2023 CPSM Program

October 2023

Overview

The 2023 Central Plains Society of Mammalogists Meeting will be held on 12 October 2023 at the National Parks Service Midwest Regional Office, Omaha, NE, and by Zoom. We have set of exciting talks and posters by students covering shrews, rodents, and carnivores.

The Zoom link is here. You can register for the meeting to receive the passcode to view and participate.

After registering, you will receive a confirmation email containing information about joining the meeting.

Hosted by the Lewis and Clark National Historic Trail at the NPS Midwest Regional Office

NPS Contact: Mitchell Meyer, phone: (402) 661-1812; email: mitchell_meyer@nps.gov

Friday 13 October 2023:

Opening Social 6:00 p.m. – 8:00 p.m.

Country Inn and Suites by Raddison
Address: 2210 Abbot Dr, Carter Lake, IA 51510
Phone: (712) 283-4133, press 2 for front desk

Saturday 14 October 2023

Lewis and Clark NHT Visitor Center at the NPS Midwest Regional Office
Address: 601 Riverfront Drive, Omaha, NE 68102
Phone: (402) 661-1804

Schedule

Time	Activity
8:30-9:00	Poster Set up and Coffee
9:00-9:15	Welcome and & Announcements
9:15-9:45	NPS Presentation
9:45-11:30	Oral Presentations
11:30-12:00	Poster previews
12:00-1:30	Lunch and Board Meeting
1:30-2:30	Posters
2:30-3:30	Members Meeting & Adjournment

Contributed Oral Presentations

Time	Presenting Author	Title
9:45am	Rebecca K. Hawkins	Online photo-guided key to the skulls of Kansas mammals
10:00am	Loryn Smith	Methylation Patterns Across Tissue Type and Time in *Peromyscus leucopus*: A Targeted Museum Study
		15-minute break & Poster Set up
10:30am	Matthew T. Turnley	A fine-scale examination of parturition timing in two temperate ungulates
10:45am	Kenneth Damper	Small Mammal Community Survey in Spring Creek Watershed, Northern Missouri
11:00am	Tabitha A. Hughes	Spatial ecology of elk in Nebraska
11:15am	Marcos O.R da Cruz	Tracing the origins of adaptive genomic variation in bank voles from Great Britain

Contributed Poster Presentations

Poster Number	Presenting Author	Title
1	Zoe M. Buffington	Diet of Kansas bat communities using mini-barcodes and Illumina sequencing: Preliminary results
2	Andrew J. Hughes	Shape-shifting squirrels: investigating morphological variations in fox squirrels under climate change and urbanization
3	Basant Sharma	Bats of Nepal: Laying a foundation for future mammalian phylogeography through the Himalayas
4	Miranda K. Theriot	Go big or go small? Building a mechanistic understanding of body-size variation in collared pikas (*Ochotona collaris*)
5	Jacob Humm	Hidden Markov models to predict black bear dispersal patterns in eastern Oklahoma
6	Courtney N. Dotterweich	American black bear resource and space use in a recolonizing population in southeastern Oklahoma
7	Dawson V. Kosmicki	Great-horned Owl diet at Merrihew Cave, Oklahoma, at a major roost of Mexican Free-tailed Bats
8	Joseph W. Paysen	Roost Sites of Eastern Red Bats and Evening Bats in the Great Plains
9	Kailey R. Meacham	Predicting the impacts of a century of anthropogenic change on genetic diversity in collared pikas, a climate-sensitive species
10	Keith Geluso	Survey on the status of Northern Long-eared Bats in western Nebraska

Poster Number	Presenting Author	Title
11	Noah Lemons	Morphological analysis of a masked shrew (Sorex cinereus) population to establish age distribution from size variation
12	Morgan G. Skinner	The Kansas State Biorepository: Developing specimen resources for long-term research
13	Emilyn Gilmore	Predicting the Sensitivity of Oklahoma's Small Mammals to Habitat Fragmentation: A Trait-Based Approach

Abstracts - Oral Presentations

Online photo-guided key to the skulls of Kansas mammals

Rebecca K. Hawkins* (MS Student)

Affiliation at time of project: Museum Studies Program, University of Kansas; Current affiliation: Sam Noble Museum, University of Oklahoma

