurate and robust systematic framework. This prevents efficient communication, effective conservation, and meaningful study of this highly imperiled and ecologically important group. Traditional Sanger-based barcoding approaches have been unsuccessful in elucidating the diversity and relationships of pleurocerids owing to unusually high rates of mitochondrial sequence divergence. Consequently, the family has been largely ignored from a molecular systematics point of view and has received limited attention since the advent of high-throughput sequencing. We used a target-capture approach to sequence 625 nuclear genes for 192 individuals representing over 70 species sampled from across the eastern United States, including from river systems of peninsular Florida, the Atlantic slope, the Mobile River basin, the Tennessee River basin, and the lower Mississippi River system. Our results confirm that all pleurocerid genera represented by more than a single species are polyphyletic, but that many clades likely merit recognition at the genus rank. Thus, the current classification does not adequately reflect phylogenetic relationships within the family and will require extensive revision. The analysis also reveals many surprising biogeographic implications and confirms the utility of the family for elucidating phylogeographic patterns. Our results support phylogenomics, and our probe set specifically, as a promising avenue in pleurocerid research.

Repeated Loss of Vision and Sensory Compensation in Deep-Sea Gastropods

Lauren Sumner-Rooney*¹, Nathan V Whelan², and Suzanne Williams³

¹Oxford University Museum of Natural History, University of Oxford

²Queen's University Marine Laboratory, Queen's University Belfast

³Life Sciences, Natural History Museum, London

Vision and colour have fascinated biologists for centuries, and represent some of the most impressive and complex evolutionary innovations. Nowhere, perhaps, is this more evident than in molluscs, where eyes and vision have evolved multiple times. Molluscs possess such great and varied structures as the chiton shell eyes, the cephalopod camera eye and the ark clam compound eye, and exhibit a wealth of light-guided behaviours including those mediated by vision. The molluscan central nervous system, inextricably linked to visual processing, also demonstrates a large functional range, from very simple cordal structures up to the complex brains of coleoid cephalopods. As such, molluscs are an enviable study system for visual ecologists and evolutionary biologists alike, offering an unparalleled opportunity to study unique visual systems, parallel evolution, and the appearance of complexity. This talk will examine several examples of molluscan photoreception and vision at different evolutionary scales, including a paedomorphic photoreceptor in plesiomorphic chitons, the evolution of eye loss in deep-sea gastropods, and the relative investment in eyes and associated central nervous systems in cephalopods. Across these three classes and a broad spectrum of complexity, mechanisms to sense and respond to light aptly reflect the seemingly endless molluscan propensity for innovation and flexibility. The wealth of wider evolutionary patterns that can be studied through photoreceptor and visual development places molluscs as a critical model system in the study of macroevolutionary processes.

The Scaly-Foot Snail Genome and the Ancient Origins of Biomineralized Armor

Jin Sun*¹, Chong Chen², Norio Miyamoto², Julia D. Sigwart³, and Pei-Yuan Qian¹

¹Hong Kong University of Science & Technology

²Japan Agency for Marine-Earth Science and Technology

³Marine Laboratory, Queen's University Belfast, Portaferry, N. Ireland

The appearance of biomineralized skeletons in the Cambrian precipitated an evolutionary arms race and the explosive diversification of animal forms(1). Understanding the genomic toolkit that enabled such innovations is critical to reconstructing animal phylogeny(2, 3). The Scaly-foot Snail, *Chrysomallon squamiferum*, combines a mosaic of biomineralized features reminiscent of enigmatic early fossils, but in a recently-diverged living species(4, 5). Using a whole-genome and tissue-specific transcriptomics, we show that its iron-infused scale and shell formation employ independent subsets of 25 highly-expressed transcription factors, and illuminate potential deep homology for its biosynthesis of nano-scale iron. Comparisons with other lophotrochozoans indicate that this biomineralisation toolkit is ancient, and the ability of molluscs to generate a diversity of hard parts draws on a capacity to dynamically modify and redeploy elements across the genome.

Developing Resilience to Ocean Acidification in Abalone Aquaculture

Daniel S. Swezey*^{1,3}, Sara E. Boles^{1,2}, Kristin M. Aquilino¹, Doug Bush³, Tessa M. Hill^{1,5}, Brian Gaylord^{1,7}, Cynthia A. Catton^{1,4}, Laura Rogers-Bennett^{4,6}, Andrew Whitehead², Jim Moore^{1,4} and Eric Sanford^{1,7}

¹ Bodega Marine Laboratory, University of California, Davis, 2099 Westshore Road, Bodega Bay, CA, 94923, USA

² Department of Environmental Toxicology, University of California, Davis, 1 Shields Ave, Davis, CA 95616, USA

³ The Cultured Abalone Farm, 9580 Dos Pueblos Canyon Road, Goleta, CA 93117, USA

⁴ California Department of Fish and Wildlife Marine Region, Bodega Marine Laboratory, 2099 Westshore Road, Bodega Bay, CA 94923 USA

⁵ Department of Earth and Planetary Sciences, University of California, Davis, 1 Shields Ave, Davis, CA 95616, USA

⁶ Karen C. Drayer Wildlife Health Center and Bodega Marine Laboratory, University of California Davis, Bodega Bay, CA 94923, USA

⁷ Department of Evolution and Ecology, University of California, Davis, 1 Shields Ave, Davis, CA 95616, USA

dswzey@culturedabalone.com

Recent research has demonstrated that most commercially harvested shellfish are sensitive to low pH conditions resulting from oceanic absorption of anthropogenic CO₂, i.e. ocean acidification (OA) with consequences including reductions in growth, calcification, reproduction and survival. In order to maintain yields of farmed shellfish under increasing global OA, industry-academic partnerships will be needed to assist growers with adaptation measures to stem the increasing threat posed by this global change. Over the past three years, the University of California at Davis' Bodega Marine Laboratory has forged an industry-academic partnership with commercial abalone growers in California, USA and the National Oceanic and Atmospheric Administration to examine potential ocean acidification impacts to abalone aquaculture and broader abalone restoration and conservation. This work has included experiments assessing impacts to both the red abalone (*Haliotis rufescens*) and the endangered white abalone (*H. sorenseni*). As part of this work, we are examining the hypotheses that differences in regional oceanography could select for variation in OA tolerance among populations of abalone, and that through examination of selective processes, adaptive variants could be identified for aquaculture and conservation in future OA conditions. In experiments to date, we have observed strong negative effects of OA on the survival of young abalone, but also substantial variation in this mortality response associated with settlement environment, maternal provisioning and both maternal and paternal genetic background. These results suggest that adaptive OA resilience strategies could be developed and applied to the continuing commercial and conservation culture of these iconic and economically valuable species.

Genomic Factors Involved in Sex Determination and Differentiation in a Protandrous Hermaphrodite Bivalve, the Pearl Oyster *Pinctada margaritifera*

Vaihiti Teaniniuraitemoana¹, Céline Reisser¹, Jérémie Vidal-Dupiol², and Gilles Le Moullac¹

¹Ifremer, UMR 241 EIO, Labex CORAIL, BP 49, 98719 Taravao, Tahiti, Polynésie française.

²IHPE, Univ. Montpellier, CNRS, Ifremer, Univ. Perpignan Via Domitia, Montpellier, France.

In the animal kingdom, sex determination can be genetic (GSD), environmental (ESD), or the result of an interaction of both (mixed sex determination, MSD). These genetic and/or environmental factors lead to sex differentiation where specific molecular cascades transform an undifferentiated gonad into a testis or an ovary. Although these mechanisms are well known in vertebrates, data on sex determination and sex differentiation in mollusks are still scarce especially in species displaying hermaphroditic features, where sex changes can occur later in adult life. The blacklip pearl oyster *Pinctada margaritifera* (Mollusca, lophotrochozoa) is a protandrous hermaphrodite species, in which a MSD system has been strongly suspected: some individuals appear to never change sex and would be genetically determined “true” males, while the other would be hermaphrodites, whose sex is epigenetically determined, under environmental influence.

Using long term sex monitoring of a pearl oyster population, whole genome sequencing, and whole genome bisulfite sequencing, we investigated the presence of potential true males, uncovered candidate SNP mutations that could control this phenotype, and analyzed the epigenetic modifications taking place in the gonads of hermaphrodite individuals, with the aim to identify the molecular processes involved in the sexualization of *P. margaritifera*. We identified 884 candidate SNPs between true males and hermaphrodites, and 2,471 differentially methylated regions (DMR) between male and female gonads. Some SNPs and DMRs impacted genes known to be involved in sex determination/differentiation.

Our results provide candidate genomic markers to be used in breeding experiments, and help to better understand the molecular processes involved in gonad reprogramming during the sex change in sequential hermaphrodites.

The Mitogenomic Phylogeny of West African Cone Snails (Gastropoda: Conidae) has Taxonomic and Conservation Implications

Manuel J. Tenorio*¹, Samuel Abalde², Jose R. Pardos-Blas², Rafael Zardoya², and Carlos M. L. Afonso³

¹Universidad de Cadiz, Dept. CMIM y Química Inorgánica – INBIO, SPAIN

²Museo Nacional de Ciencias Naturales-CSIC, Departamento de Biodiversidad y Biología Evolutiva, Madrid, SPAIN

³Universidade do Algarve, Centre of Marine Sciences (CCMAR), Faro, PORTUGAL.

A worldwide risk assessment under the IUCN Red List standards of 632 species of cone snails was carried out in 2011 indicating that most species could be classified in the Least Concern category. However, in the West African region, where hotspots of endemism occur, 43 % of the 98 cone snail species evaluated were classified from Near threatened to Critically endangered. In the following years, there has been a very sharp increase in the number of descriptions of new species of West African cone snails, particularly from the Cabo Verde archipelago, raising the number to 171. The overall quality of the descriptions for many of these new species is rather poor, and often the validity of some of these species is doubtful. This leads to a case of potential taxonomic inflation, which could certainly complicate future monitoring and eventual updates of risk status. Therefore, in order to clarify the status and validity of the species of cone snails along the West African coasts, we reconstructed a robust phylogeny based on mitogenomes of more than 100 individuals covering the species diversity of eight genera endemic to this biogeographical region. According to the reconstructed tree and pairwise sequence divergence comparisons, the number of valid West African cone species is drastically cut into almost one half, and the distribution ranges for many of the endemic species are modified accordingly. This affects directly to the Red List risk status for the remaining valid species, which will eventually require re-evaluation for proper downgrade or upgrade of their respective risk classifications.

Ampullariidae of the Midwest Region of Brasil: Hydrographic Basin Tocantins-Araguaia and Paraguay River Basin

Silvana A R Thiengo*¹, Robert H Cowie³, Monica Ammon Fernandez¹, Kevin Portilho Barbosa¹, and Kenneth A Hayes²

¹Laboratório de Malacologia, Instituto Oswaldo Cruz, Fundação Oswaldo Cruz, Rio de Janeiro, Brasil

²Bishop Museum, Honolulu, Hawaii 97822, USA.

³Pacific Biosciences Research Center, University of Hawaii, 3050 Maile Way, Honolulu, Hawaii 97822, USA.

Ampullariidae are freshwater gastropods that occur in tropical and subtropical regions of Africa, Asia and the Americas, often in dense populations. In addition to their undeniable ecological importance, they are also agricultural pests and disease vectors. Ampullariids exhibit their highest diversity in Brasil, with about 50 species of *Pomacea* found in all parts of the country. Three additional genera, *Asolene*, *Felipponea*, and *Marisa* are also found in Brasil. Here we report on the ampullariid species present in two important hydrographic basins in the central western region of Brasil, the Tocantins-Araguaia and the Paraguay basins. Both basins have been negatively impacted by increasing development of dams in the region, as well as the damaging effects of intense agriculture, deforestation and mining. The results from several regional surveys undertaken by our team, in addition to data from the Mollusc Collection of the Instituto Oswaldo Cruz, recorded four ampullariid species: *Pomacea maculata*, *Pomacea scalaris*, *Pomacea lineata* and *Marisa planogyra*. *Pomacea maculata* has the widest distribution, occurring from north-central Brasil south into Paraguay, Uruguay, and Argentina. *Pomacea scalaris* and *M. planogyra* are endemic to the Paraná-Paraguay and Prata basins, while *P. lineata* occurs along the coast of Brasil in the northeast region with some reports further south. Records of *P. lineata* in the Midwest region are probably due to anthropogenic dispersal. Detailed distribution of these species, including first records in this region are presented, with notes and illustrations of the morphology (shell and anatomy) of all four species.

How the Famous Nudibranch *Hexabranchnus sanguineus* (Rüppell & Leuckart, 1830) has Fooled Everyone – Preliminary Results

Yara Tibiriçá*¹, Manuel António E. Malaquias², Marta Pola³, Terrence M. Gosliner⁴, Juan Lucas Cervera¹

¹Universidad de Cádiz, Departamento de Biología

²University Museum of Bergen, Department of Natural History

³Universidad Autónoma de Madrid, Departamento de Biología

⁴California Academy of Sciences, Department of Invertebrates, Zoology and Geology

The “most famous” nudibranch of the world – the “Spanish dancer” *Hexabranchnus sanguineus* (Rüppell & Leuckart, 1830) – has a confusing taxonomic history with around 27 synonym names. The most dramatic rearrangement considered that all morphs of *Hexabranchnus spp.* from the Indo-West Pacific Ocean (IWP) belonged to the same species, synonymizing 20 nominal names under *H. sanguineus*. Up to now most authors have accepted *H. sanguineus* as the only species present in the IWP realm, but on the other hand the variability found in this species is intriguing and several authors questioned the conspecificity of all IWP morphs. The most recent review of the genus was based on morphology and resurrected the Atlantic Ocean species *H. morsomus* Ev. Marcus & Er. Marcus, 1952, but has still considered all morphs of *H. sanguineus* occurring in the IWP to be the same species. In this study, molecular and morphological tools are used to test whether the various colour morphs of *H. sanguineus* are conspecific or may represent different taxonomic entities. Preliminary molecular phylogenetic and species delimitation analyses of 17 specimens from across the IWP indicate the occurrence of four species in this region. Additionally, photographic evidence suggests the possible occurrence of an additional three lineages, but this warrants confirmation. Ontogenetic colour shifts and morphological similarities between species are likely the main historical causes of taxonomic confusion. Understanding the *H. sanguineus* species-complex is essential to clarify past studies on their ecology, defensive mechanisms and pharmaceutical properties.

In the Footsteps of Edmondson: Shipworm (*Bivalvia*, *Teredinidae*) Diversity, Biology, and Ecology in the Hawaiian Archipelago

Nancy C. Treneman*¹, James T. Carlton², Regina Kawamoto³, and J. Reuben Shipway⁴

¹Oregon Institute of Marine Biology

²Williams College-Mystic Seaport

³Bernice P. Bishop Museum, Malacology

⁴University of Massachusetts, Microbiology Dept.

Shipworms, recognized for centuries as the destroyers of wooden vessels, remain a serious pest of wood pilings, piers, and docks. In nature, shipworms degrade vast amounts of wood, converting the terrestrial energy stored in lignocellulose into body mass, larvae, and feces, all of which provide food for a variety of organisms. Their postmortem burrows become habitat for other species. Historical shipworm surveys in the Hawaiian Archipelago were carried out by Charles Howard Edmondson up to the 1960s, recording teredinid diversity on Oahu, with scattered reports from the rest of the Archipelago and other South Pacific islands. Our ongoing study, commenced in 2015, revisits past survey sites as well other islands and the northern atolls, with an emphasis on shipworm diversity and biogeography. In addition, we examine the role of shipworms as ecosystem engineers, teredinid ecology, life history and reproductive strategies. Short term brooders, which release planktonic larvae, dominate ports and bays with longer water retention and reduced salinity; long term brooders that release competent pediveligers are more abundant in outer coastal habitats. Three pelagic specialists are found in long-range driftwood. We detected several cryptic species and a possible change in species diversity in comparison to historical surveys. Ongoing genetic analyses will help resolve relationships among Hawaiian taxa and provide insights into their population structure. Polynesians in wooden vessels began visiting the Archipelago more than a 1000 years ago, and European ships first arrived in the 1770s. We examine how the combined roles of maritime history and rafting by ocean-currents have shaped modern shipworm diversity in the Hawaiian Archipelago.

Transcriptome Based Phylogeny of Gastropoda

Juan E. Uribe*¹, Vanessa L. González², Yasunori Kano³, David G. Herbert⁴, Ellen E. Strong¹ and M. G. Harasewych¹

¹Smithsonian Institution, National Museum of Natural History, Department of Invertebrate Zoology, 10th St. & Constitution Ave. NW, Washington, D.C. DC 20560, USA

²Global Genome Initiative, National Museum of Natural History, Smithsonian Institution, Washington, DC 20013, USA

³Department of Marine Ecosystems Dynamics, Atmosphere and Ocean Research Institute, The University of Tokyo, Kashiwa, Chiba, Japan

⁴School of Life Sciences, University of KwaZulu-Natal, P. Bag X01, Scottsville 3209, South Africa

With origins in the Cambrian (~500 million years ago) and an estimated ~100K species, Gastropoda is the second most diverse metazoan class. The clade has colonized a broad variety of environments and generated extreme morphological and developmental diversity, which have made it difficult to trace its evolutionary history. Currently, gastropods are divided into six subclasses: Heterobranchia, Caenogastropoda, Neritimorpha, Vetigastropoda, Patellogastropoda, and Neomphaliones. However, the phylogenetic relationships between Angiogastropoda (=Neritimorpha (Heterobranchia + Caenogastropoda)), Vetigastropoda, Neomphaliones, and Patellogastropoda remain unresolved despite numerous efforts using morphological, molecular and combined approaches. Discrepancies remain in the inferred phylogenetic relationships of the gastropod subclasses using the most sophisticated molecular approaches, e.g., mitogenomic vs transcriptomic, and, even among various transcriptomic studies, depending on taxon sampling, homology search, and tree reconstruction methods used. The subclass Neomphaliones has thus far been underrepresented in transcriptome-based analyses, which may be impairing our ability to robustly reconstruct relationships among the main clades. We produced sequence data for transcriptomes derived from ten taxa selected from clades with little or no prior representation in order to infer the deeper cladogenetic events within Gastropoda and, for the first time to infer the phylogenetic relationships of Neomphaliones using a phylogenomic approach. Our preliminary results indicate that resolution of early cladogenetic relationships within Gastropoda varies depending on matrix occupancy. When using a more complete matrix (>80%), monophyly of Eogastropoda and Orthogastropoda is supported, and within Orthogastropoda, there is also support for Angiogastropoda. Our results uphold a close phylogenetic relationship between Neomphaliones (represented by *Cocculina japonica*) and Vetigastropoda, which was previously reported based on morphological and mitochondrial data.

The Genome of the Chiton *Acanthopleura granulata*: An Aculiferan Perspective of Molluscan Biomineralization

Rebecca M. Varney*¹ and Kevin Kocot¹

¹University of Alabama

Molluscan genomic resources continue to increase, but with a marked bias toward bivalves and gastropods. Chitons are models for molluscan biomineralization, producing shell valves, sclerites, and radulas with teeth coated with magnetite (iron). Here we present the first genome of a chiton, the first from clade Aculifera. A single individual of *Acanthopleura granulata* was collected from the Florida Keys and DNA was extracted from foot tissue using a phenol-chloroform-based approach optimized to provide clean, high-molecular weight DNA, with modifications that proved critical for successful nanopore sequencing. A highly cost-effective hybrid assembly strategy was employed combining Illumina short reads and Oxford Nanopore long reads in MaSuRCA followed by Bionano SAPHYR optical mapping for scaffolding. After reduction of heterozygosity with Redundans, removal of bacterial scaffolds with BlobTools, and polishing of the final assembly with 4 rounds of PILON, we produced a 605.9 Mbp assembly in 73 scaffolds with an N50 of 23.9Mbp and a BUSCO completeness score of 96.2%. Annotation was carried out with multiple strategies compared. Many (but not all) genes hypothesized to be part of the conchiferan mollusc biomineralization toolkit are also present in chitons, shedding light on the possible ancestral molluscan suite of biomineralization genes. Additionally, analysis of known iron-associated proteins determined some sequence variation in known iron-binding proteins in chitons. Future screening for iron-regulated domains in the genome will be combined with 3'-biased sequencing of transcriptomes from the developing chiton radula to determine the gene expression patterns underlying magnetite mineralization.

