



Undergraduate Research Symposium 2012

Program and Abstracts

Saturday, August 11

Lecture Hall I



PROGRAM

Welcome and Opening of the Symposium

Kenneth Angielczyk

9:00 to 9:15

Session 1

Moderator: Kenneth Angielczyk

Assistant Curator, Department of Geology

9:15 to 10:15

9:15–9:30: Evolution of the Labial Palps and Gills within the Palaeoheterodonta (Mollusca: Bivalvia)

Iqra Mushtaq, Loyola University of Chicago

9:30–9:45: Taxonomic Revision of the Namibian Fly Genus *Namadytes*

Stephanie Leon, University of California, Riverside

9:45–10:00: Wingless In Tasmania: A New Genus of Flightless Rove Beetle from Tasmania (Coleoptera: Staphylinidae: Omaliinae)

Anthony Deczynski, University of Delaware

10:00–10:15: Origin and Rise of a Giant: Phylogeography of the Neotropical Bullet Ant *Paraponera clavata*

Arista Tischner, University of Illinois at Chicago

Speaker Group Photo, Illustration and Poster Presentation

Coffee Break

10:15 to 10:45

Session 2

Moderator: Matthew Nelsen

Graduate Student, Department of Botany and University of Chicago

10:45 to 12:00

10:45–11:00: Phylogenetics of the Chewing Louse Genus *Ricinus*: Implications for the Host Specificity of a Widespread Parasite of Passerine Birds

Nathan Trautenberg, Northwestern University

11:00–11:15: Amazonian Speciation in a Ring: Phylogeographic History of the Channel-billed and White-throated Toucans

Jennie Lee, University of Chicago

11:15–11:30: Genetic Structure of *Phyllastrephus fischeri* in the Albertine Rift

Daniel Montgomery, Indiana State University

11:30–11:45: Genetic & Morphologic Structure in Midwestern Barred Owls

Mark Swanson, Illinois Wesleyan University

11:45–12:00: Skeletal Morphometrics and Phylogenetic Predictors of Body Mass in the Diverse “Waterbird” Assemblage (Aves)

Liam Heins, University of Chicago

Lunch Break

12:00 to 1:00



Session 3

Moderator: Benjamin Rubin

Graduate Student, Department of Zoology-Insects and University of Chicago

1:00 to 2:00

1:00–1:15: Morphological Characterization of Cryptic Bat Species: East African *Miniopterus* (Chiroptera: Miniopteridae)

Alexandra Weber, Loyola University of Chicago

1:15–1:30: Species Delimitation and Evolution in the Foliose Lichen Genus *Montanelia*

Bradley Loomis, Green Mountain College

1:30–1:45: Species Explosion: Using DNA Sequence Data to Detect Hidden Species in the Predominantly Australian Lichen *Cladia aggregata*

Aparna Nuttaki, University of Chicago

1:45–2:00: Elucidating Evolutionary Relationships in the Tropical Lichen Family Graphidaceae - A Difficult Group Becomes More Complex

Nell Fanter, DePaul University

Coffee Break

2:15 to 2:30



Session 4

Moderator: Kenneth Angielczyk

Assistant Curator, Department of Geology

2:30 to 3:15

2:30–2:45: Who is Anomodont A? Archiving and Reconstructing Serially-sectioned Dicynodont Skulls

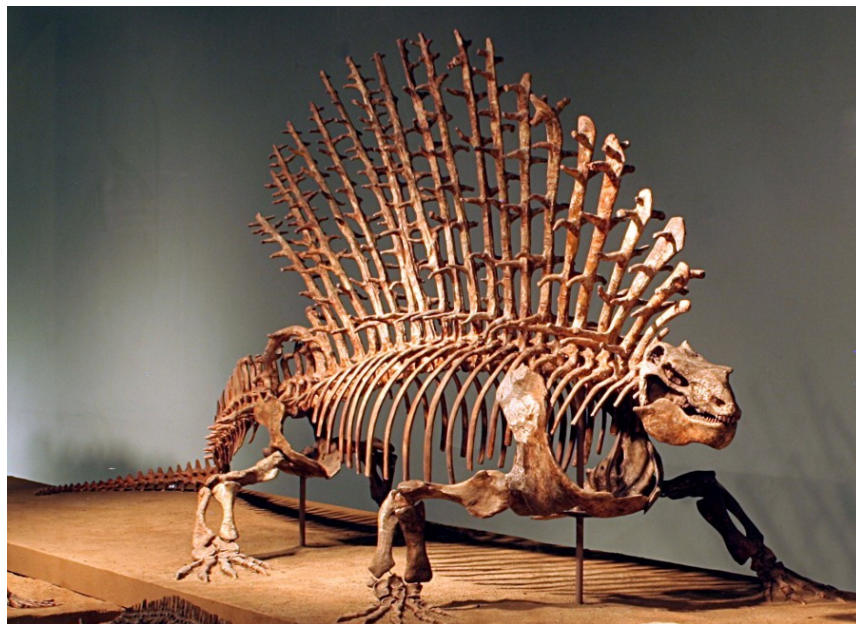
Florence Lin, University of Illinois, Urbana-Champaign

2:45–3:00: Osteohistology of *Cryolophosaurus ellioti*: Tempo and Mode of Growth in a Large-bodied Polar Dinosaur

