Special Thanks

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Contributors

The Darwin Symposium sponsored by the Natural Sciences Planning Committee, HHMI, Blakeslee Fund, Office of the President, and Smith College Lecture Committee

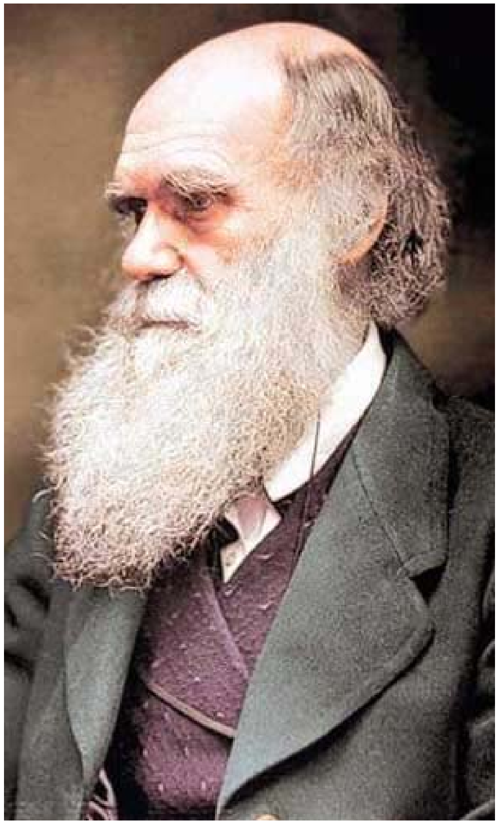
Guest Lecturers

Dr. Scott Edwards, Harvard University
Dr. Rob Knight, University of Colorado-Boulder
Dr. Elizabeth Kellogg, University of Missouri-St.Louis
Dr.Laura Katz, Smith College
Dr. Warren Allmon, Cornell University
Dr.Elliott Sober, University of Wisconsin at Madison

We are grateful to the following individuals for their contributions in planning and organizing this event

Chris Gentes, Printing Coordinator, Central Services, Smith College
Betse Curtis and staff, Dining Services, Smith College
Steve Campbell, Kathy San Antonio and the rest of the staff of the Office of College Events, Smith College

Program design by the Darwin Symposium Committee
(Robert Merritt, Gina Morrone and Bronwyn Bleakley)



The Natural Sciences Planning Committee proudly presents:

The Darwin Symposium

October 2nd & 3rd, 2009

Scientific Program

Friday, October 2

3:00 - 4:00 pm	**Dr. Scott Edwards, Harvard University** *Beyond Darwin's Dreams: Genomics of Host-Parasite Interactions* Stoddard Hall
4:15 - 5:15 pm	**Dr. Rob Knight, University of Colorado - Boulder** *Evolution of the Human Microbiome* Stoddard Hall

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Saturday, October 3

9:00 -10:00 am	**Dr. Laura Katz, Smith College** *The Tangled Branches of the Darwinian Tree of Life* Stoddard Hall
10:00 -10:30 am	Coffee Break Stoddard Hall Lower Level
10:30 -11:30 am	**Dr. Elizabeth Kellogg, University of Missouri – St. Louis** *Pigeons and Noodles and Domestication* Stoddard Hall
11:30 – 1:00 pm	**Lunch and Poster Sessions** *All Welcome* College Club
1:10– 2:45 pm	**Short Talks to be held in McConnell Hall**
3:00 - 4:00 pm	**Dr. Warren Allmon, Cornell University** *Darwin as Paleontologist* Stoddard Hall

* * *

Poster Abstracts

tion. Additionally, Flp Recognition Target (FRT) sites surround the whole rnpA-GFP operon.

The displacement of pSAVE is mediated by a second plasmid, pSWAP, which harbors phylogenetically different versions of *rnpA* and FLP recombinase. Site-specific recombination between the recombinase and those FRT sites in pSAVE excises the *rnpA* region, effectively eliminating pSAVE. The cells must now use the *rnpA* available in pSWAP.

The fitness cost of the novel versions of RNase P will be assessed by growth curves and the impact of this substitution on genome-wide is measured using DNA microarrays.

