



Undergraduate Research Symposium 2010

Program and Abstracts

Saturday, August 14

Lecture Hall II



2010 REU Projects

Name: Allen, Jessica Lynn (Eastern Washington University)^

Field Museum faculty mentor: Dr. Thorsten Lumbsch (Botany)

Project: Understanding the Evolution of Secondary Chemistry in Lichens

Name: Baker, Mairead Rebecca (Northwestern University)^

Field Museum faculty mentor: Dr. Margaret Thayer (Zoology, Insects), David Clarke, graduate student (University of Illinois at Chicago)

Project: An Island Giant: Describing a New Species of Rove Beetle from the Chatham Islands

Name: FitzPatrick, Vincent Drury (Northwestern University)^

Field Museum faculty mentor: Dr. Larry Heaney (Zoology, Mammals)

Project: Evolution and Patterns of Reproduction in Philippine Mammals

Name: Kasicky, Anna Therese (Saint Mary's College of Maryland)*

Field Museum faculty mentor: Dr. Rüdiger Bieler and Dr. André Sartori (Zoology, Invertebrates)

Project: Shell Ultrastructure in Venus Clams

Name: Loria, Stephanie Frances (Sewanee: The University of the South)^

Field Museum faculty mentor: Drs. Petra Sierwald and Thomas Wesener (Zoology, Insects)

Project: Island Gigantism or Dwarfism? Phylogeny and Taxonomy of Madagascar's Chirping Giant Pill-Millipede

Name: Melstrom, Keegan Michael (University of Michigan)^

Field Museum faculty mentor: Dr. Ken Angielczyk (Geology)

Project: Morphological Integration of the Turtle Shell

Name: Rudick, Emily Lauren (Temple University)^

Field Museum faculty mentor: Drs. Rüdiger Bieler and Sid Staubach (Zoology, Invertebrates)

Project: Comparative Gill and Labial Palp Morphology

^The REU research internships are supported by NSF through an REU site grant to the Field Museum, DBI 08-49958: PIs: Petra Sierwald (Zoology) and Peter Makovicky (Geology).

* Funded through NSF grant 09-18982 to R. Bieler

#Funded through NSF DBI-1026783 to M. von Konrat, J. J. Engel, R. Lücking, & T. Lumbsch

Name: Slowikowski, Kamil (Loyola University, Chicago)^
Field Museum faculty mentor: Dr. Scott Lidgard (Geology)
Project: Phylum Bryozoa: Developing a Global Taxonomy on the Web

Name: Zufan, Sara E. (DePaul University)^
Field Museum faculty mentor: Dr. Corrie Moreau (Zoology, Insects)
Project: The Evolution of an Ant-Plant Mutualism

Affiliated Student projects

Name: Crandall, Jake (Augustana College), **Hellert, Spencer, M.** (Augustana College)
Field Museum faculty mentor: Dr. Peter Makovicky (Geology)
Project: Antarctic Mesozoic Vertebrates

Name: Durham, Elizabeth (Anthropology, Carleton College), **Hamdan, Sara** (Anthropology, University of Illinois-Chicago)
Field Museum mentor: Dr. John Terrell (Anthropology)
Project: Befriending Strangers, Creating Communities: Using Maori Meeting Practices to Facilitate Open, Direct, and Meaningful Dialogue in American Society

Name: Gardien, Claire (Loyola University), **Iqbaluddin, Zoya** (Northeastern Illinois University), **Kochakova, Emine** (Oakton Community College), **Osborn, John** (Northeastern Illinois University), **Phan, Selina** (Northeastern Illinois University), **Rojas, Miguel** (DePaul University), **Strozier, Lynika** (Dominican University) #
Field Museum faculty mentor: Dr. Matt von Konrat (Botany, REU BRC NSF and CIRRS programs)
Project: Bringing Schuster, Standley and Co. into the Third Millennium: The Field Museum's 180K Bryophyte and Lichen Conversion & Digitization Project

Name: Grohmann, Alexander (University of Illinois at Champaign-Urbana)
Field Museum faculty mentor: Dr. Lawrence Heaney (Zoology, Mammals)
Project: Geographic patterns of Evolution in a Philippine Bird, *Brachypteryx montana*

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Name: Hannah Koepl (University of Illinois at Chicago)

Field Museum faculty mentor: Dr. Bruce Patterson (Zoology, Mammals)

Project: Behavior and Ecology of Savannah Woodland Communities in Southeast Kenya

Name: Ariadne Lumayag (DePaul University)

Field Museum faculty mentor: Dr. Corrie Moreau (Zoology, Insects)

Project: Ant Associated Fungi: Another Tier of Symbiosis

Name: Lyons, Kathleen (Nazareth College, Rochester, NY)

Field Museum faculty mentor: Dr. Torsten Dikow (Zoology-Insects, Biodiversity Synthesis Center)

Project: Taxonomic revision of *Ectyphus* and *Parectyphus* (Insecta: Diptera)

