

# AMERICAN SOCIETY OF MAMMALOGISTS

94<sup>th</sup> ANNUAL MEETING

Renaissance Oklahoma City Convention Center Hotel and Cox  
Convention Center, Oklahoma City, Oklahoma



ABSTRACT BOOK

The 2014 American Society of Mammalogists Annual Meeting logo features a Pronghorn (symbol of the ASM) with an abstracted Oklahoma City skyline, and water representing the Oklahoma River and Bricktown Canal. The arrangement suggests OKC's historic Art Deco architecture and new architecture like the Devon Tower, Scissortail Bridge, and Oklahoma River boathouses. The logo was designed by Hadley Jerman, Graphic Designer at the Sam Noble Museum in Norman, Oklahoma.

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## TABLE OF CONTENTS

Sponsor List .....	4
Abstracts .....	7
Author Index.....	83
2015 Meeting Announcement .....	Inside Back Cover

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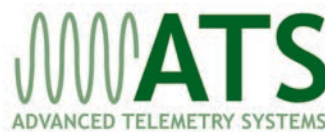


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## ABSTRACTS

E = Evaluated oral or poster presentation; TA = Student travel award; ECT = Early career travel award;

\*\*Research funded by the ASM; C = Cancelled presentation

### 1 (E,\*\*) ANNA M. JACKSON AWARD, Plenary I, Great Halls D & E, Saturday 7 June 2014

**Johanna Varner<sup>1</sup>, Mallory S. Lambert<sup>1</sup>, Joshua J. Horns<sup>1</sup>, Erik A. Beever<sup>2</sup>, M. Denise Dearing<sup>1</sup>**

<sup>1</sup>Department of Biology, University of Utah, Salt Lake City, UT 84112 USA; <sup>2</sup>Northern Rocky Mountain Science Center, U. S. Geological Survey, Bozeman, MT 59715 USA

#### Too Hot to Trot? Pika Survival in a Time of Disturbance and Global Change

Wildfires have increased in frequency and severity due to climate change, but little is known about the potential threat of altered fire regimes to mammals, particularly those with limited dispersal ability. Here, we leverage an unexpected opportunity to investigate the impact of a severe wildfire on a climate-sensitive lagomorph, the American pika (*Ochotona princeps*). Despite widespread recent interest in climate-mediated pika extirpations, little is known about how this species responds to disturbances like wildfire. In August 2011, we surveyed for pikas at several sites in the Mt. Hood National Forest. Shortly thereafter, a large forest fire burned many of these field sites, including 2 sites where data loggers were collecting temperature data in the talus interstices. In the post-fire years (2012 and 2013), we returned to measure vegetation availability and pika abundance at 24 sites on Mt. Hood. During the fire, temperatures remained cool in the talus interstices, suggesting that pikas could have survived in situ. Indeed, pikas quickly occupied all sites, even those with few food resources. However, pika abundance did not increase until a threshold of vegetation was reached. Defining these thresholds can improve distributional predictions under environmental change and identify conservation targets. Studies of this nature are impossible to plan, but may be extremely informative. This research was supported by an ASM Grants-in-Aid of Research awarded to Johanna Varner in 2011.

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### 2 (E,\*\*) ELMER C. BIRNEY AWARD, Plenary I, Great Halls D & E, Saturday 7 June 2014

**Jennifer M. Schieltz, Daniel I. Rubenstein**

Department of Ecology and Evolutionary Biology, Princeton University, Princeton, NJ 08544 USA

#### Cattle-wildlife Coexistence: How Body Size and Digestion Affect the Response of Wild Grazers to Cattle Grazing

Forty percent of Earth's land surface is used for grazing domestic animals. Grasslands and savannahs also support many of the world's wild large mammals. Consequently, conservation efforts are increasingly aimed at managing land for wildlife-livestock coexistence. Understanding the effect of cattle on different wild species could allow ranchers to adjust management plans to promote coexistence. Cattle could even be used as a tool to manage rangelands for wildlife. I investigated how body size and digestion (ruminant/non-ruminant) affected wild grazer responses to cattle grazing in Kenya. Five focal species were studied: 3 ruminants (Thomson's gazelle, hartebeest, buffalo) and 2 non-ruminants (warthog, plains zebra) spanning a range of body sizes. Results show that cattle not only change the quantity of grass but the quality of it as well, and may actually improve vegetation for several species. Small species preferred low biomass areas grazed more by cattle, while buffalo were found mostly in high biomass areas away from cattle. When grass is not limiting, zebra also are drawn to areas of high cattle use with shorter, and likely more nutritious grass. Non-ruminant species were more evenly distributed than their similar-sized ruminant counterparts. Most ruminants were found at a small number of sites while non-ruminants utilized more of the total available habitats. This research was supported by an ASM Grants-in-Aid of Research awarded to Jennifer Schieltz in 2012.

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### 3 (\*\*\*) A. BRAZIER HOWELL AWARD, Plenary I, Great Halls D & E, Saturday 7 June 2014

**John W. Doudna, Brent J. Danielson**

Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, IA 50011 USA

#### Rapid Morphological Change in the Masticatory Structures of an Important Ecosystem Service Provider

Humans have altered the biotic and abiotic environmental conditions of most organisms. In some cases, such as intensive agriculture, an organism's entire ecosystem is converted to novel conditions. Thus, it is striking that some species continue to thrive under such conditions. The prairie deer mouse (*Peromyscus maniculatus bairdii*) is an example of such an organism, and so we sought to understand what role evolutionary adaptation played in the success of this species, with particular interest in adaptations to novel foods. In order to understand the evolutionary history of this species' masticatory structures, we examined the maxilla, zygomatic plate, and mandible of historic specimens collected prior to 1910 to specimens collected after 2010. We found that mandibles, zygomatic plates, and maxilla have all changed since 1910 and that morphological development within time has shifted. We present compelling evidence that these differences are due to natural selection as a response to a novel and ubiquitous food source, waste grain (corn—*Zea mays*, and soybean—*Glycine max*). This research was supported by an ASM Grants-in-Aid of Research awarded to John Doudna in 2012.

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

4 (\*\*) WILLIAM T. HORNADAY AWARD, Plenary I, Great Halls D & E, Saturday 7 June 2014

**Abdullahi H. Ali**

*Program in Ecology and Department of Zoology and Physiology, University of Wyoming, Laramie, WY 82091 USA; National Museums of Kenya, Nairobi, Kenya; Hirola Conservation Program, Garissa, Kenya*

**Range Collapse, Demography and Habitat Selection of the Critically Endangered Hirola Antelope (*Beatragus hunteri*) in Kenya**

With a global population size of < 500 individuals, the hirola, *Beatragus hunteri*, is the world's most endangered antelope. Its extinction would constitute the 1st loss of a mammalian genus since that of the thylacine (*Thylacinus cynocephalus*) in 1936. Ecological knowledge gaps, weak local involvement, and political turmoil on the Kenya-Somali border have hindered hirola conservation since the 1970s. Unlike many endangered species, the historic range of hirola occurs entirely outside national parks and other formally protected areas, so its fate hinges on an ability to understand and manage jointly for conservation and human livelihoods. In 2010, I initiated a collaborative effort, the Hirola Conservation Program, to understand the reasons underlying hirola declines and to work with Somali communities and other stakeholders to curb these declines. Currently, I am assessing the importance of predation and deteriorating range quality for hirola demography, movements, and habitat selection. Through a combination of GPS telemetry, analysis of long-term satellite imagery, a large-scale predator exclusion zone, and sustained community outreach, the Hirola Conservation Program is informing national policy on this little-known species. In this presentation, I will discuss factors driving historic and contemporary declines of hirola and viable management options to curtail these declines. This research was supported by the ASM William T. Hornaday Award given to Abdullahi Ali in 2013.

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5 (E,\*\*) ALBERT R. AND ALMA SHADLE AWARD, Plenary I, Great Halls D & E, Saturday 7 June 2014

**Joseph R. Burger**

*Department of Biology University of New Mexico, Albuquerque, NM 87106 USA*

**Human Macroecology: Because Humans are Mammals Too**

*Homo sapiens* is the most well studied species on the planet, yet mammalogists do not typically study humans the same way we study other mammals. Like all species, humans too are constrained by the same physical, chemical, and biological laws that govern life on Earth. Yet, in less than 10,000 years humans have gone from small networks of tropical hunter-gathers to large agglomerations of global, industrial-technological, urban dwellers. I will introduce how the macroecological approach provides a rigorous framework to compare and contrast the ecology of modern humans to other mammals. First, we will discuss how thermal physiology interacts with environmental temperature to restrict the geographic distributions of all mammals and the innovations that allow modern humans to circumvent these constraints and expand geographically. Second, using the energetic equivalence rule, we will explore how hunter-gather societies and modern city dwellers compare to other terrestrial mammals in density and energy use. Hunter-gatherer abundance is statistically indistinguishable from other terrestrial mammals and is constrained by local environmental productivity. In contrast, city dwellers occur at densities much greater than hunter-gathers and comparable to mice but use more than 4 times the amount of energy required by an elephant. This talk will hopefully demonstrate how human macroecology can provide unique insights into our evolutionary past and sustainable future. This research was supported by the ASM Albert R. and Alma Shadle Award given to Joseph Burger in 2013.

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6 (E,\*\*) ASM FELLOWSHIP, Plenary I, Great Halls D & E, Saturday 7 June 2014

**C. Miguel Pinto**

*Department of Mammalogy, American Museum of Natural History, New York, NY 10024 USA*

**Mammals and Trypanosome Parasites: Searching the Origins of Chagas Disease**

Chagas disease is caused by the protozoan parasite *Trypanosoma cruzi*. Despite the public health importance of Chagas disease, there are still doubts on the evolution and biogeography of *T. cruzi* and its relatives, which form the *T. cruzi* clade. This clade has a cosmopolitan distribution, and is composed by several species of parasites of mammals—mostly bats. Here, I analyzed genetic data from multiple loci of previously known as well as newly found trypanosomes from the New and Old Worlds. I used phylogenetic model based methods, performed species delimitation, ancestral reconstruction, and historical biogeography analyses to follow the association of the parasites and their mammalian hosts. These analyses support bats as the original hosts of both—the clade and Chagas disease, also a southern super-continent (New World/Africa/Australia) biogeographic origin for the clade. In addition, the current distribution of the group is better explained as a result of long distance dispersal. Lastly, cryptic diversity is recognized within this clade. These results indicate a long evolutionary relationship between bats and their trypanosomes, suggesting a scenario where bats were key players for a radiation of trypanosomes, triggered by bat-mediated long distance dispersal of parasites and sporadic host switches to nonvolant mammals, then Chagas disease appeared in humans recently (< 15,000 years) with the colonization of the Americas. This research was

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

supported by an ASM Grants-in-Aid of Research in 2010, a Shadle Fellowship in 2012, and an ASM Fellowship in 2013 awarded to C. Miguel Pinto.

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## 7 Symposium I: The Integrative Biology of Mammalian Hibernation, Great Halls D & E, Saturday 7 June 2014

**Hannah V. Carey**

*Department of Comparative Biosciences, University of Wisconsin-Madison, Madison, WI 53706 USA*

### **Symbiotic Interactions between Gut Microbiota and Their Hibernator Hosts**

The evolution of animals with microbes has shaped multiple aspects of animal biology. In nonruminant vertebrates most microbes reside in the hindgut, and the type and amount of host diet exerts a strong influence on microbial communities. To meet metabolic needs microbes metabolize dietary components that reach the hindgut and some can utilize host-derived substrates such as mucins and nutrients in sloughed epithelial cells. Short-chain fatty acids produced by microbial metabolism can be absorbed by the host to meet energetic and nutritional needs. Seasonal changes in host diet can therefore affect the microbiota and alter the host-microbe relationship. Our studies examine the host-microbial relationship in ground squirrels that suspend feeding during their 5–6 month hibernation season. Luminal and mucosa-associated microbiotas are restructured over the annual hibernation cycle; compared to summer, phylogenetic diversity and numbers of unique species are lowest in late winter and highest after re-feeding in spring. Abundances of certain taxa change with season; hibernation increases abundance of Bacteroidetes and Verrucomicrobia, phyla with species that can metabolize host-derived substrates, and reduces abundance of several Firmicutes taxa known to prefer dietary polysaccharides. The intestinal immune system is altered during hibernation in ways that suggest enhanced tolerance between host and symbionts. The potential contributions of microbes to remodeling of physiological systems in response to seasonal or other kinds of environmental change should not be overlooked.

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## 8 Symposium I: The Integrative Biology of Mammalian Hibernation, Great Halls D & E, Saturday 7 June 2014

**Brian M. Barnes, Oivind Toien**

*Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks, AK 99775 USA*

### **Hibernation in the Extreme: Lessons from Arctic Ground Squirrels and Black Bears**

Hibernation, as an adaptation to seasonal food shortage, occurs in mammals living in diverse environments, but it is in the Arctic where conditions are coldest and duration of hibernation is among the longest. We have been investigating energetics, thermoregulation, body temperatures, metabolism, biological rhythms, and behavior in arctic ground squirrels and black bears in northern Alaska and offer the following observations. Animals anticipate food shortage and begin hibernation during times of plenty and conditions of energy surfeit. Hibernation functions to decrease metabolic demand of animals and obviates the need for food and water. During torpor entry, suppression of metabolism occurs prior to the decrease in body temperature. Metabolic suppression can be largely independent of changes in body temperature. Rates of mass specific metabolism are identical in hibernating arctic ground squirrels and black bears under average winter conditions; what happens to body temperature is a matter of physics. Hibernators eschew carbohydrates and burn fat, except when they do not (when sustaining high rates of nonshivering thermogenesis). Hibernation and reproduction are incompatible in small mammals and can co-occur in large. Torpor and sleep are incompatible in small hibernators but co-occur in large. Circadian rhythms stop but multi-day cycles of body temperatures continue for different reasons in hibernating ground squirrels and bears. Circannual rhythms rule in ground squirrels. Hibernation in ground squirrels and bears is an example of convergent evolution.

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## 9 Symposium I: The Integrative Biology of Mammalian Hibernation, Great Halls D & E, Saturday 7 June 2014

**Kenneth B. Armitage**

*Ecology & Evolutionary Biology, The University of Kansas, Lawrence, KS 66045 USA*

### **Hibernation as a Major Determinant of Marmot Life-History Traits**

During the downward trend of Quaternary global temperatures, crown-group marmots evolved to occupy harsh, seasonal environments at high latitudes and elevations. Marmots evolved hibernation and large body size to cope with a long, cold season with low, stressful ambient temperatures when food is unavailable and with a short season favorable for growth and reproduction. The short active season restricts the frequency of reproduction to no more than once a year and harsh conditions frequently cause reproductive skipping. The annual cycle is controlled by a circannual rhythm, which directs metabolic changes and fat accumulation for hibernation and reproduction. Adaptation to the low environmental temperatures of hibernation may result in heat stress and restriction of daily activity during the summer. Energy conservation characterizes metabolism: metabolic rates are lower than predicted from body size, metabolism is depressed to enter hibernation, considerable time is spent at low metabolism in deep torpor, and conductance is low. Young have insufficient time during the short active season to reach maturity and remain at home for at least 1 additional growing season. This retention of kin leads to sociality based on kinship. Both cooperation and competition occur within the social group. Competition is expressed primarily as reproductive

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

suppression, which delays the age of maturity (age of 1st reproduction), which in turn strongly affects whether a population increases or declines.

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## 10 Symposium I: The Integrative Biology of Mammalian Hibernation, Great Halls D & E, Saturday 7 June 2014

**Craig L. Frank<sup>1</sup>, Kelsey D. Howard<sup>2</sup>**

<sup>1</sup>Department of Biological Sciences, Fordham University, Armonk, NY 10504 USA; <sup>2</sup>Environmental Science Program, Fordham University, Bronx, NY 10458 USA

### The Relationship between Climate, Dietary Fatty Acid Composition, and the Over-winter Survival of Golden-mantled Ground Squirrels

Laboratory experiments demonstrated that the amount of polyunsaturated fatty acids (PUFAs) in the diet prior to hibernation influences patterns of mammalian torpor. The hibernation ability of ground squirrels is greatest (longest torpor bouts, greatest number of animals entering torpor) when dietary PUFA contents are 33–74 mg/g. The extent to which the fall diets of hibernating mammals both vary in PUFA content and influence the torpor patterns of free-ranging populations is known for a single species (*Urocyon parryii*), however. We conducted a 3-year study on the diet PUFA contents and hibernation patterns of free-ranging golden-mantled ground squirrels (*Callospermophilus lateralis*) in the White-Mountains of California. We found that fall diet PUFA contents varied by > 5 fold among individuals, and squirrels that consumed a moderate (33–74 mg/g) PUFA diet were much more likely to survive the hibernation period than those that consumed either a low (< 33 mg/g) or high (> 74 mg/g) PUFA diet during the fall. A longer (14-year) study at this site also revealed that fall soil (nest) temperatures have increased by about 2°C since 1998, and that the hibernation patterns of *C. lateralis* have shifted accordingly. The long-term changes in hibernation patterns are also associated with corresponding changes in the PUFA contents of food plant species consumed before hibernation.

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## 11 (ECT) Thematic Session I: Recent Advances in Mammalogy, Great Halls D & E, Saturday 7 June 2014

**Caleb D. Phillips, Robert J. Baker**

Department of Biological Sciences and The Museum, Texas Tech University, Lubbock, TX 79409 USA

### How Did a Vampire Bat Evolve from a Bat That Eats Insects?

Diversity and rapidity of ecological transitions by bats of the family Phyllostomidae are unparalleled among higher vertebrates. Among ecological niche leaps observed in this family, the most dramatic is the evolution of obligate sanguivory by vampire bats. Although examination reveals modifications to essentially all aspects of vampire bat anatomy and physiology, the genomic mechanisms called upon to evolve vampire bats are largely unknown. Using comparative transcriptomics of vampire bats, outgroup insectivorous bats, and sanguivorous leeches, we identify genes that have been convergently recruited as secretory products of salivary glands of vampire bats and leeches. Convergently recruited homologs are from gene families that were necessarily present in the common ancestor more than 500 million years ago. Comparisons of vampire bat to lineages maintaining the primitive chiropteran condition of insectivory disclosed recruitment of alternative splice variants, and 5' exon evolution, as the mechanisms producing secretory expression in vampire bats, but not in the insectivorous bats *Macrotus* and *Myotis*. Established biochemical functions of convergently recruited genes explain adaptive benefits to sanguivory by modulating multiple host hemostatic pathways and neural disruption. It has been difficult to identify how complex phenotypic change and rapid ecological transition, such as that observed in vampire bats, has evolved over a short evolutionary timescale. Current results indicate that evolution of tissue-specific alternative splicing has been an important component of successful evolution to blood feeding.

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## 12 Thematic Session I: Recent Advances in Mammalogy, Great Halls D & E, Saturday 7 June 2014

**Jessica E. Light**

Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, TX 77843 USA

### Ecological and Population Genetic Assessments of Host-parasite Associations

Over the past 5 years, research in my laboratory has been broadly focused on understanding the associations between hosts and their parasites from the perspectives of ecology, phylogenetics, and population genetics. Research has been focused on 2 main projects in southeastern Texas: ecological associations among small mammals, ticks, and tick-borne pathogens and population genetics of pocket gophers and their chewing lice. Tick-borne diseases are emerging worldwide and are of particular concern in the southern United States due to high tick species diversity and longer periods of seasonal tick activity. I will present results on 2 tick-borne pathogen studies, both involving mark-recapture sampling of the small mammal community, tick-drag sampling, and molecular diagnostic analyses in the laboratory. Both tick-borne pathogen studies have the potential to better understand disease risk and can be useful for public health protection in Texas. The population genetics studies were performed in an effort to better understand the long-term associations between distantly related organisms. I will present results

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

from analyses using microsatellite data to examine gene flow across various spatial scales in both the Baird's pocket gopher (*Geomys breviceps*) and their parasitic chewing lice (*Geomydoecus ewingi*). Examination of population processes occurring within and among pocket gopher and chewing louse populations may reveal which factors play crucial roles in the establishment and maintenance of host-parasite associations.

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### 13 Thematic Session I: Recent Advances in Mammalogy, Great Halls D & E, Saturday 7 June 2014

**William J. Murphy**

*Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX 77843-4458 USA*

#### **Future Prospects for a Fully Resolved Mammal Tree of Life**

Recent advances in mammalian molecular phylogenetics have converged on a well-resolved phylogeny at the family level, and even the generic level for some orders (i.e., primates, carnivores). Despite these advances, the majority of species are not placed in a comprehensive phylogeny based on adequate genomic sampling that is conducive to divergence time estimation for the analysis of diversification patterns and character evolution. Most phylogenies in the literature are based on mitochondrial DNA and may not reflect the true species tree, therefore new tools and methods are needed for examining phylogenetic concordance across the nuclear genome to understand regional variation in signal that might highlight regions influenced by hybridization and reproductive isolation. Here, I will present the results from 2 genomic approaches used to achieve well resolved nuclear and mitochondrial phylogenies at the species level. The 1st approach describes the application of genome-wide single-nucleotide polymorphism (SNP) arrays to produce a comprehensive nuclear phylogeny of felids, characterize whole and regional chromosomal discordance in phylogenetic signal, and develop a historical biogeographic scenario for the early evolution of cats. The 2nd approach highlights the application of low-coverage genome sequencing and capture hybridization approaches on DNAs extracted from archived museum specimens, with a focus on widely distributed Southeast Asian mammals, hidden biodiversity, and the promise of applying museum-based sequencing to produce a fully resolved tree of life for mammals.

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### 14 (C) JOSEPH GRINNELL AWARD, Plenary II, Great Halls D & E, Sunday 8 June 2014

**Ricardo A. Ojeda**

*Grupo de investigaciones de la Biodiversidad, Instituto Argentino de Investigaciones de Zonas Áridas (IADIZA), Consejo Nacional Investigaciones Científicas y Técnicas (CONICET), Mendoza 5500, Argentina*

#### **Towards a Research Training Program in Temperate Aridlands**

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. My presentation will highlight different aspects of the development of our mammal research program in temperate aridlands of Argentina, answering questions and discussing some of the approaches we have taken towards a better understanding of particular ecological-evolutionary processes, species' biology or the structure of mammal communities. I discuss the ecological background or context of our research and highlight some results as well as the consolidation of a research training program oriented towards a more comprehensive understanding of animal biology and ecology of aridlands. I also discuss issues related to the scientific context where our research is carried on 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.

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### 15 ALDO LEOPOLD AWARD, Plenary II, Great Halls D & E, Sunday 8 June 2014

**Joel Berger**

*Organismic Biology and Ecology, University of Montana, MT 59812 USA; Wildlife Conservation Society, Bozeman, MT 59717 USA*

#### **Conservation's Unwieldy Path — Big Animals in an Increasingly Peopled World**

The world's mammals occupy amazingly diverse landscapes – polar, temperate, and tropical – all increasingly humanized. Although 95% of the world's people live below 1,000 m, all environments certainly have their own impediments to conservation. Using a gradient of human density and extreme environments I offer 3 vignettes to explore the progressively complex interactions between humans and wildlife. 1) In the Siberian and Alaska Arctic, where climate might be expected to be a critical driver of muskoxen persistence, it is the indirect effects of humans that may be playing a larger role. 2) In Central Asia, endemic wildlife including wild yak, saiga, snow leopards, and chiru persist where human densities are among the lowest on the planet. Nevertheless, despite strong protection from poaching, populations are being exploited indirectly through interactions that involve western cultural preferences for cashmere steeped inevitably in the multibillion dollar garment industry; hence, the challenge—economics and humans. 3) In the comparatively more peopled American West, pronghorn are an ecological surrogate of Asia's saiga. Pronghorn are also the longest migrants of any terrestrial mammal between Canada and

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

Tierra del Fuego. During migrations they confront fragmented landscapes, suburban expansion, and energy development. A science-based initiative resulted in statutory protection of their migration corridor. The extent to which on-the-ground studies facilitate messaging for conservation and its limitation will be prominent in this presentation.

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## 16 C HART MERRIAM AWARD, Plenary II, Great Halls D & E, Sunday 8 June 2014

### **Rudy Boonstra**

*Centre for the Neurobiology of Stress, Department of Biological Sciences, University of Toronto Scarborough, Toronto, Ontario M1C 1A4 Canada*

#### **Of Memory and Mammals: The Effect of Individual Experience on Population Processes in Nature**

Severe life experiences may create permanent memories, both acting directly on the individual but also through maternal effects, on future generations. The potential explanatory role of stress to understand population demography of animals in nature was invoked over 60 years ago. The exact cause proposed, social stress, was largely a failure, but it set in motion a research direction that has succeeded in helping us to understand the implications of stress at level of the individual and population. The stress axis is key in permitting mammals to cope with both predictable and unpredictable challenges in their environment. A key question in understanding individual response is whether these stresses cause organizational changes in the “memory” of an animal. One of the best explanations for this memory is that they result from epigenetic changes to the DNA. If such memory changes affect virtually all members of the population, it may change the course of the demography of the entire population. Epigenetic changes are a plausible explanation for the low phase of the snowshoe hare cycle. The critical thing in testing the significance and role of epigenetic changes is to avoid artifacts. Thus, Lamarck may have also been right after all, and so to, broadly interpreted, may have Christian and Chitty been right.

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## 17 Symposium II: Xenarthrans as Model Species in Mammalogy, Great Halls D & E, Sunday 8 June 2014

### **Bryson Voirin<sup>1</sup>, Martin Wikelski<sup>2</sup>, Niels C. Rattenborg<sup>1</sup>**

<sup>1</sup>*Sleep and Flight Group, Max Planck Institute for Ornithology, Seewiesen, 82319 Germany;* <sup>2</sup>*Department of Migration and Immuno-Ecology, Max Planck Institute for Ornithology, Radolfzell, 78319 Germany*

#### **Sleep in Wild Xenarthrans**

Sleep is a behavioral state common to all animals, yet its actual function remains unknown. One approach to examining the function of sleep is to compare how animals with different ecological and physiological characteristics sleep. Until recently, the vast majority of all sleep research has been conducted on captive or caged animals, which may provide limited insight into how animals normally sleep in the wild. In the following study, sleep was recorded in 3 species of wild xenarthrans by using miniature electroencephalogram (EEG) loggers. We found that wild *Bradypus* sloths slept over 6 hours less per day than captive ones. To examine the role of predation on sleep, we compared sloths living under starkly different predation pressures. We found that sloths facing high levels of nocturnal predation were less likely to be awake and active at night than sloths facing no nocturnal predation. We also recorded sleep and behavioral activity in wild two-toed sloths. We found that they slept 10.9 ( $\pm 0.6$ ) hours per day, and head-mounted accelerometers showed that the sloths were inactive and motionless 15.4 ( $\pm 0.8$ ) hours per day. This likely explains why behavioral studies report high amounts of sleep in sloths. As many studies focus on immobility as a basis for sleep, our findings highlight the need for EEGs in calculating animal sleep quotas in indolent animals such as xenarthrans.

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## 18 Symposium II: Xenarthrans as Model Species in Mammalogy, Great Halls D & E, Sunday 8 June 2014

### **W. J. Loughry, Colleen M. McDonough**

*Department of Biology, Valdosta State University, Valdosta, GA 31698 USA*

#### **Ten Burning Questions about Armadillos**

Like all xenarthrans, the unique and distinctive features of armadillos have inspired scientific curiosity for centuries. Even so, a review of the literature indicates considerable taxonomic, geographic, and topic biases. Thus, there are many opportunities for mammalogists to make substantial contributions to our understanding of this group. Not only that, but recent analyses suggest that even relatively well-studied phenomena may require re-examination. While there are certainly not exactly 10 burning questions that need to be answered about armadillos, some prominent issues include 1) the taxonomic composition of extant Cingulata; 2) ecological energetics, particularly with regard to maternal investment in offspring; 3) the evolution of polyembryony within the genus *Dasybus*; 4) documentation of sensory abilities; 5) impacts of pathogens in wild populations, perhaps most notably of leprosy in nine-banded armadillos (*Dasybus novemcinctus*); 6) the population biology of all species of armadillos; 7) the role of armadillos as potential harbingers of environmental change or degradation in terrestrial ecosystems; and so on. Although the main benefit of answering these questions may be to increase our knowledge of armadillos, many of the findings, as well as the techniques used in studying the animals, should have important implications for those studying other species of mammals.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 19 Symposium II: Xenarthrans as Model Species in Mammalogy, Great Halls D & E, Sunday 8 June 2014

### **Frédéric Delsuc**

*Institut des Sciences de l'Evolution, CNRS-Université Montpellier 2, Montpellier, France*

#### **A Decade of Advances in Xenarthran Molecular Phylogenetics**

Armadillos, anteaters, and sloths belong to Xenarthra and represent 1 of the 4 major clades of placental mammals. In the last decade, the reconstruction of xenarthran phylogenetic relationships has been revolutionized by molecular data. In this talk, I will review advances in xenarthran molecular systematics that allowed the reconstruction of their phylogenetic relationships at the genus level. I also will present ongoing efforts aimed at building a reference phylogenetic framework and timescale for the 31 living xenarthran species based on shotgun Illumina next-generation sequencing of complete mitochondrial genomes. This data set will serve as the basis for incorporating recently extinct species using ancient DNA. Finally, I will describe recent phylogenomic results pertaining to the debated question of the position of Xenarthra within placental mammals.

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## 20 Symposium II: Xenarthrans as Model Species in Mammalogy, Great Halls D & E, Sunday 8 June 2014

### **Mariella Superina<sup>1</sup>, Agustín M. Abba<sup>2</sup>**

*<sup>1</sup>Laboratorio de Endocrinología de la Fauna Silvestre, IMBECU, CCT CONICET Mendoza, Mendoza, Argentina;*

*<sup>2</sup>División Zoología Vertebrados, Facultad de Ciencias Naturales y Museo, UNLP, La Plata, Argentina*

#### **What Can We Learn from Xenarthrans about the Conservation of Mammals?**

Due to their unusual appearance and a wealth of extraordinary characteristics, the Xenarthra have awoken interest and curiosity since their discovery. They constitute 1 of the 4 basal clades of placental mammals, and their entire evolutionary history, which took place exclusively in the Americas, is concentrated in 31 extant species. This in itself would be an argument to study them and ensure their long-term survival. Nevertheless, many Xenarthra remain poorly known, which makes it difficult to realistically assess their conservation status and develop effective conservation strategies. A higher proportion of armadillos are listed as Data Deficient or Near Threatened than other South American terrestrial mammals, while proportionally more sloths and anteaters are listed as Vulnerable or Critically Endangered. Hunting seems to be a more significant threat for Xenarthra than for other South American terrestrial mammals; land use change and roadkills also are taking a heavy toll on them. Two decades ago, existing conservation efforts for Xenarthra and the number of researchers dedicated to studying them were rather limited. However, the present situation paints a more promising future for these unusual mammals. In this talk we will revise the conservation status of and threats to Xenarthra and compare them with other South American taxa, discuss experiences made over the past 10 years, and provide suggestions that may help other mammalogists develop conservation strategies for their species.

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## 21 Technical Session 1, Meeting Room 16, Sunday 8 June 2014

### **Steven R. Sheffield<sup>1</sup>, Carlos A. Iudica<sup>2</sup>, John W. Wenzel<sup>3</sup>**

*<sup>1</sup>Department of Natural Sciences, Bowie State University, Bowie, MD 20715 USA; College of Natural Resources and Environment, Virginia Tech, National Capital Region - Northern Virginia Center, Falls Church, VA 22043 USA;*

*<sup>2</sup>Department of Biology, Susquehanna University, Selinsgrove, PA 17870 USA; <sup>3</sup>Powdermill Nature Reserve, 1847 Rt. 381, Rector, PA 15677 USA*

#### **Gone with the Wind: Effects of a Tornado Blowdown and Subsequent Forest Management on the Small Mammal Assemblage Inhabiting Eastern Deciduous Forest**

Tornados are common natural weather phenomena that have been shown to highly influence ecosystem structure and function. In eastern deciduous forests, tornados often cause a substantial amount of physical damage, which greatly decreases the spatial heterogeneity of the forest. A tornado struck the area of Ligonier, Pennsylvania on 1 June 2012, creating a path of severe canopy damage about 8 miles long and affecting about 90 acres of forest. Following the tornado, experimental forest management for each blowdown area was initiated which included salvage logging, no salvage logging, and control (unaffected forest). In November 2013, we established a small mammal live-trapping grid across both forest treatments and control forest, with trapping occurring seasonally (4 times per year). Initial trapping of 120 trap-nights yielded 41 total individuals (34.2% trap success). The forest small mammal assemblage is composed mainly of *Peromyscus leucopus*, *Clethrionomys gapperi*, and *Blarina brevicauda*. All species were trapped both in open areas as well as forested cover areas. Overall, 34% of small mammals were trapped in non-salvaged areas, 29% in salvaged areas, and 37% in control areas. The number of mammals trapped in open areas was slightly higher in the no salvage logging areas where coarse woody debris covered the ground. Although these mammals all strongly prefer forested habitat, the added complexity of the ground cover seems to make the non-salvaged blowdown area a favored habitat.

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 22 Technical Session 1, Meeting Room 16, Sunday 8 June 2014

**Paul Stapp<sup>1</sup>, Melissa Fowler<sup>1,2</sup>, Christopher Moore<sup>1,3</sup>**

<sup>1</sup>Department of Biological Science, California State University, Fullerton, CA 92831 USA; <sup>2</sup>CH2M HILL, Santa Ana, CA 92707 USA; <sup>3</sup>Program in Ecology, Evolution, and Conservation Biology, Department of Biology, University of Nevada, Reno, CA 89557 USA

### Post-fire Recovery of Rodent Communities and Vegetation in High-elevation Mojave Desert

Wildfires can have catastrophic effects in arid ecosystems. In 2005, lightning strikes ignited fires in the Mojave National Preserve, California, burning 286 km<sup>2</sup> of high-elevation sagebrush-juniper vegetation. Since 2006, we have studied the recovery of rodents and vegetation in and adjacent to a large remnant of sagebrush-juniper vegetation. We live-trapped rodents along a 200-m transition from burned to unburned vegetation to determine how fire affects population densities. We also investigated how changes in rodent assemblages affected patterns of granivory by quantifying seed removal in artificial trays. Lastly, we monitored changes in plant cover and species richness in a series of wire cages that excluded herbivores of different body sizes. Kangaroo rats, especially *Dipodomys panamintinus*, increased in abundance in burns, whereas cricetid rodents, notably woodrats (*Neotoma*) and deermice (*Peromyscus*), remained much rarer than in the unburned vegetation. Rates of seed removal were highest at the burn edge, and were depressed by moonlight in the open burned areas. Large herbivores reduced plant cover but only in the burn, whereas effects of small granivores were seen only at the edge. Excluding large and all herbivores combined reduced species richness in the burn relative to the edge, suggesting that herbivores may mediate plant competition. These effects were modest however, implying that, in such an unproductive system, effects of herbivores on vegetation recovery may not be manifest for many years.

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## 23 Technical Session 1, Meeting Room 16, Sunday 8 June 2014

**Andrew J. Edelman**

Department of Biology, University of West Georgia, Carrollton, GA 30118 USA

### Response of Small Mammals to Fire-based Restoration of Montane Longleaf Pine

Longleaf pine (*Pinus palustris*) forests of the southeastern United States are a disturbance-adapted ecosystem that requires frequent low-intensity fires to maintain an open, park-like savanna. Regionally, significant efforts are being implemented to restore this once widespread ecosystem through use of prescribed fire. My research objective was to examine how the small mammal community responds to fire-based restoration activities in montane longleaf forests of Alabama. I measured small mammal abundance and species richness on live-trapping plots across 3 restoration treatments: 2–3 year fire frequency, 8–12 year fire frequency, and areas with no recent fire history. Preliminary results suggest small mammals were most abundant and species rich on plots associated with a 2–3 year fire frequency compared to plots with less frequent fire intervals; although, several small mammal species were only found on plots with little to no prescribed fire. These patterns of small mammal diversity are likely driven by dramatic habitat differences among restoration treatments. Plots with 2–3 year fire frequency were characterized by dense ground cover and open canopies, likely providing more cover and food for many small mammal species. Restoration of montane longleaf pine through prescribed fire has the potential to locally increase small mammal diversity. At the landscape scale, however, a mosaic of forest management regimes should be implemented to provide a variety of habitats for different small mammal species.

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## 24 (E) Technical Session 1, Meeting Room 16, Sunday 8 June 2014

**Marie-Eve Jacques<sup>1</sup>, Stephen W. Hallgren<sup>1</sup>, Duncan S. Wilson<sup>1</sup>, Karen McBee<sup>2</sup>**

<sup>1</sup>Department of Natural Resource Ecology and Management, Oklahoma State University, Stillwater, OK 74078 USA;

<sup>2</sup>Department of Zoology, Oklahoma State University, Stillwater, OK 74078 USA

### Low Basal Area Practices Alter Small Mammal Communities in Oak-Pine Forests of Southeast Oklahoma

Small mammals exercise key ecosystem functions, such as seed dispersal and germination, mycorrhizal fungal spore dispersal, and soil aeration. Therefore, it is important to assess the effect of land management practices on their communities. We determined how low basal area (BA) practices influenced small mammal communities in oak-pine tallgrass prairies in southeast Oklahoma. We compared the small mammal communities at 4 sites where frequent prescribed fires followed thinning (low BA), with those at 4 sites that have not been thinned within the past 20 years and where prescribed fires were less frequent (high BA). During the preliminary phase of this study, we captured 138 individuals over 4,313 adjusted trap nights. Small mammal community composition differed between both types of sites. Of the 10 species captured, least shrew (*Cryptotis parva*), hispid cotton rat (*Sigmodon hispidus*), fulvous harvest mouse (*Reithrodontomys fulvescens*), and eastern harvest mouse (*R. humulis*) were found only in low BA; house mouse (*Mus musculus*), Texas mouse (*Peromyscus attwateri*), and cotton mouse (*P. gossypinus*) were found only in high BA. To interpret these results, a microanalysis of habitat preferences was performed. Based on these preliminary results, we recommend that land managers in southeast Oklahoma maintain habitat patches with low and



# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

high BA to retain a diversity of small mammal communities and to maximize the number of small mammal species present.

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## 25 Technical Session 1, Meeting Room 16, Sunday 8 June 2014

### **Erika L. Barthelmess**

*Biology Department, St. Lawrence University, Canton, NY 13617 USA*

### **Spatial Distribution of Road-kills and Factors Influencing Road Mortality for Mammals in Northern New York State**

The aims of this study were to examine the spatial pattern of mammal-vehicle collisions (MVCs), identify and examine factors that contribute to MVCs, and determine whether the factors that increase the odds of MVCs are similar between species. On 103 road surveys that covered 7,094 total km, I recorded the location of each MVC along the survey route. I measured landscape and roadway features associated with each MVC and used kernel density and network analysis tools to identify road mortality hotspots and measure spatial clustering of MVCs. I used logistic regression to model the likelihood of MVCs in relation to specific habitat variables for all mammal data and separately for porcupine (*Erethizon dorsatum*), raccoon (*Procyon lotor*), skunk (*Mephitis mephitis*), muskrat (*Ondatra zibethicus*), and cottontail (*Sylvilagus floridanus*) data sets. I identified MVC hotspots and found spatial clustering of MVCs for porcupines, raccoons and skunks. Two landscape variables, distance to cover and the presence of an ecotone, as well as 2 road variables, width and topography, appeared as broadly important predictors of mammalian road mortality. Further, field-measured variables were more important than remotely-measured variables in predicting the odds of MVCs. Conservation implications are that mitigation of landscape features associated with higher risk of vehicle-collisions may reduce the number of MVCs in general, but species-specific research is required to more carefully tailor mitigation efforts for particular species.

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## 26 (E) Technical Session 1, Meeting Room 16, Sunday 8 June 2014

### **Marcus E. Blum<sup>1</sup>, Kelley M. Stewart<sup>1</sup>, Cody Schroeder<sup>1,2</sup>, Tony Wasley<sup>2</sup>**

*<sup>1</sup>Natural Resources and Environmental Science, University of Nevada Reno, Reno, NV 89557 USA; <sup>2</sup>Nevada Department of Wildlife, 1001 Valley Road, Reno, NV 89512 USA*

### **Impacts of Mining on Mule Deer Migrations in Nevada**

Over the past century, mule deer (*Odocoileus hemionus*) have suffered dramatic declines throughout the western United States due, in part, to loss of migratory corridors. An increase in mineral exploration across Nevada has raised the level of concern over protection of ungulate migration routes throughout the state. In January of 2012 and 2013, the Nevada Department of Wildlife and University of Nevada, Reno captured and applied radio collars to 43 female mule deer in proximity of an active mine in the Ruby Mountains of eastern Nevada. Collars were scheduled to collect locations at 1-hour intervals during migrations to give an accurate depiction of migratory behavior in and away from mining facilities. We used Brownian Bridge Movement Models to delineate stopover sites for each individual during both fall and spring migration periods. We calculated efficiency of movement and movement rate between stopover locations and throughout the mining area to determine the effects of the mine on movement patterns. We also used resource selection functions to determine if mule deer are avoiding specific levels of disturbance when navigating through the mine complex. We hypothesized that mule deer would show higher efficiency of movement and movement rates between stopovers than through the mining complex. In addition, we hypothesized that mule deer would avoid higher levels of disturbance when traversing through the mine.

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## 27 Technical Session 1, Meeting Room 16, Sunday 8 June 2014

### **Chris Lowrey, Kathleen Longshore**

*U.S. Geological Survey, Las Vegas Field Station, Henderson, NV 89074 USA*

### **Effects of Cumulative Human Disturbance on the Habitat Use of Desert Bighorn Sheep in the River Mountains, Nevada**

Human activity may mimic predation risks for wildlife by forcing abandonment of foraging sites and increasing expenditure of energy. Animals that can tolerate nonlethal disturbance may minimize these fitness costs. We examined a risk-disturbance hypothesis by comparing responses of desert bighorn sheep that were subjected to differing levels of recreation activity, suburban encroachment, and the addition of water and foraging resources between 2 time periods, 30 years apart. Animals were tolerant of suburban activity when a consistent forage resource (municipal park grass) was provided. However increased recreation activity resulted in shifts from otherwise suitable habitat that had been occupied decades earlier, reducing habitat availability. Habitat loss and tolerance to human activities may have detrimental effects on this important population that serves as a translocation source throughout the west.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 28 (E) Technical Session 1, Meeting Room 16, Sunday 8 June 2014

**Rachel E. Eguren, Karen McBee**

*Department of Zoology, Oklahoma State University, Stillwater, OK 74078 USA*

### **Investigating Chiroptera from Tar Creek Superfund Site: Community Structure, Metal Levels, and Behavioral Assays**

Bat communities within the contaminated Tar Creek Superfund Site were compared to bats from uncontaminated reference sites within Oologah Wildlife Management Area for 1) community composition and population structure; 2) behavioral impacts on willingness to fly and maneuverability; and 3) levels of lead, zinc, and cadmium in fur, liver, and kidney tissues. *Lasiurus borealis* (eastern red bat;  $n = 43$ ) was the most common species captured at all sites, followed by *Perimyotis subflavus* (tricolored bat;  $n = 2$ ), and a single *Lasiurus cinereus* (hoary bat), *Myotis lucifugus* (little brown bat), and *Nycticeus humeralis* (evening bat). Thermographic flight videos on *L. borealis* ( $n = 19$ ) were scored for 3 variables: number of obstacles touched, movement between marked sections of the cage, and flight time(s). Results from reference bats showed a predicted correlation between flight time, movement between sections, and number of obstacles encountered that was not present in contaminated bats. Hair, liver, and kidney were analyzed to determine tissue metal levels for comparison with results from flight cage assays. This study provides the 1st assay measuring behavioral impacts of metals for chiropterans. These results give us a better understanding of the anthropogenic impacts on bats living within a Superfund Site, and will inform decisions on both remediation and reclamation of contaminated habitats for the conservation of bats.

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## 29 Technical Session 2, Meeting Room 17, Sunday 8 June 2014

**Bruce D. Patterson, Nathan S. Upham**

*Integrative Research Center, Field Museum of Natural History, Chicago, IL 60605 USA; Committee on Evolutionary Biology, University of Chicago, Chicago, IL 60637 USA*

### **A New Family of Mammals Endemic to the Horn of Africa: The Heterocephalidae (Rodentia: Hystricomorpha)**

Relationships of the African mole rats (Bathyergidae) have long perplexed systematists; this group possesses hystricognath jaws but the reduced infraorbital foramina and distally fused tibia and fibula that characterize the myomorph clade. Further, their prominent adaptations to subterranean life have apparently overwritten their synapomorphies with related groups. We assembled sequence data for 5 genes across 17 families of hystricomorphs plus *Pedetes* (outgroup), producing a supermatrix of 199 species and 5194 base pairs of DNA. Bathyergidae is recovered as strongly monophyletic and sister to the African rock rats (Petromuridae) + cane rats (Thryonomyidae). Dating the tree with 22 well-documented fossils, the Bathyergidae appear by the Late Eocene (36.2 Ma). Its basal member, the naked mole rat *Heterocephalus*, separated from other African mole rats 31.2 Ma, at a time when the 4 caviomorph superfamilies were just appearing in South America. Rank-equivalence of taxonomy and the recovered chronology argue for distinguishing the naked mole rat in the monotypic family Heterocephalidae Landry, 1957, sister to Bathyergidae in the superfamily Bathyergoidea.

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## 30 Technical Session 2, Meeting Room 17, Sunday 8 June 2014

**Link E. Olson<sup>1</sup>, Kristen M. Scholten<sup>1,2</sup>, Neal Woodman<sup>3</sup>, Eric J. Sargis<sup>4</sup>**

<sup>1</sup>*Department of Mammalogy, University of Alaska Museum, Fairbanks, AK 99775 USA;* <sup>2</sup>*Department of Biology and Wildlife, University of Alaska Fairbanks, Fairbanks, AK 99775 USA;* <sup>3</sup>*U.S. Geological Survey Patuxent Wildlife Research Center, National Museum of Natural History, Smithsonian Institution, Washington, D.C. 20013 USA;*

<sup>4</sup>*Division of Vertebrate Zoology, Yale Peabody Museum, New Haven, CT 06520 USA; Department of Anthropology, Yale University, New Haven, CT 06520 USA*

### **"The" Treeshrew in Biomedical Research: An Evolutionary Reality Check**

For much of the 20th century treeshrews (Order Scandentia) were incorrectly classified as basal primates. Because of this and their tractability in captivity they have featured prominently in biomedical research. Of the 23 currently recognized species, 2 (*Tupaia glis* and *T. belangeri*) have accounted for nearly 80% of the > 12,000 treeshrew-related biomedical publications. These same species are currently undergoing extensive taxonomic revision, with several formerly synonymized names recently re-elevated to species status. In addition to their implications for conservation and biogeography in Southeast Asia, these findings call for a re-examination and possible reinterpretation of much of the treeshrew biomedical literature. We review the use of treeshrews in biomedical research, persistent misunderstandings about their relationships to primates and other mammals, and the need for incorporating evolutionary biology in biomedicine.