Cortisol Levels from Hair and Saliva in Dogs, *Canis familiaris*

Alyssa B. Ward and Virginia Hayssen
Department of Biological Sciences, Smith College, Northampton, MA 01063

Hair shows promise as a non-invasive cortisol collection medium compared with blood and provides a more accurate view of long-term hormone levels than point samples of blood, saliva, urine, or feces. Here we validate hair sampling in dogs (*Canis familiaris*) as a method of measuring basal cortisol values in a non-stressful environment. We predicted that hair and salivary cortisol levels measured over the same time period would be positively correlated. Hair and saliva samples were collected from 23 Labrador Retrievers and 25 German Shepherd Dogs in their homes. We determined basal hair cortisol values using a wash, powder, and methanol extraction protocol established for Rhesus Macaques. Cortisol levels were compared between a new hair growth sample and several concurrent saliva samples. We report a significant positive correlation between salivary and hair cortisol ($R^2 = 24.2\%$, $p = 0.001$), validating hair sampling as a means to measure basal hypothalamic-pituitary-adrenal (HPA) activity.

identified. Using starch gel electrophoresis, this study sought to augment the mtDNA data with information from nuclear genes by comparing allele frequencies at six polymorphic allozyme loci among populations of *D. ocoee* at and around the contact zone. Previous studies have found allozyme frequencies tend to corroborate mitochondrial sequence data, indicating similar patterns of geographic differentiation among populations. However, the allele frequencies determined by this study do not correlate with the mtDNA data. They show little differentiation between populations in excess of that expected from isolation by distance, suggesting that they belong to the same biological species.

Experimental Evolution of RNase P: focus on the protein subunit

Paula Turini
Department of Biological Sciences, Smith College, Northampton, MA 01063

RNAse P is essential for the *in vivo* cleavage of the 5' end of tRNAs in bacteria and consists of a protein subunit (*rnpA*) and a ribosomal catalytic subunit. My master's thesis involves the investigation, at the molecular level, of the fitness costs inherent to the distinct versions of the *rnpA* gene in *E.coli* cells.

In order to get *E.coli* cells to rely on phylogenetically different versions of *rnpA*, we knocked out the single chromosomal copy of the gene and artificially engineered a plasmid (pSAVE) to express the essential protein. Subsequently, pSWAP – a plasmid containing a diverse *rnpA* gene - displaces pSAVE by site-directed recombination (FLP-FRT recombination) resulting in a cell where RNase P is composed of its wild-type RNA subunit in combination with a heterologous protein subunit.

The deletion of the single chromosomal copy of *rnpA* was made using a modified version of the Datsenko and Wanner (2000) method. In this method, the plasmid pKD46 promotes homologous recombination between the target region and a PCR-generated linear fragment comprising a selective marker. The antibiotic marker replaces the target gene and the construction can then be selected. In our case, the target gene is *rnpA* and pSAVE must be expressed in advance for cell survival. pSAVE was previously constructed in our laboratory and consists of the wild type *rnpA* gene under the *lacZ* promoter and an artificial ribosome binding site (RBS). For screening purposes, a GFP gene was inserted as part of the same operon. Finally, a terminator sequence ensures the end of operon transcrip-

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The Natural Sciences Planning Committee
&
The Darwin Symposium Committee

request the pleasure of your company
at a Wine and Cheese Reception
for

The Darwin Symposium

Friday, October 2, 2009
5:30 — 7:00 pm
Ford Hall

ID Required

1:10 - 1:30pm	103	**Bronwyn H. Bleakley (Chair)** *Application of an interacting phenotype model of cannibalism in an endangered isopod*
	B 05	**Meaghan Hall (Chair) & Laura Katz** *On the nature of species: insights from ciliates*
	B 15	**Laura Wegener Parfrey (Chair) & Laura Katz** *Nuclear dynamics during the life cycle are influenced by food source in* Allogromia laticollaris *strain CSH (Foraminifera)*
1:35 - 1:55pm	103	**David Lahti, Norman Johnson*, & members of the Relaxed Selection and Trait Loss NESCENT working group** *Relaxed selection in the wild*
	B 05	**Mark A. Farmer & Andrea Habura** *Using Protistan Examples to Dispel the Myths of Intelligent Design*
	B 15	**Zhiyi Sun** *Evolutionary Forces Driving Genome Reduction in* Prochlorococcus
2:00- 2:20pm	103	**L. David Smith** *The role of phenotypic plasticity in a marine biological invasion: taking cues from the environment*
	B 05	**Mark Aldrich** *From Darwin to Dayton: Cartoonists Interpret Evolution, 1860-1925*
	B 15	**A.M. Kovner & L.A. Katz** *Multiple origins of scrambled coding domains within rapidly evolving germline sequences in ciliates*
2:25- 2:45pm	103	**Jesse Bellemare** *Proximate Environmental Correlates and Ultimate Evolutionary Sources of Species Richness Gradients in Temperate Deciduous Forest*
	B 05	**Michele L. Aldrich & Alan E. Leviton** *Darwin and the Gardener's Chronicle, 1841-1877*
	B 15	**Amy T. Toulson Wimmer & Robert Merritt *** *Genetic structure in the Mohave Desert endemic* Yucca brevifolia

* speaker / presenter

All short talks will be held in McConnell Hall

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losing support as molecular technologies are applied more frequently to study the biogeography and distribution of microorganisms (Foissner, 2006). Previous molecular biogeographic studies show that ciliate diversity is in fact much larger than anticipated (Katz et al., 2005). The aim of this project is to evaluate the levels of diversity in Oligotrich and Choreotrich ciliates (two subclasses of the class Spirotrichea) in near coastal sediments over space and time to determine spatial and temporal scales of microbial diversity.

