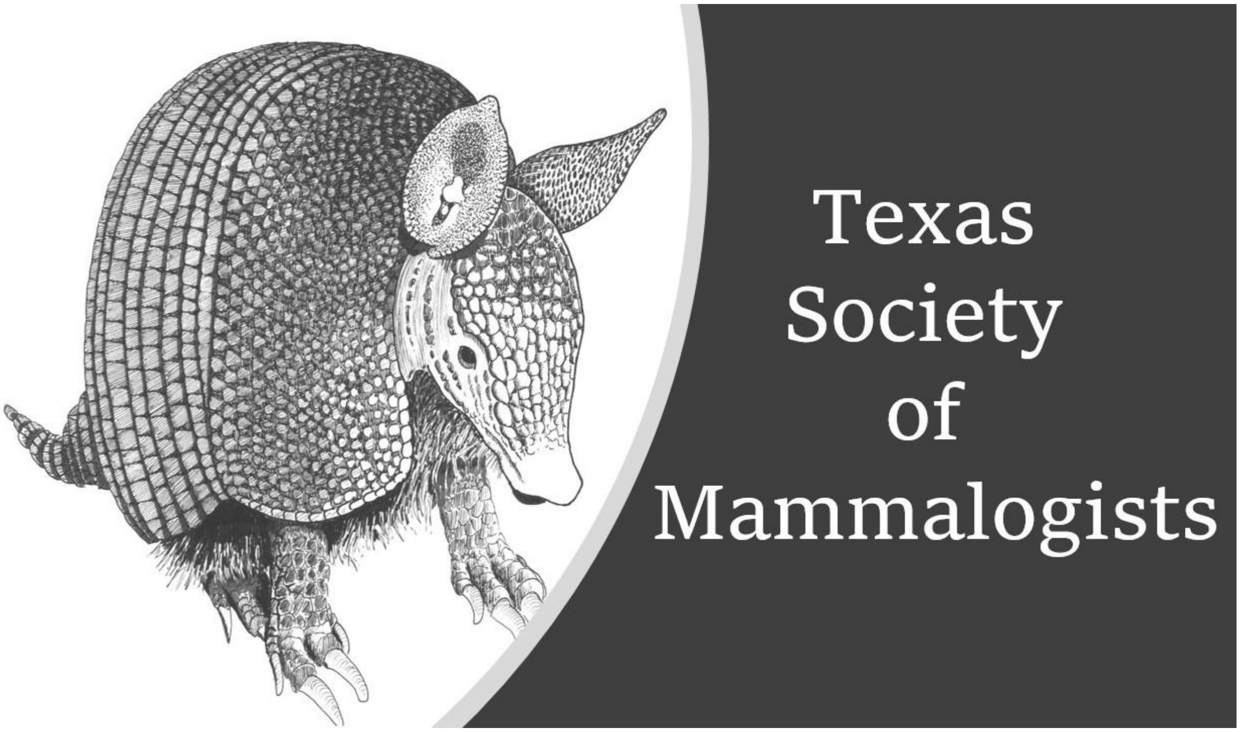

Student Presentation Abstracts
The 44th Annual Meeting
2026

Oral Presentation Abstracts

Paper 1 is to be considered for the Packard Award.

Paper 1

BLUBBER METABOLITE PROFILES REVEAL ENVIRONMENTAL ADAPTATIONS IN NORTHERN GULF OF MEXICO DOLPHINS Makayla Guinn[1], Dara N. Orbach[1], and Hussain Abdulla[2] **-** [1]Department of Life Sciences, Texas A&M University – Corpus Christi; [2]Department of Physical and Environmental Sciences, Texas A&M University – Corpus Christi (mguinn1@islander.tamucc.edu)

Common bottlenose dolphins (*Tursiops truncatus*) inhabit bays, sounds, and estuaries along US coastlines that are influenced by varying levels of anthropogenic impact. Biochemical changes can accumulate in dolphin blubber over several weeks to months, making blubber metabolites informative biomarkers of molecular adaptations to variable inshore conditions. This study investigated the metabolomic signatures of four free-ranging bottlenose dolphin stocks inhabiting the inshore waters of Mississippi and South Texas. Untargeted metabolomics was performed on blubber samples (n = 67) using ultra high-performance liquid chromatography mass spectrometry. Pathway enrichment analyses comparing detected metabolites revealed five major metabolite groups that were regulated significantly differently between each stock, including lipid and energy metabolism, inflammatory and immune signaling, membrane integrity and cellular signaling, endocrine regulation, and protein and amino acid turnover. Our results suggest dolphins in each stock exhibit distinct metabolic and physiological responses to environmental and anthropogenic stressors and warrants the use of blubber biomarkers to measure biochemical adaptations in cetaceans. An improved knowledge of habitat-specific physiological responses will offer critical insights into how cumulative impacts may affect the health and adaptive capacity of vulnerable species in dynamic coastal ecosystems.

Papers 2-9 are to be considered for the William B. Davis Award.

Paper 2

EIGHT YEARS OF SMALL MAMMAL MARK-RECAPTURE RESEARCH IN WESTERN OKLAHOMA: TRENDS AND HANTAVIRUS PRESENCE Claire Wiley[1], Francisca M. Mendez-Harclerode[2], Gloria M. Caddell[1], Chad B. King[1], and Michelle L. Haynie[1] **-** [1]Department of Biology, University of Central Oklahoma; [2]Department of Biology, Bethel College (cwiley6@uco.edu)

The purpose of this project is to monitor changes in small mammal populations and communities over multiple generations to determine what factors affect how the populations and communities change over time. In March of 2018, a permanent trapping web was established at the University of Central Oklahoma's Selman Living Lab (SLL). Two additional permanent webs were established in June of 2018. SLL is located in the gypsum hills of Woodward County in western Oklahoma. Surveys of the 3 webs are conducted for 3 nights, 4 times a year, and include collection of mammalian and vegetation data. Climate data also is obtained for each day of the trip; monthly and yearly climate data also will be assessed. To date, 28 mammalian and 27 vegetation surveys have been conducted. During processing, each small mammal is subject to species identification, weighing, ear clipping for DNA samples, a unique mark (e.g., toe clip or ear tag), fecal sampling, and a viral oral swab. Thus far, 19 individuals have tested positive for hantavirus, as shown by polymerase chain reactions (PCRs) and gel electrophoresis. Preliminary Shannon Diversity models constructed using R have shown fluctuations in values over time across all three webs, peaking for Web I in 2021 (1.93), Web II in 2019 (1.73), and Web III in 2024 (2.12). In the future, the animal, climate, and vegetation data will be used to build mathematical models that can be used to determine which factors have the largest impact on population and community persistence.