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 31 (E) Technical Session 2, Meeting Room 17, Sunday 8 June 2014

**Victor C. Mason<sup>1</sup>, William J. Murphy<sup>1</sup>, Kristofer M. Helgen<sup>2</sup>**

<sup>1</sup>Department of Veterinary Integrative Biosciences, Interdisciplinary Program in Genetics, Texas A&M University, College Station, TX 77843 USA; <sup>2</sup>Smithsonian Institution, National Museum of Natural History, Washington, D.C. 20560 USA

### **Reassessing Colugo Phylogeny, Taxonomy, and Biogeography with Next Generation Sequencing Data from Museum Specimens**

Colugos are nocturnal arboreal mammals that have poor dispersal capabilities outside of forested areas, have the largest patagium (gliding membrane) of any mammal, and are widely distributed across the Southeast Asian mainland and archipelago. They represent their own order, Dermoptera, and under current taxonomy 2 species are recognized, *Galeopterus variegatus*, the Sunda colugo, and *Cynocephalus volans*, the Philippine colugo. Preliminary studies indicated that Sunda colugos harbor multiple potential species with about 13% mitochondrial DNA (mtDNA) sequence divergence across populations. Therefore we revisited colugo taxonomy and implemented 2 methods for obtaining orthologous sequences from museum specimens using Illumina sequencing: 1) capture-hybridization to enrich specific nuclear DNA segments and 2) low-coverage genome sequencing (~0.3x) of raw genomic DNA extracts from museum specimens to recover complete mtDNA genomes from 86 Sundaic and Philippine colugos. Evidence for deeply divergent colugo populations/species endemic to distinct geographic regions is supported by maximum likelihood phylogenetic reconstructions. Divergence time estimation suggests complex biogeographic patterns from the Miocene through the Pleistocene. We recovered mtDNA genomes from 8 pangolins (genus *Manis*), and 19 mouse deer (genus *Tragulid*) and compare their phylogeographic patterns to colugos. Finally, we analyze targeted nuclear sequence capture of biparental loci, Y-chromosome loci, and genes predicted to underlie adaptations within colugos. Our results suggest future avenues to utilize museum approaches to explore colugo specific adaptive biology, and the complex biogeography of the Southeast Asian archipelago.

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## 32 Technical Session 2, Meeting Room 17, Sunday 8 June 2014

**Kathryn M. Everson<sup>1,2</sup>, Sharon A. Jansa<sup>3</sup>, Steven M. Goodman<sup>4</sup>, Link E. Olson<sup>1</sup>**

<sup>1</sup>Department of Mammalogy, University of Alaska Museum, Fairbanks, AK 99775 USA; <sup>2</sup>Department of Biology and Wildlife, University of Alaska Fairbanks, AK 99775 USA; <sup>3</sup>Department of Ecology, Evolution, and Behavior and Bell Museum of Natural History, University of Minnesota, St. Paul, MN 55108 USA; <sup>4</sup>Field Museum of Natural History, Chicago, IL 60605 USA; Association Vahatra, Antananarivo, Madagascar

### **Colonization, Adaptive Radiation, and Evolutionary Constraint: The Natural History of Madagascar's Small Mammals**

Madagascar is a natural model system for studying evolution and diversification. It has a long history of isolation (88 million years) and supports remarkable levels of both species richness and endemism, including 100% endemism of its native nonvolant mammals. This striking degree of endemism can be explained by infrequent, asynchronous colonization events followed by adaptive radiation. Madagascar's 2 small mammal lineages, tenrecs (Tenrecidae) and nesomyine rodents (Nesomyinae), each originated from a single common ancestor between 18-65 million years ago and have since undergone spectacular diversification. Tenrecs include semiaquatic, semifossorial, and scansorial ecomorphologies; heterotherms as well as homeotherms; velvety pelage to stout, barbed, detachable spines; and body sizes spanning 3 orders of magnitude (2–2,000 g). Similarly, nesomyine rodents vary widely in size and morphology and have radiated to occupy arboreal, terrestrial, and semifossorial niches. Because tenrecs colonized Madagascar about 10 million years before nesomyines, it has been hypothesized that their adaptive radiation constrained the subsequent diversification of nesomyines. We tested this by comparing rates of diversification in the most speciose genus of tenrec (*Microgale*) and nesomyine (*Eliurus*) based on multiple unlinked molecular markers. Our results reveal a complex historical relationship between the 2 taxa and improve our understanding of small mammal evolution on Madagascar.

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## 33 (E) Technical Session 2, Meeting Room 17, Sunday 8 June 2014

**Peter J. Galante<sup>1</sup>, Robert Muscarella<sup>2</sup>, Steven M. Goodman<sup>3</sup>, Robert P. Anderson<sup>1,4,5</sup>**

<sup>1</sup>Department of Biology, City College of New York, City University of New York, New York, NY 10031 USA;

<sup>2</sup>Department of Ecology, Evolution and Environmental Biology, Columbia University, 1200 Amsterdam Avenue, New York, NY 10027 USA; <sup>3</sup>Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, IL 60605 USA; Association Vahatra, BP 3972, Antananarivo 101, Madagascar; <sup>4</sup>The Graduate Center, City University of New York, New York, NY 10016 USA; <sup>5</sup>Department of Mammalogy, American Museum of Natural History, New York, NY 10024 USA

### **Comparing Optimally Complex Niche Models of a Malagasy Rodent Using Two Selection Techniques: AICc vs. Jackknife**

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

Ecological Niche Models (ENMs) are widely used, yet optimal complexity and violation of modeling assumptions remain outstanding issues. We analyzed 2 strategies for selecting optimal ENMs (AICc and a jackknife approach) while simultaneously lessening sampling bias via spatial filtering. We did so for a species with few records, the endemic Malagasy rodent *Eliurus majori* (subfamily Nesomyinae), using 19 bioclimatic variables and MaxEnt. We varied model complexity, employing various combinations of feature classes and regularization-multiplier values. For the jackknife approach, we calculated the average omission rate and AUC of the withheld (test) records for each feature-class/regularization-multiplier combination. In contrast, AICc uses internal testing to balance complexity and goodness-of-fit. For each dataset, the models selected as optimal by AICc were less complex models than for the jackknife. With the unfiltered dataset, AICc (but not jackknife) selected a model that had high omission, indicating overfitting to training data. In contrast, using the filtered dataset, both techniques selected models with similar (low) omission rates. However, despite this similarity in performance of the filtered dataset, the respective optimal settings led to predictions that were only 85% similar in geographic space. These results highlight the sensitivity of AICc to violation of the assumption of unbiased sampling, and suggest that the jackknife approach may be more robust in this regard.

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### 34 (E) Technical Session 2, Meeting Room 17, Sunday 8 June 2014

**Robert A. Boria<sup>1</sup>, Robert P. Anderson<sup>1,2,3</sup>**

<sup>1</sup>Department of Biology, City College of New York, New York, NY 10031 USA; <sup>2</sup>The Graduate Center, City University of New York, NY 10016 USA; <sup>3</sup>American Museum of Natural History, New York, NY 10024 USA

#### **A Single-algorithm Approach to Creating an Ensemble of Ecological Niche Models and Generating Maps of Uncertainty**

This study aims to create a consensus ecological niche model (ENM) using a single-algorithm approach, while adjusting model parameters to maximize performance. Generally, a single model from 1 algorithm or an ensemble of different algorithms is used to generate a prediction. Additionally, several recent studies have shown the need to tune model settings for a single algorithm. Nevertheless, uncertainty cannot be measured with a single model, and multiple settings may lead to essentially co-optimal models. To address this issue, we used MaxEnt, 19 bioclimatic variables, and occurrence records of a Malagasy tenrec, *Microgale gracilis*. We calibrated and evaluated preliminary models using a jackknifing approach, tuning 2 model settings (feature classes and the regularization multiplier) to estimate optimal model complexity. Based on omission rates and AUC, we chose the top 10 performing preliminary models, and then generated a consensus prediction by averaging the values for each grid cell. Furthermore, we calculated the standard deviation to obtain a map showing variation in geography. These models were 56–95% similar in geographic space (D-statistic), falling into 2 clusters; models made with the same feature classes were similar, whereas cross-cluster comparisons showed much lower similarity. In conclusion, a consensus model allows researchers to use several high-performing models, which may vary in geography, to generate a useful prediction and detect areas of discrepancy.

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### 35 Technical Session 2, Meeting Room 17, Sunday 8 June 2014

**Jacob A. Esselstyn<sup>1</sup>, Anang S. Achmadi<sup>2</sup>, Maharadatunkamsi<sup>2</sup>, Thomas C. Giarla<sup>1</sup>, Kevin C. Rowe<sup>3</sup>**

<sup>1</sup>Museum of Natural Science and Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803 USA; <sup>2</sup>Museum Zoologicum Bogoriense, Lembaga Ilmu Pengetahuan Indonesia, Cibinong 16911 Indonesia; <sup>3</sup>Sciences Department, Museum Victoria, Melbourne 3001 VIC, Australia

#### **New Perspectives on Sunda Shelf Biogeography**

The Sunda Shelf is an expansive region of shallow water encompassing many islands, large and small. These islands were united by dry land with the Asian mainland numerous times during the Pleistocene and earlier periods. This historical geographic template once provided a seemingly intelligent model for estimating rates of extinction and processes of community disassembly as land area was reduced by rising sea level. However, recent genetic studies of multiple mammalian groups reveal deep interisland genetic isolation and within-island speciation, raising questions regarding past assumptions of a once homogeneous community of mammals on the Sunda Shelf. We will discuss the implications of these findings in a context of an improving understanding of the systematics of shrews and rodents in the region.

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### 36 Technical Session 2, Meeting Room 17, Sunday 8 June 2014

**Nelish Pradhan<sup>1</sup>, Ajay N. Sharmo<sup>2</sup>, Charles A. Woods<sup>1</sup>, C. William Kilpatrick<sup>1</sup>**

<sup>1</sup>Department of Biology, University of Vermont, Burlington, VT 05605-0086 USA; <sup>2</sup>Center for Molecular Dynamics, Kathmandu, Nepal

#### **Molecular Examination of the Mountain Voles of the Genus *Neodon***

Recent molecular systematic studies of arvicoline voles of the genera *Neodon*, *Lasiopodomys*, and *Phaiomys* from Tibet, Qinghai, and Sichuan further question the recognition of these 3 genera and the number of species recognized

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

within the genus *Neodon*. Analysis of cytochrome b sequence data strongly supports the inclusion of the smoky vole (*L. fuscus*) and Blyth's mountain vole (*P. leucurus*) in the genus *Neodon* but also supports the removal of the juniper vole (*N. juldaschi*) from this genus. Sequencing of cytochrome b of material collected from Pakistan and Nepal contributes additional data for analysis. Sequences from arvicoline voles collected from 7 localities in northern Pakistan verify the presence of juniper voles at 6 of these localities and the Middle East vole (*Microtus transcaspicus*) at the other. Inclusion of these additional sequences of juniper voles supports the removal of this taxon from the genus *Neodon* and placement of this species in the genus *Blanfordimys*. Sequences collected from 2 individuals identified as *N. sikimensis* from Nepal do not cluster with sequences in GenBank of *N. sikimensis* from Tibet, but form a monophyletic clade within a clade containing the other forms of *Neodon*. Individuals identified as *N. sikimensis* have been sequenced from populations from both north and south of the Himalayas; however, these sequences fail to form a monophyletic clade suggesting that they represent 2 different phylopecies.

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### 37 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

**Rachael A. Van Essen, Angelo Capparella**

*School of Biological Sciences, Illinois State University, Normal, IL 61761 USA*

#### **Using Deuterium and GIS Tools to Estimate Geographic Extents of Source Populations of Tree Bats Killed at a Central Illinois Wind Farm**

Bats are killed at an astonishing rate by wind facilities, an estimated 600,000 nationwide in 2012. Approximately 75% of these bats are of 3 species, the eastern red (*Lasiurus borealis*), hoary (*Lasiurus cinereus*) and silver-haired (*Lasionycteris noctivagans*). While the number seems large, we have little understanding of the impact of this high mortality on these species' population persistence, in part because we have poor knowledge of their breeding sites and migration pathways. The use of stable isotopes in body tissues to determine both summer range and migration pathways of animals is an increasingly successful method for elucidating geographic patterns. In my research, I focus on the eastern red and hoary bats using the method of deuterium isotope ratio ( $\delta D$ ) analysis in a novel way through combining ecological niche modeling (GARP: Genetic Algorithm for Rule-set Prediction) with a web-based isotope modeling program (Isomap: Isoscapes Modeling, Analysis, and Prediction). My goal is to determine whether the bats being killed at an Illinois wind facility are coming from a large portion of their summer geographic range or from only a small segment. This will serve to help understand autumn migration patterns through central Illinois in terms of their northern extents. It will also be an important stepping stone towards understanding population and long-term impacts that the high mortality suffered at wind facilities will have on these two species.

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### 38 Poster Session I, Great Hall C, Sunday 8 June 2014

**Victoria J. Bennett<sup>1</sup>, Amanda M. Hale<sup>2</sup>, Ali J. Schildt<sup>2</sup>, Dean A. Williams<sup>2</sup>**

<sup>1</sup>*School of Geology, Energy and the Environment, Texas Christian University, Fort Worth, TX 76129 USA;*

<sup>2</sup>*Department of Biology, Texas Christian University, Fort Worth, TX 76129 USA*

#### **Evidence that Bats Utilize Wind Turbines as a Foraging Resource**

There are increasing concerns about the large numbers of bat fatalities reported at wind facilities across North America. Wind turbines may be attractive to bats because they provide 1 or more resources. From 2011 to 2013, we undertook surveys to explore whether wind turbines were a foraging resource for bats. First, we conducted night vision and acoustic surveys to assess the extent to which bats exhibited foraging behavior at turbines. Second, we conducted light trapping and malaise surveys to sample the invertebrate community at turbines. And third, we collected fecal samples from bat carcasses found in fatality surveys, from live-caught bats, and from systematic searches of the wind turbines themselves. We extracted DNA from these fecal samples and amplified the mitochondrial barcoding region of both bats and their invertebrate prey. We also amplified the mitochondrial DNA from invertebrates collected at the turbines. We then compared the composition of invertebrates found in bat feces to the invertebrate community at the turbines. Our results revealed that 1) bats were observed and acoustically recorded foraging at turbines; 2) invertebrates found at the wind turbines, including those resting on the turbine surfaces, were present in the bat feces; and 3) feces belonging primarily to *Lasiurus borealis* bats (59% of fatalities) were commonly found in door slats and transformers, suggesting that bats were using these areas as night roosts.

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### 39 Poster Session I, Great Hall C, Sunday 8 June 2014

**Anica Debelica-Lee<sup>1</sup>, Baoqing Ding<sup>1</sup>, Patrick Danley<sup>1</sup>, Kenneth T. Wilkins<sup>2</sup>**

<sup>1</sup>*Department of Biology, Baylor University, Waco, TX 76798 USA;* <sup>2</sup>*College of Arts & Sciences, Baylor University, Waco, TX 76798 USA*

#### **Using Pyrosequencing to Determine Diet of the Tri-colored Bat, *Perimyotis subflavus***

Determination of diet has long been a focus of many bat ecologists. Traditionally, diet was determined by examination of either gut contents or feces under the microscope. However, this approach usually reveals diet only to the levels of order or family, and excludes detection of prey items that are visually hard to detect (small size or easily degraded).

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

In recent years, great strides in DNA technologies have led to novel approaches for dietary studies. Using pyrosequencing (DNA sequencing technique based on the detection of released pyrophosphate during DNA synthesis) of a single fecal pellet belonging to the tri-colored bat (*Perimyotis subflavus*) netted in the pineywoods of eastern Texas, we were able to identify 51 different prey species. Three orders, Lepidoptera (53.8%), Diptera (15.8%), and Coleoptera (18.3%), accounted for nearly 88% of all identified prey. In addition, 12% of the sample was identified to belong to tri-colored bat. Surprisingly, as previous studies demonstrated that this bat prefers softer prey, 18% of sequences belong to the coleopteran June bug (*Phyllophaga crinita*). Our study provides rare insight into the diet of tri-colored bats and reveals that this species exhibits a much wider prey base than previously thought. This project also demonstrated the feasibility of using pyrosequencing as an effective and a non-invasive technique to study bat diets.

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### 40 Poster Session I, Great Hall C, Sunday 8 June 2014

**Lucas K. Hall<sup>1</sup>, Connor T. Lambert<sup>1</sup>, Randy T. Larsen<sup>1</sup>, Robert N. Knight<sup>2</sup>, Brock R. McMillan<sup>1</sup>**

<sup>1</sup>Plant and Wildlife Science Department, Brigham Young University, Provo, UT 84602 USA; <sup>2</sup>Environmental Programs, US Army Dugway Proving Ground, Dugway, UT 84022 USA

#### **Competition among Desert Bats at Water Sources: Influence of Surface Area and Habitat Complexity**

In arid environments, competition for water can shape communities. Small desert bats are particularly vulnerable to water loss and are thus highly reliant on water. However, there is limited information regarding competition for water among desert bats. Two alternate hypotheses exist that likely influence competition for bats at water: surface area (SA) and habitat complexity (HC). Our objectives were to evaluate: 1) support for the SA and HC hypotheses and 2) competition by experimentally manipulating SA. During May to Aug 2010–11, we randomly sampled water sources ( $n = 60$ ) with acoustic detectors in the Great Basin and Mojave Deserts of Utah. For our SA experiment, we employed a crossover design with 2 water tanks and used acoustic detectors and infrared video to record species and drinking behavior. We used generalized linear regression to model activity, richness, and diversity from our random samples and compared the 2 hypotheses using AIC model selection. Richness and activity were primarily explained by SA, whereas diversity was best explained by HC. Our experiment revealed that bats exhibited fewer successful drinking passes with reduced SA. Furthermore, our experiment demonstrated evidence of temporal partitioning between the most abundant species *Parastrellus hesperus* and all other species. Our findings support the hypothesis that SA is associated with activity and richness, but also that the competitive influence of a dominant species can drive local diversity.

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### 41 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

**Kate P. Ingram**

Wildlife Fish and Conservation Biology Department, University of California, Davis, CA 95616 USA

#### **Ecosystem Services of Bats in California Agriculture: Bats as Natural Enemies of Codling Moth in Walnut Orchards**

Agricultural pesticide use is a major source of environmental contamination and poses a health risk to society. Practices that increase the abundance of natural insect predators such as bats can reduce pesticide use and save farmers money. However, the adoption of such practices, while obviously beneficial, can be slow, and the reasons for lack of adoption are not well understood. The goals of the present study are to 1) assess the ecosystem service provided by bats in California's Central Valley; 2) quantify pest consumption by bats to create an economic model of costs and benefits for farmers; and 3) evaluate the factors that influence the willingness of farmers to adopt techniques that encourage bat residency on farms. Preliminary results from this study indicate that at least 8 species occur in California walnut orchards, and 5 of these actively forage in orchards, suggesting a potential role in conventional as well as organic agriculture. Acoustic data on the activity patterns of bats on organic and conventional walnut orchards, with and without bat housing structures will be discussed.

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### 42 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

**Chase Voirin<sup>1</sup>, Melanie Culver<sup>2</sup>**

<sup>1</sup>Department of Wildlife Management and Conservation, University of Arizona, Tucson, AZ 85719 USA; <sup>2</sup>Department of Wildlife Conservation Genetics, University of Arizona, Tucson, AZ 85719 USA

#### **Mule Deer Diet Analyses: Comparing Past with Present Techniques**

Past studies have used microhistological diet analyses of wild ungulates to answer questions pertaining to ungulate biology and habitat use. DNA-based techniques present new avenues for studying wildlife, such as using next-generation sequencing to analyze wildlife diet. Additionally, few studies have compared microhistological and next-generation sequencing diet analyses for any species of animal. The objective of my study is to compare both microhistological and next-generation sequencing diet analyses through fecal matter for mule deer, *Odocoileus hemionus*, over both summer and winter seasons on the Navajo Reservation. I will compare and contrast both diet

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

analyses through presence or absence and quantifiable amounts of plant genus. Management implications from this study may present innovative methods for determining ungulate diet and also offer new insight into investigating habitat use.

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### 43 Poster Session I, Great Hall C, Sunday 8 June 2014

Rita M. Blythe, Nathanael I. Lichti, Timothy J. Smyser, Robert K. Swihart

Department of Forestry & Natural Resources, Purdue University, West Lafayette, IN 47907 USA

#### Selection, Caching, and Consumption of Hardwood Seeds by Forest Rodents: Implications for Restoration of American Chestnut

Attempts to restore the American chestnut (*Castanea dentata*) to eastern forests are forthcoming with the successful cultivation of a hybrid tree (BC<sub>3</sub>F<sub>3</sub>). However, seed predation by vertebrate consumers, especially rodents, may impede dispersal if novel BC<sub>3</sub>F<sub>3</sub> seeds are preferentially consumed over other currently available mast. Also, it remains unknown whether pure American and hybrid chestnut seeds represent equivalent food resources for rodent consumers. We evaluated seed selection and use by 5 rodent species by presenting both types of chestnut seeds in preference trials along with other common seed types and recording fates of tagged seeds. Discrete choice models revealed that mice, chipmunks, and flying squirrels showed a preference for chestnut seeds over larger, tougher seed types (e.g., walnut, hickory, red oak), whereas tree squirrels preferred these seeds to chestnut. In some cases, rodents displayed a significant preference for pure American chestnuts over hybrid chestnuts. In general, rodents tended to consume more chestnut than other seed types, but hybrid seeds removed by tree squirrels were recovered in significantly lower proportions than American chestnut, suggesting that they may be dispersed farther and cached more often. Our results indicate that most rodent consumers would hinder chestnut dispersal through consumption of seeds. In addition, we have demonstrated that, from the perspective of mammalian granivores, hybrid chestnuts are not ecologically equivalent to pure American chestnut.

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### 44 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

Kathryn A. Preston, Ned A. Dochtermann

Department of Biological Sciences, North Dakota State University, Fargo, ND 58102 USA

#### How are Density Dependence, Population Variability, and Extinction Risk Related in Mammals?

The preservation and persistence of many mammalian species are affected by anthropogenic related activities. In this study, we used mammalian population data from the Global Population Dynamics Database to test for relationships among population size variability, the strength of density dependence, and risk of extinction. Based on theoretical expectations, populations with greater fluctuations in abundance can be predicted to have increased risks of extinction. Because strong density-dependence (DD) might be expected to dampen fluctuations in abundance, increases in DD can be predicted to be associated with decreases in extinction risk. We tested these predictions and the relationship of these population parameters with current conservation status, average mass at maturity, and average age at reproductive maturity. Statistical modeling demonstrated that as the strength of density dependence increases, extinction risk decreases, and population size variability decreases. This suggests that populations with strong density dependence are at or close to their carrying capacity which allows for population stability over time. Mammals with larger mass sizes had higher population size variability. We also found that age to sexual maturity was positively associated with decreased rates of population size variability and increased extinction risk.

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### 45 Poster Session I, Great Hall C, Sunday 8 June 2014

Donald W. Kaufman<sup>1</sup>, Glennis A. Kaufman<sup>1</sup>, Dawn M. Kaufman<sup>2</sup>

<sup>1</sup>Division of Biology, Kansas State University, Manhattan, KS 66506 USA; <sup>2</sup>Department of Biology, King's College, Wilkes-Barre, PA 18711 USA

#### What Have We Learned About Small Mammals In Tallgrass Prairie After 32 Years of Sampling? Dynamics and Drivers of Community Patterns

We have completed our 32-year study of small mammals in tallgrass prairie, which was conducted as part of the Konza Prairie Long-Term Ecological Research Project. Using standardized procedures, we live-trapped small mammals in 14 permanent sites in autumn and spring during October 1981–March 2013. Our goal was to assess spatial-temporal variation in population and community characteristics as well as possible drivers (weather, fire, grazers, land cover) of observed patterns. The regional pool includes 13 rodent species and 2 shrews; all were recorded during at least 1 sampling period. As expected for grasslands in Kansas, deer mice (*Peromyscus maniculatus*) dominated the 14 species recorded in autumn (33% of 6,564 individuals) and 13 in spring (46% of 3,884). In our macro-site (ca. 10 km<sup>2</sup> represented by the 14 sites), community abundance and species richness varied widely over 32 years (autumn: 58–453 individuals, 6–12 species; spring: 22–379, 4–9). No significant unidirectional changes in abundance and richness were evident, which was unexpected as woody vegetation increased significantly over the study period. In contrast, species composition changed over time owing to a

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

significant increase in white-footed mice (*Peromyscus leucopus*). This increase in white-footed mice was particularly obvious in individual sites that increased most dramatically in the areal coverage of woody vegetation; a compositional change that occurred especially at the expense of deer mice.

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### 46 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

**Sarah L. Hale, John L. Koprowski**

*School of Natural Resources and the Environment, University of Arizona, Tucson, AZ 85721 USA*

#### **Re-establishment of a Potential Keystone Species: Initial Impacts of Black-tailed Prairie Dogs on Woody Species and Small Mammal Species Assemblages**

Many tests of the keystone species concept have only assessed areas occupied by these species or the effects of their removal on the ecosystem. We have had the opportunity to assess effects of the addition of a potential keystone species to an ecosystem from which they have been extirpated for at least 50 years. The black-tailed prairie dog (BTPD; *Cynomys ludovicianus*) has been commonly described as a keystone species and, over the past 6 years the Arizona Game and Fish Department, has re-established the BTPD at Las Cienegas National Conservation Area in southeastern Arizona. We assessed small mammal species diversity on, off, and at edges of colonies through live-trapping, and determined if prairie dogs suppress woody plant growth (i.e., mesquite and acacia) by use of experimental enclosures. We found that species diversity and richness increased between 2012 and 2013, and the greatest diversity of small mammals was on edges of colonies (compared to on and off colonies). We also found that woody plants placed in enclosures on prairie dog colonies grew at a greater rate than those left exposed to prairie dogs. Our early results suggest that these re-established prairie dogs may not have resumed their keystone role yet, but they are beginning to change the environment in ways that suggest resumption of this role in the future.

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### 47 (E,TA) Poster Session I, Great Hall C, Sunday 8 June 2014

**Anne-Marie C. Hodge, Jacob R. Goheen**

*Department of Zoology & Physiology, University of Wyoming, Laramie, WY 82071 USA*

#### **The Effect of Invasive Prickly Pear Cactus (*Opuntia stricta*) on Mammalian Diversity in Central Kenya**

Seed dispersal by native mammals can facilitate spread of invasive plants, creating significant management problems on wildlife conservancies. Introduced plant species may also be used as food or water sources for native mammals, resulting in localized increases in mammalian activity in "invaded" areas. We investigated the effects of the prickly pear cactus (*O. stricta*) on the diversity of wild mammals within multiple land-use settings across central Kenya's Laikipia Plateau (i.e., conservancies, fenced ranches, and community ranches). We used remote cameras to compare species diversity and activity in control and invaded plots at 100 m intervals from riverbanks between property types. Activity was defined as the cumulative time spent within a plot by all individuals of each species in a 24-hour period. We also recorded cactus density and vegetation structure, plant species diversity, maximum height of non-*Opuntia* plants, and percent cover. Species richness of wild mammals was higher in invaded plots than the control plots on all land-use settings. Species composition differed between conservancies and the 2 types of ranches, with conservancies exhibiting the highest species diversity, while invaded areas on fenced ranches had higher species diversity and visitation rates than those on community ranches. Heightened diversity and activity of mammals in invaded areas is likely to increase dispersal of *O. stricta*, the spread of this introduced plant throughout conservancies and other wildlife-friendly properties.

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### 48 Poster Session I, Great Hall C, Sunday 8 June 2014

**Mariela G. Gantchoff, Jerrold L. Belant**

*Carnivore Ecology Laboratory, Forest and Wildlife Research Center, Mississippi State University, Mississippi State, MS 39759 USA*

#### **Anthropogenic and Environmental Effects on Invasive Mammal Distribution in Northern Patagonia, Argentina**

European hare (*Lepus europaeus*) and wild boar (*Sus scrofa*) are 2 widespread mammalian invaders in Argentina. We looked for support for the disturbance hypothesis, which states that anthropic disturbance facilitates invasive species, and compared the relative importance of anthropic and environmental factors in hare and boar occurrence. We established 80 camera stations, from February to May 2012 and January to April 2013, along hiking trails. We characterized land cover, horizontal cover, herbaceous vegetation, distance to nearest human settlement, distance to nearest road, and average daily number of people at each station. We used likelihood-based occupancy modeling, with the site descriptive variables affecting occupancy. We ranked models with Akaike Information Criterion for small sample sizes (AICc), and used model averaging to estimate parameter coefficients, unconditional SEs, and 85% CIs for each variable in competing models ( $\Delta AICc < 2$ ). Hare occupancy gave support for the disturbance hypothesis, being greater closer to human settlements and in denser horizontal cover, which might reduce predation risk. On the contrary, boar occupancy was greater farther from human settlements, likely a result of hunting pressure, and in



## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

humid forests, more abundant in food. As hares and boars had an opposite response to the presence of anthropic disturbance, we suggest the influence of environmental or anthropogenic factors can vary based on each species' life history traits and role in human society.

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### 49 Poster Session I, Great Hall C, Sunday 8 June 2014

**Anna Weyers<sup>1,2</sup>, John S. Scheibe<sup>1</sup>, Brad Pendley<sup>2</sup>**

<sup>1</sup>Department of Biology, Southeast Missouri State University, Cape Girardeau, MO 63701 USA; <sup>2</sup>Mingo National Wildlife Refuge, Puxico, MO 63960 USA

#### The Distribution and Abundance of Feral Hogs (*Sus scrofa*) at Mingo National Wildlife Refuge

Within the past 2 years, there has been a dramatic increase in feral hog activity on Mingo National Wildlife Refuge, a bottomland hardwood forest/swamp in southeastern Missouri. This project was designed to develop a baseline dataset of seasonal habitat use by feral hogs, so that cost effective strategies for hog control can be implemented. To do this, we established 30 camera trap stations across the refuge. Camera trap locations were divided into groups using a cross classification design. Groups included control sites on a transect established using ArcGIS, sites with hog sign (rooting, wallowing, and scat), sites that were baited, and sites at both high and low elevations. Camera trapping was initiated in November 2012 and completed in December 2013. More than 73,250 images were obtained, with 19 of 30 cameras capturing hogs. We present data on the expansion of the hog population at Mingo, the effects of bait, and elevation on hog habitat use.

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### 50 Poster Session I, Great Hall C, Sunday 8 June 2014

**Ana L. Trujano-Alvarez<sup>1</sup>, Miguel A. Briones-Salas<sup>2</sup>, Mario C. Lavariega-Nolasco<sup>2</sup>**

<sup>1</sup>Department of Biological Science, University of Tulsa, Tulsa, OK 74119 USA; <sup>2</sup>Recursos Naturales, CIIDIR Oaxaca, Oaxaca C.P. 71230 Mexico

#### Effects of Anthropogenic Activities on *Liomys pictus* Populations in the Tropical Forest of the Oaxaca Coastal Plain

We evaluated the effects of anthropogenic activities on *Liomys pictus* populations in the tropical forest of the Oaxaca coastal plain in Mexico. Home ranges, individual movement distances, intraspecific interactions, population density, and habitat preference were evaluated in 2 areas with different levels of anthropogenic perturbation. Females of the non-perturbed area had a larger average home range than males, while in the perturbed area, home range size was similar in both sexes. Analogous results were obtained for average individual movement distances. We found no significant differences in home range size and movement distances between the areas evaluated. Intraspecific interactions were high; capture sites for females and males overlapped during the rainy season in both areas. The population inhabiting the disturbed area demonstrated a tolerant social structure, whereas individuals in the non-perturbed area were more territorial. Females had higher site fidelity to their areas than males. Population density in the perturbed area was significantly higher than in the non-perturbed area. This study demonstrates that *Liomys pictus* populations are successful in perturbed habitats, and anthropogenic activities elicit changes in the behavior and ecology of this species of heteromyid.

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### 51 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

**Richard W. Dolman, David M. Leslie, Jr.**

Oklahoma Cooperative Fish and Wildlife Research Unit, Department of Natural Resource Ecology and Management, Oklahoma State University, Stillwater, OK 74078 USA

#### Small Mammal Response to Habitat Loss and Fragmentation in the Lower Rio Grande Valley

Few regions in the United States are as unique ecologically as Tamaulipan brushlands of the Lower Rio Grande Valley (LRGV) in southern Texas. Following the escalated conversion to agricultural and urban use beginning in the 1920s, native brushland in LRGV has been reduced by > 95%. In 1979, the U.S. Fish and Wildlife Service created the Lower Rio Grande River Valley National Wildlife Refuge (LRGVNWR) to serve as a corridor to connect fragmented native habitats and reclaim/restore agricultural lands along the Rio Grande. No studies have examined the refuge and surrounding agricultural/urban matrix providing a true landscape perspective. We surveyed small mammal diversity from 14 refuge tracts, as well as 4 agricultural fields directly adjacent to refuge tracts, to assess species diversity relative to landscape structures and habitat characteristics and to determine the extent to which small mammals use surrounding agricultural matrices for dispersal and/or habitat. Based on 8,251 trap nights over 4 seasons and 5,115 captures (62%) of 9 species, preliminary results show higher species richness in larger tracts and interior versus edge habitat. Very little use of agricultural matrix fields was documented. Maximum species richness was 10, with 2 species dominating in most tracts: white-footed mouse (*Peromyscus leucopus*) and hispid cotton rat (*Sigmodon hispidus*).

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

52 Poster Session I, Great Hall C, Sunday 8 June 2014

**Thomas S. Jung**

*Yukon Department of Environment, Whitehorse, Yukon Y1A 2C6 Canada*

## **Short-term Effect of Fire on Habitat Use by Little Brown Bats (*Myotis lucifugus*) in Northwestern Canada**

Fire is 1 of the most pervasive disturbances in the boreal forest, yet the effect of fire on bats is not well known. Bats may benefit from fire, because the reduction of vegetative clutter may increase foraging opportunities and result in an abundance of dead trees. Activity levels of little brown bats (*Myotis lucifugus*) were acoustically monitored at lacustrine and upland sites in burned and mature boreal forest. I monitored 8 replicates of each of 4 treatment types. Activity levels were significantly greater in unburned forest than in burned forest. The relative use of edges created by fire, and those created by lakeshores and road corridors, also was investigated. In this study, 6 sampling sites for each of the 3 edge-type treatments was sampled. Bats used edges at lakeshores significantly more than fire-created edges or edges created by roads. Similar to logged stands elsewhere in the boreal forest, little brown bats avoided these very open habitats. Thus, large areas of burned boreal forest appear to provide little foraging habitat for little brown bats, despite the reduction of structural clutter and creation of abundant snags. Distinct edges created by fire, however, may be useful to little brown bats as travel corridors and foraging habitats. Further research is needed to examine the influence of fire severity and time since fire on habitat use.

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53 Poster Session I, Great Hall C, Sunday 8 June 2014

**Thomas S. Jung**

*Yukon Department of Environment, Whitehorse, Yukon Y1A 2C6, Canada*

## **Dominance and Diversity in Shrew Assemblages in Logged Boreal Forest of Northwestern Canada**

Shrews contribute substantially to mammalian diversity in the boreal forest. Yet, they are often overlooked when considering the impact of logging on biodiversity. I used pitfall trap arrays to sample shrews in 3 habitat types (logged forest, mature forest, and the forest-logged edge) in the boreal forest of southeastern Yukon, Canada. I captured 370 shrews during 43,875 trap-nights. Captures were dominated by *Sorex cinereus* (69%); other species captured included *S. monticolus*, *S. hoyi*, and *S. palustris*. All trapping sites had  $\leq 2$  species present, which always included *S. cinereus*. Species richness, abundance, evenness, and diversity were greatest in the logged sites and least in the edge sites. Shrew communities were most similar between mature forest and edge habitats ( $P_s = 89.91\%$ ), and least similar between mature forest and logged habitats ( $P_s = 61.55\%$ ). Despite some species being found in much higher abundance in logged stands, all 3 species in this study had relatively high niche overlap values ( $> 70\%$ ), suggesting that all species could be found in similar habitats. We suggest that shrew communities differ dramatically after logging, as larger-bodied species (*S. monticolus*) exploit modified habitats and likely compete with smaller-bodied species that otherwise are more numerically dominant.

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54 Poster Session I, Great Hall C, Sunday 8 June 2014

**Leah M. Andresen-Everatt<sup>1</sup>, Kristoffer T. Everatt<sup>1</sup>, Thomas S. Jung<sup>2</sup>**

<sup>1</sup>*Department of Biology, Vancouver Island University, Nanaimo, British Columbia V9R 5S5 Canada;* <sup>2</sup>*Yukon Department of Environment, Whitehorse, Yukon Y1A 2C6 Canada*

## **Monitoring Collared Pikas (*Ochotona collaris*) as an Indicator Species for Climate Change: Modeling Patch Occupancy in Northwestern Canada**

Collared pikas (*Ochotona collaris*) have been proposed as an indicator species for climate change in northwestern Canada, because of the anticipated loss of their alpine habitat and changes in the timing and amount of snowfall. Therefore, monitoring pika populations should be of interest. However, a standardized sampling protocol that can produce robust population indices is needed to detect long-term changes in pika distribution and abundance. Occupancy models, which incorporate detection probability by using readily collected presence data, produce population indices that can be used to infer population trends, based on the proportion of occupied sites. In this study, we used a detection/non-detection sampling protocol to estimate initial occupancy and detection probabilities for collared pikas in Tombstone Territorial Park, Yukon, Canada. We sampled 59 talus patches 2-3 times for pikas or their haypiles. Selected characteristics of each survey site were measured and we applied model selection techniques to ascertain habitat characteristics associated with patch occupancy. Overall patch occupancy was estimated at 0.5637 (SE = 0.0181) with detection probabilities of 0.91. Elevation, patch area, rock size and patch perimeter were the covariates that best predicted pika occupancy across all sites. Our pilot results suggest that occupancy-based methods are suitable for large-scale, long-term assessment of collared pika abundance and distribution and describe the characteristics of sites that should be monitored.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 55 Poster Session I, Great Hall C, Sunday 8 June 2014

**Kristina Ernest<sup>1</sup>, Jill Hooghkirk<sup>2</sup>, Bryant Sawada<sup>1</sup>, Amanda Tompkins<sup>1</sup>**

<sup>1</sup>Department of Biology, Central Washington University, Ellensburg, WA 98926 USA; <sup>2</sup>Washington Department of Transportation, 2809 Rudkin Rd., Union Gap, WA 98903 USA

### **Pikas in a Human-altered Landscape: Temporal and Spatial Patterns of Patch Occupancy in the Central Washington Cascades**

Talus and other rocky areas of mountain ranges of the western United States and Canada are the primary habitat for American pikas (*Ochotona princeps*), but pikas have also been documented to use other layered habitat types such as log piles and human-constructed rock slopes. In the central Cascades of Washington State, human alteration of the landscape by a major interstate highway (I-90), active and former railways, Forest Service roads, and a reservoir have changed both the habitats pikas occupy and those through which they disperse. We mapped, measured, and monitored > 100 potential pika habitat patches in our study area over the past 6 years. Overall patch occupancy has varied between 75% and 95% over the study period. Most sites were occupied by pikas in all years, but 10–15% of sites show dynamics in occupancy, with apparent local extinctions and re-colonizations. Distances between pika-suitable habitat patches are often within reported pika dispersal distances (and documented movement distances in our study area), and may be a factor in the relatively high rate of occupancy by pikas. Combined, these spatial and temporal factors are predicted to result in relatively rapid colonization of new rocky habitat that becomes available as a result of construction activities along I-90.

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## 56 Poster Session I, Great Hall C, Sunday 8 June 2014

**Justin T. Pynne, Andrew J. Edelman, Amalia Hernandez**

Department of Biology, University of West Georgia, Carrollton, GA 30117 USA

### **Influence of Pine Forest Fragmentation on Southeastern Fox Squirrel Occupancy Patterns**

Alabama's Talladega National Forest (TNF) has adopted thinning and burning management regimens to promote restoration of montane longleaf habitat (*Pinus palustris*) forests. The objective of this study is to determine occupancy for southeastern fox squirrels (*Sciurus niger*) in TNF. Little is known overall about how southeastern fox squirrel populations are responding to the dramatic changes in forest cover, so studies like this 1 can be used to determine suitable habitat. Studies have observed that fox squirrels are food generalists but are limited by habitat selection; they usually select habitat that is predominantly pine, especially longleaf, but with some hardwood component. Fox squirrel home ranges are affected by forest fragmentation; ranges are smaller in more isolated habitat. We used baited remote cameras to document fox squirrel occupancy in varying quality forested patches. Sites were selected using a stratified random design based on quality of identified fox squirrel habitat from USGS GAP Analysis Data. Potential habitat was placed into 3 categories for site selection based on quality of pine-dominated areas: high quality (most continuous areas); medium quality (moderately continuous areas); and low quality (isolated areas). At each site we placed 2 remote cameras and recorded fox squirrel occupancy during 4 survey periods over 2 weeks. Preliminary occupancy for fox squirrels in different forested patches will be estimated using detection/non-detection data obtained from camera surveys.

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## 57 Poster Session I, Great Hall C, Sunday 8 June 2014

**Dawn M. Kaufman<sup>1</sup>, Glennis A. Kaufman<sup>2</sup>, Donald W. Kaufman<sup>2</sup>**

<sup>1</sup>Department of Biology, King's College, Wilkes-Barre, PA 18711 USA; <sup>2</sup>Division of Biology, Kansas State University, Manhattan, KS 66506 USA

### **Expansion of the Semi-Arboreal White-footed Mouse in Tallgrass Prairie: Three Decades of Fire, Woody Invasion, and Land-Cover Change**

Since its inception in 1981, temporal variation in the experimental "application" of fire as part the Konza Prairie Long-Term Ecological Research Project has maintained native tallgrass prairie with varying success. Konza is comprised of a patchwork of treatment units that vary in prescribed fire frequency (annually or quadrennially burned, or long-term unburned), occurrence of native grazers (bison), topography, and weather conditions. Over much of the last century (since 1939) and especially during the last 3 decades (since 1981), a documented increase in woody vegetation has occurred across the ~3,500-ha site; furthermore, during the last 30+ years, woody expansion has occurred in treatment units that undergo fire less frequently. Concurrently, we have assessed the community and population dynamics of small mammals at Konza, among 14 sampling sites in 7 treatment units. Concomitant with the increase of woody vegetation, the semi-arboreal white-footed mouse (WFM; *Peromyscus leucopus*) has generally expanded its presence at Konza during the last 3 decades. Furthermore, WFM has increased sharply at sites with less frequent burns (> 4 years between fires) and, in some cases, has become the dominant species. At the same time, its prairie cousin, the deer mouse (*Peromyscus maniculatus*), has tended to decrease at these sites, suggesting that some degree of ecological replacement in small mammal communities has accompanied the land-cover change.

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 58 Poster Session I, Great Hall C, Sunday 8 June 2014

**Daniel C. Corral, Stephanie A. Trewitt**

*Department of Biological Sciences, San Jose State University, San Jose, CA 95192 USA*

### **A Comparison of Small Mammal Community Structure in Burned and Unburned Aspen Stands, Warner Mountains, California**

In the western United States, aspen forests have undergone a drastic decline due to disturbance from grazing, fire, and prevailing forest management practices. Individual aspen stands can serve as natural firebreaks impeding the spread of wildfires. However, aspen also rely on fire for regeneration and overall stand health. Small mammals serve as an important bio-indicator of aspen stand condition. We conducted a mark-capture-release study from 2011-2013 within burned and unburned aspen stands located in the Warner Mountains, Lassen and Modoc Counties, California. Two stands were chosen, 1 that intensely burned in 2001 and another that has not burned since around the 1900's. Both stands were trapped for 4 days each month from May through September each year using 200 Sherman live traps for a total of 16,800 trap nights. For each stand, we collected data on the age structure, sex and reproductive status, distribution and movement patterns of each species. We also compared species richness between stands and the overall abundance of each species. Each stand was characterized using data collected on stand class (based on height), canopy cover, groundcover, and large woody debris. Species richness differed between stands with the burned stand being more diverse than the unburned stand. Overall abundance was greater in the burned stand compared to the unburned.

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## 59 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

**Ty Sprayberry, Andrew J. Edelman, Shelby Lewis, Matthew Rouse**

*University of West Georgia, Carrollton, GA 30118 USA*

### **Influence of Prescribed Fire Management on Mesocarnivore Occupancy in Montane Longleaf Pine Forests**

Longleaf pine (*Pinus palustris*) is 1 of the most endangered ecosystems in North America. This fire-adapted ecosystem once covered an estimated 90 million acres of the southeastern United States but has now been reduced to less than 5% of its original range due to human alterations from logging, clearing land for development/agriculture, and suppression of fire. Longleaf pine forests are disturbance-dependent, requiring frequent burning and thinning to maintain an open canopy with an herbaceous understory. In the most northern ecoregion of longleaf pine, known as montane longleaf, the U.S. Forest Service is actively restoring this ecosystem through prescribed fire management. We used remote cameras to estimate occupancy of mesocarnivores on different prescribed fire management plots in montane longleaf pine forest of north-central Alabama. Remote cameras were placed for 2 week periods at 21 plots across 3 different fire frequencies: 2-3 year burn interval; 8-12 year burn interval; and a no recent fire history (> 25 years since last fire). Baited remote camera stations were located at opposing ends of each 75m by 75 m plot. Typical characteristics of the 2-3 year burn interval plots are open canopies and dense understory vegetation as existed under historical conditions, while the 8-12 year interval and no recent fire history plots have closed canopies with little understory vegetation. Preliminary results of mesocarnivore occupancy across fire treatments will be discussed.

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## 60 Poster Session I, Great Hall C, Sunday 8 June 2014

**Brittany A. Mixon, Colleen M. McDonough**

*Department of Biology, Valdosta State University, Valdosta, GA 31698-0015 USA*

### **Can Fecal Pellet Size Indicate Population Structure in Nine-banded Armadillos?**

Armadillos are difficult to study because of their nocturnal and solitary habits. Signs or artifacts, such as burrows or fecal pellets, may be more evident and easier to collect than capturing the animals themselves. If fecal pellet size can give some indication of a population's demography, then this information could facilitate conservation decisions regarding many armadillo species listed as threatened or endangered. To determine if pellet size reflects an individual's body size, age or sex, we collected 102 fecal remains deposited naturally or during capture of the commonly occurring nine-banded armadillo (*Dasypus novemcinctus*). Age, sex and body weight were recorded. For the 65 samples with defined pellet formation, volume was calculated from the average length and width of each dried pellet. The largest pellet from each sample was used for analyses. Males and females did not differ in pellet size in any age class. Body weight did predict pellet volume, but when age classes were considered separately, only juvenile weight correlated positively with volume. Pellet width may be the best indicator of an individual's body size and age. Width was significantly smaller in juveniles than both adults and yearlings. Even looking at all pellets, the smallest pellet for adults tended to be wider than the largest pellet for juveniles. Pellets may be able to identify juvenile recruitment in a population.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

61 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

**Amanda E. Cheeseman, Jonathan Cohen**

*Department of Environmental and Forest Biology, State University of New York College of Environmental Science and Forestry, Syracuse, NY 13210 USA*

## **Survival and Home Range of New England Cottontail (*Sylvilagus transitionalis*) in Response to Hunting, Competition, and Habitat Composition**

The New England cottontail (*Sylvilagus transitionalis*) is a shrubland obligate lagomorph. Historically common throughout New England and eastern New York, the New England cottontail has experienced range-wide declines. This decline has prompted the U.S. Fish and Wildlife Service to consider the New England cottontail for listing under the Endangered Species Act. Loss of early successional forest is widely recognized as the driving factor behind the decline of New England cottontail. Presence of eastern cottontails also is suggested to limit colonization of new habitat patches by New England cottontail. Programs throughout the Northeast have been instated to restore early successional forest, with the goal of increasing New England cottontail populations in the region. However, it is unknown if this species can effectively recolonize newly restored early successional forest patches. Furthermore, hunting of New England cottontail is permitted in New York and ongoing in areas targeted for habitat restoration. Hunting pressures could lower New England cottontail survival and success of restoration efforts. Our study examined survival and home range of New England cottontail in response to habitat structure and composition, presence of eastern cottontails, and hunting. Results from this study will inform managers of effective ways to manage habitat to increase New England cottontail populations, as well as provide much needed data on the biology of a declining species.