Name: Montag, William (Bowdoin College)

Field Museum faculty mentor: Drs. Corrie Moreau and Stefanie Kautz (Zoology, Insects)

Project: Evaluating Methods to Estimate Bacterial Diversity in Ants

Name: Yao, Lu (Northwestern University)

Field Museum faculty mentor: Dr. Robert Martin (Anthropology) and Edna Davion

Project: Revelations About "The Hobbit" From Flores, Indonesia

2010 Phylogenetic workshop

Instructors: Drs. Joshua Drew and Karen Cranston, postdoctoral fellows, Biodiversity Synthesis Center, Field Museum of Natural History

^The REU research internships are supported by NSF through an REU site grant to the Field Museum, DBI 08-49958: PIs: Petra Sierwald (Zoology) and Peter Makovicky (Geology).

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PROGRAM

9:00 – 9:15 am Opening of the Symposium, Welcome, Petra Sierwald

Session 1

Moderator: David Clarke

University of Illinois at Chicago and Zoology, Insects, Field Museum

9:15 – 9:30am **An Island Giant: Describing a New Species of Rove Beetle from the Chatham Islands** (Coleoptera: Staphylinidae)
Mairead Rebecca Baker, Northwestern University

9:30 – 9:45am **Island Gigantism or Dwarfism? Phylogeny and Taxonomy of Madagascar's Chirping Giant Pill-Millipede** (Diplopoda: Sphaerotheriida)
Stephanie Frances Loria, Sewanee: The University of the South

9:45 – 10:00 am **Taxonomic revision of *Ectyphus* and *Parectyphus*** (Insecta: Diptera: Mydidae: Ectyphinae)
Kathleen Lyons, Nazareth College

10:00 – 10:15am **Geographic Patterns of Evolution in a Philippine Bird, *Brachypteryx montana*** (Aves: Passeriformes: Turdidae)
Alexander Grohmann, University of Illinois at Champaign-Urbana

10:15-10:45am **Speaker Group Photo**
Coffee Break



Session 2

Moderator: Erika Arnold

University of Illinois at Chicago and Zoology, Insects, Field Museum

- 10:45 – 11:00am **Befriending Strangers, Creating Communities: Using Maori Meeting Practices to Facilitate Open, Direct, and Meaningful Dialogue in American Society**
Elizabeth Durham, Carleton College & Sara Hamdan, University of Illinois at Chicago
- 11:00 – 11:15am **Evolution and Patterns of Reproduction in Philippine Mammals**
(Mammalia: Rodentia: Muridae)
Vincent Drury FitzPatrick, Northwestern University
- 11:15 – 11:30 am **Behavior and Ecology of Savannah Woodland Communities in Southeast Kenya** (Mammalia: Carnivora: Felidae)
Hannah Koeppl, University of Illinois at Chicago
- 11:30 – 11:45pm **Revelations about "The Hobbit" from Flores, Indonesia**
Lu Yao, Northwestern University
- 11:45- 12:00noon **Early Land Plants: The Forgotten Flora** (Plantae: Machantiophyta)
Zoya Iqbaluddin, John Patrick Osborne, Selina Phan (Northeastern Illinois University), *Claire Gardien* (Loyola University)
- 12:00 – 1:00pm **Lunch Break**



Session 3

Moderator: Dr. André Sartori

Zoology, Invertebrates, Field Museum

- 1:00 – 1:15pm **Species delimitation in melanelioid lichens** (Ascomycota: Lecanorales: Parmeliaceae)
Jessica Lynn Allen, Eastern Washington University
- 1:15 – 1:30pm **Ant Associated Fungi: Another Tier of Symbiosis**
Ariadne Lumayag, DePaul University
- 1:30 – 1:45pm **Comparing Methods to Assess Bacterial Diversity in Ants. What does cultivating tell us?**
William Montag, Bowdoin College
- 1:45 – 2:00pm **Evolutionary Histories of Bacterial Endosymbionts and their Ant Hosts**
Sara E. Zufan, DePaul University
- 2:00 – 2:15pm **Coffee Break**

Session 4

Moderator: Nathan Smith

University of Chicago and Geology, Field Museum

- 2:15 – 2:30pm **Bryozoan Biodiversity on the Web** (Lophotrochozoa: Bryozoa)
Kamil Slowikowski, Loyola University, Chicago
- 2:30 – 2:45pm **Morphological Integration of the Turtle Shell**
(Vertebrata: Reptilia: Testudines)
Keegan Michael Melstrom, University of Michigan
- 2:45 – 3:00pm **Shell Ultrastructure in Venus Clams** (Mollusca: Bivalvia: Veneridae)
Anna Kasicky, Saint Mary's College of Maryland
- 3:00 – 3:15pm **Comparative Gill and Labial Palp Morphology** (Mollusca: Bivalvia)
Emily Lauren Rudick, Temple University
- 3:15 **End of Symposium**