Paper 3

PRELIMINARY FINDINGS ON HABITAT PREFERENCES OF DAVIS MOUNTAIN COTTONTAILS (*S. HOLZNERII ROBUSTUS*) IN THE DAVIS MOUNTAIN RANGE

H. A Shapiro[1], C. Wzientek[1], D. Karelus[2], and A.M. Martin[1,3] - [1]Caeser Kleberg Wildlife Research Institute, Texas A&M University – Kingsville, Kingsville, TX 78363 USA; [2]Texas Parks and Wildlife Department, Austin, TX 78744 USA; [3]Department of Biology, Grand Valley State University, Allendale, MI 49401 USA (hannah.shapiro@students.tamuk.edu)

Little is known about habitat requirements of Davis Mountain cottontail rabbits (DMCR); however, they are assumed to be montane specialists. DMCR have been documented to use dense thickets of evergreen woody plants and rocky crevices as refugia. Our objective was to determine habitat use of DMCR in the Davis Mountains region of Texas. We conducted vegetation sampling during May-August 2025 at sites where rabbits were visually observed and at randomly located points within the same area to gain understanding of plant associations. Preliminary woody plant data indicate that catclaw mimosa (*Mimosa aculeaticarpa*) and prickly pear (*Opuntia* sp.) were found at 8.3% and 12.5%, respectively, of the locations where DCMR were observed during the dry-to-wet intermediate season (May-June). For herbaceous plant usage, preliminary assessments indicate that during the dry-to-wet intermediate season, DMCR were always associated with sand dropseed (*Sporobolus cryptandrus*); however, during the wet season (July – September), they used a wider variety of species, with Grama varieties (*Bouteloua* spp.) making up about 40% of usage, and sand dropseed was not used. Locations were also categorized in five ways: bare, rocky, plant cover, plant litter, and other. Rabbits were associated with plant ground cover during the dry-to-wet intermediate season; however, during the wet season when herbaceous plants were more productive, rabbits were associated with bare and rocky ground cover. This preliminary observation may be due to seasonal differences in availability of escape cover; availability will be accounted for in future analyses. We also observed rabbit habitat utilization during flee behavior at two sites: one dominated by grassland and one categorized as urban. Of the 7 rabbits observed, 6 of the rabbits (85.72%) fled to vegetation structures, while 1 (14.29%) rabbit fled to rock structures. These are the first fine-scale data to assess plant associations and habitat utilizations in DMCR.

Paper 4

BATS AND WATER: GUZZLER DESIGN INFLUENCES BAT ACTIVITY IN THE TRANS-PECOS OF TEXAS

Manuel Quispe-López[1], Bonny McKinney[2], and Richard D. Stevens[1,3] - [1]Department of Natural Resources Management, Texas Tech University; [2]El Carmen Land & Conservation Company; [3]Natural Sciences Research Laboratory, Museum of Texas Tech University (mquispel@ttu.edu)

Bats are among the most imperiled mammals in Texas, with 23 species listed as Species of Greatest Conservation Need. In the arid Trans-Pecos of the Chihuahuan Desert, man-made water sources are often installed to benefit game species, but little is known about benefits to non-target species such as bats, or how benefits vary among water-source designs. We evaluated whether man-made waters increase bat activity and which guzzler designs are most effective. We conducted our study on property managed by El Carmen Land and Conservation Company in the Trans-Pecos region. We examined 37 man-made water sites across six water types (large earthen tanks plus five wildlife guzzler designs). At each site, we deployed paired acoustic detectors, with one placed ~15m from the water source and the other placed 200m away to measure ambient bat activity. Detectors recorded for 18 nights per site in rotating deployments from September 2022 to August 2023. Bat calls were identified using Kaleidoscope, and activity was quantified as the summed number of bat passes across all nights. We recorded 331,227 bat calls in total. Generalized linear mixed models showed higher total calls at water sources than at paired controls, but the magnitude depended on water type and guzzler design. Earthen tanks consistently had higher call rates than all guzzler types, for total calls and across species-level models. Among water-present guzzlers, designs with larger water surface areas had the highest call rates, whereas those with smaller water surface areas had significantly lower call rates. Species-level patterns mirrored these

results, with strong design-dependent contrasts in *Antrozous pallidus*, *Parastrellus hesperus*, and several *Myotis* species, whereas molossids showed weaker differences. Our results highlight that man-made water architecture can influence bat activity and which architecture to employ may be an important management decision when aiming to benefit game and non-target species alike.