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62 Poster Session I, Great Hall C, Sunday 8 June 2014

**Ralph P. Eckerlin<sup>1</sup>, Walter Bulmer<sup>1</sup>, Alfred L. Gardner<sup>2</sup>, Suzanne C. Peurach<sup>2</sup>**

<sup>1</sup>*Natural Sciences Division, Northern Virginia Community College, Annandale, VA 22003 USA;* <sup>2</sup>*U.S. Geological Survey Patuxent Wildlife Research Center, National Museum of Natural History, Smithsonian Institution, PO Box 37012, MRC 111, Washington, D.C. 20013-7012 USA*

## **West Virginia Rock Voles**

The Rock Vole, *Microtus chrotorrhinus*, has a northern distribution in eastern North America. It occurs across southern Canada from Ontario to Labrador and in the United States through the New England states southward to isolated populations in the Appalachian Mountains. There are few records of the Rock Vole from West Virginia where the species is listed as state imperiled (S2). In the National Museum of Natural History collection, only 30 specimens of Rock Voles from 3 localities in Pocahontas County are represented. We had previously trapped a single Rock Vole on a talus slope at high elevation (ca. 1120 m) in Pocahontas County. We are attempting to determine an estimate of the population size and its boundaries in the more than 1 km-long talus slope. In October 2013, we established a 0.5-ha plot on the slope using 60 Sherman live traps 10 m apart in a 100 m by 50 m array. The following day, 4 transects of 20 traps each were set, 1 at the base of the 0.5-ha plot and 3 others at 100 m intervals upslope of the plot. A single Rock Vole was caught in a transect 300 m up from the plot. Thus in 200 trap nights, 1 target species was caught. Ecological associates of the Rock Vole are *Blarina brevicauda*, *Sorex fumeus*, *Myodes gapperi*, *Peromyscus maniculatus*, *P. leucopus*, *Synaptomys cooperi*, and *Napeozapus insignis*. Efforts will continue.

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63 Poster Session I, Great Hall C, Sunday 8 June 2014

**Cary D. Chevalier, Trevor Boyd, Tyler Lee, Cody Phillips, John Powell, Jarrett Rowland, Erin Stith, Mary Kate Wiley**

*Biology Department, Missouri Western State University, St. Joseph, MO 64507 USA*

## **Summer Den Site Selection by Male Raccoons (*Procyon lotor*) in an Urban Habitat in Northwest Missouri**

Raccoons are an important member of the mammalian fauna native to Missouri. However, we know little about their modes of resource selection in urban areas of northwest Missouri or the characteristics of their den site choices. The purposes of this study were to: 1) determine if male raccoons choose 1 den site over any possible alternative site and 2) determine the spatial distribution and use of summer den sites by male raccoons. Male raccoons were captured with live traps, fitted with radio transmitters and released. During the day, we located the raccoon in their den sites. Twenty-two variables were measured at each den site and its 2 randomly associated satellite sites. Of these variables, statistical differences (Wilks' Lambda; F-Test;  $P < 0.05$ ) between mean values for raccoon dens and alternate satellite sites occurred for 9 variables measured. Four models were constructed using stepwise discriminate function analysis and evaluated for efficiency in identifying male raccoon dens, as well as identifying the most important variables keyed on by male raccoons in selecting den sites during the summer season. All models were significantly effective at differentiating between real raccoon dens and randomly selected sites in the environment ( $P < 0.05$ ). Model efficiencies equaled or exceeded 80%. Models such as these can be useful in predicting habitat "richness" for resources such as den sites.

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 64 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

Melissa A. Mills<sup>1</sup>, Robert Denkhaus<sup>2</sup>, Michael C. Slattery<sup>3</sup>, Victoria J. Bennett<sup>1</sup>, Julie K. Young<sup>4</sup>

<sup>1</sup>School of Geology, Energy and the Environment, Texas Christian University, Fort Worth, TX 76129 USA; <sup>2</sup>Fort Worth Nature Center & Refuge, Fort Worth, TX 76135 USA; <sup>3</sup>Institute for Environmental Studies, Texas Christian University, Fort Worth, TX 76129 USA; <sup>4</sup>Wildland Resources Department, Utah State University, Logan, UT 84322 USA

### Monitoring Urban Bobcats (*Lynx rufus*) in Fort Worth/Dallas Area, Texas

Wildlife monitoring programs often require the ability to accurately identify individuals within a population. Non-invasive techniques that use pelt markings in photographs taken by camera traps have proven to be useful in population studies. This method may be particularly advantageous to urban wildlife managers that are often logistically constrained in their abilities to assess local carnivore populations. Utilizing these techniques may therefore be a cost-effective alternative. Thus, we set out to determine whether camera trapping methods could effectively be used in urban mesocarnivore studies. Beginning in September 2013, in 2 study sites in the Fort Worth/Dallas Metroplex in Texas, we randomly placed 25 motion triggered Moultrie M-880 Mini Game Cameras at 50 locations (25 on a 3-month rotation). In addition, we recorded all signs of carnivore presence incidentally found during habitat ground-truthing surveys conducted at our sites. From photographs collected, we used a standard procedure of spot identification for mammals, which included the detection of at least 3 unique pelt characteristics, the patterns among clusters of spots, and the presence of marks, such as scarring. To date, we have identified at least 8 individual bobcats (*Lynx rufus*) in each study site recorded on multiple cameras, suggesting it may be possible to monitor specific individuals in an urban population and estimate the range size and habitat use of these individuals.

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## 65 Poster Session I, Great Hall C, Sunday 8 June 2014

Victoria L. Jackson<sup>1</sup>, W. Sue Fairbanks<sup>2</sup>, Sara B. Lyda<sup>3</sup>

<sup>1</sup>Department of Biology and Agriculture, University of Central Missouri, Warrensburg, MO 64093 USA; <sup>2</sup>Department of Natural Resource Ecology and Management, Oklahoma State University, Stillwater, OK 74074 USA; <sup>3</sup>Oklahoma Cooperative Fish and Wildlife Research Unit, Oklahoma State University, Stillwater, OK 74074 USA

### A Comparison of Black Bear Home Ranges in Two Distinct Populations in Oklahoma

Distribution and abundance of black bears has increased in Oklahoma over the past 2 decades. An understanding of the relationship of home range dynamics and land-use practices is critical in effectively managing this species. In 2001–2002, demographic characteristics and habitat use of black bears were studied in the Ouachita National Forest of Oklahoma, where human impacts are low. We compare the home ranges of black bears in the Ouachita National Forest to those of bears in east-central Oklahoma, which exists on primarily private land with many more anthropogenic factors. We used ArcView 3.2 and the Animal Movement Extension to estimate Minimum Convex Polygon (MCP) at 100% and 95% as well as to estimate Adaptive Kernel Home Ranges (AKHR) at 95% and 50% for 9 female bears in east-central Oklahoma and 13 female bears from the Ouachita National Forest. Due to high variability of home range estimates, non-parametric tests were used to look at differences. There was no significant difference in the 50% AKHR estimates, but significant differences existed in 100% MCP, 95% MCP, and 95% AKHR (Mann-Whitney U Test,  $p < 0.008$ ). Differences may exist due to the increased number of locations of bear in east-central Oklahoma ( $\bar{X} = 719$  vs  $\bar{X} = 53$ ) due to the use of GPS collars. Differences in habitat fragmentation may also influence the differences in home range estimates.

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## 66 Poster Session I, Great Hall C, Sunday 8 June 2014

Anthony P. Bush<sup>1</sup>, Kelley M. Stewart<sup>1</sup>, Vernon C. Bleich<sup>2</sup>, Neal Darby<sup>3</sup>

<sup>1</sup>Dept of Natural Resources and Environmental Science, University of Nevada, Reno, NV 89504 USA; <sup>2</sup>California Department of Fish and Wildlife, Bishop CA, USA; <sup>3</sup>Mojave National Preserve, National Park Service, Barstow, CA, USA

### Effects of Perennially Available Water on Home Range Size of Mule Deer in Mojave National Preserve, California

Mule deer (*Odocoileus hemionus*) populations have been in decline for several decades. Water is an important, and often limiting, factor in habitat suitability for wildlife in arid regions. In the southwestern United States, installation of water developments to benefit wildlife has been practiced since the 1940s. Despite its widespread use in wildlife management, few studies have shown the benefits of providing water for wildlife. Previous research suggests that during hot dry months deer will expand home ranges to include more sources of perennial water. During a 4-year period, we investigated the effects of available water on the size of home ranges of radio collared adult female mule deer in Mojave National Preserve, California. Using 3 study areas with differing levels of water provisioning, we assessed home range size, as well as distance from the center of home range and core area of use to the nearest perennial water source, seasonally, and annually for each individual. We analyzed these data to identify variations between those with relatively more or less available water contained in their home range. We found distance to

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

nearest water source to be strongly significant during the summer months. A significant effect of study area was found annually, as well as in spring. Additionally, deer were found to have the smallest home ranges during summer and largest during winter.

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### 67 (E,TA) Poster Session I, Great Hall C, Sunday 8 June 2014

**Brett R. Jesmer<sup>1,2</sup>, Jacob R. Goheen<sup>1</sup>, Matthew J. Kauffman<sup>3</sup>, Kevin L. Monteith<sup>1,2</sup>**

<sup>1</sup>Department of Zoology and Physiology, University of Wyoming, Laramie, WY 82072 USA; <sup>2</sup>Wyoming Cooperative Fish and Wildlife Research Unit, University of Wyoming, Laramie, WY 82072 USA; <sup>3</sup>U.S. Geological Survey, Wyoming Cooperative Fish and Wildlife Research Unit, University of Wyoming, Laramie, WY 82072 USA

#### Linking Climate and Habitat with Nutritional Condition and Recruitment in Moose

A major goal in population ecology is to understand the factors underlying density-dependent shifts in demography. Life-history theory predicts that nutritional reserves of long-lived mammals should be allocated to reproduction in a state-dependent manner because survival is highly conserved. Consequently, variation in reproductive effort and recruitment strongly influences population dynamics of large herbivores. Because nutritional reserves integrate climatic and habitat conditions, both climate and habitat should influence the reproductive decisions that underpin recruitment rates. Therefore, life-history theory provides a framework for testing hypotheses related to density-dependence and bottom-up limitation. Recruitment rates in most moose (*Alces alces*) populations of the Intermountain West are declining, even in areas lacking large carnivores, strongly suggesting bottom-up limitation. From 2011–2013, we evaluated climate, habitat condition, nutritional condition, reproduction and recruitment in 6 populations of moose across Wyoming and northern Colorado. Our results indicate that climate and habitat combine to influence nutritional condition and pregnancy rates, but not always recruitment rates, in these areas. Our results suggest that changes in nutritional state should preempt shifts in recruitment during the early stages of density-dependence. Life-history theory provides a useful conceptual framework through which to link habitat and nutritional condition to reproduction in ungulates experiencing bottom-up limitation.

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### 68 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

**Margaret E. Sackrider<sup>1</sup>, Susan G. Clark<sup>1</sup>, Isaac M. Ortega<sup>2</sup>**

<sup>1</sup>School of Forestry and Environmental Studies, Yale University, New Haven, CT 06511 USA; <sup>2</sup>Department of Natural Resources & the Environment, University of Connecticut, Storrs, CT 06269 USA

#### Exurban Residents' Perceptions of Naturally Returning Predators: Connecticut Case Study

As a result of reforestation, growth of exurban areas and wildlife adaptation, it is believed that the public is currently encountering more human-wildlife conflicts than ever before. Balancing wildlife conservation and human development is key to understanding the dynamic relationship between humans and carnivores. Gaining insight into the complexity of this relationship will aid in the creation of more effective conservation policy and outreach. Connecticut reforestation has supported a tremendous population growth of prey species and subsequently the growth of predator populations including coyotes (*Canis latrans*), black bears (*Ursus americanus*), and potentially pumas (*Puma concolor*) in the future. Prior to this study, there was limited knowledge regarding residents' perceptions of these predators, making it difficult to implement management strategies reflexive of residents' beliefs and opinions. The goals of this project were to explain the social context regarding large predators in Connecticut, as well as work toward bridging the gap between ecological and social science disciplines. An explanatory sequential grounded theory approach was taken to achieve these goals. Qualitative data collected through interviews and participant observation was used to create of a case specific survey. Quantitative data was collected through surveys of 1,000 randomly identified Connecticut residents. Finally, a spatial representation of perceived threats was developed and compared to human-carnivore conflict sites.

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### 69 (E) Poster Session I, Great Hall C, Sunday 8 June 2014

**Gael A. Sanchez<sup>1</sup>, Charlotte R. Milling<sup>2</sup>, Janet L. Rachlow<sup>2</sup>**

<sup>1</sup>Department of Biology, New Mexico State University, Las Cruces, NM 88001 USA; <sup>2</sup>Department of Fish and Wildlife Sciences, University of Idaho, Moscow, ID 83844-1136 USA

#### Evaluating a Method for Sensing Ambient Temperature and Its Effect on Behavior of Mountain Cottontails

Activity in mammals is strongly influenced by ambient temperature because energy required to thermoregulate can limit when organisms are active. Leporids are particularly constrained by high temperatures because they lack mechanisms for efficient brain cooling. We evaluated the efficacy of temperature sensors (ibuttons) attached to collars on mountain cottontails (*Sylvilagus nuttallii*) to monitor ambient temperature experienced by the rabbits, and then we used this technology to evaluate the effects of ambient summer temperatures on activity of cottontails in captivity. We expected that the ibuttons would be influenced by body temperature such that the difference between the ibutton reading and ambient temperature would decrease with increasing ambient temperatures. The difference between the 2 (mean = 11–13°C, *n* = 4) was relatively consistent among individuals in a temperature-controlled room

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

at 22°C. In trials conducted during July in outdoor pens, the temperature difference decreased significantly with temperature and reached approximately zero as the ambient temperature approached body temperature. We used cameras to monitor activity of rabbits throughout the day and night in the outdoor pens. Rabbits were most active at ambient temperatures between 5.5–15°C. This study evaluated a technique that can be used to assess selection of thermal resources by free-ranging mammals, and it highlighted the influence of temperature on activity in leporids.

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### 70 (E,\*\*) Poster Session I, Great Hall C, Sunday 8 June 2014

**Hae Yeong Ryu**

*Ecology and Evolution, Stony Brook University, Stony Brook, NY 11794 USA*

#### **Natal Dispersal of the Golden Mantled Ground Squirrel**

The golden-mantled ground squirrel (*Callospermophilus lateralis*) is an asocial, hibernating species that is found in the subalpine regions of the Rocky Mountains. The life history traits of the species are characterized by high mortality during natal dispersal, low survival during hibernation, and high predation over its life-time. These factors are thought to drive the overall population dynamics of the species in the Rocky Mountains. However, the dispersal behavior of *C. lateralis* is poorly understood making it difficult to model population dynamics at the metapopulation level and project the future fate of the species under the influence of climate change. Therefore, I used radio-telemetry on 20 juveniles to determine dispersal distances and characterize the pattern of movement. Based on the location data obtained from radio-telemetry, juveniles moved short distances at a time, though in rare cases, some stayed in the same territory until the very end of the active season and moved a long distance at once. For the individuals that successfully settled down into a new territory, the overall dispersal distance did not exceed 3 km. The movement paths were generally formed along meadow areas which are known to be preferred by the species. Radio-telemetry data also revealed that more than 50% of the juveniles are killed by predators before they even initiate the movement. This research was supported by an ASM Grants-In-Aid of Research awarded to Hae Yeong Ryu in 2013.

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### 71 (E,\*\*) Poster Session I, Great Hall C, Sunday 8 June 2014

**Allyssa L. Kilanowski, John L. Koprowski**

*School of Natural Resources and the Environment, University of Arizona, Tucson, AZ 85721 USA*

#### **Do Behavioral Phenotypes Affect the Exploration Stage of Juvenile Dispersal in a Fossorial Rodent (*Tamias dorsalis*)?**

Climate and anthropogenic forest change creates numerous conservation challenges. Understanding the impact of such change on key population processes can influence potential conservation strategies. One of the most important processes is the dispersal of juveniles. Behavioral phenotypes (BPs), a set of observable behaviors in an individual that are the result of its genotype interacting with the environment, may influence a juvenile's exploration method as it disperses. We described BPs of a fossorial rodent population (*Tamias dorsalis*) on Mount Graham in the Pinaleno Mountains, AZ, and examined how personality differences influence the exploration of juveniles. We captured juveniles after emergence from the natal nest, performed 2 behavioral tests to measure activity/exploration and sociality/aggression, and radio collared individuals to track exploratory movements as individuals dispersed. In 2013, we found that BPs exist in our population and that subtle differences exist between males and females. We also found that BPs affected the path distance individuals moved during exploration with highly active individuals exploring longer path distances than less active individuals. This work will be continued in 2014 to further elucidate the effect of BPs on natal exploration. This research aids our understanding of a key population process, natal dispersal, which affects conservation efforts in environments affected by climate and anthropogenic changes. This research was supported by an ASM Grants-in-Aid of Research awarded to Allyssa L. Kilanowski in 2013.

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### 72 (E,TA) Technical Session 3, Meeting Room 16, Sunday 8 June 2014

**Samuel H. Hirt<sup>1</sup>, Cheryl Rosa<sup>2</sup>, Wendy Hood<sup>1</sup>, Troy Best<sup>1</sup>**

*<sup>1</sup>Biological Sciences, Auburn University, Auburn, AL 36849 USA; <sup>2</sup>U.S. Arctic Research Commission, Anchorage, AK 99501 USA*

#### **Analyses of Stable Isotopes, Hormones, and Minerals of Baleen from Bowhead Whales (*Balaena mysticetus*)**

Bowhead whales inhabit an ecosystem undergoing dramatic changes in sea ice and temperature and are of great importance to indigenous people of the North Slope of Alaska. Information on reproduction, however, has been difficult for researchers to acquire because of inaccessibility of bowhead whales in their environment. Baleen is an inert tissue that is formed from keratinized epithelium similar to nails, claws, or hair. My analyses have determined differences between reproductive groups by analyzing hormones and minerals at the proximal end of baleen. Concentrations of calcium in baleen were significantly lower in mature pregnant females than in non-pregnant females, (Tukey-Kramer adjusted  $p = 0.022$ ). Correlation between length of whale and concentration of calcium was significant ( $r = -0.503$ ,  $p < 0.001$ ), but not significant in sexually mature whales that were over 14 m in length ( $\rho = 0.721$ ). Stable isotopes of baleen correlate with annual migratory events of bowhead whales and thus provide a



## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

timeline for mineral and hormonal analyses along the length of the baleen. Concentrations of estrogen and progesterone were measured in 5 cm increments along the length of adult female whales. Results from these analyses will provide estimates of calving interval that will be important for management of this endangered species.

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### 73 Technical Session 3, Meeting Room 16, Sunday 8 June 2014

**Gail R. Michener**

*Biological Sciences, University of Lethbridge, Lethbridge, AB T1K 3M4 Canada*

#### **Lifetime Reproductive Success in Richardson's Ground Squirrels**

For short-lived highly-seasonal breeders, both failure to wean a litter in a reproductive season and failure of daughters to reach reproductive age have costly impacts on reproductive success. From 1987 through 2011, I assessed the annual and lifetime reproductive success of females in a population of Richardson's ground squirrels (*Urocitellus richardsonii*) in southern Alberta, Canada. Richardson's ground squirrels are obligate hibernators that attain sexual maturity on emergence from their 1st hibernation. Females survive for an average of 1.8 adult years and are limited to producing a single litter per year. Of about 1,700 females still alive in the litter-weaning period (60 days post hibernation emergence), 89% weaned a litter. Reproductive failure was more likely to occur during lactation than during pregnancy; 98% of females were impregnated and 91% of those weaned a litter. Although average litter size at weaning was 6.2, of which 3.1 offspring were daughters, on average only 0.9 daughters per litter survived to maturity (range 0–7). Mothers with completely known lifetime reproduction weaned a lifetime average of 5.0 daughters (range 0–19), of which 1.5 (range 0–9) survived to maturity. Lifetime number of daughters weaned was a stronger predictor of daughter recruitment ( $r^2 = 49\%$ ) than lifetime number of litters produced ( $r^2 = 38\%$ ). Post-weaning mortality of daughters had a greater negative impact on lifetime reproductive success than did pre-weaning reproductive failure.

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### 74 (E, \*\*,TA) Technical Session 3, Meeting Room 16, Sunday 8 June 2014

**Rebecca E. Green**<sup>1,2</sup>, **Kathryn L. Purcell**<sup>2</sup>, **Craig M. Thompson**<sup>2</sup>, **Douglas A. Kelt**<sup>3</sup>, **Heiko U. Wittmer**<sup>3,4</sup>

<sup>1</sup>*Ecology Graduate Group, University of California, Davis, CA 95616 USA;* <sup>2</sup>*U.S. Forest Service, Pacific Southwest Research Station, 2081 E Sierra Ave, Fresno, CA 93710 USA;* <sup>3</sup>*Department of Wildlife, Fish, and Conservation Biology, University of California, Davis, CA 95616 USA;* <sup>4</sup>*School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand*

#### **A Comparison of Fisher (*Pekania [Martes] pennanti*) Reproductive Parameters in the Southern Sierra Nevada Relative to the Broader Geographic Range**

Identifying basic reproductive parameters for rare species is essential to inform and facilitate regional conservation efforts. However, parameters associated with reproduction may vary across the range of a species due to factors such as body size, diet, habitat, and environmental conditions. Here, we summarize available reproductive parameters for fisher (*Pekania [Martes] pennanti*) from across the range in North America to provide context for data collected in the southernmost portion of the range in the Sierra Nevada. Between 2008 and 2013, we located 224 reproductive dens of 34 female fishers in the Sierra National Forest. On average, 84% (range 71–93%) of adult females in the southern Sierra Nevada reproduced annually with a range of 71 to 93% across years. The earliest documented date of parturition in our study area was 23 March, with a mean of 30 March. Mean litter size was 1.6 kits (range 1–3). Although the proportion of females that reproduced annually was comparable to or even higher than reported elsewhere, parturition dates were slightly later, and mean litter size was smaller in the southern Sierra Nevada relative to other geographic areas. We discuss potential explanations for variation in fisher reproductive parameters across the range and implications for conservation of this isolated population. This research was supported by an ASM Grants-in-Aid of Research awarded to Rebecca Green in 2011.

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### 75 Technical Session 3, Meeting Room 16, Sunday 8 June 2014

**Diane M. Post**<sup>1</sup>, **Kathleen Callicot**<sup>1</sup>, **James A. Eldridge**<sup>2</sup>

<sup>1</sup>*Department of Biology, University of Texas-Permian Basin, Odessa, TX 79762 USA;* <sup>2</sup>*Department of Kinesiology, University of Texas-Permian Basin, Odessa, TX 79762 USA*

#### **The Effects of Access to Anthropogenic Resources on Reproductive Schedules in *Neotoma micropus***

For some species, occupancy in a wildland-urban interface area can provide access to new resources. For example, anthropogenic food sources can provide year-round access to food waste and other consumable agricultural products. Such access might free interface occupants from the effects of dependence on seasonal natural food supplies. We obtained monthly high-resolution scans and external condition observations to assess the reproductive status of female Southern Plains woodrats (*Neotoma micropus*). We used our data to determine the effect of access to anthropogenic resources on the pattern of reproduction on female *N. micropus*. Our results suggest that females occupying the interface are reproductively active throughout the entire year and, as a result, may enjoy greater reproductive success than females in wildland environments.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

76 Technical Session 3, Meeting Room 16, Sunday 8 June 2014

**Tyla S. Holsomback**

*Epidemiology Division, Tarrant County Public Health, Fort Worth, TX 76196 USA*

## **Rare, Morphometric Data for Texas *Oryzomys palustris* (Marsh Rice Rat) Dams, Embryos, and Fetuses**

*Oryzomys palustris* (Harlan, 1837) is a long-distance terrestrial and aquatic disperser, occurring in riverine and marsh grassland habitats throughout the southeastern United States and the Atlantic Coast. Based on available data, litter sizes of Texas *O. palustris* appear to range from 2–7 pups/litter with an average of 4. Our coastal marsh study indicates somewhat less variability in litter sizes (3–7 pups/litter) and more pups per litter compared to other Texas populations (mean = 4.69, 95% CI [4.07, 5.32],  $t = 2.42$ ,  $d.f. = 12$ ,  $P = 0.03$ ), but comparable results to Virginia populations [4.63 ± 1.39 (mean ± SE). Pearson's product moment revealed a significant, positive correlation ( $R^2 = 0.71$ , 95% CI [0.088, 0.934]) between embryoid–/fetal widths and dam weights ( $t = 2.67$ ,  $d.f. = 7$ ,  $P = 0.03$ ). Other correlation analyses did not detect relationships between numbers of embryos/fetuses and weights of dams ( $R^2 = 0.46$ ,  $P = 0.11$ ) or numbers of embryos/fetuses and total length of dams ( $R^2 = 0.21$ ,  $P = 0.49$ ). Embryoid/fetal lengths and dam weights were not correlated ( $t = 2.02$ ,  $d.f. = 7$ ,  $P = 0.08$ ,  $R^2 = 0.61$ , 95% CI [-0.096, 0.906]). Interestingly, total length of pregnant females was significantly shorter (229.1 mm) compared to the published value (245.0 mm—95% CI [221.6, 236.7],  $t = -4.55$ ,  $d.f. = 12$ ,  $P = 0.0007$ ).

77 Technical Session 3, Meeting Room 16, Sunday 8 June 2014

**Kent E. Edmonds, Jalina Mueller**

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## **Effects of Photoperiod, Melatonin, and Environmental Enrichment on Reproductive Function in the Female Marsh Rice Rat (*Oryzomys palustris*)**

Animals must continuously adjust physiologically to their current environment. The present studies coupled photoperiod or melatonin administration with an enriched cage environment to examine growth and reproductive function, Harderian gland (HG), spleen, and brain masses of females of various ages. Environmental enrichment refers herein to the alteration of a standard (typically bedding only) housing environment and included the addition of various items into the cage. The treatment groups included standard or enriched housing on either a long photoperiod (14L:10D) or a short photoperiod (12L:12D). In adults, long photoperiods stimulated and short photoperiods inhibited reproductive function and HG mass. Environmental enrichment enhanced the mass of the ovaries, HG, and brain, regardless of photoperiod. There was no effect of any treatment on spleen mass. In juveniles exposed to a long photoperiod both enriched and super-enriched environments inhibited only ovarian development. In aged females on a long photoperiod only, there were no significant effects of 11 weeks of enrichment on any variable examined. Melatonin implants decreased ovary and uterine masses, but enrichment failed to override any effects of melatonin. Taken together, these data suggest that some physiological responses to photoperiod can be altered, both positively and negatively, by environmental enrichment (although the effect may be dependent upon several factors) and the utilization of environmental enrichment (instead of standard housing) into experimental design may want to be considered in future studies.

78 (E) Technical Session 4, Meeting Room 17, Sunday 8 June 2014

**Cibele G. Sotero-Caio<sup>1</sup>, Fengtang Yang<sup>2</sup>, Marianne Volleth<sup>3</sup>, Robert J. Baker<sup>1</sup>**

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## **Karyotypic Megaevolution on Phyllostominae Revisited: Chromosomal Rearrangements in the Bat *Tonatia saurophila***

The term karyotypic megaevolution was coined in the early 1980s to describe major repatterning of the synteny of genomic segments presented by some species. The phyllostomid bat *Tonatia saurophila* was used as an example of extreme chromosomal reorganization. Because no homology could be found among its chromosomes and those of closely related species, *T. saurophila* is considered 1 of the bats with the most rearranged karyotype described so far. Changes on the Phyllostomidae classification have redefined the taxonomy of *Tonatia* and the intergeneric relationships of Phyllostominae. Additionally, the development of molecular cytogenetic techniques that can identify chromosome homologies based on DNA sequence provides a new landscape to study the magnitude of chromosomal change of species with highly rearranged karyotypes. In this context, we used chromosome painting to access the chromosome homologies between *T. saurophila* and 6 phyllostomid species and integrated the results with recent molecular phylogeny findings. We proposed the ancestral karyotype for the subfamily Phyllostominae and found, for the 1st time, correspondence among *Tonatia* and other phyllostomid chromosomes. We calculated the minimal number of rearrangements required to derive the extant karyotype of *T. saurophila* from the ancestral Phyllostominae condition. Rates of chromosomal evolution were estimated and the probability of fixation of

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

chromosome rearrangements is discussed in terms of long-term effective population sizes, selection coefficients for specific rearrangements, and natural history aspects of the species.

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### 79 (E) Technical Session 4, Meeting Room 17, Sunday 8 June 2014

**Julie A. Parlos, Robert J. Baker**

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#### **Phylogenetic Reconstructions of *Dermanura*: Incongruence of Multiple Markers**

Morphological studies have failed to yield congruent resolution for the number of species within the genus *Dermanura* (Chiroptera: Phyllostomidae). Species delineated based on morphological characteristics have ranged from 1 to 10. Recent evaluation of the cytochrome b gene recovered 11 statistically supported monophyletic species groups that were correlated with morphological characters. Because of the lack of congruence among previous morphological methods, we selected the genetically defined monophyletic bat genus *Dermanura* to test for congruence of previous morphological and mitochondrial DNA data with nuclear datasets (amplified fragment lengths polymorphisms (AFLPs) and microsatellites) to delineate species boundaries. Morphological and mitochondrial DNA datasets were incongruent with the 2 nuclear datasets. A previous allozyme study (Koop and Baker 1983) found very few fixed differences among species groups of *Dermanura*. These contrasting results may be due to incomplete lineage sorting at the nuclear level (i.e., microsatellites) or reticulated evolution of sympatric population (i.e., AFLPs). In an effort to further understand the lack of congruence among these datasets, we have chosen to investigate molecular variation at a locus on the y chromosome.

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### 80 Technical Session 4, Meeting Room 17, Sunday 8 June 2014

**Kelly A. Speer, Zachary Quicksall, David L. Reed**

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#### **Estimating Genetic Diversity, Dispersal, and Population Structure Across Island Populations of Brazilian Free-tailed Bats**

The Bahamas provide a unique system where dispersal can be evaluated in a relatively controlled setting compared to mainland communities. Previous research indicates the oceanic channel separating the Great and Lesser Bahama Banks acts as a barrier to gene flow between bat populations. It is unclear whether characteristics specific to this oceanic channel or habitat and resource differences between the Great and Lesser Bahama banks are most important in deterring dispersal. To identify factors influencing gene flow and test the effects of this barrier on an excellent disperser, we examined the population structure of *Tadarida brasiliensis* within islands, between islands of the same bank, and across the 2 banks. We collected tissue from a total of 90 individuals from localities on Grand Bahama and Abaco of the Lesser Bahama Bank, and Eleuthera and Long Island of the Great Bahama Bank. We amplified 9 variable microsatellite loci, which were analyzed using Structure to test for population cohesion and Migrate to estimate movement between populations. Preliminary mitochondrial sequence data shows *T. brasiliensis* populations are distinct across the Great and Lesser Bahama banks. By characterizing dispersal within islands and between islands of the same bank, we can potentially identify attributes important in maintaining structure across these banks. These attributes may provide novel information for elucidating key mechanisms underlying biogeographic processes (e.g., colonization, speciation, extinction).

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### 81 Technical Session 4, Meeting Room 17, Sunday 8 June 2014

**Cassandra M. Miller-Butterworth<sup>1</sup>, Maarten J. Vonhof<sup>2</sup>, Joel Rosenstern<sup>1</sup>, Greg G. Turner<sup>3</sup>, Amy L. Russell<sup>4</sup>**

<sup>1</sup>*Penn State Beaver, Monaca, PA 15061 USA;* <sup>2</sup>*Department of Biological Sciences and Environmental Studies Program, Western Michigan University, Kalamazoo, MI 49008 USA;* <sup>3</sup>*Pennsylvania Game Commission, Harrisburg, PA 17110 USA;* <sup>4</sup>*Department of Biology, Grand Valley State University, Allendale, MI 49401 USA*

#### **Genetic Structure of Little Brown Bats (*Myotis lucifugus*) Corresponds with Spread of White-nose Syndrome among Hibernacula**

Until recently, the little brown bat (*Myotis lucifugus*) was 1 of the most common bat species in North America. However, this species faces a significant and immediate threat from white-nose syndrome (WNS). The aims of this study were to examine the population genetic structure of *M. lucifugus* in Pennsylvania (PA) and to determine whether that population structure may have influenced the pattern of spread of WNS through PA and into neighboring states. Samples were collected from 198 individuals from hibernacula located throughout PA, as well as from 2 sites in West Virginia and Vermont. Both mitochondrial (cytochrome oxidase I) and nuclear (8 microsatellites) loci were examined. No substructure was evident from nuclear DNA, however female-mediated gene flow was restricted between hibernacula in western PA and the remaining colonies. This mitochondrial genetic structure corresponded with topographical variation across the region: 3 hibernating colonies located on the western Appalachian plateau were significantly differentiated from colonies located in the central mountainous and eastern lowland regions. This suggests that gene flow between these clusters of colonies may be reduced. Consistent with the hypothesis that

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

WNS is spread primarily through bat-to-bat contact, these same 3 hibernating colonies in western PA remained WNS-free for 1–2 years after colonies throughout the rest of the state were infected, suggesting that female migration patterns may influence the spread of WNS across the landscape.

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### 82 (E) Technical Session 4, Meeting Room 17, Sunday 8 June 2014

**Mallory E. Jones<sup>1,2</sup>**, Link E. Olson<sup>1</sup>

<sup>1</sup>Department of Mammalogy, University of Alaska Museum, Fairbanks, AK 99775 USA; <sup>2</sup>Department of Biology and Wildlife, University of Alaska Fairbanks, Fairbanks, AK 99775 USA

#### Northern Range Extension of Keen's Myotis and Other Bats in Alaska

Bat research in Alaska has lagged behind that in southern Canada and the contiguous United States due in large part to the relative inaccessibility of much of the state. The greatest diversity is found in the southeast temperate rainforest, which is known to support 6 species. These include, Keen's Myotis (*Myotis keenii*), which has 1 of the smallest geographic ranges of any North American bat, and the Yuma Myotis (*M. yumanensis*), which was only recently documented in extreme southeast Alaska. Recent and ongoing field surveys as well as re-examination of historical museum specimens has extended the known ranges of these and other bat species in the state, nearly doubling the latitudinal range of *M. keenii*. We also present the 1st evidence of bats seasonally migrating over mountain passes between the continental interior and coastal rainforest in Alaska. These and other findings highlight the need for continued field research at the northern distributional limits of North America's bats.

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### 83 Symposium III: The United States Biological Survey and North American Natural History, Great Halls D & E, Monday 9 June 2014

**Alfred L. Gardner**

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#### History of the Bureau of Biological Survey, U. S. Department of Agriculture

"The indefatigable chief of the division [C. Hart Merriam]...may be congratulated on having at last realized his hope of establishing in effect a Biological Survey of the United States." This statement appeared 114 years ago in the *The Auk* (vol. 7, p. 414, 1890), in reference to an 1889 biological survey of a 5,000 square mile region in northern Arizona conducted by the Department of Agriculture's Division of Economic Ornithology and Mammalogy. This unit, whose 1st day of business was 1 July 1885, as the Branch of Economic Ornithology (in the Division of Entomology) and renamed the Division of Economic Ornithology and Mammalogy in 1886, became the Division of Biological Survey in 1896 and the Bureau of Biological Survey in 1905. Transferred to the Department of the Interior in 1939 and absorbing the Wildlife Division of the National Park Service in February 1940, the Bureau of Biological Survey and the Bureau of Fisheries (from the United States Department of Commerce) were merged on 30 June 1940, to create the Fish and Wildlife Service. The Survey's original emphasis on research underwent major change in 1900 with the passage of the Lacey Act, followed by law-enforcement responsibilities, international treaty obligations, land management, control of injurious wildlife, wildlife restoration, food habits analysis, fur research, bird banding, and other functions further increased diversity within the agency.

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### 84 Symposium III: The United States Biological Survey and North American Natural History, Great Halls D & E, Monday 9 June 2014

**Keir B. Sterling**

Richmond, VA, USA

#### C. Hart Merriam, Pioneering Mammalogist

In the summer of 1872, 16-year-old naturalist C. Hart Merriam, a protégé of Smithsonian Secretary Spencer F. Baird, began his scientific career as expedition naturalist for the Hayden Survey in Wyoming. Following completion of his formal preparation at Yale and medical school in New York, he published several important regional bird and mammal studies. As chair of the American Ornithologists' Union's (AOU) Migration Committee in 1884, Merriam requested federal aid for an AOU migration study. Congress responded by establishing the position of Ornithologist in the Agriculture Department, to which Merriam was appointed in 1885. This was among the earliest instances of Congress underwriting scientific inquiry. In 1905, Merriam's office evolved into the Bureau of Biological Survey. Working within the context of his Life Zone theory of plant and animal distribution (superseded decades later by more advanced concepts), Merriam undertook numerous regional biological surveys in the western United States. The agency also published the influential *North American Fauna* series, including important monographic studies of mammalian genera and species. During Merriam's quarter century with the Survey, he and his small scientific staff helped establish the foundations of modern mammalogy.

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## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

**85 Symposium III: The United States Biological Survey and North American Natural History, Great Halls D & E, Monday 9 June 2014**

**David J. Schmidly**

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### **Vernon Bailey and the U. S. Biological Survey Federal Agents**

To realize his vision for the United States Biological Survey (USBS), C. Hart Merriam needed talented assistants for the field and museum related work. Part of his genius was his ability to attract a number of capable men and bring them into his organization. Among those, 3 (Vernon Bailey, A. K. Fisher, and T. S. Palmer) joined Merriam's staff early on and remained with the organization for more than 4 decades. Both Fisher and Palmer had formal college educations but Bailey's education was through an apprenticeship with Merriam. But it was Bailey who developed a close relationship with Merriam, marrying his sister and forging a life-long friendship. Merriam obviously had great confidence in Bailey because when he reorganized the Biological Survey into a Bureau in 1905, he placed Bailey in charge of investigations in geographic distribution, 1 of 3 major responsibilities of the Survey, the only 1 that Merriam had created, and the 1 that sustained most of Merriam's interest during his years as Survey Chief. After Merriam left the USBS, and its mission expanded beyond scientific interests, all 3 men adjusted their roles and continued to make enormous contributions to the agency. Other USBS employees of note to mammalogists included Wilfred H. Osgood, E. W. Nelson, E. A. Goldman, Hartley H. T. Jackson, and A. Brazier Howell. The USBS was clearly the primary influence on mammalogy outside of academia in the United States.

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**86 Symposium III: The United States Biological Survey and North American Natural History, Great Halls D & E, Monday 9 June 2014**

**Rodrigo A. Medellín<sup>1</sup>, Xavier López-Medellín<sup>2</sup>**

*<sup>1</sup>Instituto de Ecología, UNAM, Mexico; <sup>2</sup>Universidad Autónoma del Estado de Morelos, Mexico*

### **Two Lives and Their Influence: Nelson, Goldman, and a Universe of Mammals**

The borderlands between Mexico and the United States have a long and complicated history in many ways: biogeographical boundaries, wars, poignant migrant stories, brilliant biological discoveries, enhanced international cooperation, and much biological history. Two individuals have contributed more than most other characters to the understanding, knowledge, and documentation of this area and much of Mexico beyond the borderlands: Edward William Nelson and Edward Alphonso Goldman. Over 14 years at the turn of the 20th century, they carried out an impressive biological survey, with detailed field notes reflecting mammals, birds, and ecosystems they encountered. This all occurred in the context of the social turmoil that would turn into the Mexican revolution. They collected thousands of specimens, and described dozens of new taxa. Their influence goes well beyond mere specimen collection: Goldman contributed to the 1st-ever environmental treaty between Mexico and the USA: the Convention for the Preservation of Migratory Birds and Game Mammals was signed in Mexico City in 1936. One can only imagine the intertwining, friendship, and kinship that would develop between 2 men, 18 years of age apart, embarking in such an adventure and more. Their legacy lives on in both countries and beyond, where the seeds of the study of Mammalogy were sowed. What we see today as Mexican mammalogy clearly shows the fingerprints of these 2-of-a-kind, unparalleled individuals.

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**87 Symposium III: The United States Biological Survey and North American Natural History, Great Halls D & E, Monday 9 June 2014**

**Michael J. Robinson**

*Center for Biological Diversity, Silver City, NM 88062 USA*

### **The Predator Wars between the Biological Survey and American Society of Mammalogists**

Following C. Hart Merriam's 1910 retirement, the Biological Survey increasingly prioritized agricultural service over scientific research and conservation. Maddeningly, predators that preyed on livestock had survived private, local, and state bounties. In 1915, Congress 1st appropriated funds (\$125,000) for the Biological Survey to destroy "wolves, coyotes, and other animals injurious to agriculture and animal husbandry." A. K. Fisher's Division of Economic Investigations hired hundreds of hunters and paid their salaries through Federal appropriations and private, local- and state-donated funds, not only augmenting revenues but also building a potent political network and cementing the loyalties of the Biological Survey to its livestock industry patrons. With nobody objecting, the Biological Survey trapped and poisoned almost every wolf in the West by the mid-1920s then blamed coyotes for increasing depredations and poisoned them extensively along with nontarget animals such as skunks and badgers. Ungulate, rodent and even invertebrate irruptions followed decreases in predators, spurring the Biological Survey to kill more prairie dogs, ground squirrels, and porcupines. Commercial trappers, mammalogists, and animal lovers tried in vain to stop the poisoning. Fisher's replacement, Stanley P. Young, a trapper talented in administration and public relations, in the 1920s and 1930s fended off criticisms, disclaiming the Biological Survey's true actions and expanding

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

and institutionalizing its funding, leading to the broad-scale eradication of wolves, grizzly bears, jaguars, blackfooted ferrets, prairie dogs, and other wildlife.

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## 88 Technical Session 5, Great Halls D & E, Monday 9 June 2014

**J. Delton Hanson, Eric J. Rees**

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### Evaluation of NexGen Sequencing Technology for Mammalian Genomes, Part 2

Last year we examined the usefulness of, NexGen Sequencing and the Ion Proton system specifically for sequencing mammalian genomes. Since then the technologies have changed, opening new opportunities. We examined new chemistry (V3) on the Ion Proton system as well as new chemistry (2 x 300) on Illumina's MiSeq that gets longer reads. We will also provide a brief overview of other approaches that have used NexGen sequencing to examine mammalian biology.

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## 89 (E) Technical Session 5, Great Halls D & E, Monday 9 June 2014

**Jeremy E. Wilkinson<sup>1</sup>, Eric J. Rees<sup>1</sup>, Michelle L. Haynie<sup>2</sup>, J. Delton Hanson<sup>1</sup>**

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### Comparison of Two Approaches for Microsatellite Library Development Using the Illumina MiSeq Platform

Microsatellites are among the most widely used molecular markers for population genetic studies. However, the identification and development can be time consuming and costly with little amount of data produced. Microsatellite development is typically performed by Sanger sequencing and has also been done using NextGen platforms. NextGen methods include screening the entire genome or enrichment approaches that target known repetitive regions. Even though enrichment approaches are limited to known repetitive regions, their cost savings outweigh the benefits of whole genome approaches. The recent emergence of new Illumina MiSeq chemistry has significantly reduced the cost of reads while increasing ease of use. In this study, using *Onychomys* as a model, we compared the output of 2 enrichment methods for microsatellite discovery, inter-simple sequence repeat PCR (ISSR-PCR) and a multiplex DNA enrichment method, using the Illumina MiSeq platform.

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## 90 (E,\*\*,TA) Technical Session 5, Great Halls D & E, Monday 9 June 2014

**Emma K. Roberts<sup>1</sup>, Daniel M. Hardy<sup>2</sup>, Robert D. Bradley<sup>1,3</sup>**

*<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409 USA; <sup>2</sup>Graduate School of Biomedical Sciences, Texas Tech University Health Sciences Center, Lubbock, TX 79430 USA; <sup>3</sup>Natural Science Research Laboratory, Museum of Texas Tech University, Lubbock, TX 79409 USA*

### Is Zonadhesin a Useful Molecular Marker for Determining Ordinal Relationships among Mammalian Orders?

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 protein that is crucial in species specific fertilization. The mRNA for this protein spans more than 7 kb in most taxa with 3 domains that are directly related to 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 taxa and conserved in others. The VWD domain mRNA sequences (> 6kb) for 15 different orders of mammals, including 44 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, Artiodactyls, Perissodactyls, etc. each were recovered as monophyletic groups. However, some results were unusual, such as Afrosorocida grouping with Sirenia. Based on this study, baseline information suggests that variability among *Zan* sequences in mammals is phylogenetically informative. This research was supported by an ASM Grants-in-Aid of Research awarded to Emma K. Roberts in 2012.

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## 91 Technical Session 5, Great Halls D & E, Monday 9 June 2014

**Robert J. Baker<sup>1</sup>, Caleb D. Phillips<sup>1</sup>, Jeffery Wickliffe<sup>2</sup>, Faisal Anwarali Khan<sup>3</sup>, Sergey Gaschak<sup>4</sup>, Kateryna Makova<sup>5</sup>, Ben Dickens<sup>5,6</sup>**

*<sup>1</sup>Department of Biological Sciences and Museum, Texas Tech University, Lubbock, TX 79409 USA; <sup>2</sup>Department of Global Environmental Health Services, Tulane University, New Orleans, LA 70118 USA; <sup>3</sup>Department of Zoology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Kota Samarahan, Sarawak, 94300, Malaysia; <sup>4</sup>International Radioecology Laboratory, Kiev Region, Slavutych, Ukraine; <sup>5</sup>Department of Biology, Penn State University, Old Main, University Park, PA 16801 USA; <sup>6</sup>School of Science and Technology, Nottingham Trent University, Nottingham, United Kingdom*

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

### Multigenerational Exposure to the Chernobyl Environment in Bank Voles Alters the Mitochondrial Genome

Using the bank vole (*Myodes glareolus*) as a model system, we tested the hypothesis that 40 generations of exposure to the Chernobyl environment will not significantly alter the mitochondrial genome. We compared mitochondrial genomes from 131 individuals including populations from sites with radioactive contamination comparable to that present in Northern Ukraine before the 26 April 1986 meltdown to populations living in the most radioactive sites (Red Forest and Glyboke Lake) created by the meltdown. Using a variety of population genetic measures, we found multiple statistical differences in our comparisons of the populations from contaminated and uncontaminated localities. Therefore, we rejected the hypothesis of no significant genetic effect from 40 generations of exposure to Chernobyl radiation. Contaminated localities were found to be more diverse than uncontaminated localities, exhibiting greater numbers of haplotypes, polymorphic loci, and increased genetic diversity, and these differences were not attributable to sample size artifacts. The observed pattern of diversity is contrary to predictions of a source-sink demographic scenario and is consistent with low-dose radiation producing an accelerated mutation rate. This study is the 1st to demonstrate this phenomenon. However, bank voles from contaminated localities are not distinguishable from those collected in uncontaminated localities, compatible with the hypothesis that the cost of living in the most contaminated site does not have profound health effects.