Diana Boudreau, Augustana College

3:00–3:15: Competitive Exclusion in North American Theropods–Insights from Tooth Enamel and Morphology

Franco Gallastegui, University of Chicago



ABSTRACTS

Osteohistology of *Cryolophosaurus ellioti*: Tempo and Mode of Growth in a Large-bodied Polar Dinosaur

DIANA BOUDREAU, Augustana College

The Early Jurassic theropod, *Cryolophosaurus ellioti* (Dinosauria: Theropoda), was discovered in 1991 in the Hanson Formation of Antarctica. To date, it is the most complete dinosaur skeleton found in Antarctica. Histological examination is essential to understanding the life-history and developmental patterns of extinct taxa. My goal is to study bone microstructure in the rib and long bones of *C. ellioti* and discuss histological variance both at the individual level and across dinosaur phylogeny. Thin sections were made in the histology lab at The Field Museum. Examination of histological slides under a light microscope with polarizing lens revealed mild to strong presence of lines of arrested growth (LAGs) and primarily lamellar bone structure. The femur, fibula, and radius showed signs of moderate to severe remodeling, diminishing the amount of microstructure preserved. Based on these results, the estimated age of *C. ellioti* is 12-13 years old, classifying it as a juvenile theropod. These data match well with other skeletal indicators of subadult status (e.g., closed, but visible neurocentral sutures in the vertebrae), increasing the evidence that *C. ellioti* represents the largest known Early Jurassic theropod. Correlating age estimation with mathematically estimated body mass measurements will provide insight into the growth rate of *C. ellioti*. Plotting this growth curve with closely related theropods from non-polar regions, such as *Dilophosaurus*, *Allosaurus* or *Tyrannosaurus*, will allow me to visualize variation in growth between polar and non-polar dinosaurs. The description and analysis of additional histological features (e.g., vascularity amount, dominant canal orientation, vascular canal anastomoses, osteocyte density) will allow for the osteohistology and growth patterns of *C. ellioti* to be placed within the larger phylogenetic context of dinosaur evolution.

Wingless In Tasmania: A New Genus of Flightless Rove Beetle from Tasmania (Coleoptera: Staphylinidae: Omaliinae)

ANTHONY DECZYNSKI, University of Delaware

The family Staphylinidae – the rove beetles – is the largest family of beetles in the world and also one of the least understood. There are currently over 57,000 described species in over 3,600 genera and more are still being discovered at a rapid rate. In this project we describe a new flightless staphylinid genus from Tasmania belonging to the tribe Omaliini of the subfamily Omaliinae, extending knowledge of the highly endemic Australian fauna. We studied the beetles whole as dry specimens and in alcohol as well as cleared and dissected in permanent or temporary microscope slides. Scanning electron microscopy (SEM) allowed us to examine and image selected characters not clearly visible with optical microscopy. Using these sources of data we prepared descriptions and images of the beetles including species-specific genitalic structures and compiled all known distributional and ecological data. We added the genus into an ongoing phylogenetic analysis of World Omaliini by the second author to infer its phylogenetic placement. While we initially believed that this genus consisted of a single undescribed species from Tasmania we discovered that there are actually two species inhabiting different areas of that island. Several other genera of Omaliini have austral disjunct distributions that probably reflect an ancient origin on Gondwana. Our new genus needs to be compared carefully with several undescribed species of wingless Omaliinae known from southern New Zealand to assess whether they are all phylogenetically close – representing another disjunct genus – or convergently wingless.

Elucidating Evolutionary Relationships in the Tropical Lichen Family Graphidaceae - A Difficult Group Becomes More Complex

NELL FANTER, DePaul University

The lichen family Graphidaceae occurs mainly in tropical habitats. It consists of small crusts growing on tree trunks, soil, rocks and even leaves. The generic classification has always been a problem. Traditional taxonomists proposed a simple classification based on the ascospore type. This is resulted in a highly unnatural system of classification, in which closely related species were placed in different genera if their spores were different. Subsequently, the margins of the fruiting bodies were used for classification, but again the classification was highly arbitrary. My project is part of a larger scale project using DNA sequence data to test previous classifications and also to try to circumscribe natural groups and find morphological characters to recognize these groups. My new DNA sequence data and the data generated in the project, however, show that in some cases, the evolution of morphological characters is quite complex. This will be illustrated using the genus *Chapsa* as an example. The genus is shown to be highly polyphyletic. To conclude, these results indicate the limitations of using morphology to circumscribe genera in Graphidaceae.

Competitive Exclusion in North American Theropods—Insights from Tooth Enamel and Morphology

