95TH ANNUAL MEETING
OF THE
AMERICAN SOCIETY OF MAMMALOGISTS

12-16 JUNE 2015

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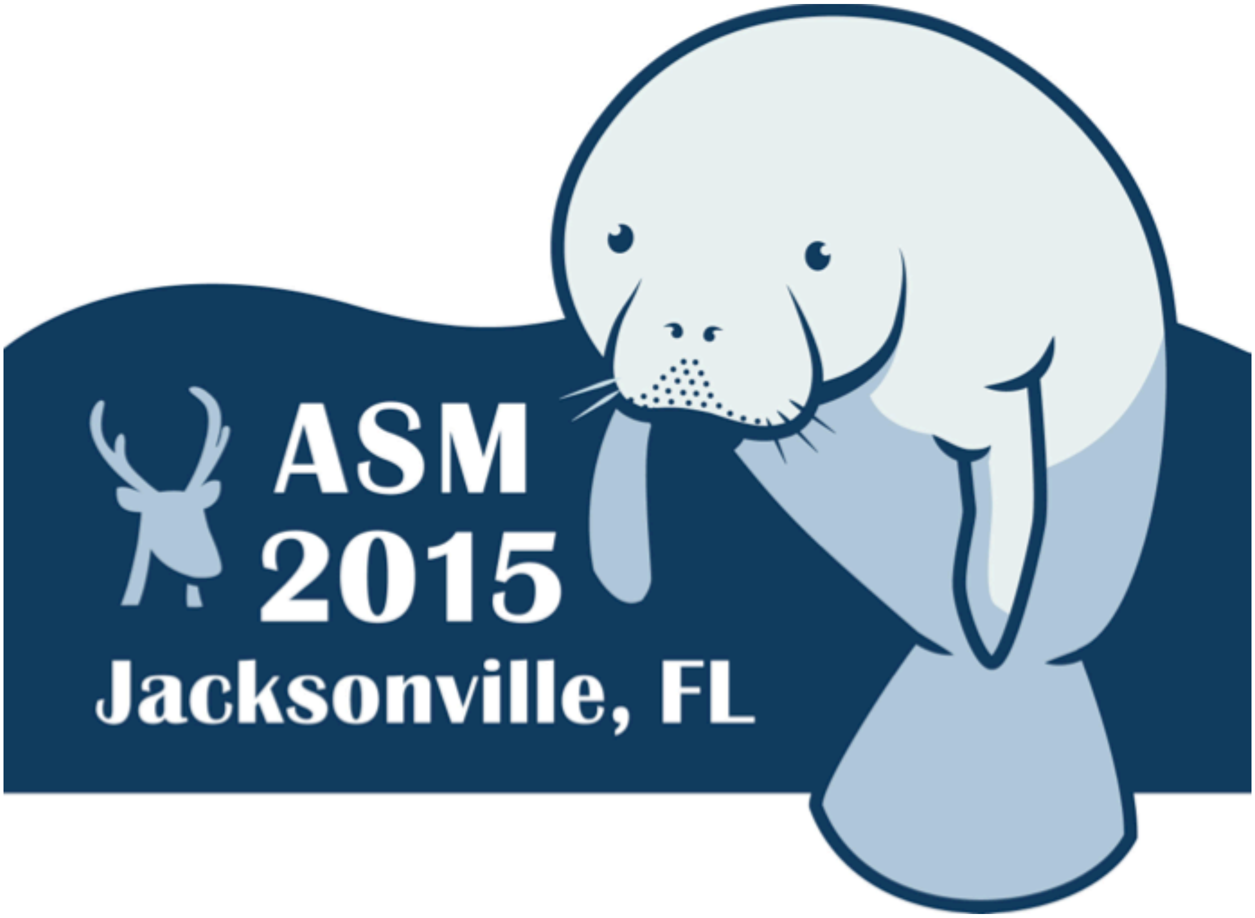
-JACKSONVILLE, FLORIDA-



ABSTRACT BOOK

The 2015 American Society of Mammalogists Annual Meeting logo features a Florida Manatee, an endangered mammal that inhabits waters of Jacksonville. t also includes a silhouette of a pronghorn, the symbol of ASM. The waves in the background represent the St. Johns River and Trout River as well as accentuate the city's costal location. The logo was designed by Cheng 'Lily' Li, a designer and illustrator.

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AMERICAN SOCIETY OF MAMMALOGISTS (ASM)

The American Society of Mammalogists (ASM) was established in 1919 for the purpose of promoting interest in the study of mammals.

AN OVERVIEW

In addition to being among the most charismatic of animals, mammals are important in many disciplines from paleontology to ecology and evolution. We, of course, are mammals and thus are in the interesting position of studying ourselves in quest of a greater understanding of the role of mammals in the natural world.

The ASM is currently composed of thousands of members, many of who are professional scientists. Members of the Society have always had a strong interest in the public good, and this is reflected in their involvement in providing information for public policy, resources management, conservation, and education.

The Society hosts annual meetings and maintains several publications. The flagship publication is the *Journal of Mammalogy*, a journal produced 6 times per year that accepts submissions on all aspects of mammalogy. The ASM also publishes *Mammalian Species* (accounts of individual species) and *Special Publications* (books that pertain to specific taxa or topics), and we maintain a mammal images library that contains many exceptional photographs of mammals.

We encourage you to peruse the ASM web site for information about mammals and the American Society of Mammalogists. Check out our interesting history by clicking on the Our History tab on the Archives Committee page. We hope it will stimulate your interest in mammals and further your appreciation of their importance.

ASM LEADERSHIP

The ASM is led by a group of scientists who are elected by the membership.

ASM COMMITTEES

Much of the work that the ASM does is accomplished through a large number of volunteer committees. These committees work to further the aims of the Society and the science of mammalogy as a whole.

ASM ENDORSES HUMAN DIVERSITY

The ASM is dedicated to ensuring the opportunity for active, equal participation in all ASM functions by all members, regardless of gender, race, ethnic background, age, physical disabilities, or sexual orientation.

http://www.mammalsociety.org/

TABLE OF CONTENTS

WELCOME

Welcome to the 95th annual meeting of the American Society of Mammalogists!

The next few days promise to be exciting, busy, and fun. In addition to a full slate of contributed papers and talks covering the latest research in mammalogy, we have scheduled symposia on two important themes: the conservation of Caribbean mammals and the application of emerging technologies to collections-based research. The first is very geographically relevant and will include researchers from Cuba and the Dominican Republic, providing a great opportunity to interact with colleagues from these countries while learning about some cool critters like hutias and solenodons. The second will demonstrate how use of emerging technologies such as genomic sequencing, stable isotope analysis, and CT-scanning to study museum specimens can generate important new insights into mammalian biology.

As part of our Society's commitment to research training and professional development, we are again hosting several pre-meeting workshops, which will take place the day before the regular meeting program begins. These events will provide important opportunities to learn how to publish peer-reviewed papers, how to capture and use digital collections data, and how to incorporate genomic sequencing and bioinformatics into your research. To read more about these workshops, please see the information posted on the meeting website.

In terms of oral presentations, we have a great roster of plenary session speakers. During the first plenary session, we will hear from some of our outstanding student members, including the 2014 recipients of the Hornaday Award (Erin Baerwald), the Shadle Fellowship (Nicté Ordóñez-Garza), and the ASM Fellowship (Melissa Merrick). At the second plenary, we will hear from a stellar group of more established mammalogists, including the 2014 recipients of the Merriam Award (Denise Dearing), Leopold Award (Lawrence Heaney), and Grinnell Award (Troy Best). In addition, we have a bonus presentation from the 2013 recipient of the Grinnell Award (Ricardo Ojeda). The meeting will conclude with a capstone presentation by Dr. Wayne Clough, whose career has integrated his passion for conservation with leadership of important national resources such as the Smithsonian Institution.

And, of course, there will be socializing! This important component of the meeting will begin with an event for new members and first time attendees on Friday night, followed by our traditional opening night social, when you greet old friends and meet new fellow mammalogists. On Saturday night, we will hold a student mixer, which is an important opportunity for this group of attendees to get together and share ideas and experiences. Sunday is the picnic, which will take place at Fionn McCool's Irish pub and will include live music. Monday night is our annual auction, which is always an entertaining event and which supports our Future Mammalogists Fund. Come, have some beer, and bring your checkbook…. The meetings will close with something new … rather than a formal closing banquet, we will be holding a Closing Social and Awards Ceremony at the River City Brewing Company. With this change, we hope that more meeting attendees will participate in our closing event and thus be present when we honor outstanding achievements in mammalogy.

In closing, I would like to thank our sponsors, exhibitors, and advertisers. Their support is critical to the success of many of our annual functions. Please take some time during the breaks and socials to stop by their tables and displays and be sure to let them know how much you appreciate their participation. Pick up a book, souvenir, or some mammal art.

And yes, there should be manatees!

Enjoy the meetings,

Eileen Lacey
President, American Society of Mammalogists

ACKNOWLEDGEMENTS

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ABSTRACTS

1^{E,TA}: A matter of toxins and fiber: selection of plant parts by sympatric herbivores

M. M. Crowell*, L. A. Shipley, J. S. Forbey, and J. L. Rachlow.

School of the Environment, Washington State University, Pullman, WA 99164 USA (MMC, LAS); Department of Biological Sciences, Boise State University, Boise, ID 83725 USA (JSF); Department of Fish and Wildlife, University of Idaho, Moscow, ID 83844 USA (JLR)

Mammalian herbivores face inherent risks from potentially toxic chemicals and fiber when consuming plants. However, the relative risk of toxins and fiber likely depends on the physiological adaptations of the forager. To better understand how mammalian herbivores respond to these risks, we collected fecal pellets from free-ranging pygmy rabbits (sagebrush specialists, *Brachylagus idahoensis*) and cottontails (generalists, *Sylvilagus nuttallii*) from 3 field sites in Idaho to investigate the proportion of sagebrush and the proportion of leaves (high toxin/low fiber) and stems (low toxin/high fiber) in their diets. We also conducted captive feeding trials during which rabbits were offered a choice between sagebrush leaves or stems. Free-ranging and captive pygmy rabbits consumed a greater proportion of sagebrush, and a greater proportion of sagebrush leaves relative to stems, than did cottontails. This result is supported by field observations of pygmy rabbits cropping smaller stem diameters of sagebrush than cottontails, which often clip off leaves and leave them on the ground. Our findings suggest that pygmy rabbits perceive fiber as a higher risk than toxins in sagebrush, whereas cottontails perceive toxins as a higher risk than fiber. This difference may reduce competition for food resources by these rabbits within sagebrush communities. Understanding how sympatric herbivores partition forage resources may help land managers focus on specific sagebrush communities that are best able to support sustainable diverse herbivore communities.

2^{E,TA**}: Genetic diversity in captive populations: the impact of inbreeding, drift, and selection

Janna R. Willoughby*, Nadia B. Fernandez, Maureen C. Lamb, Jamie A. Ivy, Robert C. Lacy, and J. Andrew DeWoody

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The goals of captive breeding programs are often to prevent extinction and extirpation while maintaining genetic diversity and fitness until reintroductions or supplementation of wild populations can occur. However, due in part to genetic changes in captive populations, approximately one-third of reintroduction programs fail. We evaluated such genetic changes in captive populations using pedigrees, microsatellites, and mtDNA. We bred six populations of white-footed mice (*Peromyscus leucopus*) for 20 generations using two replicates of three protocols: minimizing mean kinship (MMK), random mating (RAN), and selection for docility (DOC). After 20 generations, pedigree-calculated inbreeding increased in all 6 captive populations, most quickly in the first five generations. MMK resulted in the slowest loss of microsatellite diversity compared to RAN and DOC. However, the loss of mtDNA haplotypes was not consistent among replicate lines. By comparing simulated populations to empirical data, we found no evidence of selection via genetic hitchhiking of neutral microsatellites to nearby genes under selection. Our results suggest that although the effects of drift may not be fully mitigated, MMK reduces the loss of alleles due to inbreeding more effectively than random mating or docility selection. Therefore, MMK should be preferred for captive breeding. Furthermore, our simulations show that incorporating microsatellite data into the MK framework reduced the magnitude of drift, which may have applications in long-term or extremely genetically depauperate captive populations. This research was supported by a Grant-in-Aid of Research awarded to Janna Willoughby in 2014.

3^{E,TA**}: Understanding range shifts by chipmunks in Yosemite: importance of interspecific spatial overlap and habitat use

Rachel E. Walsh* and Eileen A. Lacey

Department of Integrative Biology, University of California, Berkeley, CA 94720-3160 USA (REW, EAL); Museum of Vertebrate Zoology, University of California, Berkeley, CA 94720-3160 USA (REW, EAL)

Despite substantial evidence that global climates are changing, predicting organismal responses remains challenging, as responses can vary dramatically, even among closely related species. To explore ecological reasons for this variation, we compared patterns of spatial overlap and habitat use in two chipmunk species (genus *Tamias*) that have shown markedly different patterns of elevational range change over the past century: the alpine chipmunk (*T. alpinus*) experienced a significant elevational range contraction, while the elevational range of the partially sympatric lodgepole chipmunk (*T. speciosus*) did not change appreciably. To quantify interspecific spatial overlap and contrast patterns of habitat use, we combined live-trapping and radio-tracking of chipmunks with analyses of vegetation cover (Normalized Difference Vegetation Index). We found considerable spatial overlap between these species, indicating that interspecific competition may play a role in mediating range responses in these animals. In areas of sympatry, habitat use differed between the study species, with *T. alpinus* typically found in habitats with lower NDVI values than those associated with *T. speciosus*. The range of habitats used by *T. alpinus* was also less than that used by *T. speciosus*. These results are consistent with emerging evidence that greater ecological specialization by *T. alpinus* may be associated with stronger response to environmental change. Our work underscores the importance of integrating information on multiple biotic factors when attempting to explain responses to climate change. This work was supported by an ASM Grant-in-Aid of Research awarded to Rachel E. Walsh in 2012.

$4^{E,TA}$: Biotic responses of canids to the terminal Pleistocene megafauna extinction

Melissa I. Pardi* and Felisa A. Smith
Department of Biology, University of New Mexico, Albuquerque, NM 87131 USA

The largest consumers across ecosystems have become rare or extirpated, leading to concern over losses in ecosystem function. This phenomenon, trophic downgrading, is not a uniquely modern phenomenon. The extinction of 34 genera of megafauna from North America about 13,000 years ago must have led to widespread changes in terrestrial ecosystem function. Studies that have examined the consequences of the event address impacts on vegetation, small mammal communities, nutrient cycling, and fire regimes. Less attention has been paid to effects higher in the food chain. We modeled the climatic niche of canids, including the extinct *Canis dirus,* over the last 20,000 years. Quantifying the climatic niche accounts for changes in climate fluctuations over time; deviations from expected responses likely reveal changing biotic factors. We quantify relative niche conservatism and interspecific overlap to assess species and community responses among canids. We also include in our analyses an invasive predator, *Canis lupus familiaris*. We find that endemic canid species display low niche fidelity through time, but do not expand into niche space presumably vacated by the large extinct carnivores. We find that survivors increasingly partition niche space throughout the Holocene. The loss of megaherbivores and human impacts likely outweighed the advantages conferred from the loss of competitors. Apparent overlap between domestic dogs and humans, but not wolves, suggests a distinctive relationship between wolves, dogs, and man.

5^{TA}: Bat migration and wind energy: making the most of destructive sampling

Erin F. Baerwald
Department of Biological Sciences, University of Calgary, Calgary, Alberta T2N 1N4, Canada

Across North America each year, hundreds of thousands of bats are killed at wind energy facilities, the majority of which (~80%) are migratory bats. Although these fatalities are troubling, they offer insights into bat migration and the basic biology of migratory bats. We have used bat carcasses to investigate use of migration routes, catchment area of migration routes, and the influence of environmental conditions on activity and fatality rates at wind turbines and used this knowledge to successfully reduce fatalities. We have also used carcasses to learn about foraging ecology, background rabies prevalence, and reproductive biology of migratory bats. We are currently using carcasses of hoary bats (*Lasiurus cinereus*) and silver-haired bats (*Lasionycteris noctivagans*) from 4 wind energy sites across 4 Canadian provinces to study the population genetic structures across Canada. We used a highly polymorphic portion (HVII) of the mitochondrial DNA control region (D-loop) and calculated haplotype diversity (*h*), nucleotide diversity (π), AMOVAs, and Mantel tests. For both species, we found high levels of *h* coupled with low levels of π. Both AMOVAs suggest subtle population genetic structure among groups across Canada in both species. In silver-haired bats this population structure is influenced by geographical distance, but in hoary bats, structure was not influenced by geographic distance, as determined by Mantel tests. Additional analyses will further help elucidate genetic structure and help guide conservation strategies.

6**: Reconstructing the evolutionary history of small mammals in Nuclear Central America

Nicté Ordóñez-Garza* and Robert D. Bradley
Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409-3131 USA (NOG, RDB); Museum of Texas Tech University, Natural Research Laboratory, Lubbock, TX 79409-3191 USA (RDB)

Several species of terrestrial small mammals of the family Cricetidae are co-distributed in the sparse highlands of Middle America. The objective of this study was to investigate the tempo and mode of diversification in widely distributed highland cricetid rodents in Nuclear Central America, using phylogenetic analyses of the mitochondrial cytochrome-*b*. Phylogenetic analyses of mitochondrial DNA of different species of *Reithrodontomys*, *Peromyscus*, and *Neotoma* were used to determine levels of inter-specific differentiation, and to compare the phylogeographic signal of these taxa to aid in the interpretation of historical biogeographic events that may have broadly impacted these taxa across their distribution. Sequences of *Cyt-b* gene from samples collected in Mexico and Central America supported the taxonomic status of the *P. beatae* northwest of Isthmus of Tehuantepec-IT, and suggests that *P. beatae* southeast of the IT is a separate genetic unit. For *Neotoma ferruginea*, our results suggest it as a genetic unit different from *N. mexicana*, distributed west of the IT. A similar phylogenetic pattern occurs in other species co-distributed across the IT. Studies on several species of vertebrates of the same region are congruent with the lineage diversification during the end of the Pliocene and mostly during the Pleistocene, suggesting that climate change and geologic events related to the Isthmus of Tehuantepec have an effect on the bio-diversification across the Mesoamerican highlands. This research was supported by an Albert R. and Alma Shadle Fellowship awarded to Nicté Ordóñez-Garza in 2014.

7**: Natal dispersal on the edge: why they leave, why they stop, how they get there

Melissa J. Merrick* and John L. Koprowski
University of Arizona School of Natural Resources and the Environment, Wildlife Conservation and Management, Box 210043, Tucson, AZ 85721 USA

Understanding factors that influence natal dispersal and settlement is necessary to predict gene flow, functional landscape connectivity, recruitment, and population persistence, particularly in the face of anthropogenic disturbances and habitat fragmentation. Peripheral, isolated populations provide unique opportunities to compare how ecological processes like natal dispersal differ from populations in contiguous landscapes. My dissertation research documents natal dispersal in an endangered forest obligate, the Mt. Graham red squirrel (*Tamiasciurus hudsonicus grahamensis*), constrained to a single mountain in southeastern Arizona. We test hypotheses regarding factors that influence dispersal movements and settlement, assess degree of landscape connectivity, and identify likely dispersal corridors within an altered forest landscape in an effort to answer important and often understudied questions surrounding natal dispersal: why do some juveniles leave, what influences where they decide to stop, and how do they get to their settlement destinations? We radio-collared juvenile Mt. Graham red squirrels, quantified individual and extrinsic variables hypothesized to influence dispersal (including individual behavior, mother mass, and local density), tracked dispersal distances, settlement, and survivorship. We also examine biotic and abiotic landscape variables associated with use and movement and use circuit theory to model likely corridors for long-distance dispersal. We present our attempts to answer questions related to the why, what, and how of natal dispersal and document support for habitat imprinting, and the importance of mother resources and individual behavior variation. This research was supported by an ASM Grant in Aid of Research (2010) and ASM Fellowship (2014) awarded to Melissa J. Merrick.

8: The role of transposable elements in mammalian genome evolution

David A. Ray*, Sarah Mangum, and Roy N. Platt II

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Transposable elements (TEs) comprise around 50% of most mammalian genomes. Thus, understanding TE diversity is one avenue to understanding the diversity of mammals as a whole. We have recently completed and are involved in ongoing analyses of multiple non-model mammal taxa and have identified unique patterns of TE evolution within each. These taxa include ground squirrels, which exhibit a total lack of TE activity in the recent past and bats, with high levels of TE activity from multiple transposable element classes and families. We will discuss the TE identification, genomic landscapes and TE utilization in these taxa and others. In our first example, we will describe the unique TE landscape of vespertilionid bats and the implications for their genome and organismal evolution. These bats harbor TEs that are, to date, unique among mammals suggesting that they are subject to evolutionary forces that may not be influencing other mammal clades. In our second example, we describe the apparent extinction of the most common mammalian TE lineage in the genome of *Ictidomys tridecemlinatus* genome, with no identifiable activity occurring in the past 5 million years. Such extinction events in mammals are rare, with only four other documented cases. This finding makes *I. tridecemlineatus* in particular and sciurids in general critical taxa for understanding the genomic defense mechanisms employed to protect against unchecked TE activity.

9: Phylogenomics of hybridization using whole genome data.

William J. Murphy*, Gang Li, Brian W. Davis, and Eduardo Eizirik.
Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX 77843 USA (WJM, GL, BWD); Faculdade de Biociências, PUCRS, Porto Alegre, RS 90619-900 Brazil (EE).

Interspecies hybridization has been recently recognized as potentially common in wild animals, but the extent to which it shapes modern genomes is still poorly understood. Distinguishing historical hybridization events from other processes leading to phylogenetic discordance among different markers requires a well-resolved species tree that considers all modes of inheritance, and overcomes systematic problems due to rapid lineage diversification by sampling large genomic character sets. Here we investigate these questions by analyzing phylogenetic variation across all members of a diverse mammalian family, Felidae (cats) using high-density genotyping arrays and whole genome sequencing. We present the first robust felid time tree that accounts for unique maternal, paternal, and biparental evolutionary histories. Using multiple measures of phylogenetic discordance, we find that signatures of ancient hybridization are abundant in the genomes of modern cats. Our results highlight the mosaic origin of modern felid genomes and the influence of sex chromosomes and sex-biased dispersal in post-speciation gene flow. These findings further emphasize that the complete resolution of the mammalian tree of life will require comprehensive genomic sampling to identify and control for phylogenetic conflict caused by ancient admixture and sex-biased differences in genomic transmission.

10: Genomic and ecological interactions in woodrat contact zones: next-gen enabled insights into hybridization and diet

Marjorie D. Matocq*, Peter J. Murphy, Christopher Jeffrey, Lora Richards, and Tom Parchman
Program in Ecology, Evolution and Conservation Biology, University of Nevada, Reno, NV 89557 USA

When closely related species meet on the landscape a wide range of ecological and genetic interactions can occur. Next-generation sequencing technologies can provide new insights into this broad array of potential species interactions and their outcomes. We have been using new approaches to quantify hybridization and diet breadth in areas of contact between species of the genus *Neotoma* (woodrats). We highlight our studies of *Neotoma lepida* and *Neotoma bryanti* and contrast patterns of hybridization and diet breadth in this system to that found at a contact zone between *Neotoma macrotis* and *Neotoma fuscipes*. Using genotype-by-sequencing approaches, we find that both contact areas are characterized by hybridization with approximately 15% of contact populations being of hybrid descent. To gain insight into diet breadth, we use high-throughput sequencing of the *trnL* gene from fecal pellets. While woodrats do hybridize at these sites, we find that they maintain distinct diets, and in the case of *N. macrotis* and *N. fuscipes*, even show evidence of diet displacement upon contact. The primary food plants used by each woodrat species are dominated by distinct toxic compounds that likely require different metabolic specializations. We suggest that adaptation to different plant toxins may play an important role in determining species interactions at woodrat contact zones, providing a novel mammalian example of how ecological adaptation contributes to the maintenance of species boundaries.

11: The role of geography in the adaptive radiation of sigmodontine rodents in South America

John J. Schenk and Scott J. Steppan*
Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, LA, 70118 USA (JJS); Department of Biological Science, Florida State University, Tallahassee, FL, 32306 USA (SJS)

Ecological opportunity occurs when a lineage disperses into a new region and can lead to an adaptive radiation. Although adaptive radiations are thought to be an important mechanism producing biodiversity, little is known about the role of biogeography in this process, especially for continents where most terrestrial species occur. Consequently, we quantified the relationship between lineage and biogeographic diversification patterns in the South American Sigmodontinae, one of the few demonstrated adaptive radiations in mammals. A time-calibrated phylogeny was inferred from four nuclear and one mitochondrial genes for 77% of sigmodontine diversity. Historical biogeography was reconstructed among 14 regions with S-DIVA and Bayesian binary MCMC, to which we applied a novel approach to estimate biogeographic transition rates through time. We compared these rate patterns and applied community-assemblage phylogenetic-approaches to determine the level of phylogenetic clustering among regions. Following initial colonization of South America around 7 Ma, multiple expansions from northern regions correlated with a burst of speciation. Subsequently, both diversification and dispersal rates slowly decreased. Nearly all regional communities were phylogenetically clustered. We conclude that biogeographic complexity and partitioning played a profound role in producing the adaptive radiation of Oryzomyalia (Sigmodontinae), the degree to which is determined by the relative scales of spatial variation and dispersal abilities.

12^{E}: Determining spatial and temporal overlaps of endangered small mammals and their invasive predators

Michael Cove*, Ted Simons, Beth Gardner, and Allan O’Connell
USGS, NC Cooperative Fish and Wildlife Research Unit, Department of Applied Ecology, North Carolina State University, Raleigh, NC 27695 USA (MC, TS); Department of Forestry and Environmental Resources, North Carolina State University, Raleigh, NC 27695 USA (BG); USGS Patuxent Wildlife Research Center, Laurel, MD 20707 USA (AO)

The Lower Keys marsh rabbit (*Sylvilagus palustris hefneri*) and the Key Largo woodrat (*Neotoma floridana smalli*) are both federally endangered subspecies endemic to the Florida Keys. Although a variety of confounding broad-scale factors (e.g., sea level rise, climate change) presumably threaten these two species, invasive predators such as domestic cats (*Felis catus*) are believed to be a major threat to these small mammals. Management strategies have focused on habitat restoration and variable amounts of predator control over the years; however, research on predator population dynamics and their interactions with these endangered sub species is limited and has not yielded strong inference. Thus, our objectives were to integrate noninvasive sampling and modeling procedures to estimate marsh rabbit and woodrat occurrence and their co-occurrence with predator populations. We used camera traps set to specifically target the small mammals and separate but concurrent surveys of predators to determine direct and indirect effects. Preliminary results reveal that the endangered small mammals exhibit high spatial and temporal overlap with the invasive predators, suggesting high potential for negative interactions. As invasive predator management continues, we will use dynamic occupancy models to determine these relationships and evaluate its effectiveness for endangered species recovery.

13^{E}: Biogeography and population genetics on Sulawesi, Indonesia: a case study of the shrew *Crocidura elongata*

Ryan A. Eldridge,* Anang S. Achmadi, Thomas C. Giarla, Kevin C. Rowe, and Jacob A. Esselstyn
Department of Biological Sciences and Museum of Natural Science, Louisiana State University, 119 Foster Hall, Baton Rouge, LA 70803, USA (RAE, TCG, JAE); Museum Zoologicum Bogoriense, Research Center for Biology – LIPI, Cibinong, 16911, Indonesia (ASA); Sciences Department, Museum Victoria, Melbourne, VIC 3001, Australia (KCR)

Due to its mountainous terrain, peculiarly peninsular shape and unique geological past, the island of Sulawesi, Indonesia, presents a fertile opportunity for examining biogeographical processes. Earlier work hypothesized the existence of distinct areas of endemism (AoEs) on Sulawesi, but the relevance of these zones to a broader set of taxa has not been investigated, nor the reasons for their existence fully explored. Here, we use population genetic analyses on the endemic Sulawesi shrew, *Crocidura elongata,* to assess biogeographic partitioning according to the putative AoEs. We uncover significant cryptic diversity within *C. elongata* that imperfectly aligns with AoEs, while also identifying patterns consistent with divergence along elevational gradients. The effect of intra-island climatic variation on Sulawesi biogeography, relative to the conventional “island coalescent” hypothesis, is considered.

14: The newcomers follow the old rules: body size evolution in mammals introduced onto islands

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Museum of Geology and Paleontology, National and Kapodistrian University of Athens, Panepistimiopolis, 15784 Zografou, Greece (GAL); Netherlands Centre for Biodiversity Naturalis, Postbus 9517, 2300 RA Leiden, The Netherlands (AAG); and College of Environmental Science and Forestry, Syracuse, NY 13210 USA (MVL)

On islands, mammals often exhibit patterns of body size evolution consistent with the island rule – a graded trend from gigantism in small species to dwarfism in larger species. While common for extant insular species, the pattern is more marked – sometimes to spectacular levels of gigantism and dwarfism – for palaeo-insular mammals isolated for hundreds of thousands to millions of years. Here we capitalize on the unplanned experiments of species introductions onto islands over periods ranging from a few decades up to several millennia to assess the time-scale of body size evolution in insular mammals. We present the preliminary results of a comprehensive analysis of 26 introduced mammalian taxa from over 200 insular populations worldwide. Mammals that were introduced during the period of European expansion exhibit limited change in body size, whereas more ancient introductions show significant size change. As anticipated, this size change is still less pronounced than that for the native palaeo-insular species and, in addition to time in isolation, body size evolution appears to be influenced by characteristics of the islands including their area, latitude (climate) and perhaps their isolation as well.

15: Unraveling the ecosystem consequences of the terminal Pleistocene Megafaunal Extinction

Felisa A. Smith*, S. Kathleen Lyons, Emma A. Elliott Smith, Seth D. Newsome, Thomas W. Stafford, and Catalina P. Tome
Department Of Biology, University Of New Mexico, Albuquerque, NM 87131 USA (FAS, EES, SDN, CPT); Department Of Paleobiology, National Museum Of Natural History, Smithsonian Institution, Washington D.C. 20013 USA (SKL); Department Of Physics & Astronomy, University Of Aarhus, Aarhus, Denmark (TWS)

Recent studies connecting the decline of large predators and consumers with the ‘unraveling’ of ecosystems overlook that this natural experiment already occurred. As recently as 14 ka, tens of millions of large-bodied mammals were widespread across the American continents. Within 1,000 years of the arrival of humans, ~80% were extinct including all species >600 kg. While the cause of the extinction remains contentious, what has been largely overlooked is the consequence of the loss of millions of large-bodied animals. Here, we examine the influence of the extinction at a local community. Our study site is Hall’s Cave in the great plains of Texas, which has unparalleled fine-grained temporal resolution over the past 20ka, allowing characterization of the community before and after the extinction. This site experienced catastrophic loss of 80% of large-bodied herbivores and 20% of the apex predators in the ecosystem. Using a series of tightly constrained temporal windows spanning the full glacial to the modern and comprehensive faunal lists, we reconstruct mammal associations and body size distributions over time. We find changes in alpha and beta diversity and the statistical moments associated with periods of climate change as well as with the extinction event. Moreover, employing the null model program PAIRS to our data reveals interesting temporal patterns in the disassociation or co-occurrence of species through the terminal Pleistocene and Holocene.

16: New records of *Microtus chrotorrhinus* (rock vole), westerly range limit, and the Rainy glaciation lobe

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Knowledge of geographic range limits is important for understanding the ecology, evolution, persistence, vulnerability, and conservation of species. The rock vole (*Microtus chrotorrhinus*) reaches the western limit if its range in northern Minnesota where it has been enigmatic. The 1st specimen was secured in 1921 and no others were taken until the 1970s. Subsequently, Christian and Daniels (1985) documented its occurrences at 60 sites in northeastern Minnesota, and Jannett et al. (2007) reported it at 2 sites further west. Here we report an additional 54 sites where we secured rock voles across Cook, Lake, and St. Louis counties in various types of rocky habitat, as well as their absence at sites further west. The distribution of rock voles in northern Minnesota corresponds to the Rainy Lobe of the Wisconsin glaciation.

17: Interannual variation in the magnitude and outcome of competition among grassland rodents

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Competition between species can vary temporally with changes in the abundance of competing species and their environment. The impact of competitive interactions is dependent on both the magnitude of competition and carrying capacity. Therefore it seems likely that the outcome of competition varies due to change in environmental factors. We used a long term dataset (1974-2002) to estimate the magnitude and predicted outcome of competition between two species (the hispid cotton rat, *Sigmodon hispidus*, and the prairie vole, *Microtus ochrogaster*) and tested if competition was related to environmental factors. We used Lotka-Volterra models to produce annual estimates of competition coefficients (α) and carrying capacity (K) and determined the projected outcome of competition. We then used correlation analysis to assess environmental effects on competition and logistic regression to assess effects on the projected outcome of competition. Both the magnitude of competition and the predicted outcome of competition was affected by precipitation in the previous growing season. The effect of cotton rats on prairie voles was positively associated with precipitation the previous year while competitive exclusion of cotton rats by prairie voles was negatively associated with precipitation in the previous year. Our results suggest higher levels of precipitation increased the ability of cotton rats to compete with prairie voles in the following year and promoted unstable coexistence between the two species.

18TA: The potential role of a native grazer and keystone species in managing woody encroachment

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Woody encroachment is a widespread phenomenon affecting grasslands and savannas worldwide. While its effects vary widely depending on local conditions, encroachment often can have adverse effects on an ecosystem. Several causes have been proposed in the literature, such as grazing of domestic livestock, fire suppression, climate change, and increasing atmospheric CO_2 levels; however, the widespread removal of a native grazer and keystone species, the prairie dog (*Cynomys* spp.), is one potential cause that has received little attention. Because woody encroachment has coincided with the removal of prairie dogs across their former range, we hypothesized that prairie dogs actively suppress woody plant growth on their colonies. To test this hypothesis, we installed exclosures around woody plants, and conducted artificial sapling experiments on and around 4 recently reestablished black-tailed prairie dog (*Cynomys ludovicianus*) colonies in southeastern Arizona. We found that, on colonies, woody plants inside exclosures grew faster than those left exposed to prairie dogs, and artificial saplings were rapidly destroyed. Our findings suggest that the reestablishment of this highly persecuted, yet ecologically

critical, species could simultaneously function as a management tool for widespread woody encroachment across the North American west.