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### 92 (E) Technical Session 5, Great Halls D & E, Monday 9 June 2014

**Roy N. Platt II**<sup>1,2,5</sup>, **Michael W. Vandeweghe**<sup>1</sup>, **Colin Kern**<sup>3</sup>, **Carl J. Schmidt**<sup>4</sup>, **Federico G. Hoffmann**<sup>1,2</sup>, **David A. Ray**<sup>1,2,5</sup>

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### Large Numbers of Putative miRNAs Originate from DNA Transposons and are Coincident with a Large Species Radiation in Bats

Vespertilionid bats experienced a rapid radiation around 36 million years ago that resulted in the 2nd most species rich mammalian family. Coincident with that radiation was a burst of DNA transposon activity that has continued in some species. Extensive and recent DNA transposon activity has not been seen in any other mammal. Deep sequencing of the small RNAs from *Eptesicus fuscus*, dog and horse revealed large numbers of putative microRNAs (p/miRNAs). While the origination rate of p/miRNAs is similar in all 3 taxa, 61.1% of species-specific p/miRNAs in *Eptesicus* are derived from transposable elements (TEs) compared to only 23.9% in dog and 16.5% in horse. The majority of TE-derived p/miRNAs are associated with retrotransposons in dog and horse. In *Eptesicus*, 58.7% of the TE-derived and 35.9% of the total p/miRNAs arose not from bat-specific DNA transposons. The DNA transposon expansion and introduction of novel p/miRNAs coincides with the diversification of Vespertilionidae. Furthermore, potential targets of the DNA transposon-derived p/miRNAs are identifiable and enriched for genes that are important for regulation of transcription. We propose that lineage specific DNA transposon activity lead to the rapid and repeated introduction of novel p/miRNAs. Some p/miRNAs are likely functional and may have influenced the diversification of Vespertilionidae. Our observations suggest a mechanism for introducing functional genomic variation via the expansion of DNA transposons.

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### 93 (ECT) Technical Session 5, Great Halls D & E, Monday 9 June 2014

**Jason L. Malaney**<sup>1,2</sup>, **Chris R. Feldman**<sup>2,3</sup>, **Mike Cox**<sup>4</sup>, **Peregrine L. Wolff**<sup>4</sup>, **Marjorie D. Matocq**<sup>1,2</sup>

<sup>1</sup>Department of Natural Resources and Environmental Science, University of Nevada, Reno, NV 89557 USA; <sup>2</sup>Program in Ecology, Evolution, and Conservation Biology, University of Nevada Reno, Reno, NV 89557 USA; <sup>3</sup>Department of Biology, University of Nevada, Reno, NV 89557 USA; <sup>4</sup>Nevada Department of Wildlife, 1100 Valley Rd., Reno, NV 89512 USA

### Translocated to the Fringe: Genetic and Niche Variation in Bighorn Sheep of the Great Basin and Northern Mojave Deserts

Conservation biologists use various approaches to augment imperiled populations to supplement genetic variation, conserve diversity, and restore ecological function. The bighorn sheep of North America (*Ovis canadensis*) provide a classic example of restoration biology, where management programs re-established extirpated populations via translocations. In the process, translocated individuals may have faced novel conditions, including the opportunity to interbreed with previously isolated and divergent populations. Our goal is to integrate genetic and ecological analyses to assess, retroactively, some of the evolutionary ramifications of translocation. We focus on the Great Basin and northern Mojave deserts where a high number of transplants have occurred. We quantified genetic variation using 16 microsatellite loci ( $n = 350$ ) and a mitochondrial locus ( $n = 91$ ) and explored niche variation using 26 ecological variables to test if repatriated populations occur in similar environmental conditions found in source areas. We documented hierarchical genetic and ecological variation among 3 groups that are concordant with taxonomy,

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

biogeographic expectations, and management units despite some admixture. Niche-based analyses revealed that clusters occupy different environments but translocated populations now occur in environments different from source ranges. This study highlights the importance of considering both genetic and ecological variation when implementing translocations that may help minimize the potential for hybridization and mitigate challenges of managing populations experiencing novel environments. More broadly, these results have implications for similar restoration programs including managed relocation.

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### 94 (ECT) Technical Session 5, Great Halls D & E, Monday 9 June 2014

**Michael R. Buchalski<sup>1</sup>, Walter M. Boyce<sup>2</sup>, Maria Cecilia T. Penedo<sup>3</sup>, T. Winston Vickers<sup>2</sup>, Daphne A. Gille<sup>4</sup>, Holly B. Ernest<sup>2</sup>**

<sup>1</sup>Wildlife and Ecology Unit, Veterinary Genetics Laboratory, University of California, Davis, CA 95616 USA; <sup>2</sup>Wildlife Health Center, University of California, Davis, CA 95616 USA; <sup>3</sup>Veterinary Genetics Laboratory, University of California, Davis, CA 95616 USA; <sup>4</sup>Department of Animal Science, University of California, Davis, CA 95616 USA

#### **Genetic Diversity and Gene Flow among Recovery Regions of the Federally Endangered Peninsular Bighorn Sheep (*Ovis canadensis nelsoni*)**

Peninsular bighorn sheep (*Ovis canadensis nelsoni*, PBS) represent a federally endangered population segment of desert bighorn sheep endemic to the Peninsular Ranges of southern California. The population segment is currently managed as a series of recovery regions approximating ewe group home ranges. We examined 39 microsatellite loci and a 515 base pair fragment of the mitochondrial DNA control region from PBS ( $n = 165$ ) sampled from 1992 to 2013 to assess genetic diversity and the extent of gene flow among selected recovery regions. Structure analysis clustered sheep into 2 distinct genetic groups (north versus south). Significant pairwise  $F_{ST}$  estimates (0.03 to 0.12) generally supported the presence of 2 genetic groups, with the possibility of additional substructure in the north. Mitochondrial DNA analyses revealed 5 distinct haplotypes and indicated a similar pattern of north versus south population structure. Considerable microsatellite diversity was found within both groups (mean  $H_O = 0.496$ ; allelic richness = 3.47;  $F_{IS} = 0.02$ ), comparable to accounts for desert bighorn sheep in other localities. We identified 1st-generation migrants of both sexes using geneClass2, but significantly lower assignment indices among rams suggested dispersal was male biased. Despite past declines, PBS has retained substantial genetic variation and gene flow among recovery regions. Future conservation efforts should focus on maintaining functional connectivity so the recovering population can expand into available habitat throughout the Peninsular Ranges.

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### 95 (E) Technical Session 5, Great Halls D & E, Monday 9 June 2014

**Matthew S. Leslie<sup>1,2</sup>, Frederick I. Archer<sup>2</sup>, William F. Perrin<sup>2</sup>, Phillip A. Morin<sup>2</sup>**

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#### **Using Next Generation Genetic Tools to Define Stock Boundaries for the Recovery of Significantly Depleted Pelagic Dolphins in the Eastern Pacific**

Over 6 million dolphins were killed in tuna nets in the eastern Pacific Ocean in the mid-20th century. Spinner (*Stenella longirostris*) and spotted dolphins (*S. attenuata*) show no signs of recovery. Determining population genetic structure is vital to setting meaningful mortality limits that ensure the recovery of these depleted stocks. Two endemic spinner dolphin subspecies - Central American and eastern spinners - and 1 endemic subspecies of coastal spotted dolphin were described based on morphology and behavior. A 3rd form of spinner dolphin, the whitebelly, is thought to be a transitional form between the eastern and pantropical subspecies. Molecular studies have failed to verify these subspecies due to a lack of statistical power. We collected mitochondrial genomes (mtDNA) and nuclear single nucleotide polymorphisms (SNPs) from 111 spinner and 89 spotted dolphins to test for genetic structure using DNA capture arrays and next-generation sequencing. MtDNA shows differences between whitebelly and both eastern and Central American spinners, but not between the latter 2 (accepted subspecies). SNP analyses show differences between all 3 forms. Structure was not detected between spotted dolphin subspecies in the mtDNA; SNP analyses are ongoing. Our results support current management boundaries for spinners, and suggest the need for additional data to determine the stocks of spotted dolphins. We are now collecting restriction site associated markers to test subspecies hypotheses in spotted dolphins.

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### 96 Technical Session 6, Meeting Room 16, Monday 9 June 2014

**Ana D. Davidson<sup>1,2</sup>, Kevin T. Shoemaker<sup>1</sup>, Ben Weinstein<sup>1</sup>, Gabriel C. Costa<sup>3</sup>, Volker C. Radeloff<sup>4</sup>, Carlo Rondinini<sup>5</sup>, Gerardo Ceballos<sup>6</sup>, Catherine H. Graham<sup>1</sup>**

<sup>1</sup>Department of Ecology and Evolution, Stony Brook University, New York 11794 USA; <sup>2</sup>Institute for Wildlife Studies, Arcata, CA 95521 USA; <sup>3</sup>Departamento de Ecologia, Universidade Federal do Rio Grande do Norte 59072, Brasil; <sup>4</sup>Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, Wisconsin 53706 USA; <sup>5</sup>Global



# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

*Mammal Assessment program, Department of Biology and Biotechnologies, Sapienza University of Rome, Roma 00185 Italy;* <sup>6</sup>*Universidad Nacional Autonoma de Mexico, Instituto de Ecologia, México D.F. 04510 México*

## **Geography of Global Mammal Extinction Risk**

Identifying which species are at greatest risk, what makes them vulnerable to extinction, and where they are distributed are central goals for biodiversity conservation. Here, we model extinction risk to fill in these information gaps and flag species that are especially vulnerable, based on their intrinsic (i.e., biological) traits and extrinsic environment (i.e., habitat and threats). We applied a predictive model and new geospatial and species' trait data to unravel the geography of global mammal extinction risk, and determine: 1) which species are at greatest risk; 2) why they are most at risk; and 3) where they occur globally. We found that about 10% of mammals that are not currently recognized as threatened under the International Union for Conservation of Nature and Natural Resources Red List are at risk of extinction. These species will be among the most vulnerable as human impacts expand. Each extinction driver exhibited critical thresholds and distinct ranges associated with high risk, and varied in their geographic contribution, providing guidance for conservation efforts across the globe. We found a suite of areas that have both high numbers of species at current and latent risk and are projected to experience rapid warming with climate change. Many of these regions are not currently recognized as hotspots of extinction risk for mammals, suggesting that risk in a warming world will look considerably different than it does now.

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## **97 Technical Session 6, Meeting Room 16, Monday 9 June 2014**

### **Michael J. Robinson**

*Center for Biological Diversity, Silver City, NM 88062 USA*

#### **Will Science or Politics Determine the Mexican Gray Wolf's Future?**

The U.S. Fish and Wildlife Service has botched reintroduction of the endangered Mexican gray wolf to the Blue Range Wolf Recovery Area in Arizona and New Mexico. The recovery area consists of 2 national forests totaling 4.4-million acres that could support an estimated 468 wolves. The 1996 environmental impact statement on reintroduction projected 102 wolves including 18 breeding pairs in the wild by 2005, but at last count just 83 wolves including only 5 breeding pairs survived. Far worse, the genetic heritage stemming from just 7 Mexican wolves captured decades ago and bred in captivity—the source for reintroduced wolves—has been squandered, with numerous genetically valuable wolves killed by the government or captured alive but not bred. The U.S. Fish and Wildlife Service has only released a single wolf from the captive breeding pool into the wild over the past 5 years, and removed that wolf 3 weeks later although he had not depredated. Inbreeding depression in the wild population is reducing litter sizes and lowering pup-survival rates. In response to litigation, the U.S. Fish and Wildlife Service is revising the reintroduction rule to facilitate a resumption of releases, and allow wolves to establish territories over a broader area. But its proposed rule would prevent wolves from occupying the Grand Canyon and southern Rocky Mountains ecosystems, needed for recovery, and broaden loopholes allowing wolf killing.

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## **98 Technical Session 6, Meeting Room 16, Monday 9 June 2014**

### **Michael J. Robinson**

*Center for Biological Diversity, Silver City, NM 88062 USA*

#### **Inadequate Recovery Planning for Northern Jaguars**

Paleontological remains show that the jaguar inhabited North America before colonizing South America. In historic times, jaguars were reported on the South Rim of the Grand Canyon, southern California mountains, along grassland rivers in northeastern New Mexico and the Texas panhandle, and in the forests of Louisiana, Kentucky, and North Carolina (among other locales). Jaguars disappeared from their U.S. ranges due to clearing of forests, draining of wetlands, and killing to protect livestock. The last female jaguar in the United States was shot in 1963 at 9,000 feet elevation on the Mogollon Plateau of Arizona, her stomach elk-filled. Despite jaguars' catholic use of habitat, modeling that suggests extensive extant jaguar habitat and prey on the Mogollon Plateau in Arizona and New Mexico, and a declining and semi-isolated jaguar population in northern Mexico that could benefit from connectivity with a future jaguar population in the southwestern USA, the U.S. Fish and Wildlife Service's recovery effort for this endangered mammal might permit delisting with few or no jaguars in the USA, and would only conserve arid, "sky island" habitats recently occupied by male jaguars emanating from Mexico, excluding the Mogollon Plateau. To help save jaguars in Sonora and to ensure representation in more of its evolutionary range, the Mogollon Plateau should be designated a jaguar recovery area along with the Sky Island Mountains near the United States–Mexico border.

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## **99 (ECT) Technical Session 6, Meeting Room 16, Monday 9 June 2014**

**Daniel Thornton<sup>1</sup>, Kathy Zeller<sup>2</sup>, Carlo Rondinini<sup>3</sup>, Luigi Boitani<sup>3</sup>, Kevin Crooks<sup>4</sup>, Chris Burdett<sup>4</sup>, Howard Quigley<sup>5</sup>**

<sup>1</sup>*School of Environment, Washington State University, Pullman, WA 99164 USA;* <sup>2</sup>*Department of Environmental Conservation, University of Massachusetts, Amherst, MA 01003 USA;* <sup>3</sup>*Department of Biology and Biotechnologies,*

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

*Sapienza University of Rome, Rome, Italy;*<sup>4</sup>*Department of Fish, Wildlife, and Conservation Biology, Colorado State University, Fort Collins, CO 80523 USA;*<sup>5</sup>*Panthera, New York, NY 10018 USA*

## **Evaluating the Umbrella Value of a Range-wide Conservation Network**

The umbrella species concept, whereby conservation strategies designed to protect 1 species will incidentally maintain co-occurring species, has a long history in ecology and conservation biology. Empirical evaluations of this concept have found highly variable results, for both the utility of the umbrella concept, and the characteristics of an “ideal” umbrella species. However, most previous studies were limited in spatial scale (e.g., comparing 1 or a few reserves where an umbrella species was present to where it was absent). Recently developed range-wide conservation strategies and global habitat suitability models offer the opportunity to evaluate the umbrella concept across much larger spatial scales. We evaluated the umbrella value of Panthera’s Jaguar Corridor Initiative, which consists of a series of reserves linked by corridors that extends across the entire known range of jaguars (*Panthera onca*). We overlapped these corridors and reserves with habitat suitability and fragmentation models for over 1,500 Neotropical mammals. Our results reveal that jaguar reserves and corridors function as effective umbrellas for a large number of co-occurring species, although this result is variable across major mammalian families. This finding suggests that range-wide conservation strategies for large carnivores, which take advantage of the charismatic nature of these species for funding and implementation, may have additional benefits by acting as an umbrella for the conservation of numerous co-occurring species.

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## **100 (ECT) Technical Session 6, Meeting Room 16, Monday 9 June 2014**

**Maria Sagot<sup>1</sup>, Gloriana Chaverri<sup>2</sup>**

*<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409 USA; <sup>2</sup>Universidad de Costa Rica, Golfito 60701, Costa Rica*

### **Roost Specialization Increases Extinction Risk in Bats**

Ecological specialization is defined as the use of restricted range of resources or habitats. Understanding specialization is necessary for conservation purposes because specialist species are particularly vulnerable to human activities; if their resources are depleted or lost, specialists may be unable to exploit alternative food items or habitats and therefore suffer population losses. Here, we provide evidence that roost specialization is an important correlate of extinction risk in bats. We test the hypothesis that species that use fewer roost types are at greater risk of extinction, as defined by the International Union for Conservation of Nature and Natural Resources Red List of Threatened Species. This is the 1st study that investigates the relationship between resource specialization and extinction risk in bats worldwide, accounting for phylogenetic nonindependence. We found a significant correlation between the Red List category and the number of roost types used. Species using fewer roost types had a higher risk of extinction. Twenty percent of the species using natural roosts exclusively, showed to be Critically Endangered, Endangered or Vulnerable. On the other hand, the only 2 species that use human-made roosts exclusively are categorized as Least Concern. Furthermore, only 5% of the species using both human-modified and natural roosts are Endangered or Vulnerable. Our study suggests that roost loss, particularly for species that rely on a single roost type, is in fact a major cause of extinction risk.

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## **101 (E,\*\*) Technical Session 6, Meeting Room 16, Monday 9 June 2014**

**Kendra L. Phelps, Tigga Kingston**

*Department of Biological Sciences, Texas Tech University, Lubbock, TX 79424 USA*

### **Anthropogenic and Environmental Factors Influencing Cave Bat Diversity in the Philippines: Implications for Conservation Agendas**

Caves are critical roosting sites for many bat species, housing some of the largest and most diverse aggregations of bat species in the world. However, cave-dependent bat populations are declining globally, with human disturbance at caves identified as the leading cause of these declines. In the Philippines, caves are protected under the National Cave Act, yet implementation of the Act is hindered by a lack of information to identify caves to protect. Thus, to prioritize caves to conserve cave bat assemblages, it is vital to identify factors that influence bat diversity in caves. No studies to date have explicitly quantified factors, both anthropogenic and environmental, that may shape assemblages of cave-dependent bats in the Philippines. Anthropogenic (visitation rate, hunting intensity, mining, etc.) and environmental (cave dimensions, microclimate, roost area) factors were assessed at 60 caves, and compared with species diversity and composition of bat assemblages documented over 2 consecutive nights on Bohol Island in the central Philippines. Between July 2011 and June 2013, we captured 7,419 individuals comprising 24 bat species. We used nonmetric multidimensional scaling to elucidate the primary drivers of cave bat diversity and composition. Results will be used to evaluate the significance of individual caves for maintaining viable populations of cave-dependent bats, a priority under the National Cave Act. This research was supported by ASM Grants-in-Aid of Research to Kendra L. Phelps in 2010 and 2012.

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

102 (E,\*\*,TA) Technical Session 6, Meeting Room 16, Monday 9 June 2014

**Emma P. Gomez-Ruiz, Thomas E. Lacher, Jr.**

*Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, TX 77843 USA*

## **Modeling the Nectar Corridor Followed by the Endangered Bat *Leptonycteris nivalis* in Mexico and USA**

The Mexican long-nosed bat (*Leptonycteris nivalis*) is a nectarivorous bat with a distribution from central Mexico to the southwestern United States. Currently it is listed as endangered in both countries and globally by the International Union for Conservation of Nature and Natural Resources (IUCN), due to a 50% reduction in its population size in the last 10 years. Evidence suggests that mainly pregnant females migrate north at the beginning of spring each year, following the blooms of paniculate *Agave*. The objective of this study was to model the potential distribution of this "nectar corridor". We used occurrence data of the paniculate *Agave* distributed within the known northern distribution of the bat, and computer algorithms to predict the geographic distribution of the corridor. Findings suggest that areas with a higher number of agave species coincide with the occurrence data of the bat and in particular the location of known maternity caves. We are using the model results to target areas for field assessments to determine the status of foraging and roosting sites used by *L. nivalis*. This information is fundamental to direct conservation actions to priority sites for *L. nivalis* and maintain the pollination service that they provide to key plants in arid and semiarid ecosystems. This research was supported by a Latin American Student Field Research Award awarded to Emma P. Gomez-Ruiz in 2013.

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103 (E,TA) Technical Session 6, Meeting Room 16, Monday 9 June 2014

**Hsiang Ling Chen, John L. Koprowski**

*School of Natural Resources and the Environment, University of Arizona, Tucson, AZ 85721 USA*

## **Barrier Effects of Roads for an Endangered Forest Obligate: Gap, Edge, and Traffic Avoidance**

Anthropogenic habitat fragmentation and destruction caused by infrastructure development of roads and bridges are recognized as major threats to biodiversity. Roads and traffic can act as barriers by restricting movement of animals, especially for small-bodied forest obligates. In this study, we examined barrier effects of roads and traffic on space use of an endangered, endemic forest obligate, the Mount Graham red squirrel (*Tamiasciurus hudsonicus grahamensis*; MGRS). To identify effects of traffic volume, edge, and gap avoidance, we used generalized linear mixed models to compare probability of MGRS home ranges that cross linear features between random lines in forests, road edges, lines with low to high degree of canopy cover, and road sections with varied traffic volume. Roads significantly inhibited MGRS movements. Compared to random lines in forests, MGRS were 80% less likely to include roads in their core area of home ranges, and 59% less likely to cross roads. Increasing traffic volume did not decrease probability of road crossing. Degree of canopy cover was positively correlated with probability of crossing. Increasing road width as well as road clearance (distance between forest boundaries) decreased probability of crossing. Our results demonstrate that even small roads with low traffic volume are barriers for small mammals such as endangered red squirrels and suggest that gap avoidance plays an important role in road avoidance of forest dependent species.

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104 (E,TA) Technical Session 7, Meeting Room 17, Monday 9 June 2014

**Han Li, Kenneth T. Wilkins**

*Department of Biology, Baylor University, Waco, TX 76798 USA*

## **Responses of Urban Bats to Various Levels of Nighttime Illumination**

Many insects are attracted by artificial nighttime illumination, forming a highly concentrated food source for their predators under city lights. Theoretically, insectivorous bats may follow prey and utilize urban lights as foraging grounds. However, only limited research has attempted to demonstrate how insect communities and bat activity respond to variation in lighting conditions. Whether level of bat activity under the light is mainly related to concentrations of insect prey is still not clear. Between September 2011 and October 2012, we conducted an experimental survey to record bat acoustic activity and to collect insects at a series of locations with levels of lighting intensity within a relatively small, homogenous area (Baylor University campus, Waco, Texas). Overall we found that the number of bat passes (all species combined) was not different at sites with different levels of illumination. But the proportion of foraging calls was always higher at sites with higher light intensity. Insect biomass was greater at brighter sites except during the winter. This suggested that bats responded to prey availability, foraging more where prey was more abundant. This foraging pattern lasted all year around even though during the winter prey availability was not greater under stronger illumination. The proportion of foraging calls could be predicted by insect biomass for Mexican free-tailed bats, red bats, and silver-haired bats.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 105 Technical Session 7, Meeting Room 17, Monday 9 June 2014

**Jorge F. S. Menezes<sup>1,2</sup>, Guilherme M. Mourão<sup>2</sup>, Burt Kotler<sup>3</sup>**

<sup>1</sup>Instituto de Biologia, Universidade Federal do Mato Grosso do Sul, Campo Grande, Mato Grosso do Sul 79070-900, Brazil; <sup>2</sup>Empresa Brasileira de Pecuária e Agricultura - Corumbá, Mato Grosso do Sul- Brasil – ZIP:79320-900; <sup>3</sup>Mitrani Department of Desert Ecology, Jacob Blaustein Institute for Desert Research, BGU, Midreshet Ben-Gurion 84990, Israel

### **Predation Risk and Cover from Bushes: Agoutis, Like Small Rodents, Use Bushes as Protection, While Other Medium-sized Rodents See Bushes as Dangerous**

Avoidance of open habitats as anti-predator behavior has been well documented in rodents. However, few studies have addressed predation risk in medium-sized rodents such as maras, porcupines, and agoutis (*Dasyprocta*), and none were conducted in the Neotropics. Studying medium sized mammals may greatly contribute to theoretical developments. Meta-analysis studies have shown that body mass increases the number of predators; it also makes animals more conspicuous. On the other hand, larger animals are faster and have fewer predators in certain environments. Given that contrasting evidence, we tested whether predation risk, as perceived by agoutis, increased with distance to caraguatá (a thorny bromeliad) bushes. To do so, we deployed 30 trays each with 20.5 g of peanuts mixed in 200 mL of sand. These trays were grouped in 5 by 6 grids, with stations separated by 5 m. We quantified agouti foraging using the amount of peanuts left after a night, also known as giving-up densities (GUDs). Assuming it is correlated with predation risk, we regressed GUDs with distance to caraguatá. As expected, we found that GUDs increased with distance to caraguatá ( $t_{22} = -0.443$ ,  $P = 0.662$ ). Other studies with medium-sized mammals, albeit not testing the same question directly, suggested that maras and capybaras have increased risk near bushes. This indicates that medium-sized rodents fall in between small-sized rodent and artiodactyls, the 1st using shrubs as protection while the latter rely on outrunning its predators.

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## 106 (E,TA) Technical Session 7, Meeting Room 17, Monday 9 June 2014

**M. M. Crowell<sup>1</sup>, Meghan J. Camp<sup>1</sup>, Lisa A. Shipley<sup>1</sup>, Janet L. Rachlow<sup>2</sup>, Jennifer S. Forbey<sup>3</sup>**

<sup>1</sup>School of the Environment, Washington State University, Pullman, WA 99164 USA; <sup>2</sup>Department of Fish and Wildlife Sciences, University of Idaho, Moscow, ID 83844 USA; <sup>3</sup>Department of Biological Sciences, Boise State University, Boise, ID 83725 USA

### **Perceived Risk of Predation by a Specialist and Generalist Herbivore: Behavioral Responses to Concealment and Distance from a Refuge**

Security cover is critical for the survival of small prey mammals, like pygmy (*Brachylagus idahoensis*) and cottontail (*Sylvilagus nuttallii*) rabbits. To better understand the perceived value of security cover to rabbits, we measured their relative intake in food patches in relation to the amount and arrangement of concealment cover and distance from burrow systems (refuge). We conducted a series of double-choice experiments with captive rabbits in which they were given a choice of 2 foraging patches that varied in: 1) percentage of concealment cover (0–100%); 2) arrangement of concealment cover (i.e., random, aerial, or horizontal); and 3) distance from a refuge (1.5–8.5 m). We then varied both concealment and distance from a refuge to determine the marginal rate of substitution between each measure. Both rabbit species preferred patches with  $\geq 75\%$  cover and patches closer to a refuge. As concealment cover at the patches increased, rabbits consumed a greater proportion of their diet further from the refuge. The smaller pygmy rabbits preferred horizontal to aerial cover, whereas the larger cottontails preferred aerial to horizontal cover. Our results demonstrated that rabbits responded in a complex way to the interaction between the amount and arrangement of security cover. This study provides a functional link between properties of cover and habitat selection that facilitates a biologically relevant means for evaluating effects of habitat change and management.

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## 107 (E,\*\*) Technical Session 7, Meeting Room 17, Monday 9 June 2014

**Sarah A. Smiley<sup>1</sup>, Terence M. Farrell<sup>2</sup>, H. Lisle Gibbs<sup>1</sup>**

<sup>1</sup>Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, OH 43210 USA; <sup>2</sup>Department of Biology, Stetson University, DeLand, FL 32723 USA

### **Perceived Risk in a Dangerous Environment: Response of Foraging Cotton Mice (*Peromyscus gossypinus*) to Pygmy Rattlesnakes (*Sistrurus miliarius*)**

We investigated the behavioral response of cotton mice (*Peromyscus gossypinus*) to presence of pigmy rattlesnakes (*Sistrurus miliarius*) in experimental foraging trials. Trials were conducted in seminatural enclosures in the winters of 2012 and 2013. Twenty-eight mice were individually placed in enclosures for a 5-night period (a trial). Each trial consisted of 1 night acclimation, 2 nights with exposure to a caged rattlesnake, and 2 nights without rattlesnake presence. The addition of snakes to field enclosures was performed randomly in a balanced design. Additionally, we investigated whether mice response to predators depended on the complexity of the environment; one-half of the enclosures had a higher degree of structural complexity. In all enclosures, mice could forage in trays of millet seed mixed with sand at high and low heights. The perceived risk response of mice to snake presence was measured by

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

examining the amount of seed eaten each night of the trial. Preliminary analyses suggest that, on average, cotton mice consume more seeds in snake absence than in snake presence, but this result is not significant. Mice prefer foraging at ground level when compared to elevated trays. Higher order interactions suggest that the presence of a sit-and-wait predator may have a larger impact on foraging behavior in novel environments than in familiar ones. This research was supported by an ASM Grants-in-Aid of Research awarded to Sarah Smiley in 2012.

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### 108 (E) Technical Session 7, Meeting Room 17, Monday 9 June 2014

Paula L. Perrig<sup>1</sup>, Emiliano Donadio<sup>2</sup>, Arthur D. Middleton<sup>3</sup>, Jonathan N. Pauli<sup>1</sup>

<sup>1</sup>Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, Madison, WI 53706 USA; <sup>2</sup>INIBIOMA-CONICET, National University of Comahue, Junin de los Andes, Neuquén 8371 Argentina; <sup>3</sup>Yale University of Forestry & Environmental Studies, New Haven, CT 06511 USA

#### Puma-camelid Predator-prey Relationship as a Mechanism of Food Provisioning to Andean Condors

Apex predators can have strong positive effects on scavengers by increasing both the spatial and temporal availability of carrion. To explore the importance of the trophic relationship between pumas (*Puma concolor*) and its native ungulate prey, vicuñas (*Vicugna vicugna*) and guanacos (*Lama guanicoe*), in food provisioning for Andean condors (*Vultur gryphus*) within a functionally intact ecosystem, we evaluated the cause of mortality for camelid carcasses, quantified carcass-use by condors and estimated the reliance of condors on native food items at San Guillermo National Park, Argentina. During January–July, 2013, we conducted field necropsies and then monitored 45 fresh camelid carcasses. Eighty-nine percent of these showed signs of puma predation and 98% were scavenged, at least 45% by condors. Additionally, from the 183 condor pellets that were inspected for the identification of prey remains, we found that camelids represented 88% of the prey items. Our preliminary isotopic analyses also revealed that the majority of condor diet is obtained from camelid carcasses. Our results suggest that functional linkages between these 3 species and trophic levels are tight, and highlight the importance of conserving communities of interacting species for the long-term maintenance of biodiversity.

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### 109 (E,TA) Technical Session 7, Meeting Room 17, Monday 9 June 2014

Nicholas L. Smith<sup>1</sup>, Seth D. Newsome<sup>1</sup>, Brian L. Cypher<sup>2</sup>, Katherine Ralls<sup>3</sup>, Timothy J. Coonan<sup>4</sup>, Angela Guglielmino<sup>4</sup>

<sup>1</sup>Biology Department, University of New Mexico, MSC03-2020, Albuquerque, NM 87131 USA; <sup>2</sup>Endangered Species Recovery Program, California State University Stanislaus, P.O. Box 9622, Bakersfield, CA 93389 USA; <sup>3</sup>Smithsonian Conservation Biology Institute, National Zoological Park, Washington, D.C. 20008 USA; <sup>4</sup>National Park Service, Channel Islands National Park, 1901 Spinnaker Drive, Ventura, CA 93001 USA

#### Habitat Specific Dietary Preferences of San Miguel Island Foxes

The endemic San Miguel Island (SMI) fox (*Urocyon littoralis littoralis*) was removed from its habitat in 1999 due to near extinction population numbers, and was released back into the wild in 2005. The most recent assessment of population size suggests SMI foxes are at or near carrying capacity. In this study, we quantified SMI fox habitat composition and associated diet preferences through a variety of methods using data collected from 2009–2013, a period of continuous island-fox population growth where local habitat changes and intraspecific competition may have led to habitat-specific diet specialization. Habitat differences were quantified by both above-ground vegetation volumes, and ground-cover surveys in 3 different habitat types where fox densities are quantified via mark-recapture analysis. The 3 habitats types recorded were grassland, lupine shrubland, and an intermediate habitat ranging across grassland to lupine–shrubland gradient. Fox dietary preferences were quantified via scat analysis and stable isotope analysis of fox vibrissae and potential prey items. Results show differences in above-ground shrub species' densities and volumes among habitats; ground cover also significantly varies among habitats. Island fox diet preferences vary among habitats supported by scat analysis and stable isotope analysis. Local population densities of SMI foxes also vary among habitats. Results provide evidence that island foxes are generalist consumers, but prefer deer mice (*Peromyscus maniculatus*), Coleoptera, and Orthoptera when locally available.

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### 110 (E,\*\*,TA) Technical Session 7, Meeting Room 17, Monday 9 June 2014

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#### Black Bear Use of Human-derived Foods in Northern Wisconsin

As long-lived opportunistic omnivores, American black bears (*Ursus americanus*) exhibit great plasticity in their diet and habitat selection, and can become quickly habituated to human resources. How their reliance on such novel resources affects individual and population dynamics remains largely unknown. In Wisconsin, most harvested black bears are hunted by use of baiting. Because baits are deployed before and during the hunting season, such calorically-rich and novel food items could be widely available throughout summer and fall. To quantify the relative

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

importance of these baits to black bears, we are using stable isotope analyses of tissues collected from hunter-harvested bears. We collected hair and blood from harvested bears at registration stations in north-central Wisconsin ( $n = 189$ ), and sampled representative diet items in the area. Using isotopic mixing models parameterized with the potential diet items, we estimated proportional contributions of broad dietary groups. Male and adult black bears are, on average, enriched in both  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$ , indicating a greater consumption of both bear bait and animal matter. Hair (summer-early fall diet) was also enriched in  $\delta^{13}\text{C}$  compared to blood (fall diet), suggesting bait consumption by bears did not increase during the fall hunting season. Understanding these patterns of age and sex class resource use will have important implications for long-term management. This research was supported by an ASM Grants-in-Aid of Research awarded to Rebecca Kirby in 2013.

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### 111 (E) Technical Session 7, Meeting Room 17, Monday 9 June 2014

Wynne E. Moss<sup>1</sup>, Mathew Alldredge<sup>2</sup>, Jonathan N. Pauli<sup>1</sup>

<sup>1</sup>Department of Forest & Wildlife Ecology, University of Wisconsin-Madison, Madison, WI 53706 USA; <sup>2</sup>Colorado Parks & Wildlife, Fort Collins, CO 80526 USA

#### Dietary Shifts of Mountain Lions (*Puma concolor*) in Response to Urbanization

Mountain lions (*Puma concolor*) are 1 of the most widely distributed mammals in North America and an ecologically important top predator. Once extirpated from much of their distributional range, mountain lion populations are recovering in some areas of North America and, as both human and mountain lion populations expand, the ecology and behavior of this species is changing. Though mountain lions are increasingly found within urban areas, it is not known whether these populations are viable, nor what behavioral adaptations might enable population persistence. We examined the foraging ecology of mountain lions in both near-urban and wildland habitats of Colorado. Through use of stable isotope analyses, we found that near-urban mountain lions exhibited greater plasticity in their foraging strategy compared to their wildland counterparts. Primary prey, or native ungulate species, comprised nearly all of the biomass ingested by wildland individuals (95% CI: 93-100%), whereas near-urban mountain lions relied less upon primary prey (95% CI: 62-78%), and acquired about one-fourth of their diet from human-associated prey, like synanthropic mesocarnivores and domesticated animals. Notably, individuals that used urban areas more specialized less upon primary prey ( $R^2 = 0.21$ ;  $p = 0.006$ ). Despite a greater use of human-associated prey items, these “urban opportunists” did not experience an increased risk of mortality, suggesting such a strategy may be contributing to mountain lion persistence in these highly developed and novel landscapes.

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### 112 Symposium IV: Museum Resources in Undergraduate Education, Great Halls D & E, Monday 9 June 2014

Eileen A. Lacey

Museum of Vertebrate Zoology, University of California, Berkeley, CA 94720-3140 USA

#### AIMING UP: Museum Resources in Undergraduate Education

Natural history collections represent tremendous investments in scientific infrastructure by numerous researchers, institutions, and funding agencies. ASM has a long tradition of supporting such collections. Although natural history collections have been central to research and graduate student training in mammalogy and related disciplines, they have been comparatively underutilized in undergraduate instruction in biology. AIM-UP! is an NSF-funded Research Coordinating Network dedicated to promoting the use of natural history collections data in undergraduate education. To launch this symposium, I will briefly outline the need for fundamental changes to undergraduate biology education described in documents such as Vision and Change (AAAS, 2011) and Engage to Excel (PCAST, 2012).

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### 113 Symposium IV: Museum Resources in Undergraduate Education, Great Halls D & E, Monday 9 June 2014

Joseph A. Cook

Museum of Southwestern Biology and Biology Department, University of New Mexico, Albuquerque, NM 87131 USA

#### Advancing the Integration of Museums into Undergraduate Education

AIM-UP! is a NSF-sponsored Research Coordinating Network that is exploring and developing new educational opportunities related to further integrating museum collections and associated data into undergraduate education. Natural history collections are huge research assets for mammalogy and also provide critical material for educators. New digital resources, freely available online, provide an opportunity to transform curricula to include more authentic and inquiry-driven educational experiences. Collections are especially well suited for introducing web-based discovery and for teaching fundamental concepts related to complexity, spatial and temporal scaling, integration of biotic and abiotic perspectives, and integrating from molecules to organisms to ecosystems. By incorporating natural history specimens and their associated data into undergraduate curricula, educators can promote participatory learning and foster understanding of essential interactions between mammals and their environments.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 114 Symposium IV: Museum Resources in Undergraduate Education, Great Halls D & E, Monday 9 June 2014

**Kayce C. Bell**

*Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM 87131 USA*

### **Engaging Biology Students Through Digital Data**

Increasingly, large web-based databases for genomes, environmental attributes, and biodiversity data are the basis for comparative scientific investigations. These databases provide an unprecedented opportunity for biology education to harness the vast amounts of abiotic and biodiversity data to engage in experiential learning. Accessibility, although it still needs some improvement, allows undergraduate students to investigate original questions of both local and global significance. Museum specimens are critical to tying these databases together and museum databases make the specimen data, and often media, available even in institutions that do not house local collections. Currently, over 4.5 million mammal specimen records are available on-line. These records allow students to explore occurrences through space and time and incorporate other types of data to engage in active learning. As undergraduate education works to incorporate more inquiry-based learning activities, museum and other digital databases provide a wealth of resources that can be utilized to enhance understanding of multiple biological disciplines.

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## 115 Symposium IV: Museum Resources in Undergraduate Education, Great Halls D & E, Monday 9 June 2014

**Lois F. Alexander**

*Department of Biological Sciences, College of Southern Nevada, Henderson, NV 89002 USA*

### **AIM-UP! Educational Modules in Undergraduate Classrooms**

Most undergraduate institutions do not have museums or collections. Members of AIM-UP! have been developing educational modules that incorporate museum data into a diverse array of undergraduate activities. These activities are structured to give the student an introduction to the vast resources that are available to them without requiring a physical visit to an institution that maintains a collection. The modules are used to demonstrate the critical role that museums serve as repositories for natural history data and expose some of the diverse possibilities, value, and accessibility of these resources. Some of these educational modules are presented along with a discussion of a few of the responses from undergraduate students (both biology major and non-major students) that have used these resources. These archives have been the basis for renowned research and graduate training programs, but generally have been less integrated into undergraduate biology education. By utilizing natural history collections in undergraduate education, future generations will begin to see the tremendous value of natural history collections and preserve and contribute to them far into the future.

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## 116 Symposium IV: Museum Resources in Undergraduate Education, Great Halls D & E, Monday 9 June 2014

**Enrique P. Lessa**

*Departamento de Ecología y Evolución, Facultad de Ciencias, Universidad de la República, Montevideo 11400 Uruguay*

### **Learning about Phylogenetics using Collections and Public Databases**

I present a module on phylogenetics that has been developed as part of an undergraduate course on evolution. Small groups of students choose 1 of a few problems presented to them, and work through the semester to collectively produce a term paper involving: a review of background information on the taxa and historical ideas about the problem; hypotheses to be tested; phylogenetic expectations under the hypotheses; sampling design (taxa, DNA sequence data), results, and discussion. All the resources necessary for these projects are available through internet access to public databases. Remote access to museum vouchers is possible through digital imaging but is currently limited. In part, this can be substituted by use of local teaching collections and alternative teaching resources. Future directions include: a) greater emphasis on cross-references between sequence data and museum voucher specimens (allowing use of associated data); and b) increased use of genomic data.

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## 117 Symposium IV: Museum Resources in Undergraduate Education, Great Halls D & E, Monday 9 June 2014

**Corey Welch**

*Biology Scholars Program, Department of Integrative Biology, University of California, Berkeley, Berkeley, CA 94720 USA*

### **Using Museum Specimens for Engaging Students from Underrepresented Groups**

Broadening access and promoting diversity in science remains a substantive challenge across STEM fields, but important progress has been made in how to best attract and retain underrepresented populations (1st generation, economically disadvantaged, and/or minority) in the biological sciences. This talk will address some of the traditional barriers that limit underrepresented students from succeeding in the biological sciences, in general, and museum specimen-based research, in particular. The 2nd part of the talk will describe on-going research on how to engage

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

these students in STEM fields and how these approaches can be adapted to museums and undergraduate education. Specific examples will address the strengths of using place-based exercises or labs (i.e., those specifically designed to tackle local environmental or public health issues) to engage students from underrepresented groups.

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### 118 (E,\*\*,TA) Technical Session 8, Great Halls D & E, Monday 9 June 2014

**Adam W. Ferguson<sup>1</sup>, Richard E. Strauss<sup>1</sup>, A. Townsend Peterson<sup>2</sup>, Robert C. Dowler<sup>3</sup>**

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409 USA; <sup>2</sup>Department of Ecology & Evolutionary Biology, The University of Kansas, Lawrence, KS 66045 USA; <sup>3</sup>Department of Biology, Angelo State University, San Angelo, TX 76909 USA

#### **Skunks at the Crossroads: Assessing the Interplay between Environmental, Morphological, and Genetic Variation in the American Hog-nosed Skunk**

Understanding how variation is distributed within and among populations and across geographic space can provide insight into the evolutionary history of an organism. We set out to test multiple hypotheses (i.e., stochastic events, environmental variation, and biogeographic history) as explanations for genetic and morphological variation in the American hog-nosed skunk, *Conepatus leuconotus*. Genetic variation based on mitochondrial sequence data for the ND5 and D-loop regions from 153 individuals indicated a minimal amount of genetic structure for *C. leuconotus*, with only 3 weakly supported subdivisions within the mtDNA lineage and 13 unique haplotypes. Morphological variation of the area of the dorsal white stripe/body length ('Whiteness Index'; WI) using digital photographs of over 300 museum specimens indicated that there is a significant relationship between WI values and environmental variation across the species range. Results for environmental variation through time (i.e., biogeographic hypotheses) based on Paleoecological Niche Models indicated the presence of 4 potential Pleistocene refugia that could have shaped the evolutionary history of *C. leuconotus*. Preliminary analyses indicate that phenotypic and genotypic variations appear not to have been driven by biogeographic history or stochastic processes, although there does appear to be a relationship between modern environmental conditions and morphological variation. This research was supported by an ASM Grants-In-Aid of Research and the Elizabeth Horner Award awarded to Adam W. Ferguson in 2011.

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### 119 (E) Technical Session 8, Great Halls D & E, Monday 9 June 2014

**Allison Marcella Loveless, Monica Papes**

Department of Zoology, Oklahoma State University, Stillwater, OK 74078 USA

#### **Bobcats across their Geographic Range: Combining Ecological Niche Modeling and Morphology to Assess the Population Genetic Structure of *Lynx rufus***

Despite a broad distribution, general habitat requirements, and large dispersal potentials, the bobcat (*Lynx rufus*) exhibits a distinct genetic segregation that longitudinally transects the central United States with limited population overlap. In order to understand the evolution and maintenance of this population structure, we must use an integrative approach that incorporates genetic, morphological, and environmental aspects in a historical and contemporary framework. My research aims to determine: 1) if the climate of the Last Glacial Maximum (LGM) isolated bobcats into refugia that expanded post glaciation and 2) if strong lineage delineation is manifested in the cranial morphology of the bobcat in addition to geographic variability across their range. Ecological niche models (ENM) were created using bioclimatic parameters and have revealed a northward expansion of occupancy following the recession of the LGM, yet the models were unable to limit the range of the disparate populations to their known contemporary geographic distributions or uncover locations of refugia. Geometric morphometric methods were used to evaluate variations in the cranium and mandible. These shape analyses have revealed significant variations in the shape in association with geography and genetic identity. By using ENMs to simulate the contemporary and LGM geographic distributions, and shape analyses to quantify local adaptations, we can begin to reveal what causes and maintains the genetic structure of a wide-ranging, generalist species, in the dynamic climate of our planet.

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### 120 Technical Session 8, Great Halls D & E, Monday 9 June 2014

**Marjorie D. Matocq<sup>1</sup>, Peter J. Murphy<sup>1</sup>, Lora A. Richards<sup>2</sup>, Christopher S. Jeffrey<sup>3</sup>**

<sup>1</sup>Department of Natural Resources and Environmental Science; Program in Ecology, Evolution and Conservation Biology, University of Nevada, Reno, NV 89557 USA; <sup>2</sup>Department of Biology, University of Nevada, Reno, NV 89557 USA; <sup>3</sup>Department of Chemistry, University of Nevada, Reno, NV 89557 USA

#### **Diet Specialization across a Woodrat Hybrid Zone**

Hybrid zones set across sharp ecotones provide an unparalleled opportunity to identify genotype-phenotype-environment relationships and the underlying mechanisms that contribute to adaptive divergence and perhaps speciation. The distributions of *Neotoma lepida* and *N. bryanti* meet at a sharp ecological boundary in southern California. Although the species hybridize at this location, they exhibit strong habitat segregation with *N. lepida* occupying the xeric Mojave scrub flatlands and *N. bryanti* being restricted to the relatively mesic, boulder strewn slopes. The 2 habitats are characterized by distinct vegetation communities, so we sought to characterize the diets of



## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

the 2 species where they meet. We used Illumina sequencing of the trnL gene to identify diet plants from fecal pellets collected at woodrat houses. The diets of both species are dominated by single, but distinct plants, each comprising 59% and 62% of each diet, respectively. Even including the supplemental plants used by each taxon, the species maintain highly distinct diets with a Bray-Curtis dissimilarity of 0.86. Further, the primary food plants used by each taxon are dominated by distinct toxic compounds that likely require different metabolic processing. Because of the potentially substantive metabolic challenge that would be experienced by individuals switching habitats and having to eat an alternate diet, we suggest that the striking habitat segregation and minimal hybridization across this site are at least partly the result of diet specialization.

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### 121 (E) UNDERGRADUATE STUDENT RESEARCH AWARD, Technical Session 8, Great Halls D & E, Monday 9 June 2014

**Andy Kulikowski II<sup>1</sup>, Jay Storz<sup>2</sup>, Hayley Lanier<sup>1</sup>**

<sup>1</sup>Department of Zoology and Physiology, University of Wyoming-Casper, Casper, WY 82601 USA; <sup>2</sup>School of Biological Sciences, University of Nebraska, Lincoln, NE 68588 USA

#### Using Species Distribution Modeling to Elucidate the Origin of High Altitude Hemoglobin-oxygen Affinity in Deer Mice

Strong environmental pressures often give rise to convergent evolution among populations. However, not all shared traits can be attributed to convergence. When a novel trait is observed repeatedly within modern populations, the question arises as to what type of evolutionary mechanism is responsible. High altitude populations of deer mice, *Peromyscus maniculatus*, show a greater oxygen affinity in their hemoglobin than their lowland relatives. These molecular adaptations may have occurred several times during the evolution of *P. maniculatus*, suggesting strong selection on hemoglobin. To fully understand whether these adaptations represent recurrent ecologically-mediated selection or are the result of shared history among high-altitude populations, we developed a geographic framework for how this species has moved over time using species distribution models (SDMs). We created SDM models using comprehensive *P. maniculatus* occurrence data and 19 BioClim environmental layers to determine the likely extent of suitable habitat for each major clade. We then project these models into the Last Glacial Maximum (21,000 years ago), to determine if past population connectivity can explain current population hemoglobin adaptation. These data show that population movements over the last 21,000 years have played an important role in shaping genetic novelty in modern *P. maniculatus* adaptation.

