



Undergraduate Research Symposium 2009

Program and Abstracts

Saturday, August 15

BioSynC Conference Room



REU Projects 2009

Project: The Early Evolution of Sea Turtles

Name: *William Adams* (Junior, Biology, Loyola University)

Field Museum faculty mentors: Dr. Ken Angielczyk (Geology), and Dr. James Parham (BioSynC)

Project: Bryozoan Biodiversity on the Web

Name: *Bryan Quach* (Freshman, Bioinformatics, Loyola University)

Field Museum faculty mentor: Dr. Scott Lidgard (Geology)

Project: Species recognition in tropical lichen-forming fungi

Name: *Gabrielle Lopez* (Freshman, Biology, Roosevelt University)

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

Project: Do some nocturnal primates and bats see in color?

Name: *Austin Hicks* (Junior, Molecular Biology, Loyola University)

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

Project: Ants of the rainforests of South America. Why are some species only found in some places?

Name: *Elizabeth Loehrer* (Senior, Molecular Biology, Loyola University)

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

Project: Vampires on vampires?: Coevolution of bats and bat flies

Name: *Anna Sjodin* (Sophomore, Biology and Ecology, Loyola University)

Field Museum faculty mentor: Drs. Patterson and Dick (Zoology)

Project: Giant Pill-Millipedes and Fire-Millipedes from Madagascar, taking stock of a hidden diversity

Name: *Iouliia Bespalova* (Sophomore, Biology, Mount Holyoke College)

Field Museum faculty mentor: Drs. Sierwald (Zoology) and Wesener (Zoology)

Project: One species, or more? Is *Stenomalius helmsi* really a widespread austral species?

Name: *Kristin Kalita* (Sophomore, Biology, Loyola University)

Field Museum faculty mentor: Dr. Margaret Thayer (Zoology)

The undergraduate 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).

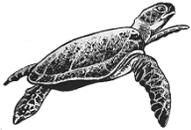


PROGRAM

9:00 AM Opening of the Symposium, Welcome, Petra Sierwald and Peter Makovicky

Session 1: Oral presentations: Evolution and Biodiversity

Moderator: Dr. Torsten Dikow, BioSynC



9:15 – 9:30 am

A Geometric Morphometric Analysis of Plastron Morphology in Marine Chelonioids and Their Relatives (Chordata: Reptilia: Testudines: Chelonioida)

William Adams



9:30 – 9:45am

Do Hipposiderid Bats See in Color?

(Chordata: Mammalia: Chiroptera: Rhinolophidae)

Austin Hicks

9:45 – 10:00am

Bryozoan Biodiversity on the Web (Lophotrochozoa: Bryozoa)

Bryan Quach



10:00 – 10:15 am

Molecular phylogeny of lichenized fungi in *Dothideomycetes* and *Arthoniomycetes* (Fungi: Ascomycota: Pezizomycotina)

Joelle Mbatchou

10:15 – 11:00 am



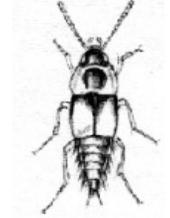
Session 2: Oral presentations: Speciation

Moderator: Edna Davion, Anthropology

11:00 – 11:15am

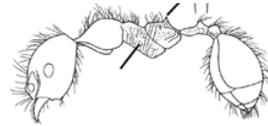
One Species, or More? Is *Stenomalium helmsi* Really a Widespread Austral Species?
(Arthropoda: Hexapoda: Insecta: Coleoptera: Polyphaga: Staphylinidae: Omaliinae)

Kristin Kalita



11:15 – 11:30am

Patterns of Diversification in South American *Pheidole* (Insecta: Hymenoptera: Formicidae): A Molecular Approach
Elizabeth Loehrer



11:30 – 11:45 am

A Phylogenetic Study of the Genus *Lecanora* (Fungi: Ascomycota: Lecanoromycetes: Lecanorales)
Gabrielle Lopez