19^E: The effects of carcass size, habitat type, and season on vertebrate scavenging community dynamics

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Carrion is a valuable nutrient resource that is used by a diversity of organisms encompassing all biological kingdoms. Despite the importance of carrion to vertebrate communities, scavenging ecology is complex and many knowledge gaps still exist. The purpose of this study was to address how mammalian carcass size and location influence scavenging community dynamics. We quantified the seasonal composition and efficiency of vertebrate scavengers among a range of carcass sizes and habitat types to elucidate differences among scavenging communities. Trials were conducted at the Savannah River Site in Aiken, South Carolina during both a warm and cool season. During each season, 12 each of rat (*Rattus*), rabbit (*Sylvilagus*), and feral hog (*Sus scrofa*) carcasses were placed in each of 4 habitat types (clearcut, hardwood forests, immature pine stands, and mature pine stands; 96 total trials per size) and monitored using remote cameras. Among carcass sizes and seasons, mammalian and avian species were observed scavenging 60.8% and 48.3% of carcasses, respectively. Among mammals, mesopredators were the dominant scavengers, occurring at 59.3% of all carcasses and more often than any other scavenger group on all carcass sizes during the cool season. Understanding the interactions that influence scavenging communities, especially in environments altered by land use, will allow researchers to further understand the role of carrion in ecosystem health.

20^E: Selection of wetland habitats by bats in coastal South Carolina: an acoustic study

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Selection of habitats by bats can be affected by many variables, including presence of water, level of vegetative clutter, availability of prey, and influence of habitat structure on echolocation calls. Most research in South Carolina has focused on how bats select terrestrial habitats in the Upper Coastal Plain. These studies have determined that landscape-level variables tend to have less of an influence on how bats select habitats than do microhabitat variables. An exception is the landscape-level variable of proximity of habitat to water, with bats more likely to be present in habitats that are near water. Because presence of water is so important to bats, we are investigating variation in activity of bats over wetlands in the Lower Coastal Plain of South Carolina, which is a region that has not been studied previously. We monitored bats using acoustic detectors that recorded echolocation calls. These calls were then identified to species and compared across habitats. Preliminary results demonstrate that activity of bats, both of individual species and overall, varies with characteristics of the wetland. The goal of our study was to provide coastal land managers with information useful in promoting healthy populations of bats at a time when bats are experiencing high rates of mortality due to white-nose syndrome and degradation of habitats.

21: Understanding the trophic role of marsupial predators in Australia's deserts

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Australia has lost several large marsupial predators during the Holocene and gained three species of eutherian carnivore. These species now co-occur in arid Australia with a range of small (body mass <200 g) marsupial mesopredators. Given the significant upheaval in the composition of mammalian predator communities in arid Australia, understanding the trophic ecology of native mesopredators and the degree of overlap in diet with introduced carnivores is important. Here we quantify the diet of four of the larger

marsupial mesopredators from arid Australia. We chose species from a diversity of environments; kowari, brush-tailed mulgara, crest-tailed mulgara and kaluta. We quantified diet by carrying out microscopic examination of the content of scats collected during fieldwork covering a dry phase from 2007 to 2011. We examine dietary diversity, the level of predation on vertebrates, and the degree of dietary overlap with the three carnivores. The diet of the four species was dominated by invertebrates particularly insects with spiders, scorpions and centipedes also consumed. Each species consumed vertebrates but the importance of vertebrates in the diet ranged from insignificant in the kaluta (<5% volume) to relatively important in the crest-tailed mulgara (30% volume). Rodents were the main vertebrate prey for kowari and brush-tailed mulgaras with rodents and dasyurids being taken by crest-tailed mulgara. Our results are of relevance for understanding the functioning of Australia's arid ecosystems.

22: Diet composition of meadow voles in postagricultural wetlands

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Small mammal diet can have a significant influence on native habitat restoration efforts. To assess the influence of small mammal diet on plant succession and restoration within post-agricultural cranberry bogs, we examined the diet composition of the most abundant small mammal within the system, the meadow vole (*Microtus pennsylvanicus*). Microhistological analysis of fecal samples revealed that meadow voles feed on a wide variety of food sources with grasses, sedges, rushes, mosses, and shrub leaves being major forage components. Although diet composition was similar among different plant communities, abundance of food types fluctuated among habitat sites. Seasonal foraging shifts were related to plant availability. These data highlight the role that meadow voles can play in the assembly of plant communities undergoing succession in postagricultural wetlands.

23[E,TA]: Seasonal circadian rhythm shift and lunar chronobiology of the nine-banded armadillo (*Dasypus novemcinctus*)

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Nine-banded armadillos are nocturnal, fossorial, insectivorous mammals that historically live in warm climates but have been moving northward over the past 150+ years. As armadillos move into more temperate climates, they must make behavioral adjustments in order to survive the winter. They do not store fat for the winter, cache food, hibernate, or have seasonal migrations. Observations of armadillos in northern latitudes have noted that they seem to be more active during the daytime in the winter, indicating a shift in circadian rhythm. Such behavioral plasticity may be an adaptation that allows individuals to forage during the warm part of the day when the ground is less likely to be frozen. We recorded observations of armadillo activity for six months using game cameras. Data were sorted according to photoperiod, temperature, and lunar illumination. We created indices for nocturnal, crepuscular, and diurnal activity, and then plotted these indices as functions of time to illustrate the change in activity. Analysis suggests that a seasonal shift in circadian rhythm does occur ($p<0.0005$). In addition, armadillos seem to be most active during the full and new moon phases ($p<0.0005$). Although armadillos have previously been reported to have lunar phobia, to our knowledge studies have not described an increase in activity during full moon periods.

24[TA]: An examination of regional variation in southern flying squirrel ultrasonic communication

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Recently ultrasonic communication was reported for southern flying squirrels (*Glaucomys volans*), and the species' calls now have been described and classified in Ontario, Canada, and in the southeastern U.S.A. with notable differences in many call frequency and time characteristics, suggesting regional variation in

G. volans communication. We evaluated this observation of regional variation by examining *G. volans* communication in a little studied portion of their range, the Central Hardwoods Region of the U.S. We recorded calls of wild *G. volans* near West Point, Indiana with Anabat II ultrasonic recorders. We used program AnalookW to describe eight frequency and time characteristics of recorded calls for statistical analysis in SAS. We categorized calls into types using discriminant function analysis and UPGMA cluster analysis. From the recordings classified by our analysis, we identified several call types with characteristics significantly different from any previously described *G. volans* calls. At least one call type is similar to calls found in both Ontario and the southeastern U.S. Our findings suggest that *G. volans* either communicates in several distinct dialects across its range, or the species possesses a much wider repertoire of calls than previously recognized. Our call classification and descriptions increases feasibility and accuracy of passive acoustic monitoring of *G. volans* populations in the Central Hardwood Region, providing a useful noninvasive tool for the research and management of this species.

25**: Agonistic interactions in harbor seals (*Phoca vitulina concolor*) vary with density on haul-out ledges

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Due to successful conservation efforts, several marine mammal populations have increased in the past 40 years, leading to the possibility of increased competition for resources. We evaluated competition for haul-out space in West Atlantic harbor seals (*Phoca vitulina concolor*) by assessing agonistic interactions at two haul-out sites in Casco Bay, Maine, USA. We predicted: intensity and rate of interactions increase as density increases, larger seals win more interactions than smaller seals do, adult seals win more interactions than juveniles do, seals with prior residency win more interactions than intruders, and higher intensity of interactions during molt but higher rates during post molt. During molt at Gunpoint Ledge, one of the two sites, intensity of interactions decreased as density increased, but the pattern reversed during post molt. Rate of interactions peaked at intermediate density. Size and age class did not affect outcomes of interactions, but seals with prior residency won more interactions than expected by chance. Interaction rate was higher during molt versus post molt seasons. Harbor seals may experience increased competition for limited haul-out space as populations continue to grow, with seals with prior residency outcompeting intruders. This research was supported by a Grant-in-Aid of Research awarded to Anne Honeywell in 2013.

26: Predation risks and oak dispersal by squirrels: Do predators direct the seed dispersal process?

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Previously, we showed that Eastern gray squirrels (*Sciurus carolinensis*) cache seeds in more open vegetation where the probability of pilferage is lowest but predation risk is presumed higher. Here, we experimentally evaluate rodent perception of predation risks at preferred cache sites and other sites for comparison by measuring giving-up densities (GUDs). Rodent GUDs were measured with small trays containing 3 L of fine sand mixed with sunflower seeds. In experiment I, we relied on a 2-year, seed dispersal study in a natural forest to identify caches of gray squirrels and then measured GUDs at (1) these caches (2) comparable points near cover where rodent activity was assumed highest, and (3) random points. GUDs and, presumably, predation risks, were higher at both cache and random points than those with cover. In experiment II, we measured GUDs of gray squirrels in an open park system and found that GUDs were consistently lowest at the base of the tree and increased with distance from the tree, where previous studies show caching by squirrels to be highest and pilferage rates by naïve competitors to be lowest. We argue that predation risks can influence rodent scatter-hoarding decisions in these and other systems, and that such decisions, especially when followed by predation of the scatter hoarder could be a major factor shaping the temporal and spatial patterns of seedling establishment.

27: The effects of North American porcupine (*Erethizon dorsatum*) herbivory on forest diversity

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While typically considered a generalist species, North American porcupines (*Erethizon dorsatum*) survive harsh winters by specializing on a selective diet of bark and coniferous needles. This feeding behavior disturbs forests by damaging trees, sometimes lethally. The intermediate disturbance hypothesis states that biodiversity is maximized in habitats that experience moderate levels of ecological disturbance. Some researchers suggest that porcupine herbivory, as an agent of intermediate disturbance, plays an important role in stimulating forest biodiversity. We tested this hypothesis by comparing areas in forests actively inhabited by porcupines with control areas in the same forests with little to no indication of porcupine foraging. Research sites were established in state forests in Northern New York between 2011 and 2015. At each site we established a $1{,}000^2$ meter plot and identified every tree taller than 1.5 meters, recording species, diameter at breast height, vitality, and age class. We also examined the selectivity and severity of winter foraging by assigning each tree a wound score that reflected the degree of damage caused by porcupine feeding. This information was then used to assess the effects of porcupine foraging on the structural, compositional, and functional diversity of the study forests. While changes in biodiversity were observed, additional studies are important to establish if these results are replicated in other regions and to determine if porcupine foraging has the potential to promote biodiversity long-term.

28[E,TA]: Body size patterns in pikas *(Ochotona)* reflect ecology

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Body size is important. It strongly influences life history, behavior and physiology, including climatic tolerance. Bergmann's rule describes the pattern that species within a genus generally have larger body sizes at higher latitudes, supposedly as a proxy for temperature variation. The underlying mechanism for Bergmann's rule, and how well it holds between biological levels is not well understood. Here, we test whether pikas *(Ochotona)* conform to Bergmann's rule and which climate variables correlate with body mass both for species within the genus, and populations within the widely distributed species, *O. princeps*. We compared the body mass of georeferenced *O. princeps* and *Ochotona* ranges with numerous bioclimatic variables in a GIS. Our results reveal that no group significantly conforms to Bergmann's rule in response to temperature. However, we found that burrow dwelling and rock dwelling species exhibit significantly different patterns in response to climate. Burrow dwelling pikas are smaller in areas of increased annual precipitation, while rock dwelling pikas respond most strongly to precipitation in the warmest quarter. *O. princeps* also tends to be larger in areas with increased precipitation in the warmest quarter. Burrow dwelling pikas are more responsive to climate variables than rock dwelling pikas, suggesting that they are more influenced by the physical environment. It appears that the timing of precipitation and thus available forage may influence body size trends.

29: Mammalogy at Wildsumaco Biological Station: The first five years

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Wildsumaco Biological Station (WBS) is a new research and education facility that opened in 2012, on the east Andes slope of Ecuador in lower montane rainforest (S 00.67145° W 077.59865°, 1,450 m elevation). WBS property is leased from Wildsumaco Wildlife Sanctuary (WWS), a private, ca. 500 ha ecotourism and conservation preserve, and is near Sumaco Napo-Galeras National Park, the core area of the larger Gran Sumaco International Biosphere Reserve. The geological and biogeographical centerpiece of the Park is the 3,732 m Volcán Sumaco, a stratovolcano isolated from the main Andes chain. WBS's location within lower montane rainforest at the volcano's base places it in the middle of an unbroken elevational transect, from páramo on Sumaco's peak to lowland tropical moist forest in the Amazon. WBS trails traverse a variety of habitats, from disturbed pasture to secondary and primary forest, providing abundant opportunities for mammalogy teaching and research. Mammalogy research at WWS began in December 2008; we summarize the results here. Camera trapping has documented more than one-third of all Ecuadorian terrestrial mammalian carnivore species in the preserve, and the highest trap success ever reported for the near-threatened margay (*Leopardus wiedii*). Current research addresses mammalian beta diversity at different elevations on the volcano. WBS is open to undergraduate classes under the direction of faculty, and graduate and faculty researchers from accredited institutions.

30: A novel use of Specify Database Software for museum collections

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In June 2014, the mammalogy collections at the Florida Museum of Natural History (FLMNH) moved from an Access database to one powered by Specify database software, joining the ichthyology and herpetology collections, which had previously transitioned into this new format. We present an aggregated collection web portal developed at FLMNH, based on Specify Database Software. For the 1st time, Specify Software’s full-featured web interface for accessing specimen data is configured to search multiple collections simultaneously. We discovered that the steps to build and export a web portal in Specify may be interrupted and data from multiple collections aggregated at a database level. The process may then be resumed to produce a web portal containing the aggregated data. As Specify software’s common data model for storage of collection data controls for disparities in data typing across collections, the Specify Web Portal is ideally-suited for aggregating databases of disparate collection types. Search results of an example aggregation using mammal and fish records are presented to demonstrate functionality. The FLMNH envisions the completion of a “Digital Florida” aggregated collection web portal for all FLMNH data-based natural history specimens, including fossils. We envision this method could facilitate comparative biogeographic and phylogeographic studies spanning across classes. This new methodology has been shared with the Specify Project and collaborative efforts toward inclusion in the Specify application are ongoing.

31^{E,TA}: Comparative phylogeography of parasites reveals the history of North American pikas

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Mammals are often parasitized by multiple independent lineages of ecto- and endoparasites. The evolutionary histories underlying parasite diversity are not thoroughly explored, but are essential to our understanding of basic ecological processes that structure faunal communities through time. Molecular investigations into codistributed, host-specific parasite lineages provide a unique opportunity to elucidate novel aspects of host history, and assessment of independent parasite lineages allows general histories to be distinguished from taxon-specific patterns. Nearctic pikas (genus *Ochotona*) and their endoparasitic helminths provide an excellent study system to investigate these interactions. Pikas have a narrow temperature tolerance, so have experienced historical range fluctuations in response to climatic oscillations. This has produced five major lineages distributed throughout the mountain systems of the American West. Parasites have been thoroughly sampled across this host’s range and we investigate 2 major lineages, the tapeworm genus *Schizorchis*, and the nematode subgenus *Labiostomum* (*Eugenuris*). We see that both include species with concordant distributions, yet are not concordant with pika lineages. We use multi-locus datasets to uncover the reasons for this pattern, and further analyze the intraspecific phylogenetic and demographic structure of these two taxa. We reveal novel patterns of gene flow and isolation, and evaluate the range of possible histories of this host-parasite assemblage relative to the timing of glacial cycles, landscape specific corridors and barriers to dispersal.

32: Occurrence of deer mice on high-elevation peaks in Colorado

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The presence of deer mice (*Peromyscus maniculatus*) was determined for various Colorado "fourteeners" (= peaks over 4,267 m above sea level) to gain insight on the ubiquity of this species at high elevation.

Dedicated trapping, opportunistic observation, and field records revealed the occurrence of deer mice on several high peaks, representing different mountain ranges in Colorado. The deer-mouse populations on these geographically disparate peaks presumably represent independent colonizations from low-altitude populations, with subsequent convergent adaptations to the hypoxia and cold of the high-altitude environment.

33^{E**}: Effects of hemlock woolly adelgid on small mammal community assemblages in eastern hemlock forests

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Eastern hemlock is declining in abundance from the effects of the invasive sap-sucking hemlock woolly adelgid (HWA). Loss of forests may impact community composition of associated small mammals. Small mammal assemblages were censused at Harvard Forest's replicated two-block experimental design. Each block consists of four-0.81ha canopy treatments: hemlock control, hardwood control, girdled treatment (simulate HWA), and logged treatment (simulate pre-emptive forest management). Sherman trap grids of 0.49 ha were placed within each canopy treatment. During the months of June and July 2012-2014, multiple season occupancy modelling with spatial replication was used to quantify the distribution of small mammals among the four canopy treatments. To date, a total of 11,403 trapping nights resulted in captures of 8 species of rodents and 3 species of shrews. Species richness (n = 11) did not vary among treatments, but species abundance and community assemblage may differ. In hemlock and hardwood controls, *Peromyscus spp.* were more abundant than *Myodes gapperi,* but *M. gapperi* were more abundant in manipulated canopy treatments. These preliminary data suggest that HWA infestation may affect small mammal composition and occupancy, but not species richness. This research was supported by an American Society of Mammalogists Grant-In-Aid awarded to Allyson Degrassi in 2014.

34: Small mammals from three mountain ranges in Nuclear Central America

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Small mammal ecology and natural history are poorly known in Nuclear Central America. In an effort to gain information on small mammals (insectivores, marsupials, and rodents), we sampled three cloud forest habitats in mountain ranges in Honduras (Cerro Celaque and Sierra de Agalta) and Guatemala (Sierra de las Minas). Small mammals were collected using removal trapping. Trapping effort varied among sites, with a total of 18117 total trap-nights utilized. A total of 789 specimens representing 21 species of small mammal was recorded from seven trapping sites. Habitat at each trapping site is described. Species diversity, relative abundance, sex ratios, reproductive activity, and other natural history information are reported. In general, cloud forests in the three mountain ranges contained different communities of small mammals. Three species (*Heteromys desmarestianus, Peromyscus oaxacensis,* and *Scotinomys teguina*) occurred in the cloud forests of all three mountain ranges.

35: Similarity of mammalian abundance and richness among four sites in Western Central Georgia

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Habitat fragmentation threatens biodiversity by reducing the trophic chain length altering species interactions. Mammalian abundance and richness was assessed at four sites, two urbanized and two rural locations, to examine the resulting dissimilarity. Game cameras were utilized from July 2014 to December 2014 to determine species abundance among four sites in Western Central Georgia. Cameras were visited every 24 hours during a 48 hour period of sampling to re-bait stations. The combined data for

all four sites yielded 425 successful identifications. On the species level, the differences between sites was significant (p = 0.003). The largest average dissimilarity was found between site 3 and site 4 (68.94%). For analysis, mammals were divided into functional groups based off of dietary needs. When divided this way, there were 11 carnivores, 275 omnivores, and 138 herbivores. The two way nested analysis of similarity found the difference in functional groups between sites to be significant (p = 0.002). The largest average dissimilarity was found between site 3 and site 4 (59.61%). Although analysis between urban and rural sites was not significant, the largest average dissimilarity was found between an urban and rural site for both analyses. In order to conserve trophic chain length and minimize the impact of habitat fragmentation on specialist species, emphasis should be placed upon the management of original habitat patches to support native wildlife.

36: Patch size effects and functional diversity thresholds: A small mammals approach

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Functional diversity (FD) is a measure of the roles that species play within an ecosystem. Factors that shape the FD of a community include the dynamics of the community (i.e. competition) and size, shape and context of a community's environment. In particular, patch size appears to be one of the prime environmental factors driving on FD. However, growing evidence suggests that FD of mammals can change abruptly at certain size thresholds. This suggested there are ecologically relevant sizes of a particular habitat patches that will enhance stability and function of the system. Here we investigated two questions using non-volant small mammal communities of Atlantic Forest hotspot in Brazil. We were interested in understanding 1) if patch size drove small mammal FD, and 2) if there were certain patch size thresholds that lead abrupt changes in FD. We used 125 published accounts and theses to identify 283 small mammal communities across a gradient of patch sizes. We used species traits to calculate the FD for each community. Using a generalized linear model we found that FD increased with an increase in patch size, and identified two thresholds when FD changed abruptly. These abrupt changes occurred when patch increased to < 40 ha and > 500 ha. Understanding when FD increases can be critically important to maintaining healthy and stable forest communities in highly fragmented systems.

37: The effect of ecology, allometry, and phylogeny on reproduction patterns in Canidae and Leporidae

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In arctic habitats predator-prey dynamics have been well studied, especially with respect to how population fluctuations are correlated. But do predator-prey reproductive patterns have similarities in other habitats? To examine this question, data were compiled for 2 families with fairly similar habitat distributions and biodiversities: canids and leporids. Reproductive, allometric, and habitat data were obtained from various sources. Reproductive data included litter size, neonatal mass, gestation, and lactation. Allometric data were primarily for females using either head-body length or body mass. For habitat, each species was categorized into one of the following: dune-desert, forest, grassland, lowland, montane, open plain, savanna, scrubland, and tundra-boreal. Separate analyses were conducted a) lumping similar habitats according to temperature and precipitation; b) using canids and leporids of similar body mass, and c) using the most diverse genera in each family: *Canis*, *Vulpes*, *Lepus*, and *Sylvilagus*. Overall, habitat has a significant contribution to explaining the variation in reproductive parameters. Savanna species have longer gestations and lactations while scrubland species have shorter gestations and lactations. Habitat makes less of a contribution to reproduction for neonatal mass that has a very tight correlation with female mass. Thus, although the interactions between the reproductive patterns of predators and prey have long been studied in arctic habitats, our results suggest that reproductive patterns of predators and prey may be related in other habitats.

38: Importance of the field biology EXPERIENCE: undergraduates in the forests of northern New York

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While at St. Lawrence University, I led an eager group of undergraduate students in a census project to assess mammal activity in the North Country of New York (St. Lawrence County). This included a short-term trapping effort (conducted in October, November, and December 2012), as part of the Mammalogy course, established at a nearby field station that included coniferous species (such as red and white pine, hemlock) along with deciduous trees. In addition to taking students out for a hands-on experience with live mammals and actual habitats, as well as involving them in creating a methodology to assess the mammals present, our project yielded a number of interesting results. First, I developed a new relatively low-cost, easy-to-implement method for live-trapping in trees (with large Sherman traps, on trunks 2 meters aboveground). Second, students experienced eye-opening behaviors and results firsthand, as we recorded a substantial "arboreal" complement of species and very different mammal faunas in trees and on the forest floor. Furthermore, there were surprises; by trapping in the trees, we found a much higher density of flying squirrels than expected and both species (*Glaucomys sabrinus* and *G*. *volans*) were trapped side by side and relatively common. This project underscores the value of even small-scale census projects to add to our mammal knowledge, but also the importance of getting undergraduates out to experience field biology.

39^{E}: Food habits of black bears in urban versus rural Alabama

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Little is known about the food habits of the black bears (*Ursus americanus*) in Alabama. A major concern is the amount of human influence in the diet of these bears as humans and bear populations continue to expand in a finite landscape, and bear-human interactions increase. To better understand dietary habits of bears, 145 scats were collected during the fall months of 2011-2014. Food items were generally classified into the major categories of vegetation, animal prey, and human (cultivated) food. Plant items were classified down to the lowest possible taxon via DNA analysis, as this category composed a majority of the scat volumes. Frequency of occurrence and volumetric weight was also calculated for each of the food items. Interestingly, despite the proximity of these bear populations to urban and suburban locations, we estimated that their diet composition, at least during the period sampled, remained mostly composed of wild plant matter instead of human food. Also, dietary composition did not differ between bears living close to urban areas compared to bears occupying more rural areas.

40: First specimens of *Pekania* (*Martes*) *pennanti* (Fisher) from Virginia

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Fishers (*Pekania [Martes] pennanti*) are believed to have occurred in portions of western Virginia before being extirpated in the late 1800s. However no specimen of *P. pennanti* from Virginia has ever been reported in a museum collection, and we were unable to find any museum records for specimens from Virginia, despite extensive electronic searches of museum databases in August 2014 and January 2015. Here we document the presence of this species in Virginia with verified photographic records and with voucher specimens deposited in the Mammal Collection of the Virginia Museum of Natural History. These animals probably have dispersed from populations that are expanding from western Maryland and northeastern West Virginia, following translocation of fishers to northeastern West Virginia in 1969. This report provides a benchmark for future studies of the distribution and abundance of fishers in Virginia.

41: Genetic structure assessment of the Ryukyu wild boar populations in the Ryukyu Archipelago, Japan

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In Japan, there are two subspecies of wild boar: the Japanese wild boar (JWB) (*Sus scrofa leucomystax*) on the Honshu, Kyushu, and Shikoku islands, and the Ryukyu wild boar (RWB) (*Sus scrofa riukiuanus*) on the Ryukyu Archipelago. In this study, we investigated the genetic structure of the RWB populations using 23 microsatellite (MS) marker polymorphisms. Samples from 299 RWBs were collected from five Ryukyu islands (Iriomote, Ishigaki, Okinawa, Tokunoshima, and Amami) and compared with reference samples of 21 JWBs from Kyushu and 114 domestic pigs. Principal coordinate analysis (PCoA) was performed by GenAIEx 6.5, and population cluster analysis was conducted by STRUCTURE 2.3.3. The PCoA revealed that the summed PC in 1 (x-axis; 40.66 %) and 2 (y-axis; 24.63 %) accounted for 65.29 % of the total variation. Two RWB populations, on Iriomote and Ishigaki, were clearly separated from the other RWB populations by PC1. These results suggest that the genetic differences between the populations are related to geographical distance. Structure analysis by MS clearly distinguished the five RWB populations from each other. Our results demonstrate that the RWB population on each island is genetically distinct and individually structured. They also suggest that there have not been substantial gene flows between these RWB populations.

42: Evaluation of growth hormone gene haplotyes between domestic pigs and wild boars in Japan

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Genetic introgression due to crosses between domesticated pigs and wild boars is a risk to preserving natural wild boar populations. In order to better understand the genetic differences we evaluated the differences in growth hormone (GH) gene haplotypes between domestic pigs and wild boars. The GH genes relate to growth, fat content and milk productivity traits in pigs, and wild boars have considerably slower growth rates than domesticated pigs. We compared the GH gene haplotypes of Ryukyu wild boars (RWB), the smaller of two Japanese wild boar species, and domestic pigs. We sampled 29 Landrace and 45 Large White domestic pigs, and 39 RWB, from Iriomote Island in Okinawa. We found 29 mutations containing six amino acid substitutions, and we reconstructed 101 GH gene haplotypes (77 domestic pigs and 24 wild boars) by estimation using ARLEQUIN version 3.5. Structure analysis indicated a rough division between domestic pigs and wild boars. Also, principal coordinate analysis and phylogenetic tree analysis revealed a general divergence into domestic pig and wild boar groups suggesting that these two populations had different GH gene characteristics. Therefore, this study indicates that during the breeding advances of domestic pig livestock a difference has developed between the GH genes of domestic pigs and wild boars. It is likely that these population will split completely in the future on domestic pig breeding advances.

43: Genetic characterization of wild boar populations in Japan, based on SRY gene haplotypes

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There are two subspecies of wild boar in Japan: the Japanese wild boar (JWB), and the Ryukyu wild boar (RWB) which inhabits the Ryukyu Archipelago. In this study to reveal the genetic property of Sex-determining region Y (SRY) gene variations on Y chromosome among wild boars inhabiting in Japan, we performed haplotype analysis using the polymorphisms in SRY gene. Samples of 139 RWB (from Iriomote, Ishigaki, Okinawa, Tokunoshima and Amami) and 32 JWB (from Kyushu and Honshu areas) were compared against 83 reference samples of European and Asian domestic pigs (Landrace, Large White, Duroc, Middle Yorkshire, Berkshire and Meishan). Primers were designed to cover the exon 1156 bp, including 3'UTR, and the promoter region of about 3000 bp. Four novel and two known polymorphisms (5 SNPs and one deletion) were detected and we reconstructed nine haplotypes of the SRY gene. The haplotype analysis indicated differences in the genetic background of paternal inheritance between the Asian domestic pigs, European domestic pigs, JWB and RWB populations. The RWB populations could be categorized into Central Ryukyu (Amami, Tokunoshima, and Okinawa) and South Ryukyu (Ishigaki, Iriomote) populations on the basis of a difference in only one polymorphism. Overall, our study suggests that the SRY gene characteristics of the RWB and JWB populations differ from those of European and Asian domestic pigs.

44: Influence of manatee diving on watercraft collision risk

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Watercraft pose a major threat to endangered Florida manatees. To assess factors that contribute to the risk of watercraft strikes on manatees, we studied diving behavior of nine manatees carrying GPS tags and time-depth recorders in Tampa Bay, Florida during winters 2002–2006. We applied a Bayesian formulation of Generalized Linear Mixed Models to depth data to model the probability (P_t) of manatees being above a depth threshold (1.25 m) as a function of behavioral and habitat covariates. When manatees were above the threshold, they were considered to be within "striking distance" of a watercraft. Overall, 78% of depth records (individual range 62–86%) were less than this threshold (mean=1.09 m, max=16.2 m depth) illustrating how vulnerable manatees are to strikes. In shallow waters (<0.91 m), the probability of a manatee being within striking distance was 0.96 (CI=0.93–0.98); the probability decreased as water depth increased. Probability of being within striking distance was greater over seagrass (P_t=0.96, CI=0.93–0.98) than over non-seagrass substrates (P_t =0.73, CI=0.58–0.84). Overall, manatees were at higher risk of being within striking distance in shallow water, over seagrass, during night, and while stationary or moving slowly; they were less likely to be within striking distance when ≥50 m of a charted waterway. Quantitative approaches to assessing risk can improve effectiveness of manatee conservation measures by helping identify areas for protection.

45: Peripheral isolation promotes diversification while increasing risk of extirpation among North American red squirrels

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North American red squirrels (genus: *Tamiasciurus*) are now of conservation and management concern due to their obligate association with mature forested regions. As a consequence of their dependence on healthy forests, isolated peripheral populations are under increasing risk of extirpation due to fire, disease, logging or some stochastic combination of factors. Their history of diversification, the distribution of genetic diversity, and evolutionary relationships among regional lineages are now being studied more intensively. Based on mtDNA and nuDNA markers, we demonstrate that red squirrels constitute multiple previously unrecognized lineages reflecting prolonged isolation in peripheral areas. In addition to a previous focus on refugial persistence occurring in the vicinity of Vancouver Island, BC, we report a distinct lineage associated with coastal refugia in Southeast Alaska – an important region for mammalian endemism – as well as multiple distinct sky-island forest isolates distributed throughout the desert Southwest. Conversely, widespread continental lineages indicate a propensity for rapid and extensive dispersal through continuous forested habitats with broad regions of secondary contact among lineages. Isolation-reconnection dynamics exemplify the history of diversification among red squirrels, further evidence for common processes influencing evolution of boreal mammals through North America. We highlight populations warranting critical conservation action, and assess taxonomic relationships among current species.

46^{E**}: Resistance of cotton mice (*Peromyscus gossypinus*) to pigmy rattlesnake (*Sistrurus miliarius*) venom

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Understanding how traits of prey vary between and within species is important for understanding ongoing evolution in predator-prey systems. Cotton mice (*Peromyscus gossypinus*) are eaten by the pigmy rattlesnake (*Sistrurus miliarius*), a generalist predator which uses venom to subdue its prey. Here we explore how resistance to venom in the native *P. gossypinus* differs from non-native model mammals and how the predator-prey interaction changes between geographically separated populations. We show that cotton mice display elevated resistance to pigmy rattlesnake venom compared to model species. Specifically, based on median lethal dose (LD50) assays, cotton mice are approximately 4x more resistant to pigmy rattlesnake venom than *Rattus norvegicus* and 5.5x more resistant than *Mus musculus*. We conducted additional toxicity tests with lab born offspring of wild caught rodents from two Florida populations (ANF and LWNWR). Pigmy rattlesnake venom was also obtained from field caught snakes at both sites. Pairs of mice (often siblings) were injected with venom from ANF and LWNWR at doses near the LD50. Preliminary results show that venom from LWNWR snakes caused quicker decline and higher levels of mortality at 24 and 48 hours compared to venom from ANF. These results demonstrate that species that are not natural prey may not be good models for assessing venom toxicity and that interactions between snakes and mice may differ across populations suggesting possible local adaptation. This research was supported by a Grant-in-Aid awarded to Sarah A. Smiley in 2012.

47: De novo identification of transposable elements recovers lineage-specific transposable element families

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Transposable elements (TEs) occupy large portions of eukaryotic genomes, are highly variable, and may have significant impacts on the biology and evolution of organisms. Therefore a proper and thorough annotation of newly sequenced genomes is of utmost importance. Often the repetitive portion of the genome is ignored in favor of protein coding genes or their regulators. In most cases TEs are identified based on homology to known TEs from related taxa. Unfortunately for these projects, TE annotations via homology are, by definition, only able to identify TEs homologous to known elements. Lineage specific subfamilies or even entire classes of TEs deposited via horizontal transfer may be missed, giving an inaccurate picture of the TE landscape. To demonstrate this, we preformed de novo TE analyses in 2 rodent genomes, the prairie vole (*Microtus ochrogaster*) and the naked mole rat (*Heterocephalus glaber*). Age distributions and overall TE content identified in each species varied based on distance to *Mus musculus* and *Rattus norvegicus*. In *M. ochrogaster*, 27.8% of the genome was derived from TEs with more than 110 Mb of lineage specific L1 identified through de novo analyses. Similarly, an additional 90 Mb of TEs were identified in the *H. glaber* genome overlapping 380 exonic regions, representing potential exaptation events. These observations demonstrate the necessity for de novo TE annotations in order to understand the activity of lineage specific TEs.

48: Preliminary data on the taxonomic status of the Everglades mink (*Neovison vison evergladensis*)

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The Everglades mink (*Neovison vison evergladensis*) is listed as a Threatened subspecies in the state of Florida. The Everglades mink appears to be geographically isolated in south Florida and is threatened by water level changes in suitable habitat, heavy metal toxicity, and canine distemper. The taxonomic status of the Everglades mink based on morphological data has resulted in different conclusions, thus it remains unclear whether the Everglades mink represents a valid subspecies. To begin to address this taxonomic uncertainty, I sequenced 943 base pairs of DNA from cytochrome-*b* for a sample of mink tissues from Florida (Everglades (n = 6) and Massachusetts (*Neovison vison mink*, n = 5) and aligned them against two published sequences of mink. I found a single haplotype in the samples from the Everglades and all samples shared one fixed difference from all other samples in the data set. Samples from Massachusetts had three haplotypes from eight variable sites and greater nucleotide diversity than the Everglades. Phylogenetic trees produced similar results with strong bootstrap support for a separate clade containing all samples from the Everglades. Preliminary data supports the designation of the Everglades mink as a distinct subspecies but nuclear markers and additional samples from mink in the southeast, including the two other subspecies of mink in Florida (*N. v. lutensis, N. v. hallilimnetes*), will be important in confirming these results.