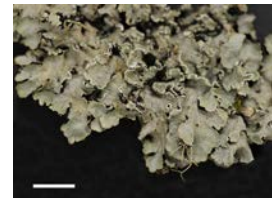
Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago, IL 60605

ABSTRACTS

Species delimitation in melanelioid lichens (Ascomycota: Lecanorales: Parmeliaceae)

Jessica Lynn Allen, Eastern Washington University, and Department of Botany, Field Museum of Natural History, Chicago, IL

Recent estimates of the number of fungal species worldwide range from 700K to 1.5 M. However, only about 100K fungal species have been described thus far, which is partially due to species circumscription not reflecting natural relationships. Molecular data have shown that traditional morphology-based species delimitation generally underestimates the number of actual taxa. This is partially due to traditional species circumscription working under the assumption that the “everything is everywhere” hypothesis applies to lichenized fungi, so biogeographical patterns were largely ignored. However, recent studies have shown that geographically isolated populations of lichens are in fact distinct lineages. In this study we focus on species circumscription in melanelioid lichens, a group within the large family Parmeliaceae, and specifically investigate whether populations on different continents are separate species. Fifty-four new nuclear ITS rDNA sequences were generated, and these sequences were combined with 55 others downloaded from GenBank to form our complete dataset. Maximum likelihood analysis revealed that members of some currently circumscribed species from different continents appear to form distinct lineages. These findings are promising and further studies using multiple loci, extended sampling and a variety of analyses will allow confident delimitation of the species in this group of lichens as well as aid in developing empirical methods to test species boundaries in other lichenized fungi.



An Island Giant: Describing a New Species of Rove Beetle from the Chatham Islands (Coleoptera: Staphylinidae)

Mairead Rebecca Baker, Northwestern University, and Department of Zoology, Insects, Field Museum of Natural History, Chicago, IL

The Chatham Islands, located approximately 800 km from the New Zealand mainland, host a myriad of thriving habitats populated with a rich insect biodiversity and numerous giant plant species. Currently there are roughly 300 beetle species residing on the islands, 65 of which belong to the diverse family Staphylinidae – the rove beetles. One genus, *Omaliomimus*, inhabits this archipelago in a quite specialized habitat: the beach. Currently, three *Omaliomimus* species are found on the Chathams: *O. robustus*, *O. actobius*, and *O. giganteus* sp. nov. This new species, as its name suggests, is a physical giant. Consistent with the giant plant species endemic to the Chathams, this new organism appears to be a result of the biological phenomenon island gigantism. Our measurements support this hypothesis as *O. giganteus* appears to be roughly 15% larger than the next largest Chatham Island *Omaliomimus* species and 30% larger than the largest New Zealand mainland *Omaliomimus*. Additionally, our extensive examination, including numerous dissections and clearings, has shown that this giant is not by any means an inflated morph of the neighboring *Omaliomimus* species, but a new species altogether. Due to certain morphological constraints, the giant cannot afford a generalist approach to habitat selection like its relatives and neighbors, *O. robustus* and *O. actobius*. It seems to be restricted to substantially more stable environments, where it is protected by boulders and cliffs. The species-specific characters of *Omaliomimus giganteus* include vestigial wings, and consequent lack of wing-associated structures such as the palisade fringe and abdominal wing folding patches. Among other characters, this flightlessness separates *O. giganteus* from the other Chathams *Omaliomimus* species. From the unusual size, unique habitat, and several distinctive characters, it is quite evident that this species is certainly new to science and evidence of island gigantism. Therefore, *Omaliomimus giganteus* will become the twelfth, and possibly the most remarkable, species of its genus.



Befriending Strangers, Creating Communities: Using Maori Meeting Practices to Generate Open, Direct, and Meaningful Dialogue in American Society

Elizabeth Durham, Carleton College & *Sara Hamdan*, University of Illinois at Chicago, and Department of Anthropology, Field Museum of Natural History, Chicago, IL

In an age where email, Skype, texting, and cell phones make it possible to talk to anyone, anywhere, anytime, it is still difficult to have meaningful, face-to-face conversations. Consequently, people often feel disconnected from each other and from the communities to which they supposedly belong (if they even consider themselves a part of any group at all). The Maori of New Zealand have developed an effective method for dealing with this social isolation: two groups of people come together on a *marae*, an open, neutral space in front of a communal meeting house, to discuss the issues affecting their lives and their identities as members of communities. The Pacific Anthropology program's *marae* encounter process is rooted in this traditional Maori system of communication, and has been adapted for use in American society. Each encounter features two groups of people, a host community and a guest community, and revolves around a mutually selected topic. Groups currently working with museum staff to organize their own *marae* encounters include the Quaker community of Chicago, South African peacemakers, and the African-American transgender community.