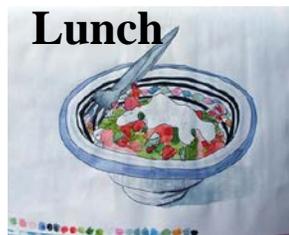


11:45 – 12:00noon

Discovery of Six New Species of Giant Pill-Millipede from Madagascar (Arthropoda: Diplopoda: Sphaerotheriida)
Ioulia Bepalova



12:00 noon – 1:00 pm



Session 3: Oral presentations: Co-Evolution

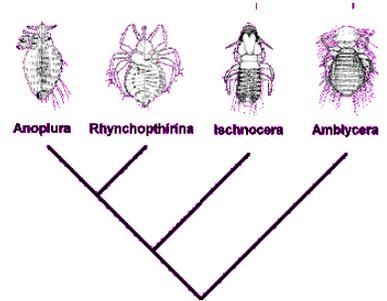
Moderator: Dr. Thomas Wesener, Zoology

1:00 – 1:15pm

Evolutionary History of *Myrsidea* Chewing Lice on Toucan Hosts

(Hexapoda: Insecta: Phthiraptera: Amblycera: Menoponidae; Chordata: Aves: Piciformes: Rhamphastidae)

Joseph Cacioppo



1:15 – 1:30pm

The Vampire's Vampire: Bats and Blood-Feeding Fly Parasites (Chordata: Mammalia: Chiroptera: Phyllostomidae; Arthropoda: Hexapoda: Diptera: Hippoboscoidea)

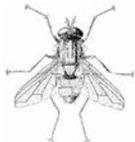
Anna Sjodin



1:30 – 1:45pm

A New Phylogenetic Hypothesis for the Axymyiidae and Nymphomyiidae based on Four Nuclear Genes (Arthropoda: Hexapoda: Insecta: Diptera)

Kathleen Lyons



1:45 – 2:00pm

Homoplasy, Atavism and Phylogeny in Gavialoid Crocodylians (Chordata: Reptilia: Crocodylia: Gavialidae)

Andrea Jaszlics



ABSTRACTS

A Geometric Morphometric Analysis of Plastron Morphology in Marine Chelonioids and their Relatives

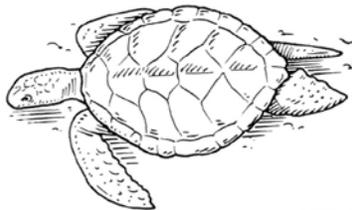
(Chordata: Reptilia: Testudines: Chelonioidea)

William D. Adams

Department of Biology, Loyola University Chicago, IL

Department of Geology, Field Museum of Natural History, Chicago, IL

Chelonioid turtles include the extant sea turtles and extinct taxa extending back to the Cretaceous. A distinguishing feature of chelonioids is the reduction of their plastron or ventral shell. The shape and proportions of chelonioid plastra have been examined in the past as a source of information for inferences about the process of marine adaptation in sea turtles. Previous research was based on simple sets of linear measurements that only provided a crude picture of plastral shape variation. We examined the plastra of several genera of extinct chelonioids and compared them to those of extant cheloniids, extant chelydrids (snapping turtles), and kinosternids (mud turtles and musk turtles) to determine whether marine turtles are characterized by a distinctive plastron shape, and how that shape differs from those of other turtles. We used landmark-based geometric morphometrics to quantify plastral shape variation, and also conducted an extended eigenshape analysis of the outlines of the extant specimens and the best preserved extinct specimens to determine if the plastral outline preserved additional relevant information. Our results indicate that plastron shape can be used to differentiate between advanced marine forms and their less-derived relatives. Advanced marine turtles have reduced plastra that are longer and narrower than those of non-marine turtles, with large central fontanelles almost completely separating the plastra into two halves. More basal chelonioids have robust plastra with little or no central fontanelle. Plastra of protostegids, advanced marine turtles that may not be chelonioids, resembled the cheloniidae plastra. This similarity emphasizes the link between plastron shape and ecology. Finally, our shape data are highly correlated with the “plastral index” used by previous workers, showing that the latter metric captures similar shape information.