Ciliates: Diverse Microorganisms

Gladys Palaguachi[1], Meaghan Hall[1], Laura Katz[1, 2]

[1]Department of Biological Sciences, Smith College, Northampton, Massachusetts, 01063; [2]Program in Organismic and Evolutionary Biology, University of Massachusetts, Amherst, Massachusetts, 01003

Every organism plays an important role in nature, including the often overlooked microbial lineages such as ciliates. Although we have gained a great deal of information about ciliate diversity, additional investigation is needed to understand more about these complex microorganisms. We hypothesize that the unique genome architecture of ciliates (i.e. nuclear dimorphism) plays a role in their evolution, consequently obscuring our taxonomic understanding. Further analysis of nuclear and mitochondrial genes of ciliates is essential in order to continue to reconstruct evolutionary trees of ciliates. Here we present our initial research on the use of mitochondrial characters to discern phylogenetic relationships among the ciliates. We collected different samples from nature, including from water in the Lyman Plant House, and isolated Loxophyllum sp., Coleps sp., and Blepharisma sp. Images of single cells of these ciliates were photodocumented and then the genome of the same cells were amplified for molecular studies. Through traditional PCR we examined their mitochondrial and nuclear small subunit ribosomal DNA (SSU rDNA) for further understanding of evolutionary patterns.

Allozyme analysis of a contact zone between two mtDNA haplotypes in Desmognathus ocoee (Amphibia: Plethodontidae)

Noëlle K. J. Bittner[1], Stephen G. Tilley[1] and Joseph Bernardo[2]

[1]Department of Biological Sciences, Smith College, Northampton, MA, [2]Cornell University, Ithica, NY

Recent phylogenetic analyses of mitochondrial DNA (mtDNA) sequences by Yoke et al. (in prep) have revealed five distinct well supported clades within the salamander species traditionally called *Desmongnathus ocoee* Nicholls. This information suggests that the organisms currently recognized as *D. ocoee* may belong to more than one species. In the Blue Ridge Mountains of northeastern Georgia, a contact zone between two mtDNA haplotypes has been

MDA, a mosquito had a 7.0% probability of infection. In addition to monitoring the progress of the treatment program in Kirare, the information being collected in this study is extremely important in providing comparisons and evaluations of the monitoring tools available over the entire course of the treatment period.

Exploring Phylogenetic Relationships of the Testate Lobose Amoebae

Jian Hua Lin[1], Truc B. Nguyen[1], Daniel J. G. Lahr[2], and Laura A Katz[1,2]

[1]Department of Biological Sciences, Smith College, Northampton, MA 01063, USA [2]Program in Organismic and Evolutionary Biology, University of Massachusetts, Amherst, MA 01003, USA

The testate lobose amoebae (Arcellinida), a monophyletic subgroup in the 'Amoebozoa,' are defined by the presence of a test. Although Arcellinida makes up a large portion of amoeboid species, the reconstruction of the evolutionary history of Arcellinida based on molecular data is still at its beginning. Here we aim to broaden the organisms sampled in order to test the traditional classification that is based on shell characters. We reconstruct the relationships of Cryptodifflugia operculata, Arcella hemisphaerica and Arcella vulgaris among other 'Amoebozoa' based on a preliminary analysis of the small subunit ribosomal DNA (SSU-rDNA). Our analysis shows many genera as non-monophyletic, which suggests that the relationships within the Arcellinida are prone to major modifications using molecular approaches. Our ultimate goal is to sample protein coding genes and more taxa representing other families in order to fully test the morphology-based classification.