49^E: Using fecal DNA to examine social structure in the North American porcupine

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The North American porcupine (*Erethizon dorsatum*) is a nocturnal mammal found throughout much of North America. It is often considered a pest by people but very little is known about its social structure. Nocturnal species can be difficult to observe directly so genetic data is valuable in determining behavioral information about the species. Using genetic data can be helpful as a way to determine behavioral information about a species such as mating systems, parentage, and relatedness. North American porcupines can be difficult to trap, however, because they typically excrete feces outside of their dens, there is ready access to fecal genetic information. Some researchers suggest that porcupines communally use winter dens when dens are in short supply. Others found that porcupines share winter dens based on relatedness. We used a common fecal DNA extraction technique that was adjusted for porcupine feces to address if North American porcupines den communally. By finding the best method of fecal DNA extraction for North American porcupines, we were able to access DNA for individuals and assess individuals across several microsatellite loci. Using this technique will help explain genetic variation, mating systems, and relatedness in North American porcupine populations and importantly help resolve the question of communal denning.

50^E: Drivers of morphological diversity in *Peromyscus leucopus* populations of northern Michigan

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How a species responds to climate change is likely to be a major determinant of success. Short-term responses to a changing environment may be accomplished via plastic development rather than genetic adaptation. For populations of white-footed mice (*Peromyscus leucopus*) in Michigan's Lower Peninsula, cranial shape is expected to have an effect on fitness at the individual level due to its importance for both feeding and sensory input. The baseline level of cranial shape diversity for *P. leucopus* is unknown, and it is also not known what factors may contribute to this diversity. I hypothesize that ecological effects such as forest type and presence of a congener will have a relationship with the morphology of the skull via plasticity, regardless of underlying genetic variation. In this study three populations of *P. leucopus* in different ecological circumstances are compared; the ecological scenarios correspond to forest type (boreal or temperate) and the presence of congeneric *P. maniculatus gracilis*. Mice were sampled at Cheboygan (boreal, *P. m. gracilis* present), Montmorency (boreal, *P. m. gracilis* absent), and Livingston (temperate, *P. m. gracilis* absent) populations. Genetic and shape data were analyzed using pairwise statistics, and categorical regressions were used to determine effect relationships with *P. leucopus* morphology. This study provides a mechanistic view of how small mammals respond to climate change and on the diversity of plastic development in wild populations.

51^E: Ontogenic development of *Akodon montensis*: a geometric morphometric approach

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Ontogenesis focuses on the developmental changes of an individual from the earliest stages of development to adulthood. Cranial ontogeny analyses provide improved understandings of the function in developmental, ecological, and evolutionary perspectives. Small rodents, such as the montane akodont (*Akodon montensis*), a sigmodontine species limited to a western region of the Atlantic Forest, makes an ideal study group given is relatively high abundance in forest remnants, large litter size, and quick population turnover yet little information exists in regards with the natural history or population ecology, In this study, we examined the postnatal ontogeny of the skull in montane akodont employing geometric morphometrics. We analyzed cranial ontogeny on skull photography, and implemented a 2-dimentional procrustes analysis for homologous landmarks. Principal component analysis (PCA) was used to identify the major latent variables of variation between age groups. Discriminant Function Analysis was used to test differences between age classes and between genders. Allometric variation was tested via a multivariate regression of the Procrustes coordinates against the log-transformation centroid size. We did not find evidence for sexual dimorphism. We found significant differences between age groups. Allometric variation was best associated with the braincase and the auditory bullae versus the rostrum, which best described allometry using traditional morphometrics. Multiple approaches to understanding ontogenic variation are valuable to improve understanding of allometry, as traditional morphometrics might be limited in applications.

52^E: Cranial ontogenetic variation patterns in *Oligoryzomy nigripes* from eastern Paraguay

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Cranial ontogenies of mammals are important for identifying the connection of function and form in ecological, developmental, and evolutionary contexts. The patterns of skull ontogeny and development are not well studied in most Sigmodontine rodents, including the genus *Oligoryzomys. O. nigripes* is a small Neotropical Cricetid rat found in the Cerrado and Atlantic Forest, (AF) in central, coastal, and southeastern Brazil, to eastern Paraguay. These rats are habitat generalists residing in primary, secondary, and forest vegetation, and in the AF is extremely important as this is among the top three most abundant species in remnants of eastern Paraguay. In this study we examined skull ontogeny development ranging from five age classes for both males and females. Discriminant Function Analysis and MANOVA were implemented to test significance between age classes and genders. Principal Components Analysis was implemented on twelve cranial variables to understand latent variables, which describe ontogenic variation. Finally, bivariate regressions were used to assess algometric skull patterns. Our preliminary analysis showed significant sexual dimorphism and significant differences between age classes. Major ontogenetic changes are associated with dental and rostrum characters. This study is important as improved understanding of morphology of *O. nigripes* will also aid in improvements in the micro-ecological and macro-ecological variation, evolutionary history, and biogeographic patterns of this taxa prevalent in important habitat such as the quickly disappearing AF.

53^E: Seasonal sex ratio variation of Gray Bats *(Myotis grisescens)* near a hibernaculum in southwest Missouri

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Sex ratio data of a *Myotis grisescens* population at a single large hibernaculum were studied across the winter and following fall and spring hibernating season by month. During the fall of 2013, a trend was observed skewing the expected 1:1 sex ratio. The ratio of males in early fall outnumbered that of females by 2:1 in September (N=40) and then reversed one month after in October to a 1:5 ratio (N=48). The previous hibernation season, December 2012-February 2013, the ratio of males to females was close to a 1:1 ratio and remained that way until early spring. From March to April of 2014 a trend of declining male presence was observed, changing from 4:1 in March (N=22) to 1:4 sex ratio in April (N=27). This trend suggests that males arrive first in fall in order to have first male advantage to breed, and leave first in order to establish territory in male summer and reduce competition with females for spring resources.

54: Changes in distribution and phenology of mammals in the Greater Gila Ecosystem

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The Greater Gila ecosystem supports high biotic diversity due to its confluence of multiple biomes and great elevational relief. This region has undergone natural transitions as well as anthropogenic modifications. Climate projections suggest the region will be heavily impacted by drying conditions in the future. To provide rigorous baselines to assess potential response of mammals to changing conditions, I am conducting literature, museum, and field surveys of the mammal fauna of the Greater Gila Ecosystem in New Mexico. For this study I have gathered data on mammal occurrences, community composition, habitat affinities, elevational distributions, migration-hibernation timing, and reproductive timing and success. With increasing threats to biodiversity, there is a growing need for natural history data and increased sampling to provide the critical materials that will be needed for new investigations of changing conditions. As the climate becomes warmer and drier documenting changes in species' distributions, phenology, and reproduction will be invaluable contributions in terms of conservation.

55: Investigating nutritional status of the West Indian manatee (*Trichechus manatus*)

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Insulin growth factor (IGF)-I and its associated binding proteins (IGFBP) are sensitive to nutritional status and plays a major role in somatic growth. Multiple IGFBP control the bioavailability of IGF-I, exerting both stimulatory and inhibitory effects on target tissues. In domestic animals under positive nutritional status, IGF-I and IGFBP-3 concentrations are elevated whereas IGFBP-2 concentrations are decreased. Under negative nutritional status, the reverse scenario occurs. The objective of this study was to investigate the nutritional status of the West Indian manatee (*Trichechus manatus*) by measuring IGF and IGF-BP in Florida, Puerto Rico, and Belize populations. Due to the low quality and quantity of available food to Belize and Puerto Rico populations when compared to Florida, we predicted that the Florida manatee would have adequate nutrition indicated by an increase in IGF-I and IGFBP-3 with a decrease in IGFBP-2. Serum samples were collected from adults during summer [Florida (n = 12), Puerto Rico (n = 20), and Belize (n = 21)]. The concentrations of IGFBPs were quantified using Western ligand blot and expressed as digital light units (DLU). Serum concentrations of IGF-I were quantified using heterologous radioimmunoassays. Puerto Rico (121.7 ± 9.4ng/ml) had reduced IGF-I concentrations compared with Florida (164.0 ± 12.1ng/ml, p = 0.01) and Belize (144.5 ± 8.7ng/ml, p = 0.08). As predicted, IGF-I levels in Florida populations were increased when compared to Belize and Puerto Rico populations suggesting that energy intake is greater in Florida populations.

56^E: Antler and body size in black-tailed deer: retrospective analysis of cohort effects

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For large mammalian herbivores, extreme climatic events and high population densities decrease forage availability and create cohort-wide declines in fitness. We examined harvest data from a previous study to determine potential cohort effects on body and antler size of 450 male black-tailed deer (*Odocoileus hemionus columbianus*) in central California, USA. Two models were created, each with numerous extrinsic variables to predict a single intrinsic variable (body or antler size). Extrinsic factors such as weather, specifically annual precipitation, during parturition and the first year-of-growth are often cohort specific, and have lasting effects on antler and body size in males. Female population density can affect forage availability greatly during critical stages of growth and development of offspring, and thereby also influence size of males later in life. In our study, female population density during the first year-of-growth had a more dominant effect than did precipitation on those male traits. Harvest of female deer resulted in increases in the overall size of males, even during years of drought. Extrinsic factors during gestation were important in determining antler size of male deer, but not their body size. Temperature during the year prior to harvest influenced both body and antler size of male deer. The insights that our study offers about the interactions between density-dependent and independent factors will enhance our understanding of the variable growth cervids exhibit among cohorts.

57: Synchronous changes in bush and rock hyrax abundances over 13 years in the Matopos, Zimbabwe

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Bush (*Heterohyrax brucei*) and rock (*Procavia capensis*) hyraxes (Hyracoidea: Procaviidae) are abundant small mammals and important prey for vertebrate carnivores in the Matobo Hills (Matopos), southwestern Zimbabwe. We monitored hyraxes at 20 observation stations in the 424-km^2 Rhodes Matopos National Park over a 13-year period (1993-2005). Hyraxes were identified to species, and counted and aged. For each species we used yearly counts to compute an index of relative abundance (AI – individuals/km^2) and age distributions to estimate productivity (proportion of the sample comprising juveniles). Time series analysis showed that annual fluctuations in AI were marked, but not cyclic, with ranges of 0.4-113.8% (median = 30.0%) for *H. brucei* and 3.7-64.7% (median = 11.0%) for *P. capensis*. Cross-correlation function revealed interspecific synchrony in annual fluctuation in numbers of individuals. A positive relationship existed between AI of *H. brucei* and rainfall of the previous austral summer, suggesting that annual precipitation contributes to fluctuations in abundance of this species. Synchronous fluctuation of the two species suggests a common response to other regulating factors in the Matopos. Potential causes of marked annual changes in AI of both species include parasitism/disease and wildfire. Presumed sampling bias in at least one year contributed meaningfully to variability in the AIs we report.

58: Body size and reproductive characteristics of deer mice in anthropogenic and native habitats in Kansas

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Body size is an important variable that has been used to examine effects of abiotic and biotic factors on species of small mammals. Often, a standard value has been used for a species, but we were interested in how plastic body size could be when examined in different environments. We used a common species in native prairies, the deer mouse (*Peromyscus maniculatus*), to examine factors that influenced body size and reproductive characteristics in north-central Kansas. In summer 1976, we collected 302 deer mice on 34 traplines, whereas in summer 1977, we collected 314 deer mice on three large grids. The first environmental factor examined was amount of precipitation present; March-June precipitation in 1976 was only ~40% of that in 1977, which was close to the 30-year average (1941-1970). The second environmental factor was habitat; we trapped deer mice in crop fields, old fields, planted grass and grazed upland and lowland native mixed grass prairies. We also examined number of males and females and their body size (indexed by both body length and mass) as biotic factors relative to environmental drivers. Our preliminary data suggest that body size is plastic and one size does not fit all and that reproductive characteristics are affected by both biotic and abiotic factors.

59^E: Intra- vs. Inter- generational tradeoffs in mammalian life histories

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Reproduction is thought to be costly for female mammals due to high energetic costs associated with pregnancy and lactation. Such costs are particularly high for young females, who are less experienced and smaller than fully-grown adults. These costs can manifest themselves within or between generations. Using lifetime survival and reproductive histories of 416 female golden-mantled ground squirrels (*Callospermophilus lateralis*) in Colorado, we tested for evidence of intra- and inter-generational trade-offs between age of first reproduction and fitness and its components. Females who waited to begin reproduction lived longer, yet, they did not experience a greater number of lifetime reproductive events, have larger litters, or have higher fitness than those females who began reproduction at age one or two. However, daughters had higher lifetime reproductive success if their mother delayed age of first reproduction, were born into smaller litters, or were born in one of the first litters of their mother. Daughters also had higher individual fitness when their mothers waited to begin reproduction, and when they were born into one of their mother's first litters. Thus, in our study system, the daughters, not the

mother themselves, bear the cost of their mothers' reproductive choices. These findings suggest that costs of reproduction can transcend a generation, and that inter-generational trade-offs should not be ignored when testing for costs of reproduction on survival or reproductive output.

60^E: Molecular systematics of *Geomys* based on two nuclear and two mitochondrial genes

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Phylogenetic relationships among members of the genus *Geomys* have been difficult to discern because of the conservation of morphological characters, presumably as a result of their fossorial lifestyle. Early studies of chromosomes and allozymes generated a few phylogenetic hypotheses, but most were hindered by taxonomic sampling and low resolving power of characters due to homoplastic events. In recent years, DNA sequence data has been obtained from two mitochondrial genes, 12S ribosomal RNA (12S rRNA) and cytochrome-*b* (*cyt*b) and one nuclear gene, retinoid-binding protein 3 (*Rbp*3), and used to generate phylogenetic relationships for all members of the genus. Herein, we utilize a combined dataset and include a second nuclear marker, the coding region of the alcohol dehydrogenase gene (*Adh-1*). Using a combination of molecular techniques and phylogenetic analyses, we were able to include many samples of *Geomys* and several *Cratogeomys* samples, a sister genus. Although this study is preliminary with only twelve species examined, the data appears to be useful for addressing phylogenetic relationships among the genus *Geomys*. However, more taxa and species of *Geomys* need to be further examined to obtain better resolution of the phylogenetic relationships in this group.

61^E: The prevalence of *Borrelia burgdorferi* in prairie dependent rodent species of northern Illinois

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Over the past twenty years, there has been a marked increase in the number of cases of Lyme disease in the United States. While the northeastern United States is known as an area of high Lyme prevalence, other parts of the country have also seen marked increases in cases. One such region is the area of northern Illinois and southern Wisconsin. This area is home to numerous prairie dependent rodent species including the primary reservoir of Lyme disease, *Peromyscus leucopus*. Studies have suggested that non-Peromyscine rodents may also serve as reservoirs of the disease, particularly among prairie dependent species. In this study tissue samples were collected from 307 rodents during the summer of 2014 on a prairie restoration in Boone County, Illinois. Four species were sampled (*Microtus ochrogaster, Microtus pennsylvanicus, Spermophilus tridecemlineatus, Zapus hudsonius*) with *M. pennsylvanicus* being the most abundant species. The presence of *Borrelia burgdorferi,* the causative agent of Lyme, was verified in all four species via PCR amplification of Flagellin B and Outer Surface Protein B, using *Borrelia* specific primers. Lyme disease was found in over 28% of animals tested with species-specific rates ranging from 18% to 37%. These data demonstrate that several prairie dependent rodent species harbor Lyme disease in appreciable numbers, and that at least some of these (*Microtus* spp.) may represent major reservoirs of the disease.

62^E: Prevalence of *Baylisascaris procyonis* in Southern California paratenic hosts

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Raccoons (*Procyon lotor*) are the definitive host for the roundworm, *Baylisascaris procyonis*. These parasites can infect paratenic hosts, such as small mammals, via fecal-oral contamination. Infection occurs when paratenic hosts forage at raccoon latrines containing *B. procyonis* eggs. Habitat fragmentation influences the abundance of raccoons and the prevalence of this parasite in both raccoons and paratenic hosts. Agriculturalization and urbanization increase landscape fragmentation and transmission of *B. procyonis* among its hosts. We aim to determine the prevalence of *B. procyonis* in several paratenic hosts in Southern California. Small mammals within a 50-mile radius of La Mirada, California were collected and necropsied to check for *B. procyonis* presence. Liver, lung, and brain tissue from the paratenic hosts were isolated and analyzed via light microscopy. We recorded the presence of *B. procyonis* in the animals, and calculated prevalence in the different species collected. Preliminary results indicate that *B. procyonis* prevalence is high in small mammals from highly urbanized areas of Southern California. Habitat fragmentation, resulting from urban development, increases transmission of *B. procyonis* among hosts. Disturbances in parasite-host relationships may influence health of all host populations.

63: Genetic variation and subspecific status of the grey wolf (*Canis lupus*) in Saudi Arabia

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This work represents the most extensive genetic study of the grey wolf (*Canis lupus* Linnaeus, 1758) in Arabia and the first considering genetic data from multiple locations within Saudi Arabia. Previous suggestion of the occurrence of two subspecies of wolves in Arabia is not supported by this study. The genetic evidence suggests that the wolves of Saudi Arabia are genetically variable and more closely related to the Eurasian wolf *Canis lupus* group (dog included) than to the Indian wolf *C. l. pallipes*. The genetic diversity observed for *C. lupus* in Saudi Arabia indicates that the subspecific status *C. l. arabs* should be retained for the Arabian wolf. What remains unclear is the degree to which genetic introgression from domestic dogs has influenced the composition and integrity of *C. lupus* in Saudi Arabia.

64: Towards a training research program in arid land mammals

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The education and training of undergraduate and graduate students is linked, among other factors, to the development of research programs and infrastructure within a given social, political, and economic context. The purpose of my presentation is to highlight different aspects related to the development of mammal research in temperate arid lands of Argentina, and the questions and approaches to explore particular ecological- evolutionary processes, the biology of a species or the structure of mammal communities. I discuss the ecological background or context of our investigations, highlight some results and the consolidation of a research program in animal biology and ecology of arid lands. I also discuss issues related to the scientific context in which we develop our research, and pinpoint some of the scientific gaps and critical environmental issues which deserve urgent consideration by the scientific community (*Partially supported by CONICET and SECYT grants PIP 5944 and PICT- 0455*).

65: Multi-use management of lands in southeastern New Mexico: some impacts of “development” on flora and fauna

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Semi-arid grasslands, characterized by shinnery oak (*Quercus havardii*) and honey mesquite (*Prosopis glandulosa*), occur in sandy-soiled portions of southeastern New Mexico and adjacent Texas. From at least the times of Clovis and Folsom cultures >10,000 years ago, Native Americans occupied this region into the 1800s. By the late 1800s, the area primarily was used for grazing cattle. Following discovery of oil in the 1900s, impacts of extraction of oil and gas initially spread slowly across the region with drilling of wells, construction of access roads, and installation of pipelines. However, as our needs for oil and gas have increased during the past 50 years, there have been significant changes over much of this habitat. While grazing cattle is still common, facilities used to extract oil and gas are conspicuous on the

landscape; e.g., access roads, oil and gas wells, storage tanks, compressors, power lines, pipelines, caliche pits, and hydraulic-fracturing ponds. Many species have been impacted by overgrazing, use of herbicides to remove native vegetation, and by removal of native habitat for installation of facilities used in extraction of oil and natural gas, potash mining, a nuclear waste disposal site, hazardous-waste disposal sites, and for other purposes. Not only are there impacts from direct removal of habitat, but there are significant impacts from noise and air pollution.

66: Models and mammals: the role of biogeography in promoting the conservation of mammalian diversity in the Philippines

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With over 100 million citizens in an area the size of Arizona, over 200 native species of mammals, and having suffered extreme deforestation (about 8% old-growth forest remains), the Philippine archipelago presents cause for great concern about biodiversity conservation. The models of biogeography that have been used in recent decades raise very different questions that lead research in different directions, and the results have great implications for conservation planning. Our recent studies on Luzon have shown that while the 70+ bats mostly occur in the lowlands and are widespread, most non-volant mammals are endemics occurring above 1000 meters elevation on isolated mountain-tops where the climate is cooler and wetter than in the lowlands. Native small mammals are competitively superior to exotic rats in primary and secondary forest. Persistence over geological time-scales has been the norm for many lineages, and speciation has produced about seven times as many species as direct colonization. Discovery of many previously unknown species has often resulted in designation of new protected areas, and empirical data from field surveys have been used by the government to assess priorities for protecting species. The increasing number of protected areas, steady growth in the number of young field-oriented biologists, and a markedly improving economy provide reason for cautious optimism about a country once derided as a "conservation basket case".

67: Eating and not dying: how mammalian herbivores cope with plant toxins

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Herbivory is a common feeding strategy among mammals; approximately 80% of all mammalian species include some plant material in their diets. Yet, at every meal, herbivorous mammals are faced with the prospect of being poisoned by naturally occurring toxins in plants. In my research group, we have been using a combination of approaches to understand the assorted ways in which mammals deal with plant toxins. Through these investigations, we have found that detoxification of plant secondary compounds is energetically costly, and that generalist herbivores are able to regulate intake of toxins at the level of a meal to avoid over-ingesting toxins. To understand differences in the detoxification abilities that exist between populations of the same species (*Neotoma lepida*), we have been characterizing specific detoxification enzymes and also examining patterns of gene expression in the liver. In addition to liver detoxification, we have discovered that degradation of plant toxins by gut microbes plays a key role in facilitating the ingestion of dietary toxins, and that these microbes and their function can be transferred to other populations and even other species of rodents. Finally, we have discovered behavioral mechanisms that mammalian herbivores use to manipulate plant toxins in order to circumvent toxicity. The mechanisms that herbivores employ in dealing with plant toxins may provide novel treatments for improving human health.

68: Assessing monkeypox prevalence in small mammal communities at the human-animal interface in DR Congo

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During 2012 and 2013, we collected small mammals in and around the villages of Baleko, Quatorze, Bokungu and Boende in the district of Tshuapa, Equateur Province, in the Democratic Republic of the Congo. The prevalence of monkeypox in this area is unknown; however cases of human infection have been previously confirmed near these collection sites. Samples were collected from 591 mammals (rodents, shrews, bats, pangolins, elephant shrews and a hyrax). Some rodents and shrews were captured from inside of houses where human *Monkeypox virus* (MPXV) cases were recently identified, but the majority of samples were collected from forested areas near these villages. The collection near Bokungu was conducted two months after a MPXV outbreak had been detected in the area and was part of the outbreak investigation. Real-time PCR and a modified enzyme-linked immunosorbent assay (ELISA) were used to investigate evidence of MPXV and other *Orthopoxvirus* infections in these small mammals. A summary of the animal samples collected and laboratory results from these samples will be presented and discussed.

69: Laboratory investigations of pouched rats (*Cricetomys*) and dormice (*Graphiurus*) as potential monkeypox reservoir species

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Post smallpox eradication, *monkeypox virus* (MPXV) has emerged as the most important human health threat within genus *Orthopoxvirus*. Thus far the natural reservoir(s) of MXPV has eluded identification; however several rodent species including African pouched rats (*Cricetomys* spp.) and African dormice (*Graphiurus* spp.) have been implicated. *Cricetomys* and *Graphiurus* are often found living in close proximity to humans (and invading homes); additionally *Cricetomys* spp. serve as a food source within Africa. It is important to utilize laboratory methods to examine the course of MPXV infection within these animals and thus determine these rodent species' competence as a viral host. We challenged *Cricetomys* with MPXV ($4X10^4$pfu) and assessed clinical symptoms and molecular markers of disease. Our results show that *Cricetomys* can be infected with MPXV and shed high loads of virus (with only 1 of the 8 animals perishing after MPXV challenge); thus, supporting the hypothesis of their involvement in the maintenance and transmission of MPXV. In comparison, African dormice challenged with 10^5pfu of MPXV had high levels of morbidity and mortality (5 of the 6 challenged dormice perished after infection). The results from this study indicate that African dormice are highly susceptible to MPXV and may not be a plausible reservoir of the virus within Africa. Our findings highlight the necessity of laboratory studies to examine potential reservoir host species.

70[**]: Bats, bedbugs, and Chagas disease: an olinguito connection

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The pop culture website "Urban Dictionary" defines an olinguito as "something hiding in plain sight." Here, we uncover an olinguito connection—one striking but overlooked—between a group of parasites, and their vector and mammal hosts, that explains the evolutionary origins of *Trypanosoma cruzi*, the parasite that causes Chagas disease. We conducted surveys of trypanosome DNA in mammalian tissues archived in museum collections, revealing that *T. cruzi* is nested in a cosmopolitan, diverse, and understudied clade of bat parasites. In addition, we analyzed published information to clarify the evolution of vector and mammal host preferences in *T. cruzi* and its close relatives. Triatomine bugs are insects widely associated with mammals including bats, and are the natural vectors of *T. cruzi*. However, at least experimentally, bedbugs are also able to transmit *T. cruzi*, and batbugs—close relatives of bedbugs—can transmit trypanosomes within bats. Taken together we draw upon this information to hypothesize that two host switches explain the origins of *T. cruzi*: 1) a vector host switch from batbugs to triatomine bugs, and 2) a vertebrate host switch from bats to terrestrial mammals. Both switches necessarily involved bats, emphasizing their important role in linking trypanosome parasites with their vectors, and suggesting a deeper time dimension for the role of bats in the origins of human diseases, compared with more recent bat-mediated emergence of viral pathogens. This research was supported by an ASM Fellowship in Mammalogy awarded to C. Miguel Pinto in 2013.

71^{E}: The role of prescribed fire in a region recently recolonized by black bears

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Black bear diets vary seasonally, especially throughout the summer, as various soft mast species produce fruits at different times. Measures of soft mast availability are an important component of assessing black bear habitat use, particularly in response to forest management practices, which are often designed to mimic natural disturbance regimes. To investigate the role of prescribed fire in black bear habitats, I measured soft mast production in the Ouachita National Forest in Oklahoma where bears encounter forests shaped by mechanical thinning and prescribed fires, rather than wildfires. I calculated Bray-Curtis dissimilarity indices based on percent cover of soft mast-producing species in relation to burning and thinning history. Burns 1– 2 years old are an average of 52% similar to each other. Burns 3–4 years old are an average of 28% similar to each other. Burns >5 years old are an average of 36% similar to each other. When recent thinning history is accounted for, burns of the same age but different thinning histories are on average 35% similar to each other. There is a lot of variability in soft mast production between areas with different recent thinning and burning histories, which makes it difficult to model soft mast production in the forest as a whole. Modeling soft mast production will ultimately be important in assessing the seasonal distribution of black bears in response to prescribed fire.

72^{E**}: Differences in day-roost habitat characteristics of *Artibeus lituratus,* between two disparate landscapes

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Habitat selection is neither arbitrary nor random, as both survivorship and fitness depend on animals evolving to make the best possible decision for maximizing both. Therefore, day-roost selection in bats should be for the optimal roosts available of this density-dependent resource. The great fruit-eating bat *(Artibeus lituratus)* occurs as an abundant bat species across both contiguous and matrix landscapes in the interior Atlantic Forest of eastern Paraguay. We examined differences between contiguous forest and a fragmented area based on measurable characteristics of roosts. We selected numerous habitat variables to characterize roosts based on previous studies. Roost characteristics included tree or vine species, whether the roost tree was alive or dead, diameter at breast height (dbh), tree height, location, aspect, and presence or absence of vine knots. Stand-level habitat characteristics included canopy height, canopy cover, grade and aspect of slope, distance to nearest taller tree, number of trees (≥ 10 cm dbh) within 10 m, vines (≥ 2 cm dbh) within 5 m, and quantity of trees (total and ≥ 70 cm dbh) recorded from a ten-factor prism timber cruise. Differences were significant; findings show disparities regarding several day-roosts variables, based upon the landscape in which *A. lituratus* occurs. Those differences suggest *A. lituratus* is selecting suboptimal habitat based on a roost-limited landscape. Understanding plasticity regarding habitat use is critical for mitigating ecological degradation, as contiguous habitat becomes increasingly scarce or marginal. This research was supported by a Grant-in-Aid awarded to Garret D. Langlois in 2014.

73^{TA,**} Socio-spatial organization and kin structure in ocelots from integration of camera trapping and noninvasive genetics

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Kin selection theory predicts that under certain conditions animals will tolerate related individuals in their home ranges. We examined the relationship between spatiotemporal overlap and genetic relatedness in ocelots (*Leopardus pardalis*) to determine if kin selection plays a role in structuring ocelot populations. We used 3 years of camera trapping to examine the spatial organization of an ocelot population on Barro Colorado Island in Panama, and we placed camera traps on ocelot latrines to match photographs of individual ocelots with microsatellite genotypes from feces. Male ocelots overlapped with ≤ 11 females, and females overlapped with ≤ 7 males. We detected no clear evidence of strict intersexual territoriality in either sex. Mean overlap among males was > 5 times more than overlap among females; however, spatiotemporal overlap was strong between some female pairs. Overall, overlapping individuals were more related to one another than was the sample population as a whole, consistent with the hypothesis that kin selection influences ocelot spatial organization. Additionally, we compared estimates of ocelot population density from noninvasive genetics with density estimates from camera trapping. Density estimates from the 2 techniques were highly comparable (1.74/km^2 from noninvasive genetics and 1.56/km^2 from camera trapping). These estimates represent the highest reported ocelot density within the species range. This research was supported by a Grant-In-Aid of Research awarded to Torrey Rodgers in 2012 and 2013.

74^{E}: Territorial calls analysis insights in the broad tailed bat (*Nyctinomops laticaudatus*)

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In addition to echolocation sounds bats produce social calls, conformed by 3 element types: chirps, trills, and buzzes. Some bat families perform vocalizations called “songs” to mate, and also those might be territorial warning calls; but its syntax remains to be understood. Our goal is to get information about mating calls’ patterns and its clarified function for a molossid bat species. We used ultrasound microphones to record vocalizations from a colony of *Nyctinomops laticaudatus*, during 3 periods through 2013–2014. We performed spectrogram analysis to characterize vocalizations with chirp number, duration, and acoustic frequency measurements. Results show males perform structured and complex songs. Vocal repertoire features 2 chirp types, trills and buzzes as in other species. Chirp A is a short descendent frequency modulated pulse of 8.05 milisec (*SD* = 3.53 ms); chirp B is a downward FM larger than A with an upward final segment of 43.93 ms total length (*SD* = 14.85 ms). Distinctively *Nyctinomops laticaudatus* performs songs of a series of 3 to 9 compound chirps, starting with B element of high plasticity. Additionally structure is modified by the syntax, with shorter phrases when the 1st element is a trill or a buzz.

75: Effects of coyotes on sympatric mesopredator activity patterns

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Coyotes are expanding their range in eastern North America and are likely to shift food web dynamics and behavior of other predators through interference competition and intraguild predation. We analyzed activity patterns of spatially overlapping coyotes (*Canis latrans*), red foxes (*Vulpes vulpes*), gray foxes (*Urocyon cinereoargenteus*), and bobcats (*Lynx rufus*) across the mid-Atlantic region using camera trap data from 29 parks. Camera traps were deployed at about 2,400 sites and captured 5,975 detections of the 4 predator species. Activity patterns of predators in areas of high and low coyote and bobcat relative abundance were used to test the effects on smaller predators. Red foxes shifted morning activity 4.4 hours earlier in high coyote abundance areas, although evening activity was unchanged. Bobcats shifted both morning (4.3 hours earlier) and evening activity (1.8 hours later) in areas of high coyote abundance compared to low abundance areas. Red foxes also shifted peak evening activity 1 hour later in areas of high bobcat abundance. Gray foxes did not change their activity patterns in areas of high and low red fox abundance. Smaller predators consistently shifted activity farther away from sunrise or sunset in areas with higher abundance of larger predators. Our results show how coyotes can change behavior patterns of other predators and show the potential for coyotes to have cascading effects on food webs in the eastern United States.

76^{E} Long-term radio tracking of pangolin

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The cryptic behavior and burrow-dwelling lifestyle make Taiwanese pangolins (*Manis pentadactyla pentadactyla*) difficult to study. In this study, we improved the method of fixing radio transmitters to the scale on their rump using antiwear screws and elastic straps. This significantly extended the periods of tracking. We were able to retrieve radio-tracked individuals about every 2 months to check or replace, if out of battery, the transmitters. From June 2009 to December 2014, we radio-tracked a total of 38 pangolins for various durations within an area of 24 km^2 on the Coastal Mountain Range in southeastern Taiwan. We also successfully monitored 4 (1.3) sub-adults and 4 (2.2) adults for a period ranging from 19- to 66-months. Long-term monitoring revealed that pangolins were extremely bound to their home ranges; not leaving the area once settled. Adult home range size did not change significantly between years. We confirmed 9 losses during the study period, which were attributed to poaching (*n* = 5) and deaths due to individuals accidentally stuck in the burrow (*n* = 4). One female was observed to have her 1st birth at approximately 36-months old, and subsequent camera-trap monitoring showed that the transmitter attachment did not impede the mother’s ability to carry the baby on her rump while travelling. Long-lasting radio tracking is of significant value to improving our knowledge of the pangolin.

77^{E}: Occupancy and distribution of carnivores within the Chernobyl Exclusion Zone

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Although it is widely recognized that acute radiation exposure can have negative impacts on wildlife, significant data gaps exist regarding effects of chronic exposure. The landscape surrounding Chernobyl is an ideal model to investigate chronic radiation effects on wildlife, as populations have been exposed to radiation for 29 years. Carnivores are of particular interest as their position at high trophic levels may facilitate accumulation of radionuclides in their tissues. Several carnivore species are reported within Chernobyl Exclusion Zone (CEZ), but little is known about these populations and no studies have used camera surveys to quantify distribution or relative abundance as a function of radiation intensity. Our research aimed to elucidate the relative influence of contamination and habitat variables on site occupancy rates of carnivores across the CEZ. During fall 2014, we deployed 93 scent stations spaced ≥ 3km apart, sampling of a range of habitats and contamination levels. From these trials we observed several carnivore species: raccoon dog (*Nyctereutes procyonoides*), gray wolf (*Canis lupus*), red fox (*Vulpes vulpes*), European badger (*Meles meles*), and pine marten (*Martes martes*), which were observed at 33.3%, 16.12%, 9.68%, 9.68%, and 7.53% of scent stations, respectively. Our results suggest several carnivore species are relatively abundant and widely distributed throughout CEZ. These findings represent a critical first step towards elucidating potential effects of chronic radiation exposure for wildlife inhabiting contaminated environments.

78TA: The absent niche: a historical perspective on the ecology of *Enhydra lutris* in California

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Historic ecology is increasingly relevant and important, allowing scientists to quantify ecological shifts and establish baselines for conservation efforts. Sea otters are key members of nearshore communities, which are highly productive and threatened ecosystems. Here, we use stable carbon (δ^{13}C) and nitrogen (δ^{15}N) isotope analysis of ancient sea otter bone collagen from four archaeological sites in southern and central California— San Nicolas Island (SNI), San Miguel Island (SMI), Monterey Bay (MBY), and Año Nuevo (ANU)— to quantify long-term changes in sea otter dietary ecology. We compared these data to δ^{13}C and δ^{15}N of modern sea otter whiskers from the same locations where data were available (SNI and MBY). We found ancient otters occupy much larger isotopic space, and likely had a higher degree of population dietary diversity than their modern counterparts. Additionally, at all sites but MBY, a large proportion of ancient otters had high □^{13}C values, implying a reliance on kelp-based prey. These data suggest that historically, kelp played a greater role as a food source for sea otter prey. Given the role of sea otters as a keystone species, it is possible that their local extirpation lead to a 'deforestation' of kelp in these systems and a collapse of local food webs. In the future we hope to expand this study in California, the Aleutian Islands and southeastern Alaska.