Animal skulls are occasionally found in nature, sparking curiosity in those that discover them and desire to know their identities. Skulls can be identified to species using dichotomous keys, which guide users through a series of choices between alternative characters to reach an identification; however, there are barriers to understanding and accessing dichotomous keys by the general public. As such, this project endeavored to create an easy-to-understand, accessible dichotomous key to the skulls of Kansas mammals. After examining existing identification resources and best practices for creating dichotomous keys, this goal was achieved through the development of the website "What's This Skull?", which features a photo-guided dichotomous key and browsable list of skull photographs representing 90 mammals in Kansas, including wild and domestic species. Trial testing shows that the key meets usability benchmarks, is quick to use, and generally satisfies users. Beyond fulfilling curiosity, "What's This Skull?" also serves to advocate for the broad utility of museum collections and can be used in education and research.

Methylation Patterns Across Tissue Type and Time in Peromyscus leucopus: A Targeted Museum Study

Loryn Smith* (MS Student), Nicholas Stewart, Alexandra DeCandia, Lorelei Patrick

Fort Hays State University (LS), Southern Oregon University (NS), Georgetown University (AD), Fort Hays State University (LP)

Museum specimens are a vital data source for many types of studies. One relatively new use includes studying methylation patterns. Methylation patterns are a form of epigenetics or how gene expression changes without alteration of the genetic code. These patterns have been examined in many mammals. However, the focus has previously been on overall epigenetic patterns. Few studies have investigated whether methylation patterns differ across tissue types and time. In this study, we compared methylation patterns in muscle, liver, toepads, and nasal bones in *Peromyscus leucopus* (white-footed mouse) museum specimens collected in 2022, 2018, 2014, and 2008 using reduced-representation bisulfite sequencing. We found methylation patterns are most similar within an individual and there was little to no clustering of methylation patterns based on tissue type or collection year. Additionally, tissue preservation in ethanol had no effect on methylation patterns. This study illuminates the role of tissue type in methylation patterns in P. leucopus, and thereby provides an important resource for researchers seeking to study DNA methylation in museum specimens.

A fine-scale examination of parturition timing in two temperate ungulates

Matthew T. Turnley* (PhD Student), Tabitha A. Hughes, Randy T. Larsen, Kent R. Hersey, Matthew S. Broadway, M. Colter Chitwood, W. Sue Fairbanks, Robert C. Lonsinger, and Brock R. McMillan

Department of Natural Resource Ecology and Management, Oklahoma State University (MTT, MSB, MCC, WSF, RCL); School of Natural Resources, University of Nebraska-Lincoln (TAH); Department of Plant and Wildlife Sciences, Brigham Young University (RTL, BRM); Utah Division of Wildlife Resources (KRH); U.S. Geological Survey, Oklahoma Cooperative Fish and Wildlife Research Unit, Oklahoma State University Stillwater (RCL)

Parturition timing has long been a topic of interest in ungulate research. However, few studies have examined parturition timing on a scale < 1 day. We monitored parturition events and early-life survival of elk (*Cervus canadensis*) and mule deer (*Odocoileus hemionus*) in Utah, USA from 2018-2021 to better understand diel timing of parturition in temperate ungulates. Diel timing of parturition was highly synchronous among conspecifics and influenced by environmental variables on the date of parturition. For elk, parturition events were most common during dawn and diel timing of parturition was influenced by moon illumination and temperature. For mule deer, parturition events were most common during the day and diel timing of parturition was influenced by temperature and precipitation. Diel timing of parturition did not influence neonate survival, but we recommend that larger data sets be analyzed to verify the apparent lack of influence. Although more work is required, we offer a rare, fine-scale examination of parturition timing and provide evidence that ungulates can adjust diel timing of parturition in response to their environment.

Small Mammal Community Survey in Spring Creek Watershed, Northern Missouri

Kenneth Damper* (Undergraduate Student), Stephanie Fore, Autumn Winslett

Department of Biology, Truman State University

Biological diversity is crucial in defining the function of an ecosystem. Small mammals less than 35 grams, such as mice and voles, in Missouri function as herbivores and insectivores, and are prey for larger animals. The objective of my research was to assess the diversity of small terrestrial mammals in four habitats at Union Ridge Conservation Area within Spring Creek Watershed in northeast Missouri over multiple seasons. Over two years, mammals were captured, identified, and released. I compared the number and abundance of each species in each habitat. The results of this diversity survey showed that the prairie site was the most diverse habitat. Across the watershed, Peromyscus and Reithrodontomys were the most common species.