Genetic Diversity of Ciliates in Coastal Sediment

Hannah Jaris, **Danielle Vazquez[1]**, Maiko Tamura, and Laura Katz[1,2]

[1]Program in Organismic and Evolutionary Biology, University of Massachusetts, [2]Department of Biological Sciences, Smith College

Planktonic ciliates play an important role in both the food webs and health of the world's oceans as these organisms: 1) provide a critical link between bacteria and larger zooplankton and 2) are important grazers on harmful algal bloom species (Katz et al., 2006). However, little is known about their distribution. Martinus Willem Beijerinck's famous metaphor says that "in microorganisms, everything is everywhere, the environment selects." And yet this hypothesis is quickly

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Insights into the Evolution of Heterolobosea from Multigene Molecular Analyses
Dominique Barbeau, Jessica Grant, Laura Wegner Parfrey, and Laura A. Katz

Differential proteome profiling analysis of male and female murine skeletal muscle following a single bout of exercise
Yutian Gan, Mohini Kulp, Laura Smith, Stylianos P Scordilis

Identifying the life cycle and classification of a novel organism with similarities to Vampyrellidae
Anastasia Gant, Laura Wegner Parfrey, Jessica Grant and Laura A. Katz

Genetic Diversity of Ciliates in Coastal Sediment
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Comparing PCR and Mosquito Dissection for Monitoring the Progress of Mass Drug Administration Programs for Elimination of Lymphatic Filariasis in Tanzania.
Sandra J. Laney, Stephen Magesa, Erling M. Pedersen, Paul E. Simonsen, Deus Ishengoma, Theophil Rwegoshora, Lea T. Occhialini, Caitlin J. Buttaro, Jenna D. Lovaas, and Steven A. Williams.

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Alyssa B. Ward and Virginia Hayssen

Posters will be presented in the Smith College Club.
Lunch will be served. All welcome.

From Darwin to Dayton: Cartoonists Interpret Evolution, 1860-1925

Mark Aldrich
Department of Economics, The Gables, Smith College, Northampton, Massachusetts, 01063

Darwin's writings coincided with the rise of a mass popular press and technical improvements that allowed low cost cartooning. The man and his work proved to be a cartoonist's dream and the illustrators in turn, introduced evolution to a popular audience, both criticizing and defending it. While few cartoons focused on evolutionary mechanisms, a central theme was human descent, and many images trace the increasing skepticism with which the Americans viewed the idea of progress. Artists also employed evolution as a humorous gimmick and to comment on a wide range of social and cultural issues. Sometimes it might be subversive -- spoofs of monkeys in tuxedoes skewered the pretensions of the nouveau riche. But by the Scopes trial evolution had become a symbol for all of science, and belief came to symbolize cultural enlightenment.

2:00—2:00 pm, McConnell Hall B05

Darwin and the Gardener's Chronicle, 1841-1877

Michele L. Aldrich[1] and Alan E. Leviton[2]
[1]Department of Biological Sciences, Smith College, Northampton, Massachusetts, 01063 [2]Department of Herpetology, California Academy of Sciences, 55 Music Conservatory Drive, Golden Gate Park, San Francisco CA 94118

In January 1841, the *Gardener's Chronicle* (GC), a weekly horticultural newspaper, began publication. The botanist John Lindley edited GC until his death in 1865, when botanist Maxwell Masters took over; both shared scientific interest with Charles Darwin (orchids and teratology respectively). Darwin first published an item in GC in August 1841. Across his life, a plurality of his printed articles appeared in the GC. In 1869, *Nature* started publishing and Darwin shifted allegiance to publish many short papers there (in part to address a wider range of topics), although he continued to send occasional pieces to the GC until 1877 Among the advantages of GC publication for Darwin were its fast turn-around (many of his articles were published within a week of submission) and large circulation (6,000 subscribers, reflecting the passion of Victorian England for gardening but nonethess remarkable for its time). Darwin published notes and queries in GC on double flowers, mould formation, soils, manures, and other horticultural topics. Several of his articles related to major topics addressed in his books, such as on orchids, hybrids, bees and fertilization of flowers,

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contents. Rather, it feeds by ingesting algae. This suggests that this new isolate is related to the Vampyrellidae but represents a new clade. An SSU-rDNA genealogy supports this hypothesis. The new isolate is sister to other sequenced representatives of the Vampyrellidae, but the SSU sequence is 8% divergent. With further analysis and observational study, we will describe this new clade of amoebae.

Comparing PCR and Mosquito Dissection for Monitoring the Progress of Mass Drug Administration Programs for Elimination of Lymphatic Filariasis in Tanzania.