Discovery of Six New Species of Giant Pill-Millipede from Madagascar

(Arthropoda: Diplopoda: Sphaerotheriida)

Ioulia Besimalova

Biology Department, Mount Holyoke College, South Hadley, MA

Department of Zoology, Insects, Field Museum of Natural History, Chicago, IL

Madagascar houses a very unique mix of dry to rain forest climates and high mountain range habitats, which provide ecosystems for a wide array of millipede species. These ecosystems are rapidly being destroyed by deforestation. Description of newly discovered species at least ensures that they will not disappear unnoticed. This project focuses on the descriptions of new species of the enigmatic Malagasy giant pill-millipedes. The Malagasy giant pill-millipedes are all endemic and belong to the order Sphaerotheriida which is distributed all over the Southern hemisphere. Its members superficially resemble pill bugs, and possess the unique ability to roll into a fully closed ball. Six new species of the genus *Zoosphaerium* as well as the females of two other *Zoosphaerium* species, *Z. pseudoplatylabum* and *Z. xerophilum*, are described. Four of the newly described species belong to pre-existing species-groups, while two show surprising characteristics – one species from Torotorofotsy possesses male sexual organs that have not yet been seen in any other giant pill-millipede, and one new species from the montane rainforest of Andringitra which shows a linkage to two species which live in a different ecosystem, the southwestern sub-humid forest. This study focused on producing images (both hand drawn with camera lucida and ink, as well as Scanning Electron Microscopy) and descriptions of the specimens, detailing morphological characters discovered in earlier studies which can be later used in a larger phylogenetic analysis of *Zoosphaerium*. These characters include various features of the male and female sexual organs, features of the leg, anal shield, endotergum, and antenna. In general the identification and phylogenetic analysis of organisms has been a project that has been worked on since the early 18th century, and in this endeavor Myriapoda have been vastly ignored. This project is another incremental step forward towards that goal.



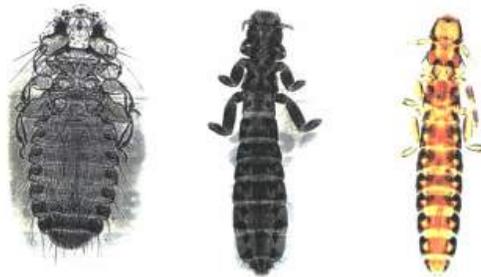
Evolutionary History of *Myrsidea* Chewing Lice on Toucan Hosts

(Hexapoda: Insecta: Phthiraptera: Amblycera: Menoponidae; Chordata: Aves: Piciformes: Rhamphastidae)

Joseph Cacioppo

Biological Sciences Collegiate Division, University of Chicago, Chicago, IL
BioSynC, Field Museum of Natural History, Chicago, IL

A number of characteristics make chewing lice choice models for studying coevolutionary history. First, lice in general have a relatively simple life history in comparison to many other parasite groups and live their entire life cycle on a single host. Second, they are primarily transmitted between mates and between parents and their offspring. Third, they infrequently disperse. Lastly, they are often host specific. Thus one can often compare phylogenies of lice and their hosts to reconstruct the evolutionary history of their associations. *Myrsidea* (Phthiraptera: Amblycera) chewing lice are one of five louse genera that parasitize toucan hosts and also are known to parasitize a wide variety of perching birds (Passeriformes) and some barbets (Piciformes). Furthermore, some toucan species host two species of *Myrsidea*. Thus one logical question is whether toucans have acquired their *Myrsidea* chewing lice once or multiple times over evolutionary times scales. I am using DNA sequences to reconstruct the phylogenetic history of *Myrsidea* chewing lice to draw inferences about their evolutionary history and associations with their toucan hosts. I will use these phylogenetic data to test whether *Myrsidea* from toucans are monophyletic. If they are monophyletic then it suggests that toucans acquired these parasites only once. However, if toucan *Myrsidea* are paraphyletic it suggests that toucans have acquired these parasites multiple times. Through phylogenetic reconstructions I will determine which *Myrsidea* species hosted by passeriform (perching) birds are closest to the toucan *Myrsidea* and thus can make inferences regarding how toucans may have acquired their parasites. Lastly, I will conduct cophylogenetic comparisons of the *Myrsidea* and toucan phylogenies to establish whether or not they exhibit significant levels of cospeciation. If there is significant cospeciation I can use these cospeciation nodes to calibrate the trees to reconstruct the timing of other coevolutionary events such as host switching, duplication, or failure to speciate.