FRANCO GALLASTEGUI, University of Chicago

Tyrannosaurids are the subclade of coelurosaurian dinosaurs that include *T. rex* and its closest relatives. While notorious for achieving colossal body sizes, tyrannosaurids evolved from small-bodied Asian precursors and did not become a dominant predator until the latest stages of the Mesozoic (Campanian and Maastrichtian). Based on observations from the Asian record, it has been suggested that allosauroids competitively excluded tyrannosauroids from the top-predator niches in North America during most of Cretaceous. Support for this hypothesis, however, consists of a small number of temporally and geographically disparate body fossils. Theropod teeth, because they are abundant across several well-correlated sections in NA, provide a richer source of data for which to test this hypothesis. In addition, studies have established that the 3D arrangement of enamel crystallites (the schmelzmuster) is a character that exhibits a strong phylogenetic signal in theropods, which allows for isolated teeth to be taxonomically diagnosed with family and even genus-level precision. In this study, I measured variables pertaining to size, shape, and serration density for a number of tooth samples from three Lower Cretaceous formations in western NA. In addition, I coded the teeth for several morphological characters used in a previous analysis of theropod phylogeny. Since enamel visualization requires destructive sampling, representatives were chosen from clusters based on morphological similarity as well as on rough taxonomic affinity. Teeth were sectioned in longitudinal and transverse planes and their enamel examined using scanning electron microscopy. Together, the microstructural and gross morphological characters will be used to assign teeth to different theropod groups. The size distribution of teeth referable to allosauroids and tyrannosauroids will be compared to determine whether they support the competitive exclusion hypothesis.

Skeletal Morphometrics and Phylogenetic Predictors of Body Mass in the Diverse “Waterbird” Assemblage (Aves)

LIAM HEINS, University of Chicago

Assessing correlations between skeletal measurements and body mass allows for the estimation of body sizes of fossil forms, and provides information on the evolution of morphometric traits, body size, and ecology in different taxa. The diverse “waterbird” clade (including e.g., pelicans, loons, herons) serves as a useful system for studying

such correlations, as many different body sizes, skeletal proportions, and ecological niches are represented. The group has a rich fossil record, and includes giant forms such as *Giganhinga* and *Icadyptes*. A database of skeletal measurements will help to reveal which skeletal predictors of body size hold up across large taxonomic and morphological disparity. I measured nine skeletal traits (femur length, femur circumference, tibiotarsus length, tibiotarsus circumference, humerus length, humerus circumference, skull length, synsacrum length, and synsacrum width across the antitrochanters) in 39 waterbird taxa represented by 137 specimens. Ordinary least squares regressions were performed between these measurements and taxon-averaged body sizes drawn from the literature. Measurements were log-standardized prior to analyses. To account for non-independence between character traits and phylogenetic relatedness, subsequent phylogenetic independent contrasts analyses were performed using three different phylogenies for the waterbird clade. Preliminary results show strong, significant correlations between these skeletal measurements and body mass, with tibiotarsus circumference as the strongest skeletal correlate with body mass. Tibiotarsus length showed one of the weakest (though still significant) correlations. Correlations were found to be robust to different estimates of waterbird phylogeny. These results suggest great potential for estimating body mass in fossil taxa represented by even fragmentary remains. Multiple regression models and clade-specific analyses will ultimately provide a more nuanced picture of body size evolution and morphological change in the waterbird assemblage.

Amazonian Speciation in a Ring: Phylogeographic History of the Channel-billed and White-throated Toucans

JENNIE LEE, University of Chicago

Toucans are among the most prominent symbols of New World tropical forests and have attracted the attention of biologists for centuries, notably for their gaudy plumage coloration patterns and large bills. The Amazonian *Ramphastos* toucan species are a particularly interesting system for several reasons. First, throughout Amazonia two species of *Ramphastos*, one in the smaller-bodied Channel-billed Toucan complex (*Ramphastos vitellinus*) and the other in the larger-bodied White-throated Toucan complex (*Ramphastos tucanus*), overlap in geographic range. Second, each of these toucan species complexes includes multiple morphologically differentiated subspecies, and these subspecies hybridize to produce populations bearing intermediate or novel coloration patterns. This study focuses on uncovering the patterns of introgression (movement of different classes of genes between these differentiated populations) across these two overlapping hybrid zones. Using standard laboratory techniques and tissue samples from specimens obtained from toucan populations across the Amazon, I collected sequence data from two mitochondrial loci, cytochrome-*b* (cyt-*b*) and cytochrome oxidase I (COI) to reconstruct patterns of phylogeographic history. Phylogeographic analyses were performed on the resulting nucleotide alignments with the goal of comparing and contrasting patterns of hybridization and introgression in these two co-distributed toucan species. Future work in this system will include nuclear loci to form a more complete picture of gene flow and hybridization in these species complexes across evolutionary time.

Taxonomic Revision of the Namibian Fly Genus *Namadytes*

STEPHANIE LEON, University of California, Riverside

Flies are the most ecologically diverse of all insects. They are typically easily collected and available for research. The family Mydidae—or mydas flies—has a very short annual activity period. They are seldom collected, and usually unavailable in museum collections. Not much work is done on mydas flies because of this, thus little is known about their biology and taxonomy. There are 66 genera and 473 species of mydas flies. We reviewed the genus *Namadytes* Hesse, 1969. There are five described species of *Namadytes*, all from Namibia. Our goal was to create

redescriptions of each of these species, generate a detailed dichotomous key, and provide accurate distribution maps. Using holotypes and non-type specimens, we gathered data on the external morphology, internal characteristics of the male and female genitalia, and geographic distribution for each species. We were able to generate more detailed redescriptions by coding for a variety of characters, which also helped us identify and define the different species we were studying. Wing length, presence of pubescence, size and structure of setae, and antenna shape and size were just some of the characters we looked at which provided useful information about our genus. Our new descriptions revealed that the previously described species *N. vansoni* and *N. prozeskyi* were exactly the same, making *N. prozeskyi* a junior synonym. We were also able to find several characters which had not been seen in other Mydidae genera before (i.e., tuft of setae below metathoracic spiracle, an indented anterior pronotum). We also found that these flies extended beyond the borders of Namibia into north-western South Africa. By studying these flies in detail, we can provide more information about the biodiversity of southern Africa. We can also attempt to understand and explain the interesting behavior that is the short activity periods of the Mydidae. Ideally, the goal of every taxonomist and systematist is to provide more answers about the biology and evolutionary relationships of life.