Sandra J. Laney, Stephen Magesa, Erling M. Pedersen, Paul E. Simonsen, Deus Ishengoma, Theophil Rwegoshora, Lea T. Occhialini, Caitlin J. Buttaro, Jenna D. Lovaas, and Steven A. Williams.
Department of Biological Sciences, Smith College, Northampton, MA 01063

Delivery and coverage of mass drug administration (MDA) is vital to the effectiveness of the lymphatic filariasis elimination effort. Equally important is determining when transmission has been reduced below sustainable levels. Thus, easy, effective and accurate monitoring of infection levels is critical to the elimination program. This study provides preliminary evidence of effective monitoring using the mosquito as an indicator (xenomonitoring) and aims to produce a comparison of measures across a longitudinal survey in Kirare Village, Tanzania before and after a treatment program. The baseline pre-MDA mosquito infection rates were determined by the collection of mosquitoes during the period of November 2003 through September 2004 by placing light traps in 50 randomly selected houses once per week. The dissection of 5,396 mosquitoes yielded a 1.4% rate of infectivity as determined by the presence of Wuchereria bancrofti L3 stage larvae. The post-MDA dissection results of 6,608 mosquitoes collected from Oct. 2004 through Sept. 2005 yielded a 0.4% infectivity rate. This 71% decrease in infectivity rate is significant with a ÿ2 = 37.30, $p<0.0001$. In addition to monitoring by dissection, 1,514 mosquitoes collected from January-July 2004 were tested in 135 pools using the molecular xenomonitoring (MX) PCR assay for W. bancrofti. The PCR assay estimates the mosquito infection rate by determining the presence of any stage of the parasite. Post-MDA collections of 2,374 mosquitoes collected from Jan-Oct. 2005 were tested by PCR in 201 pools. After only one round of MDA a decrease of 55% in the mosquito infection rate was found as assessed by MX. Pre-MDA, a mosquito had a 15.6% probability of infection with W. bancrofti estimated by Poolscreen v.2.0.2). Post-

single bout of eccentrically-biased exercise in skeletal muscle will shed light on the molecular mechanisms underlying adaptation, as well as their gender specificity. Exercise-naïve male and female mice ran downhill (-15°) on a treadmill at 25 m min^{-1} for 15 min and 800 mg of total biceps brachii extract was electrophoresed on pH 5-8 2-D gels. The resulting spots that changed at least +/- 2-fold and were significantly different ($p<0.05$) relative to unexercised controls of the appropriate gender using PDQuest 8.0 were analyzed by LC/MS-MS and identified using BioWorks 3.3.1. This analysis showed significant proteome remodeling subsequent to downhill running. The expression change patterns were followed at 0, 24, 48, 72 and 168 hrs post-exercise (PX) and significant changes were observed in 4 NCBI KOG groups. Both myofibrillar and cytoskeletal protein remodelings were noted, as well as decreased expression of creatine kinase. Nearly all of the glycolytic enzymes were up-regulated. The cellular heat shock protein responses were significant and specific. Roughly the same number of protein spots changed in females and males, but the females peaked at 24 hr PX, whereas in males the peak was at 72 hr PX.

Identifying the life cycle and classification of a novel organism with similarities to Vampyrellidae

Anastasia Gant[1,2], Laura Wegner Parfrey[3], Jessica Grant[1] and Laura A. Katz[1,3]
[1]Department of Biological Sciences, Smith College, 44 College Lane, Northampton, MA ; [2]Department of Chemistry, Smith College, 44 College Lane, Northampton, MA ; [3]Program in Organismic and Evolutionary Biology, University of Massachusetts, 611 North Pleasant Street, Amherst, MA

Often times we work with just a certain organism's DNA, and examine sequences without ever actually observing the organism itself. However, having an understanding of both the genetic information and the physiological and morphological characteristics of the organism studied is ideal. We isolated a unique amoeba from local environmental sampling and have established cultures of this organism. Distinct physiological, morphological, and life cycle characteristics suggest that this organism is closely related to the Vampyrellidae, a group of filopodial (thin pseudopodia) amoeboid protists. Through my observations, we established a model of the organisms' life-cycle, feeding behaviors, and its reaction to varying environmental conditions. While there are many similarities between this new amoeba and vampyrellids, it does not share the defining characteristic of the group—drilling holes in cells and sucking out there

and natural selection. Darwin used GC readers to collect data and to try out ideas that were more fully developed in his longer articles in scientific journals published by the Linnaean Society and the Geological Society of London. Arguably his most sustained reporting (1852-57) in GC involved seed viability across time and under conditions such as salt-water immersion, questions important for theories of species dispersal and longevity that related to evolution. Darwin worked to ensure favorable reviews of his books in the GC, and usually succeeded in obtaining them.
2:25—2:45 pm, McConnell Hall B05

Proximate Environmental Correlates and Ultimate Evolutionary Sources of Species Richness Gradients in Temperate Deciduous Forests

Jesse Bellemare
Department of Biological Sciences, Smith College, Northampton, Massachusetts, 01063