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### 122 (E,TA) Technical Session 8, Great Halls D & E, Monday 9 June 2014

**Michael W. Holmes<sup>1</sup>, Genevieve K. R. Boykins<sup>2</sup>, Miriam L. Zelditch<sup>3</sup>**

<sup>1</sup>Department of Integrative Biology, University of California, Berkeley, CA 94720 USA; <sup>2</sup>College of Natural Resources, University of California, Berkeley, CA 94720 USA; <sup>3</sup>Museum of Paleontology, University of Michigan, Ann Arbor, MI 48109 USA

#### Morphological Impacts of Environmental Change: Elevational and Temporal Variation in Cranial Structure and Body Size in *Peromyscus maniculatus*

Cranial morphology can reflect several selective pressures from an organism's environment, ranging across factors as diverse as its diet to its perception of surroundings. Using specimens collected in the Grinnell Resurvey Project, a recent massive resampling effort of California's vertebrate fauna, we seek to understand how crania of *Peromyscus maniculatus* have responded to environmental change over the last century. We show that crania have undergone significant, albeit subtle, morphological shifts in 3 sampled transects in California, suggesting a shift in diet and possibly habitat. Further, we show that in 1 area of California, *P. maniculatus* is adhering to Bergmann's and Allen's rules, growing in body size and decreasing tail length in an area of intense warming. These results provide insight into the evolutionary implications of small mammals to recent anthropogenic environmental disturbance such as land use and climate change.

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### 123 (E) Technical Session 8, Great Halls D & E, Monday 9 June 2014

**Howard M. Huynh<sup>1,2</sup>, Jessie Norman<sup>1</sup>, Donald F. McAlpine<sup>2</sup>, Karen J. Vanderwolf<sup>2</sup>, Robert J. Baker<sup>1</sup>, Robert D. Bradley<sup>1</sup>**

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409 USA; <sup>2</sup>Department of Natural Science, New Brunswick Museum, Saint John, New Brunswick E2K 1E5 Canada

#### On the Identity of *Peromyscus* on Grand Manan Island, New Brunswick, Canada

Grand Manan Island (GMI) is the largest island (137 km<sup>2</sup>) in the Grand Manan Archipelago and is situated 15 km off the southern coast of New Brunswick in the Bay of Fundy, Canada. A series of 23 deer mice, *Peromyscus maniculatus*, collected from GMI in September 1905, was subsequently described as the subspecies, *P. m. argentatus*, by M. Copeland and M. L. Church in 1906. In studies examining the molecular systematics and morphological variability in mainland and island forms of *P. maniculatus* in Atlantic Canada, we collected material to

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

re-evaluate the taxonomic status of *P. m. argentatus*. Surprisingly, our molecular genetic studies have revealed the presence (mitotype) of the white-footed mouse, *P. leucopus*, on GMI. This is the 1st reported occurrence of *P. leucopus* for the province of New Brunswick and confirms the need to reassess the taxonomic validity of *P. m. argentatus*. Our research also highlights the importance and utility of molecular systematics in identifying morphologically cryptic species. The natural history, ecology, and wildlife management issues pertaining to the discovery of *P. leucopus* on GMI also are discussed.

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### 124 (E,TA) Technical Session 8, Great Halls D & E, Monday 9 June 2014

**Emma Shubin, Christy M. McCain**

*Department of Ecology & Evolutionary Biology; University of Colorado Museum of Natural History, University of Colorado, Boulder, CO 80309 USA*

#### **Robust Discrimination of *Microtus longicaudus* and *Microtus montanus***

Montane and long-tailed voles (*Microtus montanus* and *Microtus longicaudus*) are notoriously difficult to distinguish through external and osteological characteristics, particularly among juveniles and subadults. Here we aim to present a definitive set of characteristics to distinguish the 2 species where sympatric regardless of age class. Three external characteristics and 9 cranial measurements were used in discriminate function analyses (DFA) to detect the most robust measurements for species identification using 82 *M. longicaudus* and 100 *M. montanus* museum specimens from a region of sympatry (Colorado, USA). Newly collected, difficult to distinguish specimens were sequenced with DNA to test model accuracy ( $n = 16$ ). All known-identity museum specimens were precisely identified to species with all 12 measurements (-loglikelihood = 0.23; 0 misclassifications), and with 3 key measurements (tail length, prelambeoidal breadth, mastoidal breadth; -loglikelihood = 0.33; 0 misclassified). In contrast, models with only external measurements or cranial measurements were considerably less accurate. Model identifications were verified with DNA at 100% accuracy and the remaining unknown identity specimens, mostly juveniles, were precisely identified with an average classification fit of 99.8%. These models and key characteristics can be applied widely in other regions of sympatry for accurate and precise identifications.

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### 125 (E) Technical Session 8, Great Halls D & E, Monday 9 June 2014

**Christopher D. Dunn<sup>1</sup>, Matthew R. Mauldin<sup>1</sup>, Robert D. Bradley<sup>1,2</sup>**

<sup>1</sup>*Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409 USA;* <sup>2</sup>*Museum of Texas Tech University, Lubbock, TX 79409 USA*

#### **Phylogeography and the Origin of Free-ranging Elk (*Cervus canadensis*) in Texas**

The historic range of Elk (*Cervus elaphus*) included much of the western United States. Natural distributions of this species decreased substantially in the early 20th century presumably eliminating the Texas population. In the last 20 years, several herds of free-ranging elk have appeared in the Trans-Pecos region of Texas. It is not known if these herds were the result of introduction from captive herds or if they represent natural migrants from New Mexico or Colorado. The main objective of this study is to determine the origin and genetic affinities of free-ranging *C. elaphus* in Texas. DNA sequences from the mitochondrial cytochrome b locus will be used to generate haplotype networks to compare *C. elaphus* samples from Texas with those from New Mexico and Colorado. In addition, 6 microsatellite loci will be used to examine the phylogeography and genetic divergence of the various aforementioned populations, which will help determine the origin and the relatedness of the *C. elaphus* herds in Texas. Preliminary results suggest that most individuals from Texas, when compared to Genbank reference samples, cluster together when using the cytochrome b gene.

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### 126 Technical Session 9, Meeting Room 16, Monday 9 June 2014

**Felisa A. Smith<sup>1</sup>, S. Kathleen Lyons<sup>2</sup>, S. K. Morgan Ernest<sup>3</sup>, IMPSS RCN**

<sup>1</sup>*Department of Biology, University of New Mexico, Albuquerque, NM 87131 USA;* <sup>2</sup>*Department of Paleobiology, Smithsonian Institution, National Museum of Natural History, NHB MRC 121, P.O. Box 37012, Washington, D.C. 20013-7012 USA;* <sup>3</sup>*Department of Biology and Ecology Center, Utah State University, Logan, UT 84322 USA;* Additional authors: A. G. Boyer, J. H. Brown, D. P. Costa, A. R. Evans, M. Fortelius, J. L. Gittleman, M. J. Hamilton, L. E. Harding, K. Lintulaakso, J. G. Okie, J. J. Saarinen, P. R. Stephens, J. Theodor, M. D. Uhen, and R. M. Sibly

#### **Mammal Community Structure over the Cenozoic**

What factors act to influence the structure of mammal communities and how persistent are these over geological space or evolutionary time? Our research coordination network (IMPSS RCN) constructed a database of local community assemblages from each continent for each epoch over the entire Cenozoic and used it to investigate the consistency of patterns over both time and space. We characterized the local distributions using the statistical moments. Our analyses clearly demonstrate that the factors regulating mammalian local community composition have a deep history. The highly consistent patterns of local community assembly seen across continents today 1st developed approximately 40 million years ago coincident with the trajectory of mammalian body mass evolution

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

reaching a plateau. Local body size distributions were only slightly influenced by changing environmental conditions and/or habitats over the Cenozoic, despite considerable variability over both time and space. Because we find consistent patterns across the Cenozoic for both modern and archaic mammal faunas, we suspect the fundamental rules regulating energy flow within communities have remained consistent across evolutionary history.

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### 127 (E,TA) Technical Session 9, Meeting Room 16, Monday 9 June 2014

**Marlee Tucker, Terry Ord, Tracey Rogers**

*Evolution and Ecology Research Centre, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, N.S.W. 2052 Australia*

#### **Re-examining Predator-prey Relationships across Mammals**

Terrestrial carnivorous mammals shift to feeding on larger sized prey when their body size is above 21 kg, to meet increasing energetic requirements. What happens to this relationship when marine carnivorous mammals are included as the differences associated with an aquatic lifestyle (increasing body mass and changes to prey types used) may have altered that relationship. We investigate the relationship between predator and prey body mass, in addition to energetic requirements, more broadly, across 107 carnivorous mammals including 51 terrestrial and 56 marine mammal species. We found that marine and terrestrial carnivores have evolved opposing predatory behaviors likely to minimize energy expenditure while maximizing energy intake. Despite the high energetic requirements of large body mass, marine carnivores (> 12,000 kg) feed on small prey up to several magnitudes smaller than themselves. To meet energetic requirements large marine carnivores consume enormous quantities of small prey using specialized feeding apparatus (such as baleen) and specialized behaviors (such as bubble netting) to corral prey schools. We demonstrate that the relationship between prey size and predator body mass is not uniform but differs between marine and terrestrial mammals due to the differences in prey type, predator morphology, and behavior.

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### 128 Technical Session 9, Meeting Room 16, Monday 9 June 2014

**Christy M. McCain**

*Ecology & Evolutionary Biology, University of Colorado Museum of Natural History; University of Colorado, Boulder, CO 80309 USA*

#### **North American Mammals: Who is Most at Risk from Anthropogenic Climate Change?**

Over 120 populations of North American (NA) mammals have been examined for responses to recent climate change. Larger, diurnal, montane, and arctic mammal species are responding at a higher rate, particularly to increasing temperatures. Here we examine differences in responses rates among mammal orders and rodent suborders. With these trends, we construct a predictive model for all NA mammals and the 50 mammal species of conservation concern to pinpoint those species that will be most likely to respond to climate change and be at higher risk for population extirpations, range contractions, and decreases in abundance. Sixty-five mammal species are predicted to be the strongest responders, including muskox, polar bears, and various larger, montane, diurnal mammals, predominately marmots, pika, chipmunks, and ground squirrels. Twenty percent of these predicted species already have shown responses to climate change. Twelve species of concern fall within the highest predicted responders, one-half of which are critically endangered or endangered. Any negative population perturbations from anthropogenic climate change could be perilous for these species. More monitoring of climate change responses is needed for these species in particular as well as a dire need for more research on tropical mammal species, which encompass the majority of mammal diversity and globally endangered species.

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### 129 (ECT) Technical Session 9, Meeting Room 16, Monday 9 June 2014

**Sean P. Maher<sup>1,2</sup>, Steven R. Beissinger<sup>1,3</sup>**

<sup>1</sup>*Environmental Science, Policy & Management, University of California Berkeley, Berkeley, CA 94720 USA;*

<sup>2</sup>*Berkeley Initiative in Global Change Biology, University of California Berkeley, Berkeley, CA 94720 USA;* <sup>3</sup>*Museum of Vertebrate Zoology, University of California Berkeley, Berkeley, CA 94720 USA*

#### **Community Models of Small Mammals Yield Site Level Patterns of Response to Climate Change in the Sierra Nevada**

Recent work has examined species' responses to 20th century climate change in the Sierra Nevada by comparing elevational profiles between historic and modern surveys. These approaches compared species-specific occupancy probabilities with elevation to demonstrate distributional shifts, and tested whether climate change was a predictor of shift. We extended these analyses to quantify effects of climate change on persistence and colonization in the small mammal community through a Bayesian multispecies, multiseason occupancy model. Using data collected as part of the Grinnell Resurvey Project, we identified paired sites and modeled historical occupancy as function of elevation. Occupancy during the modern era for these sites was modeled as a function of climate change for a series of variables representing patterns of temperature and precipitation. An inclusion parameter was used to evaluate

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

support for the effect of change on persistence and colonization. Our results show that without accounting for detection variability, estimates of richness at each site during each period would be under-estimated, thus influencing perceived changes in richness. Estimates of the probability of persistence generally were 0.72–0.78, whereas colonization estimates were 0.01–0.05, suggesting that at most of the paired sites, richness values became depressed. The change in annual mean temperature was more relevant than change in annual mean precipitation in single variable models, based upon the frequency the inclusion parameter, although full models yielded equivocal results.

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### 130 Technical Session 9, Meeting Room 16, Monday 9 June 2014

**Rebecca J. Rowe<sup>1</sup>, Kate E. Jenks<sup>1,2</sup>, Rebecca C. Terry<sup>3</sup>, Eric A. Rickart<sup>4</sup>**

<sup>1</sup>Department of Natural Resources and the Environment, University of New Hampshire, 56 College Road, Durham, NH 03824 USA; <sup>2</sup>Minnesota Zoo, 13000 Zoo Boulevard, Apple Valley, MN 55124 USA; <sup>3</sup>Department of Integrative Biology, 3029 Cordley Hall, Oregon State University, Corvallis, OR 97331 USA; <sup>4</sup>Natural History Museum of Utah, University of Utah, 301 Wakara Way, Salt Lake City, UT 84108 USA

#### **Small Mammal Community Similarity over Space and Time in the Great Basin**

Anthropogenic activities are rapidly changing natural environments, threatening the persistence of ecosystems and species. Temporal comparisons at the decadal to centennial scale have increased in an effort to understand ecological impacts of past environmental change and to anticipate future changes. Here we examine small mammal community similarity using paired survey data spanning an 80-year interval in 2 mountain ranges in the Great Basin: the Ruby Mountains of northeastern Nevada and the Toiyabe Range of central Nevada. These mountains extend from desert shrubland to alpine tundra, share many species in common (60%), and have similar land use and climate histories. We applied a multi-species hierarchical community model using era, trap effort, and trend (for removal trapping) as covariates for detection, and mountain range, elevation, elevation<sup>2</sup>, era, era x elevation, and era x elevation<sup>2</sup> for occupancy. These detection-corrected occurrence data were then used to compute measures of community similarity within and among time periods for each mountain. Comparisons of community similarity with climate similarity (temperature and precipitation, 800 m) were conducted using mantel tests. Preliminary results suggest that communities today are less similar to one another than they were in the past, and that greatest community stability is at high elevations. Finally, we emphasize the importance of interpreting temporal changes against the backdrop of spatial variation in community structure along each elevational gradient within each time period.

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### 131 Technical Session 9, Meeting Room 16, Monday 9 June 2014

**Robert P. Anderson**

*Department of Biology, City College of the City University of New York, New York, NY 10031 USA*

#### **Expanding Hutchinson's Concept of Scenopoetic Variables: When Can Biotic Interactions be Included in Grinnellian Niche Models?**

How to integrate biotic interactions represents a thorny problem for ecological niche modeling. I focus on models of Grinnellian niches defined by density-independent factors not affected by the presence of the focal species (termed scenopoetic by Hutchinson). In contrast, models of Eltonian niches include density-dependent factors represented by variables that are affected by the focal species. Because biotic interactions can have strong effects on species distributions, including them in niche models might lead to substantially more realistic predictions. I here consider the logic of whether each particular class of biotic interactor could be considered scenopoetic. By definition, some classes of biotic interactors can be classified as scenopoetic or nonscenopoetic, but others require additional information regarding the pair of species involved. Completely superior competitors, facilitators, and harming ammensals are always scenopoetic (and important to the focal species). In contrast, completely inferior competitors, commensals, and suffering ammensals are never scenopoetic (but are irrelevant). All other classes require species-specific information (and may be important): competitors of intermediate effects, mutualists, and all positive/negative interactions (predators/prey, consumers/resources, parasites/hosts). Of these latter classes, some interactors may only be trivially affected by the population level of the focal species; in such cases, the interactor represents a scenopoetic variable. Future research should address how nonscenopoetic biotic interactors can be taken into account (e.g., included in post-processing; or via Eltonian models).

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### 132 (TA) Technical Session 9, Meeting Room 16, Monday 9 June 2014

**Angela D. Hornsby, Marjorie D. Matocq**

*Program in Ecology, Evolution, and Conservation Biology, University of Nevada, Reno, NV 89557 USA*

#### **Using Approximate Bayesian Computation to Compare Demographic Estimates from Ecological Niche Models and Subfossil Abundances**

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

Species in regions with dynamic climatic and geological histories often undergo major shifts in range and demography as a function of their environment. Much of our understanding of these processes through the late Quaternary comes from modeling approaches offering indirect evidence of reactions to climate change; however, some taxa have extensive subfossil records offering more direct evidence of these reactions. The purpose of this study is to determine whether indirect evidence (ecological niche models, ENMs) and direct evidence (subfossil abundance) can accurately reflect changes in population sizes of *Neotoma cinerea* and *N. lepida* since the last glacial maximum. To address this, we convert ENMs and subfossil abundances to quantitative hypotheses of effective population size, and use approximate Bayesian computation to model these scenarios and compare them to observed genetic patterns. We find that both the ENMs and subfossil abundances may be converted into quantitative demographic hypotheses that perform well against null models, indicating that both methods may accurately capture relatively fine-scale population size changes. This process makes many assumptions about the subfossil record, but attempts to continue expanding the amount of information derivable from this important resource.

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### 133 (E) Technical Session 10, Meeting Room 17, Monday 9 June 2014

**R. Craig Bland<sup>1</sup>, Katrina M. Morris<sup>2</sup>, Steven B. Castleberry<sup>1</sup>**

<sup>1</sup>Daniel B. Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA 30606 USA;

<sup>2</sup>Georgia Department of Natural Resources, Nongame Conservation Section, Social Circle, GA 30025 USA

#### **Roosting Habitat Selection of the Northern Yellow Bat (*Lasiurus intermedius*) on Two Georgia Barrier Islands**

In the southeastern USA, northern yellow bats (*Lasiurus intermedius*) roost primarily in Spanish moss (*Tillandsia usneoides*) but also are known to roost under the fronds of cabbage palms (*Sabal palmetto*). Although hardwood habitats are important in roost site selection, specific habitat composition that provides optimal roosting habitat is unknown. We examined roosting habitat selection of the northern yellow bat on 2 Georgia barrier islands, 1 dominated by pine/mixed pine-hardwood habitats and 1 dominated by hardwood habitats. We captured and radiotagged 34 adult males, 3 adult females, and 2 juvenile females. We tracked bats to their diurnal roosts daily and measured site characteristics at roosts and random trees. Out of 408 roosts, 97% were located in Spanish moss on hardwood trees and 3% were located under palm fronds. Consistent with previous research, our preliminary analyses indicated that roost trees had a larger diameter at breast height (DBH) than surrounding trees. Additionally, we found that the mean distance was greater between midstory height and roosts (mean = 3.4 m) than between midstory height and randomly selected Spanish moss clumps (mean = 2.4 m). Our results support the general supposition that hardwood habitats are important roost locations but, management actions that promote large-diameter hardwoods and reduce midstory clutter may provide suitable roosting habitat.

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### 134 (\*\*,TA) Technical Session 10, Meeting Room 17, Monday 9 June 2014

**Melissa J. Merrick, John L. Koprowski**

School of Natural Resources and the Environment, Wildlife Conservation and Management, University of Arizona, Tucson, AZ 85721 USA

#### **Factors Influencing Expanded Sex-biased Natal Dispersal in an Isolated, Peripheral Mammal**

Understanding factors that influence natal dispersal is necessary to predict gene flow, functional landscape connectivity, recruitment, and population persistence, particularly in the face of anthropogenic disturbances and landscape fragmentation. Peripheral, isolated populations provide unique opportunities to compare how ecological processes like natal dispersal differ from populations in contiguous landscapes. Herein we document natal dispersal and examine factors that influence dispersal movements in an endangered forest obligate, the Mount Graham red squirrel (*Tamiasciurus hudsonicus grahamensis*), restricted to a single mountain in southeastern Arizona. We compare natal dispersal in this population to range-wide observations and apply established mammalian dispersal theory to explain differences between dispersal observed on Mt. Graham and other areas. From 2010–2013, we radio collared 93 juvenile Mount Graham red squirrels, assessed individual behavior, and tracked natal dispersal, settlement, and survivorship. We quantified intersexual differences in natal dispersal distance and explored these as a function of intrinsic (individual body condition, behavior trial scores) and extrinsic (mother's body condition, sibling sex ratio, local density, neighborhood sex ratio) factors. In Mount Graham red squirrels, natal dispersal is sex biased and distances are greater than reported for other North American red squirrel populations (North American red squirrel mean dispersal distance: 106.8 m, this study: males 969.4 m; females 339.0 m). For both sexes, models including mother's body condition and individual behavior were most supported. This research was supported by an ASM Grants-in-Aid of Research awarded to Melissa J. Merrick in 2010.

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### 135 Technical Session 10, Meeting Room 17, Monday 9 June 2014

**Catherine M. Johnson<sup>1</sup>, Larissa L. Bailey<sup>2</sup>, Allan F. O'Connell, Jr.<sup>3</sup>, Winston P. Smith<sup>4</sup>**

<sup>1</sup>Monongahela National Forest, 200 Sycamore Street Elkins, WV 26241 USA; <sup>2</sup>Colorado State University, Department of Fish, Wildlife and Conservation Biology, Campus Delivery 1474, Fort Collins, CO 80526 USA; <sup>3</sup>U.S. Geological

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

Survey Patuxent Wildlife Research Center, 10300 Baltimore Avenue, Beltsville, MD 20705 USA; <sup>4</sup>Institute of Arctic Biology, University of Alaska-Fairbanks, 2571-3 Douglas Highway, Juneau, AK 99801 USA

## Ecological Correlates of Occupancy by West Virginia Northern Flying Squirrel (*Glaucomys sabrinus fuscus*)

The northern flying squirrel (*Glaucomys sabrinus*) is a forest obligate that achieves its highest density in old growth and facilitates critical symbiotic relationships; its sensitivity to isolation renders it an ideal indicator of landscape connectivity. Results of numerous studies across its range reveal acute sensitivity to disturbance at multiple spatial scales, rendering the squirrel an effective sentinel of forest ecosystem condition and processes. However, little information exists regarding endemic populations native to high elevation red spruce (*Picea rubens*) forests in the Appalachians. Catastrophic disturbances historically caused extensive habitat loss; climate change with associated shifts in forest communities is expected to further displace and fragment naturally isolated red spruce forests and *G. s. fuscus* populations. We used survey data from trapping grids and nest boxes over a 4-year period with both open and closed occupancy models to investigate ecological correlates of colonization and occupancy rates. We developed hypotheses according to published habitat relationships and models. *G. s. fuscus* was detected on 21 of 40 grids (52%) with 95 captures of 78 individuals. More trapping captures occurred in spruce-dominated sites (0.6%) than northern hardwood sites ( $\leq 0.1\%$ ). Initial occupancy probabilities were higher in spruce-dominated sites and at lower elevations; sites in closer proximity to historical populations had higher local colonization probabilities. Our results can inform efforts to restore red spruce forest communities and *G. s. fuscus* habitat.

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### 136 Technical Session 10, Meeting Room 17, Monday 9 June 2014

#### Steve K. Windels

Voyageurs National Park, International Falls, MN 56649 USA

#### Hydrologically-connected Systems Facilitate Long Distance Dispersal in Beavers

Beavers typically disperse from natal areas between 2–3 years of age. Mean dispersal distances reported in the literature have generally not exceeded 10 km in northern systems, as predation risk from wolves and bears limit overland travel. Six hundred thirty-five (635) beavers were ear-tagged from 2006–2012 in Voyageurs National Park (VNP); an 88,000-ha protected area dominated by large, interconnected lake systems. Trapping is not allowed in VNP and beaver densities exceed 1.0 lodges/km<sup>2</sup>. Fifty-five (55) ear-tagged beavers were reported legally trapped outside of the park between 2008 and 2012, of which 48 were determined to be dispersal events. Mean ( $\pm SE$ ) estimated dispersal distance by water was 31.4 km ( $\pm 3.8$ ). Maximum dispersal distance was 99.9 km, with 10 others also exceeding 50 km. Dispersal was female-biased (62.5% of events), and females also dispersed farther than males (35.0  $\pm$  5.0 km versus 24.2  $\pm$  5.0 km). Timing of dispersal events by beaver age class and time of year will be discussed. Results suggest that long-distance dispersal by beavers is facilitated in hydrologically-connected systems.

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### 137 (E) Technical Session 10, Meeting Room 17, Monday 9 June 2014

#### Savanna M. Summers<sup>1</sup>, Florent Bled<sup>1</sup>, Jerrold L. Belant<sup>1</sup>, Deb Martell<sup>1</sup>, Dean Beyer<sup>2</sup>

<sup>1</sup>Carnivore Ecology Laboratory, Forest and Wildlife Research Center, Mississippi State University, Mississippi State, MS 39762 USA; <sup>2</sup>Michigan Department of Natural Resources, Wildlife Division, Marquette, MI 49855 USA

#### Spatial and Temporal Variations in Habitat Selection by Bobcats (*Lynx rufus*)

Investigation of spatial and temporal variations of habitat selection can advance our understanding of population ecology and improve wildlife responses to management measures. Factors affecting habitat selection can vary in time and space. Although species' seasonal ranges might be controlled by a particular factor (e.g., forest coverage), spatial use within this range might change across fine temporal resolutions due to other factors (e.g., prey availability). We studied variation in habitat selection by bobcats (*Lynx rufus*) in the Upper Peninsula of Michigan with data collected from January to March 2012–2013. Camera survey data was compiled from 64 baited sites in a 20 by 20 km area. Using a hierarchical model, we estimated how occupancy was related to prey abundance and presence of roads. We also identified the relative importance of those covariates across 3 spatial scales: seasonal (January–March winter home range); daily (estimated range occupied within a day); and point (influence of local covariates on camera site occupancy). Our results lead to a better understanding of how habitat selection in bobcats is controlled by different factors at various scales. This understanding could help to improve management decisions by targeting conservation measures at appropriate temporal and spatial scales depending on the objectives for the population.

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### 138 (C) Technical Session 10, Meeting Room 17, Monday 9 June 2014

#### Casey R. Taylor, Sarah J. Corey-Rivas, Jesús A. Rivas

Department of Biology, New Mexico Highlands University, Las Vegas, NM 87701 USA

#### Does a Bear Live in the Woods? An Analysis of Urban Black Bear Populations in Northern New Mexico

Conflicts between humans and black bears (*Ursus americanus*) have increased in the recent decades, with little change in sight. These conflicts have arisen due to habitat degradation, human expansion into black bear habitat,

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

and anthropogenic attractions in urban areas. Urban bears are rather common in New Mexico, where bears are often seen in town and around dumpsters. Conventional wisdom states that once a bear has come to town they do not leave. These bears stop being a participant of the rural ecosystem and become urban animals. The purpose of this study is to assess the magnitude of the urban bear problem by determining the abundance, and movements of these urban populations, in comparison with rural populations. Transects were randomly assigned within the city limits and in the neighboring areas to determine relative abundance of black bears by counting scat and bear sign. Scat and hair samples were collected to determine individuals through the use of microsatellite analysis, as well as tracking movement patterns. Telemetry was used to track the movements of 2 sows (1 with 2 cubs) through the summer and fall of 2013. I found more scat in town than in the neighboring areas ( $t = 2.98$ ,  $d.f. = 13$ ,  $p = 0.005$ , 1 tail). Both sows were collared in town but moved to rural areas in the fall, presumably seeking hibernation dens.

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### 139 (C) Technical Session 10, Meeting Room 17, Monday 9 June 2014

#### Ronny Forney

*Geography, New Mexico State University, Las Cruces, NM 88011 USA*

#### **The Effects of Diurnal Patterns on the Spatial Distribution of Female Desert Bighorn Sheep (*Ovis canadensis mexicana*)**

This research explored variation in the distribution of desert bighorn sheep between day and night, specifically in elevation, slope, and aspect of desert bighorn locations. The data used in this study are of 6 adult female desert bighorn sheep captured from the Cabeza Prieta mountains, Arizona, in 2002. Female locations were mapped, allowing for inferences of spatial patterns. I generated a Minimum Convex Polygon around all female point locations to estimate home range size and determine movement. Data points within this polygon were considered areas of use and were compared with an equal number of random points to indicate areas of availability and determine habitat. To model the surface of the mountain range, I obtained 10 m, 1/3 arc second elevation data, which was overlaid with point locations. The elevation data was used to create a slope map using percent slope as the output, as well as an aspect map using preferred azimuth categorizations as the output. Whether surfaces were convex (curving outward) or concave (curving inward) were also considered. To determine if there was a significant statistical difference in the means in the 6 samples of each of the 3 dependent variables, given 2 independent variables, MANOVA was applied. It was predicted that variation exists in female desert bighorn sheep use of slope, aspect, and elevation between night and day, and between samples (females) in the population.

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### 140 Technical Session 10, Meeting Room 17, Monday 9 June 2014

#### Floyd W. Weckerly

*Department of Biology, Texas State University, San Marcos, TX 78666 USA*

#### **Population Irruption by Roosevelt Elk**

Population irruptions by large herbivores are associated with animal introductions to oceanic islands, absence of predators, food supplies unexposed to prior ungulate herbivory, and severe winter conditions. None of these conditions existed in an irruption by Roosevelt elk (*Cervus elaphus roosevelti*) in Redwood National and State Parks, California. I examined whether a sudden availability of discrete patches of forage habitat and the existence of elk in the area near the new forage habitat could facilitate the irruption. These conditions allow for ingress of adult elk onto a new food resource that fuels rapid population growth which is needed for the eventual exhaustion of the food supply by elk herbivory and overshoot of K carrying capacity. After 100 years of cattle grazing Davison meadows became available to elk in 1991 and the elk inhabiting Davison have since undergone the 4 stages of population irruption: rapid growth; overshoot; decline; and ostensibly, lower K carrying capacity. Simulations showed that colonization of Davison meadows by 2 adult females and high rates of survival and recruitment did not result in abundance observed during the peak of the overshoot. Ingress of adult females during the rapid growth phase was needed to match female abundance estimated during the peak of the overshoot. Ungulate population irruptions may need, in part, conditions that foster rapid population increase during the initial growth phase.

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### 141 (E) Poster Session II, Great Hall C, Monday 9 June 2014

#### Jocelyn P. Colella

*Department of Biology and Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM 87106 USA*

#### **Molecular Analysis of Species Limits and Hybridization of Ermine (*Mustela erminea*) in Southeast Alaska**

Secondary contact zones provide a unique opportunity to investigate introgression, reinforcement and divergence. This study examines DNA sequence variation and species distribution models to understand the evolutionary history and contemporary consequences of climate-induced range shifts on the North American ermine (*Mustela erminea*). Ermine are the most widespread terrestrial carnivore in the Arctic and are represented in southeast Alaska by 3 genetically and morphologically distinct groups or clades (Holarctic, Continental and Island). Preliminary genetic data

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

indicate that these ermine clades may be the result of isolation during the last glacial maximum (~22,000 years ago), including a hypothesized North Pacific coastal refugium. Extended isolation, followed by massive range expansion likely led to secondary contact where hybridization may be occurring between some of these diverged clades. Here, mitochondrial and nuclear loci are examined across all clades for 120 individuals to form robust phylogenies, resolve taxonomic limits, and refine distributional boundaries of representatives of the clades in the region and also to assess potential hybridization. *Mustela erminea haidarum*, an endemic subspecies that roughly corresponds to the island clade, has previously shown to be distinctive from other clades. Whether this forms a distinct species will require further characterization. The Canadian Federal Government already has listed this subspecies as vulnerable.

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### 142 Poster Session II, Great Hall C, Monday 9 June 2014

**Jon C. Pigage<sup>1</sup>, Jeremy M. Bono<sup>1</sup>, Peter J. Wettstein<sup>2</sup>, Stephanie A. Herlik<sup>1</sup>, Helen K. Pigage<sup>1</sup>**

<sup>1</sup>Biology Department, University of Colorado Colorado Springs, 1420 Austin Bluffs Parkway, Colorado Springs, CO 80918 USA; <sup>2</sup>Departments of Surgery and Immunology, The Mayo Foundation, Rochester, MN 55905 USA

#### **Preliminary Investigation of Evolutionary Genetics of Abert's Squirrels (*Sciurus aberti*) Using Restriction-site Associated DNA Sequencing (RAD-Seq)**

Abert's or tassel-eared squirrels (*Sciurus aberti*) are found in montane Ponderosa pine (*Pinus ponderosa*) forests in the southwestern United States and northern Mexico. Six subspecies of *S. aberti* are currently recognized by variations in pelage coloration and distribution in ponderosa pine forests. These observations have led to questions about the status of the species; that is, have sufficient genetic changes occurred to lead to the formation of new species? Lamb et al. (1997) have drawn a geographical east/west split in the phylogeny of these squirrels based on mitochondrial DNA (mtDNA) analysis. We propose to further define the phylogeny of the subspecies as well as examine the possibility of current speciation using Restriction-site Associated DNA (RAD-Seq).

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### 143 Poster Session II, Great Hall C, Monday 9 June 2014

**Danny Follett, Jon C. Pigage, Helen K. Pigage**

Biology Department, University of Colorado Colorado Springs, 1420 Austin Bluffs Parkway, Colorado Springs, CO 80918 USA

#### **Seasonal Habitat Selection by Non-migratory Female Mule Deer (*Odocoileus hemionus*) in a Semi-arid Environment**

Twenty-three non-migratory female mule deer (*Odocoileus hemionus*) at Fort Carson Military Reservation, Colorado, were fitted with GPS/VHF collars and tracked for the 2011 winter (January–March) and summer (July–September) seasons. Fixed points were taken every 3 hours and used to make Kernel Density Estimations (KDE). Based on the KDEs, home (95%) range and core (50%) areas were determined and compared on the size of area, vegetation available, and vegetation used. Differences in habitat utilization between the seasons were observed. Overall, coniferous areas made up the majority of habitat use on both home and core areas. Winter core areas included a higher percentage of grassland (32.7%) than summer core areas (22.9%). Riparian and shrubland habitats were used more in the summer core area (12.1%, 12.5%) than in the winter core area (8.76%, 7.16%). In summer, the deer utilized a higher percentage of grassland in the home range compared to the core area (38.0% versus 22.8%). The treed and riparian areas of the summer core had a higher use (48.16%, 12.12%) than the home range area (41.45%, 6.88%). This information has management implications for habitat conservation in light of expanding military training.

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### 144 (E,\*\*,TA) Poster Session II, Great Hall C, Monday 9 June 2014

**Nelish Pradhan<sup>1</sup>, C. William Kilpatrick<sup>1</sup>, Priya Joshi<sup>2</sup>, Ajay N. Sharma<sup>2</sup>, Saurav Chhetri<sup>3</sup>**

<sup>1</sup>Department of Biology, University of Vermont, Burlington, VT 05405 USA; <sup>2</sup>Center for Molecular Dynamics-Nepal, Kathmandu, Nepal; <sup>3</sup>American Community School, Amman, Jordan

#### **Phylogeny and Biogeography of *Apodemus***

Species of the genus *Apodemus* are widely distributed throughout the broadleaf forests in temperate zones of Eurasia and are among the oldest extant lineages of murid rodents. Examination of chromosomal rearrangements, allozymic and DNA sequence data has resulted in the placement of the taxa of *Apodemus* into 4 groups (*Apodemus*, *Sylvaemus*, *Argenteus*, and *Gurkha*). However, the phylogenetic relationships among the 4 lineages are not fully resolved. This study used concatenated sequences of 3 mitochondrial and 5 nuclear genes to construct a phylogeny in parsimony, likelihood and Bayesian frameworks for 17 species of *Apodemus* with all 4 major lineages represented. Additional cytochrome b sequences were obtained from 29 specimens of *A. gurkha* collected from 3 localities to expand sampling for the monotypic *Gurkha* group. Considerable polymorphism was observed with the detection of 19 cytochrome b haplotypes as well as geographic variation among the 3 localities sampled. The phylogenetic analyses suggest 2 distinct lineages within the genus rather than 4, with *Argenteus* being the basal taxon in the *Apodemus* clade and *Gurkha* being the basal taxon in the *Sylvaemus* clade. The 4 groups of *Apodemus* diverged between 6.5



## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

and 9.2 million years ago which coincides with global climactic changes that resulted in change in vegetation across Eurasia and rapid uplift of the Himalayas that occurred in the late Miocene and early Pliocene. This research was supported by an ASM Grants-in-Aid of Research awarded to Nelish Pradhan in 2013.

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### 145 Poster Session II, Great Hall C, Monday 9 June 2014

**Alyssa M. Kiesow<sup>1</sup>, Hugh B. Britten<sup>2</sup>**

<sup>1</sup>Math and Science Department, Northern State University, Aberdeen, SD 57401 USA; <sup>2</sup>Department of Biology, University of South Dakota, Vermillion, SD 57069 USA

#### **Phylogeography of *Glaucomys sabrinus* and *Tamiasciurus hudsonicus* Populations: A New Perspective in the Insular United States**

Northern flying (*Glaucomys sabrinus*) and red squirrel (*Tamiasciurus hudsonicus*) populations are distributed in northern North America, including the Black Hills. The Black Hills populations are considered disjunct from other populations within their range. We examined insular populations to determine whether arboreal squirrels in the Black Hills each represent a unique subspecies. We trapped and collected ear samples from northern flying and red squirrels in the Black Hills and in areas of Montana, Wyoming, Idaho, Utah, Minnesota, and Wisconsin to infer population phylogenies with special consideration of the Black Hills population. Microsatellite loci and 2 mtDNA sequences were used for phylogenetic data analyses, such as neighbor-joining, maximum parsimony, and likelihood trees and percent divergence and nucleotide diversity. For both squirrels, all phylogenetic trees (for each gene) group the Black Hills and Bear Lodge Mountain populations together, thereby, demonstrating lack of genetic exchange with other nearby mountain ranges. Sequence divergence among studied populations is relatively small (0 to 0.85% [northern flying] and 0 to 2.4% [red]), so divergence may be from a historical event. Nucleotide diversity is higher than other ranges (0.1 to 0.7 [northern flying] and 0.5 [red]); however, genetic structure data indicate low heterozygosity in the Black Hills populations. These data suggest that northern flying and red squirrel populations in the Black Hills and Bear Lodge Mountains be reclassified and/or maintained as its own subspecies.

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### 146 Poster Session II, Great Hall C, Monday 9 June 2014

**Andrew G. Hope<sup>1</sup>, Eric Waltari<sup>2</sup>, Jason L. Malaney<sup>3</sup>, David C. Payer<sup>4</sup>, Joseph A. Cook<sup>5</sup>, Sandra L. Talbot<sup>1</sup>**

<sup>1</sup>U.S. Geological Survey, Alaska Science Center, 4210 University Drive, Anchorage, AK 99508 USA; <sup>2</sup>Aaron Diamond AIDS Research Center, 445 First Avenue, New York, NY 10016 USA; <sup>3</sup>Department of Natural Resources and Environmental Science, University of Nevada-Reno, Reno, NV 89557 USA; <sup>4</sup>U.S. Fish and Wildlife Service, Arctic National Wildlife Refuge, 101 12th Ave, Rm 236, Fairbanks, AK 99701 USA; <sup>5</sup>Department of Biology and Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM 87131 USA

#### **Small Mammal Comparative Phylogeography in the Arctic: Evolutionary, Ecological and Human Land-use Implications**

Culminating from 15 years of phylogeographic studies on small mammals distributed across the northern continents through Beringia, we present a comparative methodological approach to understand the evolutionary processes associated with environmental change across the Arctic landscape, and how these perspectives may be applied for land management, conservation, and the dynamics of suture zones. This integrated multi-disciplinary research relies on extensive specimen-based archives of georeferenced specimens across time, including both genomic resources and fossils. Phylogeographic assessments revealed lineages from each species for which taxon-specific molecular substitution rates were scaled to assess the relative timing of demographic trends across the community. Population size changes were tested using coalescent simulations and distributional shifts of lineages through time were assessed with species distribution models. Predictions of potential future distributions suggest a northward shift in Arctic mammal diversity resulting in novel species assemblages, although our models also predict key regions where ecological community components remain relatively non-overlapping. These key areas also are coincident with an increasing human footprint in the Arctic, suggesting a need for careful land-use planning to accommodate multiple management priorities. A shifting Arctic ecotone between boreal and tundra biomes has multiple implications for evolutionary processes associated with hybridization, adaptation, and exposure to novel pathogens, investigations of which are increasingly feasible considering emerging and integrated genomic and GIS-based methods.

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### 147 Poster Session II, Great Hall C, Monday 9 June 2014

**Brett Ford, Erika L. Barthelmess**

Biology Department, St. Lawrence University, Canton, NY 13617 USA

#### **The Effects of Roads on the Genetic Structure of North American Porcupine Populations**

Roadways have become an increasing conservation concern for wildlife populations. In addition to direct mortality by vehicles, wildlife is impacted by roads through habitat fragmentation, noise and chemical pollution and other factors. When roads limit movement of individuals, the result may be a decrease in genetic variation and genetic differentiation of subpopulations or individuals. We investigated the impact of high-traffic roadways on the genetic

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

structure of the North American porcupine (*Erethizon dorsatum*) in northern New York. The North American porcupine is the mammal species facing the highest vehicle-induced mortality rates in northern New York, yet the consequence of this mortality on genetic structure remains unclear. Recovery from the harmful effects brought about by roads is especially concerning for the porcupine population because their reproductive rate is slower compared to other rodent species. We assessed a population of 80 individuals across 8 microsatellite loci to determine the genetic structure of the population. We evaluated the degree of genetic variation and level of differentiation on either side of these roads and discuss our findings in this presentation.

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### 148 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Karla L. Flores, Paul Stapp**

*Department of Biological Science, California State University Fullerton, Fullerton, CA 92831 USA*

#### **Landscape Genetics of Northern Grasshopper Mice in Relation to Prairie Dog Colonies in Shortgrass Steppe**

Patterns of spatial genetic structure reflect the effects of landscape composition and functional connectivity on gene flow and effective population size. In the Pawnee National Grasslands, Colorado, northern grasshopper mice (*Onychomys leucogaster*) often occur at relatively high population densities in black-tailed prairie dog (*Cynomys ludovicianus*) colonies and have wide-ranging movements relative to their body size. However, little is known about the movements of grasshopper mice among colonies or the effects of colonies on their population structure at the landscape scale. We used the mitochondrial gene cytochrome oxidase subunit I (COI) and 11 nuclear microsatellite loci to determine the population genetic structure of grasshopper mice. An analysis of molecular variance of COI showed no significant genetic structure among locations, though a weak east-west pattern was detected. A median-joining haplotype network also revealed 2 groups corresponding to east and west clusters but no isolation-by-distance. Differentiation into east and west clusters may be a relatively recent event reflecting changes in land-use rather than historical processes. Analysis of microsatellites showed moderate levels of genetic differentiation among colonies, and genetic distances did not correlate with geographic distance. Given the high heterozygosity at colonies, the lack of an isolation by distance pattern might indicate preferential patterns of dispersal. Because grasshopper mice may spread plague to prairie dogs, understanding their movements can help predict patterns of infection risk among colonies during epizootics.

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### 149 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Vicki L. Villanova<sup>1</sup>, Phillip T. Hughes<sup>2</sup>, Eric A. Hoffman<sup>1</sup>**

<sup>1</sup>*Department of Biology, University of Central Florida, Orlando, FL 32816 USA;* <sup>2</sup>*U.S. Fish and Wildlife Service, National Key Deer Refuge, Big Pine Key, FL 33043 USA*

#### **Population Genetics of the Endangered Key Deer Using Noninvasive Sampling**

Approximately 10,000 years ago, the Florida Keys became isolated from mainland Florida due to sea levels rising. Key deer (*Odocoileus virginianus clavium*) are 1 of only 2 recognized subspecies in the Lower Keys, which are genetically isolated from the mainland taxa. In addition to their unique evolutionary history, they were hunted to near extinction in the early 1900s. The overexploitation of Key deer led to the listing of the subspecies as federally endangered in 1967. Despite their interesting history, there is a lack of research on how their past has impacted contemporary demography and genetic structure of the population. Preliminary analyses show the island population has an average allelic richness of 2.61 versus 5.94 of the mainland population. The probability of identity (PID) was estimated to be 0.00018, illustrating our ability to identify unique individuals for mark-recapture. Based on limited evidence in the literature, we expect the population size to be about 800 individuals, a sex ratio of 3:1 (male: female), and a single, panmictic population with geographic separation based on family groups. Our project aims to test these predictions using 12 microsatellite markers and sex-linked genes obtained from noninvasive sampling. Ultimately, our research will add to the advancement of noninvasive genetic sampling and to our understanding of how population demographics are modified by insularization while furthering the overall conservation of *O. v. clavium*.

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### 150 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Wesley Brashear, Gang Li, William J. Murphy**

*Department of Veterinary Integrative Biosciences, Interdisciplinary Program in Genetics, Texas A&M University, College Station, TX 77843 USA*

#### **Testis Transcriptome Divergence in Felidae: Implications for Hybrid Sterility and Reproductive Isolation**

Studying patterns in gene expression and transcriptome divergence provides a unique and necessary approach to understanding a myriad of physiological and evolutionary processes. Such studies are particularly useful when conducted within systems that not only facilitate comparisons between species, but also between their hybrids, as a means to identify the genomic basis of reproductive isolation. Recent studies have shown that within mammals, transcriptome complexity is greatest within the testes and suggest that patterns in epigenetic chromatin modification more readily allow for novel gene origination. We examined patterns of testis transcriptome divergence between

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

several members of the cat family, Felidae. This family is unique in that there are numerous interspecific hybrid crosses and most of the parent species' genomes have been sequenced. Here we present the results of an analysis of genome-anchored, testis transcriptomes of 6 felids: domestic cat, Asian leopard cat, serval, tiger, lion and snow leopard. Testis transcriptome assemblies recovered ~25,000 coding and non-coding transcripts for each species. Cross-species mapping identified patterns of novel gene evolution, including many novel, lineage-specific transcripts. An analysis of F1 hybrid transcriptomes between 4 of the species pairs (e.g. bengals, savannahs, caravals and ligers) identified some conserved patterns of genetic misregulation, particularly on the sex chromosomes. These results, together with analyses of rates of non-synonymous versus synonymous evolution, identify numerous candidate genes potentially underlying reproductive isolation.

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### 151 (E,\*\*) Poster Session II, Great Hall C, Monday 9 June 2014

**Nicholas K. Fletcher<sup>1</sup>, Jeremy B. Searle<sup>1,2</sup>**

<sup>1</sup>Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, NY 14853 USA; <sup>2</sup>Cornell University Museum of Vertebrates, 159 Sapsucker Woods Road, Ithaca, NY 14850 USA

#### **Genomic Differentiation during Refugial Isolation and Its Relevance to Speciation in the Field Vole (*Microtus agrestis*)**

Understanding the ways that climate fluctuations in the Quaternary have shaped the genetic structure of organism has important implications for processes that effect diversification both at the species level and within species. The genus *Microtus* represents 1 of the best-known cases of a rapid mammalian radiation, resulting in nearly 70 extant species throughout the Holarctic with origination of the clade only 1.2–2 million years ago. Within *Microtus*, the *agrestis* complex includes a hierarchy of differentiation, cryptic species or near-species that split at the Last Glacial Maximum and further, more recent subdivisions. Here, we present pilot data of next generation sequencing data used to resolve the relationships between populations of *M. agrestis* and quantify the amount of genomic differentiation caused by selection and drift during isolation in glacial refugia. After examining phylogeographic patterns over its entire range, we will analyze a hybrid zone between 2 within-species lineages to determine the extent to which populations have built up genetic incompatibilities that may contribute to reproductive isolation and ultimately speciation. These findings will inform us about population subdivision and the range expansion at the end of the last glaciation and will offer insights into the early stages of differentiation within a system that displays 1 of the highest speciation rates in vertebrates. This research was supported by an ASM Grants-in-Aid of Research awarded to Nicholas Fletcher in 2013.