Evolution and Patterns of Reproduction in Philippine Mammals (Mammalia: Rodentia: Muridae)

Vince Drury FitzPatrick, Northwestern University, and Department of Zoology, Mammals, Field Museum of Natural History, Chicago, IL

In most groups of animals, body size and litter size are allometrically related: the smaller the animal, the larger its litter size. This is typically true of mammals and of rodents specifically, which usually have large litters. However, anecdotal evidence obtained during field work in the Philippines has suggested that several speciose endemic clades of Philippine murid rodents (rats and mice) differ significantly from this pattern. A departure of this large set of species could have interesting implications for theories of life history and evolutionary aspects of island biogeography. Using field notes, published materials, and reproductive autopsies of about 600 specimens, we seek to document the reproductive characteristics of the Philippine murid fauna. This includes the two

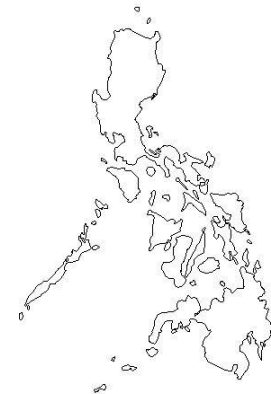


highly diverse “Old Endemic” clades (the cloud rats and the earthworm mice) which first arrived in the Philippines 12-20 million years ago, as well as several clades that arrived in the more recent geologic past, and some introduced by humans. Several species from Palawan, an area biogeographically distinct from the rest of the Philippines, were also included. Initial results suggest that the Old Endemics produce 1-2 offspring per litter, regardless of body size. This is much lower than “exotic pest” species of similar size, which are representative of continental species and have litters of 5-10 offspring. Some of the endemic clades which arrived in the Philippines more recently than the “Old Endemics” show intermediate litter sizes of 3-4 offspring. These data raise many currently unanswered questions about predation, longevity and reproductive strategies.

Geographic patterns of Evolution in a Philippine Bird, *Brachypteryx montana* (Aves: Passeriformes: Turdidae)

Alexander S. Grohmann, University of Illinois at Champaign-Urbana, and Department of Zoology, Mammals, Field Museum of Natural History, Chicago, IL

Throughout the last 30 million years the interaction between the Asian continental plate, the northward-moving Australian continental plate, the Philippine Sea Plate, and the Pacific Plate have given rise to the isolated archipelago known as the Philippines. The montane topography and isolation of the Philippines has set the stage for extensive evolutionary diversification. Recent mammalian studies conducted throughout the Philippine islands reveal high levels of endemism on the majority of the islands within the archipelago. Large percentages of endemism have been found on current landmasses that existed during the late Pleistocene era (ex. Greater Luzon and Greater Mindanao) and subcenters of endemism have been observed within these landmasses in areas of mountains and high elevations. With the phylogeography of the large endemic mammalian clades well studied, questions have been raised over how the phylogeography of avian species compares to that of the observed mammals. *Brachypteryx montana* is a montane species of ground thrush that is found throughout the Southeast Asian main land, the Indochinese Peninsula, and throughout Indonesia and the Philippine islands. *Brachypteryx montana* is a non-migratory species typically living near the forest floor within montane regions above 1500m. We examined specimens from three subspecies (*Brachypteryx montana andersoni*, *Brachypteryx montana sillimani*, and



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Brachypteryx montana polioygna) from various mountain ranges throughout the Philippines, in Luzon, Palawan and Mindanao. Phylogenetic analysis of 48 specimens was conducted using DNA sequencing of the mitochondrial genes ND3, ATPase6, CytB and CO1. These genes were selected due to their high likelihood to express evolutionary divergence occurring within the recent genealogical history of the populations. In contrast to montane mammals that exhibit high levels of diversification, preliminary phylogenetic analysis has shown very little diversification of the bird populations within Luzon. However, bird specimens collected from Palawan and Mindanao displayed distinct divergence from the Luzon populations. Our results suggest that the geographic population structure of *Brachypteryx montana* is not fully congruent with the phylogeographic patterns observed in studied mammals. The significant divergence, however, of the Palawan and Mindanao populations indicate a complex phylogeographic pattern that needs to be further studied.

Early Land Plants: The Forgotten Flora (Plantae: Machantiophyta)

Zoya Iqbaluddin^{1*}, John Patrick Osborne^{1*}, Selina Phan^{1*} & Claire Gardien²

¹ Northeastern Illinois University, ² Loyola University, and Department of Botany, Field Museum of Natural History, Chicago, IL, * Speakers

Liverworts belong to a group of green land plants technically known as bryophytes, the latter include hornworts and the more familiar mosses. Together, bryophytes are the second largest group of land plants after flowering plants. A growing body of evidence is now supporting liverworts as the earliest diverging lineage of embryophytes, i.e., as sister to all other groups of land plants. Hence, liverworts are regarded as pivotal in our understanding of early land plant evolution. Liverworts also are of great ecological and biological significance. The Field Museum has one of the largest and scientifically most significant collections of this group of plants in the world. A major NSF-funded project is outlined, involving the physical improvement of these collections, as well as databasing and digitization initiatives. Two case studies are briefly presented illustrating the utility of the collections, including molecular systematics and the *Encyclopedia of Life*. We conclude that collections are indispensable to areas of scientific research such as systematics and evolution, ecology, and biogeography.