In this study I investigated a prominent plant species diversity gradient in the Temperate Deciduous Forests of the northeastern United States to ask whether long-term evolutionary processes, such as phylogenetic niche conservatism, may ultimately explain variation in the numbers of species present along different portions of a key environmental gradient, soil pH and calcium content. Analyses of the phylogenetic 'depth' of plant communities along the soil pH/calcium gradient and parsimony-based reconstructions of the ancestral calcium niche for a number of angiosperm lineages suggests the ecological 'zone of origin' for angiosperm lineages in Temperate Deciduous Forest vegetation was on fertile, calcium-rich soils. These habitats also house the greatest angiosperm plant diversity in contemporary plant communities. This result indicates that long-term phylogenetic niche conservatism may be an important factor underlying species diversity patterns in modern forest plant communities. Additionally, I found that basally-derived or early-diverging angiosperm lineages were often most abundant and dominant on favorable, calcium-rich soils, while later-diverging angiosperm lineages were more dominant on less-favorable, calcium-poor soils. This pattern suggests the possibility of niche preemption by early-diverging angiosperm lineages in favorable, nutrient-rich habitats. The results of this study highlight the potential for long-term evolutionary and ecological dynamics to play a significant role in determining the structure and species diversity of contemporary communities.
2:25—2:45 pm, McConnell Hall 103

Application of an interacting phenotype model of cannibalism in an endangered isopod

Bronwyn H. Bleakley
Department of Biological Sciences, Smith College, Northampton, Massachusetts, 01063

Cannibalism is often modeled as a threshold trait with environmental influences triggering a cannibalistic attack. One such "environmental" influence is the body size of a potential victim. Traits that depend at least in part on the characteristics of a social partner are termed "interacting phenotypes". Interacting phenotype models of cannibalism highlight the importance of both the absolute body size of a potential victim and that of its relative body size as cues for the induction of cannibalism and are sensitive to the variance of the included traits. However, few empirical studies have explored the specific influences of the social environment on the induction of cannibalism. *Thermospaeroma thermophilum* is an endangered freshwater isopod found natively in a single thermal spring in the southwestern US. Cannibalism is thought to contribute significantly to mortality and thus poses a management difficulty for this species. We test an existing interacting phenotypes models for cannibalism and discuss the implications for cannibalistic species that are also of conservation concern.

1:10—1:30 pm, McConnell 103

Using Protistan Examples to Dispel the Myths of Intelligent Design

Mark A. Farmer[1] and Andrea Habura[2]
[1]Department of Cellular Biology, University of Georgia ; [2]Wadsworth Center, New York State Department of Health and Department of Biomedical Sciences, School of Public Health, The University at Albany

In recent years the teaching of the religiously-based philosophy of intelligent design (ID) has been proposed as an alternative to modern evolutionary theory. Advocates of ID are largely motivated by their opposition to naturalistic explanations of biological diversity, in accordance with their goal of "challenging the philosophy of scientific materialism and the false scientific theories that support it" (Discovery Institute 2003). ID has been embraced by a wide variety of creationists who promote highly questionable claims that purport to show the inadequacy of evolutionary theory, which they consider to be a threat to a theistic worldview. We find that examples from protistan biology are well suited for providing evidence of many key evolutionary concepts, and have often been misrepresented or roundly ignored by ID advocates. These include examples of adaptations and radiations which are said to be statistically impossible, as well as examples of speciation both in the laboratory and as documented in the fossil re-

Insights into the Evolution of Heterolobosea from Multigene Molecular Analyses

Dominique Barbeau[1], Jessica Grant[1], Laura Wegner Parfrey[2], and Laura A. Katz[1,2]
[1]Department of Biological Sciences, Smith College, 44 College Lane, Northampton, Massachusetts 01063, USA; [2]Program in Organismic and Evolutionary Biology, University of Massachusetts, 611 North Pleasant Street, Amherst, Massachusetts 01003, USA

The origin and diversification of eukaryotes is poorly understood, in part due to the paucity of comparable morphological characters and the limited molecular data available for many groups. The Heterolobosea are a group of amoeboflagellates that was first recognized in 1985 on the basis of shared ultrastructural characters including eruptive pseudopodia, disc-shaped mitochondrial cristae, and lack of defined dictyosomes. This group includes Naeglaria, the causative agent of primary amebic meningoencephalitis, a fatal infection of the central nervous system, although most Heterolobosea are free living. The major groups within Heterolobosea are the Vahlkampfiidae, characterized as uninucleate and having a nucleolus that persists during mitosis; the Gruberellidae, which can be uninucleate or multinucleate and whose nucleoli fragment during mitosis; and the Acrasidae, the only group known to form fruiting bodies. Additionally, there are several genera of uncertain taxonomic position within the Heterolobosea. Historically, the Valkampfiidae and the Gruberellidae have been combined as the Schizopyrenida, though its monophyly has not been supported in molecular analyses. The current classification of Heterolobosea is based on ultrastructural data—subcellular organization—and has not been rigorously tested with molecular analysis. We have sequenced SSU-rDNA and four protein-coding genes from eight species of Heterolobosea with representatives from all three major groups and several incertae sedis genera. Here we use SSU-rDNA and multigene phylogenetic analyses to specifically test the 1) sister relationship of Heterolobosea with Jakobida, 2) established classification within the Heterolobosea, and 3) monophyly of the genus Tetramitus. The resulting trees are also used to assess morphological evolution within the Heterolobosea.