79: Comparative Andean small mammal ecology, and additional records of mammals from Guandera Biological Reserve, Ecuador

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In 2014 a mammal survey was conducted in an ecotone region (including páramo and temperate forest) on the Eastern Versant of the Andes in Carchi province, Ecuador. Sherman traps, Tomahawk traps, pitfall traps, and mist nets were used to collect mammal specimens at two sites (3,340 m elevation and 3,650 m elevation). A total of 142 specimens representing 14 species were collected from the survey area. The species collected include: *Didelphis pernigra, Microryzomys altissimus, M. minutus, Nephelomys albigularis, Neusticomys monticolus, Reithrodontomys soderstromi, Thomasomys baeops, T. cinnameus, T. rhoadsi, T. ucucha, Sturnira bidens, S. bogotensis,* and *Myotis.* One additional species (*Mazama rufina*) was salvaged as a partial skull only from the forest near the biological station. A comparison of effect of elevation on Ecuadorian rodents can be made by looking at past studies. These studies reveal an ecological gradient and turnover of cricetid rodent diversity (at the taxonomic level of tribe) that occurs between 2,070 m and 2,500 m.

80: Influence of pine forest fragmentation on southeastern fox squirrel (*Sciurus niger*) occupancy patterns

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Alabama's Talladega National Forest (TNF) has adopted management regimens promoting restoration of fragmented montane longleaf (*Pinus palustris*) forests. The objective of this study is to determine occupancy for southeastern fox squirrels (*Sciurus niger*) in TNF. Little is known about how southeastern fox squirrel populations are responding to dramatic changes in forest cover, so this research can be used to determine characteristics of suitable habitat. Previous studies have observed that fox squirrels usually select habitat that is predominantly pine, but with some hardwood component. Baited remote cameras were used to document squirrel presence in varying qualities of forested patches. Sites were selected using a stratified random design based on quality of fox squirrel habitat identified from USGS Gap Analysis Project (GAP) data. Habitat covariates were measured on fixed-plot local scale at the sites, stand basal area around the plot, and GIS based landscape scale. Occupancy for fox squirrels is currently being estimated using detection/non-detection data obtained from camera surveys. Initial models for detection data show that detection is moderately high, 68%, and is unaffected by survey covariates like Julian day, temperature, and rain. The null model estimates squirrel occupancy at 11%. Measured landscape factors do not play a large role in determining occupancy. More likely, local and stand covariates will show greater effects on occupancy, once these models are processed.

81TA: The effects of urbanization on genetic variation in the cotton mouse, *Peromyscus gossypinus*

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Anthropogenic forces such as habitat fragmentation and urbanization are known to impact a number of small mammal species. Studies of habitat generalists have indicated a mixture of positive and negative impacts of urbanization and fragmentation. This study focused on the effects of urbanization on the cotton mouse, *Peromyscus gossypinus*. The cotton mouse prefers hardwood hammocks but also can utilize urban areas as habitats. Eleven populations of cotton mice were sampled in both 1988 and 2009. During that time six populations experienced urbanization while the remaining five did not. Genetic variation was assessed within populations at both time points by sequencing a 784-bp region of the mitochondrial genome and genotyping specimens at seven polymorphic microsatellite loci. At both time points several metrics of genetic variation were assessed within populations. In all areas that experienced urbanization there was a decrease in both effective population size and migration rate in and out of populations. By comparison, populations in areas that did not experience urbanization experienced an increase in both effective population size and migration rate. Increased urbanization was also associated with a decrease in allelic richness and mean gene diversity. These results suggest an overall negative impact of urbanization on genetic variation in *P. gossypinus*. This demonstrates that native habitat generalists, capable of utilizing urban areas, are still negatively impacted by habitat modification associated with urbanization and fragmentation.

82: Risk assessment of roadway crossings in radio-collared mule deer on the Air Force Academy

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From 1988 to present, the Colorado Division of Wildlife (CDOW) and USAFA Natural Resources (NR) implemented a lethal management program to reduce the resident mule deer population on the 19000-acre USAFA reservation due to concerns of winter-browse overuse, decreasing deer health and fitness, and high deer-to-vehicle collisions. These efforts resulted in a 8-fold reduction of the mule deer population estimated at 1800 animals in 1990, reduced to current levels of 250 animals. Over this period, a reduction in deer-to-vehicle collision fatalities also occurred ranging from a high of 118 in 1990 to a yearly average of 20 from 2000 to present. A correlation of deer population to deer-vehicle collisions was 0.91 with a predictive regressive equation R^2 of 0.82. In addition, the proportion of the mule deer population struck by vehicles averaged 10% from 1988-2012, with an 11% strike rate during the high population period (1988-2004) and an 8% strike rate during the low population period (2004-present). This suggests that deer movements may also account for potential risk of deer-vehicle collisions. Thus, we evaluated fine-scale temporal movements of 14 radio-collared (LOTEK Wildcell) mule deer over an 18-month period at multiple scales to assess daily and seasonal movement patterns relative to roadways to assist in developing mitigation strategies to help reduce deer-vehicle collisions.

83: Sanctuary in city: a high-density Formosan Reeves' muntjac population in an isolated tropical urban forest

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Formosan Reeves' muntjac (*Muntiacus reevesi micrurus*) normally occurs in mountain areas and preferably in primary forests in Taiwan. Recently, a small Formosan Reeves' muntjac population was documented in Shoushan National Nature Park, a small (9.3 km^2) and isolated forest surrounded by urban Kaohsiung, the second largest city of Taiwan. To understand its population status and evaluate the effects of human disturbance and habitat fragmentation, we investigated the abundance, distribution, habitat preference, food habits and potential threats using camera trapping. We established camera traps 500 m apart at 35 points in a square grid, which covered 4 habitat types: tree-shrub mixed, shrub-dominated, vine-shrub mixed, and human-disturbed area in 2014. A total of 121,909 camera-hours yielded 4,327 images of muntjacs and 5,863 for other animals. Muntjacs occurred at all sites, but its frequency of occurrence was significantly different among habitat types, and decreased from north/west to south/east. Its estimated density was $14.9 \pm 16.8/ km^2$, which was higher than most mountain areas in Taiwan. Twenty seven plant species were identified as its food items, and mostly were common in Shoushan. Domestic dogs were highly overlapped with muntjacs in both space and time, and were the primary predator of muntjac here. Our findings indicated the muntjacs were abundant and widely distributed in this isolated area. Further investigations on the interactions between domestic dogs and muntjacs are suggested.

84: Ranging patterns and habitat use of striped hyaenas (*Hyaena hyaena syriaca*) in Lebanese human-dominated landscapes

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Increase in human population density is inextricably associated with the decrease in the abundance, distribution and home range size of local carnivore populations and leads to an increase in human-carnivore conflict. Though research has been carried out on the direct humans' effect on the ranging ecology of large carnivores, few studies are available on the Hyaenidae family. Moreover, no detailed studies have been carried out on striped hyaenas living in human-dominated landscapes. In this study we investigated the home range size and habitat use by striped hyaenas in Lebanon in two human-dominated landscapes, rural and urban, and the effect of environmental correlates on their ranging ecology. We trapped and radio-collared four hyaenas, two in each landscape. Distance per hour walked by hyaenas was longer in rural sites than in urban ones as well in moonless vs. full moon nights. The home range size of hyaenas living in urban landscapes has responded to the benefits of available urban refuse, and to the challenges posed by human disturbance, by reducing their home range by a factor of 5 and by much larger home range overlap. Despite this difference in home range size, all hyaenas showed greater preference for wild and urban habitats than agricultural ones. Understanding the ranging patterns and habitat use by hyaenas could help in resolving their conflict with humans and improve their conservation.

85: Bats and rats: Mammal communities and prescribed fire in the southern Appalachians

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Longleaf pine forests of the southeastern U.S. are a disturbance-adapted ecosystem requiring frequent low-intensity fires to maintain an open, park-like savannah. Regionally, significant efforts are being implemented to restore this once widespread ecosystem through use of prescribed fire. Our research objective was to examine how the mammal community responds to fire-based restoration activities in Alabama's montane longleaf forests. We measured small mammal abundance and species richness on 48 plots across 4 prescribed fire intervals: 2-3 years, 3-8 years, 8-12 years, and areas with no recent fire history (>25 years). We also used automated ultrasonic detectors to record bat calls on many of these same plots. Plots with shorter fire intervals were characterized by dense ground cover, open canopies, and few hardwoods. Small mammals were most abundant and species rich on plots associated with shorter fire intervals compared to plots with longer fire intervals. Bats were detected at all sites, but the greatest number of calls was recorded at sites with shorter fire intervals. Species specific identification of calls indicated that species of conservation concern such as the Indiana bat and the northern long-eared bat were detected on all sites including those with shorter fire intervals. These results suggest that prescribed fire management associated with restoration of longleaf pine is compatible with the habitat needs of many mammal species.

86TA: People homogenize how wolves but not cougars perceive the landscape

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After decades of persecution, large carnivores are returning to human-occupied landscapes in many areas of North America and Europe. To ensure the safety of both people and wildlife, we need to understand how these animals perceive and select habitat as they navigate through developed areas of the landscape. Here, I investigate habitat selection by wolves and cougars in a 20,000 km^2 landscape characterized by a marked gradient of urban and industrial development. I used data from over 15,000 km of wolf and cougar movement pathways collected during the past 22 winters in Banff National Park (Alberta, Canada) and environs. Using GIS software, I created habitat selection models by comparing 'used' resources (e.g., topography, habitat type) found along movement pathways with random points located <500 m from the movement pathway. I then compared habitat selection near developed areas with habitat selection in remote areas, >5 km from towns or roads. For wolves, topography and habitat cover had strong effects on habitat selection in remote areas, but not near developed areas. For cougars, selection for topography or habitat cover was unaffected by proximity to developed areas. These results suggest that people homogenize how wolves use the landscape and that cougars may be highly vulnerable to conflict with people. These results are being used to inform policy on land-use planning in areas where large carnivores and people co-exist.

87: Is the Homosassa shrew naturally rare in most habitats?

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The Homosassa shrew, *Sorex longirostris eionis*, is a state-listed species first identified in the 1950s with a highly restricted range, but now it's expected distribution encompasses the northern two-thirds of peninsular Florida. *Sorex l. eionis* has been captured in multiple habitats from cypress swamps and hydric hammocks to xeric sandhills and scrub. To assess habitat use and relative abundance we first examined museum records for *S. longirostris* collected in Florida to attain data on capture localities and habitat associations. We also obtained data from previous herpetological surveys, which used drift-fence arrays, and small mammal surveys, which used standard live-trapping protocols. We then established a set of drift-fence arrays to sample for *S. l. eionis* in additional habitats. Across all studies there was a total of 131,626 trap nights, with most in commercial pineland (28.3%), basin swamp (21.7%) and natural pineland communities (9.7%). Only 87 *S. l. eionis* were captured (0.007 captures per trap night). Captures per site ranged from 1 to 12 (mean = 2.3, *SE* = 0.45), but Homosassa shrews were rare at most sites (median = 1). Capture rates indicated *S. l. eionis* prefer natural pineland (34.4%), hydric hammock (29.9%), and xeric sandhill or scrub (18%) communities. Further analyses have provided little indication that there are vegetative communities where Homosassa shrews occur at high densities

88^{E**}: Using bat flies to examine bat dispersal in an island system

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Mammalian dispersal can be difficult to quantify, especially when migration is rare or started occurring recently. Estimating these rare or recent events requires sampling from many individuals and loci, which can be difficult to achieve. Because host-specific parasites track the evolution of their hosts and rapidly accumulate mutations, they can act as a high resolution marker of host population dynamics. It can be much easier to collect a population-level sampling of parasite individuals compared to their hosts. To assess the facility of using parasites to infer patterns of host dispersal, we studied the connectivity between populations of 2 bat species (*Tadarida brasiliensis* and *Erophylla sezekorni*) and their associated, host-specific bat flies across a known geographic barrier in the Bahamas. I used microsatellites to genotype individuals of *T. brasiliensis*, *E. sezekorni*, and their bat flies, which belonged to 2 species of the genus *Trichobius* (Family Streblidae). Preliminary data indicate bat fly populations are panmictic throughout the Bahamas, although bat populations are structured. This data suggests that bats are able to disperse between islands of the Bahamas, but these dispersals do not result in mating or are too infrequent or recent to be detected using our sampling of bat individuals and loci. In this way, bat flies may provide a tool for assessing connectivity of populations of their bat hosts.
This research was supported by a Grant-in-Aid awarded to Kelly Speer in 2014.

89^{E**}: Phylogeography of the Himalayan wood mouse (*Apodemus gurkha*) in Central Nepal

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Apodemus gurkha belongs to an ancient lineage that diverged from other apodemus during late Miocene. *A. gurkha* inhabits temperate and coniferous forests between 2,200 and 3,600m in Central Nepal and is classified as “Endangered” by the International Union for Conservation of Nature and Natural Resources with loss of habitat and fragmentation cited as major threats. Analysis of a 690 base region from Cytochrome b sequences of 29 individuals from southern Annapurna Conservation Area (ACA) and 13 individuals from the Manaslu Conservation Area (MCA) along with the single Cytb sequence available from GenBank (North ACA) show large and significant genetic differentiation between the populations from North ACA, South ACA, and MCA. Individuals cluster by locality forming 3 distinct clades corresponding to the geographic regions in a Neighbor Joining analysis. Narrow habitat requirement coupled with geographical barriers (Kali Gandaki River valley between North and South ACA and high mountain ranges between ACA and MCA) likely prevent gene flow as suggested by the low number of migrants (< 0.02) per generation and large F_{ST} values between South ACA and MCA ($F_{ST} = 0.96273$; $p < 0.00001$), South ACA and North ACA ($F_{ST} = 0.96710$; $p = 0.04199$), and North ACA and MCA ($F_{ST} = 0.97535$; $p = 0.05273$). *A. gurkha* populations are highly structured in the sampled regions and represent 3 distinct evolutionary significant units. Identification of evolutionary significant units, especially in an endangered species, can help prioritize areas for conservation efforts to preserve genetic diversity. This research was supported by a Grant-in-Aid of Research awarded to Nelish Pradhan in 2013.

90: Spatiotemporal diversification of a low-vagility Neotropical mammal clade (short-tailed opossums, Didelphidae: *Monodelphis*)

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Marsupials of the genus *Monodelphis* are widespread in South America, ranging from high-elevations in the Andes across Amazonia to the Atlantic Forest in southeastern Brazil and the temperate grasslands of northern Argentina. These species comprise small (< 200 g), terrestrial opossums, most of which are narrowly restricted to particular vegetation formations where they inhabit ground-level microhabitats. We estimated a time-scaled phylogeny using sequence data from 1 mitochondrial and 4 nuclear genes from 100 individuals representing 23 of the 25 currently recognized species of *Monodelphis*. We used biogeographic models to estimate ancestral distributions and infer causal processes of spatiotemporal diversification. Our results suggest that the earliest cladogenetic events in the genus occurred in late Miocene, with subsequent diversification from early Pliocene to late Pleistocene. Model selection suggests an important role for founder-event speciation, a process seldom accounted for in previous biogeographic analyses of continental clades. Two equivalently optimal models reconstruct the most recent common ancestor of *Monodelphis* as occurring in both Amazonia and Atlantic Forest. Those 2 areas hosted most diversification events within *Monodelphis* and were the historical sources of lineages that subsequently colonized the Andes, the Arid Diagonal (Caatinga, Cerrado, Chaco), and other neighboring biomes during Pliocene and Pleistocene. Possible mechanisms for founder-event speciation in *Monodelphis* include historically transient connections between currently disjunct biomes and rapid reproductive isolation of populations colonizing adjacent but ecologically disparate biomes.

91: Cryptic shrew diversity and fine-scale endemism on the Asian continental shelf

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The SE Asian biodiversity hotspots of Indo-Burma, Sundaland, Wallacea and the Philippines have a long history of serving as models for testing hypotheses regarding the long-term assembly of biotic diversity. The increased availability of phylogenetic data from these regions from relatively well-studied groups such as mammals has facilitated recent efforts to integrate genetic, distributional, geomorphic, and ecological data, thereby illuminating the processes that generated the region's megadiversity. We carried out phylogenetic and population genetic analyses of shrews (genus *Crocidura*) on the continental islands of Sundaland, focusing particularly on Sumatra and Java. We find high levels of previously unrecognized intra-island endemic diversity, highlighting the crucial interactions between coalescent-based species delimitation, traditional systematics, and especially increased survey efforts. The newly recognized patterns of endemism, in which no species is widespread on the continental shelf, indicate that evolutionary processes on these islands may be more similar to those reported for oceanic archipelagoes, such as the Philippines and Wallacea, than is currently appreciated.

92[E**]: Zoogeography of bats from Ecuador

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Ecuador is categorized as a megadiverse country with high levels of species richness and endemism for several taxonomic groups. The Order Chiroptera (bats) is currently the most diverse and studied group of mammals in the country. The most recent taxonomic revision recognizes 176 species, belonging to 8 families, distributed across 9 zoogeographic ecoregions. However, no formal analysis has been conducted on the geographic and biological determinants that account for the distribution patterns of bat species in the country. The main objective of this study is to test the influence of vegetation type, elevation, and the presence of the Andes mountain range on bat species distribution in Ecuador. A database, including biological and geographic information, of more than 11,500 records was generated. Primary data were obtained from fieldwork and associated notes, natural history museum voucher collections and databases, and published literature. The records were organized and evaluated using multivariate analyses. Preliminary results suggest a relationship among vegetation type, elevation, and species composition. Our results also recognize three major bat faunas: Pacific, Andean, and Amazonian. Species richness in the Pacific and Amazonian faunas is very similar, with 116 and 125 species, respectively, whereas the Andean fauna only includes 31 species. The majority of bat species in

Ecuador occur below 1200 m. This research was supported by a Latin American Fellowship awarded to Juan Pablo Carrera-E in 2012.

93^{E}: The phylogeography of endemic Sulawesi squirrels generated from high throughput sequencing of museum specimens

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Sulawesi is the largest island in the biodiversity hotspot Wallacea—an island that is demarcated by the biogeographic breaks of Wallace's and Lydekker's lines. The endemic mammalian fauna of Sulawesi is transitional between Asiatic and Australian faunas. Sulawesi's endemic squirrels (subfamily Nannosciurinae: *Hyosciurus*, *Rubrisciurus*, and *Prosciurillus*), have evolved a variety of phenotypes that allow a range of ecological niche specializations. Here we present the most complete phylogeny of this radiation, including both species of *Hyosciurus*, *Rubrisciurus rubriventer*, and 4 species of *Prosciurillus*, incorporating 14 samples from museum collections. High throughput sequencing technology was used to generate whole mitochondrial genome sequences (WMG's), in addition to a panel of nuclear Ultra Conserved Elements (UCE's) providing a large genome-wide dataset for inferring phylogenetic relationships. Our analysis revealed deep divergences between the genera, implying a long evolutionary history on Sulawesi. WMG and UCE signals were largely congruent, and well supported, except for the placement of the large and conspicuous *Rubrisciurus rubriventer*. The mitogenome analysis placed *Rubrisciurus rubriventer* between *Prosciurillus murinus* and the other species of *Prosciurillus* included. The nuclear DNA, however, showed a deep but monophyletic history for the 4 species of *Prosciurillus*. Mitochondrial capture events may have led to these disparate results. Further research of these species is warranted to fully resolve the evolutionary history of this adaptive radiation.

94: Spatio-temporal dynamics of mammals in a woody encroached southern African savannah

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The expansion of woody cover and subsequent loss of grass in tropical savannahs causes changes of global concern. Changes in vegetation structure and composition may reduce habitat availability and animal communities. We modeled the influence of temporal and spatial covariates on species richness and abundances across a gradient of woody cover in a southern African savannah for 2 years using camera traps and multi-species hierarchical Bayesian models. Temporal covariates showed higher detection probabilities and abundances for most species during the 2nd year of sampling and the rainy season. Habitat covariate results showed woody cover did not appear to be a strong predictor of mammalian species richness or mean community abundances, but percent grass cover was. Of the 23 species detected, one showed a negative response to woody cover. Eight species showed a positive association to grass cover. Our results indicate woody encroached plots are still used by a large number of species and therefore may provide some benefit to them. However, low detection rates and abundance estimates suggest a vulnerability to woody encroachment in the area for some species. Most importantly, our study suggests that an indispensable condition for maximizing species richness and abundances of vulnerable species is the maintenance of a high number of sites with adequate grass cover.

95^{E}: Browsing, bioturbation, and biodeposition by *Brachylagus*: burrowing influences the environment through multiple pathways

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Animals influence their environments through various pathways, including direct trophic interactions and indirect effects associated with engineering behaviors. Pygmy rabbits (*Brachylagus idahoensis*) inhabit the sagebrush-steppe of the western United States and are obligate burrowers, making them an ideal species for evaluating such pathways. Rabbits rely on sagebrush for food and concentrate activities around burrow systems, which often are associated with mima mounds. Our goal was to assess how pygmy rabbits alter vegetation and soil in the sagebrush environment. We predicted that the effects of rabbits would increase over time and that the net effect on sagebrush reproduction would be positive. We measured indices of 3 habitat alteration mechanisms (browsing, biodeposition, and bioturbation) and a suite of vegetative and soil characteristics on mima mounds with burrow systems occupied for 0 to 12 years at 2 study sites in east-central Idaho. Rabbits had significant, cumulative effects via all 3 pathways. We documented a decrease in sagebrush canopy cover and an increase in cover of herbaceous and disturbance-adapted plants. Plant-available nitrogen did not increase relative to burrow system age, but nutrients were markedly higher at burrow entrances, which increased in number over time. Two measures of sagebrush reproduction (inflorescences and seedlings) increased significantly with duration of rabbit occupancy. These changes potentially alter habitat quality for sagebrush-dependent species and illustrate the multiple pathways by which rabbits affect the sagebrush-steppe ecosystem.

96^{TA,E}: Niche compression enhances competition between two reintroduced carnivores

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Reintroductions and translocations are increasingly important tools for the conservation and recovery of carnivores, but the role of interspecific competition is often overlooked when reconstructing historic communities. American martens (*Martes americana*) and fishers (*Pekania pennanti*) are the 2 most commonly reintroduced carnivores in North America, but they are also direct competitors that exhibit strong interference competition. Both species have been reintroduced to a highly modified landscape in Wisconsin, and although fishers have flourished, martens remain an endangered species in Wisconsin. We assessed the role of competition in limiting marten recovery and tested 4 general carnivore coexistence hypotheses—1) spatial niche partitioning; 2) temporal niche partitioning; 3) differential habitat selection; and 4) dietary segregation—using occupancy models and stable isotope analyses. Contrary to previous research, we found that martens fell 99.99% within the isotopic niche of fishers and exhibited no partitioning of space, time, or resources with their primary competitor. Moreover, martens and fishers aggregated in space and time with mean occupancy probabilities of 0.37 and 0.86, respectively. However, fishers responded negatively to snow cover, suggesting this interaction could be mediated by snow conditions. We propose that this unique lack of niche differentiation is ultimately limiting the recovery of martens via enhanced competition, and hypothesize that this mechanism is a function of niche compression in Wisconsin’s homogenized landscape.

97^{E**}: Does seed dispersal by olive baboons affect germination of an invasive cactus in central Kenya?

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The North American cactus *Opuntia* has become widely established across semi-arid rangelands across the globe, and is a versatile and persistent invader. *Opuntia* was introduced to central Kenya in the 1940s and 1950s, and has spread rapidly across the region, to the detriment of local rangeland quality. Olive baboons (*Papio anubis*) are known to be the primary dispersers of *Opuntia* seeds in sub-Saharan Africa. Dispersal by baboons can increase germination rates of fruiting plants, and baboon populations exhibit mesopredator release elsewhere in sub-Saharan Africa. This association of baboon abundance with both large carnivore

declines and *Opuntia* establishment creates strong potential for a trophic cascade, in which declines of large carnivores actually exacerbate the invasion success of non-native plants, as mediated by increasing populations of a seed-dispersing mesopredator. We compared the rate of germination of *Opuntia* seeds from 3 different treatments: seeds from baboon scats, cleaned seeds from fruits, and seeds from fruits with pulp attached. We tested reports that *Opuntia* seeds germinate more successfully after a minimum 1-year period of dormancy by including seeds collected from the current year (January–March 2015) as well as seeds from each source type collected the previous year (February–April 2014). We show significant differences in germination rates between treatments and between age classes within treatments. These results have important implications for ongoing wildlife conservation and rangeland management efforts in Laikipia. This research was supported by an ASM Grant-in-Aid of Research awarded to Anne-Marie Hodge in 2013.

98: **Anti-androgenic effects of fungicides on small mammals inhabiting grape vineyards in western Xinjiang Province, China.**

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We conducted a field study using the small mammal assemblage naturally occurring in grape vineyards under heavy pesticide application to examine possible negative impacts. Four grape vineyards and 2 control sites without pesticide application were trapped for 5 consecutive nights, and 133 small mammals of 6 species were captured. Small mammals were returned to the lab and standard morphometric and organ weight data were taken for each animal. The herb field mouse (*Apodemus uralensis*) was the only species caught in large enough numbers for statistical analysis. We found that significantly more males than females were captured from both grape vineyards and control sites. Mice of both sexes from grape vineyards had greater body mass and were significantly less reproductively active than those from control sites. In males, gonadal weights demonstrated why they were less active; in pesticide-exposed mammals, there was a strong correlation between lack of reproductive activity and decreased gonadal weight. Grape vineyard pesticides included at least 16 different fungicides and several insecticides-herbicides, including many that are banned in the United States and Canada. Several of the fungicides used in these grape vineyards have known anti-androgenic activity, and likely led to our findings. These pesticides exerted insidious sublethal effects on exposed small mammals, which essentially shut down reproduction of this population of *A. uralensis*.

99: 300 million years of species co-occurrence patterns reveal a shift in community structure in the Holocene

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A major focus in contemporary ecology is understanding the patterns and causes of species associations. In this paper, we describe the spatial structure of 80 replicated fossil assemblages of plants and animals to reveal the frequencies of aggregated and segregated species pairs. Aggregated species pairs dominate from the Carboniferous (307 million years ago) to the early Holocene (10,000 years before present). However, in a Quaternary fossil pollen sequence, and 2 Quaternary mammal assemblages, there was a progressive shift towards more segregated pairs in recent times. This trend is also consistent with a meta-analysis of 260 contemporary assemblages, which are dominated by segregated species pairs. The pattern cannot be attributed to effects of spatial or temporal grain and extent of sampling, simple taphonomic artifacts, whether it is an island or mainland assemblage, or to increased variability in climate toward the present. Breakpoint analysis indicates that the trend towards fewer positive associations begins approximately 6,000 years ago, and may point to the increasing influence of anthropogenic effects over the Holocene. These results suggest that the organization of contemporary and Quaternary plant and animal assemblages may differ from those of deeper time slices.

100: The last ones standing: why mammalogists should care about Caribbean bats

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Counting a total of 58 extant species, many of them closely related, if not conspecific, with continental populations the Caribbean bat fauna seems at first depauperate and indistinct. Further, lacking key continental ecomorphs such as carnivorous, sanguivorous, or strictly nectarivorous lineages, its ecological diversity may appear massively reduced too. Species composition and beta-diversity, however, are poor guides to the value of this fauna. I analyzed the diversity of this mammalian fauna using new, dated phylogenies of major groups of Caribbean bats —including noctilionoids, natalids, and vespertilionoids— coupled with new metrics to quantify phylogenetic diversity and endemism. These approaches reveal the unique contribution of the West Indies, and in particular the Greater Antilles, to neotropical diversity. Despite low richness relative to the continent, the Caribbean harbors key paleo and neo-endemics without continental equivalents. These quantitative approaches reveal the extent to which West Indian bats contribute to overall diversity, and highlight islands and regions of unique conservation concern.

101: DNA barcoding of bats from the Dominican Republic: implications to Neotropical biodiversity

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Recent molecular studies have documented at least a 25% underestimation of biodiversity in bats from throughout the world. Bats comprise the majority of mammalian diversity in the Antillean islands but few molecular studies have compared the genetic diversity across the Neotropics. The International Barcode of Life (iBOL) project identifies the Caribbean as one noticeable gap in geographic coverage for

mammals. Our study looks at the first comprehensive barcoding survey of bats from the Dominican Republic and compares the genetic variation on the island to similar species on the continental mainland of South America and Central America. Of the 18 known extant species reported from the Dominican Republic, 14 species were DNA barcoded and represented by 150 individuals collected during a fieldtrip in 2015 that sampled several sites across the country. The 14 species were genetically distinct with interspecific variation greater than 15% and intraspecific variation less than 1% indicating that the barcode gap was sufficient in differentiating bat species diversity in the Dominican Republic. The low levels of intraspecific divergence indicate that the populations within each species are relatively homogeneous across the country. There were, however, several cases of high sequence divergence for widely distributed species that occur on both the Caribbean islands and the continental mainland. Further systematic study is needed to identify cases of cryptic species and implications to conservation biology.

102: Cuba's endemic mammals: current biodiversity, invasive species, and conservation threats

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The West Indies are a hotspot of biodiversity where 37.5 % of all known mammals become extinct. The current Cuban terrestrial endemic mammals are seven rodents (Capromyidae) and one soricomorph (*Solenodon cubanus*), all endemic; and 26 bats with seven endemics. The rodents belong to three genera: *Capromys*, *Mysateles*, and *Mesocapromys.* Many of the Cuban mammals in the threat category of IUCN or Red book of Cuban Vertebrates and almost all species exist in the Cuban System of Protected Areas. Of the total of the 15 current mammals, ten are Critical, Vulnerable, and Endangered. Conservation threats include invasive species, hunting, and habitat destruction. In particular, 150 vertebrates have been introduced in Cuba in the last 523 years, with 87 invasive vertebrates. The 35 invasive mammals (79.5% of mammals introduced) are the principal threat for Cuban mammals due to competition, predation and diseases. Cats, dogs, pigs, mongooses and rats, are the worst, with wide distribution. There is evidence of the predation of *Solenodon* and hutias by cats and dogs, and rats are present in all habitats, producing ecological perturbation and transmitting parasites and disease. Hunting is a problem for Cuban hutias, including threatened, isolated and smallest *Mesocapromys* species. Mining, tourism and deforestation also reduce the habitats of species. In the long term climate change could affect coastal habitats. The conservation condition and threats for each Cuban mammal are analyzed.

103: Hispaniola's endemic mammals: Current biodiversity, conservation threats and invasive species

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After searching many remote regions on the island of Hispaniola, The Last Survivors Project discovered that the island's last two endemic mammals, formerly believed to be rare, are in fact common in many areas. However, Hutia (*Plagiodontia aedium*) and Solenodon (*Solenodon paradoxus*) are at risk from invasive mammals and human pressures, and both could soon be in serious danger of extinction unless conservation NGOs and the Government of the Dominican Republic take effective steps. Invasive species have been reported as one of the leading causes of extinction in the world, and there is evidence that their arrival has caused the decline or extinction of species on Hispaniola. Conservation groups like SOH CONSERVACION, the Island Conservation, American Bird Conservancy, CEPF, Ministerio de Medio Ambiente and other NGOs are leading programs in the Dominican Republic that will benefit these species know and in the future.

104: Assessing spatial habitat use of terrestrial and arboreal mammals in the Dominican Republic

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Understanding the management actions required to conserve endangered small mammals can be challenging, particularly when there is a lack of even basic ecological knowledge. In some cases deployment of tracking technology can help inform species' management by providing important ecological outputs relating to habitat and resource use. We deployed radio telemetry and GPS units on 2 poorly-known, ecologically contrasting endangered species, the Hispaniolan solenodon (*Solenodon paradoxus*) and hutia (*Plagiodontia aedium*), to explore habitat use in agricultural and native forest systems in the Dominican Republic. Here we demonstrate the importance of tailoring the tracking-strategy adopted to the target species and address issues with technology development and design. Hutia appear to be restricted to native forest. Radio-telemetry of solenodon showed that they have larger ranges during the wet season and habitat preferences varied between study sites and between seasons: forest was often, but not always, preferred to pasture and crop areas. Examination of denning patterns indicated that den site availability is unlikely to be a limiting factor in the study landscapes, there being high numbers of used dens across different habitats. Furthermore, there were extensive movements of animals between dens, regardless of the season, even in the relatively short periods of radio-telemetry study.

105: Endangered Cuban hutias: Population genetics and biogeography in the context of an evolutionary radiation

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The endemic radiation of hutias on Caribbean islands is remarkable among rodents for its high rate of extinction since the Holocene (>50%), yet apparently persistent diversity in areas of intact habitat throughout the archipelago. Cuba remarkably contains 11 of the 14 living species of hutia, with surviving forms also on Hispaniola, Jamaica, and in the Bahamas. In this study, we perform population genetic analyses on Cuban species of hutia in the genera *Capromys*, *Mesocapromys*, and *Mysateles* to address major gaps in our understanding of their species limits, genetic structure, and geographic distributions. Comparing sequences of two mitochondrial genes (cyt-*b*, COI) from a set of 40 individuals collected at sites across the Cuban archipelago, we find evidence supporting the morphological hypothesis that *Capromys* contains at least three living species. A broader phylogenetic analysis of four genes (12S, GHR, vWF, and RAG1) and hutia relatives from nearby islands and South America finds an affinity between hutias and Brazilian echimyids such as *Carterodon, Trinomys*, and *Clyomys*. However, poor resolution of this clade currently argues against classifying hutias as an echimyid subfamily. We note that more detailed geographic sampling of Cuban hutias is needed to better assess population structure within species. With ~15% of forest cover intact and two-thirds as primary growth, we highlight Cuba as key for biodiversity conservation in the Caribbean, though continually threatened by invasive species.

106: Fossil assemblages of cave-dwelling bats: Tracking evolution and extinction in the Caribbean

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The most dramatic late Quaternary biotic phenomenon on the Caribbean was the extinction of most species of land mammals due to major climatic and environmental change after the Pleistocene–Holocene transition (PHT; 15–9 ka). Recent evidence shows that Caribbean land mammals such as sloths, monkeys, and large rodents survived until the mid-Holocene or later, a time interval corresponding to the first human arrival in the islands but characterized by small changes in climate, sea level, and land area than during the PHT. Particularly, Bahamian islands were much larger in the Pleistocene than today because of lower sea levels. These expanded islands were inhabited by many species of bat. Using newly radiocarbon dated bat fossils from archaeological (cultural) and paleontological (non-cultural) sites in the Bahamas and the Greater Antilles, we established a chronology for late Quaternary bat faunal change. Time-scaled ecological niche models (ENM) from the Last Glacial Maximum to the present reflect overall stability in distributions, with suitable climatic habitat being present over time. This shows that while commonly regarded as late Pleistocene fossils, bats were able to persist through the PHT. Nevertheless, they did not survive the past millennium of human activities. Now we see that extirpation of bats on these tropical islands is more complex than previously thought and primarily postdates the major climate changes that took place during the PHT climate transition.