Bivalve Evolution in Time and Space (BiTS): Shell Ultrastructure in Venus Clams (Mollusca: Bivalvia: Veneridae)

Anna Kasicky, Department of Biology, Saint Mary's College of Maryland, St. Mary's City, MD, and Department of Zoology, Invertebrates, Field Museum of Natural History, Chicago, IL

The family Veneridae, commonly known as venus clams, is among the largest families of bivalves, consisting of over 800 species. Among these, some are key components of the world's fisheries, such as quahogs, butterclams, and Pismo clams. These bivalves live submerged in sand surrounded by shallow water. Venerids are not only diverse, but they have an excellent fossil record, which makes venus clams an ideal model group for the Bivalves in Time and Space (BiTS) project. BiTS is a multidisciplinary effort which aims to test molecular clock dating and to increase our understanding of spatial and temporal patterns in macroevolution. In conjunction with this project, I investigated the morphological characteristics of shell microstructure in 35 extant species of venerids. Specimens from the Field Museum's collection were photographed in standard views to verify the identification of the species. I studied shell microstructure by fracturing and immersing the shells in polyester resin and then sectioning the shells radially and comarginally using a diamond rock saw. Once these sections were polished and immersed in weak acid, I made slides from acetate peels of each of the samples. The slides were then observed under a compound light microscope. Samples with indistinct crystal structures were repolished and etched and then coated in gold to be examined further under scanning electron microscopy (SEM). For each of these species, I was able to determine microscopic crystal structures in the calcium carbonate lattice of the shells. By comparing the shell microstructure between the species, I discovered changes in crystal patterns that occur in cross-lamellar banding as well as in composite prismatic crystal structures. Once microstructure character states for the 35 species of venus clams were determined, I created a character matrix in Morphobank, which also serves as a repository for all photographs and SEM images produced during this project.



Using this data set and the computer program Mesquite, I was able to map the shell ultrastructural characters onto a published molecular tree of the group to reconstruct the evolution of observed morphological patterns. All generated data will also be incorporated into the morphological data set of the BiTS project for further analyses.

Behavior and Ecology of Woodland Communities in Southeast Kenya

(Mammalia: Carnivora: Felidae)

Hannah Koeppl, University of Illinois at Chicago, and Department of Zoology, Mammals, Field Museum of Natural History, Chicago, IL

The word Tsavo means “place of slaughter,” named for bloody battles between the East African tribes there. The name took on new meaning when lions began systematically killing railway workers, stopping the British Empire in its tracks 110 years ago. To this day, lions continue to attack people and livestock there. Curiously, most lions in Tsavo lack a mane. To understand why these lions are maneless and attack people and livestock, Dr. Bruce Patterson has conducted research in southeastern Kenya in Tsavo East National Park observing not only the lions, their behavior, the environment, seasonality, but also the community of other animals. Over the course of eight years, he and his colleagues have led 68 expeditions, driven 94,000 kilometers, and made 86,500 animal sightings. A total of 542 volunteers from all over the globe have collected these data. Summarizing this mountain of data on the biodiversity in Tsavo was the objective of my internship.

Because the data were collected over a long period and by many different people, my first task was to check the data for errors, inconsistencies and formatting. Programs such as *Microsoft Excel* and *Statistica* were utilized to create histograms, scatter-plots, and perform statistical tests to consolidate, summarize and examine the data. The data include time and location of sightings of over 100 species, from small mammals such as dik-diks to large reptiles like the Nile crocodile. Here I offer some distillations of patterns evident in the data: especially concerning daily cycles of activity and annual changes in abundance. This research will provide a clearer picture of the lions prey base and competitors, and provide the Kenya Wildlife Service with much-needed information on the biodiversity of the ranchlands surrounding its largest national park system.



Island Gigantism or Dwarfism? Phylogeny and Taxonomy of Madagascar's Chirping Giant Pill-Millipede (Arthropoda: Diplopoda: Sphaerotheriida)

Stephanie Frances Loria, Sewanee: The University of the South, and Department of Zoology, Insects, Field Museum of Natural History, Chicago, IL