Do Hipposiderid Bats See in Color?

(Chordata: Mammalia: Chiroptera: Rhinolophidae)

Austin Hicks

Department of Biology, Loyola University, Chicago, IL

Pritzker Laboratory for Molecular Systematics and Evolution, Field Museum of Natural History, Chicago, IL

Until recently, nocturnal mammals were believed to have a retina that consisted purely of rods, optimized for vision in low light conditions. These rod cells contain the photopigment rhodopsin (RH1) that responds to a single photon of light. Recent studies regarding nocturnal mammals have shown that some, including three groups of primates and some bats have not one, but two different types of cones. Contained in these cone cells are photopigments that are sensitive to light in the blue to yellow (short) wavelengths (SWS1), or to light in the green to red (medium- to long) wavelengths (M/LWS). Cones are therefore the first step in facilitating color vision. *Hipposideros* is a wide spread micro-bat that consists of approximately 55 species, all of which are nocturnal and insectivorous. The answer we seek is whether *Hipposideros* has the capacity for color vision. To answer this question, we attempted to sequence the autosomal SWS1- and X-linked M/LWS-opsin genes in *Hipposideros*. These attempts will be discussed. After sequences have been obtained, we wish to 1) establish if the SWS1 gene is functional, 2) conduct statistical analyses on the SWS1 and M/LWS opsin sequences to test for evidence of purifying, negative or neutral selective pressure on the genes, and 3) analyze these sequences in a phylogenetic context in order to draw inferences regarding the ancestral condition at various nodes in the mammalian tree of life.



Homoplasy, Atavism and Phylogeny in Gavialoid Crocodilians

(Chordata: Reptilia: Crocodylia: Gavialidae)

Andrea Jaszlics

UCB 265, CU Museum University of Colorado, Boulder, CO

The true gharial of India, *Gavialis gangeticus*, and the false gharial of Southeast Asia, *Tomistoma schlegelii*, are unique among the crocodilians as they are characterized by a highly elongate snout (longirostry) and almost exclusively piscivorous diet. This is in contrast to the rest of the crocodilians which have a blunter snout shape (Brochu 1997) and a more varied diet, consisting of mammals, amphibians and other reptiles in addition to fish. However, many extinct groups of crocodilian and crocodylomorph taxa have the morphological characteristics of the modern gharials. Understanding the evolutionary relationships of the gharials is, therefore, helpful in improving our understanding of fossil diversity, in addition to the diversification of the modern crocodilian clade. Current phylogenetic hypotheses of the relationships of crocodilians are highly controversial, as morphological approaches to the gharial taxa have found that *Tomistoma* and *Gavialis* are only distantly related, while molecular analyses show a sister relationship between the two species. *Gavialis* is a unique among the living crocodilians, and its controversial phylogenetic position is thought to be due to the great number of atavisms, or evolutionary reversals, which characterize this species (Gatesy et al. 2003). A combined analysis of morphological and molecular characters of the crocodilian supports the hypothesis of a sister-group relationship between the gharials. Furthermore, by examining the distribution of morphological characters on the species tree derived from the combined dataset, a number of characters demonstrating high degrees of both homoplasy and atavism were identified within the crocodilians. These characters have many implications for the interpretations of fossil archosaur relationships, especially in longirostrine crocodilian taxa.