107: Endemic primate extinctions in the Greater Antilles

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To date, 5 endemic Greater Antillean primate species have been described including *Xenothrix mcgregori* from Jamaica, *Antillothrix bernensis* from the eastern Dominican Republic, *Paralouatta varonai* and *P. marianae* from Cuba, and *Insulacebus toussaintiana* from western Haiti. The earliest fossil evidence comes from the Miocene site of Domo de Zaza, Cuba (14.68-18.8 million years ago). Despite this remarkably early first appearance, the vast majority of primate fossils are Pleistocene or Holocene in age with dates of last appearance occurring around 2000 years ago. Multiple causes have been suggested for rapid extinctions of native Caribbean mammals including climatic change, human hunting patterns, human mediated environmental change, and, in recent times, the introduction of invasive species. Additionally, body size may play a role in susceptibility to extinction. Given the relatively small fossil record for the primates, tracing patterns of extinction across the islands has been difficult; however, little concrete evidence for a human-mediated extinction of primates exists. Using postcranial and craniodental regression equations derived from 3-dimensional analyses of morphological shape, here, we reconstruct the body size of the Hispaniolan and Jamaican primates to be 3–5 kg and 10 kg for *Paralouatta* placing them into a body size range shown among some Caribbean taxa to increase vulnerability to extinction. Additionally, primates may have been competing with similarly sized sloths (e.g., *Neocnus*) and rodents (e.g., *Plagiodontia*; *Hyperplagiodontia araeum*).

108: Patterns of Quaternary evolution in Greater Antillean lipotyphlans

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The 2 Recent Greater Antillean lipotyphlan families (the extant Solenodontidae and recently extinct Nesophontidae) constitute the most ancient endemic land mammal clades of the insular Caribbean. Despite their general morphological conservatism, these lipotyphlans experienced substantial evolutionary differentiation during the Quaternary in terms of both cladogenesis and anagenesis. Combined morphological-molecular investigation of Hispaniolan solenodon (*Solenodon paradoxus*) samples demonstrates that distinct allopatric solenodon populations are associated with Hispaniola's 3 major physiographic provinces, with minimal levels of gene flow between populations. This phylogenetic pattern of evolutionary relationships is spatially noncongruent with that seen in Hispaniolan hutia, Hispaniola's other extant nonvolant endemic mammal. Two of Hispaniola's solenodon populations have extremely low effective population sizes, and we highlight the evolutionary distinctiveness of the "Critically Endangered" solenodon population in the Massif de la Hotte, southwestern Haiti. Newly collected *Nesophontes edithae* material from a stratified owl accumulation in Puerto Rico studied within a robust temporal framework (AMS and uranium-series dating) reveals that Holocene animals were more than twice the size of Late Pleistocene animals; stable carbon isotope analysis demonstrates that Holocene nesophontids were associated with closed tropical forests, and Late Pleistocene individuals occurred in open habitats. Late Quaternary climatically-driven biome shifts in the Greater Antilles were responsible for major body size changes in nesophontid lineages, driving considerable size variation that has been previously interpreted as sexual dimorphism or high coeval species diversity.

109: The evolutionary history of extinct Caribbean mammal radiations: insights from ancient DNA

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Until very recently, the Caribbean hosted one of the world's most diverse insular land mammal faunas, with approximately 100 endemic species of rodents, insectivores, sloths and monkeys. However, Caribbean mammals have experienced the most severe post-glacial extinctions of any mammal fauna, and today only 15 putative species, mostly highly threatened capromyid rodents, survive in the region. In order to better understand the origins and evolution of this fascinating and formerly highly diverse fauna, we have been working on the recovery and analysis of ancient DNA from a range of Caribbean mammal remains. In this talk I will discuss our ongoing work to reconstruct colonization events and the paleobiogeographic history of extinct Caribbean mammalian fauna. This will include a key component of the region's endemic fauna, the Antillean rice rats (Muroidea: Sigmodontinae: Oryzomyini), which became completely extinct within the recent historical period. Rice rats have been relatively poorly studied, but represent a potentially large evolutionary radiation. Applying an ancient DNA approach has allowed us to examine the number of rice rat species present, the number of colonisation events that occurred and the timing of these events.

110: High-contrast 3D imaging of fetal bats using microCT imaging

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Mammalian embryonic development is an exceedingly complex morphogenetic process. Comparative and developmental studies of mammalian morphology require detailed visualization of three-dimensional structures. Until recently, few methods existed for non-destructive 3D-volume imaging of mammalian anatomy. With the advent of microCT (X-ray microcomputed tomography) imaging, we can produce quantitative 3D images of small biological samples, including fetal mammals. Soft tissues are contrast enhanced with iodine staining to yield high-contrast x-ray images of a wide variety of hard and soft tissues. Images were post-processed using OsirixMD software to demonstrate tissue boundaries. The breadth of possible applications is illustrated with 3D microCT images of the head and cochlea of a series of fetal little brown bats (*Myotis lucifugus*) without destroying the specimens. Length, area, and volume measurements produce highly accurate quantitative data of morphological features. Such images are expected to yield a wealth of information useful in comparative, functional, and developmental morphology of fetal mammals.

111^{E**}: Evolution of the zonadhesin gene depicts a unique history during the origin on Eutherian mammals

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The reigning paradigm of cellular biology suggests that structure determines function with regard to protein interactions. Molecules that are directly involved in reproduction are often subject to rapid evolutionary change. Zonadhesin (ZAN) is a multi-domain sperm recognition protein that is crucial in species-specific fertilization. The mRNA for this protein spans more than 7 kb in most taxa with three domains that are directly related with facilitating the adhesion function of the protein, including a hemostatic glycoprotein called von Willebrand D (VWD) domain, mucin, and a receptor component. Mammalian VWD domains are highly variable between some taxa and conserved in others. The VWD domain mRNA sequences for sixteen different orders of placental mammals, including 54 species, were obtained from GenBank and Ensembl, aligned, and then analyzed using both Bayesian and maximum likelihood methods to generate a phylogenetic tree. In most cases, relationships corresponded to phylogenies recovered from other datasets. For example, Primates, Rodentia, Chiroptera, Perissodactyla, etc. each were recovered as monophyletic groups. Based on this study, baseline information suggests that variability among ZAN sequences in mammals is phylogenetically informative. This research was supported by an American Society of Mammalogists Grants-in-Aid awarded to Emma Roberts in 2014.

112TA: Natural selection determines palate shape and allometry constrains palate dimensions in New World leaf-nosed bats

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Why some groups of organisms are extraordinarily diverse, while others vary little in their morphology, is a key question in evolutionary biology. To date, most analyses rely on the neutral Brownian Motion (BM) model to infer how evolution has occurred. Natural selection on a continuous trait can be estimated using Ornstein-Uhlenbeck (OU) models that combine phylogeny and morphology to estimate the influence of natural selection on adaptive traits. Phyllostomid bats are an ideal system to test the role of neutral evolution or natural selection because they vary widely in palate shape and body size, and this variation correlates with dietary specialization. Using size-independent and size-dependent data sets, we tested 1) whether the BM or OU models better explained the evolution of palate dimensions, and 2) whether palate dimensions evolved independently or in a correlated fashion through allometric constraint. All analyses revealed four adaptive optima consistent with dietary specialization. However, the best-fit model for size-independent data was uncorrelated, suggesting that palate shape changes as if these elements were independent, contributing to ecological associations with plants and dietary specialization. For the size-dependent data, we found significant correlation between width, length and model parameters in the best-fit model, suggesting allometric constraints are important in phyllostomid cranial evolution. These analyses can be useful in exploring how ecological opportunity and allometric constraints affect morphological diversity in other groups of organisms.

113: Temporal patterns of diversification and disparity in opossums: a marsupial success story

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Opossums (members of the didelphimorph marsupial family Didelphidae) occur in a wide range of habitats from Canada to Patagonia and occupy a corresponding diversity of ecological niches. We recently completed a time-calibrated phylogenetic analysis of almost all (>97%) currently recognized species of opossums based on sequence data from 1 mitochondrial gene (CYTB) and 4 nuclear loci (BRCA, OGT, SLC38, Anon128, and IRBP). Our results suggest that the didelphid crown clade is descended from a South American rainforest ancestor that lived in the Oligocene, and that subsequent net diversification has been nearly linear, interrupted only by an anomalously long Miocene interval of zero net diversification, possibly attributable to a mass extinction event. Contrary to expectations from traditional scenarios of South American historical biogeography, we found no evidence that Panamanian

land bridge formation impacted the net diversification of this endemic lineage. Disparity-through-time analyses suggest that morphological differentiation was initially high but decreased sharply after the principal ecotypes represented in modern communities (arboreal frugivores, small terrestrial insectivores, large nonarboreal carnivores, etc.) made their appearance in the mid-Miocene.

114: Survey and Implication of Dental Anomalies found in Extant Sloths (Order Pilosa)

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Records of dental anomalies are known for representatives from all extant orders of tooth-bearing mammals, although the knowledge base is not always extensive or quantified. Recent recognition of supernumerary dental anomalies in two-toed sloths (*Choloepus*) has led to extensive reviews of extant sloth specimens (n = 881) to look for additional anomalies. The review revealed two primary types of anomalies, hyperdontia (extra teeth) and anodontia (loss of teeth), occurring at a rate of 2.4% (n = 21). Two-toed sloths were more likely to have hyperdontia in the anterior dentition, whereas three-toed sloths (*Bradypus*) experienced more frequent anodontia with the upper caniniforms. Both anomalies were found to occur in the two sloth genera. Most affected upper dentitions, while only three specimens exhibited mandibular anomalies. Aside from tooth positioning, anomalies were random with respect to age, sex, and geography. Specimens expressing incomplete anodontia (but not counted in the anomaly tally) indicate that the loss occurred postnatal, and was not an embryological anomaly. The findings provide new support for the hypothesis that *Bradypus* represents a neotenic lineage, and opens new possibilities about its relationship to the extinct ground sloths, with a suggested rooting above that of the basal position it typically occupies for Folivora.

115^{E}: Sexual dimorphism in skeletal indices of aggression is widespread in Carnivora

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Because lifetime reproductive success is often dependent upon the ability to compete for mates, males tend to be more specialized for physical competition than females. Among mammals, polygyny enforced by male-male competition is the most common mating system. However, variation in social structure may lead to differences in the relative importance of intraspecific aggression. Here we present a large comparative data set on sexual dimorphism in skeletal shape in Carnivora in order to test the hypothesis that male carnivorans are more specialized for physical aggression than females. We tested this hypothesis using a set of functional indices predicted to improve aggressive performance. Results from comparative analyses on 25 carnivoran species indicate that sexual dimorphism in skeletal shape is widespread and is positively correlated with sexual dimorphism in body size, a common proxy for the intensity of sexual selection. The best-fitting models for the evolution of skeletal shape dimorphism were associated with mating system as well as primary locomotor style (terrestrial versus arboreal).
Functional traits that are predicted to enhance performance in aggressive contests are more pronounced in males. Importantly, traits that enhance performance in fighting may entail functional trade offs with locomotor performance, indicating a possible conflict between natural and sexual selection in the primary locomotor system of a large set of mammals.

116^{E}: Are the pelvic-girdle and sacrum independent developmental modules?: A geometric-morphometrics analysis of integration in Rodents

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In mammals the pelvic-girdle plays an important functional role in locomotion. Resulting from the fusion between the innominate and sacrum (fused vertebrae) at the sacroiliac joint. Functionally, increased fusion in this system will dissipate more stress in the hind legs into the vertebral column at the cost of flexibility. Anecdotal accounts that the location of the sacroiliac fusion is not rigidly constrained within species prompted us to test if the sacrum and innominate persist as separate developmental modules, or

a single integrated structure. To test this a 2 species locomotory functional contrast between a quadruped rodent species *Phyllotis xanthopygus* (leaf-eared mouse), and a biped *Dipodomys ordii* (kangaroo rat) were chosen. In each species pelvic-girdle we quantified variation in sacroiliac location and pattern of modularity. Despite more sacroiliac variation in the biped, both had the same 2 module pattern separating the sacrum and innominate. To understand why there were differences in variation we tested a prediction of modularity, that if the functional relationships between modules increases, then the magnitude of integration will also increase, constraining the production of phenotypic variation. Finding greater magnitudes of integration between modules of the biped, we conclude that despite a common developmental pattern in both species, greater functional demands in bipedal locomotion has resulted in greater phenotypic constraint in the production of morphological variation in both the pelvic-girdle and sacroiliac fusion.

117^{E,TA}: Dental ecomorphology and evolution of Malagasy rodents (Muroidea: Nesomyinae)

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The native rodents of Madagascar are dentally diverse. We characterize nesomyine tooth morphology using both a developmental model that may constrain diversity and a functional model that may promote it. The Inhibitory Cascade (IC) model of molar-size development predicts that anterior molars constrain growth of posterior molars such that m1>m2>m3. The model was initially developed for murine rodents, but its predictions have never been examined for nesomyines, which exhibit substantial variation in molar size proportions. We analyzed molar size for 118 muroid rodents, including all nesomyine species and representatives of most muroid subfamilies, to test whether the IC model can predict the diversity of molar size ratios in nesomyines. We find that most nesomyines occupy a region of molar-size morphospace distinct from murines and most other muroids, suggesting that the IC model is not constraining relative tooth size in this clade. To quantify tooth crown morphology, we µCT-scanned 19 nesomyine species and extracted >250 shape measures per individual. We used these metrics to predict diets for nesomyines based on analyses of North American rodents for which we can predict diet category from tooth morphology with >95% accuracy. We find that nesomyines occupy three of six possible diet categories, with most species classified as omnivores. However, omnivorous nesomyines occupy different areas of morphospace, suggesting that dietary specialization is linked to dental diversity in this clade.

118^{E}: MHC variation and genetic population structure of *Artibeus jamaicensis* in Mexico

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The Major Histocompatibility Complex (MHC) genes are essential in pathogen recognition and triggering an adaptive immune response. These genes have become excellent models to investigate adaptive variation and natural selection because their crucial role in fighting off pathogens. Very little information on MHC patterns at geographic variation is available for bats. *Artibeus jamaicensis* is one of the most common and well-studied Neotropical mammal with generalist habits. We explored the genetic population structure and the footprints of selection in 15 collected localities of *Artibeus jamaicensis*. We assayed population genetics by using ten neutral microsatellites and one expressed MHC class II locus. We reported extensive polymorphism at both markers. Overall, 161 alleles from MHC class II gene were isolated from 193 individuals. Bayesian inference of positive selection suggest 20 amino acid sites that may have experienced positive selection (ω=4.167). Genetic diversity was relatively high in both markers (microsatellites = 0.86 and DRB gene = 0.978). In microsatellites, observed heterozygosity was 0.756±0.15 (±SD) and expected heterozygosity was 0.885±0.11 (±SD), all localities were in Hardy-Weinberg equilibrium. STRUCTURE and BAPS software detected signatures of population genetic structure assigned into five clusters. In MHC gene, we not found any genetic structure.

119^{E}: Microevolutionary analysis of large-scale dispersal patterns in the striped skunk (*Mephitis mephitis)* across Ohio

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The striped skunk (*Mephitis mephitis*) is commonly sighted mammal found throughout Ohio and the surrounding states. While not currently considered a primary reservoir species of rabies in Ohio, skunks have historically been included on that list and have the potential to become an active reservoir species in the future. This makes the skunk an important species in terms of wildlife and public health concerns. As a result we decided to use microsatellite markers to investigate the population genetics of the skunk across Ohio, looking for the microevolutionary signal of gene flow that would be indicative of long established dispersal patterns. Not only will this study help improve our baseline understanding of a widespread mammal species but evidence of historic movement patterns could provide a valuable insight to wildlife management and epidemiology should there be a major outbreak in the future. Preliminary analysis indicated a greater than expected genetic diversity among sampled skunks. We have also detected a strong East to West gradient in population differentiation as well as a division between the North-East and East Central regions of Ohio.

120: Molecular markers, modelling and morphometrics: Increasing our understanding of the platypus

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Armed with venom, electroreception, ten sex chromosomes and oviparity; the platypus (*Ornithorhynchus anatinus*) is easily one of the most bizarre and unique mammals on the planet. I will summarize the last ten years of my research on this curious mammal. I will explore the leap forward in understanding and research that followed the initiation and completion of the platypus genome project, ranging from a changed view on the movement of platypuses between adjacent rivers to the identification of genetically distinct evolutionarily significant units. The role of refugia and paleodistribution during the last glacial maximum will also be examined with regard to the impact of climate variables on the modern day occurrence patterns and genetic structuring. I will also discuss my current findings on cranial morphometrics and how these findings reinforce the differences between evolutionarily significant units. Finally, I will relate this research back to us, here in the US, and how we can apply a similar approach to gain a better understanding of our own semi-aquatic mammals. A highly vulnerable group of mammals that remain poorly understood compared to their terrestrial brethren.

121: Population genomics of a global urban invader, the brown rat (*Rattus norvegicus*)

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Brown rats (*Rattus norvegicus*) are one of the most populous mammals around the world, and their recent history is tightly coupled with humankind. However, the evolution and invasion history of rats as they established populations around the world are still poorly resolved. We are taking advantage of this massive unintentional experiment to investigate the population genomics of replicated invasions by human commensals. In this ongoing study, we are using phylogeographic inference, evolutionary clustering analyses, and demographic modeling based on genome-wide SNP data (ddRAD-Seq) to examine divergence and migration between global rat populations. Early commensalism of brown rats with humans is poorly understood, but likely included NE Asia, Japan, and major Chinese cities and agricultural centers. Brown rats later spread across Asia through Silk Road trade routes, and reached Europe in the 16th century. European colonists introduced brown rats to eastern North America in the 1750's, followed by human-assisted migration across the continent by the early 1900's. This rough historical outline presents a series of hypotheses that we examine using population genomics and phylogeographic inference. We are also using evolutionary clustering analyses and demographic modeling to investigate the number of distinct rat lineages around the world, the numbers of lineages that colonized different areas, and migration after divergence between populations.

122: Genetic variability of *Abrothrix olivaceus* (Rodentia, Sigmodontinae) among mainland and island populations of southern Chile

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Abrothrix olivaceus (Rodentia, Sigmodontinae) is characterized as being a species with a wide distributional range encompassing a distribution between southern Peru to the Patagonia. Previous phylogeographic analyses have reported that this species shows a well-marked structured pattern suggesting a strong local adaptation, with recognized subspecies, which is an interesting feature if we want to study patterns of genetic variability along distributional ranges. Previous phylogeographic studies have demonstrated that populations of the *olivaceous* mouse from the Chiloe Island in southern Chile, and from the mainland (e.g., Valdivia) would belong to the same clade, indeed to the same subspecies, *Abrothrix olivaceus brachiotis.* In this work we evaluated the genetic variability of *Abrothrix olivaceus* of the southern Chilean island of Chiloé, with populations of the mainland area of Chile. Genetic evaluation also included populations of additional subspecies of *olivaceus* in southern Chile. Specifically, we evaluated the effects that population's fragmentation of the Temperate Forests in southern Chile have had on the genetic variability of this species, as well as the historical effects of the last Pleistocene glaciation events that severely affected the biota of the study area. For the analyses, we used nucleotide sequences and microsatellite markers. Based on our results, we hypothesized a structured pattern of differentiation between fragmented populations of *olivaceus* on the island, and between the island and nearby populations of mainland Chile.

123: Spatial genetic variation and functional connectivity of Great Basin mule deer

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Quantifying the influence of climatic conditions, landscape features, habitats, and anthropogenic fragmentation on the genetic structure and variation of natural populations remains an important empirical challenge for understanding functional connectivity, and often, provides key insights for conservation and management. Biogeographic history is an important consideration when exploring geographic variation, and many species experienced Holocene admixture, especially large mammals such as mule deer (*Odocoileus hemionus*). We conducted an analysis of microsatellite genotypes and mtDNA sequences to examine the genetic structure of mule deer in the naturally complex and anthropogenically impacted landscapes of the Great Basin. We constructed genetic landscapes from spatial Principal Components Analyses (sPCA) and compared genetic variation against 5 classes of variables (distance, physiographic characteristics, climatic conditions, habitat features, and the anthropogenic footprint) using spatially explicit autoregressive approaches. Our results reveal low nDNA divergence among herds and a significant signal of isolation-by-distance, but the mtDNA reveals a signal of deep divergence among 3 geographically mixed clades, likely the result of Holocene admixture. Spatially explicit tests of observed genetic structure using information theoretic model selection revealed that multiple factors best explained the first 2 axis of variation along clines of variation. More broadly, our results highlight the power of the spatially explicit approaches in unraveling the best explanatory variables responsible for hierarchical landscape-based genetic variation and functional connectivity.

124^{E}: Inferring population structure of depleted eastern tropical Pacific spinner dolphins (*Stenella longirostris*) using RAD-seq data

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Millions of spinner dolphins (*Stenella longirostris*) were killed as bycatch in tuna nets in the eastern tropical Pacific Ocean (ETP). Despite over three decades of protection, they show little-to-no sign of recovery. Determining population genetic structure is vital to establishing biologically meaningful geographic boundaries for accurate population abundance estimates and corresponding stock mortality

limits. Until recently, molecular genetic studies had failed to verify accepted endemic subspecies due to a lack of statistical power. A number of factors (large historical population sizes, ongoing mating between subspecies, and recent divergence) combine to obscure the detection of population genetic structure in this system. Here we test for genetic structure using >1,000 neutral SNPs collected by applying restriction-site associated DNA sequencing (RAD-Seq) to 120 spinner dolphin samples. Preliminary results using traditional F-statistics and clustering analyses on neutral SNPs show significant differences between all three forms of spinner dolphins in the ETP. However, gene flow was detected between all forms, including between the endemic subspecies. High levels of asymmetrical gene flow were detected between whitebelly and eastern spinners. In addition, structure within subspecies indicates the potential for additional novel stocks. Our results support current management boundaries, and suggest fine-scale population structure might exist that warrant additional stocks within ETP spinner dolphin subspecies. We are also using these data to design single-SNP assays for genotyping degraded DNA within museum material.

125: Improving non-model mammalian genome assemblies using optical mapping technology

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Draft genome assemblies of non-model mammals typically have low N50 statistics and consist of many unplaced scaffolds and contigs. The fragmented nature of these assemblies limits downstream research applications focused on genome evolution, gene discovery and biomedical research. However, recent technological advancements allow for the rapid and accurate assembly of mammalian genomes. In particular, whole genome optical mapping can be used to drastically increase genome scaffold lengths and to examine the quality of genome assemblies more effectively than a sheer increase in sequence data. Here, we show how this technology has helped our team to improve the mouse lemur (*Microcebus murinus*) genome. We used the BioNano Irys platform to create an approximately 80x optical map assembly of the *M. murinus* genome. This assembly allowed us to perform hybrid-scaffolding and doubled our scaffold N50 statistic to over 7 Mb (longest scaffold 45.6 Mb). Moreover, we used the optical maps to screen for assembly errors and to confirm the presence of an approximately 500,000 bp inversion on the *M. murinus* X chromosome. Our results document the utility of optical mapping technology for the improvement of non-model mammalian genomes.

126^{E}: Status of swift foxes, *Vulpes velox*, in northwestern Texas

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The swift fox (*Vulpes velox*) is one of the smallest of the North American foxes. Swift Foxes were relatively abundant throughout the Great Plains through the early 1900's. Their historical range included short grass regions of the southern Canadian prairies south to Texas. They reportedly occurred in 79 counties of West Texas; now they are found only in Dallam and Sherman counties, the two most northwestern counties. We conducted surveys with sifted soil tracking stations, camera traps, and scent dogs on the Rita Blanca National Grasslands and private ranches in Dallam and Sherman counties, to determine the presence and habitats used by swift foxes and other carnivores. Three different vegetation types were surveyed: native grasslands, croplands, and exotic pastures. We found evidence of swift fox presence only on sites dominated by native short grasses. Predator avoidance by swift foxes may be a reason for them minimizing use of CRP (Conservation Reserve Program) fields and crop fields with growing crops and standing stubble left when crops are harvested. Vegetation over 25cm in height may obstruct the vision of swift foxes and increase their vulnerability to depredation by coyotes. We visited 89 natural den sites that were identified during 2002-2004 and none were being used. Swift foxes were present in the general area. The occurrence of foxes is localized in patches of native grasses.

127^{E}: Space use in a seasonal environment: antelope jackrabbits in the Sonoran Desert

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Knowledge of the basic ecology of small game species is crucial to understanding how animals use the landscape during a period of rapid and extreme changes due to human development and climate change. The antelope jackrabbit (*Lepus alleni*) is a large hare found in southern Arizona, USA and Mexico. Despite its large size and conspicuous presence on the desert landscape, little is known about the antelope jackrabbit. For this study, we tracked antelope jackrabbits across the Buenos Aires National Wildlife Refuge in southern Arizona across multiple seasons and years. Using data obtained from radio telemetry locations, we determined home range size and tracked seasonal movements of male and female animals. We used GIS to plot animal locations and overlay habitat layers to determine whether animals change their locations seasonally, possibly indicating a shift in habitat based on food or cover availability. Our results show male antelope jackrabbit home range size is smaller than female home range size and have not detected any significant seasonal movements. This study is the first to document the large but stable home range of antelope jackrabbits. This information will allow managers to more accurately anticipate seasonal antelope jackrabbit space use patterns within a unique and fragile arid environment.

128^{E}: Biodiversity assessment of small mammals, ticks, and tick-borne pathogens in South Texas

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The knowledge of biodiversity in south Texas is lacking due to large amounts of private land ownership in this area of the state that has been a barrier to conducting standardized biodiversity assessments. Through the East Foundation's stewardship program on their 218,000 acres of private land, we have the opportunity to document biodiversity of various vertebrate species, to serve as baseline data from which change can be monitored in the future given changes in land use and climate. Our primary objective is to create a baseline assessment of mammalian biodiversity of East properties across various habitat types. Because rodents are competent reservoirs for a variety of tick-borne zoonotic pathogens, we also aim to document the biodiversity of ticks and tick-borne pathogens that are associated with south Texas rodents. We utilized several capture techniques across two field seasons to document biodiversity. Here we present preliminary data of presence of tick-borne pathogens in the genera *Borrelia* (causative agent for Lyme disease and other diseases) and *Rickettsia* (causative agents for spotted fevers and typhus). Using PCR and DNA sequencing, we are screening both rodents and ticks for these tick-borne pathogens. Screening native fauna for tick-borne pathogens can create a general baseline of prevalence across the various habitats and rodent assemblages in southern Texas and could aid in determining tick-borne disease risk in the region.

129^{E**}: Characteristics of fisher (*Pekania pennanti*) reproductive dens in the southern Sierra Nevada

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Prior to the initiation of this study in 2007, only a handful of fisher reproductive dens had ever been located in the Sierra Nevada. As fishers are of particular conservation concern in the region, this lack of information made it difficult to identify and protect forest structures and habitat suitable for fisher reproduction. Between spring 2008 and summer 2014, we used ground telemetry to follow 34 adult female fishers with radiocollars to 247 successful reproductive dens on the Sierra National Forest,

California, including 74 natal dens, 173 maternal dens, and 7 assumed failed dens. Dens trees were located in elevations ranging from 1,040 to 2,070 m. As documented in other parts of the range, females used cavities in live trees and snags to shelter kits, with the exception of two hollow logs used late in the denning period. Females selected California black oaks (*Quercus kelloggii*) for natal (50%) and maternal dens (53%) more than any other tree species, followed by white fir (*Abies concolor*), ponderosa pine (*Pinus ponderosa*), incense cedar (*Calocedrus decurrens*), sugar pine (*Pinus lambertiana*), and canyon live oak (*Quercus chrysolepus*). Den trees were generally large in diameter and surrounded by relatively dense tree canopy. We present additional analyses related to fisher reproductive habitat and discuss relevance to regional conservation. This research was supported by a Grants-in-Aid Award given to Rebecca Green in 2012.

130^{E}: Photoreceptors of the Kangaroo Rat (Dipodomys ordii) and implications for UV-vision & activity patterns

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The visual system of species has far reaching implication affecting our understanding of foraging strategies, mating systems, daily activity patterns, intraspecies & interspecies interactions. ect. As part of an integrated research project aimed at determining whether the kangaroo rat (*Dipodomys ordii*) can communicate in the ultraviolet (UV), we used Immunohistochemical labeling (IHC) to identify photoreceptor proteins (Opsins) expressed in the retina. We constructed retina maps illustrating the relative densities of rod cells expressing Rhodopsin (Rho1), and of cone cells expressing Medium- Long Wavelength (MW/LW), and Short Wavelength (SWS1) Opsins. The retina of *D. ordii* has a uniform distribution and high density of Rhodopsin, high density of MW/LW opsins, and high but variable densities of the SWS1 opsin across the retina. Our data led us to conclude that *D. ordii* has some degree of UV-vision. The composition and densities of MW/LW & SWS1 expressing cone cells resemble that of a crepuscular / diurnal species thereby supporting previous authors who have suggested *Dipodomys* displays crepuscular and diurnal activity patterns. The uniform and high density of Rhodopsin also confirms that the species has visual acuity at night. Visual acuity in low light might be associated with known avoidance of activity during high moonlight intensity; we propose that the species could easily compensate for loss of foraging due to high moonlight nights by foraging during crepuscular or diurnal periods.

131: Visual modeling of the kangaroo rat (*Dipodomys ordii*) and implications for UV communication

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Potential UV-communication in the Kangaroo rat (*Dipodomys ordii*) has been validated through multiple hypotheses previously tested. Hypotheses include: (1) morphological markings reflect UV-light (2) the cornea and lens transmits UV-light (3) relatively high densities of all three mammalian retinal photoreceptor proteins (Opsins) including short-wavelength sensitive type 1 (SWS1), middle / long-wavelength (MWLW), and Rhodopsin type 1 (Rho1). Here, we present a mathematical model that includes maximum absorption (λMAX) of the three retinal Opsins along with quantitative UV-reflectivity data of morphological markings and various environmental light intensity conditions (nocturnal and diurnal) to extrapolate how each Opsin contributes to the visual capacities of the species. We found that even under nocturnal conditions, the species could utilize the SWS1 Opsin (UV-sensitive) for communication. Our diurnal model suggests the species has visual acuity during the day and supports previous anecdotal accounts of daytime activity when UV-vision would seem most adaptive. With a visual system well suited for nocturnal and diurnal activity, *D. ordii* might display a more diversified temporal activity pattern than previously thought.

132: The giant woolly rats of New Guinea (Muridae: *Mallomys*): systematics, biogeography, and natural history

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The genus *Mallomys,* the "giant woolly rats," is distributed primarily within montane forests above 1,100 meters in New Guinea's Central Cordillera. These very large murid rodents also occur in certain outlying montane areas, including the Arfak Mountains of the Vogelkop Peninsula, the Foja Mountains of the Mamberamo Basin, the mountains of the Huon Peninsula, and Mt. Bosavi in the Kikori River Basin. The status of *Mallomys rothschildi* and *M. aroaensis* as distinct biological species, recently questioned in the literature, is re-confirmed. The distribution and elevational associations of *M. aroaensis* and *M. istapantap* are clarified, and sympatric interactions between *M. rothschildi* and *M. istapantap* are shown to span most of New Guinea's Central Cordillera. Previously published records of *M. aroaensis* from the Snow and Arfak mountains are shown to represent *M. istapantap* and a new species, respectively. *Mallomys hercules* from the Huon Peninsula is recognized as a species distinct from *M. aroaensis*. In eastern New Guinea where *M. aroaensis* and *M. rothschildi* occur sympatrically, the 2 species are distinguished by different fur colors, grey and black respectively. However, in the absence of *M. aroaensis* in the western Cordillera, *M. rothschildi* presents as both black and grey color morphs. We identify three new species of *Mallomys* from isolated mountain ranges and interpret ecological and behavioral information for the genus in light of these taxonomic changes.

133: Adaptive roost selection by Rafinesque's big-eared bats (*Corynorhinus rafinesquii*) in relation to management history

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I tested the hypothesis that roost selection by Rafinesque's big-eared bats (RBEB) in South Carolina varies with site characteristics, particularly land-use history. The study was conducted at the Savannah River Site (SRS), a site that has experienced considerable disturbance for >100 years, the Webb Wildlife Management Area (WWMA), a relatively undisturbed site, and Groton Plantation (GP), a site that has received intermediate amounts of disturbance. Transects (50 m wide by 1-2 km long) were searched for trees with cavity volumes >130 dm^3 and the presence of RBEB. Eight logistic models were developed and 5 of those models were also run with a site interaction term. The Cavity*Site model had the greatest support. Similar to other studies, bats at all 3 sites selected smooth textured cavities with significantly larger volumes than unused cavities. However, cavity volumes of trees used at the WWMA were nearly 4 times as great as those used at SRS and 2.7 times greater than those used at GP. Further, at WWMA only 7.7% of the roosts were in trees other than cypress or tupelo whereas, 31.2% and 31.4% of the trees at SRS and GP, respectively, were in trees other than cypress or tupelo. These data suggest that use and selection of roost trees varies with availability and bats may be less selective in lower quality sites.

134[E,TA]: Nectar bats reliance on visual, olfactory, and acoustic cues in flower choice

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Nectar-feeding bats in the Family Phyllostomidae serve as important pollinators of wild and agricultural plants in the Neotropics, yet the manner in which these bats use their sensory systems in flower choice is not well understood. We experimentally examined the use of vision, olfaction, and echolocation in flower choice in 24 wild-caught individuals of the species *Lonchophylla robusta* at the Wildsumaco Biological Station in Ecuador. To assess the role of visual cues, individual bats were acclimated to a flight tent and presented with a 3 by 2 array of artificial flowers of 2 size classes—large (petals 35 mm in length) and small (petals 20 mm in length), and 3 colors— white, light green, and pink. Experiments on the use of olfactory and acoustic cues tested bat preferences for 3 experimental concentrations (0%, 20% and 40%) of honey-water and the presence of *Burmeistera* scent under conditions of minimal light while using an ultrasonic bat detector to monitor echolocation activity. In our tests of visual cues we found that these

bats exhibited a significant preference for large and white flowers, while our olfactory-acoustic cue tests suggest that *L. robusta* uses echolocation to locate a food source (i.e., artificial flower) but then switches to using olfaction to choose on which particular flower to feed.