The occurrence of island gigantism and dwarfism has not been extensively studied in invertebrates. On the island of Madagascar, both of these trends have been observed in the giant pill-millipede family Arthrosphaeridae (Sphaerotheriida). In particular, the genus *Zoosphaerium* contains some gigantic species, while the genus *Microsphaerotherium* consists entirely of dwarfed forms. Within the endemic genus *Sphaeromimus*, only three species have been described and none are known to display gigantism or dwarfism. However, recent collections have discovered nine new populations of *Sphaeromimus*, whose taxonomic status was unclear. These findings include specimens from localities further north than previously known, from a cave, and from isolated, azonal rainforests, as well as the first gigantic *Sphaeromimus* specimens. To determine if gigantism in Arthrosphaeridae represents a plesiomorphy, or if it evolved independently in the different Malagasy genera, we constructed a molecular phylogeny. DNA of all *Sphaeromimus* populations, including all undescribed forms,



was extracted and fragments of the CO1, 28S and 16s, as well as the entire 18S gene (>4000 bp in total) were sequenced. Our results indicate high microendemism within the genus, particularly in southeastern populations, with populations only 1 km apart belonging to distantly related species. Other southeastern *Sphaeromimus* species consist of a single population located in an extremely small area of distribution. Such sharp species boundaries are probably due to abrupt changes in habitat, including changes in soil type which suggests that speciation within the genus has occurred as a result of environmental change. Our phylogeny also reveals that our basal most species has the widest distribution and is found in the southwestern dry spiny forests, the only *Sphaeromimus* species adapted to such a habitat. Scanning electron microscope images taken of the antennae and endotergum of the various *Sphaeromimus* populations agree with our molecular data providing further support for our phylogeny. Finally, our results indicate that gigantism is an apomorphic character inside the genus *Sphaeromimus* and therefore has evolved multiple times on Madagascar.

Ant associated Fungi: Another Tier of Symbiosis

Ariadne Lumayag, DePaul University, Chicago, Illinois, and Department of Zoology, Insects, Field Museum of Natural History, Chicago, IL

Although a vast amount of research has been done on ants, the possible mutualisms between ants and fungi are a subject still being developed. One prime example of an ant-fungus mutualism is the alliance between leaf-cutter ants and the fungus gardens they cultivate. In comparison to this external ant-fungus mutualism, little research has been done on internal ant-fungus mutualisms. This project focuses on the existence of symbioses between endosymbiotic fungi and their ant hosts. We dissected specimens from six different ant species and cultivated samples from internal parts of the ants (i.e. hindgut, intrabuccal pocket, and brain) in a series of Petri dishes in order to isolate fungi samples. The fungi were identified by sequencing the ITS region of their DNA. Sixty-three fungi samples from seventeen fungi genera were identified. The identified fungi included *Fusarium*, *Cladosporium*, *Cordyceps* and *Pestalotiopsis*. Most of the identified fungi, except *Cordyceps* (an endoparasitoid), are known to be plant or plant-animal pathogens. However, the functions these fungi are commonly known to have may not be the same as the functions they may have in the internal organs or systems of the ants - this is still unknown. Our results show that cultivation is a useful way of determining endosymbiotic fungi in ants. Based on this finding, future research will focus on identification of fungi according to specific internal organs in ants, as well as species-specific differences of ant-fungi symbiosis.



Taxonomic revision of *Ectyphus* and *Parectyphus* (Insecta: Diptera: Mydidae: Ectyphinae)

Kathleen Lyons, Department of Biology, Nazareth College, Rochester, NY, and Department of Zoology, Insects, Field Museum of Natural History, Chicago, IL

Mydidae is a family of large flies with less than 500 species. Mydas-flies probably feed from flowers, although little else is known about them. They tend to inhabit harsh and arid environments where collection is difficult, and may only emerge for a few weeks out of the year. The two genera I studied are represented by very few specimens. *Ectyphus* and *Parectyphus* are two genera of mydas-flies known in southern Africa. Only a few species of *Ectyphus* have been classified from the coastal regions of South Africa. *Parectyphus* is even less studied; a single specimen was identified from Namibia, and a few similar specimens have since been collected. My research focused on studying individual specimens to confirm species published by Hesse in 1969 and determining if new species were present. Interestingly, a few specimens of *Ectyphus* were collected in Kenya, far from the known distribution of this genus. My goal was to determine whether the Kenyan *Ectyphus* represent a new species, and to classify the few *Parectyphus* specimens as either *P. namibiensis* or a new species

I photographed, dissected, and drew specimens to observe differences in morphology between the type specimens of each species and the new unidentified flies. I entered morphological data into a character matrix using the program Lucid, and created a dichotomous key from this information and a matrix-based online key incorporating the specimen photos. I also georeferenced the collection localities of all the specimens to create distribution maps of *Ectyphus* and *Parectyphus* across the Afrotropical region. The Kenyan *Ectyphus* specimens were determined to represent a new species, while a number of *Ectyphus* species from South Africa were placed into other species based on a lack of significant morphological variation. Although striking differences in coloration were observed in the *Parectyphus* specimens, their overall similarities make them all members of *P. namibiensis*. The information I obtained about both recognized and new species of *Ectyphus* and *Parectyphus* are incorporated into species pages on the Encyclopedia of Life website. Descriptions of the new species will also be included in a scientific publication, along with a key to all 10 species of the subfamily Ectyphinae.