Spatial ecology of elk in Nebraska

Tabitha A. Hughes* (Undergraduate Student), Todd Nordeen, Luke Meduna, John F. Benson

School of Natural Resources, University of Nebraska-Lincoln (TAH & JFB); Nebraska Game and Parks Commission (TN & LM)

Recovering populations of ungulates can provide ecological value to ecosystems and increased opportunities for hunters, but may also increase conflict with humans. Rocky Mountain elk (*Cervus canadensis*) recolonized Nebraska, USA in the 1960's and their populations have subsequently expanded across western Nebraska. Managers require basic information about the spatial ecology of elk to guide harvest management and mitigate crop damage. Furthermore, there is a high proportion of cropland in Nebraska relative to other regions within elk range, providing a novel opportunity to examine the influence of agriculture on space use. Accordingly, we tracked 131 male and female elk with GPS telemetry to estimate seasonal space use and movements. Males used larger home ranges than females during calving season (spring-summer) and fall, whereas females used larger ranges in winter. During calving and fall, females with greater access to forage used smaller home ranges. Males and females used smaller winter home ranges in areas with greater access to cover. Males in areas with greater road density during the winter used larger home ranges. Our results highlight the importance of forage availability and efficient space use during calving and fall for females, who experience increased energy costs due to lactation.

Tracing the origins of adaptive genomic variation in bank voles from Great Britain

Marcos O.R da Cruz* (Undergraduate Student), Silvia Markova, Marco A. Escalante, Jeremy B. Searle, Petr Kotlík, Hayley C. Lanier

Sam Noble Museum, University of Oklahoma, 2401 Chautauqua Ave, Norman, OK 73072(MORC, HCL); Laboratory of Molecular Ecology, Institute of Animal Physiology and Genetics of the Czech Academy of Sciences, Rumburská 89, 277 21 Liběchov, Czech Republic (SM, MAE, PK); Department of Ecology and Evolutionary Biology, Cornell University, Corson Hall, Ithaca, NY 14853 (JBS)

Identifying the factors that shape adaptive variation is important for predicting the response to future environmental change. We investigated this in bank voles (*Clethrionomys* [*Myodes*] *glareolus*) from Britain, where previous work indicated two end-glacial colonization events, the second involving a hemoglobin variant associated with adaptation to warmer climates. We used genome-wide SNPs identified in 153 whole genomes to evaluate the following hypotheses: (1) variation at the majority of adaptive loci originated in mainland Europe rather than Britain, (2) both mainland refugia contributed to adaptive variation, but (3) the presumably warmer (western Europe) and (Carpathian) colder refugia, contributed alleles that are adaptive under different climatic regimes. We identified loci subject to selection based on genetic-environment association, inferred the origin of these polymorphisms using allele frequency and gene genealogy analyses, and tested whether alleles from the two refugia were associated with different temperatures. The results show that most of the adaptive SNPs found in Britain are polymorphic in both

mainland refugia. However, for a subset of loci, the polymorphism appears to originate from a single refugium, with the Carpathian refugium contributing more unique SNPs than the western refugium. Furthermore, Carpathian alleles are significantly correlated with wetter conditions while Western alleles were more correlated with acute heat, which may reflect past selection in different climatic conditions. Our results highlight the importance of biogeographic history, and past selective regimes, for the geographic distribution of genome-wide adaptive variation and thus future adaptive potential.