One species, or more? Is *Stenomalium helmsi* really a widespread austral species?

(Arthropoda: Hexapoda: Insecta: Coleoptera: Polyphaga: Staphylinidae: Omaliinae)

Kristin Kalita

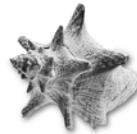
Biology Department, Loyola University, Chicago, IL

Department of Zoology, Insects, Field Museum of Natural History, Chicago, IL

Currently, the beetle family Staphylinidae (rove beetles) includes more than three percent of all described animal species and occupies virtually all terrestrial habitats. Among those inhabiting lands of the southern hemisphere, most are endemic to a single area. *Stenomalium helmsi* appears to be an exception to that pattern, having been collected in Australia, New Zealand, and southern Chile and Argentina. Typically, divergent evolution after the breakup of Pangaea resulted in various austral lands having similar yet distinct species, so the existence of a widespread species would demand other distributional explanations.

A specimen from the middle of the range of distribution in New Zealand was chosen as a reference specimen of *S. helmsi*. Through the study of 69 morphological characters, including detailed genitalia and macrosetae analyses, the supposed *S. helmsi* specimens were compared to the reference specimen. Ten other species of *Stenomalium* and related genera of Omaliini were also coded in order to generate a phylogenetic tree using TNT and to examine character distribution in WinClada.

The examination of 28 *S. helmsi* specimens provided no significant evidence of more than one species being involved. Furthermore, the tree search produced two most parsimonious trees, each of length 136. Each tree placed *S. helmsi* two nodes up from the group of other *Stenomalium*, a well-supported group with a Bootstrap value of 92. Thus, *Stenomalium* does not include *S. helmsi*. Possibly, *S. helmsi* represents an undescribed genus that is characterized by three synapomorphies. Because *S. helmsi* has been more widely and more abundantly collected in New Zealand than in other austral locations, the species may have originally dispersed from New Zealand. Regardless of the cause of dispersal, the fact that *S. helmsi* defies the area-endemic pattern reveals that the distribution of all austral Staphylinids is not the result of a single set of causes.



Patterns of Diversification in South American *Pheidole*: A Molecular Approach

(Arthropoda: Hexapoda: Insecta: Hymenoptera: Formicidae)

Elizabeth Loehrer

Department of Biology, Loyola University, Chicago, IL
Pritzker Lab for Molecular Systematics and Evolution, Department of Zoology, Field Museum of Natural History, Chicago, IL

Though the Amazon is known to be a rich and diverse ecosystem, much of the origin and evolution of the Amazonian biota is still unclear. Using the most speciose ant genus, *Pheidole*, as my study system, I tested two of the Amazonian origin of species hypotheses, specifically I examined the river barrier hypothesis and the uprising of the Andes hypothesis. The two hypotheses suggest that speciation events occur in accordance to the formation of natural barriers (e.g. a major river or mountain range respectively) that would prevent two populations from mating and thus lead to diversification (Haffer 2008, Cracraft & Prum 1988). My supervisor, Dr. Corrie Moreau collected *Pheidole* specimens from various locations in Ecuador, Peru, and Venezuela prior to the commencement of my project. I extracted the DNA from ninety-five specimens and amplified two different genes, EF-1 α -F2 and COI. I used the bioinformatics program, Sequencher® to perform a multiple sequence alignment of my data and TNT® and DNAPars® to construct molecular phylogenetic trees of *Pheidole*. I then examined the correlation between branching patterns on the tree and the geographic collection site of each specimen to determine the validity of the river barrier hypothesis and the uprising of the Andes hypothesis. Initial findings with the EF-1 α -F2 data did not reveal definitive patterns between geographic location and speciation events, particularly due to multiple polytomies within the tree. Finishing the data set for COI as well as amplifying additional genes may improve tree resolution, which would allow for a better analysis of the connection between diversification and geographic barriers.