Morphological Integration of the Turtle Shell

(Vertebrata: Reptilia: Testudines)

Keegan Michael Melstrom, University of Michigan, and Department of Geology, Field Museum of Natural History, Chicago, IL

The turtle shell is one of the most distinct evolutionary novelties among tetrapods. Though the shell is a recognizable feature of all turtles, there is significant variation in the function and morphology of the shells of various species. One of these differences is the presence of a hinge on the plastron or ventral shell. Using landmark-based geometric morphometrics our research sought to explore the link between plastral hinging and the organization of modules within the shell. We digitized over 1,800 turtles, from the families of Emydidae, Geoemydidae, and Kinosternidae, from photographs. A principal components analysis was then run which demonstrated that a major component of variation in plastron shape was correlated with presence or absence of a hinge. This is an expected result because the evolution of a hinge typically accompanies the replacement of the bony bridge between the carapace and plastron by a ligamentous connection. Using canonical variates analysis confirmed this result by showing that plastra of kinetic and akinetic turtles could be classified with a high degree of accuracy. We then used the method of Klingenberg (2009) as implemented in the program MorphoJ to test *a priori* hypotheses for the presence of different modules. The number of modules varied from two to four, and we tested their locations throughout the plastron. The majority of turtles possessing a kinetic hinge had two distinct modules, one in the anterior portion of the shell, the second in the posterior. This line of separation is the location of the hinge. Given that most turtles with a kinetic hinge have this particular modular placement, despite belonging to several distantly related clades, one may conclude that plastron shape is independent of phylogeny. This analysis and others demonstrate that plastral kinesis has a strong effect on plastron shape, and this effect seems to extend to patterns of modularity, but to a lesser degree. This may indicate that functional selection, in the case for plastron shape, is less strongly affected than the modules in the plastron.



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Comparing Methods to Assess Bacterial Diversity in Ants. What does cultivating tell us?

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Background. -- Symbiotic bacteria play a vital role in maintaining the diversity and distribution of ants. Many species of ants may be dependent on bacteria to provide nutrients that they cannot extract from their environment or to produce chemicals that protect the ants against parasites. Other ants suffer from the presence of bacterial parasites that steal resources or change the behavior of their hosts. We estimated bacteria diversity in *Cephalotes varians*, *Pseudomyrmex ferrugineous*, and *Pseudomyrmex seminole* using two different methods, cultivation and environmental PCR and cloning. Our aim was to determine which method most accurately represents the bacterial community within the ants.

Results. -- The two methods for assessing bacterial diversity produced very different results. Cultivation showed a large proportion of Enterobacteria, Pseudomonadales, and Actinomonadales bacteria, with a few representatives of the orders Bacillales, Sphingomonadales, and Rhodospirillales. The environmental PCR and cloning method showed the presence of many species including representatives of several other orders, including the Xanthomonadales and the Rhizobiales.

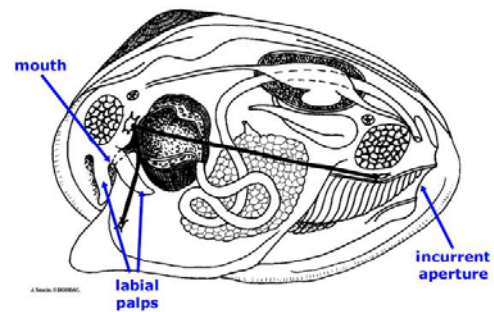
Conclusion. -- The cultivation method failed to match the estimate of bacterial diversity provided by the environmental PCR and cloning method. There are at least two explanations for these differences. Most importantly, less than 1% of all bacteria species can be cultured on a media plate due to special nutrient requirements and environmental adaptations. In addition, captive ants may lose some of their bacterial diversity if members of the symbiotic bacterial community must be reacquired at certain intervals. Our results provide evidence that cultivation, though useful, does not accurately represent the diversity of the symbiotic bacterial community in ants. Cultivation alone shows an amazing diversity of ant-associated bacteria, but multiple methods are needed to estimate total diversity.



Comparative Gill and Labial Palp Morphology (Mollusca: Bivalvia)

Rudick, Emily Lauren, Temple University, and Department of Zoology, Invertebrates, Field Museum of Natural History, Chicago, IL

Bivalves, with 20,000-30,000 living species, are the second largest class of mollusks next to gastropods. They are aquatic, bilaterally symmetrical and characterized by a laterally compressed body enclosed in a bivalved shell. In addition, they play important ecological roles in marine and freshwater ecosystems during the process of filter feeding, and economic roles in fisheries and health sciences. Funded by the National Science Foundation, the BivATOL (Assembling the Bivalve Tree of Life) Project aims to reconstruct the evolutionary history of bivalves using molecular and morphological approaches. In our study, we used scanning electron microscopy to investigate the anatomical structures of gills and labial palps. Besides the shell and stomach, gills and palps are one of the most important character complexes for phylogenies based on morphological characters. They are also a highly functional character system in regard to feeding, respiration, sensory function and breeding. The Bivalvia are divided in two major clades, the Protobranchia, which retain a number of plesiomorphic characters, and the Autolamellibranchiata. Here, we will compare the morphological characteristics of gills and labial palps in seventeen different species and eight different orders of bivalves (two protobranch and six autolamellibranch orders) to determine character polarity. We will test if the assumed monophyly of each major clade and order is supported by the gill and labial palp morphology. Additionally, our phylogeny consisting of 41 morphological characters will be compared with bivalve phylogenies derived from other independent character suites in order to postulate preliminary hypotheses about the evolution of specific characters.