Abstracts - Poster Presentations

Diet of Kansas bat communities using mini-barcodes and Illumina sequencing: Preliminary results

Zoe M. Buffington* (Undergraduate Student), Lorelei Patrick

Fort Hays State University

Bats hold important ecosystem roles through their feeding habits. Their diet consists of insect species that may be agricultural pests or vectors for disease. To date, no studies have been done on the diet of bats in Kansas. This study provides an important first step in quantifying the ecosystem role provided by Kansas bats. DNA extracted and sequenced from guano samples collected directly from bats at five community sites around Kansas were used to examine whether bats were partitioning food (insect) resources. Guano samples collected from five caves allowed us to determine the species of bats using the caves and what they were eating. A CO1 mini-barcode was sequenced for all samples on the Illumina platform. The Qiime2 bioinformatics platform was used to confirm the identity of bat species and their insect prey from raw DNA sequencing data. Shannon's index and Jaccard similarity index analyses were performed with the species data, finding significant variability in the diets of bats at cave sites. Bats from the different communities sampled were clustered close together, indicating that they feed on similar prey. These preliminary results suggest that bat species may not be specializing on specific species of insects.

Shape-shifting squirrels: investigating morphological variations in fox squirrels under climate change and urbanization

Andrew J. Hughes*, Miranda K. Theriot, Hayley C. Lanier

Sam Noble Oklahoma Museum of Natural History, University of Oklahoma, Norman, OK, USA

In our time of rapid global change, evaluating how wild animal populations respond to the multifaceted effects of habitat change is crucial. Rising ambient temperatures have been hypothesized to drive declines in body size consistent with Bergmann's Rule (a biogeographic pattern in which smaller body sizes are observed in warmer, lower-latitude environments). Additionally, recent research suggests that skull morphology of urban-dwelling animals differs from their rural counterparts, potentially mirroring the effects of domestication syndrome. Here, we evaluated the effects of temperature and urbanization on skull shape in fox squirrels (*Sciurus niger*), an apt candidate for assessing morphological patterns over space and time as they are widespread and are well represented in museum collections. We conducted landmark analysis on 106 specimens to assess the factors contributing to skull shape variation. Splitting the sample into two geographic groups (one covering Oklahoma, the other northeastern Arkansas, and the surrounding area) revealed significant differences in skull shape by region. To assess predictors of skull shape, we focused on the larger regional sample (Oklahoma specimens collected from 1930-2019). Overall, skull shape differed significantly by overall skull size, latitude, and over time; however, neither habitat type nor mean annual temperature had a significant effect,

suggesting that other factors—such as land use (at a finer scale than "urban" or "rural") or competition with Eastern grey squirrels—influence temporal variation in skull morphology. Evaluating these effects is important to understanding how animals respond to human alteration of the environment.

Bats of Nepal: Laying a foundation for future mammalian phylogeography through the Himalayas

Basant Sharma* (PhD Student), Andrew G. Hope

Division of Biology, Kansas State University (BS, AGH)

The Himalayan Mountains of Nepal represent an extreme latitudinal elevation gradient, reflected by topographic, climatic, and ecological diversity. Numerous deep canyons also dissect this region across longitude. This dramatic geography has fueled mammalian evolution, resulting in a biodiversity hotspot. The Kaligandaki Canyon of central Nepal is the deepest gorge in the world, and separates eastern and western Himalaya. We present a first assessment of bat biodiversity and elevational composition of species as related to the Kaligandaki as a biogeographic feature shaping bat diversity across Himalaya. We hypothesize that latitudinal gradients shape bat communities, whereas longitudinal features influence intra-specific diversification. Preliminary bat surveys were conducted in low and high elevational zones with use of both netting and acoustic surveys in caves and forest habitats. Species range maps (IUCN) were used to model the distribution of bat richness as well as regional bat faunas. A total of 23 species were detected where composition varied significantly between elevational zones. Bats at lower elevation were Indomalayan (eastern and southern) whereas bats at higher elevation were Palearctic (western and northern) reflecting regionally distinct community assembly. This is the first biogeographic assessment of bats through Nepal and a first step to investigating existing bat diversity and evolution. Future studies will focus on building specimen resources through field surveys to enable modern genetic analyses through an understudied center of mammal biodiversity.