135^{E,TA}: Vocal ontogeny in grasshopper mice (*Onychomys*)

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Isolation calls produced by mammalian neonates are a fundamental form of acoustic communication. However, the relationship between pup calls and vocalizations produced later in life under different social contexts is poorly known. We investigated the ontogeny of vocalizations in 3 species of grasshopper mice (*Onychomys arenicola*, *O. leucogaster*, and *O. torridus*), a genus renowned for its audible long-distance advertisement calls. We identified 4 call types, 2 of which appear to be precursors to the adult long-distance call and ultrasonic vocalizations produced in close-distance mating contexts. Pups were highly vocal during the 1st weeks of life, but greatly reduced call production prior to weaning. In addition, many pup vocalizations exhibited strong nonlinearities (subharmonics and deterministic chaos) rarely found in adult calls. We discuss our findings in relation to developmental milestones to highlight how shifts in signal form correspond to distinct selection pressures throughout life.

136: How ecological variables influence social network structure and fitness in *Octodon degus*

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Within a population, animal social structure can influence the types and extent of competitive and socio-sexual interactions with conspecifics. Thus, understanding social structure is critical to developing a comprehensive understanding of the evolution of sociality and cooperation. Ecological variation is an important driver of social interactions that influence social structure. Evidence suggests social interactions are beneficial to species that live in unpredictable environments where ecological conditions cause some years to be more "harsh" than others. Across taxa, social network analyses are repeatable and comparable methods to examine how social structure relates to environmental variation. The objective our study was to determine if environmental conditions influence social network structure in the degu (*Octodon degus*), a semifossorial rodent endemic to Chile. To achieve this objective, we conducted social network analyses using live-capture data from multiple seasons and across 8 years. We are determining if sociality is increased in years with low food abundance, high animal density and high burrow density. We also examine if increased interactions among group members enhance the direct fitness of adults by examining the slopes of regressions of social network structure and direct fitness across years. Funding: NSF IRES, UTC PRSA

137: Comparative phylogeography of a Beringian mammal-parasite assemblage

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Mammals exhibit complex histories of dispersal and diversification across the Holarctic, with Beringia playing a central role in mediating these histories. Parasites offer independent perspectives that can refine our understanding of mammalian histories. For example, red-backed voles (genus *Myodes*) represent a diverse group of rodents with both deep and shallow histories of colonization across Beringia into North America. Several species of *Myodes* are parasitized by the tapeworm *Arostrilepis macrocirrosa*, and examining population histories of this parasite may allow tests of histories inferred for *Myodes.* This study aims to resolve the phylogeographic history of *A. macrocirrosa* and compare this history to that of its rodent hosts. We use molecular tools to evaluate patterns of geographic isolation, dispersal, and change in effective population size. Our data reveal that *A. macrocirrosa* tracked its host *Myodes rutilus* across Beringia from Eurasia. Once in North America, new host associations resulted in

host-switching. Thus, this study is illuminating the dynamics of complex host-parasite systems during episodes of range expansion and community reshuffling.

138^{E}: Exploring arvicoline colonization history across Beringia: a molecular phylogenetic analysis of a tapeworm species complex

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Beringia, the region spanning eastern Siberia and northwestern North America, was uniquely impacted by climatic oscillations of the Quaternary with the opening and closing of the Bering Land Bridge. The land bridge facilitated the exchange of species between Eurasia and North America, and phylogeographic investigations of mammalian histories are revealing the direction and timing of faunal movements. For example, studies investigating arvicoline rodents (e.g., *Myodes*, *Microtus*, *Lemmus*) have revealed deep and shallow colonization events across Beringia, with complex histories of expansion, contraction, and diversification. These northern rodents are parasitized by a tapeworm species complex (genus *Arostrilepis*) that has tracked its hosts throughout the Quaternary and provides a window to the ecological dynamics of shifting host distributions. We use a molecular phylogenetic approach to examine the history of *Arostrilepis* in light of hypotheses for transberingian dispersal events by its rodent hosts. As predicted from host histories, we reveal multiple Nearctic colonization events by *Arostrilepis* species, but we also identify signatures of complex co-evolutionary processes such as missing-the-boat and host-switching. These events highlight the complex history of faunal assembly associated with Beringian mammal-parasite assemblages.

139: Phylogeography of Mongolian pika

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Central Asia is a dynamic landscape that contains diverse fauna and ecosystems. Broadly distributed mammal taxa in Mongolia can provide insight into the role of landscape in shaping diversity. Current ranges of pikas, genus *Ochotona*, in Mongolia are poorly understood due to difficulties in morphological identification and overlapping distributions. In this study, we are examining diversity and distributions in *O. hyperborea, O. pallasi, O. alpina,* and *O. dauurica*, the four species present in Mongolia today. Using a phylogeographic approach, we address questions regarding structure and demography of current pika populations across a climatically and topographically diverse landscape, namely: 1) Is there gene flow between what appear to be disjunct populations? and 2) What is the geographical distribution of species and diversity of current populations? Preliminary results based on our sampling suggest that our current understanding of species ranges do not accurately reflect the distributions of pikas in Mongolia. *Ochotona hyperborea* and *O. alpina* show possible range extensions, *O. hyperborea* eastward and *O. alpina* westward with some genetic structure in each species. *Ochotona pallasi* has genetic structure, however it does not appear to be driven by geography as several distinct lineages occur sympatrically. These results suggest that divergence within *O. pallasi* predates the formation of their current distribution, but more sampling is necessary to fully resolve the distribution, diversity, and relationships of Mongolian pikas.

140: Phylogeography of the North American meadow vole (*Microtus pennsylvanicus*)

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The Nearctic endemic meadow vole (*Microtus pennsylvanicus*) inhabits a wide latitudinal and longitudinal gradient across North America, covering Alaska, Canada, much of the NE United States and along the Rocky mountains into northern New Mexico. Isolated populations have been identified in Washington, Florida, and Mexico with insular populations in Alaska and along the Atlantic Coast. This study aims to increase phylogenetic resolution and historical biogeography of this species. There have been many studies noting the distribution of the meadow vole, but little is known of the evolutionary history. Here we present preliminary phylogeographic analysis of *M. pennsylvanicus* based on mitochondrial data. Genetic

structure suggests recent post-glacial expansion north with established populations found in the south, this based on lower levels of genetic variation found in northern latitudes. In the future, we will include multiple nuclear loci to better understand the distribution of genetic variation within this species. This phylogeographic study will aid in understanding the colonization of northern latitudes following the Pleistocene, shedding light on possible glacial refugia, colonization corridors, and distinct genealogical lineages that can be compared with other northern colonizers to better understand the effects of climate change on mammals. Our study will aid in the proper management of populations of significant genetic variation that are geographically restricted, emphasizing insular populations and continental isolates located along the southern limits of the meadow vole.

141: Small mammal communities in experimentally manipulated sites within the Flint Hills tallgrass prairie

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In 1981, we initiated the Konza Prairie Small Mammal Research Project focused on tallgrass prairie that was manipulated by fire and grazers, varied in topography, and experienced highly variable weather within and among years. We used standardized procedures to sample small mammals in 14 local sites during autumn and spring (autumn 1981–spring 2012). During the 32 years, we captured $\geq$ 1 individual of each species present (13 rodents; 2 shrews) in this region of Kansas. Total species recorded over the study period varied noticeably among local sites (autumn: 9–13; spring: 6–9). Average richness per sampling period in each local site was much lower than the total (autumn: 2.3–4.7; spring: 1.2–2.5). Average local richness was lowest in ungrazed, annually burned prairie as compared to sites that were less frequently burned, bison grazed, varied in topography, or some combination of these. Within local sites and seasons, communities typically were temporally nested through the 32 years. *Peromyscus maniculatus* was the most frequently recorded species in prairie sites; *P. leucopus* was the most frequently occurring species in woody-encroached long-term unburned sites. In contrast, other species (autumn: 5; spring: 10) were recorded only infrequently (< 5% of the total 448 site-years). Many ecological lessons can be learned from understanding long-term patterns of abundance, composition, and richness of local small mammal communities and their possible drivers.

142: Effects of deer exclosure fences on population estimates and niche breadths of small mammals.

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A small mammal capture-recapture study was conducted in 2013-2014 utilizing two 0.65 hectare deer exclosures constructed in the oak-maple-eastern hemlock forest of northeastern Pennsylvania. On exclosure (old) was constructed in 1995 and a second (new) in 2011. Forty Sherman trap locations were established in each exclosure and in two adjacent old and new control sites. Both the new exclosure and control trap grids contained amounts of lumbering slash (downed limbs and branches). The old sites did not. Jolley-Seber population estimates calculated for white-footed mice (*Peromyscus leucopus*) for the four trap grids were not significantly different. Population estimates calculated for eastern chipmunks (*Tamias striatus*) for the two new grids were also not significantly different. Too few chipmunks were captured in the old exclosure and control grids to permit the calculation of population estimates. Niche breadth estimates for the chipmunks suggest that the likelihood of chipmunk captures is positively associated with the abundance of lumbering slash. Significantly more northern short-tailed shrews (*Blarina brevicauda*) and masked shrews (*Sorex cinereus*) were captured in the new exclosure and control sites than in the old. Niche breadth estimates suggest that captures of both shrew species were significantly associated with the abundance of herbaceous plant cover.

143^{E}: Time as a niche dimension: An examination of temporal partitioning in two Paraguayan bat communities

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Community ecologist have long been interested in the patterns and processes involved in the structure of assemblages. Often times aspects of the food niche are closely and statistically scrutinized to examine patterns of overlap and whether biotic interactions can possibly account for them. Another relevant dimension involves time and whether species are interacting along a temporal niche axis. Biotic interactions could produce low overlap in situations where species experience much interspecific competition. We examined temporal overlap of bats from 2 communities in interior Atlantic Forest of eastern Paraguay. We analyzed temporal patterns of species using the TimeOverlap Program. Pianka and Czechanowski indices demonstrated a high degree of overlap among species at both sites. Constrained permutation tests demonstrated that degree of overlap was highly significant but opposite of what would be predicted by competition theory. At both interior Atlantic Forest sites bats overlaped more along the temporal axis than expected by chance. Future studies are aimed at examining the generality of these findings across a number of other Neotropical sites as well as determining the mechanistic basis to these patterns.

144: Increasing the dimensions of human diversity: approaching the next 100 years of North American mammalogy

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Over the last 2 decades, the Human Diversity Committee (HDC) has sought to monitor and promote the participation of under-represented groups in the American Society of Mammalogists (ASM), as well as its meetings and publications. From the starting point of an almost exclusively male, Caucasian membership (of primarily European descent), the diversity of ASM eventually grew, with the rising role of women in the society throughout the last one-third of the 20th century and an increasing presence of Latin American mammalogists. The last twenty years have seen greater efforts (via HDC and ASM) to promote inclusivity and further increase the dimensions of diversity. This has led not only to a more prevalent role for students and young mammalogists, but also giving a voice to other members who may have felt disenfranchised at times *(with discussions like the 2012 "LGBT and Friends Roundtable and Mini-mixer")*. In addition to continuing to support and promote all types of human diversity and the future of ASM, it seems fitting to continue to strive to encourage the participation of young mammalogists, new members, and first-time meeting attendees. In order to accomplish these goals, we must be able to continue to assess where we stand and how our diversity is changing, as well as understanding the needs of our current, future, and potential membership.

145^{E}: Regional differences in bobcat (*Lynx rufus*) occupancy in Connecticut

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Throughout the second half of the twentieth century, bobcats (*Lynx rufus*) in Connecticut (CT) were uncommon and restricted primarily to the less developed northwest corner of the state. Over the last twenty years or so, this species seems to be re-expanding and is now thought to be widespread throughout CT. However, it is not known if the probability of occupancy is equal throughout the state or if occupancy is higher near the historic source population. We estimated occupancy (Ψ) of bobcats in areas with young forests and shrublands from twenty-three sites in two regions (western CT and southeastern CT) using automatically-triggered cameras. Model evaluation in PRESENCE indicated that bobcat occupancy was not constant across all sites and that site occupancy was higher in western CT (Ψ=0.69, SE=0.22) than in southeastern CT (Ψ=0.11, SE=0.11). Such differences in occupancy suggest that bobcats may still be much less common in southeastern CT which could be due to geographic barriers such as interstate highways and the Connecticut River, which bisect the state.

146^{E}: Small mammals and associated ectoparasites occupying distinct south Texas ecoregions

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Texas is a large state with more than 10 distinct ecoregions. However, organismal biodiversity across ecoregions in the southern portion of the state is poorly known due to widespread private land ownership. Through the use of various live trapping techniques, we investigated the diversity of small mammals on private properties owned by the East Foundation, which are found in the South Texas Sand Sheet, South Texas Brush Country, and Gulf Coast Prairies and Marshes ecoregions. Our efforts documented the presence of multiple mammal species, with those belonging to order Rodentia being the most abundant. Small subsets of captured mammals were retained as museum voucher specimens and inspected for ectoparasites, which were placed in ethanol and stored for quantification and identification. To date, several ectoparasite taxa have been collected and identified, the majority of which belonging to subclass Acari (mites and ticks). Assessing mammal and ectoparasite biodiversity across these various ecoregions will aid in broadening the knowledge of general biodiversity in southern Texas.

147^{E}: Den use and activity patterns of *Spilogale putorius* in the Talladega National Forest, Alabama

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Eastern spotted skunks (*Spilogale putorius)* are small (*ca.* 0.5-1.5 kg) omnivorous mephitids that inhabit rocky and shrubby forested areas with closed canopies and extensive vegetation cover. Historically, eastern spotted skunks were widely distributed throughout most of the eastern United States. However, since the 1940s this species has experienced precipitous population declines. While the exact reasons for their range-wide decline is unknown, a variety of possible mechanisms are suspected including anthropogenic factors such as habitat loss, pesticide use, overharvesting, and natural causes. The basic ecology and habitat requirements for the eastern spotted skunk is poorly understood and rarely researched. We are conducting a telemetry based research project in the Shoal Creek ranger district in Talladega National Forest, located in Alabama, to examine the den and space use requirements of this species. We tracked radio-collared skunks to dens and placed remote cameras to monitor the skunks' activity patterns. This method also allows us to see how often they use each den and how many dens each skunk uses. Dens are often located in burrows dug into the ground, holes in stumps, or under rocks. We will also determine at what time spotted skunks leave and return to their dens throughout the day. These data will assist in designing management actions and policies for maintaining habitat for closed canopy adapted species, such as the eastern spotted skunk.

148: Inferring the demographic history of Florida black bears: Fragmentation, bottlenecks or both?

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The Florida black bear (*Ursus americanus floridanus)* historically ranged throughout Florida and into southern portions of Georgia and Alabama. The current range of the Florida black bear is highly fragmented and genetically differentiated. Using a combination of approaches (Bayesian clustering analysis, Bayesian estimates of gene flow, and approximate Bayesian population modeling) we test alternative historical demographic scenarios for the Florida black bear. Data from 10 sampling areas representing 7 bear management areas, comprising approximately 1000 bears and 6 to 12 microsatellite loci, were examined to determine whether black bears in Florida were once effectively a large contiguous (i.e. panmictic) population, and whether the current level of genetic variation could be attributed to habitat fragmentation and persecution during the 20th Century. Most black bear populations, with few exceptions were highly differentiated based on Bayesian clustering, reflecting previously reported differentiation based on F-statistics. Recent historical gene flow has been low (directional migration rates have been effectively zero for the past few generations), although there is good evidence of recent translations

among management areas. Current effective population sizes (N_e) range from approximately 2 to over 240. Based on these data, we will present the demographic model that best predicts the observed genetic pattern for black bears in Florida.

149^E: Phylogeography and population genetics of North American wolverine (*Gulo gulo*)

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Boreal biomes are ideal for studying phylogeography due to their dynamic history. Glacial and interglacial periods caused range expansions and contractions in high-latitude species, impacting genetic structure of mammals across northern North America. As a wide-ranging Holarctic carnivore, the wolverine (*Gulo gulo*) is an ideal system for studying diversification due to glacial refugia and post-glacial recolonization. The large range and high mobility of wolverines are thought to be limited primarily by climate, and not topographical boundaries, so this species should track or respond primarily to changing climatic conditions. Because distributional changes and loss of genetic variability can inform conservation strategies, we attempt to identify regions of greatest concern, and also explore potential barriers to gene flow in the future under scenarios of changing conditions. We use a combination of mitochondrial and nuclear loci to resolve phylogeographic history, determine areas of greatest genetic diversity, and begin to develop a landscape genetics approach to understand gene flow and connectivity in these low-density carnivores. Preliminary results suggest three refugial populations other than Beringia were recolonization sources: California, Nunavut, and Ontario. Currently, incomplete lineage sorting between New and Old World wolverines support a division at the subspecies level. Nuclear markers and further sampling will illuminate hypotheses relating to movement and diversification of evolutionary lineage across North American and Eurasian wolverines.

150: Effective rehabilitation techniques contributing to successful release of the Florida Panther (*Puma concolor coryi*)

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The Florida panther is a highly endangered large felid species that was on the brink of extinction in the 1990s before being saved by genetic restoration through the addition of genes from Texas cats. Currently there are 120–180 individuals, each playing a crucial role in the growth and sustainability of the species. White Oak Conservation is the only facility rehabilitating injured or orphaned panthers for release into south Florida. As the small population grows, the Florida panthers are threatened with human encroachment and habitat loss. In recent years, the number of panthers hit by vehicles or injured in intra-specific aggression has led to an increased need for rehabilitation. Large, remote, naturalistic enclosures promote natural behaviors in the panthers, while camera traps and radio telemetry collars minimize human contact and prepare them for release into the wild. Panthers are 1st offered a balanced commercial raw meat diet and progress to natural prey items, culminating in live prey. White Oak has rehabilitated and released 14 Florida panthers in the past 27 years. Of the 8 females released, it has been confirmed that 6 of those females produced litters. As the genetic contribution from each individual is critical for long-term sustainability of small populations, rehabilitated and reintroduced panthers play a crucial role in supporting this small population of endangered carnivores.

151: Drinking water as a source of environmental DNA for the detection of terrestrial species

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Use of environmental DNA for species detection is a field of research that has seen rapid growth in recent years, however, the majority of research to date has been focused on aquatic species. Here, we propose and test a novel new source for the detection of terrestrial species with environmental DNA: drinking water from watering holes and wildlife water developments. We hypothesized that when terrestrial animals drink from a water source, DNA from saliva and buccal cells is shed and can be isolated for species identification. We tested this hypothesis by filtering drinking water supplied to coyotes (*Canis latrans*) at a captive coyote research facility. DNA was successfully extracted from filters, amplified by the

polymerase chain reaction, and sequenced, and sequences were positively identified as belonging to coyotes. We believe this exciting environmental DNA based approach holds great promise for the detection of terrestrial species of conservation concern.

152^{E}: Patterns of genetic diversity in wild and domesticated cane rats (*Thryonomys swinderianus*) from Southwestern Nigeria

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Cane rat (*Thryonomys swinderianus*) is a large (up to 10 kg) rodent, widely distributed in sub-Saharan Africa. As a valued source of protein, it is hunted extensively throughout West Africa. Concerns associated with unsustainable hunting pressures on wild populations led to domestication efforts in the 1970s in select West African countries. Genetic information (a valuable resource) which guides management decisions for both wild and domesticated populations are limited for this species. The purpose of this study was to quantify and compare genetic diversity among wild cane rat populations from distinct vegetation zones (Guinea savannah, derived savannah, rain forest and swamp forest) and also among domesticated populations in Southwestern Nigeria. We examined whether populations are genetically structured based on vegetation zone, and whether there have been neutral genetic signatures of domestication on this species (e.g., patterns of genetic drift or reduced effective population sizes). We genotyped 250 individuals (89 domesticated and 161 wild) at twelve highly variable microsatellite loci and present results quantifying regional genetic structuring and the relative patterns of diversity among wild and farmed cane rat populations. Analysis of molecular variance (AMOVA) was used to test the significance of variation among eco-zones and between wild and farmed cane rat populations. Understanding the patterns of genetic diversity of this species serves as a valuable resource to guide management decisions for both wild and domesticated populations.

153^{E}: Evaluating performance of GPS technology to quantify space use by a semi-fossorial small mammal

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Global positioning system (GPS) technology has enhanced the temporal and spatial resolution at which animal location data can be collected, and recent advances in GPS receivers permit their deployment on mammals weighing < 500 g. Our goal was to evaluate performance of GPS telemetry on a small, semi-fossorial mammal, the pygmy rabbit (*Brachylagus idahoensis*), to examine how errors might influence conclusions about fine-scale patterns of space use and resource selection. We performed both stationary and free-ranging animal trials to quantify the effects of habitat on GPS location accuracy and fix-success rates. We predicted that cover provided by shrubs, snow, and burrows would reduce performance of the GPS collars in increasing magnitude. We fitted adults with collars that carried both VHF and GPS telemetry units programmed to collect locations at 15-min intervals in east-central Idaho during winter; summer trials are on-going. As expected, fix success of GPS collars in burrows was significantly reduced relative to above ground. Accuracy of locations varied markedly during winter, and preliminary evidence suggests that snow cover had a larger effect on location accuracy than fix success. Effects of shrub cover on GPS performance also were variable, but less pronounced than either snow or burrow cover. These trials will be used to quantify errors to inform the scale at which interpretations of resource selection and space use patterns are appropriate.

154: A novel break-away device for use with radiocollars on small carnivores

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Radiotelemetry is a valuable technique in the toolbox of methods available to wildlife biologists. In some cases, it is the only known or logistically feasible approach to collect specific data to aid in the conservation of a rare species or address an important research question. However, the attachment of radiotransmitters to animals is not always without negative effects; in some cases researchers may need to find ways to minimize potential impacts of transmitters on individual species while still obtaining data to answer research questions. The fisher (*Pekania pennanti*) is a species that presents some challenges to radiocollar attachment due to its slender morphology, tendency for neck size of males to fluctuate according to age and season, and inclination to use tight spaces and forested habitats with elements that can snag collars. On the Kings River fisher project in the southern Sierra Nevada, we developed and used handmade breakaway devices that could be attached to radiocollars in an effort to reduce potential neck injuries (especially on young males that were still growing), provide an opportunity for animals to break free from the collar if stuck, and eventually allow the collar to drop off if the animal was never recaptured. While the basic pattern and materials used were designed for fishers, this break-away pattern has the potential to be adapted for use with other species.

155: Effects of habitat disturbance on small mammal communities associated with Kibale National Park, Uganda

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Disturbance in the form of logging and fragmentation may lead to local extinction of native forest-dwelling species, while altering the environment in ways that may be more suitable for grassland-associated, invasive, or peridomestic species. To improve our understanding of this process, we surveyed terrestrial small mammals along a habitat disturbance gradient in and around Kibale National Park (KNP), western Uganda. We collected 327 small mammals from seven distinct habitats, including intact forest, forest areas logged at low and high intensity, forest edge, two forest fragments, and human dwellings. In total, 23 species were identified. Ten of the species were previously unreported in this region; *Dasymys incomtus, Mastomys natalensis, Oenomys hypoxanthus, Praomys misonnei, Scutisorex somereni, Crocidura dolichura, C. fuscomurina, C.* cf. *littoralis, C. maurisca*, and *C. olivieri*. We found community structure to be sequentially altered along a gradient of disturbance. We identified the highest levels of species richness and diversity in areas that experienced moderate levels of disturbance outside KNP (i.e. forest edge and fragments). High species richness was positively associated with increased coexistence of both grassland and forest-dwelling species. Finally, we compared our species diversity results within the boundaries of KNP to historical records and found them to be similar. Anthropogenic disturbance in forested Uganda was associated with alterations in small mammal community composition creating higher species richness and coexistence in habitats of intermediate disturbance.

156: Quartz sand and the origin of crown cementum in horses.

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Cementum is a calcified material that usually covers tooth roots. We call it crown cementum when it extends onto the enamel of a tooth. In high-crowned (hypsodont) teeth with elongated cusps and lophs (as in many herbivorous dinosaurs, rodents, proboscideans, and equids), crown cementum supports enamel ridges as they wear. The hypsodonty exhibited by horses involves elongation of upper crown features reinforced by crown cementum. Assuming a single origin for this condition in horses, a new species of *Parahippus* from the early Miocene of Florida possesses the most primitive form of crown cementum. Its teeth are not hypsodont, but are similar to those of *Parahippus pawniensis* of Colorado and Nebraska, a low-crowned equid lacking crown cementum. Some have proposed increasing amounts of abrasive volcanic ash in soils during the Miocene as the proximate cause for the evolution of hyposodont, cemented teeth in horses. But volcanism was not present in the Gulf Coast in the middle Cenozoic. An alternate source to increase tooth abrasion is quartz. Starting about 25 million years ago, accelerated rates of erosion in the Appalachians produced vast amounts of quartz sand that were transported south to turn island Florida into a peninsula. Ingestion of quartz sand with plant foods would increase rates of tooth wear, which in turn would select for more durable teeth, starting with the spread of enamel-supporting crown cementum.

157^E: Genetic microstructure as possible explanation of philopatry

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Philopatry is a biological trait, which refers to the behavior of an individual remaining in its birthplace even after having reached maturity and independence from parents. In species with philopatric females, a pervasive trait is the need to have access to a resource that allows the female to rear the offspring. Dominance interactions are important elements of the life history traits and necessary to mediate priority of access to resources and the associated consequences for individual variation in fitness. By means of setting a hierarchy, females may monopolize resources to remain philopatric. The genetic microstructure study of the sandy pocket mouse *Chaetodipus siccus* has shown that there is a wide variety of unique cytochrome-b haplotypes (31) in the extremely small distribution range (~270 km^2) of this rodent. To explore relationships between genetic microstructure and philopatry in females, we examined patterns of aggressive-submissive behaviors among females of *C. siccus*, based on: direct dominance, dominance along the time and dominance based on the defense of food resource. Preliminary findings suggest the presence of a relation dominant-dominated, which remained constant through the time and a strong hierarchy of dominance by highly aggressive behaviors between individuals. These facts could be linked to a strong territorial behavior that permits the formation of family nuclei that are related with genetic microstructure.

158: Phylogenetic analysis of *Myotis peninsularis* (Chiroptera: Vespertilionidae) blending geometric morphometrics and molecular datasets

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Myotis peninsularis is an endemic bat from the Cape Region in Baja California Sur, Mexico. Its taxonomic status is unclear, either as a valid species or as a subspecies of *M. velifer*. In order to assess its taxonomic status, the phylogenetic relationship of *M. peninsularis* was performed, using molecular and geometric morphometric data. Cytochrome oxidase subunit I and cytochrome *b* were analyzed. Phylogenetic analysis showed that *M. peninsularis* and *M. velifer* are sister groups, collectively forming a monophyletic assemblage. We observed less than 2% of genetic distance with both mitochondrial genes, which is considered an interval at the subspecies level. The geometric morphometric analysis showed differences in skull shape. We obtained three morphotypes: *M. peninsularis* (Cape Region), *M. velifer incautus* (northern population) and *M. v. velifer* (southern population). The most important differences were located in the braincase, the sagittal crest area and in the rostral slope. Morphologically, the three lineages tend to possess the same normal variation between Mexican population of *M. velifer*; but with specific morphotypes associated to its distribution. In a combined molecular and landmark configurations phylogenetic analysis, the monophyletic assemblage was confirmed. The ancestral shape corresponded to an intermediate shape between *M. peninsularis* and *M. velifer*, presenting similar variation to the intra-specific level in *M. velifer*. We propose *M. peninsularis* to be considered a junior-synonym of *M. velifer*.

159^E: An analysis of pleiotropic effects of the agouti gene in the genus *Peromyscus*

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A mutation in the Agouti gene may not only determine a deer mouse's coat color but may also have an effect on its body size, making the Agouti gene pleiotropic in nature. *Peromyscus maniculatus gracilis* that are homozygous for the non-agouti alleles have a melanistic coat color and an increased tendency towards obesity (Hayssen 2001 Comp Biochem Phys 130:311). If the non-agouti allele exerts its pleiotropic effects across species, then species which are melanistic due to this allele could also be heavier. Melanism can also be caused by the extension locus which codes for the pigment cell's melanocortin receptor, but has no effect on body size. Thus assessing the degree of association between body size and coat color across deer mice is one way to assess the use of the agouti versus the extension locus to achieve melanism. To this end, data on coat color and body size were assessed via digital photographs from over 7300 museum specimens representing 45 species of deer mice. The data were analyzed across the genus and within species. Darker coat color and larger body size were evident at both taxonomic levels but the relationships were not always significant. The strength of the relationships varied as well. In general, these findings suggest that the evolution of melanism via the non-agouti allele may be more common then via the melanocortin receptor.

160: Ontogenic variation of *Akodon montensis,* an extremely successful rodent in the Atlantic Forest

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Ontogenic studies aim to understand morphological variation of organisms throughout their lifecycle from an evolutionary and ecological framework. *Akodon montensis* is the most abundant terrestrial rodent species found in the Atlantic Forest (AF) of South America. Recently, *Akodon paranaensis* has been shown to also be extremely abundant in these forests also. Identification between these species is difficult in the field. Understanding ontogenic variation can be valuable to understanding both evolutionary and ecological correlates which allow for the species to be so successful in the AF, and additionally what distinguishes this species from other sympatric species. We evaluated the skulls using traditional morphometrics for males and females in 5 age classes from juveniles to adults. A multivariate approach was implemented for 17 variables to identify the highest latency among age classes and gender. Discrimintate Function Analysis was conducted to test significance between age groups and gender. We did not find evidence of sexual dimorphism, and age classes were easily discriminated. Our analysis revealed the highest allometric variation was related to the nasal passage and incisors width. Given this preliminary data, we intend to compare these morphological trends with *A. paranaensis* in future studies. This information is valuable to improve our understanding of the ecological and evolutionary role of this species in the AF, which is a rapidly disappearing forest system by anthropogenic disturbances.

161^{E}: Cranial morphology of the variegated squirrel (*Sciurus variegatoides*)

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Central America is a region harboring an incredible amount of biodiversity, including many endemic species, likely due to a variety of geographic features and habitat types. One of these endemic species, the variegated squirrel (*Sciurus variegatoides*), is one of the most variable mammal species, featuring a large display of pelage patterns across its range from southern Mexico to central Panama. Hypotheses for the variable pelage of this species include possible adaptations to primary habitat and consequences of the variable climatic ranges seen in the region. The last revision of this species in 1937 identified 15 subspecies with cranial and dental morphological variation among many of them. Unfortunately, this revision neglected to further analyze this cranial and dental variation, instead focusing on the pelage differences among the subspecies. Given the variation seen in this species, we will undertake a study of the cranial morphology of *S. variegatoides* across its geographic range. Both traditional morphometrics and 2-dimensional geometric morphometrics of the cranium will be used to determine any possible variation among subspecies and geographic areas. Preliminary results from this study will be discussed. Elucidating the patterns of morphological variation seen in this species can help to pinpoint overarching patterns of mammalian variation and better inform future biogeographical studies in this region.

162: A morphological phylogeny of the genus *Molossus* (Chiroptera, Molossidae)

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Many phylogenies of different molossid bats genera have been proposed in the last few years based both on morphological and molecular data. Nevertheless, intra-generic phylogenetic relationships are not well understood even for some relatively common and diverse taxa, such as the genus *Molossus*. Although most authors regard *Molossu*s as monophyletic and the position of the genus in the family Molossidae as sister group of *Promops* is well established, phylogenetic relationships among species within the genus remain undefined. In this study we propose a phylogeny of the genus *Molossus* using morphological data. 485 specimens belonging to *Molossus, Eumops* and P*romops* were analyzed, including a new species of *Molossus* from the Brazilian caatinga. External morphology, skull and dental characters were included. A parsimony analysis using the program Tree Analysis Using New Technology was performed to evaluate the congruence between the characters. The relationship between *Molossus* + *Promops* and the monophyly of *Molossus* have strong support in both Bootstrap and Bremmer values. Relationships among species were not well supported, however by these data diversification of *Molossus* occurred in a dichotomous sequence, and not in two major clusters as hypothesized by previous authors sing similarity matrices. Even a general lack of definitive morphological characters at the generic level, a molecular phylogeny within *Molossus* could reveal important new relationships to clarity the overall process of adaptive radiation.

163: Taxa centered versus content centered view of mammalogy from undergraduate students

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Science educators often create assignments requiring students to develop a deeper understanding of a topic by searching the primary literature and summarizing results. Students, on the other hand, may be more interested in particular taxa than in specific content. We gathered assignments for 3 years from sophomore students in a wildlife biology program to determine if students have taxa centered or content centered view. Students searched the primary literature for a paper and were asked to provide the abstract of the paper, summarize the research, the key words the students used to find the paper, and the title of the lecture in which they first encountered the topic. Our results show that students were more likely to choose papers about Artiodactlya or Carnivora than other Mammalian orders. Students may select content oriented topics within these orders; however, key words used to chose these papers were more likely to include the name of a particular species than key words from the lecture in which they first encountered a topic suggesting that sophomores are more likely to be taxa centered in their approach to a mammalogy course than content centered. The implication of this is that there are ample opportunities to foster academic maturity and appreciation of deeper topics than a student's affinity for taxa.

164^{E}: Habitat use on a fragmented landscape by *Peromyscus polionotus,* an early successional species

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Natural disturbances are an essential component for maintaining or creating early succession habitat. Oldfield mice (*Peromyscus polionotus*) are commonly found in areas affected by storms, fire, and agriculture. Studies on the response of oldfield mouse populations to disturbance from hurricanes are well documented, however movement patterns following fire disturbance is less understood. Low intensity, prescribed fire alters the habitat enough to remove ground cover and thin mid-story vegetation. Three wild populations of oldfield mice in southeastern Georgia were tracked using radio telemetry before and after a prescribed fire. Habitat variables and overall small mammal population density were measured before and after managed burns. We predict that movement distances will not change as a result of ground cover reduction. However, we predict that the number of burrows used will increase and that movement patterns will be altered as a result of limited cover.

165: The future of ASM meetings: 2016 and beyond

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The Annual Meeting of the American Society of Mammalogists (ASM) is our premier event each year. Globally, this is the most important annual conference regarding the science of mammalogy. For a 4-day period, an international community of hundreds of mammalogists and professionals from related disciplines gather to exchange scientific information, discuss new research opportunities, enhance their professional training, and network with colleagues. Traditionally, the Annual Meeting was held at universities and museums, rotating among 5 geographic regions within the United States and Canada. Since 2012, the Annual Meeting has been held at hotels and convention centers in Reno, Nevada, Philadelphia, Pennsylvania, Oklahoma City, Oklahoma, and most recently, Jacksonville, Florida. The “convention center model” was an experiment undertaken to determine if this type of venue would enhance member attendance at the annual meeting. However, based on a vote by attendees at the 2014 Annual Meeting, the 2016 meeting will move to a modified “university model” in which the Kansas State University Global Campus will partner with the University of Minnesota, Minneapolis. As ASM approaches its centennial, the Program Committee welcomes input from members regarding the ongoing evolution of our annual meeting. By hosting scientifically exciting, collegial, and fun conferences, ASM will ensure the future of our society as we move into our second century of promoting the understanding of mammals.