A Phylogenetic study of the genus *Lecanora*

(Fungi: Ascomycota: Lecanoromycetes: Lecanorales)

Gabrielle Lopez

Department of Biology, Roosevelt University, Chicago, IL

Department of Botany, Field Museum of Natural History, Chicago, IL

Species recognition in lichen-forming fungi is difficult at best when considering the different methods used in classification. Historically, chemical and morphological characters are implemented to produce phylogeny. In this study, a phylogenetic tree of the genus *Lecanora* is produced using morphological and molecular data. Techniques that were applied include DNA extraction, PCR amplification, gel electrophoresis, DNA sequencing, and alignment. Analysis of the molecular data was performed using Garle. The tree positioned the specimens in the group *subfusca*, which was supported with bootstrap analysis. Morphological characters of the specimens were studied and photographed to confirm placement on the tree. This study could be improved by incorporating more genes in the analysis, along with morphological characters for all taxa. The integration of morphological and molecular data, like those used in this study, could lead to a more complete phylogenetic tree of the lichen genus *Lecanora*.

**A new phylogenetic hypothesis for the Axymyiidae and Nymphomyiidae based on four nuclear genes**

(Arthropoda: Hexapoda: Insecta: Diptera)

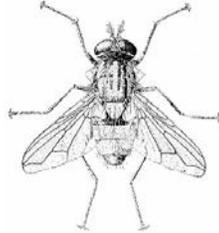
Kathleen Lyons

Department of Biology, Nazareth College, Rochester, NY

The hallmark of a good phylogenetic analysis is its repeatability. A paper that postulates new taxonomic relationships between species should be clear on how the authors arrived at their conclusions. Taxonomic relationships among the lower Diptera (formerly the suborder Nematocera) have been analyzed and reinterpreted multiple times, most recently by Bertone in 2009. I have attempted to reanalyze this most recent study using four sequenced genes and 70 taxa. Using the programs TNT and POY, I have produced a phylogenetic tree that proposes a new position for the families Axymyiidae and Nymphomyiidae and shows the suborders



Culicomorpha and Brachycera as paraphyletic. While Bertone's analysis proved difficult to repeat, much of the tree topology was conserved in my results. The new placements of certain groups, however, may be significant in studying the course of evolution of the lower flies from other Diptera.



Molecular phylogeny of lichenized fungi in *Dothideomycetes* and *Arthoniomycetes*

(Ascomycota: Pezizomycotina)

Joelle Sophya Mbatchou

Department of Biology, De Paul University, Chicago, IL

Department of Botany, Field Museum of Natural History, Chicago, IL

The morphological taxonomic classification of lichenized fungi was evaluated by testing for congruency with molecular phylogeny analysis. The phylogenetic position of lichenized fungi in two fungal classes, *Dothideomycetes* and *Arthoniomycetes*, was studied. Previous studies have shown that molecular data can alter the classification based on morphological characters. The accuracy of the classification scheme of families containing lichenized fungi was investigated. The phylogeny was examined using two different loci: mtSSU and TEF1 α . The phylogenetic reconstruction, based on maximum likelihood, was used to assemble a hypothetical phylogenetic tree. The genus *Herpothallon* as is currently defined is not monophyletic. The phylogenetic placement of the family Chrysotrichaceae is confirmed. The results show that change is necessary for the current classification system. The placement of several lichenized fungal species may need to be revised



The Vampire's Vampire: Bats and Blood-Feeding Fly Parasites

(Chordata: Mammalia: Chiroptera: Phyllostomidae; Arthropoda: Hexapoda: Diptera: Hippoboscoidea)

Anna Sjodin

Department of Biology, College of Arts and Sciences, Loyola University, Chicago, IL
Department of Zoology, Field Museum of Natural History, Chicago, IL

Bats constitute a single, extensive radiation of evolutionary lineages, trophic strategies, roosting structures, and social behaviors, and are parasitized by blood-feeding flies that vary in the reduction and loss of eyes and wings, flattening or narrowing of bodies, and the development of holdfast organs. Coupled, bats and bat flies represent a model system for evolutionary studies. My research included a morphometric study of the bat genus *Sturnira*, and a study of how bat fly eyes vary among the roosting structures utilized by their hosts.

