

SYMPOSIUM ABSTRACTS



Summer Systematics Institute



Internship in Biological Illustration

**Thursday, August 6, 2015
Board Room**



CALIFORNIA
ACADEMY OF
SCIENCES

Summer Systematics Institute Symposium
9:30 AM Thursday, August 6, 2015
Boardroom

Speaker order:

- ◆ Mosquito vector biodiversity across habitats in Costa Rica, Thailand, and California
Victoria Pimentel (California State Univ., CA), Shannon Bennett (Micro)
- ◆ Getting a grip on size, shape, and evolution of ophicephalous pedicellariae in sea urchins
Meghan Yap-Chiongco (Diablo Valley Coll., CA), Rich Mooi (IZ&G)
- ◆ Sand dollars and the sands of time: Patterns of scutelline (Clypeasteroidea, Echinoidea) evolution in the Cenozoic North Pacific
Alexandra McCoy (Cabrillo Coll., CA), Rich Mooi (IZ&G)
- ◆ Phylogenetic analysis of gorgonian and pennatulacean corals from the Verde Island Passage, Philippines
Makaila Kowalsky (Univ. of Maine., ME), Gary Williams (IZ&G)
- ◆ Deep sea mysteries: A molecular phylogeny of newly discovered nudibranchs (genus *Halgerda*) from low light Philippine reefs
Shaina Villalobos (Univ. of Maryland College Park, MD), Gosliner (IZ&G)

LUNCH
BREAK

We will begin again at 1:00 PM

- ◆ A revision of male ants of the Malagasy region (Hymenoptera: Formicidae): A key to genera of the subfamily Formicinae
Veronica Sinotte (Univ. of Scranton, PA), Brian Fisher (Ent)
- ◆ Assembling the puzzle: Morphology and biogeography of short-range endemic Japanese and Californian harvestmen (Opiliones: Laniatores: Travunioidea)
Stephanie Castillo (San Diego State Univ., CA), Charles Griswold (Ent)
- ◆ Barcoding for braincases: Computed tomography-enabled landmark analysis of pipid frog crania
Isaac Krone (Univ. of Chicago, IL), Dave Blackburn (Herp)
- ◆ Morphological character analysis of infrageneric clades of the wintergreen group (Ericaceae) for the delimitation of the clade *Brossea*
Ian Mounts (San Francisco State Univ., CA), Peter Fritsch (Bot)
- ◆ Scientific illustration: Using the imagination to communicate accurate science
Tom Davis (California College of the Arts, CA), Tom Daniel (Bot)

Assembling the puzzle: Morphology and biogeography of short-range endemic Japanese and Californian harvestmen (Opiliones: Laniatores: Travunioidea)

Stephanie Castillo

Darrell Ubick

Charles Griswold

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Opiliones (harvestmen) are the third largest order of arachnids (spiders and kin) after the Acari (mites and ticks) and Araneae (spiders). Previous studies demonstrate that the diversification of many groups of Opiliones is closely associated with historical geographic processes. Harvestmen typically have low dispersal capability and high endemism, and are therefore excellent models for biogeographic research. Laniatores comprise the most diverse suborder of harvestmen, with over 4000 described species. Phylogenetic data support an early-diverging north temperate clade within Laniatores—Travunioidea, with short-range endemic taxa distributed on three continents: east Asia, North America, and southern Europe. However, the current classification is problematic at higher levels since it relies heavily on tarsal claw morphology which is argued to be homoplastic. Preliminary multilocus phylogenetic data indicate that travunioidea are monophyletic and that the Californian genus, *Zuma*, is nested within a Japanese clade. As part of the SDSU-CAS joint project devoted to species delimitation of Laniatores harvestmen, homology and variation among this clade were assessed by obtaining a standard set of images of both male and female genitalia, as well as somatic morphology, using a scanning electron microscope (SEM). Both Japanese and North American travunioidea have remained mostly unstudied since the 1970s and were never examined with SEM. Morphological analysis will be used to increase confidence of clade support, resulting in phylogeny-based reclassifications of deeper phylogenetic nodes. Travunioidea are habitat specialized and have very small geographic distributions. Therefore, they hold tremendous promise as biogeographic models that warrant conservation.