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### 152 Poster Session II, Great Hall C, Monday 9 June 2014

**Charlene Belew, Brandon K. McDonald**

Cameron University, Department of Biological Sciences, Lawton, OK 73505 USA

#### **UV-reflective Morphology in the Rodent Families Heteromyidae, Geomyidae, and Dipodidae: Results from UV-photography**

Reflection of ultraviolet light (UV) by morphological markings in the kangaroo rat, *Dipodomys ordii*, has been confirmed. This UV-reflective morphology has been validated quantitatively through UV-VIS photospectrometry and subsequently corroborated qualitatively with UV-photography. We have developed a UV-photography protocol that incorporates a UV-reflective standard (Fluorilon) to visually discriminate between UV-reflectivity and absorption while also allowing us to estimate the degree of reflectivity observed. Using this approach, we examined UV-reflective morphology in congeners of *D. ordii*, other heteromyid genera, several genera in the family Geomyidae, as well as morphological equivalents of kangaroo rats, jerboas in the family Dipodidae. We present UV-reflective morphology in gophers (Geomyidae) due to white patches similar to those seen in kangaroo rats (*Dipodomys* spp.) We also discovered cryptic UV-reflective patterns in 1 specimen of the gopher *Geomys tropicalis*. While this project was exploratory in nature, we conclude that UV-reflective morphology might be a conserved trait common to the heteromyids and geomyids due to common ancestry (i.e., superfamily Geomyoidea). We also found UV-reflective morphology in jerboas (family Dipodidae) highly similar to those seen and measured in kangaroo rats. We conclude that these similarities amongst jerboas and kangaroo rats are the products of convergent evolution.

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### 153 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Cybil Nicole Cavalieri<sup>1</sup>, David C. Druskins<sup>1</sup>, Lauren T. Phillips<sup>2</sup>, Kay E. Holekamp<sup>1</sup>, Barbara L. Lundrigan<sup>1,3</sup>**

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#### **What's in a Bite: Skull Ontogeny and Dietary Challenge**

Developmental constraints can delay the timing of morphological maturity, which in turn affects an individual's ability to compete with conspecifics. Here we compare ontogeny of the cranium and mandible in 6 species of carnivores,

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

representing a range of dietary preferences. We test the hypothesis that trade-offs exist between dietary challenge (i.e., “take down” difficulty and food consistency) and the rate and timing of skull development, such that species with more “difficult” diets reach morphological landmarks (e.g., age at adult skull morphology) later relative to other life-history events. Skulls of each species representing individuals ranging from 1 day to several years of age were photographed and digitized in 3 views (ventral cranium, lateral cranium, and lateral mandible). Ontogenetic change in skull size (centroid size) and shape (Procrustes distance from the average for the youngest specimens) were plotted for each species and the ages at maturity compared. To estimate age at maturity for skull size and shape, we used the 95% of the asymptotic (adult) value from nonlinear growth models selected using Akaike Information Criterion. Interspecific differences in skull ontogeny were interpreted in the context of life history events (e.g., age at 1st reproduction). Preliminary data suggest a positive relationship between dietary challenge and the timing of skull maturity. Carnivores with “difficult” diets mature later relative to life history events than do those with less “difficult” diets.

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### 154 (E) Poster Session II, Great Hall C, Monday 9 June 2014

Jerry H. Scrivner<sup>1</sup>, Craig A. Johnson<sup>2</sup>, Camron A. Segó<sup>1</sup>

<sup>1</sup>Department of Biology, Brigham Young University-Idaho, Rexburg, ID 83460 USA; <sup>2</sup>Department of Mathematics, Brigham Young University-Idaho, Rexburg, ID 83460 USA

#### Use of Cementum Annuli and Eye-lens Weight for Aging Coyotes

We used 29 known-aged coyotes (*Canis latrans*) to evaluate 2 different aging techniques: cementum annuli analysis (CAA) and eye-lens weight. Two lower canines and eye lenses were collected from each coyote. Canines were sent to Matson's laboratory for estimation of age by CAA. The lab was unaware that duplicate teeth were submitted for each coyote. We compared the estimated ages from the lab to the known ages to determine accuracy. Precision was measured by how often canines from individual coyotes yielded the same age estimate. The lab correctly determined age using CAA for 52 of 56 (93%) teeth. There was a correlation between the mean estimated age using both canines and the known age. The estimated age,  $y$ , is given by the equation  $y = 0.7179 + 0.9565(x)$ , where  $x$  is the mean age based on annuli counts for both lower canines. There also was a correlation between estimated age based on right and left tooth. Age predictions based on the left tooth matched the right tooth 25 of 28 (89%) occasions. A curvilinear relationship was found between known ages and eye-lens weight: eye lenses grew more rapidly in animals < 1 yr old than in animals > 1 yr old. Age based on eye-lens weight was more variable and less accurate than when estimated using CAA.

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### 155 Poster Session II, Great Hall C, Monday 9 June 2014

Jeffrey Berens<sup>1,2</sup>, Ned A. Dochtermann<sup>1</sup>

<sup>1</sup>Biological Sciences, North Dakota State University, Fargo, ND 58108 USA; <sup>2</sup>Environmental and Conservation Sciences, North Dakota State University, Fargo, ND 58108 USA

#### Morphological Differences within and among *Peromyscus* spp.

The white-footed mouse (*Peromyscus leucopus*) and the deer mouse (*P. maniculatus*) are 2 of the most widespread members of the genus *Peromyscus* in North America. *Peromyscus* species are typically very abundant and comparatively easy to capture, handle, and mark, which has made them 1 of the most common genera to use in research. By using landmark-based geometric morphometric techniques, we sought to determine if *P. maniculatus* displayed patterns of geographic variation in skull morphology in North Dakota and Minnesota. We also sought to determine if skull shape variation could be used to help determine species differentiation between *P. maniculatus* and *P. leucopus* in this region. We analyzed 43 specimens from Minnesota and 246 specimens from North Dakota that were obtained from the skull collection at North Dakota State University. Our results show ecological patterns associated with geographic position of *P. maniculatus* and some species differentiation between *P. maniculatus* and *P. leucopus*.

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### 156 (E) Poster Session II, Great Hall C, Monday 9 June 2014

Amy R. Rutter<sup>1,2</sup>, Jesus Maldonado<sup>2,3</sup>, Kristofer M. Helgen<sup>2</sup>, Eliécer E. Gutiérrez<sup>2</sup>

<sup>1</sup>Department of Ecosystem Science and Management, The Pennsylvania State University, University Park, PA 16802 USA; <sup>2</sup>Division of Mammals, National Museum of Natural History, Smithsonian Institution, Washington, D.C. 20013 USA; <sup>3</sup>Center for Conservation and Evolutionary Genetics, Smithsonian Conservation Biology Institute, National Zoological Park, Washington, D.C. 20008 USA

#### Neotropical Deer: Morphometrics and Taxonomy of the *Mazama americana* Species Complex (Mammalia: Cervidae)

Molecular studies have shown that the genus *Mazama* (brocket deer) is not monophyletic and has extreme molecular and chromosomal variability, indicating the need for taxonomic work at both the genus and species levels. In this study, we investigated the morphological variability of species in the *Mazama americana* complex using linear

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

morphometrics. We took 16 measurements from 61 adult (i.e., those having complete dentition) skull specimens. After transforming the raw data utilizing the natural logarithm, we conducted a cluster analysis based on Euclidian distances and a principal component analysis (PCA) employing the covariance matrix. The 1st principal component of the PCA largely captured differences in size, explaining 84.22% of the variation among analyzed specimens. Both a bivariate plot of the 1st and 2nd principal components and the cluster analysis showed separation of taxa with several atypical exceptions. Our analyses have several taxonomic implications. *Mazama zetta*, a taxon traditionally treated as a synonym of *M. americana*, was found to be morphometrically distinct. Similarly, our results support the recognition of *Mazama temama* at the species level. This species was previously considered a synonym of *M. americana* and raised to the species level based mainly on karyotypic data. Specimens provisionally assigned to *M. americana* embedded in several clusters, demonstrating the urgent need for a comprehensive taxonomic revision in this group.

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### 157 Poster Session II, Great Hall C, Monday 9 June 2014

#### Virginia L. Naples

Department of Biological Sciences, Northern Illinois University, DeKalb, IL 60115-2861 USA

#### **How Did the Mandible in *Hippopotamus amphibius* Get its Hook?**

*Hippopotamus amphibius* famously gapes widely, and the natural upward curve of the lips give these animals their amusing smiles. When their mouths are closed, hippos show large, fleshy, rounded “jowls,” formed by the presence of a portion of the masseter muscle that inserts on the massive anteroventral projection of the mandible, the mandibular flange. Together, these structures form cheeks that bulge ventrolaterally when the mouth is closed, creating the characteristic dorsoventrally deep hippo head shape. In hippos there is both a superficial and a deep masseter muscle, as in many other mammals. Detailed dissections of the masticatory musculature of 2 *H. amphibius* heads demonstrated that the superficial division of this muscle differs from anterior to posterior, with a parallel-fibered structure that maximizes the ability of the anterior portion to stretch to assist in increasing gape. In contrast, the more posterior sections show increased mass and complex pennation that help maximize muscular force generation during mandibular closing. The longest and most anterior superficial masseter fibers arise from an anteroposteriorly elongated, ridge-bounded scar on the lateral surface of the zygomatic arch, and occupy approximately one-third of the entire ridge. Fibers of this muscle portion insert on a triangular region of the “hook,” wrapping around ventromedially and anteriorly, an arrangement that allows at least a 20% increase in fiber excursion, and a similar additional increment of gape.

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### 158 Poster Session II, Great Hall C, Monday 9 June 2014

#### Barbara J. Shaw

Colorado State University, Fort Collins, CO 80523 USA

#### **Does Size Matter? Isometric vs. Allometric Scaling in Armadillos, Pamphateres, and Glyptodonts (Order Cingulata)**

Members of the Order Cingulata (armadillos, pamphateres, and glyptodonts) are generally power diggers. The extant species of Cingulata are tiny compared to their extinct relatives. They range in size from the 12 cm *Chlamyphorus* (fairy armadillos) to the more than 3 m glyptodonts, like *Panochthus*. One factor in evaluating the biomechanics of a species is to establish an accurate estimate of body mass, however armored organisms defy the usual estimates. To better understand the locomotion of glyptodonts and pamphateres, the best model, therefore, is using extant but small armadillos, which also are armored. This calls into question isometric versus allometric scaling. If armadillos are closer to an isometric scale, the more fit the model, and thus better able to estimate the body mass and emulate the locomotion of their giant, extinct relatives. Because of the digging lifestyle, the bones in some of the small extant species are very robust. This study examines isometric and allometric scaling of humeri and femora among the extinct and extant cingulatan by comparing a morphometric analysis to a log transformed regression of these same specimens. The data indicate that *Priodontes* and *Cabassous* armadillos are a good isometric model when examining their larger extinct relatives.

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### 159 Poster Session II, Great Hall C, Monday 9 June 2014

#### Laureano R. González-Ruiz<sup>1</sup>, Sandrine Ladevèze<sup>2</sup>, Ross D. MacPhee<sup>3</sup>

<sup>1</sup>Laboratorio de Investigaciones en Evolución y Biodiversidad, Universidad Nacional de la Patagonia “San Juan Bosco”, CONICET, Esquel 9200 Chubut, Argentina; <sup>2</sup>Muséum National d’Histoire Naturelle, UMR7207 CR2P CNRS/MNHN/UPMC, Paris, France; <sup>3</sup>Vertebrate Zoology, American Museum of Natural History, New York, NY 10024 USA

#### **Dental Anomalies in *Euphractus sexcinctus* Wagler (Mammalia: Xenarthra: Dasypodidae)**

Dental anomalies in Dasypodidae (Mammalia: Xenarthra) have never been thoroughly examined. For this contribution, we analyzed anomalies in 66 *Euphractus sexcinctus* (six-banded armadillo) specimens housed in the Department of Mammalogy, American Museum of Natural History (New York). Group 1 ( $n = 50$ ) consists of wild-

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

caught specimens collected in Argentina, Bolivia, Uruguay, and Brazil. Group 2 ( $n = 16$ ) consists of captive specimens donated to the AMNH by the Wildlife Conservation Society (Bronx Zoo and Central Park Zoo). *Euphractus sexcinctus* exhibits a dentition consisting of monophyodont, homodont, and euhypsodont molariforms. The typical dental formula is 9/10 (Mf/mf), with 1st Mf in the premaxilla. As in xenarthrans generally, the homology of molariforms to typical eutherian tribosphenic cheek teeth has not been established. Group 1 specimens display supernumerary teeth in the maxilla (2%) as well as the dentary (4%), whereas Group 2 specimens show supernumerary teeth in the dentary only (12.5%). Only 6% of Group 1 had missing teeth, compared to 18.75% showing tooth loss in Group 2. Two captive specimens exhibited abnormally high crowns. One had normal mandibular occlusion, indicating that the tooth grew very fast and/or suffered very little wear. The other possessed an abnormal dentary, resulting in irregular occlusion and, thus, unequal attrition. Although dental anomalies were recorded in both captive and wild specimens, the proportions of those variations are proportionally greater in captive individuals.

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### 160 (E,TA) Poster Session II, Great Hall C, Monday 9 June 2014

**Kristy L. Tuttle**

*Department of Biological Sciences, Northern Illinois University, DeKalb, IL 60115 USA*

#### **Form Following Function? Shared Linear and Shape Dimensions of the Humerus and Femur in Two Disparate Locomotor Guilds**

Members of a locomotor guild, a group of species that habitually practice a particular form of locomotion, share a suite of musculoskeletal features based on the mechanical demands placed on the skeleton during locomotion. This study examines convergent osteomorphology of the distal humerus and proximal femur in 2 disparate locomotor guilds. ANOVA, MANOVA, regression, and PCA are used to compare humeri in 7 fossorial and 4 ricochetal genera and femora in 9 fossorial and 5 ricochetal genera, all within the order Rodentia. Differences and similarities are compared between non-weight bearing, manipulative humeri and weight-bearing high-loading humeri, and between quadrupedal high-loading femora and bipedal high-loading femora. In ricochetal groups, forearm rotation and hand manipulation, with the humeri held in habitual dorsiflexion, produces elbow morphology similar to that seen in fossorial forelimb flexion under high-loading. Femora of both groups share similar morphologies related to thigh abduction under high-loading, with ricochetal groups displaying a markedly enlarged greater trochanter and a proximally shifted midshaft.

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### 161 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Melissa Sutton**

*Department of Biological Sciences, California State University-Chico, Chico, CA 95926 USA*

#### **Assessment of Sexual Dimorphism in Cranial Morphology in Western Gray Squirrels**

The presence or absence of sexual dimorphism can be a valuable indicator of selective pressures, including sexual selection, acting on a species. Sexual dimorphism is most often attributed to sexual selection, which is expected to exert more pressure on species whose mating system is non-monogamous. The type of sexual dimorphism most commonly seen in mammals is size dimorphism in which males are larger than females. Published literature on species within *Sciurus* indicates that most species are polygynous. I predicted from this that western gray squirrels (*Sciurus griseus*) might be expected to be polygynous and, therefore, display some degree of sexual dimorphism. This study aimed to determine if sexual dimorphism occurs in western gray squirrels. To determine this, I photographed a sample ( $n = 57$ ) of western gray squirrels collected in Butte County, CA, USA. Using the freeware program, ImageJ, I measured 20 cranial features of each of the specimens. I performed multivariate analysis of variance to determine if males and females differed significantly from each other with respect to the measured features. I found no evidence ( $p = 0.359$ ) that males and females differed significantly from one another. These results indicate that either sexual selection is not an important selective pressure for or another selective pressure is acting to maintain monomorphism in the western gray squirrel.

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### 162 Poster Session II, Great Hall C, Monday 9 June 2014

**David W. Hale**

*Department of Biology, U.S. Air Force Academy, CO 80840 USA*

#### **Elevational Record for Deer Mice**

Sherman live traps were set on the summit of Mount Elbert (4401 m ASL), the highest peak in Colorado and the second-highest peak in the contiguous United States, to ascertain whether deer mice (*Peromyscus maniculatus*) were present at this high elevation. The 15 traps yielded 7 deer mice, all of which were adults. The presence of deer mice on the summit of Mount Elbert represents an elevational record for this species.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

163 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Yeong-Seok Jo<sup>1</sup>, John L. Koprowski<sup>2</sup>, Byung-Jin Choi<sup>3</sup>, John T. Baccus<sup>1</sup>**

<sup>1</sup>Department of Natural Resources Management, Texas Tech University, Lubbock, TX 79409 USA; <sup>2</sup>School of Natural Resources and Environment, University of Arizona, Tucson, AZ 85721 USA; <sup>3</sup>Korea Natural Environment Institute Co. LTD, Seoul 122-837 Korea

## **Mammals of Korea: A Guide to the Korean Mammals**

The Korean peninsula with associated islands located between the Pacific Ocean and Asian Continent has a distinctive mammalian fauna. Unfortunately, facts about Korean mammals are relatively unknown in other countries. Therefore, we plan to introduce this mammalian assemblage through the 1st rigorous guidebook on Korean mammals produced in English. Chapters on taxonomic status, fossil history, distribution, natural history, species accounts, management, and conservation of 132 species in 8 orders and 31 families of both terrestrial and marine mammals with illustrations, range maps, color plates, and field sign will comprise this tome. We will present the history of Korean mammalogy and include sections on recent trends in research on Korean mammals, diversity hotspots for ecotourism and current endeavors on conservation of endangered mammals in Korea. Our volume will highlight the splendid diversity of mammals of Korea in a colorful and informative compendium.

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164 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Amanda K. Jones<sup>1</sup>, Joseph A. Cook<sup>1,2</sup>**

<sup>1</sup>University of New Mexico; <sup>2</sup>Museum of Southwestern Biology, Albuquerque, NM 87131 USA

## **Mammals of the Gila**

As the threats to biodiversity grow, there is also a growing need for natural history data, which establishes baselines for comparisons regarding changes in species' distributions, phenology, and reproduction. This is especially true with the trend towards a warmer, drier climate. I am conducting a survey of the mammals of the Gila Wilderness of New Mexico, which includes gathering data on species occurrences, habitat affinities, elevational distributions, migration timing (for bats), and reproductive timing and success. This data will not only be used for my thesis, but all specimens and associated data will be interred at the Museum of Southwestern Biology for use in future studies.

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165 Poster Session II, Great Hall C, Monday 9 June 2014

**Susan C. Loeb<sup>1</sup>, Thomas J. Rodhouse<sup>2</sup>, Laura E. Ellison<sup>3</sup>, Cori L. Lausen<sup>4</sup>, Thomas Ingersoll<sup>5</sup>, Jonathan Reichard<sup>6</sup>, Kathryn Irvine<sup>7</sup>, Wayne E. Thogmartin<sup>8</sup>, Jeremy T. H. Coleman<sup>9</sup>, John R. Sauer<sup>10</sup>**

<sup>1</sup>Southern Research Station, U.S. Forest Service, Clemson, SC 29634 USA; <sup>2</sup>National Park Service, Bend, OR 97701 USA; <sup>3</sup>USGS Fort Collins Science Center, Fort Collins, CO 80526 USA; <sup>4</sup>Wildlife Conservation Society, Kaslo, B.C. V0G 1M0 Canada; <sup>5</sup>Department of Defense, Aberdeen, MD 21001 USA; <sup>6</sup>U.S. Fish and Wildlife Service, Hadley, MA 01035 USA; <sup>7</sup>USGS Northern Rocky Mountain Science Center, Bozeman, MT 59715 USA; <sup>8</sup>USGS Upper Midwest Environmental Sciences Center, LaCross, WI 54603 USA; <sup>9</sup>U.S. Fish and Wildlife Service, Hadley, MA 01035 USA; <sup>10</sup>USGS Patuxent Wildlife Research Center, Laurel, MD 20708 USA

## **NABat — The North American Bat Monitoring Program**

Bats in North America are facing unprecedented threats including white-nose syndrome, wind energy development, habitat loss and fragmentation, and climate change. Until now, there has been no coordinated monitoring program to track changes in their populations in response to these threats. The North American Bat Monitoring Program (NABat) has been under development since 2012 and will be operational in 2014–2015. NABat will provide the statistical, biological, and administrative architecture for coordinated bat population monitoring that will promote effective decision-making and long-term viability of bat populations across North America by providing robust data on changes in bat distributions and abundance. The sampling framework is comprised of 10 by 10 km grid cells across Canada, the USA, and Mexico. The Generalized Random Tessellation Stratified (GRTS) design will be used to create a master list of spatially balanced grid cells within each state and province. The primary data sources are maternity and hibernacula counts, acoustic surveys conducted along driving transects, and acoustic surveys at stationary points across the landscape. Data will be housed and managed in the Bat Population Database at the USGS Fort Collins Science Center. Once sufficient data are available, NABat will produce periodic "State of North America's Bats" reports. This monitoring program will provide the information necessary to promote effective conservation decision-making and long-term viability of bat populations across the continent.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

166 Poster Session II, Great Hall C, Monday 9 June 2014

**Sue Ann Gardner, Paul Royster**

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167 Poster Session II, Great Hall C, Monday 9 June 2014

**Kent Smith<sup>1,2</sup>, Nicholas J. Czaplewski<sup>2</sup>, Richard L. Cifelli<sup>2</sup>**

<sup>1</sup>Department of Anatomy and Vertebrate Paleontology, Oklahoma State University Center for Health Sciences, 1111 W. 17th Street, Tulsa, OK 74107 USA; <sup>2</sup>Sam Noble Oklahoma Museum of Natural History, 2401 Chautauqua Avenue, University of Oklahoma, Norman, OK 73072 USA

**Barstovian (Middle Miocene) Carnivorans from the Monarch Mill Formation, Churchill County, Nevada**

A Barstovian-age vertebrate assemblage, the Eastgate local fauna, was discovered in the lower most part of the Monarch Mill Formation. This fauna includes the remains of fish, amphibians, reptiles, birds, and mammals; the carnivores are the focus of this study. The Canidae are represented by *Tomarctus brevirostris* (Borophaginae) and *Leptocyon* sp. indet. (Caninae). The earliest record of Ailuridae in North America is represented by a new species of *Actiocyon*. The Mustelidae are represented by a new genus of Galictinae and a new genus of Lutrinae. A 4th family of Carnivora is represented by the felid *Pseudaelurus* sp. indet. Based on nearby, contemporaneous paleobotanical evidence from fossil leaf assemblages, the vegetation in the area was mixed coniferous and hardwood forest, as well as chaparral-sclerophyllous shrubland. This suggests the altitude of the area was between 2700–2800 m in paleoaltitude before dropping later to its current elevation of 1600 m. *Tomarctus brevirostris* is limited biochronologically to the Barstovian land-mammal age and thus is consistent with the age indicated by other members of the Eastgate local fauna as well as by indirect tephrochronological dates previously associated with the Monarch Mill Formation. The Eastgate local fauna improves our understanding of mammalian successions and evolution, during and subsequent to the climatic optimum in the Miocene (17–14 Ma).

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168 Poster Session II, Great Hall C, Monday 9 June 2014

**Robert K. Rose, A. Scott Bellows**

Department of Biological Sciences, Old Dominion University, Norfolk, VA 23529-0266 USA

**Population Responses to Stomach Worms (Order Spirurida) in Hispid Cotton Rats in Southeastern Virginia**

Nematode stomach worms (*Mastophorus* and *Physaloptera*) occasionally infect herbivorous small mammals, especially hispid cotton rats (*Sigmodon hispidus*) because of their tendency to eat insects when available. Several groups of insects, including crickets, ground beetles, and earwigs, serve as intermediate hosts for the worms. During necropsy studies of reproduction in wild-caught cotton rats over 50 g, the stomachs were opened and any worms present were removed, counted and weighed to the nearest mg with an Ohaus electronic balance. We detected higher infestation rates of stomach worms in a population from an oldfield undergoing secondary succession (79.79 % of 287 animals) than in animals taken from roadsides or mowed fields (23.06%,  $n = 425$ ). Further, the parasite loads were much greater in the oldfield, with a mean of 1,293.12 mg, compared to 492.65 mg in cotton rats taken from managed fields. The largest mass of parasites was 6,200 mg from an infected animal in the successional field, whereas in the managed habitats the heaviest parasite load was 3,060 mg. An unexpected result was that the 328 parasitized cotton rats had significantly ( $p < 0.0001$ ) higher mean body mass (101.54 g) than that of the 384 animals without parasites (89.33 g). Despite analysis of other features, the cause(s) of the growth enhancement related to parasitism remain unknown.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

169 (E,TA) Poster Session II, Great Hall C, Monday 9 June 2014

**Adam A. Ahlers<sup>1,2</sup>, Mark A. Mitchell<sup>3</sup>, Jitender P. Dubey<sup>4</sup>, Robert L. Schooley<sup>1</sup>, Edward J. Heske<sup>2</sup>**

<sup>1</sup>Department of Natural Resources and Environmental Sciences, University of Illinois, Urbana, IL 61801 USA; <sup>2</sup>Illinois Natural History Survey, Prairie Research Institute, Champaign, IL 61820 USA; <sup>3</sup>College of Veterinary Medicine, University of Illinois, Urbana, IL 61820 USA; <sup>4</sup>Animal Parasitic Diseases Laboratory, Animal and Natural Resources Institute, Agricultural Research Service, US Department of Agriculture, Beltsville, MD 20705 USA

## **Human-modified Watersheds Concentrate *Toxoplasma gondii* in a Freshwater Ecosystem**

We assessed the landscape epidemiology of the parasite *Toxoplasma gondii* in a freshwater ecosystem in Illinois, USA. This agricultural region has extensive subsurface drainage systems that could transport *T. gondii* oocysts into the watershed. We used muskrats (*Ondatra zibethicus*) and American mink (*Neovison vison*) as sentinels of watershed health. We predicted individuals from larger watersheds would more likely be seropositive as they were exposed to drainage from larger areas. We also evaluated amount of urban landcover within the watershed and proximity to farmsteads in competing models of *T. gondii* infection. Antibodies for *T. gondii* were detected in 60% of muskrats ( $n = 30$ ) and 77% of mink ( $n = 26$ ). Infection rates were 1.7 times higher than those typical for mammals in upland habitats in this region. As predicted, watershed size was the most important predictor of *T. gondii* infection in muskrats. Models incorporating urban landcover and proximity to farmsteads had little support. None of our models reliably predicted seroprevalence in mink, possibly because mink are less strictly associated with riparian habitats. Transport and concentration of *T. gondii* in freshwater ecosystems is likely facilitated by modified drainage practices used worldwide.

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170 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Cassandra D. Pauling, Anna Oller, Scott Lankford, Victoria L. Jackson**

Department of Biology and Agriculture, University of Central Missouri, Warrensburg, MO 64093 USA

## **Surveying Internal Parasites and Fecal Glucocorticoid Metabolites in Captive Scimitar-horned Oryx, *Oryx dammah*, in Different Environments**

The scimitar-horned oryx, *Oryx dammah*, is an endangered species which is extinct in the wild and is currently managed in various captive management programs. Determining beneficial environmental settings will aid in maintenance of optimal herds for further establishment in captivity as well as potential future reintroductions. This can be partially accomplished by evaluating cortisol levels and parasite loads. This study aims to analyze resilience and susceptibility of the scimitar-horned oryx to the potential exposure to a variety of parasites throughout different regions, as well as determine parasite diversity including any species-specific parasites. This study also aims to determine the difference in cortisol levels between different environmental settings to help establish a baseline cortisol level and determine optimal environments. Fecal egg counts will be performed by using the McMaster method in order to determine parasite loads and wet mounts will be prepared in order to identify genera of parasite ova present in feces. Fecal glucocorticoid metabolites will be assayed using an enzyme-linked immunosorbent assay (ELISA). This study can help determine host-parasite relationships, reduce chance of introducing non-native parasites to regions of translocation, and aid in increased success of reintroductions.

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171 (E) UNDERGRADUATE RESEARCH AWARD, Poster Session II, Great Hall C, Monday 9 June 2014

**Kimberly Conway, Paul Stapp**

Department of Biological Science, California State University, Fullerton, Fullerton, CA 92831 USA

## **Determinants of Botfly Infestation of Thirteen-lined Ground Squirrels in Colorado Shortgrass Steppe**

Botfly larvae were discovered on thirteen-lined ground squirrels (*Ictidomys tridecemlineatus*) during long-term (1999–2011) population studies in north-central Colorado. Although botflies are common parasites of small mammals, there were no records of infestation of this squirrel species and the species of botfly was unknown. We examined prevalence and intensity of infestation of botflies in ground squirrels trapped in saltbush and grassland habitats in spring and summer to determine host and environmental factors that influence patterns of infestation. We also investigated possible effects of prescribed fires, a common habitat management technique in grasslands, on infestation prevalence. Squirrels had from 1–7 warbles, with 44% having only 1 warble. Infested squirrels were rarely found in saltbush sites and during spring (May–June) trapping. Across the 13 summers (July), average prevalence of infestation in grasslands was 7.9%. Infestation did not vary significantly with host sex, age, or weight. Prevalence was significantly higher (33.0%) in burned sites 1 year after a prescribed fire, and remained consistently higher in burned sites than unburned sites. Our results suggest that fires may alter the environment in ways that make parasitism of squirrels more likely. Molecular analyses of cytochrome oxidase I (COI) sequences of 3 late-instar larvae revealed that the botfly species was likely most closely related to *Cuterebra fontinella*, a species typically associated with white-footed mice (genus *Peromyscus*).

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

172 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Delina E. Dority<sup>1</sup>, Zachary P. Roehrs<sup>2</sup>, R. Scott Seville<sup>1</sup>**

<sup>1</sup>University of Wyoming, Casper College Center, 125 College Dr. Casper, WY 82601 USA; <sup>2</sup>School of Math and Sciences, Laramie County Community College, Cheyenne, WY 82007 USA

## **A New *Eimeria* (Apicomplexa: Eimeriidae) in *Perognathus fasciatus* (Rodentia: Heteromyidae) from Wyoming**

The olive-backed pocket mouse, *Perognathus fasciatus*, was captured from 4 sites in Fremont County, Wyoming, during the summers of 2011 and 2012. A total of 62 *P. fasciatus* (21 in 2011 and 44 in 2012) were captured, resulting in 48 individuals providing 59 samples (2011: 8 intestinal and 16 fecal; 2012: 35 fecal samples). Of these 48 individuals, 16 (33.3%) were positive for oocysts *Eimeria* sp. nov. (2011: 7 of 14, 50%; 2012: 9 of 34, 26.5%). Oocysts of *Eimeria* sp. nov. are ellipsoid to ovoid in shape, 23.33 by 20.68 (19.30–26.85 by 16.89–24.54)  $\mu\text{m}$ , and typically contain a residuum that is single, bubble-like, and smooth. The sporocysts are oval in shape, 10.04 by 8.16 (9.64–11.69 by 6.69–8.01)  $\mu\text{m}$ , and contain a residuum that appears similar to a cluster of grapes usually consisting of 3.45 (2.52–4.38) spheres. The oocyst has 1–2 polar granules and 2 wall layers with a mean wall thickness of 1.29 (0.73–1.78)  $\mu\text{m}$ . The *E.* sp. nov. lacks a micropyle, and the stieda body is small, appearing flattened to knobby. We provide a description of this new species based upon comparisons with other *Eimeria* morphotypes from *Perognathus* and *Dipodomys*. These *Eimeria* constitute the only records of coccidia from *P. fasciatus* and the 1st identification of an *Eimeria* from any heteromyid in Wyoming.

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173 Poster Session II, Great Hall C, Monday 9 June 2014

**Heather Martin, Polly Campbell**

Department of Zoology, Oklahoma State University, Stillwater, OK 74078 USA

## **The Chemistry of Speciation: Candidate Genes for Premating Isolation in Mice**

Behavioral barriers to gene flow between species are difficult to measure and even harder to dissect to the level of genes. However, genes required for normal reproductive behavior are compelling candidates for assortative mating between species. In rodents, chemical communication dominates, and chemoreceptors in the vomeronasal organ (VNO) are essential for reproductive and defensive behaviors. In *Mus* (house mice and their wild relatives), individual VNO receptors (VRs) are narrowly tuned to distinct chemical compounds in urine and other excretions, and different receptors are activated by conspecific versus heterospecific cues. Species differences in degree of geographic range overlap, the costs incurred by females who mate with males from the wrong species, and the prevalence of hybridization in nature, provide a natural experiment in which to study the genetics and evolution of premating isolation. We present results from a preliminary study whose goal was to quantify the acuity of VNO-mediated discrimination among male chemosignals. We exposed females from 2 subspecies of house mice to male chemical cues from either their own subspecies, the other subspecies, or a co-distributed congener, and measured the relative expression of a suite of VRs previously identified as responding with high specificity to conspecific versus heterospecific male cues. This candidate gene approach lays the foundation for whole VNO transcriptome analysis and promises key insight into the molecular basis of species recognition in mice.

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174 Poster Session II, Great Hall C, Monday 9 June 2014

**Charlotte R. Milling<sup>1</sup>, Janet L. Rachlow<sup>1</sup>, Lisa A. Shipley<sup>2</sup>, David Paul<sup>3</sup>**

<sup>1</sup>Department of Fish and Wildlife Sciences, University of Idaho, Moscow, ID 83844 USA; <sup>2</sup>School of the Environment, Washington State University, Pullman, WA 99164 USA; <sup>3</sup>Department of Movement Sciences, University of Idaho, Moscow, ID 83844-2401 USA

## **A Comparative Assessment of Thermoneutral Zones of Two Sagebrush Steppe Lagomorphs**

Although metabolic rates are well documented to scale with body size in mammals, a recent study was the 1st to examine how critical temperatures and the thermoneutral zone (TNZ) scale to body size of mammals while also controlling for phylogenetic relationships (Riek and Geiser, 2013). That study reported that both the lower critical temperature and TNZ were moderately body-mass dependent across a diversity of mammal species. We examined these 2 thermal parameters for 2 species of sympatric lagomorphs that inhabit the sagebrush-steppe ecosystem of the intermountain West, which is characterized by hot summers (> 30°C) and cold winters (< 0°C). We hypothesized that the larger-bodied mountain cottontail (*Sylvilagus nuttallii*) would have wider a TNZ and cooler lower critical temperature than the smaller pygmy rabbit (*Brachylagus idahoensis*). We used flow-through respirometry to measure oxygen consumption at temperatures predicted to bracket the TNZ of wild-caught pygmy rabbits and mountain cottontails. This research provides physiological data for evaluating the relative importance of burrows as thermal refugia to help understand differences in life history traits between pygmy rabbits (obligate burrowers) and other lagomorph species that also live in the sagebrush-steppe environment.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## 175 Poster Session II, Great Hall C, Monday 9 June 2014

**Frank Knight<sup>1</sup>, Michael Power<sup>2</sup>, Katie Murtough<sup>2</sup>**

<sup>1</sup>Division of Sciences and Mathematics, University of the Ozarks, Clarksville, AR 72830 USA; <sup>2</sup>Nutrition Laboratory, Conservation Ecology Center, Smithsonian Conservation Biology Institute, National Zoological Park, Washington, D.C. USA

### **Got Armadillo Milk**

This study focuses on the unusual armadillos' (*Dasypus novemcinctus*) most ordinary mammalian feature, milk, and its relation to the armadillos' most obvious, namesake trait, armor. This is the 1st report of milk composition for any member of the superorder Xenarthra. Because mineralization of the osteoderm occurs mostly after birth, its development and growth may depend on a unique milk formula. Six female armadillos wild-caught in Arkansas that birthed in captivity were milked at regular intervals through the lactation period, and 3 additional females were milked once each at the University of the Ozarks, producing a total of 25 milk samples. Samples were assayed following standard protocols at the Nutrition Laboratory of the Smithsonian National Zoological Park. Nutrient composition varied among individual and with lactation stage. Armadillo milk protein and ash (mineral) levels are among the highest of mammal milks so far studied (mean  $\pm$  SEM: 10.05%  $\pm$  0.44% and 2.48%  $\pm$  0.20%, respectively). Milk fat is moderate (5.20%  $\pm$  0.44%) and milk sugar levels are relatively low (2.69%  $\pm$  0.09%). The mineral content of armadillo milk is more than twice that of most mammals and the percentage of calcium and phosphorus more than doubles over the course of lactation. The high milk protein content suggests rapid growth, and the high and increasing mineral content is consistent with the undoubtedly high mineral requirement for the osteoderm.

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## 176 Poster Session II, Great Hall C, Monday 9 June 2014

**Esteban A. Actis<sup>1</sup>, Sergio Mosconi<sup>2</sup>, Graciela A. Jahn<sup>3</sup>, Mariella Superina<sup>1</sup>**

<sup>1</sup>Laboratorio de Endocrinología de la Fauna Silvestre, IMBECU, CCT CONICET Mendoza, Mendoza, Argentina; <sup>2</sup>Fundación Escuela Medicina Nuclear – CNEA, Mendoza, Argentina; <sup>3</sup>Laboratorio de Reproducción y Lactancia, IMBECU, CCT CONICET Mendoza, Mendoza, Argentina

### **Reproductive Strategy of Armadillos (Xenarthra: Cingulata): Is the Carapace a Source of Minerals during Lactation?**

Armadillos (Xenarthra: Cingulata) are well identifiable by their ossified carapace. Their offspring have rapid growth rates and require high mineral levels. However, armadillos feed on a low-quality diet mainly consisting of insects, a poor source of calcium and phosphate, which raises the question how lactating females obtain the needed minerals to provide their offspring sufficient quantities for the development and hardening of their carapace. The main objective of this study was to evaluate whether armadillos demineralize their carapace or endoskeleton during lactation. We performed computed tomography of 26 female and 13 male dead pichis (*Zaedyus pichiy*) of different age classes and reproductive status and compared bone mineral density (BMD) of their marginal scutes, compact and spongy bone of the carapace, and femoral bone. Yearlings of both genders had significantly lower BMD values than adults. BMD of marginal scutes and femoral heads, but not of other carapace regions, was significantly higher in lactating females and males than in adult females without signs of gestation or lactation. Also, lactating females tended to demineralize scutes and femora over the course of lactation. We conclude that lactating females use parts of both their carapace and their endoskeleton as mineral sources to provide calcium and phosphate to their offspring. We hypothesize that females accumulate calcium during pregnancy and require a minimum level of mineralization to successfully breed.

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## 177 (E) Poster Session II, Great Hall C, Monday 9 June 2014

**Brianne V. Boan<sup>1</sup>, Kelley M. Stewart<sup>1</sup>, Thomas D. Lohuis<sup>2</sup>, Cynthia J. Downs<sup>1</sup>**

<sup>1</sup>Department of Natural Resources and Environmental Science, University of Nevada, Reno, Reno, NV 89557 USA; <sup>2</sup>Alaska Department of Fish and Game, Anchorage, AK 99518 USA

### **Consequences of Motherhood: Relationships between Reproduction, Cortisol, and Immune Function**

In wildlife populations, fitness is often measured in terms of reproductive success by progeny recruited into the breeding population. Many intrinsic and extrinsic variables affect an individual's fitness. Dall sheep (*Ovis dalli dalli*) populations in south central Alaska have been declining for about the past 20 years. Recent studies have indicated highly fluctuating pregnancy and parturition rates without apparent cause. By focusing on intrinsic physiological interactions to answer population management questions, we were interested how stress via cortisol levels affects reproduction and how reproduction affects components of constitutive immune function (bacteria killing ability and haptoglobin). We predicted a negative relationship between high cortisol levels and pregnancy status and a negative relationship between pregnancy and constitutive immune function. Cortisol was extracted from hair samples collected from marked individuals and constitutive immune function was tested from serum samples. We did not find significant relationships between reproduction and cortisol nor immune function. In the top model, pregnancy trended a negative effect on bacteria killing ability. We did observe significant differences in immune function between study sites and age classes in the year 2013. Bacteria killing ability was significantly lower for senescent animals. Both immune

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

function components differed significantly between study sites. Cortisol had a trending negative effect on bacteria killing ability. Results suggest a greater role by extrinsic factors affecting cortisol levels and immune function.

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### 178 Poster Session II, Great Hall C, Monday 9 June 2014

**Thomas S. Jung<sup>1</sup>, Troy M. Hegel<sup>2</sup>, Shannon A. Stotyn<sup>3</sup>, Sophie M. Czetwertynski<sup>3</sup>**

<sup>1</sup>Yukon Department of Environment, Whitehorse, Yukon Y1A 2C6 Canada; <sup>2</sup>Canadian Wildlife Service, Environment Canada, Whitehorse, Yukon T6G 2H1 Canada; <sup>3</sup>Department of Renewable Resources, University of Alberta, Edmonton, Alberta T6G 2H1 Canada

#### **Co-occurrence of Reintroduced and Resident Ungulates on a Shared Winter Range in Northwestern Canada**

It is generally believed that for interspecific competition to occur species must use the same resources (e.g., food, habitat) and overlap in time and space. Bison (*Bison bison*) were reintroduced to southwestern Yukon, Canada, where they are sympatric with resident caribou (*Rangifer tarandus*), moose (*Alces americanus*), and thimhorn sheep (*Ovis dalli*). Concerns from local communities regarding potential competition between reintroduced bison and resident ungulates prompted us to test their spatial distribution for co-occurrence. We conducted multiple aerial surveys ( $n = 11$ ) to develop a presence/absence matrix (4 species by 779 cells) of the late winter spatial distribution of ungulates. Randomization procedures were used to conduct a null model analysis of co-occurrence. C-scores and V-ratios indicated that species were neither negatively nor positively associated with one another; rather their spatial distribution suggested neutral interactions between these species. The most co-occurrence, however, was between bison and sheep, suggesting that there may be a weak positive association between these species. We conclude that the overall potential for competition between reintroduced bison and resident ungulates during late winter is low, based on spatial overlap. Even though bison are reintroduced, these species had interacted for thousands of years and have likely co-evolved mechanisms to partition resources and co-exist.

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### 179 Poster Session II, Great Hall C, Monday 9 June 2014

**Thomas S. Jung<sup>1</sup>, Shannon A. Stotyn<sup>2</sup>, Sophie M. Czetwertynski<sup>3</sup>**

<sup>1</sup>Yukon Department of Environment, Whitehorse, Yukon Y1A 2C6 Canada; <sup>2</sup>Canadian Wildlife Service, Environment Canada, Whitehorse, Yukon Y1A 5X7 Canada; <sup>3</sup>Department of Renewable Resources, University of Alberta, Edmonton, Alberta T6G 2H1 Canada

#### **Dietary Overlap and Potential Competition in a Dynamic Ungulate Community in Northwestern Canada**

The potential for interspecific competition for food resources is a key consideration when newly introduced ungulates occupy a shared range with resident native species. To assess potential competition among ungulates, we examined dietary overlap of 7 species in southwestern Yukon, Canada. Diet composition at the forage class scale and composite diet indices (diversity, evenness, and niche breadth) were compared among species found at 2 elevation classes (high and low) during broad seasons (summer and winter), using diet data derived from microhistological analyses. Composite diet indices and use of major forage classes differed among species between seasons and elevations. Dietary overlap for most species pairs was low to moderate (0.10–0.70). However, for reintroduced bison (*Bison bison*) and thimhorn sheep (*Ovis dalli*), and bison and semi-feral horses (*Equus ferus caballus*), it was high ( $\geq 0.80$ ), indicating potential for food competition. Dietary overlap between species appeared to be based primarily on morphophysiological classification (i.e., browser-intermediate-grazer), rather than body size. Bison, horses, and sheep were all grazers. Intermediate species such as introduced elk (*Cervus canadensis*) had moderate dietary overlap with several species, but did not highly overlap with any other species. We conclude that the potential for competition for food resources between bison and sheep and bison and horses is high, but that for all other species pairs in our study area is low to moderate.

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### 180 Thematic Session II: Recent Advances in Conservation, Great Halls D & E, Tuesday 10 June 2014

**Fabian M. Jaksic**

Ecology Department, Catholic University of Chile, Santiago, Chile

#### **History, Ecology, and Impacts of the European Rabbit Invasion in Southern South America**

I present an overview of the invasion of the European rabbit (*Oryctolagus cuniculus*) in Chile and Argentina, firstly identifying geographical sources, agencies involved, pathways of introduction and spread, receiving ecosystems, and geographical distribution up to present. Efforts to control this exotic invasive species are commented upon, and limitations to governmental actions are mentioned. Secondly, I analyze ecological data showing what are the main impacts that rabbits have had on Chilean flora, vegetation, and fauna, noting that some impacts are indeed negative (such as fragmentation of shrublands, declines among native mammals, and spread of exotic herb species), but others are positive (such as becoming the staple food of endangered raptors and carnivores, and facilitating spread and germination of native shrubs). Thirdly, I analyze the trade of rabbit skins, and its economic value for Chile. Fourthly, I document a long-term study of a rabbit invasion since its beginning in semiarid Chile, showing temporal fluctuations in abundance and how do these affect the diet of local vertebrate predators. As a conclusion, I offer that

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

invading exotic species may be considered as a natural ongoing experiment on how do they fail or succeed and on how receiving ecosystems adjust to their presence, with cascading effects to develop novel ecosystems.

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### 181 Thematic Session II: Recent Advances in Conservation, Great Halls D & E, Tuesday 10 June 2014

**Paul C. Paquet**

*Raincoast Conservation Foundation, Box 2429 Sidney, BC V8L 3Y3 Canada; Department of Geography, Box 3060 STN CSC, University of Victoria, Victoria, BC V8W 3R4 Canada*

#### "The last word in ignorance is the man who says of an animal or plant: 'What good is it?'" - Aldo Leopold

Wildlife conservation aims to ensure populations and species survive and ecological and evolutionary processes continue. Accordingly, gray wolves (*Canis lupus*) are biologically influential, often disproportionately so, within the environments they inhabit. Mounting scientific evidence increasingly shows that wolves have a significant but idiosyncratic influence over a wide range of environments. For example, through predation and by modifying the behavior of their prey, wolves can exert strong influence on ecological systems via top-down regulation, affecting herbivores that in turn affect standing plant biomass and production. Similarly, wolves directly and indirectly affect mesopredators and therefore the community structure of small prey. Many human activities adversely affect wolves and hence community ecology. Direct effects include lethal culling, hunting, trapping, poisoning, and the destruction of prey. Indirect effects include changes to habitat or movement patterns that result in death or disrupt social relationships. When wolves are eliminated, ecological and evolutionary relationships are distorted far beyond the changes in the number and behavior of ungulates. Killing some individuals in a social group can cause indirect harms by disrupting the transfer of cultural and genetic information between generations and altering group stability and breeding structures in the population. Although direct harms are more obvious, both direct and indirect harms are important determinants of animal welfare and conservation.