Paper 5
ENVIRONMENTAL DRIVERS OF MIGRATION AND ECTOPARASITE DYNAMICS IN MEXICAN FREE-TAILED BATS (*TADARIDA BRASILIENSIS*) Kristin. E. Dyer[1], Meagan Allira[1], Bret M. Demory[1], Mackenzie G. Hightower[1], Jackson T. Wingert[2], Krystie A. Miner[3], Amanda M. Adams[3], Winifred F. Frick[3], Jeremy D. Ross[1], Kevin T. Castle[4], and Daniel J. Becker[1] - [1]School of Biological Sciences, University of Oklahoma, Norman, OK; [2]Department of Biology, University of Louisiana at Lafayette, Lafayette, LA; [3]Bat Conservation International, Austin, TX; [4]Wildlife Veterinary Consulting, Livermore, CO (kristin.dyer-1@ou.edu)

Long-distance migration can facilitate parasite transmission between seasonally connected habitats, yet the role of migration in structuring ectoparasite dynamics remains poorly understood in bats. In migratory hosts, parasites must persist through dramatic seasonal changes in host density, climate, and movement, creating complex interactions between environment, host behavior, and transmission. Mexican free-tailed bats (*Tadarida brasiliensis*) migrate annually between Mexico and the southwestern United States, forming summer maternity colonies that can exceed 20 million individuals, where dense host aggregations may promote parasite spread. We assessed seasonal and site-specific parasite dynamics through monthly and bi-monthly sampling at Selman Cave, Oklahoma ($n = 1124$), and Bracken Cave, Texas ($n = 459$) during 2023–2025. Bats were screened for ectoparasites, PIT-tagged, and assessed for body condition via mass. To examine the relationship between parasitism and migration, we radio-tagged a subset of bats and tracked fall departure using the Motus Wildlife Tracking System. Radio-tagged individuals were tracked from Oklahoma through Texas and into northern Mexico, revealing stopover and long-distance movement up to 1157 km. Using generalized additive models, we tested for seasonal patterns in ectoparasite prevalence, the influence of parasitism on migration timing, and the effects of climate on both. Flea prevalence and abundance exhibited strong seasonal patterns ($p < 0.001$), with higher rainfall corresponding to increased prevalence ($p = 0.03$) and abundance ($p < 0.001$). Temperature predicted migration departure ($p < 0.001$), while ectoparasite prevalence and richness were not significant predictors. These findings suggest that migration timing is primarily influenced by environmental factors and that migration may serve as an effective dispersal mechanism for ectoparasites.

Paper 6
WHEN ROADS BECOME BARRIERS: BOBCAT (*LYNX RUFUS*) AND OCELOT (*LEOPARDUS PARDALIS*) MOVEMENT AND LANDSCAPE PERMEABILITY IN SOUTH TEXAS Sean Kiernan[1], Simona Picardi[2], Emma Brookover[1], Elizabeth Grunwald[1], Terry Hanzak[1], Thomas Langschied[1], Daniel Scognamillo[3], Jack Towson[1], Thomas Yamashita[4,5], John Young[6], and Michael Tewes[1] **-** [1]Caesar Kleberg Wildlife Research Institute, Texas A&M University – Kingsville; [2]Department of Fish and Wildlife Sciences, University of Idaho; [3]Safari Club International Foundation; [4]Fish, Wildlife, and Conservation Biology, Colorado State University; [5]Rocky Mountain Research Station; [6]Environmental Affairs Division, Texas Department of Transportation(sean.kiernan@students.tamuk.edu)

Roads are a pervasive source of habitat fragmentation and mortality for wildlife, yet their effects on fine-scale movement patterns remain poorly understood for many carnivore species. In South Texas, ocelots (*Leopardus pardalis*) are a high-priority conservation species, but low densities and a restricted range limit direct study of their movement. Bobcats (*Lynx rufus*), which share life-history traits and occupy overlapping habitats, serve as a model for evaluating how roads influence felid movement and landscape connectivity. Using long-term GPS telemetry data from both species, I applied a barrier behavior framework to quantify road permeability and assess how road characteristics, traffic volume, and individual behavioral traits influence movement decisions. Specifically, I examined (1) whether high-traffic roads act as movement barriers, producing altered or trapped behaviors; (2) differences in movement behavior between resident and transient individuals; (3) variation in road-crossing frequency among individuals; and (4) how movement patterns can inform broader connectivity and conservation strategies for ocelots. By integrating GPS movement data with road and landscape metrics, this study identifies behavioral responses of bobcats to anthropogenic barriers at multiple spatial and individual scales. Identifying roads that limit movement, individuals that can navigate barriers, and the role of transient movements offers actionable guidance for conservation planning. This work supports evidence-based mitigation strategies, including targeted placement of wildlife crossing structures, to maintain functional connectivity for ocelots and sympatric carnivores in fragmented habitats. Ultimately, apply a barrier behavior analysis to bobcats advances our ability to predict and manage road impacts on low-density felids in human-modified landscapes.

Paper 7

WHY DID THE CAT CROSS THE ROAD? EXPLORING THE GENOMIC LINK UNDERLYING DECISION-MAKING BEHAVIOR IN WILD CATS Jack Towson[1], John Young[2], Emma Brookover[1], Brian Davis[3], Jan Janečka[4], Lucas Spetic da Selva[3], and Michael Tewes[1] **-** [1]Caesar Kleberg Wildlife Research Institute, Department of Rangeland and Wildlife Sciences, Texas A&M University – Kingsville; [2]Environmental Affairs Division, Texas Department of Transportation; [3]College of Veterinary Medicine and Biomedical Sciences, Texas A&M University; [4]School of Science and Engineering, Duquesne University (jack.towson@students.tamuk.edu)

Roads are critical infrastructures of the global economy, but they raise concerns about habitat fragmentation. Wildlife will modify their behavior in response to road-related threats by exhibiting altered movement patterns. In South Texas, bobcats (*Lynx rufus*) and ocelots (*Leopardus pardalis*) are prime roadkill candidates, vulnerable to ecological difficulties exacerbated by roads. The endangered status of ocelots in the United States amplifies the need to mitigate road mortalities to sustain its genomic diversity. Despite progress towards identifying local wildlife hotspots, limited genomic research has been conducted to understand felid decision-making around roads. In this study, bobcats and ocelots were captured at Laguna Atascosa National Wildlife Refuge and private ranches around U.S. Highway 77 and Farm-to-Market 1847. Blood samples were collected, and felids were fitted with GPS or VHF collars to assess movement patterns. Genomic DNA from nearly 450 blood samples was extracted, and whole genome sequences were developed. Single nucleotide variants (SNVs) were called for individual cats and then jointly across all cats. Additionally, SNVs were called in ten genes hypothesized *a priori* to influence decision-making. A gene ontology (GO)-esque functional categorization of the bobcat genome was performed to select the candidate genes. Genomic variation in these targeted genes was analyzed for all individuals across traits relating to road crossing probability. Population relatedness will be used to assign “genomic IDs” and construct pedigrees to ultimately determine roadkill individuals’ origin. The kinship analyses will allow us to identify inherently high-risk individuals and quantify ‘heredity of roadkill vulnerability.’ Collectively, these genomic dynamics will illuminate the functional adaptability shaping these wild cats’ persistence in an expanding urban environment. By coupling behavioral ecology with functional genomics, informed decision-making regarding wildlife crossing structures will be implemented to maximize the fitness of these species, despite the challenges roads present to their future in Texas.