Who is Anomodont A? Archiving and Reconstructing Serially-sectioned Dicynodont Skulls

FLORENCE LIN, University of Illinois, Urbana-Champaign

Anomodontia is the most successful group of extinct therapsids, surviving the Earth's largest mass extinction and occurring on every continent from the middle Permian through the late Triassic. In 1944, Everett Olson serially-sectioned several therapsid specimens and then created nitrocellulose peels from the specimens. Among the remaining peels were those from various specimens of anomodontia, cynodontia, and therocephalia. Due to the fragility of the peels, we wanted to digitally archive them to improve accessibility for researchers. Of particular interest was the specimen that Olson designated Anomodont A, which possessed an elongated snout and anteriorly-positioned canines, similar to those seen in basal anomodonts. Because basal anomodonts are rare and poorly known, it would be of great interest if we could confirm such an identity for Anomodont A. We scanned the individual peels and then stacked the slices in Amira to create a 3-D reconstruction. We labeled prominent morphological features such as the canines, external nares, and postcanine teeth, and used these characteristics in comparisons with 23 species of basal anomodonts and dicynodonts from the middle Permian. Our 3-D reconstruction of Anomodont A revealed the presence of a secondary palate and tusk. Furthermore, it possessed a shorter, very dicynodont-like snout and no premaxillary teeth, making it highly unlikely for Anomodont A to have been a basal anomodont. Instead, it shared a considerable number of similarities with basal dicynodonts such as *Brachyprosopus*, *Chelydontops*, and *Pristerodon*. The resemblance between Anomodont A and basal dicynodonts indicates that Olson's depiction is inaccurate. Correctly identifying and archiving Olson's specimens is important because it allows researchers to more accurately apply Olson's data on braincase morphology to modern phylogenetic and evolutionary questions.

Species Delimitation and Evolution in the Foliose Lichen Genus *Montanelia*

BRADLEY LOOMIS, Green Mountain College

Species circumscriptions in lichenized fungi that focus primarily or entirely on morphology often have aggregated many genetically distinct species into single taxa. Results from recent molecular studies have shown the potential for morphologically cryptic species-level diversity within some groups that are considered virtually indistinguishable based on morphological characters. To better understand diversification within the foliose brown parmelioid lichens (family Parmeliaceae), sequence data from six genetic markers from 46 specimens representing the newly

described genus *Montanelia* were analyzed within a phylogenetic context. The species of *Montanelia* occur on siliceous rocks in arctic-alpine habitats of the northern Hemisphere. The results from this research suggest that multiple traditionally circumscribed *Montanelia* species include previously unrecognized species-level diversity. Within the four traditionally circumscribed species investigated here, a total of nine candidate species were recognized. The results of this preliminary data show the limitations of using morphology to circumscribe species in *Montanelia*. Future studies investigating character evolution and the role of biogeography in the brown parmelioids will be essential to better understand biogeography and factors driving diversification in these commonly occurring lichens.

Genetic Structure of *Phyllastrephus fischeri* in the Albertine Rift

DANIEL MONTGOMERY, Indiana State University

The Albertine Rift comprises a chain of highlands stretching 1000km from north to south in East Africa. Many of the forested highland regions are isolated due to the geologic activity of the Rift. We set out to learn if the birds in these highlands have become genetically isolated. In order to assess this question, we sequenced two mitochondrial genes of 45 individuals of *Phyllastrephus fischeri* from various highland forests across the region. The results show two distinct geographic clades, one widespread clade and one limited to the Mt. Kabogo highlands in the south. Our original prediction that birds would show genetic isolation within the Albertine Rift was accurate. This research is important not only to further our understanding of evolution in the region, but also to help set conservation priorities in a region with limited conservation resources. Further research can look into other birds' genetic structure in the Albertine Rift. If more birds from the Mt. Kabogo region are shown to be genetically distinct, it will highlight the importance of these forests for the conservation of genetic diversity.

Evolution of the Labial Palps and Gills within the Palaeoheterodonta (Mollusca: Bivalvia)

IRQA MUSHTAQ, Loyola University of Chicago

Bivalves are easily recognizable animals that are known for their "two-shells" (bi-valves) connected by a hinge. They are most familiar to the public as clams, oysters, mussels, and scallops which may have come across their plate at a seafood restaurant. BivAToL is a part of the Assembling the Tree of Life initiative, a large research effort sponsored by the National Science Foundation to reconstruct the evolutionary origins of all living organisms. The BivAToL (Assembling the Bivalve Tree of Life) project aims to understand bivalve evolution by focusing on bivalve anatomy, morphology, and genetic makeup. Within the BivAToL project, my project for the summer was to reconstruct a plausible hypothesis of evolution for a specific bivalve organ system, the labial palps and gills. Labial palps and gills are very important organs in the Bivalvia as they are not only used for respiration, but are also essential for feeding and reproduction. The anatomical organization of gills is highly varied throughout the Bivalvia and an understanding of gill evolution is necessary in order to understand the evolution of bivalves in general. Using scanning electron microscopy, I investigated the labial palps and gills of seventeen species with a focus on the superorder Palaeoheterodonta and documented the most varied characters within a morphological data matrix using MorphoBank (www.morphobank.org). The morphological data matrix was used with molecular phylogenies in ancestral character state reconstruction to determine how the labial palps and gills evolved and how the labial palps and gills of ancestor species might have looked like and functioned. After reconstructing the evolution of the labial palps and gills, it is apparent that pearls are not the only prizes that can be extracted from bivalves.