Catches, Yield, Bycatch and Discards in the Small-Scale Cuttlefish Trap Fishery

Paulo Vasconcelos*¹, Fábio Pereira¹, Ana Moreno², and Miguel B. Gaspar^{1,3}

¹Instituto Português do Mar e da Atmosfera (IPMA), Centro de Olhão

²Instituto Português do Mar e da Atmosfera (IPMA), Divisão de Modelação e Gestão de Recursos da Pesca (DivRP)

³Centro de Ciências do Mar (CCMAR)

This study reports a detailed description of the catches, bycatch and discards in the cuttlefish (*Sepia officinalis*) trap fishery off the Algarve coast (southern Portugal). This markedly seasonal small-scale fishery constitutes a locally important socio-economic activity during spring and summer. Overall, 86 fishing surveys involving 6311 traps were performed during the fishing season (May–September) from 2009 to 2014, on sandy bottoms at 8–10 m depth. The gear catch rate (frequency of traps with cuttlefish) was 37%, with a mean of 0.9 cuttlefish caught per trap. A total of 5883 *S. officinalis* (1424.0 kg) were caught, corresponding to a CPUE of 46.6 individuals and 11.3 kg 50 traps⁻¹. Males (n = 3188) outnumbered females (n = 2695) producing a male-biased sex ratio (1 M: 0.85 F). On average, females were larger and heavier than males, with 89.6% females and 85.8% males accomplishing the MCRS (100 mm ML). Bycatch was caught in 1037 traps (catchability rate of 16.4%), comprising 1576 individuals belonging to 38 taxa, with an overall weight of 268.3 kg. BCPUE's were 12.5 individuals 50 traps⁻¹ and 9.4 kg 50 traps⁻¹, whereas bycatch rates accounted 21.1% in number and 15.9% in weight. A total of 34 bycatch species (89.5% of bycatch taxa) were discarded at sea, corresponding to discard rates of 19.5% in number and 11.1% in weight. This highly sustainable and low impacting fishery is characterised by undamaged and highly fresh target catches, together with low bycatch, discards and mortality rates.

Eye Morphology and the Depth Distribution of Large Heteropods (Pterotracheidae and Carinariidae) in the Northern Gulf of Mexico

Michael Vecchione*¹, Kristine A. Clark², Heather L. Judkins², and Brad A. Seibel³

¹NOAA National Systematics Lab., National Museum of Natural History

²Department of Biological Sciences, University of South Florida St. Petersburg

³College of Marine Science, Univ. of South Florida

Heteropods (Caenogastropoda: Littorinimorpha: Pterotracheoidea) are holopelagic gastropods with very strange eyes. We describe vertical distribution and eye size in five large species from the superfamily Pterotracheoidea. The specimens were collected by very extensive discrete-depth sampling with 10 m² Multiple Opening Closing Nets with Environmental Sampling System (MOC10). The family Pterotracheidae (*Pterotrachea coronata*, *P. hippocampus* and *P. scutata*) included the most abundant and largest specimens examined. *Carinaria lamarcki* and *Cardiopoda placenta* from family Carinariidae were generally smaller and less abundant than the pterotracheids but also well represented. Eye shape varies among these five species. We found evidence of diel migration only in *P. coronata* and *P. scutata*. The only evidence for possible ontogenetic shifts in vertical distribution was that the largest *C. placenta* (>30 mm) and *P. coronata* (>150 mm) were found only in the upper 600 m. We evaluated eye size (lens diameter) at capture depth for each species; there was no evidence of eye size increasing with depth among the five species. We also compared eye size with body length and found that relative eye size is species-specific. Unlike our expectation of eye size differences among migrators and nonmigrators, we determined that pterotracheids have smaller eyes than carinariids relative to their total body size.

SLIME: Citizen Science Focused on the Terrestrial Malacofauna of Southern California

Jann E. Vendetti*¹

¹Natural History Museum of Los Angeles County, 900 Exposition Blvd., Los Angeles, CA 90007

SLIME (Snails and slugs Living in Metropolitan Environments) is a community/citizen science initiative sponsored by the Natural History Museum of Los Angeles County (NHMLA) and hosted online by iNaturalist, since 2015. Its focus is the terrestrial malacofauna of southern California and has amassed nearly 12,000 terrestrial snail and slug records from approximately 1500 participants. Efforts to promote SLIME by NHMLA have included malocofauna bioblitzes, events (e.g. SnailFest and SnailBlitz), public lectures, and outreach through social media. The project's results include first occurrence records for snails and slugs in the state of California and in southern California counties (e.g. Los Angeles and Riversid), including the limacid slug *Ambigolimax nyctelius* (Bourguignat, 1861). These outcomes demonstrate the efficacy of citizen science to document molluscan biodiversity in a major metropolitan area and could serve as a model for similar initiatives at other museums or institutions.

Species Name Formation for Malacologists: A Quick and Helpful Tutorial

Jann Elizabeth Vendetti*¹ and Robert Garland²

¹Natural History Museum of Los Angeles County, Malacology Department

²Colgate University, Department of the Classics

Creating scientific names for species, and/or reviewing those created by other authors, is a necessary part of the job for malacologists working in taxonomy and systematics. Guidelines for the construction of species names for animals are outlined in the International Code of Zoological Nomenclature but many modern systematists are stymied by the Code because they are unfamiliar with Latin and/or have little experience navigating the idiosyncrasies of Linnaean binomial nomenclature. Therefore, in this talk the author will present 10 pragmatic and simplified strategies for creating zoological species names. They are intended to demystify the derivation and construction of species names and facilitate the process of naming species for a broad audience of malacologists working in systematics.

Predicting Arm Loss Patterns from Life History Traits in Eight Northeastern Pacific Octopus Species

Kelley M. Voss*¹ and Rita S. Mehta¹

¹Ecology and Evolutionary Biology Department, University of California, Santa Cruz

Octopuses are ecologically important mesopredators with eight hydrostatic arms that may be involved in myriad tasks, including locomotion, hunting, exploration, and reproduction. The radial arrangement suggests that the arms are morphologically similar with the exception of the specialized third right arm in males that is modified for copulation. Sublethal predatory events result in varying degrees of arm loss, and octopus are capable of arm regeneration after such events. In this study, we compare arm scaling patterns in museum specimens and elucidate which morphological and ecological factors may predict arm loss in our multispecies data set. We first measured morphological features of octopus (arm lengths, sucker diameter, interocular distance, mantle length) and documented arm loss for an ontogenetic series which included at least 70% of the size range for each species. We discovered that arm loss was more frequent in arm pairs 1 and 2. We also observed in arm loss patterns between the sexes, with higher numbers of amputations in the arm radially opposing the specialized reproductive arm in males. It is unknown how arm loss and regrowth affect the performance of an individual octopus in the wild. Missing arms have been shown to reduce or eliminate an octopus' opportunities for copulation, but arm loss or regrowth may also translate to a reduced efficiency in prey capture, locomotion, and evading a predator. This study is the first to show whether particular life history traits related to octopus morphology or ecology can inform the frequency of sublethal predation in important marine mesopredators.

Mollusks in Deep-Sea Chemosynthetic Habitats: Hydrothermal Vents, Hydrocarbon, Seeps, Whale- and Wood-Falls

Robert C. Vrijenhoek*¹

¹Monterey Bay Aquarium Research Institute

Clams, mussels, and gastropods dominate deep-sea hydrothermal vents and hydrocarbon seeps worldwide. Many of these mollusks host nutritional endosymbionts, or they graze directly on microbial biofilms that are sustained by reduced gasses (sulfides, methane and hydrogen) dissolved in vent and seep effluents. Obtaining their sustenance from chemosynthetic primary productivity lead some researchers to suggest that these taxa might be ancient---they are 'living fossils' that were sheltered from the catastrophic changes affecting Earth's photic zone. Initial evidence from fossilized Paleozoic and Mesozoic vent and seep deposits appeared to support the 'living fossils' hypothesis, but more recent studies have revealed major transitions of chemosynthetic faunas during the Mesozoic. Molecular phylogenetic analyses indicate that most of the dominant vent and seep vent taxa diversified following the Paleocene/Eocene thermal maximum (PETM), which led to a widespread anoxic/dysoxic events in deep-ocean basins about 45 million years ago. Thus, deep-sea chemosynthetic taxa were not sheltered from surficial processes. Instead, they appear to be particularly vulnerable to climatic shifts affecting deep-ocean temperatures and circulation, because their chemosynthetic requirements restrict them to extremely narrow redox zones where subsurface fluids laden with reduced gases contact oxygenated seawater. Contemporary vent and seep mollusks have evolved some extraordinary means to expand this boundary, but they are nonetheless susceptible to climatic shifts that would alter the breadth of the oxic/anoxic interface.

Biodiversity Research on Marine Heterobranchia in Indonesia – in the Light of National and International Regulations, Collaborations and Networking

Heike Wägele*¹, Nani Undap¹, Adelfia Papu^{1,2}, Dario Karmeinski¹, and Alexander Donath¹

¹Zoological Research Museum Alexander Koenig, Bonn, Germany

²Faculty of Mathematics and Sciences, Sam Ratulangi University, Manado, Indonesia

Studying phylogenetic relationships and understanding evolution needs the inclusion of many members of the respective taxon to get a picture as complete as possible. Indonesia is a hotspot with regard to marine Heterobranchia, and therefore a large source of potential candidates for these studies. Working with Indonesian counterparts allowed us to study several areas in North Sulawesi with regard to the species diversity and submit or publish these results. Usually we are dealing with at least 25% of undescribed species. However, regulations especially in Indonesia are very strict and thus hamper knowledge transfer or working in a network with other scientists. In this talk I will present results from our studies in North Sulawesi, but also the problems and how they affect other projects.

Biodiversity, Biogeography and Vulnerability of Hydrothermal Vents: A Case Study Using Bathymodioline Mussels

Kerry Walton*^{1,2}, Bruce Marshall², and Ashley Rowden^{3,4}

¹Department of Zoology, University of Otago

²Museum of New Zealand Te Papa Tongarewa

³National Institute of Water and Atmospheric Research

⁴School of Biological Sciences, Victoria University of Wellington

Hydrothermal vent habitats represent a very small proportion of the seafloor, yet they host diverse, unique and poorly-known faunas. Due to their formations of high-value poly-metallic deposits, many vent fields are being evaluated for mineral extraction, necessitating an improved understanding of vent communities and population connectivity patterns. Correct taxonomic determination of specimens is important to assay the sensitivity of habitats to exploitation and to accurately quantify patterns of regional connectivity. Restriction of analyses to enigmatic named species or broad genus-level identifications fails to account for the most sensitive taxa: regional endemics. We present a simple genetic dataset of bathymodioline mussels with a focus on the southwest Pacific and discuss what such datasets can tell us about the vulnerability of venting systems and, more importantly, what they cannot.

Growth Rates of Potamidid Snails in Mangroves in Northern Australia

Fred E. Wells*^{1,2} and John Keesing^{3,4}

¹School of Molecular and Life Sciences, Curtin University

²Integrative Research Center, Field Museum of Natural History

³CSIRO Oceans and Atmosphere, Indian Ocean Marine Research Centre, The University of Western Australia

⁴Oceans Research Institute, Indian Ocean Marine Research Centre, The University of Western Australia

Mudwhelks of the genera *Terebralia* and *Telescopium* dominate the sessile invertebrate epifauna of many Indo–West Pacific mangroves. They can be useful in monitoring the health of mangrove communities as they are thought to have a shorter lifespan than the trees, but there is little data on the lifespan of these snail species. To eliminate this gap, growth rates were obtained using data from tagging experiments fitted to the von Bertalanffy growth equation. *Terebralia palustris* and *T. semistriata* were tagged at Mandorah, Northern Territory in May 1999 and remeasured approximately every six months for two years; *Telescopium telescopium* was added in December 1999. *Terebralia palustris* and *T. semistriata* were tagged at two sites near Dampier, Western Australia in April 1999 and remeasured quarterly until July 2000. Both species of *Terebralia* grew faster and larger at Mandorah, near the centre of their ranges; growth and adult sizes were less in Dampier, near their southern range limit. The small (up to 6 cm) *Terebralia semistriata* matures in about four to six years, *T. palustris* (up to 19 cm) in 10 to 12 years and *T. telescopium* (up to 13 cm) in about 10 to 12 years. However, the high proportion of adults in some populations of all three species suggest the lifespans may be much longer.

Advances in Quaternary Non-Marine Molluscan Research: The View from Britain and NW Europe

Tom S. White*¹

¹Department of Life Sciences, Natural History Museum, Cromwell Road, London, SW7 5BD, UK

The rich molluscan fossil record preserved in terrestrial interglacial deposits has been an established cornerstone of Quaternary biostratigraphical and palaeoecological research in Britain and NW Europe. In the last decade, significant advances in dating techniques and new fine-grained sampling of critical fluvial and lacustrine sequences have transformed understanding of this record, particularly for the late Middle Pleistocene (the last ~500,000 years). It is now possible to examine broader patterns in these data against the backdrop of global Quaternary climate change provided by marine and ice core records, providing evidence for major environmental changes on a regional level, such as the onset of rising sea-levels during different interglacials, and the timing and extent of previously unrecognized lowland glaciations. This increasingly detailed picture of climatic and environmental change has profound implications for understanding Britain's important Palaeolithic archaeological record, as well as for modelling possible future climate change scenarios.

Shell Pigmentation In The Eastern Oyster, *Crassostrea virginica*

Michael Whiteside*¹, Suzanne Williams², Sho Ito³, Kazumas Wakamatsu³, Jessica Wade⁴, and Ximing Guo¹

¹Rutgers University, Department of Marine and Coastal Sciences

²Natural History Museum London

³Fujita Health University

⁴Imperial College London

To better understand the nature of shell pigmentation in the eastern oyster, *Crassostrea virginica*, four color morphs were described and crossed amongst each other in breeding experiments undertaken in an aquaculture facility. Proportions of color morphs in the progeny suggest color and pattern are under genetic control. A comparative transcriptome study was then conducted to identify differentially expressed genes (DEGs) between dark and light regions of mantle tissue. Several transcripts were found to be differentially expressed in common across three replicates, including several genes involved in the heme pathway. UV/visible spectroscopy results suggest that both black and brown shell colors contain two pigments, and the absence of characteristic banding patterns indicate neither pigment is a porphyrin. Raman data show no evidence of carotenoid-type pigments, but do show evidence of melanin pigments. Other pigment peaks are consistent with linear tetrapyrroles. To further analyze melanins, demineralized shells were subjected to Soluene-350 solubilization, H₂O₂ oxidation, and hydriodic acid (HI) hydrolysis. Soluene-350 solubilization yielded A₅₀₀/g and A₆₅₀/g values, which were similar and did not show evidence for relatively eumelanin- or pheomelanin-rich pigments. H₂O₂ oxidation afforded low levels of both pyrrole-2,3,5-tricarboxylic acid (PTCA) and thiazole-2,4,5-tricarboxylic acid (TTCA) levels, markers for eumelanin and pheomelanin, respectively. However, the levels of dopa in the HI hydrolysates were extremely high and high levels of 4-amino-3-hydroxyphenylalanine (4-AHP) and 3-amino-4-hydroxyphenylalanine (3-AHP), markers for pheomelanin, were found, which suggests that pheomelanin may also play a role in both black and brown pigmentation.

Systematic Revision of the Predatory Snail Genus *Paciocinebrina* Houart, Vermeij & Wiedrick, 2019 (Muricidae: Ocenebrinae) Based on Molecular And Morphological Analyses

S. G. Wiedrick*^{1,2} and D. J. Eernisse¹

¹Department of Biological Science, California State University, Fullerton, CA 92834 USA

²Department of Invertebrate Paleontology, Natural History Museum of Los Angeles County, 900 Exposition Blvd., Los Angeles, CA 90007 USA

Paciocinebrina Houart et al. (2019) is a species-rich genus restricted to western North America, with species found in the mid-intertidal to depths of 284 m. They were formerly assigned to *Ocinebrina* Jousseaume, 1880, which is now considered to be a distinct European clade. Species of *Paciocinebrina* are notorious for their phenotypic plasticity and unsettled taxonomy. The paucispiral protoconchs found in members of this group are indicative of direct development, a reason to suspect regional differences that confound species delimitation. The abundant literature contains a daunting number of misidentifications and other errors, with an overdue need for systematic revision. Because species descriptions have been based chiefly on shell features, we used these in our selection of museum or private vouchers for study, and collected new corresponding material targeted for molecular analysis from 15 California field sites ranging from Humboldt (40°N) to Orange County (37°N), and additional material (in prep.) from Washington (48°N). Spiral morphology of each taxon was recorded to compare morphological characteristics with molecular results. We estimated species limits and phylogenetic relationships across *Paciocinebrina* with a combined analysis of mitochondrial (COI + 16S) and nuclear (28S + ITS-2) sequences. Molecular results have affirmed the validity of some recognized *Paciocinebrina* species, while challenging any separation between others that are instead attributed to the influence of habitat. They have also revealed evidence for new cryptic or overlooked species. The new phylogenetic estimate is providing insight into clarifying the biogeography and evolutionary history of this endemic radiation of the northeastern Pacific, and allows for refining ecological and reproductive differences between its members.

An Integrated Approach to Unraveling the Fossil Record: Estimating the Paleontological Past, One Phylogeny at a Time

S. G. Wiedrick*¹, A. J. W. Hendy¹, and D. J. Eernisse²

¹Department of Invertebrate Paleontology, Natural History Museum of Los Angeles County, 900 Exposition Blvd., Los Angeles, CA 90007 USA

²Department of Biological Science, California State University, Fullerton, CA 92834 USA

The diverse muricid genus, *Paciocinebrina* Houart, Vermeij & Wiedrick, 2019, of the northeastern Pacific, is phenotypically plastic with a great deal of confusion associated with previously proposed taxa and historical records. Species of the genus are currently recorded from Alaska to Baja California, with most species known and described from California. The ecological role of these snails is most notable for their drilling capabilities by which they primarily prey on sessile barnacles and other marine mollusks, and partly for their richness in local intertidal zones along the northeastern coastline. A review of relevant literature, museum vouchers and the careful collection and analysis of molecular data has provided an insight to patterns of occurrence, distributions of taxa, ecological importance, and the overall clarification of taxonomic instability. Our approach utilizes the traditional use of morphological analysis, combined with, and based on, modern molecular techniques and analysis of both mitochondrial (COI & 16S) and nuclear (28S & ITS-2) loci. The mode of development of this group is thought to be direct, as indicated by the paucispiral protoconch, a trait known to support higher levels of diversification compared to planktonic dispersal and development. The extensive assemblage of Pliocene-Pleistocene fossils is remarkable and in need of major revision, with species dating back to the Oligocene of California. As a member of the Ocinebrinae, *Paciocinebrina* Houart et al. 2019 is one of a variety of clades thought to have originated from an ancestral group from the Paleogene of Europe. The absence of *Ocinebrina*-like species from the Western Atlantic suggests the migration of ancestral species was likely through the Tethys seaway during the late Paleogene, further supported by morphologically similar records from Japan. The Late Oligocene fauna of California is reported to include 5 to 6 species, with a modern record of about 20 distinct members. Additional undescribed species are expected to increase our knowledge about this expansive and diverse group. Modern molecular techniques are here leveraged to establish and estimate the relationships between members of this genus, a tool used to interpret paleontological relations and to reconstruct the biogeography and biodiversity of this large group of organisms.