Paper 8

HISTORICAL AND CONTEMPORARY DISTRIBUTION OF *MEPHITIS MACROURA* IN TEXAS

J. Clint Perkins[1], Robert C. Dowler[2], and Richard D. Stevens[1,3] - [1]Department of Natural Resources Management, Texas Tech University; [2]Department of Biology, Angelo State University; [3]Natural Science Research Laboratory, the Museum, Texas Tech University (j.clint.perkins@ttu.edu)

The hooded skunk, *Mephitis macroura*, is one of the least documented mammals in Texas, and its distribution within the Trans-Pecos ecoregion has long been characterized by sparse records, uncertain species identification, and conflicting range interpretations. Although the species may be uncommon within the region, an alternative explanation is that survey effort has been insufficient to reliably characterize its presence. To evaluate these competing explanations, we independently reviewed and verified all known preserved specimens, compiled results from regional camera-trap surveys, and conducted targeted surveys in southern Brewster County. We performed a meta-analysis across 19 independent regional surveys to assess hooded skunk presence within the local four-species mephitid assemblage. Of 23 preserved specimens historically identified as hooded skunk, four could not be confirmed, suggesting that previous distribution estimates may be inflated by as much as 44%. Across the 19 independent surveys, the other three skunk species were documented in 86% of surveys, whereas hooded skunks were detected in only 26% and restricted to four counties. A Pearson's chi-squared test did not detect spatial structure across the four-species assemblage ($\chi^2 = 9.44$, df = 24, $p = 0.998$), suggesting community-level homogeneity, whereas a Fisher's exact test rejected the null hypothesis of equal regional distribution for hooded skunks ($p = 0.008$), demonstrating a nonrandom distribution pattern. Collectively, our results indicate these surveys were sufficient to characterize the local mephitid assemblage, but that hooded skunk records were disproportionately concentrated in the broader Davis Mountains region and southern Brewster County. The paucity of hooded skunk records is more consistent with a restricted distribution and potentially low population density rather than with insufficient survey effort. Similar distributional characteristics are observed in other primarily Neotropical mammals that receive conservation consideration in Texas, suggesting that comparable attention may be warranted for the hooded skunk.

Paper 9

AN UPDATED R PACKAGE FOR ECOLOGICAL CYCLICAL DATA: AN APPLICATION EXAMPLE FOR CERVID ACTIVITY PATTERNS

Tatiana Velásquez-Roa[1], Maria A. Hurtado-Materón[2], Ángel L. Robles-Fernández[3], and Iván Castro-Arellano[1] - [1] Integrative Ecology Lab, Biology Department, Texas State University; [2]Ecology and Evolutionary Biology Program, Department of Ecology and Conservation Biology, Texas A&M University; [3]The University of Kansas. (yxh11@txstate.edu)

Temporal niche overlap can be effectively studied using null models, that are statistical tools that randomize ecological data to reveal underlying patterns. The Rosario algorithm, originally developed for a windows interface, has supported this type of analysis and has been used in more than 100 scientific publications. Most applications have focused on insect (25 studies) and mammals (21 studies), though it has also been applied to birds, anurans, and plants (i.e. phenological phenomena). Here, we present an application of a recently developed R-based *rosario* package, using the SIM Deer project dataset of approximately 85,000 images, which is freely available through Wildlife Insights platform. To ensure long-term usability and standardization, we transitioned the Rosario algorithm from Windows software to R programming environment. This transition increases accessibility and enhances compatibility with other R packages such as *activity* and *overlap*. Unlike these packages, *rosario* supports concurrent overlap analysis among multiple biological identities (e.g., individuals, species) providing a more comprehensive approach to studying cyclical ecological data. An assessment of activity patterns for three cervid species using the *activity*, *overlap*, and *rosario*, showed that all three approaches produce similar overlap estimates. This indicates that the overlap indices implemented in *rosario* (i.e., Pianka and Czekanowski) provide comparable results to those from already existing tools. In addition, the integration of a null

model framework enables a more robust assessment of significance by comparing empirical overlap values with those generated through randomization. Now, users can access *rosario* in R and work with a full suite of packages in one language, facilitating complementary insights into natural temporal patterns.

Paper 10 is to be considered for the Rollin Baker Award.

Paper 10

COMMON DOLPHINS (*DELPHINUS DELPHIS*) INCREASE *S*WIMMING SPEED AS AN AVOIDANCE RESPONSE TO VESSEL APPROACHES Soleil Delorge[1], Fadia Al Abbar[2,3], Lorenzo Fiori[1,3], and Dara N. Orbach[1] - [1]Department of Life Sciences- Texas A&M University-Corpus Christi; [2]Department of Wildlife, Ecology and Conservation & Department of Behavioral Ecology- Wageningen University; [3]Azores Delphis Project (sdelorge@islander.tamucc.edu)

Swim-with-dolphin (SWD) tourism activities expose dolphins to repeated close-range vessel maneuvers that can cause behavioral changes. Vessel presence is known to elicit short-term avoidance responses from dolphins. The effects of specific vessel approach types and repeated maneuvers during encounters remain poorly understood. We quantified the group swimming speeds of common dolphins (*Delphinus delphis*) before, during (parallel approach and three consecutive J-approaches), and after simulated SWD vessel approaches off São Miguel Island, Portugal. Dolphin group focal-follows were video-recorded at 50fps using an unoccupied aerial system (UAS). Swimming speed was calculated post hoc from 102 video segments (Before = 16, Parallel = 18, J1 = 21, J2 = 15, J3 = 16, After = 16) in which dolphin groups traveled in a straight-line trajectory. Parallel approach (trajectory matching) swimming speeds were not significantly different compared to the before-phase speeds. When the J-approach (path intersection trajectory) was the first vessel maneuver, dolphin swimming speeds increased significantly compared to the before-phase, indicating a strong avoidance response. Repeated J-approaches within a trial produced cumulative increases in swimming speed that persisted into the after-phase. These findings can provide guidance for managing vessel approach type and repetition to minimize disturbance during SWD tours.