Species Explosion: Using DNA Sequence Data to Detect Hidden Species in the Predominantly Australian Lichen *Cladia aggregata*

APARNA NUTTAKI, University of Chicago

The *Cladia aggregata* complex currently includes 9 species of lichenized fungi. These species are predominantly found in the southern Hemisphere, particularly Australia. The species in this complex are fruticose lichens, meaning that their thallus is shrubby. The color and perforations of the thallus were used to circumscribe species in the group. In addition to morphology, presence or absence of secondary metabolites were used to delimit species. The classification of the *Cladia aggregata* complex based on morphology and chemistry is highly controversial with authors accepting few and others up to 9 species. Therefore, I used molecular data to evaluate the species delimitation in this group. Molecular species delimitation began with single-gene analysis where a particular gene was sequenced to group or remove individuals from a species. The problem with this analysis was that a gene might have multiple alleles or incomplete lineage sorting might cause issues with separating species. Thus, multiple loci should be used to evaluate species delimitations. Within the multiple gene analyses two main methods are currently used: 1) the Genealogical Concordance Phylogenetic Species Recognition (GCPSR) and 2) Coalescent-based species delimitation. The latter uses factors, such as the branch length between species, the population size, and migration rates to determine the probability that different species emerged from a common ancestor. My work in the lab, however, dealt with the GCPSR applied to the *Cladia aggregata* complex. I used molecular techniques, such as PCR and Sanger sequencing to sequence multiple gene loci, such as those that code for proteins and ribosomes, in order to determine whether the 9 species actually do or do not belong in the *Cladia aggregata* complex.

Producing photographic plates for *The Bats of Kenya*

DAN PATTERSON, Lyons Township High School

East Africa is home to more than 140 different species of bats that are poorly understood. Elsewhere, bats are known to play important roles in pollination, seed dispersal, and insectivory. This project, *The Bats of Kenya*, seeks to identify, document the distribution and status, and determine the ecological roles of the 108 species known from Kenya. The book represents a collaboration of a systematist (FMNH Curator Bruce Patterson), an ecologist (Paul Webala), and a parasitologist (Carl Dick) To help identify these bat species and assess their interrelationships, we need to document the morphology of their skulls, teeth, and jaws. Each species will have a plate of photos. During the internship, I took >2000 photos of 66 Kenyan bat species represented in the FMNH mammal collection under varying lighting conditions to highlight its morphological structures. These were (1) organized and tagged in a Photoshop library, (2) the best photo in each set marked, and then (3) the background was blacked out to provide maximum contrast with the whitish bone of skulls and teeth. Using Photoshop, the different images were combined into a plate showing all aspects of the skull. The process taught me about the organization of one of the world's largest systematic collections of mammals, principles of macrophotography, and the process of organizing and editing technical photographs.

Genetic & Morphologic Structure in Midwestern Barred Owls

MARK SWANSON, Illinois Wesleyan University

Barred Owls (*Strix varia*) are ecologically important predators in forests across much of Eastern North America and can be separated into two distinct clades based on mitochondrial DNA sequences. A recent study showed these two clades intermingle in Minnesota. I gathered mitochondrial control region sequences from Barred Owls from Minnesota, Wisconsin, and Illinois. I also collected morphological data from owls of this region by using 20

skeletal measurements of nearly 100 individuals to produce a Principal Components Analysis. My results to date suggest all Illinois owls belong to a single mtDNA clade found mainly to the south. There also appears to be significant differentiation in morphology across this same region. Future research will include an increased sample size from additional localities in order to gain a clearer understanding of genetic and morphological structure in this region.

Origin and Rise of a Giant: Phylogeography of the Neotropical Bullet Ant *Paraponera clavata*

ARISTA TSCHNER, University of Illinois at Chicago

Known for their powerful sting, the giant Neotropical bullet ant *Paraponera clavata* (Formicidae: Paraponerinae) is a conspicuous member of ecosystems in lowland tropical rainforests throughout Central and South America, ranging from Honduras in the north to Brazil and Bolivia in the south. This distribution range is much larger than is typical for ants of a single species. They are the last remaining species in the genus *Paraponera*, and the only species to the subfamily Paraponerinae. We aimed at analyzing large and small scale genetic patterns in bullet ants. Firstly, on a larger scale, we investigated the phylogeography of the species using the mitochondrial gene, cytochrome oxidase I (mtCOI). More specifically, we asked whether gene flow occurs between geographically well separated sites, or on the contrary, whether populations are genetically isolated leaving room for speciation events. Methods included DNA extraction, PCR, cycle sequencing, and sequence analysis. A central question of this research topic is where the giant bullet ant has its origin and in which direction it populated its current range. Based on a mtCOI sequences, we generated a phylogenetic tree inferred from 43 individuals, including three ponerine outgroup taxa. This revealed that bullet ants arose in the Brazilian Amazon and then spread outward into Peru, Ecuador, and eventually into the Central American countries of Panama, Costa Rica, Nicaragua and Honduras. On the small scale, we investigated genetic colony structure including number of queens and number of mates per queen in a single population. To address this question, we developed microsatellite primers specific to bullet ants. So far, we were able to develop 18 primers variable for bullet ants of which 8 were variable within a single population. These primers will be used to screen 971 ants of 81 nests belonging to a single Costa Rican population.