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### 182 Thematic Session II: Recent Advances in Conservation, Great Halls D & E, Tuesday 10 June 2014

**Erik A. Beever<sup>1</sup>, Shawn Crimmins<sup>2</sup>, Johanna Varner<sup>3</sup>, Steven L. Clark<sup>4</sup>, Carlo Abbruzzese<sup>5</sup>, Solomon Dobrowski<sup>6</sup>**

*<sup>1</sup>Northern Rocky Mountain Science Center, U.S. Geological Survey, Bozeman, MT 59715 USA; <sup>2</sup>Upper Midwest Environmental Sciences Center, U.S. Geological Survey, La Crosse, WI 54603 USA; <sup>3</sup>Department of Biology, University of Utah, Salt Lake City, UT 84112 USA; <sup>4</sup>Clark College, Vancouver, WA 98663, USA; <sup>5</sup>Washington Department of Natural Resources, Vancouver, WA 98663 USA; <sup>6</sup>Department of Forest Management, College of Forestry and Conservation, University of Montana, Missoula, MT 59812 USA*

#### **Pika Density, Distribution, and Extirpations Over 80 Years: Conservation Lessons on Climate, Mammals' Behavioral Plasticity, and Ever-changing Rules**

The American pika (*Ochotona princeps* Richardson) represents a model system with which to investigate the nuanced mechanisms of how climate influences animal distribution and abundance. We have investigated pika density and abundance in the Greater Yellowstone Ecosystem, Columbia River Gorge, and hydrographic Great Basin. In the Basin, we have used microclimatic sensors, plane-mounted high-resolution radiometric-temperature and multispectral sensors, NDVI, biogeographic variables, and local-site predictors to test competing hypotheses about how and why Basin pikas are largely declining. The Gorge presents a striking apparent contrast in both status and trend of pikas: declines are modest and rare, densities are markedly higher than in the Basin (even at elevations < 100 m), and pikas exhibit dietary and behavioral plasticity considered uncharacteristic of the species. Results from research since 1994 suggest that the strongest determinants of both abundance and persistence vary across space and time; context-dependency in effects of climate is likely the norm rather than the exception. In particular, in the Basin, aspects of climate and microclimate are apparently playing an increasingly important role in local extinctions and density of pikas, and drought and climatic-water balance exert strong short- and long-term effects on pika dynamics. Using the pika as an example, we will raise a vexing problem regarding the intersection of species' taxonomy reflected in different kinds of genetic markers, with likely conservation futures under contemporary climate change.

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### 183 Technical Session 11, Great Halls D & E, Tuesday 10 June 2014

**James Ryan<sup>1</sup>, Phil Myers<sup>2</sup>, Tanya Dewey<sup>2</sup>, Roger Espinosa<sup>2</sup>, George Hammond III<sup>2</sup>, Tricia Jones<sup>2</sup>**

*<sup>1</sup>Biology Department, Hobart & William Smith Colleges, Geneva, NY 14456 USA; <sup>2</sup>Museum of Zoology, University of Michigan, Ann Arbor, MI 48109 USA*

#### **Using Quaadrvark to Enhance Critical Thinking in Mammalogy**

Quaadrvark is a large database query tool linked to species accounts in the Animal Diversity Web (ADW), a growing database including over 4,200 mammalian entries. ADW-Quaadrvark allows students to access and explore ecological and evolutionary patterns using a simple query interface. Mammalogy instructors use Quaadrvark to enhance critical thinking through active inquiry activities. Active inquiry includes approaches to learning where

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

knowledge is gained from experience. Four levels of inquiry-based learning in mammalogy can be used with the ADW-Quaardvark inquiry tool. Confirmation inquiry reinforces a previously learned concept by providing the question and query procedure, with results known in advance. Structured inquiry also provides the question and procedure, but students generate an explanation consistent with the evidence collected. In Guided inquiry, only the question is provided, and students design the query to test the question and provide a consistent explanation. Open inquiry requires students to formulate questions, design procedures, and communicate their results. Guided inquiry activities using ADW-Quaardvark will be demonstrated and future directions in the development of this database tool will be discussed.

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### 184 Technical Session 11, Great Halls D & E, Tuesday 10 June 2014

**Janet L. Rachlow<sup>1</sup>, Jennifer S. Forbey<sup>2</sup>, Lisa A. Shipley<sup>3</sup>, Matthew A. Burgess<sup>4</sup>, Peter J. Olstoy<sup>2</sup>, Charlotte R. Milling<sup>1</sup>, Jordan Nobler<sup>2</sup>**

<sup>1</sup>Department of Fish and Wildlife Sciences, University of Idaho, Moscow, ID 83844-1136 USA; <sup>2</sup>Department of Biological Sciences, Boise State University, Boise, ID 83725 USA; <sup>3</sup>Department of Natural Resource Science, Washington State University, Pullman, WA 99164 USA; <sup>4</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, FL 32611 USA

#### **Evaluating Habitat Characteristics for Mammals in the Sagebrush-steppe using Unmanned Aircraft Systems (UAS) Technology**

Use of unmanned aircraft for applications in wildlife research and conservation has increased rapidly over the past decade. In addition to counting and mapping distributions of animals or their sign (e.g., nests or tracks), unmanned aerial systems (UAS) technology is well suited for quantifying characteristics of habitat. We are evaluating and modeling tradeoffs among 4 competing habitat relationships (concealment from predators, thermal protection, nutrition, and toxicity from plants) for small mammalian herbivores in the sagebrush-steppe environment. To evaluate habitat relationships in ways that are relevant to land managers, we are interested in scaling up from individual animals and shrubs to populations and landscapes. We are using high-resolution imagery obtained via UAS during summer and winter to characterize shrub-steppe vegetation across areas of 1-2 km<sup>2</sup>. Our applications include use of: 1) color imagery to quantify overhead concealment to assess predation risk from aerial predators; 2) 3-dimensional surfaces of shrub heights derived from color imagery for modeling wind speed at the ground surface to evaluate the thermal environment and model concealment from terrestrial predators; and 3) color infrared imagery to map distribution and abundance of plant species that vary in nutrition and toxicity. These techniques provide tools for translating information about fine-scale resource selection into spatially explicit maps of habitat quality over broader spatial extents that can help evaluate consequences of habitat change or restoration.

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### 185 (E) Technical Session 11, Great Halls D & E, Tuesday 10 June 2014

**Daniel U. Greene, Lindsay M. Wagner, Robert A. McCleery**

*Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, FL 32611 USA*

#### **A Comparison of Four Methods for Detecting Fox Squirrels in the Southeastern USA**

Fox squirrels (*Sciurus niger*) in the southeastern United States are difficult to study because of large home ranges, low densities, and low capture rates. Throughout many portions of their range, populations appear to have declined, and 3 of the 10 subspecies currently have a conservation status for protection, with 2 occurring in Florida. Presently, monitoring changes in population size and distribution is difficult because a reliable method is not available to study populations in the southeastern United States. To determine which survey method is most feasible for monitoring fox squirrels, we evaluated overall detection rates (any time a squirrel was seen) and number of unique individuals identified using 4 common survey methods: live-trapping; passive infrared digital cameras; point counts; and transect surveys. Surveys were conducted over 4 seasons. Surveys using cameras produced > 4 times more detections ( $n = 355$ ) than the other 3 methods combined ( $n = 83$ ). Only live trapping and cameras allowed for individual identification, with 48 individuals through live-trapping, and 75 individuals identified using cameras.

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### 186 (E) Technical Session 11, Great Halls D & E, Tuesday 10 June 2014

**Courtney A. Tye, Daniel U. Greene, Robert A. McCleery**

*Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, FL 32611 USA*

#### **A Method to Identify Individual Fox Squirrels (*Sciurus niger*) in the Southeastern USA**

Fox squirrels (*Sciurus niger*) have proven difficult to study in the southeastern United States due to their wide distribution, large home range, and low capture success. Several survey methods have been utilized in the past to detect fox squirrels but have been largely unsuccessful, time consuming, and labor intensive. Passive infrared digital cameras have been utilized to study a myriad of cryptic mammals, and can be useful for photo-identification of individuals within a species. To test whether cameras could be utilized for individual fox squirrel identification in the southeastern USA, we: 1) inspected digital images of fox squirrels acquired through field surveys; 2) selected pelage

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

features useful for individual identification; 3) tested the ability of people to identify individuals; and 4) evaluated the success of training to improve identification. We identified 6 features to distinguish individual fox squirrels: dominate pelage color; eye ring, facial markings; amount of white on the rostrum; toe colors; and presence of leg stripes. To test the ability of people to identify squirrels using these features, we developed an identification test. One group of participant's ability to identify squirrel increased from a 73.6% success rate to 75.5% after training. A 2nd group that received the training prior to the identification test had an 80.3% identification success rate. These differences suggest that training is effective for improving accuracy of individual identification.

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### 187 (E) Technical Session 11, Great Halls D & E, Tuesday 10 June 2014

**Jonathan P. Harris, Timothy J. O'Connell**

*Department of Natural Resource Ecology and Management, Oklahoma State University, Stillwater, OK 74078 USA*

#### **Modeling Habitat Suitability for Mesocarnivores: Understanding Risk for Nesting Northern Bobwhite (*Colinus virginianus*)**

Populations of mesocarnivores have increased in temperate North America, potentially increasing predation rates on ground-nesting birds, such as the declining Northern Bobwhite (*Colinus virginianus*). The goal of this study was to identify areas of bobwhite habitat that are at high risk for nest predation by measuring predation rates of artificial bobwhite nests and mapping habitat suitability of common nest predators. We constructed 151 artificial bobwhite nests across 12 discrete patches representing 4 broad-scale cover types in western Oklahoma: upland grassland (3); riparian grassland (3); upland shrubland (3); and riparian shrubland (3). After 7 days, 76 nests (50.3%) were depredated, with rates higher in riparian grassland and conversely lower in upland grassland and both riparian and upland shrubland. MaxEnt software was used to model spatial habitat use of mesocarnivores using occurrence data collected from scent station, spotlighting, and camera trap surveys, in conjunction with fine-scale vegetation data. Coyotes (*Canis latrans*) were widespread in the study area, although density and activity levels were greater along the riparian corridor. Striped Skunks (*Mephitis mephitis*) primarily used upland grassland of little bluestem (*Schizachyrium scoparium*) and switchgrass (*Panicum virgatum*). Our results suggest that shrub cover could be important to reduce nest predation on bobwhite relative to grass cover, and that efforts to increase nesting in uplands could reduce exposure of nests to patrolling predators like coyotes.

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### 188 (TA) Technical Session 11, Great Halls D & E, Tuesday 10 June 2014

**Sheryn J. Olson, Daniel J. Harrison**

*Department of Wildlife Ecology, University of Maine, Orono, ME 04469 USA*

#### **Seasonal Influence of Vegetation on Snowshoe Hare Pellet Densities across Forest Management Types in an Eastern Acadian Forest**

Snowshoe hare is an important prey species for a suite of predators, especially federally threatened Canada lynx. Forest management regimes produce a diverse array of habitats supporting vastly different densities of hares. Despite habitat-specific seasonal migrations that affect hare survival in western North America, seasonal changes in forest selection by hares near the southeastern extent of their range are poorly understood. We analyzed semi-annual pellet counts from 2005–2012, in 3 stand types [mature (MT), selection harvest (SEL), regenerating conifer (RG)] throughout a 1,120 km<sup>2</sup> study area in northern Maine. At a stand-scale, we expected: 1) greater winter pellet densities in all stands because winter diets contain more lignin and 2) larger summer to winter differences in RG stands relative to other stand-types because of comparatively lower summer food and cover. As expected, RG stands had significantly larger seasonal differences in hare pellet densities than MT and SEL stands; however, seasonal differences were significant only for RG stands. This suggests that hares in MT and SEL may have higher winter mortality than in RG stands, or hares may migrate from MT and SEL to RG stands during winter. Conifer sapling density, total saplings, and mid-story conifer cover had the largest seasonal effects on change in hare pellet density between seasons, suggesting that regenerating conifer stands with high winter cover value vary seasonally in selection by snowshoe hares.

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### 189 Technical Session 11, Great Halls D & E, Tuesday 10 June 2014

**Nancy D. Moncrief<sup>1</sup>, Raymond D. Dueser<sup>2</sup>, John H. Porter<sup>3</sup>**

*<sup>1</sup>Virginia Museum of Natural History, Martinsville, VA 24112 USA; <sup>2</sup>Department of Wildland Resources, Utah State University, Logan, UT 84322 USA; <sup>3</sup>Department of Environmental Sciences, University of Virginia, Charlottesville, VA 22904 USA*

#### **Least-cost Path Analysis of Movement Pathways of Raccoons (*Procyon lotor*) in a Naturally Fragmented Landscape**

Predation by raccoons (*Procyon lotor*) has been implicated in the recent decline of beach-nesting and colonial waterbirds, including species that are endangered and threatened, on the Virginia barrier islands. Raccoons are established on 11 islands and occur sporadically on others. We sought a tool to help identify potential movement

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

pathways of raccoons in this naturally fragmented landscape in order to either impede movement of animals or focus removal efforts on destinations having both conservation value for birds and minimal potential for reoccupation by raccoons. To that end, we applied Least-cost Path Analysis to: 1) estimate the relative costs (i.e., difficulty) for a raccoon to reach any given island from both mainland and island sources; 2) identify potential movement pathways and source locations for focusing raccoon monitoring and removal efforts; and 3) compare the costs of potential movement pathways with observed interisland movements and the rates of immigration to islands subject to periodic raccoon removal. We estimated movement costs across upland, marsh, and open-water habitats. We conclude that interisland movements are typically less costly for raccoons than immigration from the mainland, and we identify islands where predator control is most likely to be useful in enhancing avian recruitment. A similar approach can be applied to any landscape where there are distinct differences in the costs of traversing different elements of the landscape.

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### 190 Technical Session 11, Great Halls D & E, Tuesday 10 June 2014

**John T. Baccus**

*Department Natural Resources Management, Texas Tech University, Lubbock, TX 79409 USA*

#### **Melanism in White-tailed and Mule Deer in North America**

Melanism is rare in white-tailed (*Odocoileus virginianus*) and mule (*Odocoileus hemionus*) deer in North America with less than 5 animals harvested annually during the last decade. Pelage of melanistic deer is characterized by black or brown color and absence of white body markings. Previous literature records indicate melanism in deer from only 5 states—New York, South Carolina, Wisconsin, Texas, and Idaho. In an initial study in 1990, melanism in white-tailed deer occurred in 8 counties in central Texas. Records of melanistic deer were based on photo-documentation, sightings on mobile roadside counts, harvest records, personal interviews, and data mining. After over 2 decades of record collections for melanistic deer, I have records of melanistic white-tailed deer in 30 counties in Texas, 27 states and 2 Canadian provinces. Records for melanistic mule deer are from 7 states, and confirmation for both species in only 1 state, Idaho. These records indicated that melanism in deer follows different patterns of coloration, and most deer inhabit woodlands associated with drainage systems. Although distributions of melanistic white-tailed and mule deer have been increased in North America by these records, most new documentations are single individuals or a doe with fawns; and thus, the status of melanistic deer remains rare with the exception of central Texas.

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### 191 (E,TA) Technical Session 12, Meeting Room 16, Tuesday 10 June 2014

**Juan F. Diaz-Nieto<sup>1</sup>, Sharon A. Jansa<sup>1</sup>, Robert S. Voss<sup>2</sup>**

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#### **The Onset of the Amazon River and the Early Diversification of the American Marsupial of the Genus *Marmosops***

The Miocene was the scenario of multiple historical events in the diversification of Neotropical taxa; nonetheless, probably 1 of the most impressive of all was the birth of the Amazon River. During the early Miocene, a large proportion of the continental waters in South America drained into the Caribbean in a northward direction, however, in the late Miocene, the final stages of Andean uplift produced drastic changes in the depositional system of the Amazon changing the flow pattern of this basin (from a northward direction) to an eastward direction into the Atlantic. We tested whether the “new” transatlantic flow of the Amazon influenced the diversification history of the American marsupial of the genus *Marmosops*, a clade broadly distributed in the Amazon basin from its Andean headwaters to the river mouth in the Atlantic. Based upon the most recent revisionary work on the species limits of the genus, using a multi-locus dataset, we constructed a complete species-level time-calibrated tree for *Marmosops*. Subsequently, we reconstructed the ancestral areas (north and south of the Amazon River) within *Marmosops* using the dispersal-extinction-cladogenesis (DEC) method. Our results demonstrate that the onset of the Amazon River caused a vicariant event in what once was a widespread taxon in the Amazon basin dividing populations into northern and southern clades. Comparative studies are needed to test this event in other South American clades.

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### 192 (\*\*) Technical Session 12, Meeting Room 16, Tuesday 10 June 2014

**Nicté Ordóñez-Garza<sup>1</sup>, Cody W. Thompson<sup>2</sup>, Margaret K. Unkefer<sup>3</sup>, Cody W. Edwards<sup>3</sup>, James G. Owen<sup>4</sup>, Robert D. Bradley<sup>1,5</sup>**

*<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409 USA; <sup>2</sup>Department of Ecology and Evolutionary Biology and Museum of Zoology, University of Michigan, Ann Arbor, MI 48109 USA; <sup>3</sup>Department of Environmental Science & Policy, George Mason University, Fairfax, VA 22030 USA; <sup>4</sup>Universidad Salvadoreña “Alberto Masferrer”, Apartado Postal 2053, San Salvador, El Salvador; <sup>5</sup>Museum of Texas Tech University, Lubbock, TX 79409 USA*



# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## Biogeographic Patterns and Taxonomic Implications of Small Mammals across the Tehuantepec Isthmus: *Neotoma ferruginea* Tomes 1861 as an Example

The evolutionary history of the Mesoamerican highlands has been shaped by past geological and climatic events, including the rise and fall of the Isthmus of Tehuantepec. Such events in the Quaternary have influenced in the current regional patterns of biodiversity. In order to understand the relative impacts of these historical events on diversification in montane taxa in Mesoamerica, this study used phylogenetic analyses of the mitochondrial cytochrome b gene from members of the *Neotoma mexicana* species group. Samples of *N. isthmica*, *N. mexicana*, and *N. picta* formed 3 well-supported clades, including a clade containing samples from southern Mexico and Central America that historically have been referred to as *N. ferruginea*, *N. isthmica*, and *N. mexicana*. Based on the monophyletic nature of this clade, magnitude of genetic divergence from other species of woodrats, criteria set forth in the genetic species concept, and the rule of priority of zoological nomenclature, individuals from southern Mexico, Guatemala, and El Salvador should be referred to as *N. ferruginea*, and *N. isthmica* should be subsumed into *N. ferruginea*. The phylogenetic pattern observed within this group was similar to that of other vertebrate taxa co-distributed in the region south of the Trans-Mexican Neovolcanic Belt and the highlands of Chiapas, Mexico, and nuclear Central America. This research was supported by an ASM Grants-in-Aid of Research awarded to Nicté Ordóñez-Garza in 2012.

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### 193 Technical Session 12, Meeting Room 16, Tuesday 10 June 2014

#### M. Laura Ruiz-Vega, Livia León-Paniagua

Museo de Zoología "Alfonso L. Herrera", Facultad de Ciencias, Universidad Nacional Autónoma de México, Apartado Postal 70-399, México DF 04510 Mexico

#### Phylogeography of the Osgood's Mouse (*Osgoodomys banderanus*; Rodentia: Cricetidae) Endemic to Mexico

Phylogeographic relationships were evaluated among specimens of the Osgood's mouse (*Osgoodomys banderanus*), endemic to west Mexico, along its entire distributional range using sequences of 1,331 base pairs of the mitochondrial ND3 and ND4 genes. Sequences of 102 specimens of both subspecies (*O. b. banderanus* and *O. b. vicinior*) were obtained, and we performed maximum parsimony, maximum likelihood, and Bayesian inference analysis, along with a haplotype network to assess the relationships at the intraspecific level. All the analysis assembled the samples into 2 groups or clades that showed a high divergence (~6%), corresponding, on the one hand to the localities of the north and on the other hand to those southernmost of the distributional range, in south Guerrero. The split of these 2 groups can be explained geographically by the presence of the Balsas basin, because it has been observed that it works as a geographic barrier to other mammals. Probably the most ancient haplotypes are found to the south of this barrier from which a spread to the north through the Pacific coast following the distribution of the tropical dry forest to the center and west of the Transmexican Volcanic Belt could have occurred. The results may have taxonomic and conservation implications for this monotypic species.

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### 194 Technical Session 12, Meeting Room 16, Tuesday 10 June 2014

#### Daniel E. Chávez, Santiago F. Burneo

Museum of Zoology, Pontificia Universidad Católica del Ecuador, Quito, Ecuador

#### Genetic, Morphological, and Ecological Variation of the Genus *Reithrodontomys* in Ecuador

Morphologic, genetic, and ecologic data were used to analyze the variation among populations of *Reithrodontomys mexicanus* in Ecuador. Additionally, a phylogeny of the genus *Reithrodontomys* was reconstructed including DNA sequences of Neotropical species reported in GenBank. We reviewed *R. mexicanus* as a valid name for the Ecuadorian forms. Phylogenetic results suggest that Ecuadorian specimens are not conspecific with *R. mexicanus*, and 2 separated clades of *Reithrodontomys* were discovered in the Andes of Ecuador. We propose to treat them as 2 valid species. Analysis of topotypes have allowed us to revalidate 1 clade as *R. soderstromi* endemic to inter-Andean valleys of Ecuador and the other clade as a new species never described before, endemic to the Highlands of Ecuador.

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### 195 Technical Session 12, Meeting Room 16, Tuesday 10 June 2014

#### Tanya K. Daughtry<sup>1</sup>, J. Delton Hanson<sup>2</sup>, Joshua M. Brokaw<sup>1</sup>, Thomas E. Lee, Jr.<sup>1</sup>

<sup>1</sup>Department of Biology, Abilene Christian University, Abilene, TX 79699 USA; <sup>2</sup>Research and Testing Laboratories, Lubbock, TX 79416 USA

#### Phylogenetic Relationships in *Thomasomys* (Rodentia: Cricetidae)

Phylogenetic relationships in the genus *Thomasomys* were analyzed based on sequences for the mitochondrial cytochrome b gene and the nuclear Recombination-activating Gene 1 (RAG1). The primary objective of this study was to test previous taxon descriptions for species of *Thomasomys* to facilitate creation of an updated key for the

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

mammals of Ecuador. New sequences were generated using the primers P484 and P485 for cytochrome b and newly designed primers for RAG1. Maximum likelihood (ML) searches were performed with gaps treated as missing data and each codon position treated as a separate partition. In the ML reconstruction using cytochrome b alone, nodes at the species level were well resolved, and most species of *Thomasomys* were shown to be monophyletic, with the exception of *T. baeops*. A subclade of *T. baeops* was grouped together with *T. taczanowskii* (95% bootstrap; 2.5% genetic distance), but an additional set of *T. baeops* specimens were otherwise grouped sister to the *T. baeops*—*T. taczanowskii* clade (85% bootstrap; 6% genetic distance), rendering *T. baeops* paraphyletic. In contrast, most deep nodes joining multiple species into clades had bootstrap values lower than 70%. RAG1 was consistent with cytochrome b in all strongly supported clades but did not provide as much phylogenetic resolution. The small branches at lower nodes suggest a rapid radiation early in the diversification of *Thomasomys*.

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### 196 (E,\*\*,TA) Technical Session 12, Meeting Room 16, Tuesday 10 June 2014

**Nathan S. Upham<sup>1,2</sup>, Bruce D. Patterson<sup>2</sup>**

<sup>1</sup>Committee on Evolutionary Biology, University of Chicago, Chicago IL 60637 USA; <sup>2</sup>Integrative Research Center, Field Museum of Natural History, Chicago IL 60605 USA

#### Testing for Adaptive Radiation and Ecological Constraint in a Major Lineage of Rodents (Hystricomorpha, Caviomorpha)

Ecological diversification was investigated in the rodent suborder Hystricomorpha. The main component of this clade, Caviomorpha, has radiated to 244 modern species in the Americas and Caribbean, and spans 3 orders of magnitude in body size (~60 g to ~60 kg). A molecular timetree was constructed using 22 fossil calibrations and a 5-gene supermatrix for 68% of caviomorph species, including all 54 living genera, plus related rodents in Africa and Asia. Body masses and ecological life modes of species were mapped on the timetree. Two family dyads in Octodontoidea are sister to each other with crown radiations starting about 18 million years ago, but show different histories. The southern, arid-adapted radiation of Octodontidae (degus, viscacha rats) and Ctenomyidae (tuco-tucos) shows exponentially increasing rates of both species diversification and body-size diversification beginning about 5 million years ago until the Recent. In contrast, the northern, mesic-adapted radiation of Echimyidae (spiny rats, tree rats) and Capromyidae (hutias) contains 18 lineages present since 10 million years ago, with initially high evolutionary rates that then decline. Analyses within reconstructed life modes show that burrowers have smaller and less variable body sizes than tree-dwelling or terrestrial rodents. In the context of Simpson's adaptive zones, Ctenomyidae is confined to the single zone of burrowing while Echimyidae-Capromyidae occupies at least 2 (burrowing and tree-dwelling). Thus, the latter clade may constitute an old adaptive radiation that has persisted after saturating available niches. This research was supported by an ASM Grants-In-Aid of Research to Nathan S. Upham in 2010 and an A. Brazier Howell Award to Nathan S. Upham in 2013.

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### 197 Technical Session 12, Meeting Room 16, Tuesday 10 June 2014

**Scott L. Gardner<sup>1</sup>, Jorge Salazar-Bravo<sup>2</sup>, Joseph A. Cook<sup>3</sup>**

<sup>1</sup>H. W. Manter Laboratory of Parasitology, University of Nebraska State Museum, and School of Biological Sciences, University of Nebraska-Lincoln, NE 68588-0514 USA; <sup>2</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409 USA; <sup>3</sup>Department of Biology and Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM 87131 USA

#### Phylogenetic Diversification of *Ctenomys* in South America with Focus on Bolivian Species

Tuco-tucos are subterranean rodents of the genus *Ctenomys* Blainville, 1826 (Rodentia: Ctenomyidae) that are endemic to the Neotropics, occurring in suitable habitats consisting of well-drained, friable soils from about latitude 12° S and extending south to the tip of South America in Tierra del Fuego. Ctenomyids have been the subject of evolutionary speculation and thought extending from Darwin's encounter with tuco-tucos in Uruguay in the 19th century on through to contemporary studies of behavior, morphology, and molecular evolution. In the present study, we made genetic comparisons and produced phylogenetic trees based on complete cytochrome b gene sequences (1,140 base pairs) and the 4th intron (and partial flanking exon) of the nuclear gene coding for Rhodopsin. Phylogenetic analyses of the separate genetic data and of the complete concatenated data set shows significant structure. Our analyses were based on 42 sequences from representatives of all populations of *Ctenomys* available from Bolivia and those of as many other species in the genus as possible in addition to 3 outgroup taxa. Our work shows high levels of genetic diversity among some species of *Ctenomys* and the outgroups we analyzed. Additional survey and inventory work on subterranean and cryptic species of mammals worldwide will continue to yield species new to science. Supported in part by National Science Foundation grants: BSR-8612329, BSR-9024816, DEB-9496263, DEB-9631295, DEB-0097019, DBI-0646356, BSR 89-20617, BSR 90-15454, INT-9417252, NATO-CRG 920612.

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

198 (\*\*) Technical Session 12, Meeting Room 16, Tuesday 10 June 2014

**Rafael N. Leite**<sup>1,2</sup>, **Fernanda P. Werneck**<sup>1</sup>, **Maria Nazareth F. da Silva**<sup>1</sup>, **Duke S. Rogers**<sup>2,3</sup>

<sup>1</sup>Biodiversity Division, National Institute of Amazonian Research, Manaus, AM 69067-375 Brazil; <sup>2</sup>Biology Department, Brigham Young University, Provo, UT 84602 USA; <sup>3</sup>Monte L. Bean Life Science Museum, Brigham Young University, Provo, UT 84602 USA

## **Evolutionary History of the Southeastern Amazon Basin as Revealed by the Phylogeography of a Spiny Rat, *Proechimys roberti* (Hystricognathi: Echimyidae)**

Several alternative hypotheses have been proposed to account for diversification patterns in the Neotropics, with special reference to the Amazon Basin. Traditionally, molecular studies of Amazonian taxa have been based on qualitative assessments and ad hoc explanations of phylogenetic trees that describe patterns and underlying processes of genetic variation. However, by applying coalescent methods we can now incorporate the stochasticity inherent to lineage sorting and the evolutionary processes shaping demographic structure and population divergence in order to better understand the diversification of Amazonian biota. Therefore, we employed a coalescent-based approach to investigate the phylogeographic history of the spiny rat *Proechimys roberti* (family Echimyidae), which is distributed in the southeastern Amazon Basin. We analyzed DNA sequence data from multiple loci and several individuals of this rodent to estimate divergence times and migration rates between populations, test alternative divergence models based on geological and paleoecological data, and reconstruct a spatiotemporal trajectory of the species' range. *Proechimys roberti* populations are geographically structured with respect to major topographic features such as rivers and relief. Population splitting times agree with the formation of southeastern Amazonian drainages and establishment of modern landscape configuration during the Plio-Pleistocene. Different gene flow patterns suggest a role for main rivers as well as relief variation in the historical evolution of *P. roberti*. We discuss implications of our findings for the biogeography of the Amazon Basin.

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199 Technical Session 13, Meeting Room 17, Tuesday 10 June 2014

**Erik A. Beever**<sup>1</sup>, **Kara N. Laney**<sup>2</sup>

<sup>1</sup>Northern Rocky Mountain Science Center, U.S. Geological Survey, Bozeman, MT 59715 USA; <sup>2</sup>National Academy of Sciences, National Research Council, Washington, D.C. 20001 USA

## **Free-roaming Horses in the American West: Interactions with Native Mammals and the Environment**

According to seminal social-science research by Kellert (1980), humans consistently rank mammals most favorably among all animals, especially the horse. Populations of free-roaming horses descended from escaped or abandoned animals have existed in North America since the arrival of the domestic horse with Europeans in the 16th century. Management areas for free-roaming horses and burros now span 37.78 million ha in 10 western states, plus smaller areas in 12 additional states and 2 Canadian provinces. The Bureau of Land Management recently commissioned the National Academy of Sciences to review the science surrounding numerous vexing topics germane to management of free-roaming equids in the American West: population-size estimation; population ecology; fertility control; genetics; demographic modeling; synecology (Appropriate Management Levels); and human socio-political issues surrounding equid management. We review the findings of a 14-member scientific committee on these topics, focusing particularly on equids' relationships with other, native mammals. Free-roaming equids were declared by congressional law in 1971 to constitute "an integral part of the natural system of the public lands" in western states; we illustrate the financial, demographic, practical, and human-societal challenges that accompany the management of such a charismatic mammal in an arid environment with many competing demands for resource use.

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200 (E) Technical Session 13, Meeting Room 17, Tuesday 10 June 2014

**Peter Eyheralde**<sup>1</sup>, **W. Sue Fairbanks**<sup>2</sup>

<sup>1</sup>Department of Natural Resource Ecology and Management, Iowa State University, Ames, IA 50011 USA;

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## **Seed Rain and Bison-mediated Seed Dispersal in a Tallgrass Prairie Reconstruction**

Bison-mediated seed dispersal may be a critical ecological process that has been eliminated in grassland ecosystems by the removal of this keystone species. As part of a larger study of epizoochory and endozoochory by bison, we installed funnel seed traps on fifty 50-m transects on the Neal Smith National Wildlife Refuge in south central Iowa, to compare the composition of seed species dispersed by bison with the seed rain in a tallgrass prairie reconstruction. We hypothesized that seed species extracted from bison dung would be similar to those dispersed to the collection sites by gravity and wind. Shed hair was expected to contain a greater diversity of seeds and a higher proportion of forb species than found in seed traps. Bison-transported and abiotically dispersed seeds were extracted from 180 fecal samples, 243 shed hair samples, and 300 seed trap samples collected monthly from May 2012 through October 2013. Preliminary data suggests that both bison dung and shed hair contain a greater diversity of seed species per sample than those collected from seed traps. Bison dung and shed hair also contained a greater number of forb seeds per sample than were collected in seed traps. Seed composition found in shed hair and dung

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

appeared to be influenced by both phenology of seed dispersal and the long distance movements of bison through a variety of vegetation types.

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### 201 (\*\*) Technical Session 13, Meeting Room 17, Tuesday 10 June 2014

**Adam T. Ford**<sup>1,2</sup>, **Jacob R. Goheen**<sup>1,3</sup>, **David J. Augustine**<sup>4</sup>, **Tim O'Brien**<sup>1,5</sup>, **Todd M. Palmer**<sup>1,6</sup>, **Rob M. Pringle**<sup>1,7</sup>, **Rosie Woodroffe**<sup>1,8</sup>

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#### Trophic Repatriation of a Savanna Ecosystem

Trophic cascades, or the indirect effect of carnivores on plants, can powerfully shape ecosystems and have been used to justify carnivore restoration programs across the globe. Here, we document the cascading effects of a globally endangered canid, the African wild dog (*Lycaon pictus*), following its natural recolonization to central Kenya after a 20-year absence. We predicted that wild dogs would suppress the abundance of their primary prey (Guenther's dik-dik [*Madoqua guentheri*], a 5 kg browsing antelope) and reduce herbivory on trees. We measured dik-dik abundance using line transect surveys conducted prior to (1999–2001) and following (2008–2013) the recovery of wild dogs in 2003. We then quantified the effect of dik-dik on the tree community using 2 replicated herbivore enclosure experiments, 1 established prior to ( $n = 3$ , 1999–2002), and another following ( $n = 18$ , 2009–2012), the return of wild dogs. By 2012, the abundance of dik-dik had declined by 40%, while the effect of dik-dik exclusion on trees was 66–86% lower compared to pre-wild dog recovery. We tested and then rejected several alternative hypotheses that could have generated these patterns, including variation in rainfall, decline in the abundance of other ungulates, and increased abundance of other dik-dik predators. Our findings are the 1st to document the cascading effects of a naturally-recovering carnivore population in an African savanna. This research was supported by an ASM Grants-In-Aid of Research in 2011 and an Elmer C. Birney Award in 2013 to Adam T. Ford.

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### 202 Technical Session 13, Meeting Room 17, Tuesday 10 June 2014

**Megan A. Floyd**<sup>1</sup>, **Scott C. Williams**<sup>2</sup>, **Isaac M. Ortega**<sup>1</sup>

<sup>1</sup>Natural Resource and the Environment, University of Connecticut, Storrs, CT 06269 USA; <sup>2</sup>The Connecticut Agricultural Experiment Station, New Haven, CT 06511 USA

#### Trophic Cascade Effects of Deer Overabundance on Connecticut Native Vegetation and Small Mammal Populations

Trophic cascade theory is the destabilization of 1 trophic level resulting in the disruption of others. One of the most notable impacts on trophic cascades is the top-down effect of apex predators, which can result in increased herbivore abundance and herbivory impacts. The reduction of grass–shrub layers can diminish small mammal habitat, thus reducing populations. Conversely when a predator is reintroduced, herbivore populations often decrease, reducing consumption of vegetation, resulting in an increase in small mammal populations. However, results indicate that disturbed portions of Northeast ecosystems harbor invasive plant species, which disrupt the trophic cascade. Species like Japanese barberry flourish due to the lack of competition with overbrowsed native species. This study attempted to determine the effects of invasives on trophic cascades by determining small mammal population sizes and survival rates. White-footed mice were trapped in 3 different locations. At each location, 3 plots were established; an unmanipulated barberry stand, an area where barberry was minimal or absent, and an area where barberry was managed. In program MARK, population size and survival rates were estimated using POPAN and Cormack Jolly-Seber models, respectively. No significant differences were detected between the 3 plots at the locations. Therefore, the cascade occurring in the Northeast was impeded with no effect on the small mammal trophic level. This study concluded that there is a distinctive trophic cascade occurring in the Northeast.

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### 203 Technical Session 13, Meeting Room 17, Tuesday 10 June 2014

**Michael R. Willig**<sup>1,2</sup>, **Kevin R. Burgio**<sup>2</sup>, **Laura M. Cisneros**<sup>1,2</sup>, **Lindsay M. Dreiss**<sup>3</sup>, **Bruce D. Patterson**<sup>4</sup>, **Steven J. Presley**<sup>1,2</sup>, **Brian T. Klingbeil**<sup>1,2</sup>

<sup>1</sup>Center for Environmental Sciences & Engineering, University of Connecticut, Storrs, CT 06269 USA; <sup>2</sup>Department of Ecology & Evolutionary Biology, University of Connecticut, Storrs, CT 06269 USA; <sup>3</sup>Department of Natural Resources and the Environment, University of Connecticut, Storrs, CT 06269 USA; <sup>4</sup>Center for Integrative Research, Field Museum of Natural History, Chicago, IL 60605 USA

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

## Gradients of Phylogenetic Relatedness and Size Similarity: Bats and Rodents in a Hotspot of Tropical Biodiversity (Manu, Peru)

Environmental gradients in functional and phylogenetic attributes provide insight into processes that mold the structure of assemblages. Consequently, we quantified phylogenetic relatedness and size similarity based on only nearest neighbors (nearest taxon index, NTI) or all taxa (net relatedness index; NRI) for 13 assemblages of bats and rodents along an elevational gradient. We compared elevational rates of change between perspectives and orders using orthogonal polynomial regression. We determined non-random patterns in NRI and NTI via simulation analyses. Elevational gradients of rodent phylogenetic relatedness were strong ( $R^2_{\text{NRI-Phylo}} = 0.83$ ;  $R^2_{\text{NTI-Phylo}} = 0.71$ ), whereas those for size similarity were weak ( $R^2_{\text{NRI-Size}} = 0.5$ ;  $R^2_{\text{NTI-Size}} = 0.16$ ). Elevational gradients of bat phylogenetic relatedness were stochastic ( $R^2_{\text{NRI-Phylo}} = 0.33$ ;  $R^2_{\text{NTI-Phylo}} = 0.07$ ), and those for size similarity were weak ( $R^2_{\text{NRI-Size}} = 0.67$ ;  $R^2_{\text{NTI-Size}} = 0.42$ ). Moreover, size similarity was correlated with phylogenetic relatedness for rodents, but not for bats. Species in rodent assemblages were less related and less similar in size than were species from randomly constructed assemblages in rainforest, and were more related than were species from randomized assemblages in cloud forest. Species in bat assemblages were less related than those from randomized assemblages in cloud forest and more similar in size than species from randomized assemblages in elfin forest and grassland. Differences in strength of habitat filtering and niche conservatism likely underpin distributions for bats and rodents.

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## 204 (E) Technical Session 13, Meeting Room 17, Tuesday 10 June 2014

**María Peralta<sup>1</sup>, Víctor Pacheco<sup>1,2</sup>**

<sup>1</sup>Museo de Historia Natural Javier Prado, Lima, Peru; <sup>2</sup>Universidad Nacional Mayor de San Marcos, Calle Germán Amézaga 375, Lima 15081 Peru

### Diversity and Small Mammal Assemblages of Montane Forests from Central Peru

Studies in montane forest are characterized by a high diversity of habitats causing a high diversity of small mammals. We assess the structure patterns based on the richness and diversity of rodents recognizing different kinds of habitats in Central Peru. In 2005 we surveyed 12 montane forests setting 3 transects for a total of 8,280 trap nights. Analysis was performed using true diversity and Ordination Method of nonmetrical Multidimensional Scaling (nMDS) of habitats. A total of 368 specimens representing 11 species were captured. The true diversity showed that Campamento Regional (C. Regional) and Ucumaria obtained the highest values of effective number of species ( $1D = 3.22$  and  $1D = 3.17$  respectively) and  $1D$  observed values showed that C. Regional is the most diverse field site. Campamento Ututo (92%) and C. Regional (84%) obtained the highest evenness diversity with good completeness ( $ACE > 67\%$ ). The nMDS scatter plot (0.05 significance level) distinguished 5 groups: 1 at the western and 4 at the eastern side of the Río Marañón, suggesting geographical boundaries to the distribution. The PERMANOVA and ANOSIM showed high significance differences (pairwise comparisons:  $p < 0.01$ ). Meanwhile, the SIMPER analysis showed that *Thomasomys kalinowskii*, *Akodon orophilus*, *Akodon mollis*, and *Microryzomys minutus* are the species responsible of the similarity within-groups. Our results revealed influence of geographic distance and barriers as the Rios Marañón and Huallaga in the distribution of rodents.

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## 205 Technical Session 13, Meeting Room 17, Tuesday 10 June 2014

**Aaron W. Reed<sup>1</sup>, Majid Bani-Yaghoob<sup>2</sup>, Norman A. Slade<sup>3</sup>**

<sup>1</sup>School of Biological Sciences, University of Missouri-Kansas City, Kansas City MO 64110 USA; <sup>2</sup>Department of Mathematics & Statistics, University of Missouri-Kansas City, Kansas City MO 64110 USA; <sup>3</sup>Department of Ecology and Evolutionary Biology & Biodiversity Research Center, University of Kansas, Lawrence, KS 66045 USA

### Temporal Variation in Competition among Grassland Rodents Estimated from a Long-term Dataset

Competition within a community likely has significant effects on the dynamics of populations. Traditional approaches to assessing competition (e.g., Lotka-Volterra models) often assume constant effects of competition. However, environmental variability, density, and seasonality can alter the magnitude of competition. We used a long-term dataset (1973–2003) on the abundance of 5 species of grassland rodent to examine temporal and seasonal variation in the magnitude and direction of intra- and interspecific competition among the 5 species of rodent on our study area. This was accomplished in 2 steps; linear regression models were 1st used to obtain initial estimates of the influence of intra- and interspecific competition, and then the initial estimates were optimized by minimizing the sum of the squared errors. Competition within a species was consistently negatively related to the population growth rate suggesting substantial and consistent negative effects of intraspecific competition. Interspecific competition coefficients showed considerable temporal variation in both magnitude and direction. This suggests that interaction among species is highly variable, where competition in 1 season may change to facilitation in another season. Hence there appears to be a time varying interspecific competition that may balance the long-term dynamics of these populations.

# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

206 (E) Technical Session 13, Meeting Room 17, Tuesday 10 June 2014

**Kathryn R. Rogers**

*Biological Sciences, Old Dominion University, Norfolk, VA 23529 USA*

## **Spatial and Temporal Patterns of an Old-field Small Mammal Community**

In 2005, an ongoing monitoring program of the small mammal community began on a secondary successional wetland site owned by The Nature Conservancy. The study site consisted of an 8 by 8 grid, at 12.5-m intervals, with 2 modified Fitch traps per station. We trapped for 3 days each month, averaging 4,600 trap nights per year. Microhabitat data were collected for herbaceous coverage, open ground, and dominant vegetation at each trapping station. I hypothesized the spatial distribution of the herbivorous small mammal community and populations would be related to that of vegetation. After determining the spatial distribution for each small mammal population, I used ArcGIS to map and conduct cluster analyses using a combination of LiDAR data and ground surveys, with respect to the small mammal community and population densities. With the progression of succession, this site experienced a general and parallel decline of all oldfield species, both for vegetation and the small mammal community. I will discuss the findings to the objectives of my study which include: 1) determining which of the 4 common species used and which avoided the wettest areas of the grid; 2) analyze for spatial difference between residents and transients; 3) examine how species moved across the grid in relation to other species and habitat; and 4) determine if interspecific interactions or habitat played a strong role in spatial movement.

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207 (E) Technical Session 14, Great Halls D & E, Tuesday 10 June 2014

**Jonathan A. Nations<sup>1,2</sup>, Link E. Olson<sup>2</sup>**

<sup>1</sup>*Department of Mammalogy, University of Alaska Museum, Fairbanks, AK 99775 USA;* <sup>2</sup>*Department of Biology and Wildlife, University of Alaska Fairbanks, Fairbanks, AK 99775 USA*

## **Is Climbing Behavior Reflected in the Morphology of Scansorial Voles?**

The rodent subfamily Arvicolinae provides a unique system for studying functional morphology. Despite a conserved body plan, arvicolines occupy a wide range of niches (aquatic to arboreal). We have shown that the northern red-backed vole, *Myodes rutilus*, readily climbs trees, representing the 1st account of scansorial behavior in this species and the 3rd account in this genus. Video of wild and captive *M. rutilus* reveals hind foot reversal and other behaviors that suggest morphological adaptations to scansoriality. It has been suggested that scansorial, small-bodied mammals should not possess unique postcranial specializations for climbing, as the advantages of such specializations would not compensate for the loss of broad functionality afforded by a generalized skeleton, and at the spatial scale of most small mammals, the obstacles encountered at ground level are similar to those in the arboreal niche. Most published studies, however, are based on comparisons among distantly related large- and small-bodied species. In order to better understand the morphology of climbing in a phylogenetically appropriate context, postcranial measurements were taken from 3 arvicoline species representing a continuum from arboreal to terrestrial (*Arborimus longicaudus*, *Myodes rutilus*, and *Microtus oeconomus*, respectively). Results will be used to examine morphological variation between these locomotor specialties, shedding light on features that allow for arboreal niche specialization among this diverse group of small mammals while providing insight into the evolution of climbing.

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208 Technical Session 14, Great Halls D & E, Tuesday 10 June 2014

**Manabi Paul, Sreejani Sen Majumder, Anindita Bhadra**

*Department of Biological Sciences, Indian Institute of Science Education and Research-Kolkata, Mohanpur Campus, Mohanpur, Nadia 741252, West Bengal, India*

## **Selfish Mothers and Altruistic Grandmothers: The Case of the Dog**

Cooperation and conflict are essential components of any social system, and these present interesting contexts for studying social organization across species. Free-ranging dogs (*Canis lupus familiaris*) are a good model system for addressing various questions pertaining to the eco-ethology of canids in general, and for understanding the evolution of dogs in particular. We have used natural dog groups in India to study conflict and cooperation between adults and pups during the early stages of life, when the pups are highly dependent on their mothers for sustenance. Using this model system, we have carried out field experiments to study parent-offspring conflict in the context of extended parental care. We observed females and their pups in their natural habitat for the mother's tendency to share food given by humans with her pups in the weaning and post-weaning stage. Because these dogs are scavengers, and depend largely on human-provided food for their sustenance, voluntary sharing of food by the mother with her pups is a good surrogate for extended parental care. Our behavioral observations convincingly demonstrate an increase of conflict and decrease of cooperation by the mother with her offspring over given food within a span of 4-6 weeks. We also demonstrate that though the competition among the pups in a litter scales with litter size, the conflict shown by the mother is independent of the size of her litter. During the course of our observations we have also recorded

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

alloparental care of the pups by related females during the early stages of their development, a hitherto unknown phenomenon in dogs.

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### 209 Technical Session 14, Great Halls D & E, Tuesday 10 June 2014

**Wieslaw Bogdanowicz<sup>1</sup>, K. Emmanuvel Rajan<sup>2</sup>, Arul Sundari Arasamuthu<sup>2</sup>, Ganapathy Marimuthu<sup>3</sup>, Michal Dabrowski<sup>1</sup>**

<sup>1</sup>Museum and Institute of Zoology, Polish Academy of Sciences, 00-679 Warszawa, Poland; <sup>2</sup>Department of Animal Science, School of Life Sciences, Bharathidasan University, Tiruchirappalli 620024 India; <sup>3</sup>Department of Animal Behaviour & Physiology, School of Biological Sciences, Madurai Kamaraj University, Madurai 625021 India

#### **Babysitting and Aspects of Nonmaternal Infant Support in the Carnivorous Bat *Megaderma lyra***

Out of the 1,260 extant species of bats, only a few species are documented as helping raise the offspring of others, which includes food sharing and pup guarding. We examined patterns of maternal infant support within the Indian false vampire bat, *Megaderma lyra*. We captured 189 individuals from 4 maternity colonies in southern India and genotyped them at 9 microsatellite loci. We identified the mothers in 68% of 74 young aged 1 to 27 days. In 3 cases, mothers nursed alien offspring despite their dependent young still being present in the colony. Juveniles of 1–16 days old were babysat by their mothers as well as other females (the ratio close to 1:1), whereas juveniles older than 16 days (around the age when young start practicing flights) were cared for mostly by mothers (15:1). In the present study, we document the 1st case of nanny babysitting in bats, and this phenomenon was time-dependent suggesting that babysitting is related to the guarding of pups, either assuring appropriate body temperature at the early stage of pups' development and/or avoiding predation at a time when pups are unable to fly. This finding also supports the kin selection hypothesis as nannies were more closely related to young they cared for than expected by chance.