Papers 11-14 are to be considered for the Bobby Baker Award.

Paper 11

UNRAVELLING THE DIVERSITY OF NONVOLANT SMALL MAMMALS ALONG THE PURUS RIVER, CENTRAL BRAZILIAN AMAZONIA, THROUGH FIELD WORK AND DNA BARCODING Aramide Oladiran[1], Camila Mayume[2], Joyce A. Voltolini[3], Maria Clara Ribeiro[4], Ana Lazar[4], Joyce R. Prado[2], Renato Gregorin[5], Ana Paula Carmignotto[6], Alexandre R. Percequillo[2], and Edson F. Abreu[1] **-** [1]Department of Biology, Angelo State University; [2]Universidade de São Paulo; [3]Instituto Butantan; [4]Universidade Federal do Rio de Janeiro; [5]Universidade Federal de Lavras; [6]Universidade Federal de São Carlos (aoladiran@angelo.edu)

Climate change and deforestation are altering the Amazon rainforest at unprecedented rates, increasing the urgency to document and study its biodiversity before major losses occur. Nonvolant small mammals, especially rodents and marsupials, represent a large portion of Amazonian biodiversity, yet little is known about the diversity and occurrence of small mammals across many regions of the Amazon. DNA barcoding has become an important tool for species identification by enabling accurate taxonomic assignments. In July 2024, we conducted a field expedition to the lower Purus River in central Brazilian Amazonia to survey nonvolant small mammals and generate molecular data to support species identification. Sampling was conducted at four sites using Sherman, snap, and pitfall traps, in addition to nocturnal hunting. With a total of 5,337 conventional trap-nights and 986 pitfall trap-nights, we captured 85 individuals representing 24 species, including nine marsupials and 15 rodents. Sampling success was 0.94% for conventional traps and 1.32% for pitfall traps. Sherman traps and nocturnal hunting yielded the highest number of species across methods (12 and 11 species, respectively), followed by pitfall traps (six species). To complement field identifications, rodent tissue samples were processed for DNA extraction and barcoding using the Oxford Nanopore MinION adaptive sequencing platform. Preliminary analyses indicated that optimized extraction protocols yield DNA concentration sufficient for barcode generation, with complete mitochondrial genomes obtained for multiple samples, particularly within the species-rich genus *Oecomys*. All together, these findings highlight the high diversity of nonvolant small mammals in the Purus River basin and underscore the value of integrating field surveys with DNA barcoding. Our study provides an important baseline for future taxonomic, ecological, and conservation assessments in a region of the Amazon that remains poorly studied.

Paper 12

TEST OF A NUCLEAR GENE MARKER TO DISTINGUISH BETWEEN MEMBERS OF THE *MYOTIS CALIFORNICUS/CILIOLABRUM/LEIBII* COMPLEX

Lela Faison, Halle Summers, and Loren K. Ammerman **-** Department of Biology, Angelo State University (lfaison@angelo.edu)

Recent divergence of *Myotis californicus, M. ciliolabrum,* and *M. leibii* has prompted investigation into interspecific genetic and phenotypic differentiation within this cryptic species complex. Taxonomic determination and species identification for this complex has been difficult due to intraspecific geographic variation within *M. ciliolabrum* and *M. californicus* and morphological similarities among all three species. Previous studies using mitochondrial data failed to separate species within this complex accurately, whereas past research studying SNPs within this complex was able to recover groups consistent with their taxonomic designation. Because of success using genomic data, our goal was to test the efficacy of a nuclear intron (THY) as a genetic barcode for this complex. Using Sanger sequencing, we analyzed 648 bp of THY sequence and constructed a neighbor-joining tree containing 98 *Myotis* samples from all three species, some of which were included in the SNP study. Phylogenetic analyses recovered three distinct clusters, with SNP-verified samples grouping consistently with prior taxonomic designations. These findings support the use of THY intron as a simple barcode that could be used to confirm identification of members of this complex.

Paper 13

POPULATION STRUCTURE OF BOWHEAD WHALES USING MTDNA SEQUENCES

Alexandra A.Hernandez[1], John W. Bickham[2], John Citta[3], Amy B. Baird[1] **-** [1]Department of Natural Sciences, University of Houston – Downtown; [2]Department of Ecology and Conservation Biology, Texas A&M University; [3]Department of Wildlife Management, North Slope Borough (Hernandeza258@gator.uhd.edu)

The bowhead whale (*Balaena mysticetus*) is one of 16 baleen whale species and inhabits Arctic and subarctic waters. Bowhead whales are central to the subsistence, cultural, and spiritual traditions of Indigenous Arctic communities. Accurate knowledge of population structure and genetic diversity is essential for sustainable management. In this research, we examined mitochondrial DNA variation in three genes (ND1, HVR1, and Cytb) across bowhead whales from Bering Chukchi Beaufort (BCB) seas, Eastern Canada West Greenland (ECWG), and the Okhotsk Sea (OKS) stocks. The most recent samples analyzed were from 2025 and added to a database of samples dating back several decades. Standard population genetic analyses and haplotype network construction revealed strong differentiation of the Okhotsk (OKS) stock and weaker differentiation between BCB and ECWG stocks. These findings indicate that current management strategies, including regulated harvest, are not negatively impacting the genetic diversity of the BCB stock and provide a framework for ongoing long-term monitoring and conservation.