Go big or go small? Building a mechanistic understanding of body-size variation in collared pikas (Ochotona collaris)

Miranda K. Theriot* (PhD Student), Link E. Olson, Hayley C. Lanier

Department of Mammalogy, Sam Noble Oklahoma Museum of Natural History, and School of Biological Sciences, University of Oklahoma (MKT, HCL); Department of Mammalogy, University of Alaska Museum and Department of Biology and Wildlife, University of Alaska Fairbanks (LEO)

Understanding the mechanisms underlying body-size variation can provide critical insights into responses to environmental change, particularly within climate-threatened populations. Here, we assessed the role of climate in temporal and spatial body-size variation in the collared pika (*Ochotona collaris*). These small alpine specialists survive winter by subsisting on vegetation stockpiled during the growing season, thus they are potentially vulnerable to both intensifying summer heat (limiting critical foraging time)

and increased exposure to winter cold (due to loss of insulating snowpack), making them a target for research on climate-change responses. Drawing on museum collections, we estimated size using nine measurements collectively capturing length and width at several points on the skull. These measurements tended to be negatively correlated with latitude, and weakly positively correlated with year of collection. We tested if this spatial and temporal variation can be explained by several key climate variables estimated for the time and place of collection. Generally, size was negatively correlated with both warmer summers and winters, and positively related to variables expected to be associated plant growth; however, none of the climate variables emerged as a stronger predictor of size than latitude alone. These results indicate a strong influence of geography on pika body-size variation, which may include other factors such as elevation that we did not directly test here. Additionally, pika body size may be more sensitive to finer-scale microclimatic conditions. This study demonstrates the complexity of establishing mechanistic links between climate and body-size trends, a necessary step in understanding ongoing climate-change responses.

Hidden Markov models to predict black bear dispersal patterns in eastern Oklahoma

Jacob Humm* (PhD Student), W. Sue Fairbanks

Oklahoma State University, Stillwater, OK, USA

Oklahoma's east-central black bear (*Ursus americanus*) population occupies a fragmented region with frequent anthropogenic disturbance (e.g., logging, agriculture, urban development, etc.) and small sections of forest with limited interconnectivity. Fragmentation of habitat from anthropogenic activities has been shown to limit bear recolonization in populations across North America by acting as barriers to movement and gene flow. Black bear dispersal can be divided into 3 stages: emigration, in which the animal leaves its natal home range; transience, the process of searching for suitable habitat in which to establish a home range; and immigration, the act of establishing and remaining in the adult home range. During the transient stage, the bear must navigate unfamiliar habitat, thus the costs incurred during this stage are high; it faces intraspecific competition, higher energetic costs of travel, and risk of mortality from human-wildlife conflict. Immigration through dispersal is central to population structure and recolonization success of small black bear populations. However, few studies have focused on what movement behaviors are exhibited during the transient stage. I propose to model yearling dispersal behavior using hidden Markov models. This approach provides a direct link between movement behavior and environmental characteristics by modelling those behaviors as functions of spatial covariates. This information will be used to assess the likelihood of yearling dispersal from areas with established populations to distant habitat patches without evidence of an established bear population (e.g., reproduction, parturition).

American black bear resource and space use in a recolonizing population in southeastern Oklahoma

Courtney N. Dotterweich* (PhD Student), Dr. W. Sue Fairbanks

Department of Natural Resource Ecology and Management, Oklahoma State University

Once extirpated from eastern Oklahoma due to overharvest and habitat loss, American black bears (*Ursus americanus*) are now recolonizing areas greatly altered by anthropogenic activity. While human population density in this area is relatively low, southeastern Oklahoma is largely dominated by timber plantations, agriculture, residences, and areas of outdoor recreation, all of which have been identified to contribute to altered space use of bears throughout the world. Despite this, there are still many questions regarding how anthropogenic disturbances may affect bear recolonization potential in Oklahoma. As bears continue to recolonize southeastern Oklahoma, these activities, as well as other landscape characteristics, can influence recolonization patterns, affecting the management needs required by this population. Understanding this, our objective is to utilize GPS collar data from 2014-2022 to identify factors that influence bear space and resource use within a socioecological framework, combining both the ecological and anthropogenic aspects of the landscape within resource selection functions. We hypothesize that individual bear traits, landscape characteristics, anthropogenic activity, and levels of human tolerance will explain variations in black bear space and resource use. Improving our understanding of the many nuances of space use within this recolonizing bear population will assist in establishing management goals and guidelines that can appropriately facilitate the return and persistence of this population.