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### 210 (E,TA) Technical Session 14, Great Halls D & E, Tuesday 10 June 2014

**Caitlin P. Wells, Dirk H. Van Vuren**

Department of Wildlife, Fish, and Conservation Biology, University of California, Davis, CA 95616 USA

#### **Ground Squirrels Manipulate Offspring Sex in Response to Local Population Density**

The formation of matriline is thought to be key to the evolution of sociality in several mammalian taxa, including primates, carnivores, and ground-dwelling squirrels. In ground squirrels, matriline is formed through retention of daughters in social and spatial proximity. Retaining daughters is thought to enhance maternal fitness, and may be more possible in years of low female density when competition is reduced. We used 18 years of demographic and pedigree data from a population of golden-mantled ground squirrels (*Callospermophilus lateralis*) to investigate whether females produce more daughters in years of low female density. We evaluated litter sex ratio, corrected for the role of chance in varying litter sizes, as a function of maternal condition, environmental conditions, and female density. We found that female golden-mantled ground squirrels showed predictable changes in litter sex-ratio in response to female density: squirrels produced more daughters when female density was low, and fewer daughters when female density was high. By contrast, litter sex ratio did not vary by maternal age, body condition, or food availability. Finally, females that produced female-biased litters were more likely to retain a daughter in the matriline in later years. Our results support local resource enhancement theory of offspring sex allocation, and are consistent with physiological mechanisms that bias offspring sex in female ground squirrels.

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### 211 (E,TA) Technical Session 14, Great Halls D & E, Tuesday 10 June 2014

**Megan M. Wallen<sup>1</sup>, Eric M. Patterson<sup>1</sup>, Ewa Krzyszczyk<sup>1</sup>, Janet Mann<sup>1,2</sup>**

<sup>1</sup>Department of Biology, Georgetown University, Washington, D.C. 20057 USA; <sup>2</sup>Department of Psychology, Georgetown University, Washington, D.C. 20057 USA

#### **Ecological and Fitness Consequences of Coercive Males on Female Bottlenose Dolphins (*Tursiops cf. aduncus*)**

In Shark Bay bottlenose dolphins (*Tursiops cf. aduncus*), mating is characterized by extreme sexual coercion whereby male alliances harass females to increase mating access. Physical costs of coercion have been documented, yet little is known about how male behavior affects long-term female fitness. Approximately 20% of females in the Shark Bay population have failed to produce surviving calves. Such a high failure rate makes it plausible that the combined effects of sexual conflict and extreme maternal investment exacerbate reproductive costs. Using 25 years of longitudinal data, we calculated reproductive success rates for 157 adult females. Females that experienced more consortships outside of those that lead to successful calves had lower reproductive success ( $p < 0.01$ ). This suggests that unsuccessful females remain attractive to males, are not limited by matings, and ultimately suffer more coercion. We further examined female space use as a function of male presence. A female's baseline centroid and primary habitat type were determined from survey sightings where she was not cycling nor with males ( $n = 21$  females). Primary habitat use declined when females were with males ( $p < 0.0001$ ) but was not affected by cycling status. Females were also sighted farthest from their baseline centroid when with males, regardless of cycling

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

status ( $p < 0.01$ ). Thus, in addition to direct harassment, male coercion impacts female space use and likely associated foraging and social behaviors, ultimately leading to fitness consequences.

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### 212 (C) Technical Session 14, Great Halls D & E, Tuesday 10 June 2014

**Meghan J. Camp<sup>1</sup>, M. M. Crowell<sup>1</sup>, Lisa A. Shipley<sup>1</sup>, Jennifer S. Forbey<sup>2</sup>, T. R. Johnson<sup>3</sup>, Janet L. Rachlow<sup>3</sup>**

<sup>1</sup>*School of the Environment, Washington State University, Pullman, WA 99163 USA;* *Department of Biological Sciences, Boise State University, Boise, ID 83725 USA;* <sup>3</sup>*Department of Fish and Wildlife Sciences, University of Idaho, Moscow, ID 83844 USA*

#### **Evaluating Tradeoffs in Risks by Specialist and Generalist Herbivores**

Herbivores must cope with the risks imposed by intrinsic properties of plants such as fiber and chemical defenses. When choosing what to eat, individuals often face tradeoffs between the nutritional benefits and the toxicity of chemical defenses in plants. We examined the tradeoffs that a dietary specialist and a generalist make between the risk of starvation (high fiber) and the risk of toxicity (high chemical defenses). We conducted a series of feeding trials with the sagebrush-specialist pygmy rabbit (*Brachylagus idahoensis*) and the generalist mountain cottontail rabbit (*Sylvilagus nuttallii*) to determine how individuals perceived the fiber levels in food relative to the toxicity levels. We determined the equivalence points (i.e., the levels of toxin and fiber that result in equal intake between 2 patches) for multiple combinations of fiber and toxicity levels. Then, we used the equivalence points to model trade-off curves for the 2 risks. The equivalence points occurred at higher toxicity and lower fiber levels, and the slope of the trade-off curve was steeper for pygmy rabbits than for cottontails. These results indicated that pygmy rabbits were willing to consume higher levels of toxicity to obtain lower fiber values than cottontails. Our results demonstrated that herbivores quantify and balance these 2 risks by altering their foraging behavior, and that there are differences in how a specialist and generalist balance these risks.

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### 213 Technical Session 15, Meeting Room 16, Tuesday 10 June 2014

**T. M. Linscott<sup>1</sup>, Erin A. Roche<sup>2</sup>, Ronald M. Bonett<sup>1</sup>**

<sup>1</sup>*Department of Biological Science, University of Tulsa, Tulsa, OK 74137 USA;* <sup>2</sup>*U.S. Geological Survey*

#### **The Effects of Ecology, Physiology, and Diet on the Evolution of Endotherm Gastrointestinal Tract Lengths**

Vertebrates have diversified into a wide range of habitats, and consume many forms of organic material. Consequently, vertebrates have evolved many morphological and physiological adaptations to maximize digestive efficiency. As the primary site of nutrient uptake, the intestine's size has been proposed to be influenced by metabolic demands, diet, and locomotory restrictions (lifestyle). We tested for the effect of these factors amongst mammals and birds using a phylogenetically informed approach. Diet was found to affect large intestine length in mammals and birds but only influenced small intestine length among mammals when we partitioned herbivorous groups according to fermentative strategy. Lifestyle influenced small, large and total intestine length in both mammals and birds, supporting the notion that restrictions are placed on all endotherms intestinal lengths according to the substrate they locomote within or on. Metabolism had no effect on small intestine length or large intestine length in mammals or birds. Our analyses show the relative importance of these factors on the evolution of the gastrointestinal tract of endotherms.

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### 214 Technical Session 15, Meeting Room 16, Tuesday 10 June 2014

**Sarah Vrla<sup>1</sup>, Brandon K. McDonald<sup>1</sup>, Bryce Geiger<sup>1</sup>, Joe Macedonia<sup>2</sup>, Kelsey Ellis<sup>3</sup>**

<sup>1</sup>*Cameron University, Department of Biological Sciences, Lawton, OK 73505 USA;* <sup>2</sup>*Florida Southern College, Department of Biology, Lakeland, FL 33801 USA;* <sup>3</sup>*University of Kansas, Lawrence KS 66045 USA*

#### **Potential UV-vision in the Kangaroo Rat (*Dipodomys ordii*), Evidence from Photoreceptor Proteins (Opsins) in the Retina**

Communication in the ultraviolet (UV) spectrum is known in insects, plants, fish, amphibians, reptiles, birds, and very few mammal species. UV-communication requires both signaling mechanisms and perception mechanisms. Signaling mechanisms include UV-reflective morphological characteristics such as hair, feathers, skin, and flowers. Such reflection of UV for communication is only known to occur between 350-390 nm (UV-A). For such signaling to serve as a means of communication, the vision system of the intended signal recipient must be able to perceive light wavelengths as short as 350 nm. The ability of the visual system to perceive UV-light depends on many factors including transmission of UV light by the cornea, lens and ocular media and successful absorption of UV by photoreceptor proteins (opsins) in the retina. Here, we used immunohistochemical labeling (IHC) to identify 3 major mammalian photoreceptor types in the cone and rod cells of the kangaroo rat retina. The species' retina is populated with cells expressing the short wavelength opsin (i.e., Violet/UV opsin), middle/long wavelength opsin, and Rhodopsin. Through microscopy, we constructed opsin distribution maps of the kangaroo rat retina and compared it to published results of other small mammal species. The kangaroo rat displays a relatively high density of UV-opsins directly



## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

ventral to the optic nerve. From our data, we can conclude that *Dipodomys ordii* has the potential for UV-vision although more experiments are needed to validate this.

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### 215 Technical Session 15, Meeting Room 16, Tuesday 10 June 2014

**Adrienne Wells<sup>1</sup>, Brandon K. McDonald<sup>1</sup>, Joe Macedonia<sup>2</sup>**

*Cameron University, Department of Biological Sciences, Lawton, OK 73505 USA;* <sup>2</sup> *Florida Southern College, Department of Biology, Lakeland, FL 33801 USA*

#### **Modeling of the Vision System of the Kangaroo Rat (*Dipodomys ordii*) and Implications for UV-communication**

The potential for the kangaroo rat (*Dipodomys ordii*) to communicate in the ultraviolet (UV) spectrum has been validated. Experiments carried out thus far supporting this conclusion include: 1) observation and measurements of UV-reflective morphology; 2) UV-transmittance of the cornea, lens and ocular media; and 3) high density of UV-photoreceptor proteins (opsins) in the retina. Here, we present a mathematical model that includes maximum absorption ( $\lambda_{MAX}$ ) of the 3 retinal photoreceptors (UV-opsin; middle/long wavelength opsin; Rhodopsin) known to occur in the retina along with previously collected quantitative UV-reflectivity data of morphological markings and various environmental light intensity scenarios to extrapolate how each photoreceptor contributes to both the nocturnal and diurnal visual systems of the species. We discovered that even under nocturnal conditions, with illumination from the moon, the species could fully utilize the UV-opsin for communication functions. Results of a diurnal visual model are also presented.

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### 216 (E,\*\*,TA) Technical Session 15, Meeting Room 16, Tuesday 10 June 2014

**Jennifer Wilkening, Chris Ray**

*Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, CO 80309 USA*

#### **Characterizing Relationships between Microclimate, Metrics of Physiological Stress, and Survival in a Climate-sensitive Mammal**

The American pika (*Ochotona princeps*), a sentinel species for detecting ecological effects of climate change, is declining within a large portion of its range. Pikas have a narrow thermal tolerance and rely on access to subsurface microclimates to shed heat. Because pikas behaviorally thermoregulate, it can be difficult to assess the impact of local habitat characteristics on persistence. This underscores the importance of assessing individual response, such as physiological stress or survival, to specific habitat characteristics, such as microclimate. If local habitat variables can explain individual survival, then climate change may have relatively direct effects that are contributing to local extinctions of this species. Here we related individual survival in pikas to 2 different stress metrics, the concentration of glucocorticoid (GC) metabolites in fecal samples and GC concentration in plasma samples. Blood and fresh fecal samples were collected from marked pikas during a long-term (2008-2013) demographic study in the Rocky Mountains. Annual survival was estimated via program MARK using a resight protocol, and comparative analysis of GC concentration in samples was done using Corticosterone enzyme-immunoassay kits. Structural equation modeling was explored to characterize relationships between microclimate, stress metrics and individual survival. Results suggest mechanistic effects of chronic and acute stress on pika survival, and effects of microclimate on chronic and acute stress. This research was supported by an ASM Grants-In-Aid of Research awarded to Jennifer Wilkening in 2013.

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### 217 Technical Session 15, Meeting Room 16, Tuesday 10 June 2014

**Cynthia J Downs<sup>1</sup>, Kelley, M. Stewart<sup>1</sup>, Sabrina Morano<sup>1</sup>, Peregrine L. Wolff<sup>2</sup>**

<sup>1</sup>*Department of Natural Resources and Environmental Sciences, University of Nevada, Reno, NV 89512 USA;*

<sup>2</sup>*Nevada Department of Wildlife, Reno, NV 89512 USA*

#### **Small-scale Environmental Gradients Affect Trace Mineral Levels But Not Immune Function in Mule Deer**

Environmental conditions directly affect the nutritional quality of food. Nutritional quality of food, in turn, mediates individual-level heterogeneity in physiological phenotypes. We investigated how habitat use at small scales affected constitutive immune function and trace-mineral levels in mule deer (*Odocoileus hemionus*) in the Jackson Mountain Range in Nevada. Using GPS collar data, we assigned deer to land-use groups: field (primarily used alfalfa fields), uplands (primarily used natural, upland habitat), and split (split time between habitats). We found that habitat use on a small scale resulted in differences in serum levels of selenium, magnesium, and iron, but not differences in levels of calcium, copper, phosphorous, and zinc. Levels of calcium, phosphorous, and zinc differed among study years. These results suggest that differences in environmental conditions over short ranges can affect nutritional status of individuals. Interestingly, we found evidence of immunosenescence for 1 functional measure of constitutive immune function, bactericidal capacity, but not another measure of constitutive immune function, reactive nitrogen metabolites; neither measure of immune function differed among study groups. Because physiology is regulated by a

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

complex network of responses and many aspects of physiology must be studied to understand how environmental conditions and ontogeny affect phenotypes.

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### 218 Technical Session 15, Meeting Room 16, Tuesday 10 June 2014

**Evan C. Wilson<sup>1</sup>, Stanley D. Gehrt<sup>1,2</sup>**

<sup>1</sup>*School of Environment and Natural Resources, The Ohio State University, Columbus, OH 43210 USA;* <sup>2</sup>*Max McGraw Wildlife Foundation, Dundee, IL 60118 USA*

#### **Seroprevalence of Infectious Disease among Sympatric Carnivores in the Chicago Metropolitan Area**

Infectious diseases are important factors in the population dynamics of many mammalian species. Urbanization can increase interspecific disease transmission due to clustered resources and increased population densities. Between 2008 and 2012, blood samples were obtained from coyotes, raccoons and free-roaming cats live-trapped within the Chicago metropolitan area. Among coyotes ( $n = 53$ ) and raccoons ( $n = 196$ ) serological tests were performed for 7 *Leptospira* serovars, canine distemper virus (CDV), canine parvovirus (CPV), heartworm, *Toxoplasma gondii* (IgG, IgM), anaplasmosis, *Ehrlichia*, and Lyme disease. Among cats ( $n = 99$ ) serological tests were performed for feline leukemia virus (FeLV), feline immunodeficiency virus (FIV), *T. gondii*, and heartworm. We used logistic regression to determine the influence of study site, year, sex, and age on probability of infection. Seroprevalence of *T. gondii* (IgG) varied between species ( $p = 0.03$ ) and sex ( $p = 0.002$ ). Among coyotes seroprevalence of CDV varied by age ( $p = 0.04$ ) and site ( $p = 0.01$ ). Among raccoons seroprevalence of *Leptospira grippotyphosa* and CDV varied by year (*L. grippotyphosa*  $p = 0.02$ ; CDV  $p < 0.001$ ) and age (*L. grippotyphosa*  $p < 0.001$ ; CDV  $p < 0.001$ ), while *T. gondii* (IgG) varied by site ( $p = 0.03$ ). Although seroprevalence for CDV and CPV were high in coyotes (40%, 98%) and raccoons (53%, 100%) little mortality due to these diseases was observed. The high seroprevalence of pathogens such as *T. gondii*, CPV, and CDV emphasizes the potential for transmission into domestic species and humans.

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### 219 Technical Session 16, Meeting Room 17, Tuesday 10 June 2014 [moved to Technical Session 9]

**Mariela G. Gantchoff, Nathan S. Libal, Jerrold L. Belant**

*Carnivore Ecology Laboratory, Forest and Wildlife Research Center, Mississippi State University, Mississippi State, MS 39759 USA*

#### **Small Carnivore Introductions: Ecological and Biological Correlates of Success**

Successful species introductions are not homogeneously distributed over Earth, which points to the need to understand why some introductions succeed yet others fail. We summarized information on small carnivore introductions worldwide and assessed whether correlates of invasion success supported 1 or more of the following hypotheses: preadaptation to climate; propagule pressure; inherent superiority; island susceptibility; and Darwin's naturalization hypothesis. Using the literature, we summarized: number of individuals released; mean body size; mean litter size; consumer type; latitude difference; ecoregions difference; congener presence; and mainland or island release. We used generalized linear models and ranked models using Akaike Information Criterion and Akaike weights. We identified 210 introduction events of 23 species from 4 families, most involving northern raccoon (*Procyon lotor*), American mink (*Neovison vison*), and small Indian mongoose (*Herpestes javanicus*). Overall invasion success was high, with a success rate  $> 70\%$  for 10 of the 13 represented genera. We found support for preadaptation to climate and inherent superiority hypotheses. Success was dependent on matching climatic conditions that allow survival, and a greater body size together with a smaller litter size increased the likelihood of invasion success. Islands were not more susceptible to invasion, and the number of individuals introduced did not influence success. Finally, possibly because of the scale considered, the presence of congeners in the area did not decrease the chance of establishment success.

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### 220 (E,\*\*) Technical Session 16, Meeting Room 17, Tuesday 10 June 2014

**Jonathan J. Derbridge, John L. Koprowski**

*School of Natural Resources and the Environment, University of Arizona, Tucson, AZ 85721 USA*

#### **Consequences of Syntopy between an Endangered Tree Squirrel and an Ecologically Similar Invader**

Invasive species pose major threats to isolated populations, but mechanisms of impact are unclear. In the Pinaleno Mountains, a sky island in southeastern Arizona, we used experimental removal of Abert's squirrels (*Sciurus aberti*) to determine potential effects of competition with endangered Mount Graham red squirrels (*Tamiasciurus hudsonicus grahamensis* [MGRS]). We predicted that if spatial overlap was high, post removal space use would change and reproductive success would increase, and if the native and introduced species consumed similar proportions of fungi, fungi consumption by MGRS would increase after removal of Abert's squirrels. We monitored radio-collared individuals of both species in 2 adjacent 100-ha areas of mixed conifer, spring 2011 to summer 2012. We captured and euthanized removal-area Abert's squirrels, March–June 2012. We collected hair samples from all captured animals, and diet samples (i.e., conifer seeds, fungi, inner bark) throughout the study period. Current analysis of

## American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

carbon and nitrogen stable isotopes in hairs and diet items will determine interspecific overlap in diet proportions and shifts in post removal MGRS diet. Abert's squirrels overlapped MGRS home ranges by about 40%, and post removal home ranges increased in the removal area only. Measures of MGRS reproduction increased in the removal area only. Invader removal may release MGRS from space-use restrictions, enhancing reproductive success. Our work provides new insight on mechanisms of invader impact and potential fitness consequences for isolated populations of ecologically similar species. This research was supported by an ASM Grants-in-Aid of Research awarded to Jonathan Derbridge in 2012.

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### 221 Technical Session 16, Meeting Room 17, Tuesday 10 June 2014

**Sean A. Neiswenter<sup>1</sup>, Allen Calvert<sup>2</sup>**

<sup>1</sup>*School of Life Sciences, University of Nevada, Las Vegas, NV 89154 USA;* <sup>2</sup>*Multi-Species Conservation Program, Bureau of Reclamation, Boulder City, NV 89005 USA*

#### **Implications of Population Demographics on the Management of *Sigmodon arizonae plenus***

*Sigmodon arizonae plenus* is an isolated subspecies of Arizona cotton rat that is only found along the lower Colorado River in Arizona and California. We conducted a mark-recapture study using permanent sampling grids at 3 localities along the Colorado River. In addition, we sampled vegetation characteristics at each of the localities. We used Program Mark to estimate population demographic parameters and relate the parameter estimates to the differences in habitat at each locality. Management and monitoring recommendations will be discussed.

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### 222 (C) Technical Session 16, Meeting Room 17, Tuesday 10 June 2014

**Robert A. McCleery, Chelsey Faller**

*Department of Wildlife Ecology, University of Florida, Gainesville, FL 32608 USA*

#### **Understanding the Distribution of a Rare Rodent in the Wetlands of Florida**

From 1985 to 1996 Florida's total wetland area declined by 52,000 acres. The loss has been particularly intense for emergent wetlands (marshes and wet meadows), the loss for which was 10,500 ha (9%) from 1985 to 1996. The Florida Fish and Wildlife Conservation Commission has become concerned with the status of the round-tailed muskrat (*Neofiber alleni*), an aquatic rodent endemic to Florida which utilizes freshwater wetlands. We used a stratified random survey to locate round-tailed muskrat (hereafter RTM) populations in the north-central Florida region. RTMs were detected by walking transects within a 40-m by 40-m plot searching for their distinctive floating lodges made of grass, or feeding platforms with scat. We conducted 61 random surveys for RTMs between May and September 2013. We related the distribution of RTMs to vegetation structure and water characteristics at each site to understand how local scale features influence occurrence. On a larger scale, we investigated patch characteristics and the influence of vegetative communities, land cover, anthropogenic landscape features, and hydroregime on RTM occurrence. We compared the relative influence of local and landscape variables by comparing a priori models using an occupancy modeling approach. At local scales the occurrence of RTM was influenced by lily pads (*Nymphaea*), at the landscape scale hydroperiod influences RTM occurrence.

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### 223 (E) Technical Session 16, Meeting Room 17, Tuesday 10 June 2014 [moved to Technical Session 4]

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#### **Proximate Mechanisms of Delayed Recovery in Reintroduced American Martens**

Reintroductions and translocations are increasingly important tools for the conservation and recovery of carnivores. The American marten (*Martes americana*) is Wisconsin's only endangered mammal and has been subject to multiple reintroduction attempts, the most recent of which occurred in the Chequamegon National Forest (CNF) between 2008 and 2010. Marten recovery has been slower than anticipated, yet the mechanisms limiting recovery remain unknown. To evaluate the success of this reintroduction and explore potential limitations to recovery, we noninvasively collected marten DNA using 200 randomly distributed hair snares within the CNF. Over 2 winters we collected 46 genetic samples and estimated marten abundance ( $\hat{N}$ ), survivorship ( $\hat{S}$ ), and density via genetic mark-recapture analyses. By coupling capture histories with snow-track surveys we mapped marten distribution and identified relevant habitat features via dynamic occupancy models. Models were constructed for both sampling methods using 10 site-specific habitat variables (e.g., conifer basal area per hectare) and unique detection covariates for each. We quantified the relative importance of each variable and estimated parameter values for detection ( $p$ ), occupancy ( $\psi$ ), site colonization ( $\gamma$ ), and local extinction ( $\epsilon$ ). Ultimately, our analyses will help elucidate the proximate mechanisms limiting marten recovery in Wisconsin and provide a mechanistic understanding of reintroduction biology for recovering carnivore populations as a whole.

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# American Society of Mammalogists 94<sup>th</sup> Annual Meeting—Oklahoma City, Oklahoma

224 (E) Technical Session 16, Meeting Room 17, Tuesday 10 June 2014

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## **Status of the Jaguar (*Panthera onca*) in the Mountain Pine Ridge Forest, Belize: Evidence of Family Lineage and Residency Status**

Jaguars (*Panthera onca*) inhabit a diverse array of habitats and cover a large amount of area making residency status difficult to determine, especially with a deteriorating distribution. After sighting an adult female with cub in a year-long camera trap survey in 2010, we established similar surveys (2012 and 2013) on privately owned land near the sighting, located in the northern region of the Mountain Pine Ridge Forest. In 2012, 3 camera traps yielded 28 captures of jaguars, all of which were identified as the same individuals photographed in the previous survey. During 2012, the 2010 cub was determined to be a female due to sighting with a new cub, adding to the family line. Resightings continued to occur during the 2013 campaign and were supported by local employee findings from the resort. These results are still being analyzed. We present the results of a 3-year camera trap study providing evidence inferring residency status of a jaguar family lineage within a Neotropical pine forest.

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225 Capstone: Great Halls D & E, Tuesday 10 June 2014

**Joel S. Brown**

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## **Ecology of Fear: Past, Present and Future Directions**

Predator's both kill and frighten their prey. Such effects influence trophic cascades, coexistence, habitat suitability, management, and parallel evolution on different continents. Behavioral responses bend the vegetation's, prey's, and predator's isoclines, thus altering abundances and stability properties. Fierce carnivores can be rare even as they positively influence prey and vegetation abundances without much actual killing. For management this leads to questions such as "Does Chicago have too many deer or too fearless deer?" Biodiversity gets augmented as seen in fox squirrels and grey squirrels. They do not support the predators whose fear is needed for coexistence. Double-bind fear responses enhance predator biodiversity such as the predator facilitation experienced by snakes and owl preying upon gerbils. Springbok and striped mice of South Africa show how spatial variability in food and safety create habitats that are: 1) core for the prey (safe and productive); 2) refugia (safe but unproductive); 3) unsuitable (risky and unproductive) and core for their predators (risky and productive). Finally, work with Burt Kotler uses common garden experiments to compare 2 species of Middle Eastern gerbils and 2 species of Heteromyid rodents (a pocket mouse and a kangaroo rat) as they face a Middle Eastern (horned viper) and North American (sidewinder rattlesnake) snake. What emerges from all of this? Concepts and metrics from these predator-prey foraging games matter now and into the future.

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## AUTHOR INDEX

<b>A</b>	
Abba, Agustín M. ....	20
Abbruzzese, Carlo .....	182
Achmadi, Anang S. ....	35
Actis, Esteban A. ....	176
Ahlers, Adam A. ....	169
Alexander, Lois F. ....	115
Ali, Abdullahi H. ....	4
Allredge, Mathew .....	111
Anderson, Robert P. ....	33, 34, 131
Andresen-Everatt, Leah M. ....	54
Arasamuthu, Arul Sundari.....	209
Archer, Frederick I. ....	95
Armitage, Kenneth B. ....	9
Augustine, David J. ....	201
<b>B</b>	
Baccus, John T. ....	163, 190
Bailey, Larissa L. ....	135
Baker, Robert J. ....	11, 78, 79, 91, 123
Bani-Yaghoub, Majid .....	205
Barnes, Brian M. ....	8
Barthemess, Erika L. ....	25, 147
Beever, Erik A. ....	1, 182, 199
Beissinger, Steven R. ....	129
Belant, Jerrold L. ....	48, 137, 219
Belew, Charlene .....	152
Bell, Kayce C. ....	114
Bellows, A. Scott .....	168
Bennett, Victoria J. ....	38, 64
Berens, Jeffrey .....	155
Berger, Joel .....	15
Best, Troy .....	72
Beyer, Dean .....	137
Bhadra, Anindita .....	208
Bland, R. Craig .....	133
Bled, Florent .....	137
Bleich, Vernon C. ....	66
Blum, Marcus E. ....	26
Blythe, Rita M. ....	43
Boan, Brianne V. ....	177
Bogdanowicz, Wieslaw .....	209
Boitani, Luigi .....	99
Bonett, Ronald M. ....	213
Bono, Jeremy M. ....	142
Boonstra, Rudy .....	16
Boria, Robert A. ....	34
Boyce, Walter M. ....	94
Boyd, Trevor .....	63
Boyer, A. G. ....	126
Boykins, Genevieve K. R. ....	122
Bradley, Robert D. ....	90, 123, 125, 192
<b>C</b>	
Brashear, Wesley .....	150
Briones-Salas, Miguel A. ....	50
Britten, Hugh B. ....	145
Brokaw, Joshua M. ....	195
Brown, J. H. ....	126
Brown, Joel .....	225
Buchalski, Michael R. ....	94
Bulmer, Walter .....	62
Burdett, Chris .....	99
Burger, Joseph R. ....	5
Burgess, Matthew A. ....	184
Burgio, Kevin R. ....	203
Burneo, Santiago F. ....	194
Bush, Anthony P. ....	66
<b>C</b>	
Callicoatte, Kathleen .....	75
Calvert, Allen .....	221
Camp, Meghan J. ....	106, 212
Campbell, Polly .....	173
Capparella, Angelo .....	37
Carey, Hannah V. ....	7
Castleberry, Steven B. ....	133
Cavalieri, Cybil Nicole .....	153
Ceballos, Gerardo .....	96
Chaverri, Gloriana .....	100
Chávez, Daniel E. ....	194
Cheeseman, Amanda E. ....	61
Chen, Hsiang Ling .....	103
Chevalier, Cary D. ....	63
Chhetri, Saurav .....	144
Choi, Byung-Jin .....	163
Cifelli, Richard L. ....	167
Cisneros, Laura M. ....	203
Clark, Steven L. ....	182
Clark, Susan G. ....	68
Cohen, Jonathan .....	61
Colella, Jocelyn P. ....	141
Coleman, Jeremy T. H. ....	165
Conway, Kimberly .....	171
Cook, Joseph A. ....	113, 146, 164, 197
Coonan, Timothy J. ....	109
Corey-Rivas, Sarah J. ....	138
Corral, Daniel C. ....	58
Costa, D. P. ....	126
Costa, Gabriel C. ....	96
Cox, Mike .....	93
Crimmins, Shawn .....	182
Crooks, Kevin .....	99
Crowell, M. M. ....	106, 212
Culver, Melanie .....	42
Cypher, Brian L. ....	109

Czaplewski, Nicholas J. .... 167  
Czetwertynski, Sophie M. .... 178, 179

**D**

da Silva, Maria Nazareth F. .... 198  
Dabrowski, Michal ..... 209  
Danielson, Brent J. .... 3  
Danley, Patrick ..... 39  
Darby, Neal ..... 66  
Daughtry, Tanya K. .... 195  
Davidson, Ana D. .... 96  
Dearing, M. Denise ..... 1  
Debelica-Lee, Anica ..... 39  
Delsuc, Frédéric ..... 19  
Denkhaus, Robert ..... 64  
Derbridge, Jonathan J. .... 220  
Dewey, Tanya ..... 183  
Diaz-Nieto, Juan F. .... 191  
Dickens, Ben ..... 91  
Ding, Baoqing ..... 39  
Dobrowski, Solomon ..... 182  
Dochtermann, Ned A. .... 44, 155  
Dolman, Richard W. .... 51  
Donadio, Emiliano ..... 108  
Dority, Delina E. .... 172  
Doudna, John W. .... 3  
Dowler, Robert C. .... 118  
Downs, Cynthia J. .... 177, 217  
Dreiss, Lindsay M. .... 203  
Druskins, David C. .... 153  
Dubey, Jitender P. .... 169  
Dueser, Raymond D. .... 189  
Dunn, Christopher D. .... 125

**E**

Eaton Jr., T. Scott ..... 224  
Eckerlin, Ralph P. .... 62  
Edelman, Andrew J. .... 23, 56, 59  
Edmonds, Kent E. .... 77  
Edwards, Cody W. .... 192  
Eguren, Rachel E. .... 28  
Eldridge, James A. .... 75  
Ellis, Kelsey ..... 214  
Ellison, Laura E. .... 165  
Ernest, Holly B. .... 94  
Ernest, Kristina ..... 55  
Ernest, S. K. Morgan ..... 126  
Espinosa, Roger ..... 183  
Esselstyn, Jacob A. .... 35  
Evans, A. R. .... 126  
Everatt, Kristoffer T. .... 54  
Everson, Kathryn M. .... 32  
Eyheralde, Peter ..... 200

**F**

Fairbanks, W. Sue ..... 65, 200  
Faller, Chelsey ..... 222  
Farrell, Terence M. .... 107  
Feldman, Chris R. .... 93  
Ferguson, Adam W. .... 118  
Fletcher, Nicholas K. .... 151  
Flores, Karla L. .... 148  
Floyd, Megan A. .... 202  
Follett, Danny ..... 143  
Forbey, Jennifer S. .... 106, 184, 212  
Ford, Adam T. .... 201  
Ford, Brett ..... 147  
Forney, Ronny ..... 139  
Fortelius, M. .... 126  
Fowler, Melissa ..... 22  
Frank, Craig L. .... 10

**G**

Galante, Peter J. .... 33  
Gantchoff, Mariela G. .... 48, 219  
Gardner, Alfred L. .... 62, 83  
Gardner, Scott L. .... 197  
Gardner, Sue Ann ..... 166  
Gaschak, Sergey ..... 91  
Gehrt, Stanley D. .... 218  
Geiger, Bryce ..... 214  
Giaria, Thomas C. .... 35  
Gibbs, H. Lisle ..... 107  
Gille, Daphne A. .... 94  
Gittleman, J. L. .... 126  
Goheen, Jacob R. .... 47, 67, 201  
Gomez-Ruiz, Emma P. .... 102  
González-Ruiz, Laureano R. .... 159  
Goodman, Steven M. .... 32, 33  
Graham, Catherine H. .... 96  
Green, Rebecca E. .... 74  
Greene, Daniel U. .... 185, 186  
Guglielmino, Angela ..... 109  
Gutiérrez, Eliécer E. .... 156

**H**

Hale, Amanda M. .... 38  
Hale, David W. .... 162  
Hale, Sarah L. .... 46  
Hall, Lucas K. .... 40  
Hallgren, Stephen W. .... 24  
Hamilton, M. J. .... 126  
Hammond III, George ..... 183  
Hanson, J. Delton ..... 88, 89, 195  
Harding, L. E. .... 126  
Hardy, Daniel M. .... 90  
Harris, Jonathan P. .... 187  
Harrison, Daniel J. .... 188

Haynie, Michelle L. ....	89
Hegel, Troy M. ....	178
Helgen, Kristofer M. ....	31, 156
Herlik, Stephanie A. ....	142
Hernandez, Amalia ....	56
Heske, Edward J. ....	169
Hirt, Samuel H. ....	72
Hodge, Anne-Marie C. ....	47
Hoffman, Eric A. ....	149
Hoffmann, Federico G. ....	92
Holekamp, Kay E. ....	153
Holmes, Michael W. ....	122
Holsomback, Tyla S. ....	76
Hood, Wendy ....	72
Hooghkirk, Jill. ....	55
Hope, Andrew G. ....	146
Horns, Joshua J. ....	1
Hornsby, Angela D. ....	132
Howard, Kelsey D. ....	10
Hughes, Phillip T. ....	149
Huynh, Howard M. ....	123

**I**

Ingersoll, Thomas ....	165
Ingram, Kate P. ....	41
Irvine, Kathryn. ....	165
Iudica, Carlos A. ....	21

**J**

Jackson, Victoria L. ....	65, 170
Jacques, Marie-Eve ....	24
Jahn, Graciela A. ....	176
Jaksic, Fabian M. ....	180
Jansa, Sharon A. ....	32, 191
Jeffrey, Christopher S. ....	120
Jenks, Kate E. ....	130
Jesmer, Brett R. ....	67
Jo, Yeong-Seok ....	163
Johnson, Catherine M. ....	135
Johnson, Craig A. ....	154
Johnson, T. R. ....	212
Jones, Amanda K. ....	164
Jones, Mallory E. ....	82
Jones, Tricia. ....	183
Joshi, Priya ....	144
Jung, Thomas S. ....	52, 53, 54, 178, 179

**K**

Kauffman, Matthew J. ....	67
Kaufman, Dawn M. ....	45, 57
Kaufman, Donald W. ....	45, 57
Kaufman, Glennis A. ....	45, 57
Kelt, Douglas A. ....	74
Kern, Colin ....	92
Khan, Faisal Anwarali ....	91

Kiesow, Alyssa M. ....	145
Kilanowski, Allyssa L. ....	71
Kilpatrick, C. William ....	36, 144
Kingston, Tigga ....	101
Kirby, Rebecca. ....	110
Klingbeil, Brian T. ....	203
Knight, Frank. ....	175
Knight, Robert N. ....	40
Koprowski, John L. ....	46, 71, 103, 134, 163, 220
Kotler, Burt ....	105
Krzyszczyk, Ewa ....	211
Kulikowski II, Andy ....	121

**L**

Lacey, Eileen A. ....	112
Lacher Jr., Thomas E. ....	102
Ladevèze, Sandrine ....	159
Lambert, Connor T. ....	40
Lambert, Mallory S. ....	1
Laney, Kara N. ....	199
Lanier, Hayley ....	121
Lankford, Scott ....	170
Larsen, Randy T. ....	40
Lausen, Cori L. ....	165
Lavariega-Nolasco, Mario C. ....	50
Lee Jr., Thomas E. ....	195
Lee, Tyler ....	63
Leite, Rafael N. ....	198
León-Paniagua, Livia ....	193
Leslie Jr., David M. ....	51
Leslie, Matthew S. ....	95
Lessa, Enrique P. ....	116
Lewis, Shelby ....	59
Li, Gang. ....	150
Li, Han. ....	104
Libal, Nathan S. ....	219
Lichti, Nathanael I. ....	43
Light, Jessica E. ....	12
Linscott, T. M. ....	213
Lintulaakso, K. ....	126
Loeb, Susan C. ....	165
Lohuis, Thomas D. ....	177
Longshore, Kathleen ....	27
López-Medellín, Xavier ....	86
Loughry, W. J. ....	18
Loveless, Allison Marcella. ....	119
Lowrey, Chris ....	27
Lundrigan, Barbara L. ....	153
Lyda, Sara B. ....	65
Lyons, S. Kathleen. ....	126

**M**

Macedonia, Joe. ....	214, 215
MacFarland, David M. ....	110

MacPhee, Ross D.....	159
Maharadatunkamsi.....	35
Maher, Sean P.....	129
Majumder, Sreejani Sen.....	208
Makova, Kateryna.....	91
Malaney, Jason L.....	93, 146
Maldonado, Jesus.....	156
Manlick, Philip J.....	223
Mann, Janet.....	211
Marimuthu, Ganapathy.....	209
Martell, Deb.....	137
Martin, Heather.....	173
Martinez, Roni.....	224
Mason, Victor C.....	31
Matocq, Marjorie D.....	93, 120, 132
Mauldin, Matthew R.....	125
McAlpine, Donald F.....	123
McBee, Karen.....	24, 28
McCain, Christy M.....	124, 128
McCleery, Robert A.....	185, 186, 222
McDonald, Brandon K.....	152, 214, 215
McDonough, Colleen M.....	18, 60
McMillan, Brock R.....	40
Medellín, Rodrigo A.....	86
Menezes, Jorge F. S.....	105
Merrick, Melissa J.....	134
Michener, Gail R.....	73
Middleton, Arthur D.....	108
Miller-Butterworth, Cassandra M.....	81
Milling, Charlotte R.....	69, 174, 184
Mills, Melissa A.....	64
Mitchell, Mark A.....	169
Mixon, Brittany A.....	60
Moncrief, Nancy D.....	189
Monteith, Kevin L.....	67
Moore, Christopher.....	22
Morano, Sabrina.....	217
Morin, Phillip A.....	95
Morris, Katrina M.....	133
Mosconi, Sergio.....	176
Moss, Wynne E.....	111
Mourão, Guilherme M.....	105
Mueller, Jalina.....	77
Murphy, Peter J.....	120
Murphy, William J.....	13, 31, 150
Murtough, Katie.....	175
Muscarella, Robert.....	33
Myers, Phil.....	183
<b>N</b>	
Naples, Virginia L.....	157
Nations, Jonathan A.....	207
Neiswenter, Sean A.....	221

Newsome, Seth D.....	109
Nobler, Jordan.....	184
Norman, Jessie.....	123

**O**

O'Brien, Tim.....	201
O'Connell Jr., Allan F.....	135
O'Connell, Timothy J.....	187
Ojeda, Ricardo A.....	14
Okie, J. G.....	126
Oller, Anna.....	170
Olson, Link E.....	30, 32, 82, 207
Olson, Sheryn J.....	188
Olstoy, Peter J.....	184
Ord, Terry.....	127
Ordóñez-Garza, Nicté.....	192
Ortega, Isaac M.....	68, 202
Owen, James G.....	192

**P**

Pacheco, Víctor.....	204
Palmer, Todd M.....	201
Papes, Monica.....	119
Paquet, Paul C.....	181
Parlos, Julie A.....	79
Patterson, Bruce D.....	29, 196, 203
Patterson, Eric M.....	211
Paul, David.....	174
Paul, Manabi.....	208
Pauli, Jonathan N.....	108, 110, 111, 223
Pauling, Cassandra D.....	170
Payer, David C.....	146
Pendley, Brad.....	49
Penedo, Maria Cecilia T.....	94
Peralta, María.....	204
Perrig, Paula L.....	108
Perrin, William F.....	95
Peterson, A. Townsend.....	118
Peurach, Suzanne C.....	62
Phelps, Kendra L.....	101
Phillips, Caleb D.....	11, 91
Phillips, Cody.....	63
Phillips, Lauren T.....	153
Pigage, Helen K.....	142, 143
Pigage, Jon C.....	142, 143
Pinto, C. Miguel.....	6
Platt II, Roy N.....	92
Porter, John H.....	189
Post, Diane M.....	75
Powell, John.....	63
Power, Michael.....	175
Pradhan, Nelish.....	36, 144
Presley, Steven J.....	203
Preston, Kathryn A.....	44



Pringle, Rob M. ....	201
Purcell, Kathryn L. ....	74
Pynne, Justin T. ....	56

**Q**

Quicksall, Zachary ....	80
Quigley, Howard ....	99

**R**

Rachlow, Janet L. ....	69, 106, 174, 184, 212
Radeloff, Volker C. ....	96
Rajan, K. Emmanuvel ....	209
Ralls, Katherine ....	109
Rattenborg, Niels C. ....	17
Ray, Chris ....	216
Ray, David A. ....	92
Reed, Aaron W. ....	205
Reed, David L. ....	80
Rees, Eric J. ....	88, 89
Reichard, Jonathan ....	165
Richards, Lora A. ....	120
Rickart, Eric A. ....	130
Rivas, Jesús A. ....	138
Roberts, Emma K. ....	90
Robinson, Michael J. ....	87, 97, 98
Roche, Erin A. ....	213
Rodhouse, Thomas J. ....	165
Roehrs, Zachary P. ....	172
Rogers, Duke S. ....	198
Rogers, Kathryn R. ....	206
Rogers, Tracey ....	127
Rondinini, Carlo ....	96, 99
Rosa, Cheryl ....	72
Rose, Robert K. ....	168
Rosenstern, Joel ....	81
Rouse, Matthew ....	59
Rowe, Kevin C. ....	35
Rowe, Rebecca J. ....	130
Rowland, Jarrett ....	63
Royster, Paul ....	166
Rubenstein, Daniel I. ....	2
Ruiz-Vega, M. Laura ....	193
Russell, Amy L. ....	81
Rutter, Amy R. ....	156
Ryan, James ....	183
Ryu, Hae Yeong ....	70

**S**

Saarinen, J. J. ....	126
Sackrider, Margaret E. ....	68
Sagot, Maria ....	100
Salazar-Bravo, Jorge ....	197
Sanchez, Gael A. ....	69
Sargis, Eric J. ....	30
Sauer, John R. ....	165

Sawada, Bryant ....	55
Scheibe, John S. ....	49
Schieltz, Jennifer M. ....	2
Schildt, Ali J. ....	38
Schmidly, David J. ....	85
Schmidt, Carl J. ....	92
Scholten, Kristen M. ....	30
Schooley, Robert L. ....	169
Schroeder, Cody ....	26
Scrivner, Jerry H. ....	154
Searle, Jeremy B. ....	151
Sego, Camron A. ....	154
Seville, R. Scott. ....	172
Sharma, Ajay N. ....	36, 144
Shaw, Barbara J. ....	158
Sheffield, Steven R. ....	21
Shiple, Lisa A. ....	106, 174, 184, 212
Shoemaker, Kevin T. ....	96
Shubin, Emma. ....	124
Sibly, R. M. ....	126
Slade, Norman A. ....	205
Slattery, Michael C. ....	64
Smiley, Sarah A. ....	107
Smith, Felisa A. ....	126
Smith, Kent. ....	167
Smith, Nicholas L. ....	109
Smith, Winston P. ....	135
Smyser, Timothy J. ....	43
Sotero-Caio, Cibele G. ....	78
Speer, Kelly A. ....	80
Sprayberry, Ty. ....	59
Stapp, Paul. ....	22, 148, 171
Stephens, P. R. ....	126
Sterling, Keir B. ....	84
Stewart, Kelley M. ....	26, 66, 177, 217
Stith, Erin. ....	63
Storz, Jay ....	121
Stotyn, Shannon A. ....	178, 179
Strauss, Richard E. ....	118
Summers, Savanna M. ....	137
Superina, Mariella ....	20, 176
Sutton, Melissa. ....	161
Swihart, Robert K. ....	43

**T**

Talbot, Sandra L. ....	146
Taylor, Casey R. ....	138
Terdal, Erik. ....	224
Terry, Rebecca C. ....	130
Theodor, J. ....	126
Thogmartin, Wayne E. ....	165
Thompson, Cody W. ....	192
Thompson, Craig M. ....	74

Thornton, Daniel .....	99
Toien, Oivind .....	8
Tompkins, Amanda .....	55
Trewhitt, Stephanie A. ....	58
Trujano-Alvarez, Ana L. ....	50
Tucker, Marlee .....	127
Turner, Greg G. ....	81
Tuttle, Kristy L. ....	160
Tye, Courtney A. ....	186

**U**

Uhen, M. D. ....	126
Unkefer, Margaret K. ....	192
Upham, Nathan S. ....	29, 196

**V**

Van Essen, Rachael A. ....	37
Van Vuren, Dirk H. ....	210
Vanderwolf, Karen J. ....	123
Vandewege, Michael W. ....	92
Varner, Johanna .....	1, 182
Vickers, T. Winston .....	94
Villanova, Vicki L. ....	149
Voirin, Bryson .....	17
Voirin, Chase .....	42
Volleth, Marianne .....	78
Vonhof, Maarten J. ....	81
Voss, Robert S. ....	191
Vrla, Sarah .....	214

**W**

Wagner, Lindsay M. ....	185
Wallen, Megan M. ....	211
Waltari, Eric .....	146
Wasley, Tony .....	26
Weckerly, Floyd W. ....	140
Weinstein, Ben .....	96
Welch, Corey .....	117
Wells, Adrienne .....	215
Wells, Caitlin P. ....	210
Wenzel, John W. ....	21
Werneck, Fernanda P. ....	198
Wettstein, Peter J. ....	142
Weyers, Anna .....	49
Wickliffe, Jeffery .....	91
Wikelski, Martin .....	17
Wiley, Mary Kate .....	63
Wilkening, Jennifer .....	216
Wilkins, Kenneth T. ....	39, 104
Wilkinson, Jeremy E. ....	89
Williams, Dean A. ....	38
Williams, Scott C. ....	202
Willig, Michael R. ....	203
Wilson, Duncan S. ....	24
Wilson, Evan C. ....	218

Windels, Steve K. ....	136
Wittmer, Heiko U. ....	74
Wolff, Peregrine L. ....	93, 217
Woodman, Neal .....	30
Woodroffe, Rosie .....	201
Woods, Charles A. ....	36

**Y**

Yang, Fengtang .....	78
Young, Julie K. ....	64

**Z**

Zelditch, Miriam L. ....	122
Zeller, Kathy .....	99

# 2015 Meeting Announcement

95<sup>th</sup> Annual Meeting of the  
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