Because boundaries among species of *Sturnira* are dubious, I used geometric and traditional morphometrics to evaluate shape and form of *Sturnira* skulls. Differences in cranial characters among six *Sturnira* species were clearer using traditional morphometrics, and results expanded our current knowledge regarding differences between *Sturnira* species by providing a basic comparison between the shapes and forms of the skulls of each species. Given minimal morphological data and unclear boundaries in the bat genus *Sturnira*, I was able to clarify lines between species by defining morphological characteristics.

Because several measures of parasitism are related to the roosting characteristics of bat hosts, I evaluated trends in bat fly eye complexity among hosts that varied in the roosts they utilize. I measured eye size and counted the number of facets for >120 species of Venezuelan bat flies, and correlated these variables with roost type ranked along a gradient of enclosed and durable to exposed and ephemeral. Both eye characters were negatively and significantly associated with roost type, suggesting that bat flies of bats that use dark and durable roosts have evolved less complex eyes than their counterparts on hosts roosting in locations exposed to light. This study provided insight into the evolutionary development of eyes in cave organisms, and highlighted the importance of host roosting dynamics in the evolution of bat parasites.



Bryozoan Biodiversity on the Web

(Lophotrochozoa: Bryozoa)

Bryan Quach

Department of Bioinformatics, Loyola University Chicago, Chicago, IL
Department of Geology, Field Museum of Natural History, Chicago, IL

Utilizing the internet for disseminating and exchanging biodiversity data creates new ways for scientists to collaborate and conduct research. Current online databases output queries more effectively than any non-automated searching method, allowing researchers to spend less time retrieving data and more time analyzing it. In the case of understudied taxa, this online collaboration yields faster progress toward an understanding of their biodiversity and systematics, bringing them closer to the level of better-known taxa. Bryozoans are among the more understudied taxa with a small research community, and the Bryozoan Biodiversity on the Web project aims to enhance research for bryozoan specialists by making taxonomic, systematic, bibliographic, photographic, and biogeographic data pertaining to Bryozoans accessible on a website.

The timeline for the project divides the research into five main phases: 1) Combine bryozoan data from multiple sources into one large database 2) Use the Drupal content management system to create a website that hosts the database content 3) Develop modules for the content management system using the Hypertext Preprocessor (PHP) programming language to accommodate taxonomic and biodiversity data 4) Engage an initial group of website users that will test the functionalities of the bryozoan website 5) Expand website access to the bryozoan research community and the general public. Current progress is nearing 60% completion of phase one.

Phase one relies heavily on PHP scripts to semi-automate solutions to data discrepancies and to unify the data from multiple bryozoan databases. Bioinformatics programs were created to restructure data tables that do not adhere to database design principles. Though the project remains in the initial phase, results of phase one will in be beneficial to the bryozoan research community. Having a unified database allows researchers to obtain maximal data from one source. The completion of the remaining phases will make access to this database more expedient.



Participants

Adams, William, 6431 N. Sheridan Road,
Chicago, Illinois 60626. Permanent address:
7505 S St. Louis, Chicago, IL 60652
wadams2@luc.edu

Angielczyk, Kenneth, Dept. of Geology, Field
Museum of Natural History, 1400 S Lake Shore
Drive, Chicago IL, 60605
kangielczyk@fieldmuseum.org

Bespalova, Ioulia, 1294 Blanchard Campus
Center, Mount Holyoke College, 50 College St.,
South Hadley, MA 01075. Permanent address:
345 Farrell St Apt. 312 S. Burlington, VT 05403
bespa20i@mtholyoke.edu

