

SYMPOSIUM ABSTRACTS



Summer Systematics Institute

&

Internship in Biological Illustration

**Thursday, August 10, 2017
Board Room**



**CALIFORNIA
ACADEMY OF
SCIENCES**



Summer Systematics Institute Symposium
9:30 AM Thursday, August 10, 2017

Board Room

Speaker order:

- Chasing diversity: Phylogenetic assessment of central Philippine sea pens
Sara Debić (Univ. of Zagreb, Croatia), Gary Williams (IZ&G)
- A genetic and morphological inquiry into species delineation of a stress-tolerant hermatypic coral, *Porites*
Anthony Bartoni (Los Medanos Coll., CA), Rebecca Albright (IZ&G)
- Dancing with dorids: Phylogenetic systematics of discodorid nudibranchs in the genus *Rostanga*
Janne Torres Jarin (San Diego State Univ., CA), Terry Gosliner (IZ&G)
- The hole truth: Evolutionary biology of novel features in keyhole sand dollars from the Pliocene of North America
Adamaris Muñiz Tirado (Albright Coll., PA), Rich Mooi (IZ&G)
- Communicating science: Creating a field guide of the Vizcaino Biosphere Reserve for community outreach
Ashley Sauer (San Jose State Univ., CA), Lauren Esposito (Ento)

LUNCH BREAK

We will begin again at 1:00 PM

- Chikungunya virus: A phylogenetic analysis of the 2014 Grenada outbreak
Sarah Ohashi (Carleton Coll., MN), Shannon Bennett (Micro)
- Hoot's who: A morphological comparison of eastern and western barred owl population
Esther Perisho (Indiana State Univ., IN), Jack Dumbacher (Ornith & Mamm)
- *De novo* genome assembly and annotation of the red-eared slider (Reptilia: Emydidae: *Trachemys*): Advancing our understanding of hybridization and introgression
David Manahan (Univ. of Southern Calif., CA), Brian Simison & Joe Russack (CCG)
- Unraveling fronds: An assessment of morphological characteristics of Australian fern assemblages
D'Angelo Mori (Vassar Coll., NY), Nathalie Nagalingum (Botany)

A genetic and morphological inquiry into species delineation of a stress-tolerant hermatypic coral, *Porites*

Anthony Bartoni

Rebecca Albright

Los Medanos College, CA

Department of Invertebrate Zoology and Geology, California Academy of Sciences

An estimated 50% of coral reefs have died in the last 30 years, largely due to mass coral bleaching associated with climate change. Given the recent acceleration in global coral reef decline, there is mounting interest in understanding stress-tolerant coral genera that may comprise the ‘reefs of tomorrow’. A combination of field observations and laboratory studies suggests that corals belonging to the genus *Porites* are capable of withstanding high levels of environmental pressures and often dominate marginal reef environments. As a first step towards understanding the biology and ecology of *Porites*, we need to better constrain species-level identification and geographic distribution. Historically, taxonomy in *Hexacorallia* has relied heavily upon morphological features, including whole-colony morphology and corallite morphometrics. Within the last decade, however, the introduction of novel molecular techniques has challenged species delineation in *Porites* and other coral genera. In this study, we used a combination of Scanning Electron Microscopy (SEM) and mtDNA ND1 gene sequencing to compare and contrast species delineation between morphological and genetic techniques. We analyzed a subset of *Porites* tissue samples collected from recent expeditions to the Philippines and Palau and found that identification based on genetics is distinctly different from identification based on morphology. These findings suggest that morphological plasticity in *Porites* complicates species delineation and that more studies are needed to understand fully the biological and ecological complexity of this genus.