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

Scientific illustration: Using the imagination to communicate accurate science

Tom Davis

Tom Daniel

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Scientific illustration is primarily considered a tool for communicating information within the scientific community. But for the general public, the perception of what constitutes scientific illustration doesn't necessarily adhere to scientific accuracy. Scientific illustrators are dedicated to communicating visually accurate information. However, this doesn't preclude them from using their imagination; they often must use creative license and knowledge of the subject matter to recreate environments, emphasize or remove information, and make educated decisions with incomplete information. This summer, I developed botanical plates for plants in the family Acanthaceae. I used the traditional method of graphite pencil, pen, and ink to create stippled line art of *Avicennia germinans* and *Anisotes latablensis*. Adobe Photoshop was used to create final compositions that will be included as attached figures for species descriptions in scientific publications. For my third project, I created a digital collage that conveyed the diversity of leaf morphology in the family Acanthaceae; this piece of artwork needed to communicate an idea to scientists as well as the general public, and I therefore used different visual tools and modes of representation than I did for the botanical plates. The style of representation and level of detail used in all three projects depended on the intended audience and the assumptions around what pre-existing knowledge they were bringing to their interaction with the artwork. As an illustrator interested in communicating science as well as creating fictitious worlds and characters, I will continue to balance my dedication to accuracy with using my imagination in various ways depending on the intended audience.

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

Phylogenetic analysis of gorgonian and pennatulacean corals from the Verde Island Passage, Philippines

Makaila Kowalsky
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Octocorals are distributed around the world and are found in habitats from shallow coral reefs to the deep sea. Phylogenetic relationships of octocorals have previously been understudied and much of their systematics remains unknown. Using molecular techniques, we investigated the phylogenetic relationships of individuals representing seven genera in six families of octocorals collected during the 2015 CAS Philippine Biodiversity Expedition in the Verde Island Passage. The goal of this study was to determine if there is congruence between molecular and previously published morphological phylogenies for the gorgonian and pennatulacean groups. Examination of color, branching patterns, and sclerite morphology allowed identification of the specimens to genus. Mitochondrial protein coding genes [NADH-dehydrogenase subunits 2 (ND2) and 6 (ND6) and mutS homolog (msh1)] as well as the non-coding intergenic spacer region (COI-COII intergenic spacer) in the mitochondrial genome were sequenced to derive a phylogeny of the seven genera. The molecular results of this study suggest that *Viminella* and *Pteroeides* are sister taxa, which is in contrast to the current classification. Previous studies had mentioned similarities in the morphology of these two taxa. Molecular analysis of additional material from these families must be conducted in order to further test these newly discovered relationships.

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

Barcoding for braincases: Computed tomography-enabled landmark analysis of pipid frog crania

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Despite their unassuming appearance and small size, pipid frogs, including the well-known African Clawed Frog *Xenopus*, are a diverse and evolutionarily informative group of early-diverging Anura. Though their external morphology is not ostensibly varied, pipid braincases are morphologically diverse. Their small size means that they are often recovered with three-dimensional preservation as fossils. Because molecular evidence is almost never available from fossils, placement of these taxa would normally be based entirely on morphological analyses. Our goal was to use 3D imaging and statistical analysis to analyze morphology and affinities of pipids in a less labor-intensive, faster, and more statistically robust way. Using high-energy Computed Tomography (CT) scanning, we modeled and analyzed the braincase morphology of almost two dozen extant and two extinct pipid species: *Oumkoutia anae* and a recently discovered pipid from the Oligocene of Tanzania. A 20-landmark analysis of the braincases proved highly informative. We also achieved significant and revealing results regarding allometry across pipids and *Xenopus*, and regarding the disparity of shape in different areas of the braincase across *Xenopus*. Using Principal Component Analysis (PCA), we were able to investigate the clustering of species in morphospace across the entirety of sampled taxa and use these data to estimate phylogenetic placement of the two fossil species. While the affinities of *Oumkoutia* remain unclear, the fossil pipid from Tanzania can be interpreted with confidence to be a close relative of *X. itombwensis*.