Australia's First Monoplacophoran: Diving Deep off Western Australia

Nerida G. Wilson*¹

¹Western Australian Museum, Molecular Systematics Unit

Science has not been long acquainted with the extant members of the class Monoplacophora, and their enigmatic nature is still being slowly unravelled. The lack of morphological diversity among living species has led to them being described as 'living fossils'; however, that has been contrasted with the hypothesis that the extant group may instead represent a relatively recent radiation. Despite continuing controversy around their deeper evolutionary relationships, there remain problems with lower level classification as well. The single extant family Neopilinidae contains seven currently accepted genera. To date, the monophyly of these genera has not been tested extensively, although *Laevipilina* appeared polyphyletic in previous studies. The discovery of a new monoplacophoran off Western Australia allows discussion of the limitation of currently used characters. Despite being brought up in a rock dredge from nearly 4300m, the newly collected specimen was in very good condition, and molecular data was generated to place it in a phylogenetic framework. Field-work planned for early 2020 will revisit the site of collection with a Remotely Operated Vehicle, and further study of the new species may be possible at that stage.

Clues for the Evolution of Bivalved Gastropods through Observations of *Berthelinia singaporensis* (Mollusca: Gastropoda: Sacoglossa: Juliidae)

Nur Leena Wong W.S.*¹ and Julia D. Sigwart²

¹International Institute of Aquaculture and Aquatic Sciences, Universiti Putra Malaysia, Malaysia

²Marine Laboratory, Queen's University Belfast, N. Ireland

Bivalved gastropods (family Juliidae) are a pan-tropical group of small, green, extraordinary sacoglossan gastropods with a symmetrical paired shell. Only a single species of Juliidae has been reported in Malaysia, *Berthelinia singaporensis* Hensen, 2015, feeding on multiple species of *Caulerpa* spp. green algae. *Berthelinia singaporensis* appears to be a relative generalist without preferences among available *Caulerpa* spp. that occur in suitable (micro)habitats, and were found feeding on 5 *Caulerpa* species in separate field occasions. Juliidae hatched as univalve, coiled larvae that later transform to a bivalved adult. In the presence of *Caulerpa*, swimming veligers rapidly settle and begin feeding; in a later, terminal metamorphosis the larval operculum is shed, and the teleoconch shell field splits to form a second, right valve of the adult bivalved form. By three days after hatching, settled larvae achieve a fully functional bivalved shell with working hinge. Both veligers and adults produce an unusual elastic mucous tether to maintain attachment to the food-plant. *Caulerpa* seaweed usually grow in intertidal or shallow water exposed to strong tidal wave actions. These animals are dependent on *Caulerpa* for their entire life cycle, so adults occupy environments where dislodgement may be a substantial risk. In the adult, bivalved, form, the gastropod can withdraw completely into its shell and closed the valves while maintaining the byssus-like tether, enabling the gastropod to be simultaneously anchored to the food plant and protected from dehydration during low tide within the shell. This arrangement has suggested the most plausible adaptive explanation for the evolution of the bivalved form within gastropods.

Origin of diversity by repeated hybridization in the door snail *Charpentieria itala* in the Southern Alps revealed by RADseq data

Jie Xu & Bernhard Hausdorf¹

¹Center of Natural History, Zoological Museum, University of Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany

The door snail *Charpentieria itala* is widely distributed and subdivided into several morphologically differentiated subspecies in the Southern Alps. Some of the subspecies resemble the related *Charpentieria stenzii*. We generated genome-wide double digest Restriction Associated DNA sequencing (ddRADseq) data for 166 specimens from 36 populations of the door snail *Charpentieria itala* and for 8 specimens of the other three *Charpentieria* species to reconstruct their evolutionary history and phylogeography. Phylogenetic analyses, ADMIXTURE analyses and a Neighbor-Net based on the ddRADseq data indicate that the populations were separated in western and eastern refuges by the Garda Glacier during the glacials. The populations that resemble *Charpentieria stenzii* morphologically and ecologically, the 'stenzioid' subspecies, form a clade within the western group of populations. A TreeMix analysis revealed that they originated after a hybridization event with *Charpentieria stenzii*. They are geographically concentrated in mountain areas that were not glaciated during the Last Glacial Maximum and vicariate with non-stenzioid populations at lower altitudes. The stenzioid subspecies represent relicts of an early colonization wave that survived the ice ages in isolated mountain refuges. After the retreat of the glaciers, the non-stenzioid populations colonized the valleys from refuges at the margin of the Alps. The two population groups hybridized in different regions to different degrees. In the western area, a distinct hybrid subspecies, *Charpentieria itala latestriata*, originated again by hybridization between stenzioid and non-stenzioid populations, whereas there is a continuous transition between the eastern stenzioid populations and adjacent non-stenzioid populations.

What Ammonoid Cephalopods Tell Us About Biodiversity Dynamics on a Changing Earth

Dr. Margaret M. Yacobucci *¹

¹School of Earth, Environment & Society, Bowling Green State University, Bowling Green, OH 43403

Ammonoid cephalopods experienced significantly higher rates of origination and extinction than other mollusks. It has been proposed that this evolutionary volatility was driven both by the group's sensitivity to environmental changes and developmental flexibility that fueled ecomorphological diversification. During the Cenomanian and Turonian ages (Late Cretaceous, 90-100 million years ago), greenhouse warming led to oceanographic perturbations that impacted ammonoid biodiversity dynamics. In addition to providing a system with which to test drivers of ammonoid speciation and extinction, this interval serves as a model for what modern oceans may experience due to anthropogenic climate change. Analyses of a global database of ammonoid biodiversity and biogeographic distributions demonstrate the importance of regional variations in cephalopods' response to environmental change. Warming and sea level rise led to endemic radiations within epicontinental seas for some clades and expansion of geographic ranges for others. Speciation rates remained high throughout times of environmental stress, while extinction pulses were associated with the onset of ocean anoxia and episodes of increased continental runoff. Globally, species with larger geographic ranges had lower extinction rates during both background times and across the Cenomanian-Turonian extinction event. However, within the North American Western Interior, survivor species became geographically restricted to a single refugium within the basin. The importance of refugia in some shallow seas may explain why global patterns linking geographic range and survivorship are not always seen in regional-scale studies. These results inform predictions about how modern cephalopod biodiversity will be impacted by our current climate crisis.

Loss of Shell Coiling in Trochid Snail: Adaptation to Wave-Swept Rock Surfaces and Symbiotic Life in Sea Urchin Pits

Luna Yamamori*¹ and Makoto Kato¹

¹Kyoto University, Human and Environmental studies

Flattening of coiled shells has occurred in several gastropod lineages, while the evolutionary process is little known. The subfamily Fossarininae (Gastropod; Trochidae) is unique, because the four genera of this family vary considerably in extent of shell coiling/flattening. *Broderipia* and *Roya* have zygomorphic shells that have lost coiling, while the sister genera, *Fossarina* and *Synaptocochlea* have respectively turbiniform and auriform shells. We compared biology and morphology among these four genera to detect the selection pressure which has driven the shell flattening and loss of coiling. We discovered that *Broderipia iridescens* live symbiotically in rock pits of sea urchins, and *Roya eximia* live on intertidal rock surfaces exposed to strong waves. Comparison of the morphology of soft bodies in Fossarininae revealed that the columellar muscle of flattened species has been drastically elongated as observed in the true limpet family, Nacellidae. The flattening and loss of coiling of the shell in *Broderipia* and *Roya* caused acquisition of a zygomorphic flat body, retraction of coiled visceral mass, and expansion of the foot sole. In *Roya*, these morphological changes would have improved tolerance against strong waves and the ability to cling to rock surfaces in *Roya*, and would have enabled the commensal life in narrow space in sea urchin pits in *Broderipia*.

Threatened, Endangered, and Extinct, Oh My! Growing and Using Natural History Collections in the Midst of a Biodiversity Crisis

Norine W. Yeung*¹

¹Bishop Museum, 1525 Bernice St., Honolulu, HI 96817 USA

The Hawaiian Islands support a spectacular radiation of land snails, but like most of the fauna throughout the Pacific islands, Hawaiian land snails are being lost quickly. As much as 95% of some families are already extinct, and the remaining fauna is seriously threatened or critically endangered. Our best hope for understanding this fauna, and conserving what remains is through natural history collections, such as those housed in the Bishop Museum Malacology Center, which has ~2 million Hawaiian land snail specimens collected pre-1940. These collections in combination with contemporary surveys provide the data needed to understand historical distributions, species diversity, population declines, and ultimately extinction. Over the last decade we conducted surveys in nearly 1,000 sites throughout the Hawaiian Archipelago and collected vouchers specimens and tissue samples to reveal the true extent of the extinction crisis, and begin gathering the data needed to save the remaining fauna. To minimize negative impacts from collecting, we employed multiple specimen collection protocols, including digital photography, tissue sampling (e.g. mucus, foot), vouchering of morphospecies, and enhancing population sizes via captive rearing prior to individual preservation. The combination of traditional taxonomy, modern genetic approaches, and contemporary anatomical methods (micro-CT, SEM) clearly illustrate the ever-important role that natural history collections play in biodiversity discovery, analysis, and conservation.

Scaling Volunteer Biodiversity Documentation of Molluscs through Citizen Science Programs and Technology

Alison N. Young*¹, Rebecca F. Johnson¹

¹California Academy of Sciences, Citizen Science Department

Collaboration between amateur naturalists and professional scientists in the pursuit of natural history and biodiversity discovery is not new, but in recent years has taken on a different look, mostly due to increased connectivity through technology. We can now communicate and share in ways we could not have imagined only a decade ago. The California Academy of Sciences engages volunteers in searching for and documenting species - including molluscs, primarily in the rocky intertidal - using the iNaturalist platform, creating occurrence records with photographic evidence from around the globe. We do this in many ways, from encouraging and supporting individuals in making biodiversity observations, to long-term monitoring, to coordinated and concentrated bioblitzes along the California coastline. This work addresses the need for open and available biodiversity data at scale, as the pairing of our programs with iNaturalist not only allows us to create data that are open to anyone, but also democratizes natural history, making it accessible for anyone to participate without the barrier of needing to be trained to identify species. Through our programs and iNaturalist, volunteers have uploaded more than 100,000 observations of molluscs along the California coast, tracking fluctuations in species ranges, creating species atlases for rocky intertidal sites, discovering new county records to fill in range gaps, and even documenting new records for North America. By providing tools and resources, designing programs that scale, and networking local projects together, we are generating biodiversity data on the scale we need to make informed conservation decisions, fueling meaningful science, and building strong local and global communities of naturalists.

Dipping Our Toes Into a Sea of Possibilities: Defining the Unknown Functions And Requirements of Olympia Oysters via Science-Based Restoration

Danielle C. Zacherl*¹

¹California State University Fullerton, Box 6850, Department of Biological Science, Fullerton, CA 92834 - 6850

Oyster reefs are among the most severely impacted habitats in the world, suffering declines up to 85% in habitat areal extent and biomass across the globe. These losses have spurred global restoration efforts because oyster reefs provide critically important benefits including habitat provision, sediment stabilization, and water filtration, which improves water clarity and may facilitate seagrass success. Restoration of the U.S. west coast's only native oyster species, the diminutive Olympia oyster, *Ostrea lurida*, has been underway for at least a couple of decades, but comparatively less is known about this species' basic ecological requirements and ecosystem functions provided by its much lower-relief oyster beds. Here, I review findings not only from my lab group's science-based restoration efforts and studies on the natural history of the Olympia oyster, but also findings generated by a host of other research groups across the range of the species, that collectively shed light on the ecological role this iconic oyster plays in our bays and estuaries. The recent formation of a Coast-wide Olympia Oyster Network has resulted in a powerful new research collaboration extending across latitudes and disciplines that will strengthen our understanding of this species' ecosystem functions across its range.

Phylogenomics and Macroevolution of the Venomous Gastropods Turridae (Gastropoda, Conoidea)

Paul Zaharias*¹, Yuri I. Kantor², Alexander E. Fedosov², Mark Phuong³, and Nicolas Puillandre¹

¹Institut de Systématique, Évolution, Biodiversité ISYEB – UMR 7205, CNRS, MNHN, UPMC, EPHE, Muséum national d'Histoire naturelle, Sorbonne Universités, 57 rue Cuvier, CP26, F-75005, Paris, France

²A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Leninsky, Prospect 33, Moscow 119071, Russia, Moscow, Russian Federation

³Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA 90095, USA

Turrids (Gastropoda, Conoidea) have often been referred to as a "taxonomic nightmare", because of their huge diversity (4,000 described species, with an estimate of more than 10,000 living species) and their wide variety of forms that seems to be an endless continuum where drawing lines between taxa seems unachievable. Ten years of molecular phylogenetics greatly contributed to a redefinition of the family boundaries and their relationships. In particular, the name Turridae, traditionally applied to all conoideans except auger snails and cone snails, is now used for a restricted group of 15 genera and 200 species. The classical "sanger approach", based on a few genes and often used to establish gastropod phylogenies, proved to be unable to infer robust relationships within the Turridae. We applied a transcriptome-based exon capture approach to recover ~4000 DNA loci for 120 samples. We particularly focused on rare lineages and deep-water species (most of them undescribed). We reconstructed the phylogeny using both supermatrix (IQ-TREE) and supertree (ASTRAL-III) approaches. The resulting tree is a robust phylogeny that can be used to redefine several genera and define new ones in the polyphyletic large genus *Gemmula*. We acquired morpho-anatomical features such as shell and protoconch size, radular and protoconch types and depth ranges. We particularly studied the relations of radulae features with lineage diversity and branch length, as well as shell and protoconch metrics in relation with depth range. Our analysis sheds light on the effects of morpho-anatomical traits on diversification rates and allowed the first tests of macroevolutionary hypothesis on this family.

Poster Abstracts

First Step for Demystifying *Tritia alba* Complex (Neogastropoda: Nassariidae), With Description of Four New Species to the South Atlantic.

Daniel Abbate*¹, Luiz Simone¹, and Patricia Oristanio¹

¹ Zoology Museum of University of Sao Paulo (MZUSP)

The relocation of the species contained in the traditional "*Nassarius albus*" complex to the genus *Tritia* occurred through a comparative morphological and conchological study among the species where the complex had already previously allocated, *Nassarius arcularia*, *Nassarius tiarula* and *Tritia reticulata*. For the beginning of the understanding of the species that compose the complex, were analyzed specimens of five localities; Florida, type locality of epithet *albus*; Fernando de Noronha, Pernambuco, Brazil; Guarapari, Espírito Santo, Brazil; Trindade Island, Espírito Santo, Brazil and Queimada Grande Island, São Paulo, Brazil. After detailed morpho-anatomical analysis it was concluded that each locality has a valid specific entity, *Tritia sp1*, *Tritia sp2*, *Tritia sp3*.

Freshwater Mollusc Bioresources of North-East India

Aravind Neelavar Ananthram*¹, Anushree Jadhav¹, and Nipu Kumar Das¹

¹ Ashoka Trust for Research in Ecology and the Environment (ATREE), Suri Sehgal Center for Biodiversity and Conservation

Molluscs are considered a delicacy in many parts of the World. However, in underdeveloped and developed parts of the world, wild populations of freshwater molluscs (snails and clams) are extensively harvested and consumed as a cheap source of protein by economically and socially backward communities. In North-east India molluscs are used for food and medicinal purposes. For the last one year, we are documenting the species, quantity, location of harvest and other traditional knowledge associated with freshwater molluscs. During our study, we collected data from local markets of Assam, Manipur, Meghalaya and Mizoram. We recorded ten species of freshwater molluscs belonging to 5 families and eight genera. These include six gastropods namely, *Pila globosa* (Ampullaridae), *Bellamya bengalensis* (Viviparidae), *Angulyagra sp.* (Viviparidae), *Cipangopaludina lecythis* (Viviparidae), 3 species of *Paludomus* (Paludomidae), *Brotia costula* (Pachychilidae), and two bivalves, *Lamellidens marginalis* (Uninoidae), *Lamellidens sp.* (Uninoidae). The quantity and type of species harvested vary between seasons. In the states of Assam and Mizoram freshwater, molluscs are only consumed for food whereas, in Manipur, they also have medicinal and cultural significance. Despite molluscs being of immense importance both ecologically and economically, it is highly neglected, and studies with respect to taxonomy, distribution, ecology and livelihoods of the communities need to be studies.

Morphological Evolution of *Shikamaia*, Permian Giant Bivalves (Alatoconchidae: Ambonychioidea) from Japan

Kaito Asato*¹, Tomoki Kase²

¹Faculty of Life and Environmental Sciences, University of Tsukuba

²Department of Biological Sciences, Kanagawa University

The Permian bivalve family Alatoconchidae (Ambonychioidea) consists of species that exhibit extraordinarily large shell size and antero-dorsally compressed shell shape, and are thought to have a photosymbiotic mode of life like the modern fragine bivalve *Corculum*. The alatoconchids are heretofore known in ten, widely separated areas (Croatia, Tunisia, Oman, Afghanistan, Iran, Thailand, Malaysia, Philippines, China and Japan) that are considered to have once located at low latitudes in the Panthalassan and Tethyan seas. Despite their wide distribution, the shell morphologies and taxonomy of alatoconchids still remain unclear. The Middle and Upper Members of Akasaka Limestone of central Japan yields alatoconchids abundantly, where the type species of *Shikamaia* (*S. akasakaensis*) was described. In this study, we examined additional three species from the Akasaka Limestone, and identified two new and one undetermined species of *Shikamaia*. Detailed examination of these species reveals three types of beak morphologies among them. Type one, an appressed beak, is observed in *S. akasakaensis*, *S. ozakii* and one undescribed species. Type two, a closed and crossed beak, is recognized in new species from the Middle member of Akasaka Limestone. Type three, a divergent beak, is characteristics to new species from the Upper member of Akasaka Limestone, which shells is round and thick near the beak and has a bowl-like shaped shell wing. These features may be resulted from different shell growth patterns. With this result, a trend to increase the ventral surface area of the shell with time is recognized. This trend may have been advantageous for recliner on the soft bottom.

Living In A Sponge: A Preliminary Study of the Fauna Associated to the Antarctic Sponge *Kirkpatrickia variolosa*

Conxita Avila*¹, Eduard Giralt¹, Rafael Sardà², and Carlos Angulo-Preckler¹

¹Dept. of Evolutionary Biology, Ecology and Environmental Sciences, and IrBIO, Faculty of Biology, University of Barcelona, Av. Diagonal 643, 08028 Barcelona, Catalonia

²CEAB-CSIC, 17300 Blanes, Girona, Catalonia

The particular features of Port Foster's caldera on Deception Island (Antarctica) are an interesting subject of study because of its soft and hard substrates and its peculiar volcanic features. Antarctic benthic communities here are still poorly known, particularly the communities of small-sized invertebrates living associated to other organisms, such as sponges. We studied here the fauna associated to the Antarctic sponge *Kirkpatrickia variolosa* inhabiting the rocky substrates of Fildes Point, Whalers' Bay at a shallow depth (5-15m). This sponge is characterized by being massive and intensely red, with a size up to 30 cm in height. In order to do this, four samples of the sponge were obtained by SCUBA to separate and identify the organisms inhabiting them. The collected sponges were sliced and cleaned using a 125 µm filter. Subsequently, the organisms were classified at the lowest possible taxonomic level (considering that this is a preliminary study and several groups remain to be further identified), and analyzed for abundances, species richness, and biomass. The results shown that crustaceans (isopods, amphipods, copepods, and ostracodes), nematodes, polychaeta, and molluscs, are well represented in this type of habitat. A total of 15,222 specimens were found, most of them between 1 to 3mm. Organisms living in the sponge are protected physically by the massive sponge, containing spicules, and chemically by potent natural products, thus finding a peculiar habitat and refuge.