Paper 14

GENETIC CHARACTERIZATION OF PARASITIC NEMATODES (*CRASSICAUDA*) IN BOWHEAD AND BELUGA WHALES

Tamsin L. Ward[1], Raphaela Stimmelmayr[2], David Rotstein[3], and Amy B. Baird[1] **-** [1]Department of Natural Sciences, University of Houston – Downtown; [2]North Slope Borough Department of Wildlife Management; [3]Marine Mammal Pathology Services (wardt21@gator.uhd.edu)

The *Crassicauda* genus of nematode is known to parasitize the organs, primarily urogenital system of the cetacean suborders *Mysticeti* and *Odontoceti.* Within the past 10 years, *Crassicauda sp*. have been found for the first time in BCB Bowhead (*Balaena mysticetus)* and more recently in northern beluga whale stocks (ESB; CS) *(Delphinapterus leucas)* in Alaska. Both whale species are important subsistence resources for Inupiaq and Siberian Yupik. A molecular analysis using the ribosomal ITS2 gene was performed to assess the phylogenetic relationships of unidentified nematodes taken from *B. mysticetus* and *D. leucas* kidneys. Four unique genetic lineages of nematodes were identified in total. The *D. leucas* nematodes were very diverse. All samples taken from *B. mysticetus* kidneys were genetically identical and closely related to one specimen found in two Cook inlet Belugas.

Paper 15 is to be considered for the TSM Award.

Paper 15

IDENTIFICATION OF NUCLEAR MITOCHONDRIAL INSERTIONS (NUMTS) ACROSS THE POCKET GOPHER GENUS *GEOMYS*

Haider A. Khan and Russell S. Pfau - Department of Biological Sciences, Tarleton State University (haider.khan@go.tarleton.edu)

The use of mitochondrial genes is commonly employed for species delimitation and to infer phylogeographic structure in mammals. However, this approach can be compromised by the presence of nuclear mitochondrial DNA fragments (NUMTs)—nuclear DNA sequences that were inserted from the organism's mitochondrial genome. NUMTs may be unintentionally coamplified and misinterpreted as genuine mitochondrial variation. Recently inserted NUMTs are particularly problematic because they retain high sequence identity to mitochondrial DNA and thus easily co-amplified, generating spurious signals of divergence or cryptic lineages. There is documentation of NUMTs in many mammalian species (including rodents), but no experimentally validated, whole-genome assessment of NUMTs has been conducted in the pocket gopher genus *Geomys*. In this study, we use a recently assembled genome of *Geomys bursarius* to identify NUMTs and characterize NUMTs across the genus using complementary bioinformatic and experimental approaches. NUMTs were detected within the genome assembly of *G. bursarius* using the bioinformatic tools BLAST, NUMTfinder, and LASTZ. To identify the junction between the nuclear and mitochondrial sequences, NUMTs were then aligned to the mitochondrial genome of the individual from which the genome assembly was constructed. Primers were then designed to amplify identified junctions using polymerase chain reaction (PCR). Successful amplification of these junctions was confirmed by noting size of PCR products (to match expected amplicon size) and Sanger sequencing. Sequenced amplicons were aligned to their respective nuclear contigs from the genome assembly of *G. bursarius* to validate their existence as part of the nuclear genome. PCR amplification of these junctions across multiple species of *Geomys* was conducted to determine the presence of the same NUMTs in other species. Our results confirm the existence of NUMTs in multiple species of *Geomys* that are large and of high sequence identity. These findings emphasize the importance of accounting for NUMTs when conducting mitochondrial research.

Poster Presentation Abstracts

Posters 1-2 are to be considered for the Clyde Jones Undergraduate Award.

Poster 1

GENETIC IDENTIFICATION OF *PEROMYSCUS* SPECIMENS FROM SMALL MAMMAL MARK-RECAPTURE STUDIES IN WESTERN OKLAHOMA Kayli D. Newport[1], Claire A. Wiley[1], Francisca M. Mendez-Harclerode[2], and Michelle L. Haynie[1] **-** [1]University of Central Oklahoma, Department of Biology; [2]Bethel College, Department of Biology (knewport@uco.edu)

My project will entail genetic identification of *Peromyscus* specimens collected from the small mammal mark-recapture survey. Two species of *Peromyscus* are known to inhabit each of the three webs at the University of Central Oklahoma (UCO) Selman Living Lab (SLL): *Peromyscus maniculatus* (American deermouse) and *Peromyscus leucopus* (white-footed deermouse). The purpose of this project is to confirm species identity by utilizing genetic markers from previously collected specimens as part of the small mammal mark and recapture survey conducted at the UCO SLL. The small mammal collection is performed using Sherman live traps placed in three permanent sampling grids established in March and June of 2018 at the SLL. During the first capture, each specimen will be processed. This includes identifying the species, sex, age class, body condition, and reproductive condition of the mammal. Weight and standard measurements are taken, along with taking ear clips for DNA and applying a unique identifier (tattoo, toe clipping, or ear tag). The capture date, web number, and trap number are all recorded. DNA for every sample will be extracted from ear clippings using a DNeasy Blood and Tissue Extraction Kit (Qiagen). DNA will be amplified with two different forward-specific primers, which target 159 bp fragments for *P. leucopus* (P. leuco-F-9263) and 225 bp fragments for *P. maniculatus* (P. mani-F-9197), along with the reverse primer H9375. As of Jan 1, 2026, 363 *Peromyscus* have been genetically identified, and 19 samples need to be re-extracted.