166^{E}: Population genomics of rats in New York City

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The brown rat, *Rattus norvegicus*, is one of the most common urban mammals around the world, making rats a useful model for understanding the influence of urbanization on free-living mammals. Urban development and human activity provide major resource subsidies to rat populations, and may influence the population genomic structure of rats by altering movement patterns in cities. Wild rats typically exhibit high reproductive capacities and philopatry to natal sites, but their migration through the cityscape is not well understood. Rats occupy a complex three-dimensional habitat in cities that likely influences relative movement through different types of infrastructure. In this study, we are using population genomic approaches to understand how the cityscape influences rat movements and population structure in New York City. To date, we have sampled over 300 rats from throughout Manhattan, and generated thousands of SNP markers using double-digest RAD sequencing (ddRAD-Seq). We present results on basic population genomic characteristics of Manhattan’s rat population, and examine spatial correlation of pairwise relatedness between rats at different scales. We also report results of evolutionary clustering (e.g. PCA / DAPC, fastSTRUCTURE) and genetic differentiation between large, local aggregations of rats in specific buildings and parks.

167^{E}: Evaluating scat detection rates and methods of detection for quantifying wild pig (*Sus scrofa)* abundance

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Wild pig populations are rapidly expanding in North America, necessitating more accurate estimation of abundance to aid research and management. One promising method of estimating pig abundance is use of scat-based genetic capture-mark-recapture. Knowledge of scat densities across habitat types, methods to maximize sample collection, and factors affecting scat detection may aid in performing these studies. We estimated density of pig scat in 2 common habitat types at the Savannah River Site in South Carolina, United States, compared radial search protocols to a previously used adaptive cluster sampling (ACS) method, and evaluated effects of environmental and scat characteristics on scat detection rates. Scat density was estimated through transect sampling, while the comparison of search protocols and the evaluation of factors affecting detection rates were performed using generalized linear mixed models in a model selection framework. We found higher scat densities in bottomland hardwood than upland pine, and that 15 or 20m radial searches resulted in higher scat collection rates than ACS. Scat size, number of fecal pellets, percent vegetative ground cover, and recent rain events were significant predictors of scat detection. Use of radial sampling versus the ACS method may allow researchers to maximize sample collection, allowing accurate estimation of wild pig abundance. Application of relationships between detection probabilities and predictor variables may facilitate design of more effective sampling regimes in future wild pig research programs.

168: Long-term decline of thirteen-lined ground squirrel populations in Colorado shortgrass steppe

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Thirteen-lined ground squirrels (*Ictidomys tridecemlineatus*) are the most common small rodents in semi-arid grasslands of the Great Plains, and are important sentinels of ecological change. We monitored squirrel populations in grassland and saltbush shrublands in northern Colorado over a 15-year period. We live-trapped squirrels on 3 3.14-ha trapping webs in each habitat type twice each year: spring (May), representing primarily adults that had emerged from hibernation, and summer (July), comprising mostly young-of-the-year born in June. Across all years, squirrels were 3 and 4 times more abundant in grasslands than shrublands in spring and summer, respectively. On grasslands, squirrels were most abundant in both seasons between 2002 and 2006, then declined steadily at an annual rate of 49% until 2013 and 2014, when 2 or fewer squirrels were captured across all sites. On shrublands, squirrels were most abundant in 2002, then declined steadily afterwards, especially in summer (22%/year). Because our study encompassed periods of both high and low precipitation, it is unlikely that weather alone was responsible for the observed patterns. Changes in vegetation structure, including increases in taller, mid-height grasses and shrubs that might reduce habitat quality, might have contributed to declines, although we cannot rule out mortality from plague associated with prairie dogs. The loss of ground squirrels may pose a significant threat to vertebrate predators, e.g. swift foxes, that rely on these squirrels.

169: Distribution of nine-banded armadillo and gopher tortoise burrows in south Georgia

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Competition between burrowing species may restrict distributions locally and result in spatial segregation. Two burrowing species, nine-banded armadillos (*Dasypus novemcinctus*) and gopher tortoises (*Gopherus polyphemus*) cohabit pine forests of the southeastern United States; however, the spatial relationship of the burrows between the two species has never been formally assessed. We sampled 190 armadillo burrow locations and 76 gopher tortoise burrow locations within a 13.35 ha plot on Moody Air Force Base near Valdosta, GA, USA. We used the *L*-function (i.e., a linear transformation of Ripley's *K* function) to determine the point pattern for both tortoise and armadillo burrows separately, and the cross *L*-function to evaluate the relationship between the two point patterns. Results indicated that tortoise burrows were randomly distributed, while armadillo burrows were significantly clustered at all scales of analysis. The cross *L*-function indicated repulsion of burrow types at short distances and clustering at long distances. However, when both the standard *L*-function and cross *L*-function were corrected for spatial inhomogeneity, no statistically significant pattern was detected. These results suggest that different processes may be influencing the spatial distribution of burrow locations in different parts of our study area, and subsequent work on this subject will evaluate potential spatial covariates (such as natural and anthropogenic disturbances) that may explain the observed inhomogeneity of the point patterns.

170^{E}: Factors influencing mule deer fawn survival

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Population dynamics of large herbivores are strongly influenced by juvenile survival and recruitment relative to other demographic parameters. Recruitment of young into a population is necessary to maintain or increase population numbers. Mortality can be influenced by both indirect (maternal characteristics, birth characteristics, precipitation) and direct (predation, disease, trauma) factors. Mule deer (*Odecoilius hemionus*) populations have experienced range wide declines in recent decades, and decreased survival and recruitment of young is one proposed cause. We hypothesized that the survival and recruitment of young would be affected by maternal body condition and weight of neonates at birth as well as the summer growing season measured using a normalized difference vegetation index. We examined what variables influenced fawn mortality between birth and recruitment including birth weight, birth date, and maternal body condition. Births occurred between May 23rd and June 10th with the mean date of birth being June 2nd ± 8.44 days. Fawn mortality was approximately 73% during the first 3 months of life. Predation was the leading cause of mortality, approximately 57% followed by disease at 21%. Although fawn mortality was high and with variable causes during the first 3 months, survival after that time period to recruitment remained high.

171^{E}: Patterns of genetic diversification in a widely distributed species of bat, *Molossus molossus*

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The taxonomy and evolutionary relationships of the velvety free-tailed bat, *Molossus molossus*, from Central America and South America long has been debated. Within this species, and in fact the entire genus *Molossus*, specimens have been difficult to identify and have presented several taxonomic challenges. The objective of this project was to characterize the genetic relationship among individuals representing subspecies of the widely distributed species, *M. molossus.* We tested the hypothesis that genetic patterns of diversification would reflect subspecies lineages. The mitochondrial gene, cytochrome *b* (cyt*b*) was amplified and sequenced for specimens throughout its geographic range. A Bayesian analysis of 678 base pairs of the cyt*b* gene was conducted for 63 specimens with *M. alvarezi* as an outgroup. Genetic divergence was estimated. Our results showed that some subspecies such as *M. m. daulensis* and *M. m. tropidorhynchus,* based on morphology and geographic location, are consistent with the mitochondrial lineages recovered. However, not all currently recognized subspecies of *M. molossu*s were recovered by this analysis. Overall there was low average divergence across all specimens (4.7%), however a mitochondrial lineage containing the Cuban subspecies, *M. m. tropidorhynchus*, was 7.9% divergent from the other *M. molossus* specimens. This level of divergence and the recovery of a monophyletic lineage containing all Cuban specimens was consistent with recognition of the taxon as a distinct species.

172: Environment and demography predict seroprevalence of pseudorabies in feral swine populations of Florida

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The widespread invasive species, feral swine (*Sus scrofa*), causes over $1.5 billion in damages in the United States each year through habitat destruction, crop consumption, and disease transmission. Nearly forty percent of feral swine in Florida are seropositive for pseudorabies (PRV), an emerging herpesvirus fatal to livestock, pets, and wildlife, including the endangered Florida Panther, for which feral swine are an important food source. This study analyzed 8 years of serological data from the United States Department of Agriculture (USDA) Wildlife Services to quantify the status of PRV and identify relationships between PRV seroprevalence and environmental and demographic factors in feral swine of Florida. As expected for herpesvirus, adult feral swine exhibited higher PRV seroincidence than sub-adults and juveniles. Among adult feral swine, males exhibited higher PRV seroincidence than females. PRV seroprevalence on publicly hunted properties was significantly higher than on any other land use type. PRV seroprevalence was higher in the Eastern Florida Flatwoods and Southwestern Florida Flatwoods ecoregion than in the Central Florida Ridges and Uplands ecoregion (United States Environmental Protection Agency (EPA) Level IV ecoregions). Overall, PRV seroprevalence was negatively correlated with water and urban cover. It appears that land cover and land use—particularly anthropogenic—are predictive of PRV seroprevalence in feral swine populations of Florida. Results have implications for animal health and the management of this invasive species.

173^{E}: Are raccoons (*Procyon lotor*) good sentinels of metal contamination? – A wildlife health perspective

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Anthropogenic pollutants disrupt biodiversity globally. Sentinels of pollution provide a warning system for ecosystem wide contamination. This study sought to assess whether raccoons (*Procyon lotor*) are sentinels of local exposure and health impairment associated with metal contaminants. Raccoons are a ubiquitous, generalist species with small home ranges that make them potential candidates as biosentinels. We compared metal–metalloid accumulation and health responses of animals inhabiting contaminated and uncontaminated sites of the U.S. Department of Energy´s Savannah River Site, South Carolina. Between summer and fall 2013, data on morphometry, complete blood cell count, helminth load, histopathology and liver metal/metalloid content were collected from 15 raccoons in an area contaminated with metals/metalloids, and 11 raccoons from a comparable uncontaminated site nearby. Of eight metals/metalloids analyzed, copper, arsenic, and selenium were elevated in raccoons from the contaminated site. Raccoons with higher copper concentration also had more diverse and higher parasite loads. No other adverse health effects were observed in the raccoons exposed to higher levels of

contaminants. Our results support raccoons as sensitive sentinels of metal pollution. Even when there are no obvious health effects in the host species, changes in parasite loads may be sensitive indicators of metal exposure in raccoons. Helminths of mammals are an important and overlooked component of the ecosystem and perturbations in their community may reflect changes in overall ecosystem function and host health.

174: Body temperature rhythms of Arabian oryx (*Oryx leucoryx*) in the extreme desert of the Empty Quarter and Mahazat as-Sayd, Saudi Arabia

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During 2014, twenty Arabian oryx (*Oryx leucoryx*) were fitted with iridium satellite collars along with abdomenal thermal body temperature loggers that relay to the collar to monitor the movement and body temperature patterns of two populations of Arabian oryx in the extreme challenging environment of the Uruq Bani Ma'arid (UBM) within the Empty Quarter and the relatively less challenging Mahazat as-Sayd (MS), a fenced protected area. Body temperature measurements were recorded every 10 minutes for one year and the associated ambient temperatures recorded from the collar would enable us to determine the extremes of ambient temperatures that the oryx experience and the concomitant body temperatures experienced by the animals under such environmental conditions. Preliminary results reveal that during the summer months, the Arabian oryx experiences a greater range of body temperature than those experienced in the winter (36.5-41, 37-39, respectively). It was expected that Arabian oryx employ behavioral heterothermy by potentially heating up in the day and unloading heat during the relatively cooler evenings, in much the same way as the camel; however, a related study on activity patterns and sleep in Arabian oryx have shown that the change in sleep patterns between summer and winter would allow the Arabian oryx to overcome the problems of heat overload, and, as body temperature drops during sleep, provide them with a novel way to thermoregulate in the summer.

175^{E,TA}: Mitogenomic diversity of Procyonidae genera (Mammalia, Carnivora)

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The mitochondrial genome is a circular molecule that plays a fundamental role in cellular oxidative metabolism and energy production. It has been extensively used in phylogenetic and phylogeographic studies due to its higher rate of evolution relative to the nuclear genome, matrilineal inheritance, and lack of recombination. Several studies have shown evidence of selection acting on coding mitochondrial genes in species occupying high elevations compared to related groups in low elevations. Procyonidae is one of sixteen families in the order Carnivora, comprising six genera of medium-sized mammals, with 14 recognized species. Among those species, the mountain coatis (genus *Nasuella*) and the olinguito (*Bassaricyon neblina*) are found in montane regions (mostly > 2000 m). Here we compare the mitogenomes of procyonids to evaluate the number of non-synonymous mutations shared by *Nasuella olivacea* and *B. neblina*, but absent in other procyonids. Using one mitogenome per genus, our preliminary results show 22 amino acid changes on the NAD dehydrogenase subunits 1, 2, 4L, 4, 5 and 6, ATP synthase F0 subunit 6, cytochrome oxidase subunit II and cytochrome b genes. Out of those, nine amino acid substitutions caused change in hydrophobicity, charge and/or polarity, which might alter the secondary and tertiary structure of the proteins they encode. These results might help us identify mutations under selection associated with high elevation habitats and understand more about their role in speciation.

176^{E**}: Diversity, distribution and conservation of Holarctic ground squirrels (*Urocitellus*): new phylogenetic insights

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Holarctic ground squirrels of the genus *Urocitellus* have been a model system in ecology and evolutionary biology for nearly half a century. They are also an ecologically important and widely distributed group, occupying large portions of high-latitude North America and Asia. Yet, despite having received a breadth of scientific attention, a taxonomically complete and well-resolved phylogeny of *Urocitellus* ground squirrels is lacking. To address this, we generated new multilocus data from 11 species (including 26 of 33 recognized subspecies) for phylogenetic reconstruction. We also combined these with previously published sequences to produce a data matrix in which all species and 88% of subspecies are represented, including 100% of recognized North American subspecies. Results suggest a dynamic evolutionary history for *Urocitellus*, including multiple instances of genetic introgression in western North America as well as a complex biogeography within and across Beringia. Further, while our results largely support current taxonomic arrangements, they reveal several instances of disagreement as well as intriguing patterns of genetic diversity among taxa and in space. We discuss all these findings in the context of conservation of *Urocitellus*. This research was supported by an ASM Grant-in-Aid of Research awarded to Bryan McLean in 2014.

177^{E}: Population Level Effects of Invasive Fire Ants on Cotton Rats

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The red-imported fire ant (*Solenopsis invicta*) is an invasive predator found across the southeastern United States. Few studies have assessed the effects of fire ants on small mammal population dynamics. We used cotton rats (*Sigmodon hispidus*) as model species to determine the influence of fire ants on small mammals. We stocked populations of cotton rats into eight enclosures with either ambient or excluded meso-predators and ambient or reduced fire ant numbers. We conducted monthly mark-recapture sessions from June 2012 – July 2013. We found that the relative risk of cotton rat mortality within enclosures with predators excluded was less than populations in enclosures with ambient predators (Males: b = - 0.86 +/- 0.44, P = 0.0494 Females: b = - 0.81 +/- 0.29, P = 0.006). Fire ant treatment alone did not affect cotton rat survival (P > 0.05). However, the relative risk of cotton rat mortality was lower in enclosures with reduced numbers of fire ants and predators excluded (Males: b = -1.52 ± 0.69, P = 0.0273 Females: b = -1.11 ± 0.50, P = 0.0258). We found no differences in cotton rat recruitment (P > 0.05). Our results indicate that, in the absence of other predators, fire ants decrease survival of cotton rats.

178TA: Conservation translocations as experiments: using the reintroduction of a carnivore to understand its habitat requirements

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Translocations are conservation tools used to restore and expand populations of animals. In recent years, several authors have advocated using sound science to understand and improve the success of translocations. We propose that well designed translocations also serve as powerful experiments useful for testing hypotheses concerning the basic ecology and evolution of species and systems. Here we demonstrate how the reintroduction of fishers (*Pekania pennanti*) in California onto an industrial timberland serves as a test of fisher selection of, and viability on a landscape considered marginal for their habitat needs. From 2009 to 2011, we released 40 fishers and studied their survival, reproduction, space-use, and health. We tracked 32 translocated fishers sufficiently to determine their home ranges and most (26) established home ranges at the release site. Fisher annual survival was 0.77, mean denning rate was 0.78 ± 0.10 and litter size was 1.7 ± 0.44. We documented juvenile fishers born at the study site in each year since 2010. Annual population monitoring and population viability analysis suggest the population is stable to slightly increasing. Thus, our evidence indicates that the habitat, at the time of release to present, was sufficient to establish a small population of fishers. This experiment reveals that in some situations industrial timber management does not preclude fishers. Further investigation is needed to fully understand fisher population viability on managed landscapes.

179: A model based data-fusion approach to estimate occurrence probabilities

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Using camera traps has been an effective method for surveying animal populations. Data from such surveys have been traditionally used to draw inference on occurrence probabilities for focal species. However, surveying rare and secretive species through camera traps leads to small sample sizes which make inferences on occurrence probabilities difficult, if not infeasible. Scat-detecting dogs, cued on the species of interest, can vastly improve the probability of detection even for rare and elusive species. However, due to non-standard survey routes and lack of characterization of nondetection, standard statistical procedures to estimate the probabilities of occurrence cannot be used. We present a methodology where data from camera-trap surveys provide fixed spatial points to characterize nondetection in a scat-detection dog survey. Since the latter type of survey detects individuals in continuous space, we can create an "intensity" surface over the spatial domain that quantifies the probability of occurrence. Consequently, a data-fusion model emerges where survey data obtained from disparate sources, but over the same spatial domain, can be combined and then analyzed concurrently. We demonstrate the ability of our model in capturing true parameters through a simulation study and apply this novel technique in analyzing data from an ongoing study to assess the population status of swift foxes in northwestern Texas.

180^{E}: Habitat selection by mule deer within migration corridors in Nevada

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Migration is an important ecological phenomenon that allows ungulates to increase their exposure to high quality nutrients throughout the year. However, there is a limited amount of literature describing the habitat selection process by ungulates along their migration routes. To address this we examined movement patterns and resource selection along migration routes to understand the effects of environmental stochasticity on corridor selection and the habitat preferences within the migration corridors of female mule deer, *Odocoileus hemionus*. We captured and applied radio collars to female mule deer (n=66) on their migratory pathway in the Pequop Mountains of eastern Nevada. We used Brownian Bridge Movement Models to delineate stopover sites for each individual during seasonal migrations. We used resource selection functions to determine which climatic and environmental variables individuals selected across seasons in stopover locations and along movement paths within the migration corridors. We also compared corridors annually to determine the differences that existed due to environmental stochasticity and if corridors shifted in response to these environmental changes. Our research will benefit scientists by describing mule deer habitat selection within different parts of migration corridors which will allow them to identify high priority zones along migration routes where no collar information is available. It will also give managers a better understanding of environmental impacts on migration corridor selection as well as how corridors change in these conditions.

181^{E}: Live capture and ownership of lemurs in Madagascar: extent and conservation implications

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Overexploitation represents a severe threat to biodiversity, with live capture affecting millions of animals yearly. An improved understanding of primate live capture is needed, especially for Madagascar's endangered lemurs. Our objectives were to provide the first quantitative estimates of (1) the prevalence, spatial extent, correlates, and timing of lemur ownership; and (2) procurement methods, within-country movements, and numbers and durations of ownership. Using semi-structured interviews of 1093 households and 61 transporters across 17 study sites, we found that lemur ownership was common, widespread, and affected a variety of taxa. Lemur ownership is ongoing, impacting an estimated 28,253 animals since 2010. Most lemurs were caught by owners, and kept for short (≤ 1 week) or long (≥ 3 years) periods. The live capture of lemurs within Madagascar is not highly organized, but may threaten several already-endangered species.

182: What impacts the global home ranges of wild pigs (*Sus scrofa*)?

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Home-range sizes are an important asset to the management of invasive species. A summation of a species' home range distributions can enable conservationist to surmise current management techniques, calculate potential range expansion, and plan efficient control measures. Wild pigs (*Sus scrofa*) are a widespread and highly destructive invasive species in many regions of the world. In our review, we evaluated the use of climatic factors, (the global climate database [BIOCLIM]), remotely-sensed indices of vegetation productivity (normalized difference vegetation index [NDVI]), and native mammal species richness metrics for quantifying global variations in home ranges of wild pigs. Our results showed that home range sizes tended to be larger in males (10.51 km^2) versus females (8.10 km^2) and in native (9.53 km^2) versus nonnative (9.15 km^2) ranges. Not surprisingly, wild pig home range estimates had a negative relationship with the peak growing season; there is a decrease in home range size in more productive areas. However, what was interesting was that both male and female home range sizes had strong positive relationships with overall mammal species richness. This suggests that wild pigs may be increasing home range size in biotic rich areas with many native mammal species present. Overall, climate factors did not significantly impact home range size, suggesting that wild pigs use more productivity cues for make decisions about habitat selection compared to macroclimate conditions.

183^{E,TA}: Species differences in close-distance mating vocalizations in grasshopper mice (*Onychomys*)

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Acoustic signals that facilitate mate recognition within species may also reinforce reproductive barriers between species. Grasshopper mice (*Onychomys*) are renowned for their long-distance advertisement vocalizations, but also produce a variety of calls in close-distance mating contexts. In this laboratory study, we recorded vocalizations from conspecific and heterospecific opposite-sex pairs of *O. arenicola*, *O. leucogaster*, and *O. torridus* captured from an area of sympatry near Animas, New Mexico. We identified 3 distinct vocalizations used in close-distance mating contexts, one of which appears to be produced exclusively by females. Compared to conspecific pairings, heterospecific pairs produced fewer vocalizations. We speculate that close-distance vocalizations, in combination with long-distance advertisement calls and olfactory signals, subserve mate recognition to mediate reproductive isolation.

184: Behavioral strategies used by Neotropical singing mice (*Scotinomys*) to maximize sound propagation

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The efficacy of animal communication relies on signal detection by receivers following propagation through an oft-cluttered environment. Most studies of acoustic displays used in sexual contexts focus on the role of spectral and temporal characters in signal evolution. However, animals may also advertise at particular times and locations to maximize signal conspicuousness. In this study, we explored behavioral strategies used by Neotropical singing mice (*Scotinomys*) to enhance sound propagation. Singing mice are diurnal, insectivorous rodents that inhabit montane cloud forests throughout Mesoamerica. Males commonly emit vocalizations that serve to attract mates and repel rivals, but their high frequency nature make them susceptible to degradation. We used acoustic transects, mark-recapture, environmental monitoring, and playback experiments of synthesized signals. We found that males most often sing during a narrow window at dawn when thermal regimes are conducive to sound propagation. In addition, mice advertise in particular microenvironments within their home range to minimize sound degradation caused by understory vegetation. Our data suggest a degree of signaling sophistication previously undescribed in rodents, and highlight the importance of considering behavioral adaptations in the study of animal communication.

185: Effects of predator cues on vertical foraging habits of white-footed mice

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How mammals forage at or near the ground, to reduce predation risk or competition, has been well studied; vertical partitioning when foraging has received little attention. We hypothesized that (1) *Peromyscus leucopus* would climb trees and forage at greater heights if there is coyote urine present on the ground and (2) *P. leucopus* would avoid foraging at trees where owl pellets are present. To test these hypotheses, giving-up densities (GUDs) were measured by using foraging trays mounted on trees in an oak forest located in eastern Will County, Illinois. Trays were placed at ground level, three meters above ground, and six meters above ground. Data on population size and GUD were collected for one year during four seasons. These data were analyzed using repeated measures MANOVA. There was a significant effect of owl pellets on *P. leucopus* foraging, although this was in the opposite direction of our prediction: the mice fed on the owl pellets. Coyote urine significantly altered *P*. *leucopus* foraging on the ground and among the three vertical strata. Foraging in trees could be safer because of their ability to climb or hide to escape predation.

186^{E}: Can state-dependent foraging alter endocrine-energy relationships?

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To garner understanding of energy-performance relationships, endocrinology has recently emerged as a popular tool. Endocrine markers such as glucocorticoids (GC) and triiodothryonine (T3) reflect both energy reserves and energy intake in small-bodied animals whose energy reserves can change rapidly and in concert with energy intake. It is less clear, however, whether endocrine markers reflect the same patterns in taxa that store large amounts of energy in the form of body fat. We investigated relationships among endocrine markers and metrics of energy reserves and energy intake in North American moose (*Alces alces*), a species known to store large amounts of body fat. T3 increased as energy reserves declined, and GC increased with increasing energy intake, which were opposite to that expected from well-documented relationships in other taxa. Concordant with previous research, however, T3 increased with greater energy intake. T3 patterns indicate that moose in our study modified their energy intake dependent on their energy reserves, although we are unable to confirm whether increased energy intake was a result of forage selection alone or also increased foraging activity. We hypothesize GC plays a role in regulating foraging behavior, whereby increased GC results in increased foraging and energy intake. Alternatively, higher quality forage may be available in riskier environments, resulting in greater psychological stress and increased GC.

187: Effects of population density on sexual segregation by North American Elk

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We investigated how density-dependent processes and subsequent variation in nutritional condition of individuals influenced timing and duration of sexual segregation. We experimentally created two population densities of North American elk (*Cervus elaphus*), a high-density population and a low-density populations to test hypotheses relative to timing and duration of sexual segregation and variation in selection of resources among population densities. We used multi-response permutation procedures to investigate patterns of sexual segregation, and resource selection functions to document differences in selection of resources by individuals in high- and low-density populations during sexual segregation and aggregation. The duration of sexual segregation was 2 months longer in the high-density population and likely was influenced by individuals in poorer nutritional condition, which appears to correspond with later conception and parturition, than at low density. Males and females in the high-density population overlapped in selection of resources to a greater extent than in the low-density population, probably resulting from density-dependent effects of increased intraspecific competition and lower availability of resources.

188: The relationship between *Baylisascaris procyonis* and genetic variation in *Procyon lotor*

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Genetic diversity and gene flow in the raccoon roundworm, *Baylisascaris procyonis*, may influence genetic diversity within and among host populations. *Baylisascaris procyonis* infects the raccoon, *Procyon lotor*, with prevalence ranging up to 80%. While much is known about the transmission dynamics of the parasite, the relationship between the parasite and raccoon population genetics requires further study. We investigated the correlation between genetic variation in *P. lotor* and two variables: *B. procyonis* prevalence and *B. procyonis* genetic variation. We suggest that genetic variation in the definitive host is directly proportional to *B. procyonis* prevalence. Three microsatellite loci were evaluated in *B. procyonis* and *P. lotor* populations to determine allele frequency and quantify genetic variation. Genetic evaluation was accomplished through tissue extraction, and DNA isolation, amplification, and genotyping. Raccoon allele frequencies correlated with *B. procyonis* prevalence. The heterozygosity of raccoon microsatellites decreased with an increase in *B. procyonis* prevalence, yet increased with heterozygosity of *B. procyonis* microsatellites. Parasites appear to influence host population genetics, with the presence of *B. procyonis* shaping the genetic structure of raccoon populations in many ways.

189: Visiting an old friend: Using recent data to revise expectations of white-nose syndrome spread

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In 2012, Maher et al. published a model that showed the spread of White-nose Syndrome and the associated pathogen *Pseudogymnoascus destructans* followed a route consistent with geographic characteristics and an environmental variable. Simulations from each of the models they evaluated, including the best-supported model, tended to under-predict known date of arrival in the first few winters of spread (e.g. median values of simulations showed a later arrival than observed) for many counties. This highlights the difficulty in estimation of arrival and the many outcomes possible in stochastic modelling that should be considered when using predictions for conservation decisions. Since the associated analysis of this paper, 4 winters (including 2014-2015) have passed and the pathogen

continues to move across the eastern United States and Canada. To provide an update to estimates of spread, we re-fit coefficients of models, re-examined the speed of spread, and adjusted estimates of expected spread in the contiguous United States based on these new data. We find that best supported model in Maher et al. 2012 is still supported against other less complex models of spread, but that expected year of arrival is much sooner than previously reported. The updated spread map, with 'expected window of arrival' is now available at http://dx.doi.org/10.6084/m9.figshare.1314947.

190: The role of cutaneous fatty acids in the resistance of *Eptesicus fuscus* to WNS

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White-nose Syndrome (WNS) causes severe over-winter mortality for little brown (*Myotis lucifugus* bats. It is due to cutaneous infection with the fungus *Pseudogymnoascus destructans* (*Pd*) during hibernation. Big brown bats (*Eptesicus fuscus*) are resistant to infection with *Pd*. Hibernating *M. lucifugus* normally maintain a skin temperature (T_{skin}) of 5-7°C during torpor, whereas the T_{skin} of torpid *E. fuscus* is usually 12-13°C. We conducted analyses of wing epidermis from hibernating *E. fuscus* and *M. lucifugus* to determine their fatty acid compositions, and laboratory *Pd* culture experiments at 4.0 – 13.4°C to determine the effects of these fatty acids on *Pd* growth. Our analyses revealed that the epidermis of both species contains the same 7 fatty acid types (14:0, 15:0, 16:0. 16:1, 18:0, 18:1, & 18:2), but the epidermis of *M. lucifugus* contains more stearic (18:0) acid, less myristic (14:0) acid, and less oleic (18:1) acid, than that of *E. fuscus*. The growth of *Pd* was inhibited by: a) myristic and stearic acids at 10.5-13.4°C, only, b) oleic acid at 5.0 - 10.6°C, c) palmitoleic (16:1) acid, and, d) linoleic (18:2) acid at 5.0 – 10.6°C. One set of factors that enables *E. fuscus* to resist *Pd* infections (and thus WNS) is therefore the relatively higher myristic and oleic acid contents of the epidermis.

191: Age, prion protein and chronic wasting disease status of a mule deer (*Odocoileus hemionus*) population

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To reduce the prevalence of chronic wasting disease (CWD) in deer at Fort Carson Military Reservation, the number of hunting licenses issued was increased from 50 to 150 starting in the 2012-2013 hunting season. One-hundred ninety-three mule deer (*Odocoileus hemionus*) harvested from 2012 to 2015 were examined for CWD status, prion protein (*Prnp*) genotype and age. In the 2012-2013 hunting season 20% of the population was suspect for CWD. During the 2013-2014 and 2014-2015 hunting seasons the percentage of CWD suspect deer decreased to 8.3% and 8.8%, respectively. In mule deer, *Prnp* genotype is associated with differences in susceptibility to CWD and the rate of disease progression. Specifically, previous studies showed that individuals heterozygous for a nonsynonymous polymorphism in the *Prnp* gene (designated genotype SF) suffered 30X lower infection rates, and, when infected, much slower rates of disease progression than wild-type homozygotes (designated SS). In the first two years of the study, 75% of harvested deer were wild-type homozygotes and 25% were heterozygotes. In contrast 90% of infected deer were wild-type homozygotes and 10% were heterozygotes. We did not observe any individuals with the FF genotype. As a result of hunting the age structure of the herd has shifted and now exhibits a greater number of younger animals.

192: The past and future of bat research in West Africa

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We sampled bats during multiple brief trips to Guinea and Sierra Leone between 2006 and 2008. A total of 26 species were documented from the Simandou Range in Guinea and 19 from the Seli River Valley, Sierra Leone plus suspected new species. Several new country records were documented, especially for Sierra Leone, which has been relatively poorly sampled in the past. Perhaps most notably, we documented the endangered Ziama horseshoe bat, *Rhinolophus ziama*, for the first time in Sierra Leone. Given the Ebola outbreak in this region (which is still, and its suspected origin traced to a molossid bat (*Mops condylurus*), an understanding of the ecology and natural history of West African bats has never been more critical. Yet future fieldwork on bats will be challenging in the region. In several ways, Ebola represents a fundamentally different zoonotic from others that we've faced as mammalogists such as hantavirus and rabies. I plan to provide some thoughts on the future of bat research in West Africa and ask even more questions.

193^{E}: Small mammal interactions with invasive species: implications for tick-borne disease risk

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Small mammals are a ubiquitous faunal presence, and many species are hosts for bloodfeeding ticks. As such, small mammal species may serve as possible reservoirs for tick-borne pathogens that can affect human and wildlife health. The role of small mammals in the transmission of tick-borne diseases is of major concern, but poorly understood in the southeastern United States. This may be in part due to the presence of invasive red imported fire ants (RIFA; *Solenopsis invicta*), which are known predators of both small mammals and ticks. The objective of this study was to elucidate the impact of RIFA on tick-borne disease systems. Small mammal trapping at 2 field sites in Texas, which were partitioned into treatment plots to suppress RIFA populations and control plots, was used to determine mammal and tick density, and collect samples for pathogen testing. Small mammals and ticks were examined in the field, and samples from both were processed in the lab to detect tick-borne pathogens belonging to the genera *Borrelia, Ehrlichia*, and *Rickettsia*. We captured 1,314 mammals of 8 species, 331 ticks of 2 species, and detected a low prevalence of several species of human pathogens. Our data indicate that treatment plots have higher densities of small mammals relative to control plots, suggesting that RIFA may be impacting the ecology of tick-borne disease transmission at these study sites.

194: Museums, biodiversity, and the Anthropocene

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Studies characterizing biological variation and diversity, which are enormously valuable to science and society, have for centuries been the mainstay biological usage for natural history museum collections. Even with rapidly changing technology, including ever-expanding biochemical, genomic, and imaging techniques, these traditional uses (systematics, biogeography) remain the principal collections-based disciplinary emphases for biological research programs in natural history museums. Studies relevant to modern environmental change, and health and disease, among others, also represent important uses for museum collections, but these receive less focal attention within natural history institutions, collections, or curator-led research programs. Very large economic (and other) impacts of rapidly changing environments, climates, and disease landscapes in the Anthropocene highlight a need for organized efforts to expand natural history research programs to incorporate additional uses of collections as "core business" that can complement studies of systematic biology. Indeed, critical documentation of Anthropocene impacts, and the future of natural history museums, including public impressions of their relevance, may depend on it.

195: Population genomics and museum specimens

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A fundamental goal of evolutionary biology is to understand the causes and consequences of genetic variation in natural populations. The ability to generate massive amounts of DNA sequence data easily now makes it possible to assess patterns of genetic variation on a genome-wide scale. Importantly, next-generation sequencing techniques can be applied both to frozen or freshly-preserved material and to historic specimens housed in collections for decades. I present several examples of population genomic studies that utilize collections, including our work on environmental adaptation in house mice that have been recently introduced into the Americas. A combination of exome-capture and whole-genome sequencing has identified individual genomic regions that contribute to adaptive phenotypic differences among populations from different latitudes. Notably, most of these regions do not contain any non-synonymous variants, suggesting that much of adaptive evolution is due to changes in gene regulation rather than to changes in gene structure. These examples illustrate how museum specimens offer a rich source of material for population genomics.