Description of Two New Facelinids (Gastropoda: Heterobranchia) from the Gulf of Guinea (Eastern Atlantic Ocean)

Leila Carmona Barnosi*², Aketza Herrero-Barrencua¹, Ana Karla Araujo³, and Juan Lucas Cervera^{2,3}

¹ BIOCON Research Group, IU-ECOQUA, Universidad de Las Palmas de Gran Canaria; Islas Canarias, Spain

² Campus Río San Pedro s/n, Marine Research Institute (INMAR), 11510 Puerto Real, Cadiz, Spain.

³ Departamento de Biología, Facultad de Ciencias del Mar y Ambientales, Campus de Excelencia Internacional del Mar (CEI-MAR), Universidad de Cádiz, Polígono Río San Pedro, s/n, Ap.40, 11510 Puerto Real, Cádiz, Spain

Most of the marine biodiversity of African countries is still unknown. For instance, with regard to the Nudibranch (Gastropoda, Heterobranchia) fauna of the Gulf of Guinea, only seven species are reported from São Tomé and Príncipe. Recently collected material from the expedition BIO-Príncipe retrieved two undescribed facelinids from this archipelago. The external and internal features of the undescribed species were compared with other facelinids from the Atlantic Ocean. In addition, Maximum-likelihood, Bayesian inference and species-delimitation analyses based on H3, COI and 16S genes were carried out to support the existence these new species.

The Risk Potential of the Eastern Heath Snail, *Xerolenta obvia*, in Montana

Jennifer Birdsall*¹, Jeffrey Littlefield¹, and Ann deMeij¹

¹Montana State University Department of Land Resources & Environmental Sciences

The eastern heath snail, *Xerolenta obvia* (Fam.: Hygromiidae), is a dryland massing snail centered in southeastern Europe but which occurs across Europe. In 2012, the snail was reported in Cascade Co., Montana, USA and a large population was subsequently located over an estimated 30,000 ha area. This infestation represents one of only three in North America; the others being located in Detroit and a residential/forested area in Ontario, Canada. The presence of *X. obvia* in Montana poses a potential regulatory risk for grain and hay production and for export markets. This snail is of particular concern since it is known to feed on fodder crops. Currently little is known about the biology or invasive behavior of *X. obvia*. This information is essential in assessing the potential risk of the snail to grain growing regions of North America and for developing long-term management strategies. This poster presents preliminary findings of the snail's development at three temperatures, egg laying behavior, feeding preferences, and associated mortality factors. *X. obvia* exhibits high variability but develops fastest at 20°C as determined by width, weight, and number of whorls. Individuals at both 12°C and 28°C were noticeably smaller with snails reared at 28°C experiencing high mortality. Eggs are laid both in the autumn and spring. Nematodes belonging to three genera, *Panagrolaimus*, *Plectus*, and *Rhabditia* are associated with *X. obvia* mortality in Montana.

Terrestrial Slugs as a Model Organism for Inquiry-Based Experimentation in a Majors' General Biology Laboratory

Amy C. Blair*¹ and Brenda J. Peters¹

¹ St. Ambrose University, Biology Department

Many biology educators at the undergraduate level are revamping their laboratory curricula to incorporate inquiry-based research experiences so students can directly participate in the process of research and improve their scientific reasoning skills. Slugs are an ideal organism for use in such a student-directed, hypothesis-driven experience. Slugs are inexpensive, easily collected, and, as ectotherms, require minimal care. Commonly collected slug species in the Midwest include: *Arion subfuscus* (Draparnaud), *Deroceras laeve* (Müller), and *Deroceras reticulatum* (Müller). Most students are unfamiliar with slugs, and their curiosity is piqued as they collect, observe, and classify these fascinating creatures. Project topics have ranged from feeding preference tests to examining homing behavior to measuring locomotive activity. The procedures presented here offer step-by-step instructions on how slugs are used to guide students through an inquiry-based research project for seven weeks in a majors' general biology course with approximately 125 students enrolled per semester.

Phylogenomic evidence that chiton 'shell eyes' may have recently evolved from shell eyespots

J.T. Cannon*¹, K.M. Kocot², D.J. Eernisse³, D.I. Speiser⁴, and T.H. Oakley¹

¹Ecology, Evolution, and Marine Biology, University of California, Santa Barbara

²Biological Sciences, University of Alabama

³Biological Science, California State University Fullerton

⁴Biological Sciences, University of South Carolina

Chitons possess clusters of sensory cells called aesthetes within their eight overlapping shell plates. In some polyplacophoran species, aesthetes are modified to include an eyespot, and in others, aesthetes are present in addition to eyes with a lens and retina. To address the evolution of complexity in chiton eyes, it is necessary to phylogenetically test whether Chitoninae, with eyespots, is sister to Acanthopleurinae + Tonicinae, with lenses. To address this question, we sequenced transcriptomes from sixteen chiton species and one aplacophoran with Illumina Hi-Seq. In addition to novel aculiferan data sequenced for this study, we included data from thirteen publically available transcriptomes and genomes. Our final data matrix contains 30 mollusk species and >500 genes. Overall, our phylogenomic results are consistent with previously published chiton phylogenies, with major lineages supported as monophyletic. Chitoninae is sister to Acanthopleurinae + Tonicinae, suggesting that eyespots may be the morphological precursors of 'shell eyes'. However, expanded taxon sampling is needed. To generate a more taxon-rich phylogeny for Chitonina, we are taking a target capture approach. We designed a set of 19,980 probes covering exon regions from 355 genes, using exon boundary information from three mollusk genomes (*Lottia*, *Octopus*, and *Crassostrea*). In preliminary analyses of 12 chiton species sequenced with MiSeq, the probe set recovered data from a median of 343 and mean of 294 genes using the HybPiper software package. This target-capture study will enable us to more directly address the questions of lens origins in chitons.

Evolution of vetigastropod shell shape in the Mesozoic and early Cenozoic eras

Tauana Junqueira Cunha*¹ and Gonzalo Giribet¹

¹Museum of Comparative Zoology, Harvard University

Paleontological observations have recognized significant morphological changes in the shape of gastropod shells at the later part of the Mesozoic and into the Cenozoic era. The main driver of these changes is thought to be the intensification of predation by durophagous predators such as crabs and fishes (escalation hypothesis). Several morphological traits seem to be associated with this transition, but quantitative data on the long-term evolution of shell shape remains scarce. It is predicted that short and wide, less spired shells could provide better mechanical resistance against crushing and therefore are expected to become relatively more frequent with increased predation pressure. Here we address the evolution of shell morphospace with a dataset of hundreds of fossil vetigastropods (e.g. turban snails, top shells, slit shells, keyhole limpets) from the Triassic (~250 mya) to the Paleogene (~35 mya). We find that their morphospace changes significantly through time. A core part of the morphospace is occupied across the entire interval, but the most highly spired shells become absent in the Cretaceous, while the space of shorter shells becomes denser, in agreement with predictions from the escalation hypothesis. In the Paleogene, we further observe a large expansion of the morphospace being occupied by keyhole limpets with wider openings and flat shells. Trends from the best represented families indicate that such morphospace changes were not driven by a turnover of families with different shapes, but by the independent evolution of different families towards shorter and/or wider shells.

Gastropod community assemblage between boardwalk and non-boardwalk sites in selected mangrove ecosystems in Batangas, Oriental Mindoro and Quezon, Philippines

Emmanuel Ryan C. de Chavez*¹ and Hugo Ignacio G. Salvador¹

¹Animal Biology Division, Institute of Biological Sciences College of Arts and Sciences, University of the Philippines Los Baños College, 4031, Laguna, Philippines

Gastropods have wide range of habitats including mangrove forests. They play vital roles in the food web, and many species have commercial importance. However, they are also vulnerable to natural and anthropogenic disturbance both large- and fine-scale. This study examined the variation in gastropod community assemblage between boardwalk (fine-scale disturbance) and non-boardwalk (control) sites in select mangrove ecosystems in Calatagan, Calapan, and Pagbilao, Philippines. Using a modified Beyond-BACI design, 25 m² quadrats per 100m boardwalk were established parallel to the boardwalk, and in two control locations at least 200m away. Epifaunal and infaunal gastropods were sampled through direct hand search and sediment collection. Air temperature, relative humidity, canopy cover, tree diameter, number of saplings and trees, electrical conductivity, organic matter, and pH were measured. Mangrove species were also identified. A total of 5,929 mangrove snails belonging to 43 species and 18 families were identified. Diversity indices did not show clear pattern that would prove press disturbance due to the boardwalk construction. ANOVA and ANOSIM further supported that there was no consistent significant difference in gastropod assemblages between boardwalk and control sites. Canonical correspondence analysis indicated microhabitat preference of gastropods across sampling sites. Generalized linear mixed modelling demonstrated that electrical conductivity was the most important predictor for species richness and density. This study suggests that press disturbance due to boardwalk construction had no apparent long-term negative impacts on gastropod community in a tropical mangrove ecosystem.

Survival and growth of *Cerastoderma edule* larvae reared under different nutritional regimes

Domitilia da Conceição*¹, Ana Margarete Ramos¹, Ana Rato², Cláudia Roque¹, and Sandra Joaquim¹

¹Portuguese Institute for Sea and Atmosphere, I. P., Av 5 de Outubro 8700-305 Olhão, Portugal

²Science Faculty of University of Lisbon, Campo Grande 1749-016 Lisboa, Portugal

Cockle *Cerastoderma edule* supports an important fishery in Europe. This fishery has been affected by inter-annual fluctuations in stock abundance, due to recruitment failures and diseases. Aquaculture could contribute to address these problems through the production of larvae or juveniles for stock-enhancement programs. The effects of four feeding regimes (*Isochrysis aff galbana*; *Chaetoceros calcitrans*; *I. aff galbana* + *C. calcitrans*; Unfed) on the survival and growth of *C. edule* larvae were evaluated, aiming to provide crucial information on its nutritional requirements. The larvae fed *I. aff. galbana* showed significant higher survival than those fed with the other diets. The lowest survival was found in larvae that fed *C. calcitrans*. Also, larvae fed *I. aff. galbana* showed a higher increase in shell length than larvae from the other treatments, however with statistical similarity with larvae fed with the mixed diet (*I. aff galbana* + *C. calcitrans*). The obtained results constitute an important first step in the hatchery *C. edule* larval nutrition and a prerequisite for future work on the improvement of larval rearing and on the optimization of feeding practices for larvae yield maximization and so, minimize cost in aquaculture hatcheries.

Preliminary Studies of the Phylogeography of Three *Agathistoma* Species (Vetigastropoda: Turbinidae: Tegulinae).

Ana Paula Siqueira Dornellas*¹ and Tito Monteiro da Cruz Lotufo¹

¹Instituto Oceanográfico da Universidade de São Paulo

The distribution of South American marine biota is known to have been influenced by several marine transgressions. This is the case for the Atlantic antitropical distribution. This pattern is well represented among western Atlantic species or species pairs distributed northward and southward of the combined plume of the Orinoco and Amazon rivers. Among *Agathistoma* species, three occur in Brazil: *A. viridulum* and *A. hotessierianum*, which have an antitropical distribution and *A. patagonicum*, occurring in a more restricted geographic region, but with a higher morphological variation when compared to other species of the genus. This study aims to analyze the genetic structure of *A. viridulum*, *A. hotessierianum* and *A. patagonicum*, to determine its evolutionary lineages and biogeographic patterns. The taxa samples were obtained from museum's collections and freshly collected specimens. We sequenced two mitochondrial genes: *cytochrome c oxidase* subunit I (COI) and 16S rRNA and performed a maximum likelihood analysis to build haplotype networks and infer their genetic structure. The population of *A. hotessierianum* displayed a high degree of genetic structure with a typical antitropical pattern, split in two clades: 1) Brazilian and 2) Caribbean population. The population of *A. viridulum* from Brazil showed a small degree of genetic structure, and also split in two clades: 1) southeast and 2) northeast population. Our further analysis will include more samples of *A. viridulum* from the Caribbean and more samples of *A. patagonicum* to perform a more in depth phylogeographic analysis. Those results will be discussed within the scope of different hypothesis about marine transgressions in the Atlantic Ocean.

Describing a new species of *Baptodoris* (Nudibranchia: Discodorididae) from Costa Rica, Central America based on morphological and molecular data

Kimberly García-Méndez*¹ and Yolanda E. Camacho-García^{2,3}

¹Department of Biological Sciences, California State Polytechnic University, 3801 West Temple Ave., Pomona, California, USA

²Escuela de Biología, Universidad de Costa Rica, Apdo. 11501-2060, San Pedro de Montes de Oca, San José, Costa Rica,

³Museo de Zoología, Escuela de Biología, Universidad de Costa Rica, Apdo. 11501-2060, San Pedro de Montes de Oca, San José, Costa Rica.

The genus *Baptodoris* Bergh 1884, is a rare group of heterobranch nudibranchs belonging to the family Discodorididae. According to Valdés and Gosliner (2001) *Baptodoris* is closely related to the genera *Gargamella* Bergh, 1894 and *Platydoris* Bergh, 1877. Garavoy et al. (1999) proposed a phylogenetic hypothesis in which *Platydoris* and *Baptodoris* are sister groups, and *Gargamella* is basal to this clade. To date this genus comprises only 5 valid species worldwide: *Baptodoris peruviana* (d'Orbigny, 1837) from Perú and Chile; *Baptodoris cinnabarina* Bergh, 1884 from the western Mediterranean Sea; *Baptodoris stomascuta* Bouchet, 1977 from European waters; *Baptodoris mimetica* Gosliner, 1991 from California; and *Baptodoris phinei* Valdés, 2001 from the Coral Sea close to New Caledonia. Of the five-valid species, only *B. mimetica* and *B. peruviana* have been reported for the Americas. In the present study, we describe a new species of *Baptodoris* from the Pacific coast of Costa Rica using morphological and molecular data from three different molecular markers. We also include a preliminary phylogenetic tree comparing this new species to other members of caryophyllidia-bearing dorids in order to assess its position and to test the hypothesis of the sister taxa relationship between *Baptodoris* and *Platydoris*.

Heterobranch Sea Slugs (Mollusca: Gastropoda) from Isla del Coco National Park, Costa Rica

Kimberly García-Méndez*¹ and Yolanda E. Camacho-García^{2,3,4,5}

¹Department of Biological Sciences, California State Polytechnic University, 3801 West Temple Ave., Pomona, California, USA

²Escuela de Biología, Universidad de Costa Rica, 11501-2060 San José, Costa Rica

³Museo de Zoología, Universidad de Costa Rica, 11501-2060 San José, Costa Rica

⁴Centro de Estructuras Microscópicas (CIEMIC)

⁵Centro de Investigación en Ciencias del Mar y Limnología (CIMAR)

The molluscan fauna of Isla del Coco has been relatively well documented over the years; however, its heterobranch sea slugs remain poorly known. Recent research efforts in documenting the biodiversity of this group in Costa Rica has made it possible to update the number of species known in remote locations such as this oceanic island. We report a total of 40 species of heterobranch mollusks from Isla del Coco, 13 of which represent new records for this national park and 6 of which have not been recorded along the Pacific side of the Costa Rica mainland: *Berthella californica* (Dall, 1900), *Peltdoris rubra* (Bergh, 1905), *Dendrodoris albobrunnea* Allan, 1933, *Doriopsilla* cf. *spaldingi* Valdés & Behrens, 1998, *Glaucus* cf. *marginatus* (Reinhardt & Bergh, 1864), and *Flabellina* sp. Compared to other oceanic islands in the Tropical Eastern Pacific, the heterobranch sea slug fauna from Isla del Coco is similar in number and biogeographical affinities. The lack of some common herbivorous species, which are found in the Pacific region of the Costa Rica mainland, as well as the predominance of nudibranchs, suggests that the species composition is the result of both the habitat characteristics and geographic position of this oceanic island. We suggest increasing collecting and documentation efforts in this locality to better understand the heterobranch diversity in remote tropical environments.

Cornucopia Molluscarum Profundissimarum: New Deep Sea Mollusca at SBMNH

Daniel L. Geiger*¹

¹Santa Barbara Museum of Natural History

Cornucopia Gastropodarum Profundissimarum.— The Santa Barbara Museum of Natural History recently received a donation of approximately 1,000 lots of deep water mollusks from the retiring researcher Robert Vrijenhoek at the Monterey Bay Aquarium Research Institute. Select species are illustrated and an overview of the available material is presented. Some undescribed taxa are among the holdings, which will be formally described in forthcoming publications.

McLean Memorial Volume and the Northeast Pacific Gastropods

Daniel L. Geiger*¹, Lindsey T. Groves², and Jann E. Vendetti²

¹ Santa Barbara Museum of Natural History

² Natural History Museum of Los Angeles County

James H. McLean (1936–2016) had been working on a revision of the northeast Pacific gastropods his entire career. Unfortunately, he could not complete his vision. Select families have now been treated by a number of global experts (Geiger: scissurellids, seguenziids; Geiger & Owen: Haliotidae; Tuskes: Calliostoma; Alf: Tegulidae & Turbinidae; Raines: Caecidae; Vafiadis & Stephens: Pelycidion; Collin: Calyptraeidae; Groves: Cypraeidae; Moreno: Atlantidae; Seapy: Pterotrachoidea, Janthininae; Brown: new species of *Epitonium*; deMaintenon: Columbelloidea; Clark: new species of *Buccinum*; Houart, Vermeij & Widerick: Muricidae; Valdes: benthic shelled Opisthobranchia; Janssen, Bush & Bernarsek: Pteropoda). The contributions have been published as a memorial volume in *Zoosymposia* 13, which is available via open access (or "which is openly accessible") in its entirety thanks to a generous donation by Jim's brothers Arthur and Hugh. Many more gastropod groups remain to be treated. Manuscript files that Dr. McLean compiled as a basis for thorough revision are available to researchers with expertise and interest. Please inquire with Daniel Geiger (geiger@vetigastropoda.com), Lindsey Groves (lgroves@nhm.org), or Jann Vendetti (jvendett@nhm.org).

Blaschka glass models of land gastropod anatomy in the Field Museum of Natural History, Chicago Leopold (1822–1895) and Rudolf (1857–1939)

Jochen Gerber*¹

¹Field Museum of Natural History, Gantz Family Collections Center

Blaschka were glass artisans in Dresden famous for their intricate and life-like glass models of invertebrates and plants. Produced between 1863 and 1890, invertebrate models were sold to museums, universities and private customers around the world. While the vast majority of models represent marine species, a small number of land and freshwater forms are represented as well. The Field Museum of Natural History holds about 140 invertebrate glass models from the Blaschka workshop, first purchased for the 1893 World's Columbian Exposition in Chicago. Among the most unusual are two models of land gastropod internal anatomy. One is modeled after the escargot, *Helix pomatia* (Linnaeus, 1758), the other after the European slug *Arion rufus* (Linnaeus, 1758). The two anatomy models are pictured and discussed in their historical and scientific context.