Phylogenetics of the Chewing Louse Genus *Ricinus*: Implications for the Host Specificity of a Widespread Parasite of Passerine Birds

NATHAN TRAUTENBERG, Northwestern University

Perching birds (Order: Passeriformes), which include more than half of all birds species in the world are consequently parasitized by some of the most diverse groups of avian parasites. I am conducting a phylogenetic study of the louse genus *Ricinus* (Amblycera: Ricinidae), which is one of several of the diverse chewing louse lineages found on birds. These data will provide an important comparison with data already collected for other louse genera from the families Philopteridae (*Brueelia* and *Philopterus*) and Menoponidae (*Myrsidea*) that also parasitize perching birds. These louse genera differ in a variety of life history characteristics that may affect levels of host-specificity, ability to disperse, and ultimately patterns of cophylogenetic history with their hosts. For example, the genus *Ricinus* feeds almost exclusively on blood, whereas the genus *Brueelia* feeds only on feather barbs and thus these two genera may respond to different kinds of host defenses. Thus, one can comparing patterns of host specificity and phylogenetic history among these different louse families will provide important insights into how these different parasite life histories affect the cophylogenetic history of these parasites and their hosts. I collected DNA sequences for 1034 bp of the mitochondrial Cytochrome Oxidase I and 347 bp of the nuclear Elongation Factor 1- α . I analyzed these data using maximum parsimony and Bayesian inference to reconstruct phylogenetic trees and then used these trees to look at patterns of divergence and host specificity.

Morphological Characterization of Cryptic Bat Species: East African *Miniopterus* (Chiroptera: Miniopteridae)

ALEXANDRA WEBER, Loyola University of Chicago

Bats constitute about one fifth of all mammal species, totaling 1,200 species worldwide. Nearly 10% of these (at least 108 species) are found in Kenya. Their ecological roles in insectivory, seed dispersal and pollination have large impacts on the Kenyan environment, but are poorly understood. In 1936, FMNH curator Colin C. Sanborn named two new species in the genus *Miniopterus*, but more recently both have been treated as synonyms or subspecies. Recent fieldwork showed the two emit different echolocation calls based on variances in their minimum frequency. In an attempt to resolve their status (species, subspecies or synonym), morphological measurements were taken based on those used in Paúl M. Velazco and Alfred L. Gardner's identification of a new species of *Lophostoma* d'Orbigny. A digital caliper was used to take 16 craniodental and 12 postcranial measurements on each of the 73 *M. inflatus rufus* and 108 *M. africanus* specimen. ANOVAs of the craniodental measurements show that 16 out of the 16 measurements taken were statistically significant. ANOVAs of the post cranial measurements showed 9 out of 12 measurements were statistically significant ($p < 0.05$). Principal Components Analysis factor loadings showed widespread overlap among taxa. However, this overlap was additionally evident among well-defined *Miniopterus* species and may be due in part to intergradation among species. Discriminant function analysis of the craniodental and postcranial measurements show two distinct groups. Further studies, including molecular data and other morphological measurements, will be needed to completely resolve the relationships among these purported species.



2012 National Science Foundation Research Experience for Undergraduates (REU) Interns

REU participant: *Anthony Deczynski*, junior, University of Delaware

Project: Wingless In Tasmania: A New Genus of Flightless Rove Beetle from Tasmania (Coleoptera: Staphylinidae: Omaliinae)

Advisor: Dr. Margaret Thayer (Zoology – Insects, curator)

REU participant: *Franco Gallastegui*, junior, University of Chicago

Project: Competitive Exclusion in North American Theropods–Insights from Tooth Enamel and Morphology

Advisor: Dr. Peter Makovicky (Geology, curator)

REU participant: *Jennie Lee*, junior, University of Chicago

Project: Amazonian speciation in a ring: phylogeographic history of the Channel-billed and White-throated toucans

Advisor: Dr. John Bates (Zoology – Birds, curator) & Dr. Jason Weckstein (postdoctoral fellow)

REU participant: *Bradley Loomis*, sophomore, Green Mountain College

Project: Species Delimitation and Evolution in the Foliose Lichen Genus *Montanelia*

Advisor: Dr. Thorsten Lumbsch (Botany, curator)

REU participant: *Florence Lin*, freshman, University of Urbana-Champaign

Project: Who is Anomodont A? Archiving and reconstructing serially-sectioned Dicynodont skulls

Advisor: Dr. Kenneth Angielczyk (Geology, curator)

REU participant: *Daniel Montgomery*, junior, Indiana State University

Project: Genetic Structure of *Phyllastrephus fischeri* in the Albertine Rift

Advisor: Dr. John Bates (Zoology – Birds, curator) & Dr. Jason Weckstein (postdoctoral fellow)