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Sand dollars and the sands of time: Patterns of scutelline (Clypeasteroidea, Echinoidea) evolution in the Cenozoic North Pacific

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The “Anthropocene”, the period during which geologically significant conditions have been profoundly altered by human activities, is upon us. The fossil record provides data about the past that illustrate biotic change that can be correlated with changes in global temperature and geography similar to those occurring in the Anthropocene. Sand dollars have a superb fossil record throughout the Cenozoic of the northern Pacific. They are among the most likely invertebrates to record the influence of environmental change on fauna histories. This will shed light on how anthropogenic change affects marine communities. The tropics are likely to become larger, just as they have at times during the Cenozoic. A database of 160+ sand dollar species occurring in the North Pacific since the Eocene origin of the scutellines was developed through literature review, museum collections, and online resources. Stratigraphic information, general biogeographic data, and morphological characters were added to this database. We then compared the biodiversity levels in clades (species numbers) over geologic time with a variety of factors including temperature and current regimes, as well as fluctuations in ocean pH and geologic events such as the opening of the Bering Strait and the closure of the Central American seaway. Among many correlations, there was a species radiation in the Dendrasteridae as the Bering Strait opened 4.8 - 5.5 Ma. Dendrasterids are excentric, indicating an upright, suspension-feeding behavior found in only two other scutelline groups. We suggest that the ability to suspension-feed provided advantages for this group during Pleistocene cold periods characterized by strengthened upwelling.

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

Morphological character analysis of infrageneric clades of the wintergreen group (Ericaceae) for the delimitation of the clade *Brossaea*

Ian R. Mounts

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The wintergreen group, tribe Gaultherieae (family Ericaceae), contains ~260 species. The group is distributed throughout the Americas and East Asia, and maintains a south-temperate component in South America, Australia, and New Zealand. Recent molecular phylogenetic studies suggest that an earlier infrageneric classification based on morphological and chromosomal characters was inadequate above the series level. The recent classification scheme allows for two possibilities: a) the wider “wintergreen group,” (*Diplycosia*, *Tepuia*, and *Gaultheria*) can be grouped together under the single genus *Gaultheria*, or b) the genera *Chiogenes*, *Gymnobotrys*, and *Brossaea* could be split out from *Gaultheria*, with *Diplycosia* and *Tepuia* retained. To justify splitting *Gaultheria*, morphological character support is desirable for all six genera, and all appear to have at least some support except for the large clade *Brossaea*. To determine if any delimiting characters or combinations of characters exist for *Brossaea*, character variation was scored for the 92 species included in the most recent phylogenetic analysis of the Gaultherieae. The data were taken from species descriptions and supplemented with observations on herbarium specimen. The *Brossaea* clade was found to have several characters which showed support for the clade, but there was either large amounts of homoplasy in unambiguous characters, or ambiguous as to whether they support *Brossaea* or the wider wintergreen group. In-depth analysis of characters from herbarium sheets is pending in order to augment data taken from literature descriptions. Although results are preliminary, present data suggest that *Brossaea* is not morphologically distinct enough to justify elevating its status to genus level.

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

Mosquito vector biodiversity across habitats in Costa Rica, Thailand, and California

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Mosquitoes are nearly global carriers of multiple zoonotic diseases. Diseases transmitted by mosquitoes plague humans on a daily basis. The origins of infectious microbes is key in learning how to prevent emerging outbreaks. With 41 genera in the mosquito taxon Culicidae, it is important to develop a complete understanding of the correlation between mosquito diversity and mosquito-borne pathogens. We hypothesize that as biodiversity decreases in habitats affected by ecological disturbances, invasive disease vectors and pathogens might increase. Preliminary results from samples collected in Thailand and California suggest that habitat modifications reduce diversity in mosquito communities overall in favor of invasive mosquito vectors. Thus, there is an increase in the probability of infectious diseases emerging among humans in urban areas. Moreover, mosquito identification and deep sequencing analysis demonstrate evolutionary relationships between mosquito-restricted and vertebrate-infecting viruses. To explore these patterns further in the highly biodiverse setting of Costa Rica, which also experiences dengue, yellow fever, chikungunya, and other vector-borne diseases, mosquitoes were collected from a range of urbanized to forested habitats. Polymerase chain reaction (PCR) was used to sequence mitochondrial cytochrome c oxidase I (COI) gene from 22 samples caught in 9 different Costa Rican localities to construct a preliminary phylogeny. GenBank sequences from representative genera in Culicidae were aligned to the experimental samples, resulting in a tree depicting mosquito diversity at different localities. Deep sequencing of total RNA extracts will be used to characterize their microbial communities (including infectious pathogens), providing further evidence of the ecological effects of anthropogenic change on the evolution of microbial communities and disease emergence.