Bryozoan Biodiversity on the Web (Lophotrochozoa: Bryozoa)

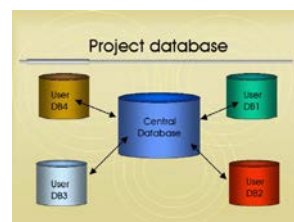
Slowikowski, Kamil, Loyola University Chicago (Bioinformatics), and Department of Geology, Field Museum of Natural History, Chicago, IL

The goal of this project is to put taxonomic, bibliographic, photographic, geographic data on the web. It should be easy for experts to contribute to or edit the data. It should also be easy to download the data or perform queries to reveal new information.

There already exist a number of personal websites with overlapping data in custom formats. They offer advantages like freedom to post anything in any format. However, there are disadvantages. For example, the existence and maintenance of the sites depends on each individual author. Also, it's not possible to perform a revealing query on the data from all such sites. So, the community would benefit from an effort to aggregate all available data into a central database.

There are a many databases that handle aggregation of taxonomic information. For the Bryozoan research community, we prefer a database that not only allows, but promotes activity by community members. After evaluating several options like MediaWiki or Encyclopedia of Life (EOL), we decided to use Scratchpads. It is the most immediately available solution that has the right balance of freedom, ownership, and customization.

During the past three months, I wrote scripts in Perl and PHP to handle names, synonyms, and authors for 2,653 taxa of rank genus and higher and 20,044 species and subspecies. There are several sources of data, so I checked, compared, and combined them into a format suitable for import into Scratchpads. This is the first step in the move to a central database for the Bryozoan research community. There are problems with the import, but once it is complete, it will serve as a foundation for the community to contribute their content.



Revelations about "The Hobbit" from Flores, Indonesia

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In 2004, a new species of *Homo* was reported from the Late Pleistocene of the island of Flores, Indonesia. This adult hominid, named *Homo floresiensis*, is different from the other two species known from that region, *Homo erectus* and *Homo sapiens*, in that it has very short stature and the smallest endocranial volume ever found in the genus *Homo*. The initial hypothesis that was proposed to explain this was island dwarfism, an empirical generalization which states that large mammals become dwarfed in body size on islands in order to reduce their resource needs. Since the Flores hominid was discovered, scientists have scrambled to search for examples of reduction in brain size. However, the assumptions and analyses in these studies are questionable, and the island rule had not previously been applied to brain size. In order to determine whether island dwarfism applies to brain size as well as to body size, I collected volumetric and linear measurements on skulls of pigs, deer, and gibbons indigenous to the Southeast Asian region. Allometric analysis of my data demonstrates that mammals do not display dwarfing in brain size. In fact, island dwarfing is not even observed in the body size of pigs and gibbons of the area. Thus, this preliminary study shows that island dwarfism cannot be invoked to explain the tiny brain size of *H. floresiensis* on the island of Flores, Indonesia.

Evolutionary Histories of Bacterial Endosymbionts and their Ant Hosts

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Many *Pseudomyrmex* ants are obligate mutualists with acacia trees, providing protection for their acacia hosts in return for shelter and food. However, the diet provided by the acacias is nutrient poor and unlikely to be sufficient for ant colonies to thrive. Recent research has found that endosymbiotic bacteria, living in the guts of ants, may supplement these nutrient poor diets. It is hypothesized that some of the bacteria found are capable of metabolizing nitrogen and synthesizing amino acids which would enable the ants to survive on plant-based diets. These studies suggest that bacterial gut symbionts may play an important role in the evolution of herbivorous ants. To describe the possible co-evolution of the symbioses between bacteria and their ant hosts, we reconstructed evolutionary histories of selected herbivorous ants and their associated bacteria. Ant species included in this study were Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago, IL 60605

primarily from the genera *Pseudomyrmex*, although *Cephalotes*, *Crematogaster*, and *Tetraponera* were also analyzed as outgroups. The barcoding region COI and the 16S rDNA gene were used to build phylogenies for the ants and bacteria, respectively. We did not find strict co-evolution between the ants and their associated bacteria, in part because our procedure for determining bacterial sequences was not as specific as we hoped. We plan to more accurately examine these relationships by developing more specific bacterial markers and reexamining the evolution of single bacterial lineages and their ant hosts.





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