REU participant: *Iqra Mushtaq*, sophomore, Loyola University Chicago

Project: Evolution of the Labial Palps and Gills within the Palaeoheterodonta (Mollusca: Bivalvia)

Advisor: Dr. Rüdiger Bieler (Zoology – Invertebrates, curator) & Dr. Sid Staubach (postdoctoral fellow)

REU participant: *Arista Tischner*, junior, University of Illinois at Chicago

Project: Origin and rise of a giant: phylogeography of the Neotropical bullet ant *Paraponera clavata*

Advisor: Dr. Corrie S. Moreau (Zoology – Insects, curator), Dr. Stefanie Kautz, & Benjamin E. Rubin (graduate student)



Affiliated Undergraduate Interns in Collections & Research

Intern: *Diana Boudreau*, sophomore, Augustana College

Project: Osteohistology of *Cryolophosaurus ellioti*: Tempo and mode of growth in a large-bodied polar dinosaur

Advisor: Dr. Nathan Smith (Geology, postdoctoral researcher) & Dr. Peter Makovicky (Geology, curator)

Intern: *Nell Fanter*, DePaul University

Project: Elucidating Evolutionary Relationships in the Tropical Lichen Family Graphidaceae - A Difficult Group Becomes More Complex

Advisor: Dr. Thorsten Lumbsch (Botany, curator)

Intern: *Liam Heins*, senior, University of Chicago

Project: Skeletal morphometrics and phylogenetic predictors of body mass in the diverse "Waterbird" assemblage (Aves).

Advisor: Dr. Nathan Smith (Geology, postdoctoral researcher)

Intern: *Stephanie Leon*, senior, University of California, Riverside

Project: Taxonomic revision of the Namibian fly genus *Namadytes*

Advisor: Dr. Torsten Dikow (Biodiversity Synthesis Center and Zoology – Insects, postdoctoral researcher)

Intern: *Aparna Nuttaki*, University of Chicago

Project: Species Explosion: Using DNA Sequence Data to Detect Hidden Species in the Predominantly Australian Lichen *Cladia aggregata*

Advisor: Dr. Thorsten Lumbsch (Botany, curator)

Intern: *Nathan Trautenberg*, sophomore, Northwestern University

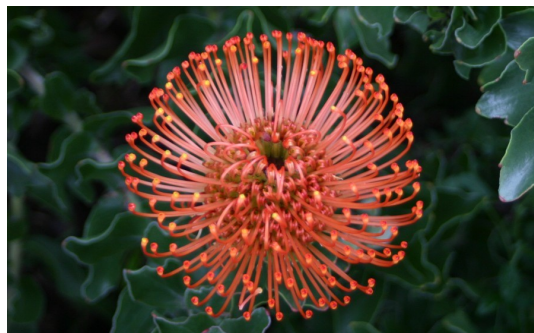
Project: Phylogenetics of the chewing louse genus *Ricinus*: Implications for the host specificity of a widespread parasite of passerine birds.

Advisor: Dr. Jason Weckstein, Zoology – Birds, postdoctoral researcher)

Intern: *Alexandra Weber*, sophomore, Loyola University of Chicago

Project: Morphological characterization of cryptic bat species: East African *Miniopterus* (Chiroptera: Miniopteridae)

Advisor: Dr. Bruce Patterson (curator, Zoology – Mammals)



Collections and Research Prince Collections Summer Interns

Undergraduate Intern: *Stephanie Garcia*; freshman, Loyola University of Chicago

Project: Insect Collection Internship: Specimen Transactions

Advisor: James Boone (Zoology – Insects, collections manager)

Undergraduate Intern: *Mark Swanson*; freshman, Illinois Wesleyan University

Project: Genetic & Morphologic Structure in Midwestern Barred Owls

Advisor: Dr. John Bates (Zoology – Birds, curator) & Josh Engel (research assistant)

High School Intern: *Niall Griffin*; senior, Glenbard West High School

Project: Documenting Coal-Forming Floras of the Late Carboniferous Period

Advisor: Dr. Ian Glasspool (Geology, adjunct curator & collections manager)

High School Intern: *Charles Griggs*; senior, Proviso Mathematics and Science Academy

Project: Ant Lab Internship: Collection Studies & Molecular Methods

Advisor: Dr. Corrie Moreau (Zoology – Insects, curator)

High School Intern: *Stacey Huynh*; junior, J. Sterling Morton East High School

Project: Insect Collection Internship: Specimen Transactions

Advisor: James Boone (Zoology – Insects, collections manager)

High School Intern: *Evan Johnson-Ransom*; junior, Brother Rice High School

Project: Reweighing, Photography & Storage of the Murchison Meteorite

Advisor: James Holstein (Geology, collections manager, Robert A. Pritzker Center for Meteoritics & Polar Studies)

High School Intern: *Katherine McDonnell*; senior, St. Francis High School

Project: Ant Lab Internship: Collection Studies & Databasing Techniques

Advisor: Dr. Corrie Moreau (Zoology – Insects, curator)

High School Intern: *Janet Morales*; sophomore, Lane Tech College Prep

Project: The Lichens of Fiji.