Poster 2

GENETIC VARIATION AND PHYLOGEOGRAPHY OF *EUMOPS PEROTIS* (WESTERN MASTIFF BAT) Daniela Childress and Loren K. Ammerman **-** Department of Biology, Angelo State University (dchildress2@angelo.edu)

The Western Mastiff Bat, *Eumops perotis*, is the largest bat in the United States, with a distribution extending into South America. They are adapted for fast flight and typically fly high above the ground resulting in low encounter rates in mistnet surveys. As a result, few specimens exist and minimal population genetic studies have been conducted on this species. Neither patterns of gene flow within this species or the genetic variation across its distribution are known. Analysis of DNA sequences can reveal phylogeographic patterns and provide a measure of genetic variation. In this research, we sequenced the mitochondrial cytochrome *b* gene and the control region to examine the phylogeography of this species and to fill in data deficiencies. Tissue samples of 30 individuals from Texas, California, Peru, and Paraguay were requested from several institutions for DNA extraction. PCR, Sanger sequencing, and haplotype analysis was performed, which revealed patterns of diversification. Our preliminary phylogenetic analysis revealed no distinct patterns of diversification relative to their collection site except some distinction between specimens in South America compared to North America.

Posters 3-7 are to be considered for the Vernon Bailey Undergraduate Award.

Poster 3

SEVEN YEARS OF CAMERA TRAPPING MAMMALS AT ABILENE STATE PARK, TAYLOR COUNTY, TEXAS Lyndsey K. Klein, Kailey F. McHenry, and Thomas E. Lee, Jr. - Department of Biology, Abilene Christian University

This is the seventh year of our camera trapping survey of Abilene State Park. This camera trapping survey of large to medium sized mammals was conducted from early September to early November 2025 as part of the Snapshot USA program. This camera trapping survey was part of a national effort in the snapshot program. In this study, we used 12 browning strike force HD cameras. Locations were chosen to avoid human interference, maximize habitat diversity and wildlife encounters. In this survey we recorded eleven species of mammals. The species encountered include *Canis latrans*, *Dasypus novemcinctus, Lynx rufus, Mephitis mephitis, Peromyscus* sp., *Odocoileus virginianus, Procyon lotor, Sciurus niger, Sus scrofa*, *Sylvilagus* sp. and *Urocyon cinereoargenteus.* The three most photographed animals were *Sus scrofa*, *Odocoileus virginianus,* and *Sciurus niger*. The park was under a drought, Lake Abilene (a reservoir in the park) completely dried up and the streams in the park had only intermittent pools. In addition to documenting mammalian species present in the Abilene State Park and their abundance, some interesting natural history findings were recorded.

Poster 4

MESOPREDATOR USE OF WILDLIFE CROSSINGS IN SOUTH TEXAS Elena Gonzales, Spencer Ferguson, Emma Brookover, and Michael Tewes - Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville (elena.gonzales@students.tamuk.edu)

Wildlife Crossing Structures (WCSs) are artificially designated structures or routes that reconnect fragmented habitats and are essential for reducing wildlife-vehicle collisions and wildlife road mortality. In South Texas, WCSs are recognized for supporting federally endangered species, such as the ocelot, a medium-sized cat found in only two isolated populations in South Texas. In addition, WCSs are also regularly used by a diverse range of wildlife, including five common mesocarnivores: bobcats (*Lynx rufus*), northern raccoons, opossums (*Didelphis virginiana*), striped skunks (*Mephitis mephitis*), and coyotes (*Canis latrans*). The presence and activity of these species at WCSs can vary depending on localized variations such as crossing design, road construction, seasonal resource availability, and proximity to developed areas. These factors influence both the frequency and nature of wildlife interactions recorded by camera traps. Researchers at Texas A&M University–Kingsville are monitoring five WCSs along Farm-to-Market Road 1847 in Willacy County, Texas. The objective of this study is to analyze how site-specific variables shape mesocarnivore passage success and behavioral interactions at each crossing. Each crossing will be evaluated based on the abundance of species-specific sightings, the proportion of Type A interactions (full crossings), seasonal trends in use, and distance from urban development. Data was collected by the Cesar Kleberg Wildlife Research Institute South Texas Ocelot Project from September 2024 to September 2025 using camera traps and a behavioral grading system to classify interaction types. Detections are counted in 30-minute intervals for each species captured by multiple cameras. Findings from this study may reveal how crossing success differs by species, season, and site, providing support for additional WCS implementation along other major highways and planned mesocarnivore conservation strategies based on species-specific trends.

Poster 5

A TEST OF RELATIVE ABUNDANCE OF GRAY FOX (*UROCYON CINEREOARGENTEUS*) AND COYOTES (*CANIS LATRANS*) IN URBAN VERSUS RURAL LANDSCAPES

Isabella Ortiz de Camargo and Thomas E. Lee, Jr. - Department of Biology, Abilene Christian University, Abilene, Texas 79699 (ixo23b@acu.edu)

Gray Fox (*Urocyon cinereoargenteus*) have been observed on numerous occasions in the city of Abilene Texas. However, a seven-year camera trapping study of Abilene State Park (which is in a rural part of Taylor County and not in the city of Abilene) found that sightings of gray fox were either rare (one or two per year) or nonexistent. It has been thought that gray fox use urban areas has human shields from coyotes (*Canis latrans*). In the Fall of 2025, we setup 12 camera traps at Abilene State Park which were part of the Snapshot USA program and nine cameras within the highway loop surrounding the city of Abilene, Texas. The city cameras were placed in riparian habitat next to Cedar Creek (walking) Trail and in residential back yards that border Elm Creek. Our hypothesis was that gray fox would be statistically significantly more common within the city than at the State Park and coyotes would be more common at the park. We ran a t-test on the two samples and found that gray foxes were significantly different with a $P < 0.02$. Whereas there were more coyote sightings in the park than within the city, the numbers were not statistically significant. We have photographic evidence that shows that gray foxes use the roofs of buildings and houses perhaps to avoid interaction with coyotes and dogs rather than that coyotes just avoid proximity to humans (which they do not).