Great-horned Owl diet at Merrihew Cave, Oklahoma, at a major roost of Mexican Free-tailed Bats

Dawson V. Kosmicki* (Undergraduate Student), Mackenzie J. Smith, Carter Kruse, and Keith Geluso

Department of Biology, University of Nebraska at Kearney 68849 (DVK, MJS, KG). Turner Institute of Ecoagriculture, Bozeman, Montana 59798 (CK)

Large aggregations of animals can attract predators to feed upon the plentiful food resources. Mexican Free-tailed Bats (*Tadarida brasiliensis*) form some of the largest aggregations of individuals of any vertebrate in North America. Herein we examined the diet of a Great-horned Owl (*Bubo virginianus*) at a cave roost for Mexican Free-tailed Bats in northern Oklahoma. Almost all (97%) of the 36 owl pellets collected from the summer of 2022 contained bat remains, whereas 67% contained remains of insects, and only 31% contained remains of small mammals (rodents and rabbits). In summer 2023, we did not find any owl pellets in the cave, although we did see a Great-horned Owl once near the cave. The summer of 2022 was extremely dry whereas the summer of 2023 was quite rainy. The incidence of insects, including grasshoppers, crickets, and cicadas, in diet of this large owl species was an interesting finding. Rodent populations were extremely low during the dry summer, and bats and insects appeared to be the main diet for this large raptor. We hope to find more owl pellets in the cave upon our return this autumn and in future years. Possibly the proportionally high percentage of bats and insects reflected local environmental conditions in summer 2022.

Roost Sites of Eastern Red Bats and Evening Bats in the Great Plains

Joseph W. Paysen* (Undergraduate Student), Mackenzie J. Smith, Carter Kruse, and Keith Geluso

University of Nebraska Kearney (MJS, JWP, KG). Turner Institute of Ecoagriculture (CK)

Eastern Red Bats (*Lasiurus borealis*) are a migratory foliage roosting species and Evening Bats (*Nycticeius humeralis*) are a migratory cavity roosting species. Deciduous and evergreen trees commonly are used for roost sites in southern and eastern U.S. by both species. Little information is known about roost sites at the westernmost parts of their distribution in the Great Plains, where both bat species generally reside in narrow wooded riparian corridors within grasslands/agricultural fields. We radio-tracked a few individuals this past summer. A single Eastern Red Bat roosted in a Green Ash (*Fraxinus pennsylvanicus*) with young for multiple days, whereas two Evening Bats roosted six very large Plains Cottonwoods (*Populus deltoides*). Roost switching was common for Evening Bats, with roost exit counts of up to 138 individuals in a single tree cavity. Roost trees had larger DBH and greater tree heights for both bat species compared to randomly selected trees and surrounding trees in plots. Knowing roost site characteristics will benefit management practices and improve conservation efforts if these species face declines, as migratory bats are vulnerable to fatalities at wind-energy facilities.

Predicting the impacts of a century of anthropogenic change on genetic diversity in collared pikas, a climate-sensitive species

Kailey R. Meacham* (MS Student), Katharine A. Marske, Vanessa Heath, Hayley C. Lanier

Sam Noble Oklahoma Museum of Natural History, University of Oklahoma; School of Biological Sciences, University of Oklahoma

The past century has been defined by an unprecedented loss in biodiversity, including species, populations, and genetic diversity. Slowing these declines requires a deeper understanding of the mechanisms which may hamper population and species' response to changing climates. Our study will use museum specimens to contrast genetic diversity in historic and modern samples to identify the main drivers of genetic loss over the past era in a climate-sensitive species, the collared pika (*Ochotona collaris*). Collared pikas have naturally fragmented populations spread across a rapidly changing landscape in Alaska and northern Canada. Here, we provide a framework for predicting relative diversity loss among potential sampling sites under three non-mutually exclusive hypotheses: habitat availability (populations with a greater proportion of suitable habitat will retain more diversity), climate velocity (populations experiencing a lower magnitude of change will retain more diversity), and habitat quality (populations with access to better food resources will retain more diversity). Broadly, this study aims to evaluate these hypotheses in order to provide insight into the genetic response to rapidly magnifying human-induced change. Our results can be applied locally to prioritize management on the leading edge of climate change and globally to inform conservation needs as biodiversity is increasingly threatened.