Advisor: Dr. Thorsten Lumbsch (Botany, curator)

High School Intern: *Dan Patterson*; junior, Lyons Township High School

Project: Producing photographic plates for *The Bats of Kenya*

Advisor: Dr. Bruce Patterson (Zoology – Mammals, curator)

High School Intern: *Sarah Pipal*; junior, Lyons Township High School.

Project: Data Cleaning for the Physical Geology Collection.

Advisor: James Holstein (Geology, collections manager, Robert A. Pritzker Center for Meteoritics & Polar Studies)

High School Intern: *Christian Valderrama*; junior, J.F. Kennedy High School
Project: Insect Collection Internship: Sorting, Specimen Preparation & Care
Advisor: Dr. Margaret Thayer (Zoology – Insects, curator)

High School Intern: *Evelina Yarmit*; senior, Highland Park High School
Project: Accession of a New Collection.
Advisor: James Holstein (Geology, collections manager, Robert A. Pritzker Center for Meteoritics & Polar Studies)

2012 Phylogenetics Workshop Instructors

Dr. Steven Leavitt (postdoctoral researcher, Botany)

Dr. Nathan Smith (postdoctoral researcher, Geology)



Photographs by Kenneth Angielczyk

Index of Participant Contact Information

- Angielczyk, Kenneth:** kangielczyk@fieldmuseum.org, Field Museum of Natural History
- Bates, John:** jbates@fieldmuseum.org, Field Museum of Natural History
- Boone, James:** jboone@fieldmuseum.org, Field Museum of Natural History
- Boudreau, Diana:** dianaboudreau10@augustana.edu, Augustana College
- Deczynski, Anthony:** adeczyn@udel.edu, University of Delaware
- Dikow, Torsten:** tdikow@fieldmuseum.org, Biodiversity Synthesis Center
- Engel, Josh:** jengel2@fieldmuseum.org, Field Museum of Natural History
- Fanter, Nell:** cefanter@gmail.com, DePaul University
- Gallastegui, Franco:** fmgallastegui@gmail.com, University of Chicago
- Garcia, Stephanie:** stephgarcia1201@gmail.com, Loyola University of Chicago
- Griffin, Niall:** niallgriffin@comcast.net, Glenbard West High School
- Griggs, Charles:** charles-griggs@kappaleaguechicago.org, Proviso Mathematics and Science Academy
- Heins, Liam:** lheins74@gmail.com, University of Chicago
- Holstein, James:** jholstein@fieldmuseum.org, Field Museum of Natural History
- Huynh, Stacey:** stacey_huynh657@yahoo.com; J. Sterling Morton East High School
- Johnson-Ransom, Evan:** ejr2013@hotmail.com, Brother Rice High School
- Leavitt, Steven:** sleavitt@fieldmuseum.org, Field Museum of Natural History
- Lee, Jennie:** jnnklee@gmail.com, University of Chicago
- Leon, Stephanie:** sleon002@ucr.edu, University of California, Riverside
- Lin, Florence:** lin.florence15@yahoo.com, University of Illinois, Urbana-Champaign
- Loomis, Bradley:** loomisb@greenmtn.edu, Green Mountain College
- Lumbsch, Thorsten:** tlumbsch@fieldmuseum.org, Field Museum of Natural History
- McDonnell, Katherine:** kitmcdonnell@hotmail.com, St. Francis High School
- Montgomery, Daniel:** dmontgomer6@sycamores.indstate.edu, Indiana State University
- Morales, Janet:** jmorales4265@yahoo.com, Lane Tech College Prep
- Moreau, Corrie:** cmoreau@fieldmuseum.org, Field Museum of Natural History
- Mushtaq, Iqra:** iqramushtaq1@gmail.com, Loyola University Chicago
- Nelsen, Matthew:** mpnelsen@gmail.com, University of Chicago and Field Museum of Natural History
- Nuttaki, Aparna:** anutakki@uchicago.edu, University of Chicago
- Patterson, Bruce:** bpatterson@fieldmuseum.org, Field Museum of Natural History
- Patterson, Dan:** dpatty545@gmail.com, Lyons Township High School
- Pipal, Sarah:** sepipal@yahoo.com, Lyons Township High School
- Rubin, Benjamin:** brubin@uchicago.edu, University of Chicago and Field Museum of Natural History
- Sierwald, Petra:** psierwald@fieldmuseum.org, Field Museum of Natural History
- Smith, Nathan:** smithnd@uchicago.edu, Field Museum of Natural History
- Staubach, Sid:** sstaubach@fieldmuseum.org, Field Museum of Natural History
- Swanson, Mark:** mswanso2@iwu.edu, Illinois Wesleyan University
- Thayer, Margaret:** mthayer@fieldmuseum.org, Field Museum of Natural History
- Tischner, Arista:** atischner@fieldmuseum.org, University of Illinois at Chicago
- Trautenberg, Nathan:** natester123@mac.com, Northwestern University
- Valderrama, Christian:** christian_valderrama@yahoo.com, J.F. Kennedy High School
- Ware, Stephanie:** sware@fieldmuseum.org, Field Museum of Natural History
- Weber, Alexandra:** aweber6@luc.edu, Loyola University of Chicago
- Weckstein, Jason:** jweckstein@fieldmuseum.org, Field Museum of Natural History
- Yarmit, Evelina:** eyarmit@gmail.com, Highland Park High School