196: High-resolution CT scanning and 3-D cranial analyses reveal hidden anatomical, phylogenetic, and functional information

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Our research team and collaborators have combined application of traditional comparative morphology and skull measurement methods with innovative non-destructive CT scanning 3-D virtual imaging and computer-based biomechanical modeling techniques in Carnivora, Anthropoidea, and extinct Meridungulata, revealing insights that cannot be garnered solely by studying external anatomy or discrete characters. Analyses focused on investigating brain evolution, inner ear structures, and inferences of locomotion, auditory acuity, and vision in fossils. Case studies will show the utility of high resolution 3-D CT imaging, geometric morphometrics (GM), and finite element (FE) biomechanical modeling analyses from our current NSF research (DEB-1257572) incorporating an integrated approach to studying phylogeny, form, and function of Carnivora and kin. Results include: 1) brain endocast reconstructions of basal carnivoramorphans to determine timing, number of events and order of acquisition of neocortex expansion features; 2) a new computational method for FE model convergence analyses (strain energy, bite force) in mastication scenarios across different sampling regimes for 1 skull; 3) evidence for strong phylogenetic signal in craniodental form and function, but also links between extant dietary groups and cranial mechanical properties after accounting for phylogeny; 4) a refined simulation approach for reconstructing dietary capability from a morpho-functional linkage model tying morphology directly to predicted dietary groups; and 5) testing correlations between bony labyrinth 3D GM landmark data and body size, phylogeny, and locomotor ecology in the Musteloidea.

197: Reconstructing animal foraging ecology and movement patterns with stable isotope analysis of archived samples

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Stable isotope biogeochemistry has been used for decades to evaluate food web interactions and reconstruct the diet and movement patterns of animals. Analysis of the δ^{13}C and δ^{15}N values from archived animal tissues to reconstruct historic trophic ecology is useful because it allows us to better understand environmental change and determine how current foraging ecology patterns relate to past trends. A relatively new biogeochemical technique, compound specific isotope analysis of amino acids (CSIA-AA), significantly augments data gained from isotope analysis of bulk tissue because baseline stable isotope values can be quantified via analysis of tissues from any organism within a food web. This is because certain "source" amino acids are minimally modified by consumers, so their analysis provides isotope values that are conserved from, and representative of, the base of the food web. Other "trophic" amino acids are isotopically fractionated as they move up a food web, and therefore reflect higher isotope values with each step in the food web. We can use the isotope differences between source and trophic amino acids to establish trophic positions of species and reconstruct variations in the baseline stable isotope values of food webs. We will illustrate the utility of these techniques on archived samples using examples from work in the Kurle lab.

198: Historical and present day mercury contamination from gold mining in three trophic levels of bats

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Artisanal mining operations use mercury as an amalgam to separate gold from river sediments. In the last twenty years the price of gold has risen and the number of small-scale gold mining operations and imports of mercury have increased in the Peruvian Amazon. Toxic mercury levels have been shown to impair reproductive, neurological and behavioral functioning of organisms. We used bats (Chiroptera) as a mammalian model system to study mercury contamination and bioaccumulation due to gold mining in the Amazon basin. Using both present day field caught and museum specimens collected between 1912 and 2001, we non-invasively measured mercury concentrations in bat hair, asking three main questions. Do higher trophic level bat species bioaccumulate more mercury than species from lower trophic levels? Do bats from mined sites bioaccumulate more mercury than bats from non-mined sites? Does mercury bioaccumulation differ over time and between mined and non-mined sites? Our findings suggest that higher trophic levels of bats bioaccumulate more mercury than bats of lower trophic levels and mercury concentrations in bats have changed over time and between mined and non-mined sites. The variety of bat feeding guilds allows for a comparison of how mercury accumulation is affected by diet within one taxonomic order. The novel use of museum specimens allows for a look back into the historical timeline of mercury contamination in the Amazon basin.

199: Conspicuous genetic structure belies recent dispersal in an endangered beach mouse (*Peromyscus polionotus trissyllepsis*)

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Anthropogenic habitat fragmentation can exacerbate the impacts on population persistence in mammals with rapid life histories and specialized habitat requirements. We investigated genetic structuring of the federally endangered (U.S.A.) Perdido Key beach mouse (PKBM), *Peromyscus polionotus trissyllepsis,* using 16 microsatellite loci. Between 2010 and 2012 we sampled the three core habitats separated by 3-5 km of developed area. One location (Gulf State Park) was re-established in 2010 by a release of 48 captive bred mice. The other two have undergone recent extirpations, translocations, and natural re-colonization. Our objectives were to assess genetic drift associated with the post-release phase at Gulf State Park over a 2 year period, and to test the hypothesis that PKBM dispersal connectivity is restricted between the three parks. The three populations were significantly differentiated in (pairwise F_{ST} from 0.135 to 0.276). However, our analyses (Bayesian clustering, assignment tests and hybridization analyses) revealed inter-park dispersal and reproduction in 2012 that was absent in 2010. The detection of dispersal was an important step in understanding the regulation of connectivity in this fragmented system. We propose recent mouse population increases combined with the concurrent re-establishment of beach-front vegetated sand berms allowed for the detected dispersal. These results provide important information for the future conservation of beach mice inhabiting northern Gulf of Mexico and Atlantic barrier islands in light of continued development pressure.

200^E: Does historical diversity contribute to regional vulnerability in Florida mice (*Podomys floridanus*)?

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The long-term survival of populations is conditioned in part by genetic diversity. In addition to anthropogenic fragmentation of habitat, historical biogeographic processes can strongly shape diversity. We applied a multilocus phylogeographic study to investigate how the late-Quaternary geological events have affected the intra-specific diversity of the Florida mouse (*Podomys floridanus*), a xeric habitat associated species that is currently undergoing status assessment in the State of Florida. Microsatellite diversity (16 loci from 361 mice representing 23 locations) indicates a high degree of geographic structuring. Samples as close as a few kms have moderately high levels of differentiation that can be due to a number of factors. Data indicate structuring is shaped by the discontinuous distribution of the ancient ridges where xeric habitats occur. Further, effects from ecological processes including population bottlenecks or “boom and bust” dynamics that would lead to a relatively strong role for genetic drift – random fluctuation in allele frequencies within populations – may overlay historical processes and lead to higher differentiation. These data provide useful insights into what may be a relatively complex biogeographic structure in Florida mice, and may influence conservation assessment decisions. Patterns of genetic differentiation may indicate that xeric ridges are distinct enough to deserve special attention for wildlife management. We present these results in addition to data collected for a further 200 mice from 15 new locations distributed across Florida.

201^E: Home ranges and habitat selection of a recently colonized population of Florida black bears

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Anthropogenic habitat fragmentation destroys habitat, severs connections among habitat patches and reduces habitat quality, and thus can influence patterns of space and habitat use by animals. Using global positioning system (GPS) location data for 16 individuals tracked during 2011–2013, we studied space and habitat use by a recently-colonized population of Florida black bears (*Ursus americanus floridanus*) in a fragmented area of north-central Florida. Average home range sizes estimated using the Kernel density method for female and male bears were 34.23 ± 5.23 km^2 and 249.91 ± 18.77 km^2, respectively, and were generally larger than those reported for bears inhabiting nearby contiguous habitats. These results are consistent with our expectations that animals would have to travel farther to acquire sufficient resources in fragmented landscapes. Compositional analysis and generalized linear mixed models revealed that bears consistently selected for riparian forests over all other habitat types and least preferred urban land-use types. These results suggest that large carnivores occupying fragmented landscapes may require more space than conspecifics occupying contiguous habitats and emphasizes the importance of riparian forests for conservation planning.

202^E: Florida panther survival before and after genetic introgression

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Species conservation increasingly deals with small and isolated populations that are at high risk for inbreeding depression. Intentional genetic introgression has been successful in increasing genetic diversity and population sizes in some cases, but the underlying demographic processes involved often remain unclear. The Florida panther (*Puma concolor coryi*) population consisted of only ~20 animals in the early 1980s and a genetic introgression program was implemented in 1995 to mimic historic natural gene flow. Using 32 years of data from radio-collared panthers and a Cox proportional hazard modeling framework, we estimated age- and sex-specific survival rates of Florida panthers and tested for the effects of several covariates on these rates. Survival rates were strongly sex- and age-specific. For females, subadult panthers had the highest survival rates, followed by prime adults and old adults, respectively. For males, prime adults had the highest survival rates, followed by subadults and old adults. Within age-classes, females always survived better than males, possibly because males experience a higher mortality risk from causes such as intraspecific aggression and vehicle collision. Genetic ancestry strongly influenced survival, with F1-admixed and non-introgressed individuals surviving the best and worst, respectively. Survival also improved with increasing heterozygosity. These results provide evidence for the postulate of hybrid vigor and suggest the positive demographic effects of genetic introgression can remain in the population many years after the event.

203: Reproduction and activity patterns in the Florida bonneted bat (*Eumops floridanus*)

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The Florida bonneted bat (*Eumops floridanus*) is a poorly known species that is endemic to south Florida. Although this bat was 1st described in 1936, most records have been incidental observations of individuals and thus little is known about its biology, including reproduction and activity patterns. In 2007 and 2008, bat houses were erected at 8 sites in the Babcock-Webb Wildlife Management Area in southwestern Florida and bonneted bats soon began roosting in the houses. In 2012, bat houses were erected at 5 additional sites. Bonneted bats roosted in bat houses at 7 of the 13 sites in 2014, and starting in April 2014 we netted bats at 6 houses each quarter and inserted PIT tags into all captured animals. In total, we captured 98 individuals (27M:70F, 1 escape). Pregnant females were captured in April and late August, but not in December when only subadult and post-lactating females were captured. In August 2014, we installed a PIT tag reader and antenna at one of the houses to monitor movement of tagged bats to and from the roost. Bats left the roost as expected soon after sunset, except on the coldest nights when they did not emerge. Time away from the roost and the number of returns to the roost varied widely among individuals and nights. Additional readers will be installed to detect movement between roosts.

204: Use of Florida hibernacula caves by tricolored bats and potential white-nose syndrome impacts

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White-nose syndrome (WNS) is the fungus-caused disease that is decimating bat populations while they hibernate in caves across eastern North America. The causative fungus, *Pseudogymnoascus destructans*, grows most actively in the cool environments of winter hibernacula caves. We have not detected *P. destructans* in any Florida cave as of February 2015, but these hibernacula maintain ambient winter temperatures that are suitable for growth of *P. destructans* (mean = 9.4ºC, *SE* = 1.03). Of Florida's resident bat species, the tricolored bat (*Perimyotis subflavus*) is the species that most frequently enters extended torpor and is thus most susceptible to WNS. In 2014 we surveyed 31 potential hibernacula caves. A total of 369 tricolored bats were recorded in 20 caves, with numbers ranging from 1-141 per cave (mean = 11.9, *SE* = 5.46). In 2015 we expanded our study and have surveyed 88 caves. A total of 983 tricolored bats were recorded in 62 caves, with numbers ranging from 1-220 per cave (mean = 11.6, *SE* =3.39). Two caves sheltered the majority of the bats in both years. But, we have currently identified no physical cave parameters that significantly affected use by the bats. Further analysis is ongoing and those results will be provided along with an assessment of potential impacts from WNS on this tricolored bat population.

205**: Spatial variation in population density affects dispersal behavior in brush mice

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Population density can influence all three phases of natal dispersal: departure from the place of birth, searching the landscape, and selecting a new site in which to settle. The direction of the effect of density on dispersal should be affected by relative costs and benefits of living in an area with high population density. Animals may benefit from high population density due to mate availability and predator risk dilution, but may also face increased competition in high density areas. These conflicting mechanisms should influence the pattern of change in population between departure and settlement: do dispersing individuals choose to move to areas of higher or lower population density than that at their natal site? We examined the influence of density on dispersal in brush mice (*Peromyscus boylii*). We documented pre- and post-dispersal locations of individuals using both radio telemetry and live-trapping, and used a spatially explicit capture-recapture model to estimate density across the landscape. Animals tended to settle in areas with higher population densities than where they were born. This pattern held when landscape-level changes in population density were incorporated: the magnitude of change in local population density between the pre- and post-dispersal locations of a given individual tended to be greater than would be explained by increasing population density across the landscape alone. Dispersal distances were shorter when local natal population density was higher. This research was supported by a Grant-in-Aid awarded to Karen Mabry in 2006.

206^E: Resource selection of a native grazer in nutritionally heterogeneous grassland

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Uncovering the behavioral mechanisms associated with the attraction of grazers to recently burned areas requires understanding at each level of the ecological hierarchy of foraging. First, this study focused on feeding in the area between steps in a foraging bout, the feeding station, as forage chemistry and vegetation architecture play central roles in fine-scale, feeding-station decisions. Next, profits at feeding stations drive plant community attraction by individuals, thus we investigated patch selection to determine the intermediate-level of the foraging hierarchy. Such decisions at these basal levels dictate where in a nutritionally heterogeneous landscape a grazer will forage; therefore, assessing foraging decisions of a native grazer at the feeding station- and patch-levels is key to understanding behavioral mechanisms behind coarse-scale distribution in a shifting landscape mosaic of fire-grazer interactions. At the feeding station-level, analysis of covariance revealed Bison (*Bison bison*) intake rate significantly increased at a greater rate in the early growing season than in mid-summer in infrequently-burned watersheds that burned in the spring prior to observation ($P<0.05$). We used logistic regression to test the hypothesis that if foraging efficiency determines selection of a feeding patch, the strength of avoidance of undesirable forbs will be greatest in highly-profitable watersheds. We found bison avoidance of forb cover was greater in burned watersheds than in unburned watersheds ($P<0.05$). These results suggest foraging efficiency is maximized in recently-burned watersheds.

207: Population genetics of two overlapping populations of tree squirrels (*Sciuris carolinesis and S. niger)*

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Many factors may influence the population genetic structure of a species including social behaviors, mating systems, and dispersal. The eastern gray squirrel (*Sciurus carolinensis)* is known to compete and exclude native squirrel species including the eastern fox squirrel (*S. niger*). These closely related species have similar generation times, population ecologies, and life-histories. I examined the population genetics of overlapping populations of Eastern grey (n = 38) and fox squirrels (n = 53) from 2012–2014. These populations are codistributed across our field site, set in a suburban landscape. I used nuclear DNA analyzed at 8 microsatellite loci with AMOVA and Bayesian analysis to estimate genetic variation, population structure and gene flow in both species. Preliminary findings suggest a lack of significant population substructure, low F_{st} values and lower genetic variation in gray squirrels than fox squirrels possibly due to social and/or mating systems or dispersal. Comparative population genetics of highly related, overlapping species can reveal differences in social and mating systems and dispersal, and interactions with a heterospecific species particularly within the structure of a human-dominated landscape.

208^{E}: Quantifying the effects of human food subsidies on black bear diet across Colorado

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Human-derived foods have become a widely available and predictable resource that can alter foraging behavior. Despite extensive research into black bears (*Ursus americanus*), little consensus exists about the relative influence of native and human food subsidies. We aimed to explore this unresolved question by analyzing the effects of landscape factors on bear diet across Colorado. We estimated assimilated diet using stable isotope analysis of harvested black bear tissues to determine the relative importance of road density and vegetative productivity on diet, as well as if use of food subsidies increased risk of conflict. Preliminary results on hunter-harvested bears (n = 296) indicate substantial use of food subsidies, particularly by eastern CO bears. The most influential covariates on δ^{13}C enrichment (as a tracer of human food subsidies) were age-sex class and road density. Adult females were the most enriched in δ^{13}C, and road density was positively related to δ^{13}C signature and thus, bear reliance on food subsidies, independent of vegetative productivity. In addition, the odds of being a nuisance bear increased by 60% for each unit increase in δ^{13}C, indicating that foraging on subsidies increased risk. While demographic differences play a role in the foraging ecology of bears, availability of subsidies coincident with varying levels of human use appears to be the principal driver in predicting diet of this behaviorally plastic species.

209^{E}: Denning ecology of American black bears (*Ursus americanus*) in southeast Oklahoma

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Denning is an essential component of the black bear reproductive cycle. Pregnant females are obligate hibernators, giving birth and nursing young while in their winter den. As climate change reshapes ecosystem dynamics on a global scale, however, the ecological drivers of denning behaviors may begin to shift. A thorough understanding of denning ecology will be necessary to anticipate the potential impacts climate change may have on black bear populations throughout the species' distribution. The populations that may be affected 1st and most dramatically are those already living at southern latitudes. To address this need, we collected measurements of den characteristics used by collared bears in southeast Oklahoma. We recorded the internal dimensions of each den, and canopy cover and vegetation density at each site. Two I-buttons were installed at each den to record den chamber and ambient temperature regimes. While we are awaiting the results of the 2015 den season, we have already found that collared bears are utilizing a wide variety of den types. We observed 6 excavated, 2 ground, 3 tree cavity, and 2 rock crevice dens. Preliminary results show internal temperature regimes to be significantly less variable than ambient temperatures at rock crevice dens compared with ground nests. Additional bears will be collared May–August 2015. Collared bears will be visited again in the spring of 2016 to collect information on additional dens.

210^{E}: Foraging strategies of *Perognathus flavus* in a nutrient limited desert ecosystem

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In a nutrient limited desert ecosystem, *Perognathus flavus* utilizes a variety of foraging strategies to partition these limited resources and maximize fitness. This research (1) quantified resource use within individual *Perognathus flavus* as either generalists or specialists, and (2) calculated the density and distribution of these mice across our study area. Mice were trapped monthly from March to October, 2014, pit-tagged, sexed, aged, bled, and reproductive status determined. We used a Bayesian mixing model to estimate the proportion of assimilated carbon that was derived from C_3 versus C_4 primary production in plasma, offset by a trophic discrimination factor. Differences in δ^{13}C and δ^{15}N values among rodents and plant functional groups (C_3 versus C_4) were assessed using Tukey post hoc tests to adjust for multiple comparisons. We used Bayesian spatial metrics to quantify isotope variation temporally across the species as measured by standard ellipse areas in δ^{13}C versus δ^{15}N bivariate space. Variation in isotopic space can be linked to individual variation in diet (specialist versus generalist). δ^{15}N values indicate the trophic breadth of the community while δ^{13}C values represent foraging preferences. By analyzing 1,570 plasma samples with > 60 individuals that were trapped and processed 4 or more times over the 8-month period, we were able to adequately quantify foraging strategies. Using the MARC mark-recapture program we calculated density and distribution across our study area.

211^{E}: Survival and cause-specific mortality of white-tailed deer fawns in urban and rural areas

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Urban populations of white-tailed deer (*Odocoileus virginianus*) are increasing in many areas throughout their range. Expansion of urban development and residential suburbs provides white-tailed deer with suitable habitat that is conducive to rapid increases in population growth along with increased risk of deer-vehicle collisions, personal property damage, and elevated incidences of zoonotic diseases. Assessment of fawn survival and cause-specific mortality is important for understanding the population dynamics in these areas. Comparisons between populations of fawn white-tailed deer in urban, suburban, exurban, and rural areas may provide additional insight about the factors that affect these populations. We captured and radio-collared 119 fawns (66 urban, 9 suburban, 8 exurban, 36 rural) in 2013 and 2014. Fawn survival was monitored during the first 6 months of life using radio-telemetry. Primary cause of mortality was vehicle collisions in urban areas, and coyote predation in suburban, exurban, and rural areas. We found that probability of survival increased as density of homes at birth sites increased. This information may help explain the population density differences in urban and rural areas, and help determine which management strategies may be the most effective.

212^{E}: Design of genetic population estimate and food preference studies of recolonizing black bears

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American black bears (*Ursus americanus)* are recolonizing parts of eastern Oklahoma they have not occupied since the late 1800s. A new population in a vastly changed part of their historic range presents new management challenges: damage caused by black bears using anthropogenic food sources, primarily corn in deer feeders, is a major source of human-bear conflict. To manage the growing population, we need an accurate population estimate for the region and a clearer understanding of what food resources the bears are using. We are supplementing traditional mark-recapture methods with genetic population estimation: we collect hair samples from barbed wire snares and identify individual bears using microsatellite techniques, accounting for “captures and re-captures” without physically trapping bears. We collected 148 hair samples from 38 hair snares and 26 hair samples from 14 live-captured bears. We are using stable isotopes obtained from hair samples to determine proportion of individual bears’ diets comprised of anthropogenic versus natural foods. We are also developing a novel experimental approach in collaboration with the Tulsa Zoo to assess directly whether bears, given equal access to different foods, preferentially choose anthropogenic or natural foods. This ongoing project demonstrates the value of several novel techniques to study a recently re-established population of large carnivores, and how we can apply the knowledge gained from these techniques to better mitigate human-bear conflict.

213: Phylogenetic and functional diversity in a highly fragmented forest system

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The Atlantic Forest is the second most biodiverse forest of South America. Metacommunity analysis of small mammals showed that effects of fragmentation were lineage specific at a biogeographical scale. In this study, we test the relationships of phylogenetic (PD) and functional diversity (FD) with a suite of bioclimatic variables, mean actual evapotransporation (AET), mean and range of elevation, and patch size for small mammal communities throughout Atlantic Forest. We calculated FD and PD for 73 communities. The metacommunity includes 42 species of rodents and marsupials and variation in forest patch size area that is representative of the Atlantic Forest biome. We evaluated relationships between PD, FD, latent gradients associated with metacommunity structure, and environmental variables via Spearman rank correlations. Spatial autocorrelation (or spatial structure) for these data was tested via Moran's I. PD and FD were significantly correlated for all taxonomic groups. Small mammal PD was significantly correlated with 17 Bioclim variables, AET, and mean elevation. FD was significantly correlated with 11 Bioclim variables and AET. Species composition along the latent gradient and PD showed significant spatial autocorrelation. However, FD did not show spatial autocorrelation. Variation in PD and FD was significantly associated with patch area only for marsupials. The effects of fragmentation are contingent on evolutionary lineage, requiring effective conservation and management practices to consider various taxa.

214: Spatially heterogeneous impact of climate change on small mammals of montane California

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Resurveys of historical collecting localities have revealed range shifts, primarily leading edge expansions, which have been attributed to global warming. However, there have been few spatially replicated, community-scale resurveys testing whether species' responses are spatially consistent. Here we repeated early 20th century surveys of small mammals by Joseph Grinnell and colleagues at the Museum of Vertebrate Zoology (UC Berkeley) along elevational gradients in northern (Lassen National Park), central (Yosemite National Park) and southern (Sequoia and Kings Canyon National parks) regions of montane California. Of the 34 species we analyzed, 25 shifted their ranges upslope or downslope in at least 1 region. However, two-thirds of ranges in the 3 regions remained stable at 1 or both elevational limits and not one of the 22 species found in all 3 regions shifted both their upper and lower limits in the same direction in all regions. When shifts occurred, high elevation species typically contracted their lower limits upslope, whereas low elevation species had heterogeneous responses. For high elevation species, site-specific change in temperature better predicted the direction of shifts than change in precipitation,

whereas the direction of shifts by low elevation species was unpredictable by temperature or precipitation. While our results support previous findings of primarily upslope shifts in montane species, they also highlight the degree to which the responses of individual species vary across geographically replicated landscapes.

215^E Shrub encroachment, habitat restoration, and mammalian diversity in longleaf pine sandhills

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The restoration of degraded longleaf pine (*Pinus palustris*; LLP) forests has focused on the use of prescribed fire and herbicide application. We investigated the effect of these 2 restoration tools on the diversity of medium and large (≥0.5kg) mammalian LLP inhabitants. We placed camera-traps at 450 points, comprising 50 grids, in herbicide treated and untreated LLP sandhills in north Florida. All sites experienced prescribed fire. We camera-trapped from January-June of 2013 and 2014, yielding 6,737 photos of mammals. We calculated the cumulative species richness (*Richness*), Shannon diversity index (*Diversity*), Shannon evenness index (*Evenness*), and Berger-Parker index (*Dominance*) for each grid. We developed 13 *a priori* models using 5 vegetative and 2 habitat management variables, selected because of their perceived importance to wildlife. We evaluated candidate models using either linear mixed-effects or generalized linear mixed models. We found that herbicide treatment best accounted for variation in *Diversity* and *Dominance* of mammals on our grids. Herbicide application decreased mammalian *Diversity* and increased *Dominance*. These findings reveal potential issues associated with using herbicide in habitat restoration, and highlight the need for further research into the effects of herbicide on wildlife inhabitants.

216^E: Morphometric and genetic variation in eight breeds of Ethiopian camels (*Camelus dromedarius*)

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Ethiopian camels (*Camelus dromedarius*) historically have been a domesticated and closely guarded economic staple to indigenous peoples located throughout the country's territorial states. Seventeen morphometric variables were utilized to determine intra-species variation within eight breeds of camels, common in these regions. In addition, DNA sequences from the mitochondrial cytochrome-*b* locus and seven nuclear microsatellite loci were examined to access genetic differentiation and to determine phylogenetic relationships. Exomorphic variation was detected in two of the breeds (Afar, and Jigjiga) using principle component analysis and linear discriminant function analysis. Cyt*b* was examined in 28 individuals and depicted some separation within the breeds. Microsatellites in 105 individuals was analyzed with Structure 2.3.4 using five of the seven markers. The data for 524 individuals were analyzed and indicated three distinct groups. Finally it appears separation of breeds is not supported with cyt*b* data and morphometric data.

217: A multi-locus history of Australo-Papuan rodents: Origins, biome transitions and species delimitation

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Rodents are the only non-volant, terrestrial mammals that have naturally colonized the Australian continent (Sahul) since its break-up from Gondwana. Extant species diversity in Australo-Papuan rodents, including nearly 160 species in 37 genera, evolved from two colonization events centered on New Guinea in the Pliocene and Pleistocene. Here we present a review of our phylogenetic analyses on this group and their neighbors across the Indo-Australian region. With fairly robust phylogenetic hypotheses we have dated colonization events and environmental transitions to reconstruct the ecological diversification of Australo-Papuan rodents on a broad-scale. Our multi-locus phylogenies also suggest unrecognized phylogenetic diversity within species suggesting that diversification in this group is ongoing.

218**: A new classification scheme for southern African gerbils (*Gerbilliscus*) based on genetic and morphological data

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Currently, 6 species are recognized for southern African gerbils of the genus *Gerbilliscus* (*G. afra*, *G. brantsii*, *G. boehmi*, *G. inclusus*, *G. leucogaster*, and *G. validus*). Historically, greater diversity was recognized for this group (e.g., 23 synonyms for *G. leucogaster*). Furthermore, recent studies of West African *Gerbilliscus* have illuminated unrecognized diversity in this group, indicating the need for careful examination for other members of this genus using both morphological and genetic data. Here, we estimate phylogenies using DNA sequence data from both nuclear and mitochondrial markers, including sequences from 3 type specimens. Additionally, we examine patterns of morphological variation between and among species groups using multivariate plots for 23 cranial measurements. Phylogenetic trees estimated using Bayesian inference and Maximum-likelihood provide support for 10 genetic lineages with 3 major clades: *G. afra* group, *G. leucogaster* group, and *G. boehmi*. Sequences from museum type specimens reveal the phylogenetic position of 3 of the oldest types in the genus: *G. boehmi* (Noack, 1887), *G. leucogaster* (Peters, 1852), and *G. schinzi* (Noack, 1889). Morphometric results appear consistent with genetic data, indicating that the observed genetic species also exhibit distinct morphological features. We therefore propose a new classification scheme for southern African *Gerbilliscus* including new insights into their geographic distributions. This research was supported by a Grant-in-Aid awarded to Molly McDonough in 2013.

219^{E}: Species Delimitation and Biogeography of the New World *Myotis* (Chiroptera: Vespertilionidae)

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Despite recent advances in species descriptions and phylogenetic relationships of *Myotis*, our understanding of the systematics and biogeography of this genus in the New World—particularly the Neotropics—is limited. Especially, species boundaries are unclear given the wide distribution of some species, and sometimes absence of reliable diagnostic character. Here, we conducted an exploratory analysis of published cytochrome b sequences together with new sequences generated from Ecuadorian specimens. We used a Poisson-Distribution Process (PTP) for species delimitation, and estimated the timing and biogeographic history of the *Myotis* of the New World. The most robust PTP delimitation resulted in 55 species of New World *Myotis*: North America (19 species), Central America (4 species), Caribbean (5 species), and South America (27 species). The historical biogeography analysis showed in greater detail the dispersal events that explain the current distribution of *Myotis* in the New World. These preliminary results—based on a single locus—show that the diversity of *Myotis* is underestimated and there is a need to continue doing inventories and systematic studies oriented to characterize the cryptic diversity of the genus in the New World.

220: Diversity and systematics of South American rodents: transitioning into the genomics era

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Much progress has been made in the last few decades in our understanding of the age, geographical origins, phylogenetic relationships, and diversity of caviomorph and sigmodontine rodents, 2 major components of the South American fauna. The transition of the field of phylogenetics and systematics into the genomic era promises new insights into the diversity of South American mammals and their functional roles in diverse ecosystems. However, the current representation of caviomorphs and sigmodontines in genomic–transcriptomic databases is too restricted for these opportunities to be realized. To address this situation, we outline a research program designed to a) obtain a set of genomes and transcriptomes that represent major groups within each of these 2 lineages; and b) link these data to voucher specimens with substantial associated data and biological materials. We envision a concerted international effort to guide and accelerate progress in the field.

221: The challenges of resolving a rapid radiation of Philippine shrews: Empirical and simulated phylogenomic approaches

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Phylogenetic relationships in recent, rapid radiations can be difficult to resolve due to incomplete lineage sorting and genetic markers that evolve slowly relative to the rate of speciation. Phylogenomic analyses aim to overcome these difficulties by analyzing hundreds to thousands of unlinked loci. Here, we attempt to resolve phylogenetic relationships among eight *Crocidura* shrews from the Philippines, a phylogenetic problem that has proven intractable with small datasets. We sequenced hundreds of ultraconserved elements and whole mitochondrial genomes in these species and estimated phylogenies using concatenation and species tree methods. The concatenated approach recovered a well-supported and fully resolved tree, in contrast to the species tree approaches, which produced similar phylogenies but with several poorly supported nodes. Using simulations, we demonstrate that the concatenated tree, with its complete support for all nodes, may be positively misleading. Our simulations demonstrate that the tree shape we tend to infer is difficult to resolve, even if substitution models are known and multiple individuals per species are sampled. As such, the low support we obtained for backbone relationships reflects an appropriate lack of certainty. Our results illuminate the phylogenomic challenges of estimating bifurcating trees in a rapid and recent radiation and provide a rare empirical example of a nearly simultaneous series of speciation events that occurred in a terrestrial mammal lineage as it spread across an oceanic archipelago.

222: Women in ASM

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The American Society of Mammalogists is approaching its 100th anniversary. Reaching this milestone provides an opportunity for us to reflect on our history, celebrate our accomplishments, and have a meaningful dialogue about the challenges and priorities that will guide us into the future. Women have had a long and rich history in our society. This session will highlight the early history of women in ASM, and examine demographic trends in society composition and participation by women from its founding up to today. By revisiting our history and the rich role that women have played in ASM, we improve our ability to move forward as a major professional society that welcomes all people interested in promoting understanding of mammalian biology.

223: A new era for biological conservation: the Smithsonian view

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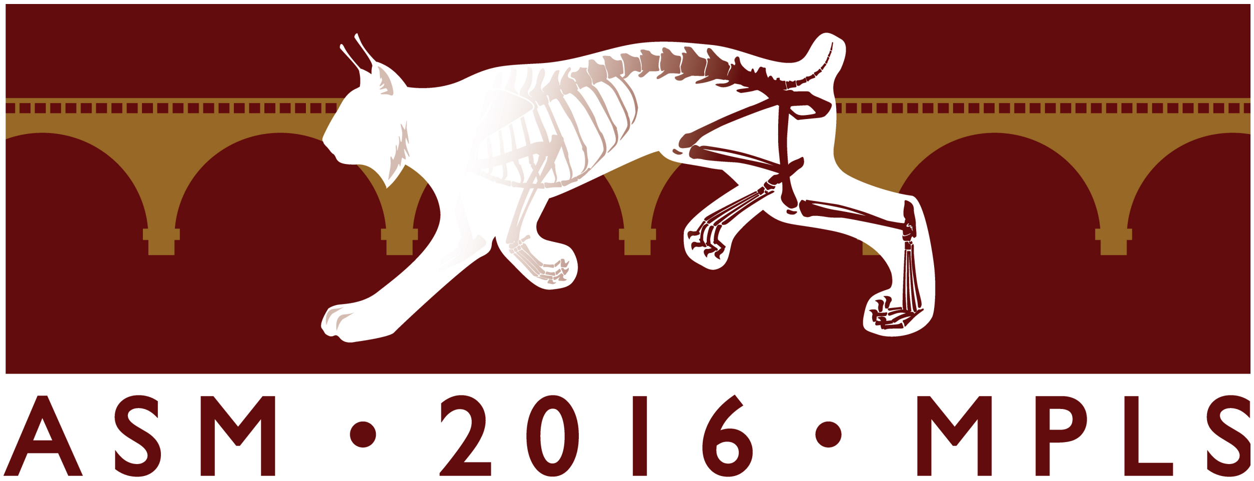
The American Society of Mammalogists was chartered on April 3, 1919. On the following day, the first meeting of the Society was held at the Smithsonian Institution in the National Museum of Natural History building, then called the U.S. National Museum. Over time the Society grew, as did the Smithsonian's Division of Mammals, with approximately 590,000 cataloged specimens in the collection. Since the origins of the formal study of mammalogy, science and general knowledge have expanded exponentially. In the field of zoology alone, there are now twenty five branches, many of them new. Disciplines, whether in science or engineering, risk losing relevance, being overshadowed by other disciplines, or being seen as out of fashion as society seeks what is new. As a mature discipline, mammalogy faces these challenges but it also has great opportunities, particularly when seen through the lens of biological conservation. Developments like biogenomics, bioinformatics, sustainability, social media, and crowdsourcing provide mammalogists new tools to build out a platform as a part of an interdisciplinary approach that will comprehensively address large-scale societal problems like anthropogenic change, habitat destruction and loss of species. In my view, mammalogy succeeds when it is seen as relevant to the issues humans face, and when it teaches young people to appreciate the challenges facing our fragile planet.

AUTHOR INDEX

NOTES

SAVE THE DATE!!!

96TH ANNUAL MEETING OF THE AMERICAN SOCIETY OF MAMMALOGISTS



Please join us June 24-28, 2016, in Minneapolis, Minnesota for the 96th Annual Meeting of the American Society of Mammalogists. The conference will be held on the campus of the University of Minnesota, home of the Golden Gophers! Come learn about the latest advances in the study of mammals and interact with researchers and educators specializing in the biology of these fascinating animals. Come and enjoy everything the Land of 10,000 Lakes has to offer!

Dorm rooms will be available in residence housing. In addition, hotel blocks will be made available to meeting attendees. Detailed conference and registration information will be made available on the conference website, which will be posted on the "Meetings" tab of the ASM webpage (http://www.mammalsociety.org).

The scientific program will include contributed oral and poster presentations as well as symposia, plenary speakers, and workshops. A full social agenda is being planned that includes multiple mixers, an awards social, a picnic, our annual Run-for-Research, and fieldtrips. Details for these events will be made available on the conference website.

For more information about the 2016 meeting, contact the chair of the Program Committee, Cody Thompson, University of Michigan Museum of Zoology (734-615-2810 or cwthomp@umich.edu), local host, Sharon Jansa, University of Minnesota (612-624-6293 or jansa003@umn.edu), or Tony Ballard, Kansas State University Conference Services (785-532-2402 or tballard@k-state.edu).

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