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

A revision of male ants of the Malagasy region (Hymenoptera: Formicidae): A key to genera of the subfamily Formicinae

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The morphology and reproductive physiology of male ants remain largely unstudied yet offer valuable insight into the phylogeny, diversity, and biology of the family Formicidae. We surveyed the morphological diversity of male ants in the subfamily Formicinae found within the Malagasy region. Generic characteristics of the eight extant genera of Madagascar (*Brachymyrmex*, *Camponotus*, *Lepisiota*, *Nylanderia*, *Paratrechina*, *Paraparatrechina*, *Plagiolepis*, and *Tapinolepis*) and the genus *Anoplolepis* of Seychelles were determined based on an examination of the mesosoma, mouthparts, and genitalia. The morphology of the mandibular teeth and maxillary palps of the mouth and the aedeagus, vosella, and paramere of the genital capsule predominately distinguish among genera. Diagnoses, illustrations, and a character matrix are provided. Further, we offer a general comparison between the tribes Plagiolepidini and Camponotini as well as a description of four subgenera (*Mayria*, *Tanaemyrmex*, *Myrmonesites*, and *Myrmotrema*) within the hyper-diverse genus *Camponotus*. This study contributes to an ongoing male-based comparative study of major ant lineages of the Malagasy region. A comprehensive understanding of male morphology will allow for pairing of males of unknown genera with their respective female worker caste. In turn, such additional characters, in conjunction with ongoing molecular studies, will contribute important features to delimit species and establish phylogenetic relationships.

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

Deep sea mysteries: A molecular phylogeny of newly discovered nudibranchs (genus *Halgerda*) from low light Philippine reefs

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During the 2014 and 2015 California Academy of Sciences expeditions to the Philippines, improved SCUBA technology allowed scientists to collect from deep reefs in what is known as the “Twilight Zone”. Formally called the mesophotic zone, this low light area from 60m-150m contains a wealth of poorly studied or completely undiscovered species. The purpose of this study was to investigate the molecular phylogeny of nine unknown nudibranch species from the genus *Halgerda* collected during this expedition, most of which were collected from the mesophotic zone. Mitochondrial fragments cytochrome c oxidase I (COI) and 16s as well as nuclear fragments H3 and 28s were sequenced from 34 samples of *Halgerda* species, including the nine unknown species and previously un-sequenced species such as *Halgerda formosa* (the type species), *Halgerda batangas*, and *Halgerda tessellata*. Outgroups were chosen from among several other discodorid species. The phylogeny was determined using maximum likelihood and Bayesian analyses. The results confirm that eight of the nine suspected new species are indeed distinct from described species. Molecular data were lacking from the ninth species owing to its fixation in a formalin-based fixative. The data also suggest that the undescribed species from the mesophotic zone form a clade nested within *Halgerda*. This also suggests a single invasion of the mesophotic zone by a shallow-water ancestor and subsequent radiation of this lineage within the mesophotic. This is different from what was found with mesophotic fish in the genus *Chromis*, in which four new mesophotic species each had a different shallow-water sister species.

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

Getting a grip on size, shape, and evolution of ophicephalous pedicellariae in sea urchins

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Pedicellariae are small, jawed structures attached to the test (calcite body wall skeleton) among the spines of many taxa in the Echinoidea (sea urchins and allies). A pedicellaria consists of a rod-like stem extending upwards from and articulating with a small tubercle upon the surface of the test. The stem terminates in a remarkable set of intricately articulating, calcite jaw pieces, or valves. There are at least 5 different types of pedicellariae, with varying functions that remain poorly understood. The order Clypeasteroidea (sand dollars and sea biscuits) shows high levels of diversity within one type of pedicellariae, the ophicephalous. Ophicephalous pedicellariae consist of 3 denticulate valves connected by hinges. Below the hinge line are calcite loops ("handles") that nest one below the other and connect to the stem through a "strap" made of connective tissue. It is believed that the strap/handle configuration is involved in increasing the gripping strength of the ophicephalous pedicellariae. Although ophicephalous pedicellariae can provide good phylogenetic characters to resolve major clades, little is known about their growth, evolution, and inter-specific variation. SEM and light microscope examination of these pedicellariae from 19 species of *Clypeaster*, several species of laganines, and related non-clypeasteroids such as the echinolampadoids, reveal important size and shape differences throughout pedicellarial evolution. Detailed analyses of three species of *Clypeaster* reveal allometric relationships among components of the pedicellariae themselves as well as the fact that pedicellariae exhibit strong negative allometry with respect to overall test size.

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