Using RNA-Seq to Investigate the Systematic Affinity and Evolution of the Pelagic Nudibranch Genus *Phylliroe* (Gastropoda: Nudibranchia: Phylliroidae)

Jessica A. Goodheart*¹ and Heike Wägele²

¹Marine Science Institute, University of California Santa Barbara

²Centre of Molecular Biodiversity, Zoological Research Museum Alexander Koenig

Transitions to a pelagic lifestyle have occurred multiple times across Metazoa, but are rare among gastropod mollusks. Understanding the relationships of pelagic organisms to closely related benthic taxa is necessary to reveal insights into the evolution of such a lifestyle. *Phylliroe* is a marine gastropod genus in a family of pelagic organisms (Phylliroidae) that has long been considered a member of Cladobranchia, a suborder of nudibranchs. Due to the pelagic lifestyle of members of this family, specimen collection has been challenging and rare, and therefore little is known about how this family is related to the rest of Cladobranchia. We address this question here with new transcriptome data collected from *Phylliroe bucephala* and data from 40 other species within Cladobranchia obtained from the Sequence Read Archive. From these RNA-seq data, we generated a supermatrix of 298 orthologous groups, which were used to construct a phylogeny of Cladobranchia. This is the first molecular phylogeny to include a member of *Phylliroe*. We found that *Phylliroe* falls within a clade of taxa previously included in the paraphyletic group Dendronotida, and this family (Phylliroidae) is closely related to Scyllaeidae and Tethyidae. We then use this phylogeny to obtain new insights into the morphological and ecological evolution associated with the transition to a pelagic lifestyle along this lineage.

Diversity at the Bottom of the Trench: First Records of Hadal Solenogastres in the Northwest Pacific

Gerhard Haszprunar*¹, Franziska Sophie Bergmeier, MSc², and Dr. Katharina Maria Jörger²

¹SNSB - Zoological State Collection Munich

²Dept. Biology II, LMU Munich

Diversity at the bottom of the trench: first records of hadal Solenogastres in the Northwest Pacific: Total absence of light, enormous hydrostatic pressure and extremely limited food availability characterize the hadal zone (i.e. marine trenches), which has long been considered void of life until first discoveries of Metazoa in the mid-20th century. Here we present the first records of hadal Solenogastres discovered in the Kuril-Kamchatka Trench in the Northwest Pacific during the German-Russian Kurambio II cruise in 2016. In total, we discovered 6 distinct morphospecies (16 specimens) at the bottom of the trench and 9 morphospecies on the slopes of the trench (11 specimens). Species are analyzed based on an integrative taxonomic approach combining data from external characteristics (i.e. scleritome features) with molecular species delineation, within a phylogenetic framework of 60 species of deep-sea Solenogastres in the Northwest Pacific summarizing data from nine cruises to adjacent bathyal and abyssal areas. Most of the discovered species are considered new to science, but allow classification among nine established families based on scleritome features. Some species, however, require comparative molecular data from their Atlantic or South Pacific congeners to exclude the presence of wide-range species. Most species have been collected as singletons and the faunal composition of the trench differs remarkably from the solenogaster fauna inhabiting nearby abyssal plains and basins. The discovery of specialized food sources in hadal Solenogastres provides some further indication that the trench fauna might not just resemble a subset of bathyal source populations but rather includes at least some endemics.

Evolutionary Diversification of Genital Morphology Among Endemic Land Snails of the Galápagos Islands

Takahiro Hirano*¹ and Christine E. Parent¹

¹Department of Biological Sciences, University of Idaho

Genital morphology can be diversified even among closely related species. This is because differences in genitalia are often a product of sexual selection/conflict. However, genital morphology has also been recognized as a taxonomic trait for clarifying phylogenetic relationships, indicating its morphological similarity among closely related lineages. Here, we focus on the hermaphroditic land snail genus *Naesiotus* on the Galápagos Islands. These snails form the most species-rich lineage of these islands (more than 65 species). A recent phylogenomic study found that these snails can be divided into two major clades, and that there is a significant linear positive relationship between clade age and island geological age. Thus, we investigated divergence patterns of genital morphology of the snails. We measured 11 traits of genitalia in more than 180 individuals representing 40 species including presumably extinct species and sister lineages from mainland Ecuador. We find that divergence patterns of genital morphology reflect phylogenetic relationships. Patterns of the genital morphology in one of the two main clades indicate that populations on older islands tend to have longer penis, flagellum, bursa stalk than that of snails found on younger islands. These results highlight the potential effects of population demographic history and a potential role for the degree of sexual selection/conflict among populations in genitalia divergence. Both phylogenetic constraints and sexual selection/conflict might affect divergence patterns of genital morphology in these snails. Although the functional role of these elongated genital structures is unclear, *Naesiotus* should be a good model for clarifying effects of sexual selection/conflict in evolutionary diversification.

Extraction of Shell DNA to Inform Conservation Biology

C.S. Hobbs*¹ N.W. Yeung², and K.A. Hayes¹

¹Bernice Pauahi Bishop Museum, Pacific Center for Molecular Biodiversity

²Bernice Pauahi Bishop Museum, Department of Malacology

Molluscs are the most threatened animal group, with many species going extinct faster than can be recorded. Fortunately, natural history collections house specimens representing many extinct and rare molluscs and represent our only opportunity to study the genetics and evolution of these species. During growth, molluscs may trap DNA within the layers of their shell, and with advanced DNA extraction and sequencing approaches these data may be utilised to yield deeper understanding of molluscan evolution, systematics, and conservation. With 209 species representing five subfamilies in Hawaii, the Achatinellidae is the second largest family of native land snails in the archipelago. Unfortunately, many of these species are now extinct, and the few remaining taxa are endangered. Nearly all 750+ Hawaiian land snail species have experienced severe population declines in the last century as a result of impacts from invasive species, habitat destruction, and climate change, yet only 44 species in the achatinellid subfamily Achatinellinae are protected under the US Endangered Species Act. Using historical shell collections of the Bernice Pauahi Bishop Museum, we are developing a DNA extraction protocol to get data from the shells of 14 extant species of Auriculellinae, a Hawaiian endemic achatinellid subfamily. Such approaches are our best hope for obtaining DNA data from extinct and rare species. These data will in turn help inform our understanding of species limits, diversity of threatened taxa, and development of effective management strategies. Once optimized, this approach can be expanded to a diverse array of specimens in museum collections globally, unlocking them as historical genetic archives for evolutionary studies and conservation.

A Mitogenomic Phylogeny of Chitons (Mollusca: Polyplacophora)

Iker Irisarri*¹, Juan E. Uribe², Douglas J. Eernisse³, and Rafael Zardoya¹

¹ Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales (MNCN-CSIC)

² Department of Invertebrate Zoology, National Museum of Natural History, Smithsonian Institution

³ Department of Biological Science, California State University Fullerton

With a rather conserved morphology and only about 1000 extant species, chitons form a discrete and comparatively understudied class of mollusks (Polyplacophora). Understanding of chitons' evolutionary history is confounded by conflicting classification systems and variable interpretations of their patchy fossil record. Furthermore, few molecular studies have addressed the phylogenetic relationships among major chiton lineages. Here, we reconstructed a phylogeny of chitons using 13 newly sequenced and six available mitogenomes, as well as mitochondrial gene sequences assembled from four RNAseq datasets. The inferred phylogenies largely agreed with the latest taxonomic system, supporting a deep split between the two extant orders, Lepidopleurida and Chitonida, and mostly supporting a split in the latter into suborders Chitonina and Acanthochitonina. However, the current classification of Callochitonidae within Chitonina has remained problematic and, as here represented by Callochiton, was instead resolved as sister to all other Chitonida in agreement with gamete characters. At lower taxonomic levels, we found evidence for major reorganizations in some families as currently defined, calling for taxonomic revisions and re-evaluation of the evolutionary history of previously studied morphological characters. Despite the generally conserved gene order in chiton mitogenomes, we found three new rearrangements that have phylogenetic utility, and reconstructed a plausible model explaining mitochondrial gene order evolution in chitons. Using a relaxed molecular clock approach with available but limited fossil calibrations, we inferred divergence times of major lineages that largely agree with the few previous molecular clock estimates and the fossil record.

Deep-Sea Biogeography Revisited with the Densest Sampling: A Tale of the Bathyal–Abyssal Snail Genus *Bathyancistrolepis* (Gastropoda: Buccinidae)

Genki Ishiyama*¹, Tsuyoshi Takano^{1,2}, Hiroaki Fukumori^{1,3}, Hajime Itoh^{1,4}, Kazunori Hasegawa⁵, Shigeaki Kojima¹, and Yasunori Kano¹

¹Atmosphere and Ocean Research Institute, The University of Tokyo

²Meguro Parasitological Museum

³Tropical Biosphere Research Center, University of the Ryukyus

⁴National Institute for Environmental Studies, Japan

⁵National Museum of Nature and Science, Tokyo

Little is known about the speciation of benthic animals in the deep sea, where few obvious barriers exist to prevent admixture of individuals. Intense environmental gradients with depth, rather than geographic separation, would thus play a central role in genetic differentiation and speciation (the depth-differentiation hypothesis). Several studies have corroborated this idea for lineages of bivalves, amphipods and octocorals. However, difficulties in sampling have hampered detailed documentation of existing diversity and hence past speciation processes in the deep sea. Here we show—with among the most extensive datasets for a clade of deep-sea benthos—that geographic distance may play as significant a role in speciation as depth-related factors do, presumably depending on the dispersal ability of individuals. Direct-developing snails of the buccinid genus *Bathyancistrolepis* are endemic to the northwest Pacific (Sea of Okhotsk to Pacific coasts of Japan to southwest of Taiwan) with a depth range from 550 to 5,300 m. Specimens from 108 localities encompassing their geographic and vertical distributions were classified into seven biological species, five of which were new to science. Sister species had either sympatric or allopatric distributions, with or without an overlap of depth ranges. Genetic distances between conspecific individuals increase with their geographic distances, but not with differences in depth, suggesting that both sympatric and allopatric speciation occurred in the evolution of this bathyal–abyssal clade. We aim in the future to time-calibrate the divergence events with their Miocene to Pleistocene fossils; the extensively uplifted areas of Japan provide an unrivaled opportunity to examine bathyal taxa of as recent as 0.6 million years ago.

Disruptive Selection on Shell Colour in Japanese Land Snails: A Mark-Recapture Study of *Euhadra peliomphala simodae*

Shun Ito*¹ and Junji Konuma²

¹Tohoku University

²Toho University

Disruptive selection is the natural selection that works on extreme traits. This selection has been studied as an important factor contributing to phenotypic divergence and ecological speciation. Few field studies have succeeded in demonstrating that disruptive selection works on a trait because it is necessary to carry out the field survey using a large number of individuals for a long time. As an example that the traits have been diversified by disruptive selection, dimorphisms of shell colour in Japanese land snails *Euhadra peliomphala simodae* are considered. This snail species diversified based on shell colour in the oceanic islands after migrating from the mainland. On Niijima Island, we conducted mark-recapture experiments during 20 field surveys from 2017 to 2018 and accurately quantified the shell colour using images and estimated survival rates using a Bayesian method. We found that black, yellow, and intermediate-coloured snails inhabit the island. These colour variations showed a bimodal distribution that the population of intermediate-coloured snails is much lower than those of black and yellow snails. The population of the three snail groups synchronously fluctuated with the changing seasons. The survival rates of the juvenile intermediate-coloured snails were lower than those of the black and yellow snails, implying that disruptive selection works on shell colour. The disruptive selection we suggested may cause a pattern of adaptive radiation in land snails.

Snails Wearing Green Heatproof Suits: The Benefits of Algae Growing on the Shells of an Intertidal Gastropod

Osamu KAGAWA*¹ and Satoshi CHIBA^{1,2}

¹Graduate School of Life Science, Tohoku University

²Center for Northeast Asian Studies, Tohoku University

Positive interactions are known to play important roles in ecological divergence but have received less attention than negative interactions in studies on intertidal communities. Here, we show that growth of the mat-forming green alga *Pseudocladophora conchopheria* on the shells of an intertidal gastropod (*Lunella coreensis*) provides them with benefits for living in intertidal rocky habitats. We found that *P. conchopheria* covered a large proportion of the shell surface in all *L. coreensis* inhabiting an exposed rocky shore habitat, but none or only a small proportion of the shell surface in *L. coreensis* inhabiting a damp boulder shore habitat. Thermal exposure experiment showed that *L. coreensis* originating from the boulder shore habitat had a higher mortality rate and temperatures inside the shell than those originating from the exposed rocky shore habitat. These differences disappeared when *P. conchopheria* was removed from the shell or was dried out, indicating that an increased coverage and dampness of the alga suppressed the increase in temperature inside the shell. These support the hypothesis that the growth of *P. conchopheria* on *L. coreensis* shells suppresses thermal stress in the hosts; the benefits of *P. conchopheria* may enable the hosts to exploit habitats where considerable thermal stress is present during air exposure.

***Trochulus hispidus* And *T. coelomphala* Interbreed Despite Distinct Genital Morphology and Genetic Differences**

Elżbieta Kuźnik-Kowalska*¹, Małgorzata Proćków², Joanna R. Pieńkowska³, and Paweł Mackiewicz⁴

¹ Department of Invertebrate Systematics and Ecology, Wrocław University of Environmental and Life Sciences, Wrocław, Poland

² Museum of Natural History, University of Wrocław, Poland

³ Department of Cell Biology, Adam Mickiewicz University, Poznań, Poland

⁴ Department of Bioinformatics and Genomics, University of Wrocław, Poland

Land snails *Trochulus hispidus* and *T. coelomphala* are poorly recognizable based on shell morphology but they differ in certain reproductive structures, i.e. length of penis and bursa copulatrix duct. Cross experiments were carried out between specimens of these species, which represented different clades in the mtDNA COI tree. The snails, originated from distant areas of ca. 700 km apart, were collected as juveniles to avoid prior mating and thus interference in stored sperm. Autogamy or parthenogenesis can be excluded since none of the snails reproduced when kept alone. The fecundity rates was 100% and 47% for the conspecific and interspecific pairs, respectively. Life history traits were highly variable within the cross types and the statistically significant differences were found for: lifetime fecundity, number of clutches per pair and survivorship of juveniles at the 300th day. The conspecific *T. coelomphala* pairs produced significantly more eggs and clutches than the control pairs of *T. hispidus* and the interspecific pairs. The intra-group variations of eggs and clutches produced by a pair were lower for the conspecific *T. coelomphala* than for *T. hispidus* and the interspecific pairs. The snails of all groups showed no statistically significant differences in mean batch size, hatching success and survivorship until the age of 150 days after hatching. The survivorship was the only life history trait greater in the hybrids than in control pairs. The results indicate that differences in the genital structure between *T. hispidus* and *T. coelomphala* are not significant enough to prevent their mating. Research was supported by the National Science Centre, Poland, Grant number: 2016/21/B/NZ8/03022.

Hungry Slugs: The Feeding Habits of an Invasive Species

Érik L'Heureux*¹, Hinatea Arie¹, and Bernard Angers¹

¹University of Montreal, Biological Sciences

Invasive exotic herbivores can have tremendous impacts on native flora. To assess these impacts, a first step is to determine the diet composition and feeding habits of these organisms. The invasive European slug *Arion fuscus* greatly expanded its distribution in northeastern North America in the last fifty years. The objective of this study is to determine the diet of this slug in North America to assess whether it is a food generalist or specialist. Slug specimens were collected in spring at eight sites characterized by the presence of wild American ginseng, a highly endangered plant. Digestive contents of specimens were extracted, and plants ingested by slugs were genetically identified. Diets were then compared spatially, and temporally while different plants emerged. Results revealed digestive contents with a single plant species per specimen for most individuals. Diet of *A. fuscus* is also strongly biased toward a few plant species compared to the species diversity present on sites. Plant species from digestive contents were compared to available plant species growing on sites to determine whether *A. fuscus* is a food generalist or specialist. This study provides guidelines to assess relevance of conservation efforts.

Habitat Selection And Invasion Success of an Exotic Slug

Érik L'Heureux*¹ and Bernard Angers¹

¹University of Montreal, Biological Sciences

The invasion success of an exotic species is often attributed to its capacity to occupy multiple habitats. Indeed, the distribution expansion of actively dispersed generalist species is not blocked by heterogeneous areas where distinct habitats are next to each other. The probability of successful introduction of passively dispersed individuals is also higher for habitat generalists, less dependant of the habitat type in which they have been transported, than for specialists. The European slug *Arion fuscus* is a relevant model to test this hypothesis. This species greatly expanded its distribution in northeastern North America in the last 50 years, likely facilitated by passive dispersal via human activities. To assess whether this species is a habitat generalist or specialist, a sampling was proceeded in five different habitat types (25 sampling sites) from natural to disturbed in southern Québec (Canada). The presence/absence of 12 gastropod species were recorded, among which a total of 363 specimens of the *A. subfuscus/fuscus* complex were collected and genetically identified. The species *A. fuscus* was detected in all habitat types sampled and could be considered as the most generalist species in the region. This contrast with the native slug species from this region that are specialists or present in much less sites. This study, coupled with a spatial transcriptomic analysis for assessing the molecular bases of generalist strategy, would help to better understand the mechanisms underlying the expansion of exotic species and guides future studies on the impacts of *A. fuscus* in various habitats.

Tiny Orange Eulimid Snails on Brittlestar Arms: A New Species of *Stilapex* Iredale, 1925 in Southern California and a Common Intertidal Ophiuroid Host

Patrick I. LaFollette*¹, Courtney Patron², and Douglas J. Eernisse^{1,2}

¹ The Natural History Museum of Los Angeles County (LACM)

² California State University Fullerton, Department of Biological Science

Eulimid gastropods are parasitic snails on particular echinoderm hosts, but they are relatively rare and mostly in subtidal depths in California, and none are known to be associated with ophiuroids. We were thus surprised in 2018 to find small (ca. 2mm) bright orange snails attached to the ventral arm surfaces of the most common brittlestar, *Ophionereis annulata* (Le Conte, 1851), at three southern California intertidal localities. The snail profile was much more stout, with fewer whorls, than most worldwide eulimids, and we tentatively identified it as a little-known Panamic species, *Stilapex cookeana* (Bartsch, 1914), whose type locality is in Baja California Sur, Mexico. However, further comparisons to Bartsch's illustrations and specimens that have been identified as this species from further south in Mexico have led us to conclude the California snails are a previously undescribed species of *Stilapex*. Elsewhere, we are describing it as new. By searching for it in the LACM (Los Angeles) collections, we found none in extensive (especially 1940-1980) microgastropod collections, but did find a 1996 specimen among forty Californian specimens of LACM *O. annulata* checked. We also found a single pair of snails on the same host from a 2017 image on iNaturalist.org, and added another intertidal specimen from 2019. Altogether, we have records for eight specimens from San Diego to Los Angeles counties, 1996 to 2019. The absence of any other records from the Eastern Pacific or elsewhere, despite considerable collective expertise of California malacologists, could imply that this is a previously undescribed and unknown species that was recently introduced to California.