Differential proteome profiling analysis of male and female murine skeletal muscle following a single bout of exercise

Yutian Gan, Mohini Kulp, Laura Smith, Stylianos P Scordilis.
Biological Sciences, Biochemistry, Center for Proteomics, Smith College, Northampton, MA

Identifying the array of proteins that change expression following a small *Prochlorococcus* share many genomic characteristics with chloroplasts and bacterial endosymbionts (Dufresne et al.2005). However as free-living bacteria, *Prochlorococcus* are not known to be subject to similar ecology constraints. In order to uncover the evolutionary causes of genome shrinkage in small *Prochlorococcus* genomes, we downloaded 17 complete genomes sequences of marine *Prochlorococcus* and *Synechococcus* from NCBI and carried out comparative genomic analyses. We first defined a comprehensive set of 1186 orthologous genes and a non-redundant gene table for all 17 genomes. Using this data we reconstructed ancestral gene states and predicted gene loss and gene gain across the phylogenetic tree. We then investigated selection and mutation rates for the set of both global orthologous genes and gene loss data. The resulting data demonstrated (1) small *Prochlorococcus* genomes were/are experiencing stronger selection than big *Prochlorococcus* and non-reductive *Synechococcus* genomes, thus rejecting the genetic drift hypothesis; and (2) the majority of lost genes in small *Prochlorococcus* genomes are in the high dN/dS ratio spectrum in extant non-reductive *Synechococcus* genomes, including some DNA repair genes. Loss of these DNA repair genes might account for observed elevated protein evolution rates in small *Prochlorococcus* genomes.

1:35—1:55 pm, McConnell Hall B15

Genetic Structure in the Mojave Dessert endemic *Yucca brevifolia.*

Amy T. Toulson Wimmer and Robert B. Merritt
Department of Biological Sciences, Smith College, Northampton, MA 01063

We used electrophoretic analysis of glucose-6-phosphate allozymes to investigate genetic structure in the Mojave Dessert endemic *Yucca brevifolia*. To test the hypothesis that, because of geographic isolation, most variation in allele frequencies would be between populations, we sampled three subpopulations from each of five populations: Arizona, Joshua Tree, Mojave, Western Mojave, and Utah. Five GPI alleles were identified with the three most common alleles present in all populations sampled. Allele frequencies differed significantly between all five populations, as well as between subpopulations in both the Joshua Tree and Arizona populations. We also tested the hypothesis that strong localized genetic structure could result from the high proportion of recruitment attributed to vegetative reproduction by some authors. Based on GPI data from an intensively sampled one-hectare plot, genotypes were randomly distributed and met Hardy-Weinberg expectations. Thus, sexual reproduction through outcrossing is likely the principal mode of recruitment in *Y. brevifolia* at this site.

cord. Because many biologists may not be familiar with the richness of the protist evolution dataset or with ID-based criticisms of evolution, we provide examples of current ID arguments and specific protistan counterexamples.

1:35—1:55 pm, McConnell Hall B05

On the nature of species: insights from ciliates

Meaghan Hall[1], Laura Katz[1,2]
[1]Department of Biological Sciences, Smith College, Northampton, Massachusetts, 01063; [2]Program in Organismic and Evolutionary Biology, University of Massachusetts, Amherst, Massachusetts, 01003

The multitude of species concepts currently accepted by the scientific community (e.g. morphological, biological, phylogenetic) are united in that they all aim to capture the process of divergence between populations. For example, the Biological Species Concept (BSC) defines a species as a natural group of organisms that is reproductively isolated from other such groups. Our conceptualization of species greatly influences our understanding of evolution. Here we synthesize nearly a century of research on two ciliate genera, Paramecium and Tetrahymena, that challenges the prevailing notions on the nature of species. In these taxa, there is a discordance between morphology, mating behavior, genetics, and perhaps even epigenetics, features assumed to be correlated under the BSC and other contemporary species concepts. We argue that the multifaceted evolutionary patterns of ciliates are not exceptions to the rule but rather vivid examples of the complexity of life and the dynamism of evolution.