***** We acknowledge generous support from the NSF REU program*****

Chasing diversity: Phylogenetic assessment of central Philippine sea pens

Sara Debić

Gary Williams

Faculty of Natural Science and Mathematics, University of Zagreb, Croatia
Department of Invertebrate Zoology and Geology, California Academy of Sciences

Octocorals are a diverse group of, for the most part, non-reef building corals accounting for almost 65% of global coral diversity. Sea pens are a highly specialized group of octocorals inhabiting both shallow and deep-water ecosystems. The evolutionary origin of sea pens and their interspecies relationships have historically been a point of contention among zoologists, with only recent molecular methods being able to elucidate systematic relationships. Here we present a molecular analysis of six sea pen genera alongside representatives from the Calcaxonia, Scleraxonia, Holaxonia, and soft coral groups using the NADH 2, NADH 6, and msh1 mitochondrial genes. All specimens were collected in the central Philippines, which is an area of extremely high marine biodiversity. We found the sea pens to be monophyletic with the calcaxonian family Ellisellidae, confirming previous studies. We also found the sea pen genera *Veretillum* and *Cavernulina* to be highly derived within the sea pen clade, refuting past hypotheses that veretillid sea pens are among the least derived. Instead, our analysis shows the genus *Virgularia*, with well differentiated polyp leaves, to be the most basal. Because the sea pen clade is monophyletic with the ellisellids, which inhabit shallow to mid-deep water, further studies are aimed at investigating whether the sea pens originated and diversified in the shallows and subsequently adapted to deep water ecosystems. A comprehensive sampling of both sea pens and calcaxonians from all depths is the next step in investigating the origin and radiation of sea pens, giving us valuable information about adaptations to different bathymetric environments in an age with rapidly rising sea levels.

***** We acknowledge generous support from the NSF REU program*****

Dancing with dorids: Phylogenetic systematics of discodorid nudibranchs in the genus *Rostanga*

Janne Torres Jarin

Terrence M. Gosliner

San Diego State University, CA

Department of Invertebrate Zoology and Geology, California Academy of Sciences

The discodorid nudibranchs are a family within Doridina, characterized by a gill plume surrounding the anus and a pair of finger-like oral tentacles. Members of the discodorid genus, *Rostanga* (Bergh 1879), can typically be identified by their red-orange to orange coloration, which they obtain from their diet of sponges. Sponge-eating species of *Rostanga* possess caryophyllidia and can be found in most of the world's oceans. Morphology and anatomy alone are often insufficient for determining evolutionary relationships within *Rostanga*. This project investigated the relationships of newly collected taxa in order to determine if there is undocumented diversity within *Rostanga* based on observed variation in coloration and the presence of caryophyllidia. In this study, we present a phylogenetic analysis of *Rostanga* using mitochondrial COI and 16S genes along with the nuclear H3 gene. Relationships were tested using known species of *Rostanga* and newly collected specimens using the outgroup *Discodoris cebuenis*. Additionally, we used scanning electron microscopy (SEM) to view characteristics of the radula such as shape, size, and number of teeth, and dissected specimens to determine orientation of their reproductive systems. Preliminary results indicate that some *Rostanga* possess morphological characters that are atypical of the genus and may not be considered a "true" *Rostanga*. There is some support for a grouping of true *Rostanga* that possess elongate outer teeth with divided tips. Increased taxon sampling, additional molecular studies, and a reevaluation of morphological characters used for description will allow for more accurate delimitation of evolutionary relationships within this group.

***** We acknowledge generous support from the NSF REU program*****

***De novo* genome assembly and annotation of the red-eared slider (Reptilia: Emydidae: *Trachemys*): Advancing our understanding of hybridization and introgression**