The Bailey-Matthews National Shell Museum (Florida, USA) Digital Imaging Project

José H. Leal*¹

¹ Bailey-Matthews National Shell Museum

The Bailey-Matthews National Shell Museum collection (BMSM), on Sanibel, Florida, currently encompasses in excess of 130,000 catalogued lots, including marine, terrestrial, and freshwater mollusks. As part of our efforts to disseminate collection data and improve their accessibility to remote users, the Museum has embarked in an ambitious project that includes acquisition, processing, storage, and distribution of images of selected collection specimens and related objects (original labels, notes). The endeavor is the logical sequel to a critical, two-phase project funded by two Institute of Museum and Library Services (IMLS) Collection Stewardship grants that allowed for the cataloguing of the entire BMSM backlog over a period of five years. We are, conforming to Darwin Core and Audubon Core standards, linking images to the BMSM catalogue via iDigBio and, ultimately, to other collection data aggregators. The main objective is to capture and distribute images of 9,240 specimens representing about 6,850 species from key areas of the collection, with distinct emphases on types, vouchers, the Colin Redfern Collection (Bahamas), Southwest Florida, and parts of the Eastern Seaboard of the US. Imaged material includes a few historical collections from Southwest Florida that provide important occurrence data for environmental studies and other types of research. The 2.5-year project, funded in 2018 by an IMLS Collections Stewardship Grant, was just launched in February 2019, with the acquisition of photographic equipment, graphics-oriented computer, image-capture and processing software, and the recent hiring and training of specialized staff.

Reproductive strategy of the squid *Lolliguncula diomedea* (Cephalopoda: Loliginidae) in the Gulf of Tehuantepec

Sairi Sarai León-Guzmán*¹, Hugo Alonso Guzmán-Intzin¹, María del Carmen Alejo-Plata¹

¹Universidad del Mar, Campus Puerto Ángel

Ovary maturation and spawning in the squid *Lolliguncula diomedea* in the Gulf of Tehuantepec, Mexico, were analysed. A total of 1525 squids were obtained from the review of the accompanying fauna of the shrimp fishery during the period of February 2017 to May 2018. Oogenesis and development were studied on histological sections of ovaries of 1351 females (19.08-90.37 mm ML, I-V maturity stages). The sex ratio (males:females) was 1:7.7, (χ^2 916.14, $P < 0.05$). The estimated size-at-50%-maturity for females was 68.54 ± 70.23 mm. The fecundity was 3120 (73.47 mm, 14g) to 8880 (74.34 mm, 15.6g) oocytes per female. The consistent presence of postovulatory follicles and the presence of oocyte of different size and development support the hypothesis that the *L. diomedea* is a multiple spawner with an extended spawning season in the study area and aggregation behavior during spawning.

Shedding Light: Evolution of Photosymbiosis in Bivalves

Jingchun Li*^{1,2}

¹University of Colorado Boulder, Department of Ecology and Evolutionary Biology

²University of Colorado Boulder, Museum of Natural History

Photosymbiotic associations between metazoan hosts and photosynthetic dinoflagellates are crucial to the trophic and structural integrity of marine ecosystems. Such associations have independently evolved in diverse metazoan lineages. However, an in-depth understanding of their ecology and evolutionary dynamics are still lacking. Among photosymbiotic host organisms, bivalve mollusks pose an evolutionary dilemma. Compared to other invertebrates that house symbionts in translucent tissues that are directly exposed to sunlight, bivalves possess opaque, protective shells that pose an inherent obstacle to expose symbionts to light. Nonetheless, at least 17 modern or extinct bivalve lineages are known, or were suspected, to form photosymbioses, and each possess(ed) distinct morphological traits that are considered adaptive to photosymbiosis. Within modern taxa, obligate photosymbiosis are found in two marine lineages: the well-known giant clams (Subfamily Tridacninae) and the heart cockles (Subfamily Fraginae). Both groups belong to the family Cardiidae and host symbionts from the same family (Symbiodiniaceae). Fraginae also includes a lineage composed of several non-symbiotic species. To date, the ecology of Fraginae, as well as the phylogenetic relationships between the two photosymbiotic bivalve lineages, are not well understood. Here, I assess bivalve photosymbiosis through ecological, morphological, phylogenetics, and genomics perspectives. In particular, I show that Tridacninae and Fraginae are likely sister clades to each other, but independently evolved photosymbiosis. There are also possible genetic/metabolic preadaptations that promoted both lineages to establish symbiotic relationships with Symbiodiniaceae algae.

Sea Slugs (Gastropoda: Heterobranchia) from Trindade Oceanic Island, South Atlantic Ocean, Brazil

Patricia O. V. Lima*¹, Hilton C. Galvão-Filho², Daniel Abbate¹, and Luiz R. L. Simone¹

¹Zoology Museum of University of São Paulo, laboratory of Malacology

²Private Address

Sea slugs possess a high variety on morphological traits and adaptive strategies that allow them to occupy multiple niches. Recently, many studies have reported new records and described new species from different regions in Brazil. Still, little is known about the diversity of marine heterobranchs from Brazilian oceanic islands. For instance, only *Berthella punctata* and *Felimare sp.* are reported for Trindade and Martin Vaz, one of the most remote islands in the country, located ~1,400 km off SE Brazil. In that isolation, 26 species of heterobranchs were found in the intertidal and subtidal zone, among them 11 possible new species, the first record of the genera *Mourgona* and *Cyerce* for the South Atlantic, the first record of *Felimare ruthae* for Brazil and the record of *Aegires absaloi* for the first time after its description. Sampling was performed in 29 spots (27 on Trindade and two on Martin Vaz) around the islands, the heterobranchs were found in 22 of them. All the specimens were collected during low tide under rocks and by scuba diving at depths up to 25m, between 2012 (January, February, June and July), 2013 (July) and 2014 (April, May and October). Besides new candidate species and new record for Brazil, this survey provide important data for future biogeographical studies, connectivity and gene flow between species of mainland and these very remote islands.

Deep Down Under: Australia's Abyssal Mollusc Fauna

Hugh MacIntosh*¹, Francesco Criscione², Anders Hallan², and Frank Koehler²

¹Museum Victoria

²Australian Museum

Australia is renowned for its molluscan diversity, and its terrestrial and shallow water fauna have been the subjects of intensive study. Australia's deep-sea environments on the other hand, have seen little coordinated sampling since the days of the Challenger expedition. This paucity of data has represented a sizeable knowledge gap for conservation planning, and for our understanding of global deep-sea biogeography. The extent of this knowledge gap has significantly reduced in the space of five years, with the completion of three major projects that aimed to quantify slope and abyssal biodiversity off southern and eastern Australia. They represent the deepest sampling in Australian waters, to 5300 m. A wide range of molluscan fauna were represented in the 100,000 total benthic invertebrate specimens retrieved in 237 operations by a variety of samplers. Taxonomic analysis to date has revealed 300 species with 60 new to science. Unsurprisingly, there was a high degree of rarity, with over a third of species known only from single specimens. Here we present a first overview of this fauna, with commentary on notable taxonomic and biogeographic results. These data are underpinning ongoing research into the processes driving Australia's deep-sea biodiversity on local, regional and global scales.

Phylogeny and Diversity of the Indo-west Pacific Gastropods *Haloa sensu lato* (Cephalaspidea: Haminoeidae): Tethyan Vicariance, Generic Diversity, and Ecological Specialization

Manuel António E. Malaquias*¹ and Trond R. Oskars¹

¹Section of Taxonomy and Evolution, Department of Natural History, University Museum of Bergen University of Bergen, PB7800 5020 Bergen, Norway

Indo-West Pacific species formally ascribed to Haminoea have been recently reassigned to the genus *Haloa*, but it was questioned whether further generic split was warranted to reflect phylogenetic relationships and morphological features. In this work Bayesian and maximum likelihood molecular phylogenetic analyses based on five gene markers were used to study an extended dataset including to our best knowledge representatives of all Indo-West Pacific species of *Haloa*, plus a large representation of Atlantic and eastern Pacific species of *Haminoea*, and several species of the closely related genus *Smaragdinella*. The results support a monophyletic Atlantic + eastern Pacific *Haminoea* clade and a monophyletic Indo-West Pacific radiation with five genera all defined by unique morphological characters and ecological traits, namely *Haloa* proper with tropical and sub-tropical species spread across the Indo-West Pacific, *Lamprohaminoea* including only colourful species of tropical and sub-tropical affinity, two undescribed genus; one with species associated with mangrove habitats across the tropical eastern Indian Ocean and western Pacific, and the second one restricted to temperate waters of Australasia, plus the genus *Smaragdinella*, which are the only cephalaspideans known to inhabit intertidal hard substrates across sub-tropical and tropical regions of the Indo-West Pacific. The results suggests the role of the closure of the Tethys seaway structuring the phylogeny of worldwide “*Haminoea*” snails and of ecology driving the phylogenetic structure of the Indo-West Pacific radiation.

A Closer Look at the Aplacophoran Biodiversity of New Zealand

Madelyn McCutcheon*¹, Kevin Kocot¹

¹The University of Alabama

Aplacophorans are shell-less, vermiform mollusks that inhabit benthic marine habitats around the world. Identifying most aplacophorans to the genus and/or species level requires characterization of internal anatomical structures, such as the radula, ventral foregut glands, and reproductive organs. Fewer than 400 species of aplacophorans have been described to date but the true number of species is estimated to be tenfold higher. New Zealand is one of the most understudied areas with only three described aplacophoran species, *Neomenia naevata*, *Neomenia trapeziformis*, and *Dorymenia quincarinata*, all of which are Solenogasters. In order to improve understanding of the biodiversity of Aplacophora in New Zealand waters, we have been studying collections from the National Institute of Water and Atmospheric Research (NIWA) and the Museum of New Zealand Te Papa Tongerawa using histology, light microscopy and SEM to identify and describe species from these collections. Here we present our preliminary data from the characterization we have been able to complete thus far. After grouping the collection into morphospecies, we estimate that there are at least 10 caudofoveates and 12 solenogasters, most of which are new to science. We will present the description of a new species of *Proneomenia*, as well as plans for future work to improve understanding of the aplacophoran fauna of New Zealand.

Fresh cucumber as a novel attractant for invasive gastropods

Rory J. McDonnell*¹, Maria Cordoba¹, and Jocelyn G. Millar²

¹Department of Crop and Soil Science, Oregon State University

²Department of Entomology, University of California, Riverside

Terrestrial gastropods cause economic damage to crops in a number of ways, including reducing yield due to consumption of seeds, seedlings, roots, and aerial parts of mature plants. Control strategies are focused heavily on molluscicides, which are ineffective under certain conditions. Thus, there is an ongoing need to develop alternative management options. One such approach is the development of novel attractants for use in traps and in attract-and-kill strategies. In contrast to insects, very little work has been done to explore the chemical ecology of gastropods, and what little work has been done has been relatively superficial. However, even these preliminary studies have clearly shown that chemical cues play a major role in a wide range of gastropod behaviors. A primary goal of this study was to develop a generic bioassay that can be used to identify novel attractants for any terrestrial gastropod species by high-throughput screening of attractant sources. The optimized method uses arrays of glass T-tubes with cameras positioned above them to record snail choices. Using the bioassay, >1500 choice and no-choice tests demonstrated that cucumber was consistently the most attractive to *Cornu aspersum* and *Deroceras reticulatum*. Our results also showed that previous feeding influenced subsequent food choice for both species, but this conditioning was not absolute and could be broken. The attractiveness of cucumber was confirmed in field trials in Oregon where both *D. reticulatum* and *C. aspersum* were significantly attracted to traps baited with cucumber. These results demonstrate the potential importance of fresh cucumber as a novel attractant for management and detection of pest gastropods.

Six or one? Study of species diversity of the genus *Ancylus* in Georgia

Levan Mumladze*¹, Nino Kachlishvili¹, Ani Bikashvili¹, and Bella Japoshvili¹

¹ Institute of Zoology, Ilia State University, Tbilisi, Georgia

Up to seven species level taxa within genus *Ancylus* have been indicated for the Caucasus including five endemics for Caucasus and eastern Mediterranean. Traditional morphological taxonomy, based on limited available materials has however failed to unambiguously delimit the species and infer biogeographical history. To overcome this problem, we applied DNA based and Geometric morphometrics approaches to investigate modern diversity and distribution of *Ancylus* species in Georgia. Our study unraveled partial discordance in morphological and DNA based classification and provided evidences of complex evolutionary pattern among local populations.

The biology of Japanese epizoic limpet *Lottia tenuisculpta*

Ryo Nakayama*¹ and Tomoyuki Nakano²

¹Department of Zoology, Division of Biological Science, Graduate School of Science, Kyoto University

²Seto Marine Biological Laboratory, Field Science Education & Research Center, Kyoto University

Patellogastropod limpets are most common inhabitants in the intertidal rocky shores. Traditionally, biology and ecology of intertidal limpets have been widely studied; however epizoic limpets receive little attention. *Lottia tenuisculpta* (Lottiidae), a tiny limpet distributed in Japan is one of the epizoic limpets that inhabit body surfaces of other molluscs. Here, we conducted whole year field observations, specimen investigations, predation experiments and larval settlement experiments to elucidate the epizoic biology of *L. tenuisculpta*. Whole year field observation and specimen investigation suggest *L. tenuisculpta* favors tegulid and muricid species as hosts. Juveniles usually attach to host and later migrate from host shell to rock surfaces as they grow to a certain size. Additionally, limpets on snail can get an early growth than it on rock surfaces. Predation experiments show limpets can reduce the predation risk by crabs when inhabiting host shells. Larval settlement experiments reveal that the larva of *L. tenuisculpta* is attracted to its host mucus. Based on our studies and previous studies concerning to the epizoic limpets, we propose two classifications of epizoic limpets based on the host-utilization duration: the “Transient type” and the “Permanent type”. “Transient type” species mainly attach to hosts in its juvenile stage and leave the host to move to rock surfaces. Whereas, “Permanent type” species attach to its host through their entire life. This study reports the epizoic biology of *L. tenuisculpta* and a general overview of the two lifestyle types of epizoic patellogastropod limpet.

A fresh look at Melanopsidae (Caenogastropoda: Cerithioidea): evolutionary systematics, biogeography and conservation genetics

Marco T. Neiber¹, Simone Cianfanelli², Fabrizio Bartolini², Thomas von Rintelen³, Matthias Glaubrecht¹

¹Universität Hamburg, Center for Natural History (CeNak)

²Università degli Studi di Firenze, Museo di Storia Naturale – La Specola

³Museum für Naturkunde Berlin, Leibniz-Institute for Evolution and Biodiversity Science

Melanopsidae occur in subtropical and temperate regions of the Western Palearctic and are also reported from Zealandia, which is an unparalleled disjunction among freshwater animals. Melanopsidae also have a rich fossil record. We sequenced nuclear and mitochondrial markers of a representative sample of species/genera covering the entire geographic range of the group. We compare the timeframe for the evolution of major melanopsid lineages with geologic events and elucidate scenarios that may have shaped distribution patterns. Our phylogenetic analyses suggest that Melanopsidae are not monophyletic. *Holandriana* is more closely related to Pleuroceridae and Semisuclospiridae than to Melanopsidae s.str. The Zealandian taxa (Zemelanopsidae) were recovered as the sister group of a clade including *Melanopsis*, *Microcolpia* and *Esperiana* (Melanopsidae s.str.). *Esperiana* branches of first, while *Microcolpia* represents the sister group of *Melanopsis*, which is comprised of three lineages: 1) western Mediterranean region, 2) eastern Mediterranean region and 3) Italy. While the Italian populations show little shell variability, the eastern and western *Melanopsis* lineages are highly variable. Several geographically coherent groups in *Melanopsis* can be ranked as species. However, in a number of cases morphologically distinct forms were not recovered as monophyletic units. The Italian narrow-range endemic *M. etrusca* was known historically from twelve populations, half of which have already gone extinct. We used AFLP markers to assess the genetic diversity in the remaining populations, which showed that the westernmost populations are genetically distinct from the remaining populations. Recovery plans, which are urgently needed to prevent a further decline of the species, ought to take population structuring into account to preserve the genetic diversity.

The Nudibranch Genus *Jorunna* in Europe with a Focus on the *J. tomentosa* Complex

Jenny Neuhaus*¹, Cessa Rauch¹, Torkild Bakken², Bernard Picton³, and Manuel A. E. Malaquias¹

¹ Section of Taxonomy and Evolution, Department of Natural History, University Museum of Bergen University of Bergen, PB7800 5020 Bergen, Norway

² NTNU University Museum, Department of Natural History, 7491 Trondheim, Norway

³ Department of Natural Sciences, National Museums Northern Ireland, Cultra, Holywood, Co. Down, BT18 0EU

Jorunna is a genus of nudibranch sea slugs in the family Discodorididae with 5–6 species recognized as valid in European waters. Among those the type species of the genus *J. tomentosa* is the only one known to occur in Scandinavian waters. This species can depict distinct colour patterns from nearly white with dark blotches scattered on the body to the more typical colouration of beige with small light-brown spots. Preliminary molecular barcoding of Norwegian specimens suggest that this taxon as currently recognised may include more than one species. In this work a combination of molecular phylogenetics and morphological approaches is used to investigate the taxonomic status of the various colour morphs found in *J. tomentosa* across its geographical distribution and to compare it with other European congeneric species. The results assembled so far point to the occurrence of a second species of *Jorunna* in Scandinavia.

Radula, Genital Structures and Shell Morphologies of the Invasive Land Species, *Achatina fulica hameliei* Petit (1859), *Achatina albopicta* E.A. Smith (1878) and *Achatina reticulata* Pfeiffer 1845 (Gastropoda : Achatinidae) in Southwest Nigeria

Alexander B. Odaibo*¹ and Suraj O. Olayinka¹

¹Department of Zoology, University of Ibadan, Ibadan, Nigeria

The aim of this study was to determine the differences in the shell, radula, and genital structures of *Achatina fulica* Bowdich, 1822 and *Achatina albopicta* E.A. Smith (1878) that have been recently been introduced into Nigeria. This is the first report of *Achatina albopicta* in Nigeria. Five to ten live specimens, with complete shell characters, of each species were used for this study. There were dark brown markings on the whorls of both species on dirty brown background for *A. fulica* and yellowish background for *A. albopicta*, and the shell of *A. albopicta* was slightly glossy on the body whorl. The whorls of *A. albopicta* were much more convex than the whorls of *A. fulica*. The columella of *A. albopicta* was truncate, moderately concave, and arched, while the columella of *A. fulica* was truncate and straight. There was significant relationship between the shell width and aperture length ($r = 0.6407$, at 5% level) of both species. The genitalia of the two species were very identical but differed significantly in the shape and size of albumen gland. The albumen gland of *A. fulica* was kidney-shaped and about one-fifth of the oblong albumen gland of *A. albopicta*. The radula could be differentiated by the structure of central teeth; *Achatina fulica* had a prominent and sharp mesocone while the central teeth of *A. albopicta* had a blunt and not very prominent mesocone.

Sequestration of Nematocysts by Aeolid Nudibranchs: A Mini-Review

Brian K. Penney*¹

¹ Biology, Saint Anselm College

There have been recent conflicting claims as to whether aeolid nudibranchs can select particular nematocysts from their prey. I surveyed the available literature and found only sixteen cases— for merely 13 aeolid species— in which both nudibranch and prey cnidomes were described in sufficient detail to see whether selection had occurred. Most nematocyst types known were sequestered by at least one aeolid, except atrichous isorhizas and spirocysts; Homotrichous isorhiza haplonemes and Homotrichous Anisorhizas were not present in prey investigated. Aeolids select particular nematocysts, although there were some prey species for which the whole cnidome was taken. Surprisingly, there are several cases in which the nematocysts taken from a prey species by a given aeolid species has differed among studies. Different aeolid species feeding on the same prey species generally take the same nematocysts, suggesting there is some functional rationale for keeping particular nematocyst types. An aeolid species generally takes different nematocysts from each of the prey species it consumes. It is unclear whether this is because the nematocysts have different functions or whether they vary in other characteristics. Therefore, while aeolids are capable of selecting nematocysts from prey species, the limits to and rationale for this ability require further investigation.