Boone, James, Dept. of Zoology, Insect, Field
Museum of Natural History, 1400 S Lake Shore
Drive, Chicago IL, 60605
jboone@fieldmuseum.org

Cacioppo, Joseph A., 5220-3 S. Kimbark Ave.,
Chicago, IL 60637
JosephCacioppo@uchicago.edu

Calwal, Tyler
tcalway@fieldmuseum.org

Czekanski-Moir, Jesse Dept. of Zoology,
Insect, Field Museum of Natural History, 1400
S Lake Shore Drive, Chicago IL, 60605,
jczekanskimoir@fieldmuseum.org

Davion, Edna Dept. of Zoology, Insect, Field
Museum of Natural History, 1400 S Lake Shore
Drive, Chicago IL, 60605,
edavion@uchicago.edu

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

Dikow, Torsten, BioSynCenter, Field
Museum of Natural History, 1400 S Lake
Shore Drive, Chicago IL, 60605
tdikow@fieldmuseum.org

Hicks, Austin, 26 East Pearson Apt 402
Chicago, IL 60611. Permanent address: 132
Oak Grove, Parchment, MI 49004
ahicks3@luc.edu

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

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

Lisa C. Hung, 600 S. Dearborn St. Apt.
1308, Chicago, IL 60605
lisahungry@gmail.com

Jaszlics, Andrea
ajaszlic@fieldmuseum.org

Kalita, Kristin, 1052 W. Rosemont Avenue
Apt. 2 Chicago, IL 60660. Permanent
address: 507 Windridge Dr., Chesterton, IN
46304, kkalita@luc.edu

Lidgard, Scott Dept. of Zoology, Insect,
Field Museum of Natural History, 1400 S
Lake Shore Drive, Chicago IL, 60605,
slidgard@fieldmuseum.org



Loehrer, Elizabeth, 1247 W. Arthur Ave, Apt. 1, Chicago, IL 60626. Permanent address: 6725 Creekside Lane, Indianapolis, IN 46220
eloehre@luc.edu

Lopez, Gabrielle, 3144 N Ridgeway Ave. Apt. 2, Chicago, IL 60618. Permanent address: 1973 Allendale Dr. Toledo, OH 43611-1701
gabrielle.lopez@mymail.roosevelt.edu,

Lumbsch, Thorsten, Dept. of Botany, Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago IL, 60605
tlumbsch@fieldmuseum.org

Lyons, Kathleen
klyons@fieldmuseum.org

Makovicky, Peter, Dept. of Geology, Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago IL, 60605
pmakovicky@fieldmuseum.org

Mbatchou, Joelle, DePaul University, 1 E. Jackson Blvd., Chicago, IL 60604
joellesophya@yahoo.fr

Newton, Alfred, Dept. of Zoology, Insect, Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago IL, 60605
anewton@fieldmuseum.org

Parham, James, BioSynC, Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago IL, 60605
jparham@fieldmuseum.org

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

Quach, Bryan, Mailbox #2791; 6431 North Sheridan Rd.; Chicago, IL 60626.
Permanent address: 301 East King Street; Fairfield, IL 62837, bquach@luc.edu

Sierwald, Petra, Dept. of Zoology, Insect, Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago IL, 60605,
psierwald@fieldmuseum.org

Sjodin, Anna, Mailbox #3335, 6431 North Sheridan Rd., Chicago, IL 60626.
Permanent address: 2085 Old North Shore Road, Duluth, MN 55804
asjodin@luc.edu

Strozier, Lyniker
Sharlice01@yahoo.com

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

Thayer, Margaret, Dept. of Zoology, Insect, Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago IL, 60605, mthayer@fieldmuseum.org

Ware, Stephanie, Dept. of Zoology, Insect, Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago IL, 60605
sware@fieldmuseum.org

Wesener, Thomas, Dept. of Zoology, Insect, Field Museum of Natural History, 1400 S Lake Shore Drive, Chicago IL, 60605, twesener@fieldmuseum.org