1:10—1:30 pm, McConnell Hall B05

Relaxed selection in the wild

David Lahti[1], **Norman Johnson[2]**, and members of the Relaxed Selection and Trait Loss NESCENT working group.
[1]Queens College; [2]University of Massachusetts , Amherst, Massachusetts, 01003

Natural populations often experience "relaxed selection", the weakening or removal of a source of selection that had been important in the maintenance of one or more traits. Here we highlight recent studies that explore the effects of such changes on traits in their ecological contexts. In a few systems, such as the loss of armor in stickleback, the genetic, developmental and ecological bases of trait evolution are being discovered. These results yield insights into whether and how fast a trait is reduced or lost under relaxed selection. We provide a prospectus and a framework for understanding relaxed selection and trait loss in natural populations.

1:35—1:55 pm, McConnell Hall 103

Multiple origins of scrambled coding domains within rapidly evolving germline sequences in ciliates

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The canonical view that genomes are fixed within species is challenged by observations of intraspecific variation in genome content. In ciliates, extensive chromosomal rearrangements occur during development of the somatic macronuclear genome. Here we show that coding domain segments in *Chilodonella uncinata* (Phyllopharyngea) are scrambled in the germline micronuclear genome. Comparing two strains of C. uncinata reveals that conserved macronuclear-destined sequences (MDSs) are embedded within rapidly evolving micronuclear sequences. Gene scrambling is only known from the distantly related class Spirotrichea, indicating multiple origins of this genomic feature. Intriguingly, the Spirotrichea and Phyllopharyngea are also united in having transient polytene chromosomes, gene-sized somatic chromosomes, and elevated rates of protein evolution. We hypothesize that this suite of characters plays an adaptive role by shaping patterns of molecular evolution in these lineages.

2:00—2:20 pm, McConnell Hall B15

Nuclear dynamics during the life cycle are influenced by food source in *Allogromia laticollaris* strain CSH (Foraminifera)

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The nucleus and the genome contained within are the defining features of eukaryotic cells. The factors that regulate nuclear size and content are beginning to be elucidated in model systems where changes in nuclear size are driven by cell size rather than DNA content. It is unclear whether these emerging models apply only to organisms with haploid/diploid life cycles such as fungi or to eukaryotes more broadly, which can vary dramatically in nuclear size and content during the life cycle. Here we show that nuclear and cell size are correlated in the amoeboid species Allogromia laticollaris CSH (Foraminifera) throughout a 6000-fold range in nuclear volume. The life cycle of A. laticollaris is an alternation between uninucleate and multinucleate adults and nuclear dynamics most likely include polyploidy and genome processing. Our results support the hypothesis that nuclear size is regulated by cell size, but intriguingly also demonstrate variation in the nuclear to cell size relationship based on food source. Further, food source has a significant impact on nuclear DNA content in A. laticollaris. Foraminifera reproduce by segregating the

parental genome into numerous daughter nuclei, thus additional DNA in the form of increased ploidy levels may increase organismal fitness by raising the number offspring produced. We hypothesize that environmental regulation of DNA content is widespread means of regulating organismal fitness for Foraminifera, and perhaps other large, single-celled eukaryotes with dynamic genomes. These results suggest that nuclear size regulation varies according to environmental factors.

1:10—1:30 pm, McConnell Hall B15

The role of phenotypic plasticity in a marine biological invasion: taking cues from the environment

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Following a biological invasion, both introduced and resident species must adjust to changes in their environment, and phenotypic plasticity (environmentally induced change in a character) provides a means for within-generation response. The role of phenotypic plasticity in marine invasions has received little study, but its influence may be great for several reasons. First, plastic phenotypes are ubiquitous in marine organisms. Second, phenotypic plasticity can impact ecological interactions between introduced and native species. Third, phenotypic responses have the potential to generate temporal and spatial patterns in ecologically important traits rapidly after an introduction. The spread of the European green crab Carcinus maenas to the northwest Atlantic Ocean provides an excellent opportunity to study post-invasion effects of phenotypic plasticity. Experiments show that claw size in C. maenas responds to natural variation in breakage resistance of the native snail, Littorina obtusata. In turn, L. obtusata builds thicker shells in the presence of the introduced crab. Latitudinal differences in water temperature in the region influence the rate and the magnitude of induced responses in both species. Taken together, our data suggest that phenotypic plasticity may explain historical shifts and biogeographic patterns in predator trophic morphology and prey defenses in this invaded system.

2:00—2:20 pm, McConnell Hall 103

Evolutionary Forces Driving Genome Reduction in *Prochlorococcus*

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A group of marine Cyanobacteria *Prochlorococcus* have the smallest genomes of any photosynthetic organism (Rocap et al. 2003). These