Survey on the status of Northern Long-eared Bats in western Nebraska

Keith Geluso*

University of Nebraska at Kearney

The Northern Long-eared Bat (*Myotis septentrionalis*) is a forest dwelling species that occurs throughout the eastern United States and reaches parts of its western-most distribution in the Great Plains. This species was listed as threatened in 2015 and endangered in 2023 by the U.S. Fish and Wildlife Service. Precipitous population declines were documented in eastern Nebraska for this species, but the population status was unknown from western parts of the state. In summer 2023, my students and I resurveyed sites with known past occurrences for Northern Long-eared Bats in western and south-central Nebraska. In about 10 nights of netting, we failed to capture any Northern Long-eared Bats in mist nets. For two nights, colleagues deployed acoustic recorders, and they also failed to detect calls of this species at netting sites. This past summer was a fairly rainy year, which is known to disperse bats in arid environments, so we plan on continuing such surveys in subsequent years pending funding to further understand the status of this species. Preliminary data suggests that Northern Long-eared Bats have also suffered significant declines in western parts of Nebraska.

Morphological analysis of a masked shrew (Sorex cinereus) population to establish age distribution from size variation

Noah Lemons* (Undergraduate Student), Miranda K. Theriot, Mariana Borras, and Hayley C. Lanier

Department of Mammalogy, Sam Noble Oklahoma Museum of Natural History, University of Oklahoma; School of Biological Sciences, University of Oklahoma

Climate change can have extensive negative impacts on population health and dynamics. Characterization of seasonal changes in age distribution is crucial to understanding these effects, such as changes in overwinter survivorship and the timing of recruitment. To that end, accurate and consistent criteria for determining age in specimens are essential. One species in which population age structure is thought to be strongly tied to seasonal change is the masked shrew (*Sorex cinereus*), in which age can be estimated based on tooth wear; unworn cusps are thought to be indicative of younger shrews and worn cusps symptomatic of older shrews. Additionally, masked shrews undergo a large and only partially reversible reduction in size during the winter (a change called Dehnel's phenomenon), therefore skull size may also provide age data. Here, we combined these two metrics to assess the age distribution of a masked shrew population from Yellowstone National Park surveyed in summer 2014. We measured skull length and quantified tooth wear using analyses of high-resolution images of museum specimens. Our results demonstrate a novel quantitative method for linking age distribution to size variation in masked shrews, which can provide a framework for assessing other shrew species and populations for indicators of population decline.

The Kansas State Biorepository: Developing specimen resources for long-term research

Morgan G. Skinner* (Undergraduate Student), Andrew G Hope

Kansas State University

The concept of FAIR (Findability, Accessibility, Interoperability, and Reuse) represents a modern standard for rigorous ecological long-term information management. We interpret the FAIR principals from the perspective of biospecimen repositories. The newly developed Kansas State Biorepository (KSB) is a publicly accessible museum, currently focused on archiving mammal and parasite specimen resources in-perpetuity, and explicitly for research and educational purposes. This facility aims to extend the value of data streams from long-term research initiatives, such as the Konza LTER program, by preserving legacies of samples and specimens for future generations, a primary directive of the LTER network. Our poster provides an overview of the mammalian specimen resources held at Kansas State University, how they are being applied to high-impact research, and our efforts to bring these collections up the highest modern standards for biodiversity science and education.

Predicting the Sensitivity of Oklahoma's Small Mammals to Habitat Fragmentation: A Trait-Based Approach

Emilyn Gilmore* (MS Student), Hayley C. Lanier

Sam Noble Oklahoma Museum of Natural History, University of Oklahoma; School of Biological Sciences, University of Oklahoma

Anthropogenic change- the process of impact by humans upon the environment- has become one of the major drivers of decline for biodiversity across the globe. Predicting how biota are impacted by anthropogenic change can be difficult and can often require detailed knowledge of systems prior to noticeable aspects of change. Assessing and ranking ecological and biological traits of mammals has been used to predict sensitivity to climate change, but is less commonly applied to other stressors. Here, we provide a framework for predicting the sensitivity to habitat fragmentation for small mammals using ecological and biological traits. We focus specifically on the small mammals of Oklahoma, and demonstrate the application using four species with statewide distributions. Our long term goal is to develop and refine a framework for predicting sensitivity which can be tested with empirical data.