David Manahan

Brian Simison and Joe Russack

University of Southern California, CA

Center for Comparative Genomics, California Academy of Sciences

The advent of globalism has been tied to an increase in the spread of destructive invasive species across continents. Among the most prominent of these is *Trachemys scripta elegans*, more commonly known as the red-eared slider. *T. s. elegans* is native to slow-moving freshwater ecosystems between Alabama and Northeastern Mexico but their involvement in the pet trade (most notably, the export of 52 million specimens between 1989 and 1997) distributed these turtles all over North America and Eurasia—consequently outcompeting native species. A current study by Dr. Brian Simison and colleagues has uncovered a population of *T. s. elegans* in the Pecos River of Texas that exhibit introgression from *Trachemys gaigeae*. This evidence of hybridization opens up the possibility that *T. s. elegans* acquires adaptive genes from native *T. gaigeae* populations, which may help explain the expansion of *T. s. elegans* into an ecosystem unlike that of their native swamps. However, before more thorough population genomic approaches can be used to assess the validity of this hypothesis, a reference genome of *T. s. elegans* is required. In this study, I drafted several *de novo* genome assemblies for *T. s. elegans*. Despite relatively noncontiguous assemblies, a BUSCO analysis has still successfully identified the presence and location of over 300 *T. s. elegans* genes in these data. The quality of this draft could be further improved by acquisition of more paired-end sequencing data to increase genome coverage. This contribution to *Trachemys* population genomics helps provide fundamental insights into the relationship between genomes and their expression into selectable traits, which are important concepts in understanding the mechanisms behind speciation and hybridization.

***** We acknowledge generous support from the NSF REU program*****

Unraveling fronds: An assessment of morphological characteristics of Australian fern assemblages

D'Angelo Mori

Nathalie Nagalingum

Vassar College, NY

Department of Botany, California Academy of Sciences

Understanding how diversity and assemblage composition is affected by climate change is of critical importance to ecological research. To this end, the morphology and the frequency of morphological diversification in plants can be used as an indicator of changing environmental conditions. Ferns, which have a broad range of both habitat preferences and trait properties, are an ideal study group for tracking ecosystem composition. My project consisted of examining 386 fern species to interpret the structure of fern assemblages based on trait properties along a latitudinal gradient. I analyzed morphological patterns in lamina dissection and length of rhizome by creating a matrix with data collected by herbaria. Our results uncovered high morphological diversification spanning the eastern border of Australia, which could be associated with the changing climate of the southeastern region of the country. While the results of this study correlate with previous results for seed plants, there is a need for further data collection. Investigation of whole assemblages along extended environmental gradients will extend this method to more morphological traits of ferns and verify the results found in this study.

***** We acknowledge generous support from the NSF REU program*****

Chikungunya virus: A phylogenetic analysis of the 2014 Grenada outbreak

Sarah Ohashi

Shannon Bennett

Carleton College, MN

Department of Microbiology, California Academy of Sciences

Chikungunya virus (CHIKV), a mosquito-borne alphavirus that causes febrile illness and severe arthralgia, has been spreading rapidly throughout the Americas since its introduction to the region in 2013. With over 1.7 million suspected cases in the Caribbean, the need to understand and track the evolution of chikungunya is greater than ever. This project utilized Next Generation sequencing to assemble complete genomes of CHIKV sampled from symptomatic patients in Grenada in 2014. Phylogenetic analysis of the sequences suggested that the chikungunya samples from Grenada group together, but distinctly from other viral strains in the Caribbean, indicating that the virus was introduced to the island in a single event. Increased sampling of infected populations is necessary in order to predict and prevent the continued spread of chikungunya virus.

***** We acknowledge generous support from the NSF REU program*****

Hoot's who: A morphological comparison of eastern and western barred owl populations