Local Ecological Knowledge on Land Snail Diversity in Mount Banahaw, Luzon Island, Philippines

Kinsley Meg G. Perez*¹, Virginia C. Cuevas², Carmelita M. Rebanco¹, Emmanuel Ryan C. de Chavez³, and Juan Carlos T. Gonzalez³

¹School of Environmental Science and Management, University of the Philippines Los Baños, College, Laguna, Philippines

²Environmental Biology Division, Institute of Biological Sciences, University of the Philippines Los Baños, College, Laguna, Philippines

³Animal Biology Division, Institute of Biological Sciences, University of the Philippines Los Baños, College, Laguna, Philippines

Local ecological knowledge (LEK) is a community-based conservation effort in sustainable management of natural resources. However, studies on LEK are very limited in the Philippines. To address this information gap, LEK on land snails in Mount Banahaw, Luzon Island, Philippines was determined. Key informant interviews and focus group discussions were conducted in the four communities (northeast- Lucban, southeast- Tayabas, northwest- Majayjay, and southwest- Dolores) of the mountain. Snail calendar served as tool for the identification of hunting season and practices of these communities on land snails. Results showed that communities were knowledgeable on macro land snails (>5mm) such as *Lissachatina fulica*, and the edible, *Ryssota otaheitana*, but were unaware of micro land snails (<5mm). Locals also showed awareness of the snails' ecosystem functions as food source for other animals, and as agents of nutrient cycling. Moreover, sustainable hunting of *R. otaheitana* in sampled communities was also noted. Only adult *R. otaheitana* was harvested, leaving the juveniles to grow and reproduce. In Lucban, the people hunt while they wait for the harvest season of their crops. In Tayabas, the community only hunts during rainy season since according to them there is plenty of *R. otaheitana* in the forest since leaf litter decomposes easily because the soil is wet and moist. In Majayjay, hunting was associated with the blooming of flowering plant, *Erythrina sp.* In, Dolores, hunting was practiced after clearing of farmlands. The present research demonstrated the importance of LEK in sustainable utilization of land snails in a tropical forest setting.

Citric acid as a potential molluscicide and deterrent for the invasive slug species *Arion subfuscus*

Brenda J. Peters*¹, Amy C. Blair¹, and Keegan A. Steele¹

¹St. Ambrose University Biology Department

Because terrestrial slugs cause significant damage in home gardens and commercial farms, physical barriers and chemical molluscicides are used to limit their impacts, yet constant maintenance and toxicity make the development of a more user friendly and safer slug deterrent appealing. Previous studies found citric acid to be less toxic to non-target species compared to current molluscicides. However, the effects of citric acid on slugs have not been explored. To determine the deterrent capabilities of citric acid, the invasive slug species *Arion subfuscus* was given a choice of Romaine lettuce sprayed with 5% citric acid or DI water. To determine the molluscicide capabilities of citric acid, slugs in no-choice trials were given lettuce sprayed with 5% citric acid or placed directly on a citric acid exposed paper towel. Lastly, Romaine lettuce was grown and sprayed with a 5% citric acid solution to examine the effects of citric acid on plant growth. The possibility of using citric acid to solve the problem of unsafe or costly slug maintenance without negatively impacting surrounding plants will be discussed.

Reassessment of *Runcina zavodniki* Thompson, 1980 as Synonym of *Runcina ferruginea* Kress, 1977 Based on an Integrative Approach

Marta Pola^{*1,2}, Ana Karla Araujo Moreira³, and Juan Lucas Cervera^{3,4}

¹ Universidad Autónoma de Madrid. Departamento de Biología

² Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM)

³ Universidad de Cádiz, Departamento de Biología

⁴ Universidad de Cádiz, Instituto Universitario de Investigación Marina (INMAR)

Runcinids are poorly known tiny marine heterobranchs inhabiting intertidal and shallow subtidal rocky shores. *Runcina ferruginea* Kress, 1977 and *Runcina zavodniki* Thompson, 1980 were first described as two distinct species from Plymouth (England) and Rovinj (Croatia), respectively. The former has a characteristic reddish-brown colour with very fine dark brown spots all over the body, three gills, denticulate rachidian teeth and smooth laterals, while *R. zavodniki*'s colour is black and presents three gills, and rachidian and lateral teeth denticulate. However, years later at the same area in Croatia, Thompson (1988) found individuals with black, red-brown and/or pale orange-brown colour and with denticulate rachidian teeth and smooth laterals. Based on this observation, he stated that the denticulate lateral teeth originally described for *R. zavodniki* was not accurate. Due to the supposed similarities between *R. ferruginea* and *R. zavodniki*, Schmekel and Cappellato (2002) considered these two species to be conspecific. In this contribution, we investigate the taxonomic status of *R. ferruginea* and *R. zavodniki* based on specimens from England and Croatia following an integrative approach combining molecular phylogenetics based on mitochondrial markers (COI and 16S) and a nuclear gene (H3), together with morphological study of the radulae. To assist with species delimitation, the ABGD analysis, p-distances and bPTP methods were employed. Our results confirm that *R. ferruginea* and *R. zavodniki* are two distinct species and, therefore, *R. zavodniki* is a valid name.

Taxonomic status of the western Balkan species *Xerocampylaea waldemari* (Gastropoda: Hygromiidae: Urticolini)

Małgorzata Proćków¹, Michael Duda², Luise Kruckenhauser³, Wim J. M. Maassen⁴, Anton J. de Winter⁴, Paweł Mackiewicz⁵

¹Museum of Natural History, University of Wrocław, ul. Sienkiewicza 21, 50-335 Wrocław, Poland, malgorzata.prockow@uwr.edu.pl

²3rd Zoological Department, Museum of Natural History Vienna, Burgring 7, 1010 Vienna, Austria

³Central Research Laboratories, Museum of Natural History Vienna, Burgring 7, 1010 Vienna, Austria

⁴Naturalis Biodiversity Center, P.O. Box 9517, 2300 RA Leiden, the Netherlands

⁵Department of Bioinformatics and Genomics, Faculty of Biotechnology, University of Wrocław, ul. F. Joliot-Curie 14a, 50-383 Wrocław, Poland

Correct species identification affects general knowledge about biodiversity and is necessary to carry out effective conservation activities, especially in biodiversity hotspot areas and former Pleistocene refugia. Such regions are represented by the Balkans, whose malacofauna is still very poorly studied. Therefore, on the basis of recently collected material and museum specimens, we assessed the taxonomic status of the endemic Balkan land snail *Fruticicola waldemari* A. J. Wagner, 1912. This species was previously classified within the genus *Trochulus* (tribe Trochulini). However, our phylogenetic analyses, based on mitochondrial markers (COI and 16S rRNA), revealed its close relationship with snails belonging to the tribe Urticolini, particularly to *Xerocampylaea erjavecii*. The anatomical and morphological data, i.e. patterns of penial plicae, shell microsculpture, umbilicus diameter, and mitochondrial markers showed that *X. waldemari* and *X. erjavecii* are separate but closely related species. The obtained results will be a reference point for further taxonomic studies of different populations of this species, as well as for detailed analyses of a highly variable *X. erjavecii*. Research received financial support from SYNTHESYS (project no. NL-TAF-4425) and the National Science Centre, Poland (project no. 2016/21/B/NZ8/03022).

Model Optimization for Prediction of the Grove Snail Colour Category

Daniel Ramos Gonzalez*¹ and Angus Davison¹

¹University of Nottingham, School of Life Sciences, Nottingham NG7 2RD, UK

We previously quantified variation in the colour of the shell polymorphism of the grove snail *Cepaea nemoralis*, and used a clustering method to bin individuals into colour categories, yellow, pink or brown. As there is high degree of discrepancy between human and computer-based colour scores, we have trialed supervised and unsupervised learning procedures with the Mclust algorithm, to define colour groups. The methods may be used in the future to standardize the collection of the colour phenotype in these land snails.

Quantification of Selection from Visual Predators on Galápagos Endemic Land Snails

Nicole K. Recla*¹ and Christine E. Parent¹

¹ Department of Biological Sciences, University of Idaho

The Galápagos Islands have been a model for studying evolutionary processes due to their isolation, and the ability to track evolutionary change over time. With over seventy species recognized in the group spanning a broad spatial distribution, endemic snails of the Galápagos Islands (genus *Naesiotus*) arguably form one of the most spectacular examples of adaptive radiation of these islands. One of the most diverse traits that has researchers both puzzled and amazed is the broad range of shell coloration of these snails. Preliminary research has suggested that the broad range of shell coloration may be a response to selection from visual predators. In this study we expand this preliminary work and test (1) whether selection from visual predators is common across islands, and (2) determine what are the factors contributing to the variation in the strength of selection in different habitats of different islands across the archipelago.

Monitoring Freshwater Mussels in Complex Rivers: Comparison of Case Studies

Joaquim Reis*¹, Daniel Garrido², and Daniel Pires³

¹MARE - Marine and Environmental Sciences Centre, Faculdade de Ciências da Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal

²University of Copenhagen, Faculty of Science, Nørregade 10, DK-1017 København K, Denmark

³BIOTA - Estudos e Divulgação em Ambiente, Lda, Rua Carlos Ramos, nº 9 A, Urbanização Jardim da Amoreira, 2620-529 Ramada, Portugal

Complex rivers present challenging conditions for sampling freshwater mussels, including flow, depth, poor visibility and large underwater structures, such as rock formations, logs and others. Some species like *Margaritifera margaritifera* live mostly in shallow clear water streams that allow sampling strategies to rely on visual searches, but even in these cases the detectability of individuals is rarely considered in population estimates. Sampling techniques have often to be adapted to the river conditions, and range from wading to scuba-diving, from visual to tactile searches. A choice of well-established sampling designs is available, from total surveys to transects and quadrats, and, less frequently, mark-recapture studies. The applicability and efficiency of each design is affected by the technique itself, and one of the main constraints is the effort needed to achieve the desired results. Here we present several case-studies applying different sampling designs and techniques to different rivers, holding typical Iberian freshwater mussel fauna. The results show the importance of choosing the appropriate technique, with scuba-diving playing an essential role in complex rivers. Different sampling designs have been successfully applied with different objectives, including total surveys and transects for population density estimates, captures per unit effort for evaluation of changes over time and space and mark-recapture for population life-history traits and detectability. We discuss the effort needed to successfully obtain the desired results with each design.

Co-evolution between predator and prey: Specific defensive behavior of *Satsuma* land snails against snail-eating fireflies in the Ryukyu islands of Japan

Nozomu Sato*¹

¹ Graduate School of Urban Environmental Sciences, Tokyo Metropolitan University

Competitive co-evolution often occurs between predators and prey in close interaction on small islands. In the Ryukyu Islands of Okinawa, Japan, the endemic land snail *Satsuma caliginosa caliginosa* (Pulmonata: Camaenidae) uses a tail autotomy defense against the endemic slug snake *Pareas iwasakii*. This defense is not observed in other *Satsuma* species inhabiting islands without slug snakes. However, tail autotomy is not effective against the snails most common specialist predator, the snail-eating firefly, *Pyrocoelia atripennis* (Coleoptera: Lampyridae), as firefly larvae predate snails through their shells. Therefore, development of an additional defense strategy should be advantageous for *S. c. caliginosa*, but this predator-prey interaction has not been investigated. Predation experiments revealed the defensive behavior by *Satsuma* land snails, specific to snail-eating firefly larvae. Land snails shake their tails while shaking the shell laterally and, further, hook the tail to remove larvae from the outer shell. This behavior reduces predation by firefly larvae and is common in snail populations exposed to *Pyrocoelia*. This behavior is not observed in populations on islands without *Pyrocoelia*, suggesting that competitive co-evolution is occurring between *Satsuma* land snails and fireflies. This study also demonstrates that land snails have adapted alternative defense behaviors to multiple specialist predators.

Molecular Evolution of Hemocyanin Genes: Adaptations to New Ways of Life That Help to Elucidate the Disarranged Systematics of Heterobranchia?

Gabriela Schäfer*¹ and Bernhard Lieb¹

¹ Institute of Molecular Physiology

The 400 kDa subunits of molluscan hemocyanins are among the largest polypeptides described in nature. In consequence, the genes, cDNA and primary structures of these oxygen transporter offer fantastic possibilities to reconstruct phylogenetic relationships within Mollusca. Presently, we use hemocyanin genes as a tool to trace phylogenetic relationships within Heterobranchia, a gastropod clade which covers over 30,000 species. Their phylogenetic relationships are far from being resolved since recent molecular phylogenetic analyses falsified the monophylies of the traditional groups “Opisthobranchia” and “Pulmonata”. So far, we analyzed several hemocyanins of Tectipleura. This extremely diverse group comprises Euopisthobranchia and Panpulmonata which live in all kinds of habitats. The variety of habitats within this clade has resulted from multiple transitions from sea to land and freshwater that took place independently within different Panpulmonata lineages. These habitat shifts required morphological and molecular adaptations including enormous changes of their respiratory systems. Thus, the evolution of hemocyanin polypeptides is strongly associated with the evolution of the animals and their living conditions. Our studies suggest that duplication events of the whole genes represent additional convergent adaptations to habitat transitions and may help to elucidate the evolution of Tectipleura. Furthermore, we identified an exon-intron architecture of hemocyanin genes which is highly conserved within Tectipleura, but differs a lot from the gene structures of other molluscan hemocyanins. These findings strongly suggest that gene structures may contain further phylogenetic signals regarding the relationships of Tectipleura.

A fresh x-ray look on old collections: Micro-CT screening of viviparity in clausiliid land snails clade

Anna Sulikowska-Drozd*¹, Piotr Duda², and Katarzyna Janiszewska³

¹University of Lodz, Department of Invertebrate Zoology and Hydrobiology

²University of Silesia in Katowice, Faculty of Computer Science and Materials Science

³Polish Academy of Sciences, Institute of Paleobiology

The oldest collections of shells appear to be a valuable source of data for modern zoological research. They provide materials for verification of broad zoogeographical and ecological hypotheses on molluscs reproduction as they include records from many territories that are no longer accessible. Here we show data on viviparous and egg-retention reproductive modes in clausiliid land snails, acquired from specimens collected since the 19th century in Pontic, Hyrcanian, and E Asian regions (subfamily Phaedusinae). X-ray imaging (micro-CT) allowed for relatively fast screening of more than 1100 individuals classified to 141 taxa; among them we discovered 205 shells containing embryos or eggs. Gravid individuals belonged to 56 species; for some of them it was the first indication of brooding reproductive strategy. Scanning was performed at Naturalis Biodiversity Centre, Leiden during Synthesis Scholarship (NL-TAF-5042), in the NanoFun laboratories, Warsaw, co-financed by the European Regional Development Fund within the Innovation Economy Operational Programme POIG.02.02.00-00-025/09, and at the Faculty X-ray Microtomography Lab, University of Silesia in Katowice.

The Cone Collector – A successful initiative

Manuel J. Tenorio*¹, António Monteiro², and William J. Fenzan³

¹Universidad de Cadiz, Dept. CMIM y Química Inorgánica – INBIO, Puerto Real, Spain

²private address, Lisbon, Portugal

³private address, Norfolk VA, USA

The Cone Collector project was launched in late 2006 as a digital newsletter dedicated to both amateur and professional malacologists sharing an interest in cone shells, aimed to exchange valuable information, and help the study and description of new cone species. The first issue was sent to less than thirty persons, with whom the editor was already in touch. The idea was received with great enthusiasm and the mailing list for the newsletter soon included over two hundred names. Moreover, the successive numbers have been uploaded to several websites, which means that the total number of readers is probably higher. Since 2006, a total of 36 numbers have been published. The newsletter itself was soon complemented by the creation of a website (www.theconecollector.com) in which a wealth of information about cone shells can be found. Besides the issues of the newsletter, sections such as Mike Filmer's work on type specimens, Paul Kersten's checklist of Cone taxa, the collections' gallery, the reproduction of the Manual of the Living Conidae in pdf format, and others provide collectors and researchers alike with invaluable information. In 2010, the 1st International Cone Meeting was held in Stuttgart, Germany. Others followed in La Rochelle, France (2012), Madrid, Spain (2014), and Brussels, Belgium (2016). The 5th International Cone Meeting will take place in Lisbon, Portugal, 13-15th September, 2019. These meetings have been extremely successful, usually with 35 to 50 participants from over a dozen different nationalities. The original goal of this citizen science initiative has been thus far successfully accomplished through the newsletter and the meetings.

An assessment of the biogeography of Chitons (Class: Polyplacophora) of the Indian Ocean

Liju Thomas*¹, Sanitha K. Sivadas², Neelesh Dahanukar³, Rajeev Raghavan¹, and Ranjeet K¹

¹Kerala University of Fisheries and Ocean Studies (KUFOS), Kochi, India, 682506

²National Centre for Coastal Research (NCCR), NIOT campus, Chennai, India

³Indian Institute of Science Education and Research (IISER), Pune, India

Chitons (class: Polyplacophora) are exclusive marine molluscs dominant in the intertidal and shallow subtidal zones with some reports from the deep sea. As prolific grazers of rocky intertidal regions, chitons are important indicators of ecological health. From an evolutionary perspective, as evident in the fossil records, chitons have not evolved much from the time of their appearance in the late Cambrian. This makes them an ideal group for understanding diversification and biogeography. Though chitons have been well studied from the Pacific and Atlantic waters, studies, especially on taxonomy, have only recently begun in the Indian Ocean region; necessitating a need to explore and better understand speciation and distribution of chitons in the region. With an aim to understand the biogeography of chitons from the Indian Ocean Rim region, extending from Western Australia to the Eastern coast of Africa, an extensive review of published data from literature and GBIF (Global Biodiversity Information Facility) database were analysed using multivariate techniques. Based on species assemblage and taxonomic classification, five geographically distinct regions were observed. Of 13 families reported from the Indian ocean region, chitonidae, acanthochitonidae, and ischnochitonidae showed wide distribution. The restricted distribution and endemism of certain species in the Indian Ocean regions were also observed. Results clearly demonstrate a need for intensifying field surveys, developing improved data collection protocols, and better understanding the geomorphology and evolutionary phylogeny to unravel species diversity and distribution of chitons in the Indian Ocean.

Who rules the abundance of *Mytilus galloprovincialis* Lamarck 1819 along the Atlantic coast of the Iberian Peninsula?

Jesus Souza Troncoso*¹, Marcos Rubal^{2,3}, Juan Moreira⁴, Ana Catarina Torres^{2,3}, and Puri Veiga^{2,3}

¹Departamento de Ecoloxía e Bioloxía Animal, Facultade de Ciencias do Mar, Universidade de Vigo, Campus Universitario Lagoas-Marcosende, 36310 Vigo, Spain

²Laboratory of Coastal Biodiversity, Interdisciplinary Centre of Marine and Environmental Research (CIIMAR/CIMAR), University of Porto, Terminal de Cruzeiros do Porto de Leixões, Av. General Norton de Matos s/n, 4450-208 Matosinhos, Portugal

³Department of Biology, Faculty of Sciences, University of Porto, Rua do Campo Alegre s/n, 4150-181 Porto, Portugal

⁴Departamento de Biología (Zoología), Universidad Autónoma de Madrid, Cantoblanco, E-28049 Madrid, Spain

Mytilus galloprovincialis Lamarck 1819 is a marine bivalve with ecological and economic relevance. Mussels are ecosystem engineers because they provide habitat for many species, enhancing biodiversity. *Mytilus galloprovincialis* is very abundant in the Atlantic coast of the Iberian Peninsula and it is used for food, being harvested in natural systems and/or cultured intensively on rafts. Aquaculture production at large scale is dependent on the abundance of mussel in the natural environment because juvenile mussels are collected in natural rocky shores and then attached to ropes on rafts. In this perspective, the objective of this study is understanding which environmental and biological drivers control the abundance of *M. galloprovincialis* along the Atlantic coast of the Iberian Peninsula. To achieve this aim, its abundance was estimated as the percentage of cover in twenty random quadrats at each of 163 different rocky shores, from Galiza (NW Spain) to South of Portugal (Sagres). Then, environmental and biological data (e.g. Temperature, Salinity) in the study area were obtained from satellite data, available online. DistLM analysis was used to ascertain the role of the studied environmental and biological drivers shaping the abundance of *M. galloprovincialis*. Results showed that twenty variables explained about 30% of mussel variability and the most significant factors were salinity, iron, maximum temperature, and primary production. Future studies should consider another factors to improve the knowledge about factors shaping *M. galloprovincialis* abundance.

Cymatiidae Salivary Glands Involved in Prey Capture

Ashlin H. Turner*¹, Christina I. Schroeder¹, David J. Craik¹, and Quentin Kaas¹

¹Institute for Molecular Bioscience, University of Queensland

Predatory marine gastropods are a source of novel bioactive compounds, yet only a few families, such as Conidae, have been studied in depth. Other less-studied families, such as Cymatiidae, are known to produce bioactive compounds in the salivary glands, despite lacking true venom glands. In this study we present the first transcriptomic and proteomic analysis of the salivary glands from members of family Cymatiidae. Species studied were *Monoplex parthenopeus*, *Monoplex pileare*, *Ranularia pyrum*, *Ranularia sinensis*, *Cabestana spengleri*, and *Turritriton labiosus*. This study further elucidates the role of Cymatiidae salivary glands in prey capture through description of the venom-like proteins produced by this family.

Size at Sexual Maturity of Commercially Important Bivalves of the Gulf of Nicoya, Pacific coast of Costa Rica

F. Villalobos-Rojas*¹, F. Vásquez-Fallas², R. Romero-Chaves¹, Y. E. Camacho-García^{1,2,3}, and I. S. Wehrtmann^{1,2,3}

¹Unidad de Investigación Pesquera y Acuicultura (UNIP), Centro de Investigación en Ciencias del Mar y Limnología (CIMAR), Universidad de Costa Rica, San José, Costa Rica;

²Escuela de Biología, Universidad de Costa Rica, San José, Costa Rica

³Museo de Zoología, Escuela de Biología, Universidad de Costa Rica, San José, Costa Rica

Bivalve extraction is an important activity in the Golfo de Nicoya, Pacific coast of Costa Rica. Basic information for the management of the extracted species such as the size at sexual maturity (L50) is practically absent. At present the legal size of capture (LSC) has only been established for *Anadara tuberculosa* ("piangua"). In this study, the L50 was estimated in four groups of commercially important bivalves of the Golfo de Nicoya: "almeja blanca" (*Leukoma asperima*, *L. ecuadoriana*, *L. grata*, *L. histrionica*), "chora" (*Mytella charruana*, *M. guyanensis*), "almejón" (*Psammotreta asthenodon*) and "almejillón" (*Tagelus affinis*). The estimated L50 for all species corresponded to a small size within the size frequency distribution of each species. So much so, that the number of specimens under the L50 also corresponded to a low percentage (1.8 - 37%) of the specimens commercialized by the shellfish extracting communities. It is hypothesized that the species studied could be maturing at smaller sizes as a compensation to factors such as fishing pressure or temperature changes due to climate change. Since fishing and aquaculture activities should be carried out in a responsible manner, it is strongly suggested to apply a precautionary size (L80) to establish the LSC of the analyzed species. Therefore, we recommend the following lengths to be used as the LSC for the analyzed species: 30.0 mm ("almeja blanca"), 25.0 mm (*M. charruana*), 32.0 mm (*M. guyanensis*), 36.0 mm (*P. Asthenodon*), and 39.0 mm (*T. affinis*). It is necessary to continue the monitoring of the L50 to assess possible changes in the size due to external factors.

Kleptoplasts of the Solar-Powered Sea Slug *Elysia crispata* Collected at Different Depths Display Similar Pigment and Fatty Acid Profiles

Xochitl G. Vital*^{1,2}, Felisa Rey^{3,4}, Paulo Cartaxana³, Sónia Cruz³, Rosário Domingues^{4,5}, Ricardo Calado³, and Nuno Simoes^{2,6,7}

¹ Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México

² UMDI-Sisal, Facultad de Ciencias, Universidad Nacional Autónoma de México

³ Departamento de Biología & CESAM – Centro de Estudos do Ambiente e do Mar & ECOMARE, Universidade de Aveiro

⁴ Centro de Espetrometria de Massa, Departamento de Química & QOPNA, Universidade de Aveiro

⁵ Departamento de Química & CESAM & ECOMARE, Universidade de Aveiro

⁶ International Chair for Coastal and Marine Studies, Harte Research Institute for Gulf of Mexico Studies, Texas A and M University

⁷ Laboratorio Nacional de Resiliencia Costera, Laboratorios Nacionales, CONACYT, México

Sacoglossan sea slugs are the only metazoans able to acquire chloroplasts from the algae they feed on and keep them functional, a process named kleptoplasty. The period of time these “stolen” chloroplasts (kleptoplasts) are maintained functional varies depending on the sea slug species. The fact that these animals can obtain photosynthates from the foreign organelles is the reason why this group of mollusks has been termed “solar-powered” sea slugs. *Elysia crispata*, the largest and most abundant species of Sacoglossa in the Caribbean, is one of the few species that can retain kleptoplasts for over a month. As photosynthesis is a phenomenon that is influenced by light, the goal of our research was to characterize the pigments and fatty acids (FA) of *E. crispata* sampled at two depths with different light conditions. Seven organisms were collected at each of two different depths, 0-4 m and 8-12 m, in the Veracruz Reef System in Veracruz, Mexico, and kept in the lab without a food source. After one month of starvation, sea slugs were freeze-dried for pigment and lipid extraction. Pigments were identified and quantified through high-performance liquid chromatography (HPLC) and FA by gas chromatography-mass spectrometry (GC-MS). We found 12 pigments and 27 FA; their concentrations and profiles were similar between depths. However, we observed a high variation between organisms within depths. As pigments reflect what sea slugs ingest, our results confirm the polyphagous regime of *E. crispata* reported in the literature and indicate that kleptoplasts were likely acquired from similar macroalgae, regardless of depth.

Unravelling circadian rhythms and depth as explanatory factors of a sacoglossan sea slug abundance and activity

Xochitl G. Vital*^{1,2} and Nuno Simoes^{2,3,4}

¹Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México

²Unidad Multidisciplinaria de Docencia e Investigación, Facultad de Ciencias, Universidad Nacional Autónoma de México, Sisal, Yucatán, México

³International Chair for Coastal and Marine Studies, Harte Research Institute for Gulf of Mexico Studies, Texas A and M University—Corpus Christi, Corpus Christi, Texas, USA.

⁴Laboratorio Nacional de Resiliencia Costera, Laboratorios Nacionales, CONACYT, México.

Light changes are one of the factors that define the circadian activity rhythms of different organisms. Some studies have analysed the mechanism that determines the circadian rhythms in molluscs, mostly in relation to their movement. However, there are few studies working with sea slugs in this subject. Sacoglossan gastropods can retain the chloroplasts of the algae they eat and get nutrients from their photosynthesis; they can be starved even for months, depending on the species. One of these species is *Elysia crispata*, the most common solar-powered sea slug in the Gulf of Mexico and the Caribbean. Some species of *Elysia* prefer particular light intensities because in that condition their chloroplasts have recorded high values of photosynthesis. However, an excess of light could affect this process and decrease the amount of photosynthesis completed. Therefore, the aim of this project is to determine the abundance and size of *E. crispata* in different light conditions at diverse localities in Southern Gulf of Mexico and Caribbean. Here, we present preliminary observations on the abundance and size of *E. crispata* recorded *in situ*, along with light intensity, using transects as a reference in four different times of the day (sunrise, noon, sunset and night) at two depths (0-4 m and 8-12 m). In its habitat, we observed a higher number of organisms during low light conditions in the day; yet, we did not notice a difference between the two depths.

Phylogeny and Pattern in Nature: wood-boring bivalves run amok

Janet R Voight*¹ and Raymond W. Lee²

¹Field Museum, Integrative Research Center

²Washington State University, School of Biological Sciences

Wood that has sunk to the seafloor can support diverse, and sometimes dramatically different communities after colonization by the quintessential wood fall taxon, wood boring bivalves of the Xylophagidae. Not only do they bore into the wood, they eat and digest it; thus they are credited with making the nutrients and energy locked in the wood available to other animals. Their actions have also been linked to reducing high sulfide levels on the surface of fresh wood. Although individual wood falls can last for years supporting diverse communities throughout, in some cases borers reduce the wood to rubble in a few short months. We document that wood destruction occurs when the colonists are members of a single clade, that of *X. dorsalis*. The clade is unified by short excurrent siphons, which deposit fecal pellets within the borehole; the accrued pellets form a “fecal chimney” which nearly fills the borehole. The chimney, compacted pellets with an inner mucus lining may be the site of sulfide oxidation, but no evidence suggests chemosynthetic microbes or precipitated electron acceptors are present. The mucus lining may, as has been shown in infaunal burrows, limit sulfide diffusion toward the bivalve. In doing so, the fecal chimney may allow their survival in lower oxygen tensions that limit other members of the wood fall fauna; it may also release larval attractants that increase recruitment. With increased recruitment, perhaps aided by fewer predators, destruction of the wood results.

An Integrated Approach to Unraveling the Fossil Record: Estimating the Paleontological Past, One Phylogeny at a Time

S. G. Wiedrick*¹, A. J. Hendy¹, and D. J. Eernisse²

¹Department of Invertebrate Paleontology, Natural History Museum of Los Angeles County, 900 Exposition Blvd., Los Angeles, CA 90007 USA

²Department of Biological Science, California State University, Fullerton, CA 92834 USA

The diverse muricid genus, *Paciocinebrina* Houart, Vermeij & Wiedrick, 2019, of the northeastern Pacific, is phenotypically plastic with a great deal of confusion associated with previously proposed taxa and historical records. Species of the genus are currently recorded from Alaska to Baja California, with most species known and described from California. The ecological role of these snails is most notable for their drilling capabilities by which they primarily prey on sessile barnacles and other marine mollusks, and partly for their richness in local intertidal zones along the northeastern coastline. A review of relevant literature, museum vouchers and the careful collection and analysis of molecular data has provided an insight to patterns of occurrence, distributions of taxa, ecological importance, and the overall clarification of taxonomic instability. Our approach utilizes the traditional use of morphological analysis, combined with, and based on, modern molecular techniques and analysis of both mitochondrial (COI & 16S) and nuclear (28S & ITS-2) loci. The mode of development of this group is thought to be direct, as indicated by the paucispiral protoconch, a trait known to support higher levels of diversification compared to planktonic dispersal and development. The extensive assemblage of Pliocene-Pleistocene fossils is remarkable and in need of major revision, with species dating back to the Oligocene of California. As a member of the Ocinebrinae, *Paciocinebrina* Houart et al. 2019 is one of a variety of clades thought to have originated from an ancestral group from the Paleogene of Europe. The absence of *Ocinebrina*-like species from the Western Atlantic suggests the migration of ancestral species was likely through the Tethys seaway during the late Paleogene, further supported by morphologically similar records from Japan. The Late Oligocene fauna of California is reported to include 5 to 6 species, with a modern record of about 20 distinct members. Additional undescribed species are expected to increase our knowledge about this expansive and diverse group. Modern molecular techniques are here leveraged to establish and estimate the relationships between members of this genus, a tool used to interpret paleontological relations and to reconstruct the biogeography and biodiversity of this large group of organisms.

Mollusca Types of Britain and Ireland: A Union Database

Harriet Wood^{*1}, Ben Rowson¹, Jon Ablett², Andreia Salvador², and Anna Holmes¹

¹Amgueddfa Cymru National Museum Wales, Dept. Natural Sciences

²Natural History Museum, Dept. Life Sciences

Mollusca Types in Great Britain: A Union Database Nomenclatural ‘types’ are the treasures of any natural history collection and are constantly sought out by researchers. Many UK curators are spread across several natural history disciplines and lack the skills or resources to attend to type research and curation and such specimens risk being 'lost' to the international scientific community. AC-NMW and NHMUK received a two year grant from the John Ellerman Foundation in 2016 to develop a jointly held, universally accessible resource connecting the Mollusca type specimens of national and regional museums for the first time. Staff at seven partner museums in six UK cities, each lacking a malacological curator, were trained to recognise, research and interpret the molluscan type specimens in their collections. The project resulted in the “Mollusca Types in Great Britain” website going live in March 2018 with over 700 type specimens fully researched, imaged and made digitally accessible (<https://gbmolluscatypes.ac.uk/>). A further 450 types were uploaded from the ACNMW collections. We have striven to maintain momentum by making additions, including a further 500 records of un-imaged type specimens from three of the partner museums that went well beyond our initial goal to cover primary types alone. The great success of this project has piqued the interest of new prospective partners. Our ambition is now to become bigger and better as the “Mollusca Types of Britain & Ireland” to encompass them. We are pushing forward with Phase II and have a funding proposal currently under consideration, which would allow us to expand this invaluable online resource further.

Comparative Seascape Genetics Revealed Contrasting Genetic Architecture and Habitat Preferences Between Co-Distributed Closely Related Marine Snails

Daishi Yamazaki*¹, Osamu Miura², Shota Uchida³, Minoru Ikeda⁴, and Satoshi Chiba¹

¹ Center for Northeast Asian Studies, Tohoku University

² Faculty of Agriculture and Marine Science, Kochi University

³ Graduate School of Life Science, Tohoku University

⁴ Graduate School of Agricultural Science, Tohoku University

Recent genetic studies have been focused on how relationships between physical and ecological factors influence on the marine biogeography. Comparative phylogeography is a powerful tool to evaluate the role of ecological traits for shaping genetic patterns of marine species. To uncover the links between ecological traits and genetic structures, a pair of closely related and co-distributed species with different habitat preferences is a good model. In the present study, ecological traits and genetic structures of sister intertidal snails genus *Monodonta* are compared. We investigated the habitat preference by measuring the degree of coastal exposure and substrate type and estimated the genetic population structure. The results showed while *M. labio* prefers a sheltered habitat, *M. confusa* can live in a habitat with a wide range of wave exposure. This indicates that *M. labio* is a habitat specialist but *M. confusa* is a generalist. We also found that these sister species showed different population genetic structures. *M. labio* had a lower level of genetic diversity and a higher level of genetic differentiation among populations. However, *M. confusa* exhibited a higher level of genetic diversity and no clear geographical genetic structure. Ecological specialization is an important process to promote genetic divergence among local populations even in a well-connected marine environment. We found distinct genetic structures between a habitat specialist and generalist, suggesting that differences in habitat preference play a key role in shaping the genetic architecture in marine species.

Draft Genome of *Neomenia Megatrapezata* (Solenogastres) as A Tool to Study Aculiferan Sclerite Biomineralization

Meghan K. Yap-Chiongco*¹, Rebecca M. Varney¹, and Kevin M. Kocot^{1,2}

¹ The University of Alabama, Department of Biological Sciences

² The University of Alabama, Alabama Museum of Natural History

Sclerites, calcareous scales and spicules, are a synapomorphy for the clade *Aculifera* (aplacophorans and chitons). This character distinguishes aculiferans from the shell-bearing conchiferans. While much is known about the genes and developmental processes behind shell formation in conchiferans, there have been no studies investigating the formation of aculiferan sclerites or whether or not sclerites are homologous to conchiferan shells. To address these questions, we are sequencing genomes from five species spanning the diversity of Aplacophora. These genomic resources will enable us to investigate the evolution of hypothesized 'biomineralization genes' and other transcription factors and conduct in situ hybridization to explore the function of these genes in the emerging model *aplacophoran Wirenia argentea*. Here, we present a draft genome assembly for *Neomenia megatrapezata* (Solenogastres). Our sequencing strategy combined one lane of Illumina HiSeq X paired-end data (90X coverage) and one flowcell of Oxford Nanopore GirdION long reads (7X coverage). MaSuRCA yielded an N50 of 31 kbp with 26,726 contigs. Through increased nanopore sequencing and optical mapping, we plan to improve this assembly to near chromosome-level. Subsequently, we will produce high-quality annotations and use established orthology- and machine learning-based approaches to identify genes likely involved in biomineralization. High quality aplacophoran genomes along with the identification of biomineralization genes will shed light on the formation of aculiferan sclerites, their homology to conchiferan shells, and the biomineralized state of the last common ancestor of Mollusca. This research will provide valuable resources that will be broadly useful within the molluscan research community.

Culturally differences cause divergent non-native and uniform native populations of *Sinotaia quadrata*

Bin Ye*¹

¹ Graduate School of Life Sciences, Tohoku University

We compared population genetic structures and estimate divergence time of the freshwater snail *Sinotaia quadrata* in source and introduced populations, with respect to their difference in biogeographic patterns driven by different influence of human activities and culture. Microsatellite data were used to estimate genetic diversity, population structures, isolation by distance and gene flow in different regions. Mitochondrial COI DNA sequence data were used to generate haplotype network and Bayesian phylogenetic tree for divergence time estimation to confirm the history of introduction. Genetic diversity and gene flow of *S. quadrata* were lower in the Japanese populations than in the continental populations. However, the genetic divergence among populations was atypically higher in Japan than on the Asian continent. Populations in Japan was introduced from the Asian continent during historical periods. We concluded that frequent human transportation of *S. quadrata* destroyed geographical variation in China, and less frequent human transportation caused genetic divergence among populations in Japan. Human activities driven by cultural differences play a dominant role in shaping the distinctive population structure between introduced and source populations.

Population ecology of the wedge clam *Donax scortum* in the Andaman Sea

Thamasak Yeemin*¹, Makamas Sutthacheep¹, Charernmee Chamchoy¹, Wiphawan Aunkhongthong¹, and Siriluck Rongprakhon¹

¹Marine Biodiversity Research Group, Faculty of Science, Ramkhamhaeng University, Huamark, Bangkok, Bangkok 10240

The wedge clam, *Donax scortum* (Linnaeus, 1758) is a marine bivalves with high economical value in the Andaman Sea, provides incomes for small-scale fishers, and promotes tourism in certain areas. A large number of *D. scortum* were collected by several hundred local people and tourists per day. However, in the past few years, the population of *D. scortum* has declined significantly. Therefore a conservation project of *D. scortum* is urgently needed for its recovery and sustainable uses. This study examined population ecology of *D. scortum* at three study sites along the Andaman coast of Thailand for baseline data to make a management plan in collaboration with government agencies, local administrative organizations, and local communities. The population densities of *D. scortum* collected from the intertidal zones were significantly different among the study sites. The highest population density of the clam was found at Hat Pakmeng, Trang Province (92 individuals.m⁻²). Management strategies include restocking, wedge clam aquaculture, size restriction, and establishment of reserve areas to increase the clam abundance along with enhancing the fishers' awareness. The achievement of *D. scortum* conservation project depends on awareness and participation of all stakeholders for managing *D. scortum* fisheries and coastal and marine resources and environment based on scientific knowledge for sustainable uses of fishery and tourism sectors.