Esther Perisho

Jack Dumbacher

Indiana State University, IN

Department of Ornithology and Mammalogy, California Academy of Sciences

Traditionally, an eastern United States species, the barred owl, *Strix varia*, has been dispersing westward for the past seventy years, and arrived in northern California 30 years ago. *S. varia* is a large, aggressive, forest generalist and performs well in its new environment. It outcompetes its close relative, the threatened northern spotted owl (*Strix occidentalis caurina*) wherever the two species have overlapping ranges. Recent museum collections of western specimens of *S. varia* suggest that there may be morphological differences between western and eastern populations. These differences may be correlated to the advent of *S. varia* in California; the species could be adapting to new habitats, or receiving new genes through hybridization with *S. occidentalis caurina*. We investigated potential differences in size, coloration, and feather pattern between the several populations of barred owls in eastern and western USA and Mexico. For each individual, we measured wing chord, length of primaries, beak length and beak depth, and scored for color. The feather pattern of the stomach, which is subject to the most variation, was scored as well. Analyses showed that while there is no significant disparity of size between the east and west, the two populations do differ in color and belly pattern. The means of assessing color and pattern variance was by eye, but still yielded promising results. Future protocols using standardized means of color and pattern analysis, possibly through utilization of spectrophotometry and/or digital imaging, will add rigor to these analyses.

***** We acknowledge generous support from the NSF REU program*****

Communicating science: Creating a field guide of the Vizcaino Biosphere Reserve for community outreach

Ashley Sauer

Lauren Esposito

San Jose State University, CA

Department of Entomology, California Academy of Sciences

Community outreach and science communication can have large and lasting impacts in regions where science education infrastructure is not well supported. Efforts to increase levels of science education are important for sustaining the health and longevity of biodiverse regions and can provide tools for the public to make informed decisions about the health and future of their unique natural environment. My project focused on the ongoing outreach in the Vizcaino Biosphere Reserve in Baja, California. "Islands and Seas", a non-profit organization co-founded by Dr. Lauren Esposito, works to create research facilities that serve as centers for science and environmental education. In the areas where this team conducts research, Islands and Seas brings outreach to local schools to help inform and advise future generations about preserving their regional diversity and resources. As a scientific illustrator, I have produced illustrations that visually communicate the biodiversity research and conservation efforts made by Dr. Esposito and her collaborators. The culmination of my work will result in an informational field guide of the Vizcaino Biosphere Reserve to represent the biodiversity of this region and communicate that knowledge to local communities. Islands and Seas will distribute this field guide during its annual community outreach. Our field guide will include informational text about each organism in Spanish to ensure accessibility to the local schools and communities. Illustrations of local reptile, insect, and arachnid species will be presented in a variety of media, including digital and acrylic. The objective of this field guide is not only to inform and educate, but to generate interest and participation in conservation for the communities of Baja, California.

***** We acknowledge generous support from the Wallace Endowment*****

The hole truth: Evolutionary biology of novel features in keyhole sand dollars from the Pliocene of North America

Adamaris Muñiz Tirado

Rich Mooi

Albright College, Reading, PA

Department of Invertebrate Zoology and Geology, California Academy of Sciences

Although there are about 250 living species of sand dollars (Clypeasteroidea: Echinoidea), there are also more than 700 fossil forms. The richness of this record makes possible detailed exploration of evolutionary change. The sand dollar family Mellitidae, common on beaches today throughout the subtropical and tropical Americas, is also well-represented in Pliocene fossil deposits along the southeastern seaboard of the U.S. The family is characterized by holes that develop in the body skeleton (test). These holes, or lunules, pass completely through the test from top to bottom, and arose as adaptations to hydrodynamic forces in wave-swept environments. All mellitids have a single lunule in each of the five rays (ambulacra), plus a single lunule in the posterior inter-ray (interambulacrum). In living members of the genus *Mellita*, the anteriormost ambulacral lunule is absent. Because mapping the occurrence of novel features in fossils can contribute to knowledge of speciation, we set out to: i) determine distribution and diversity of fossil *Mellita*; ii) determine when and where the anterior lunule was lost; iii) correlate systematics and evolutionary biology of *Mellita* with past environmental conditions to better understand how biodiversity varies with changes in factors contributing to modern biodiversity. With morphometrics, we aimed to determine if two Pliocene *Mellita*, *M. acclinensis* and *M. caroliniana* comprise one species, and to explore the possibility that a thick, round-lunuled, undescribed form constituted a new species. Morphology, phylogenetics, biogeography and stratigraphy of all mellitid genera (*Mellita*, *Leodia*, *Encope*), were examined in a synthesis of the evolution of the family.

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