Poster 6

HORMONES, HIGHWAYS, AND THE ROAD AHEAD: GENOMIC INSIGHTS INTO BEHAVIOR AND SURVIVAL OF SOUTH TEXAS WILD CATS

Denay Hernandez, Jack Towson, Emma Brookover, and Michael Tewes - Caesar Kleberg Wildlife Research Institute, Texas A&M University–Kingsville (denay.hernandez@students.tamuk.edu)

Roads are vital to economic expansion, but they act as pervasive barriers to wildlife movement and genomic connectivity. In South Texas, the bobcat (*Lynx rufus*) and ocelot (*Leopardus pardalis*) are prime roadkill candidates due to their wide-ranging dispersal. Ocelots are endangered in the United States and face reduced gene flow and population size from roads limiting dispersal and isolating individuals. Roads can disrupt hormonal pathways, resulting in infertility, altered parental care, and reduced kitten survival. Understanding hormonal genomics and its ecological consequences will help connect the hormonal activity that drives road-crossing success with overall fitness. While local road ecology research has progressed, no genomic research has examined how hormones related to stress, reproduction, and behavior affect road-crossing decisions in wild cats. In this study, bobcat and ocelot blood samples were used from across South Texas, including Laguna Atascosa National Wildlife Refuge and private ranches along U.S. Highway 77 and FM 1847. Genomic DNA was extracted, and whole-genome sequences were developed from over 400 samples collected from 1985 to present to evaluate genomic variation. Single-nucleotide polymorphisms were detected in five candidate hormonal genes to assess genomic diversity and population structure. These genes were identified in a functional categorization of the bobcat genome and selected due to their roles in stress regulation, reproductive fitness, and behavioral responses. Based on behavioral and physiological patterns, these findings will contribute to ocelot conservation by informing strategic placement of wildlife crossing structures and improving connectivity of felid populations facing increasing anthropogenic pressures in an urban environment.

Poster 7

ASSESSING THE CORRELATION BETWEEN BOBCAT PRESENCE, PREY PRESENCE, AND SURROUNDING ENVIRONMENT IN SOUTH TEXAS Emma McMillian, Spencer Ferguson, Emma Brookover, and Michael Tewes **-** Caesar Kleberg Wildlife Research Institute, Texas A&M University- Kingsville, Kingsville, Texas (emma.mcmillian@students.tamuk.edu)

In South Texas, bobcats (*Lynx rufus*) are a wild cat species commonly detected in dense brush patches. They often hunt for small prey species such as cottontail (*Sylvilagus floridanus*) and rodents (*Rodentia* spp.). Variables such as brush density, water availability, and prey abundance can generate variance in their habitat zones. Similar research has been conducted in South Texas; however, other studies focused on ecological variables such as co-occurrence, abundance, behavior, and occupancy modeling across carnivore species. This project will assess the detection of bobcats at 46 camera sites, spread over 4,400 hectares (~ 17 square miles) on a South Texas ranch. Detections are considered 30-minute intervals for each species captured by game cameras. The surrounding environment, the presence of small prey species, and comparing these findings to the presence of bobcats will be evaluated to identify the ecological correlation between bobcats and small prey. First, we will compare bobcat detections to small prey detections. Second, we will use data as input to compare the detections of bobcats and small prey species to the habitat locality and habitat containing the camera. Our research depends on these data to facilitate future research projects that rely on bobcat trapping, bobcat spatial distribution, and behavioral studies. Our results will determine which habitat is best for future bobcat research projects and will better inform conservation strategies aimed at identifying what habitat needs to be protected and managed for bobcats and other wild carnivorous species in South Texas.

Posters 8-15 are to be considered for the Vernon Bailey Graduate Award.

Poster 8

CAMERA TRAPPING IN RIPARIAN CORRIDORS WITHIN PEARL JACKSON CROSSTIMBERS PRESERVE (WIP) Teague Fox and Vicki Jackson **-** University of Central Oklahoma (tfox11@uco.edu)

The Pearl Jackson Crosstimbers Preserve is a new nature preserve that was recently acquired by The Nature Conservancy. This area is about 50 sqkm made up of rough terrain mixed with disused barb wire fences and rugged slopes. This area cannot be properly managed without knowledge of what organisms are currently utilizing the preserve. Camera trapping surveys allow for long-term, non-invasive monitoring of wildlife over a large area. Riparian corridors are contours in the landscape typically following the path of water. These corridors can act as a cross section of the overall diversity for the preserve. For this survey of the preserve we will be placing 25 cameras throughout these riparian corridors with possible locations being placed every 500 meters in each identified corridor. By placing camera traps in these areas, we will be able to get a better survey of the mammalian population. This will hopefully act as a cross section for the overall preserve. Cameras will be left out for 1 continuous year from August 2025-August 2026, with each camera being checked once a month at the minimum. The goal of this survey is to gather enough data to create occupancy models for what species are using the preserve and where they are using it.

Poster 9

EVALUATING BAT COMMUNITIES ACROSS THREE WEST TEXAS MOUNTAIN RANGES USING MOBILE ACOUSTIC SURVEYS Kennedy Berry and Loren K. Ammerman **-** Department of Biology, Angelo State University (kberry7@angelo.edu)

Acoustic mobile transects are useful for tracking activity and diversity of bat communities. Different computer programs have been developed that can automatically identify the bat species based on the acoustic recording, but manual vetting of the results is standard practice. The goal of this study was to analyze the bat activity and diversity found within three western Texas mountain ranges. For this study, we recorded along a highway transect near each of three major sky islands of west Texas - the Chisos Mountains, the Guadalupe Mountains, and the Davis Mountains. Thirty locations along each transect were sampled two nights in June, July, and August with two different types of detectors (AnabatII and Anabat Express). The calls were processed through Kaleidoscope Pro's Auto ID feature and were then manually vetted. More calls were recorded with Anabat Express compared to the AnabatII. There were 4,321 identified calls through manual vetting out of 7,614 calls recorded, while only 3,140 were identified with Auto ID. Because some call files recorded bat passes of multiple species, more calls were identified by manual ID. The species that was the most active both by month, location, and detector was *Tadarida brasiliensis*. Over all three sampling months combined the Chisos Mountains saw the highest activity. July saw the highest activity out of all three months. Results from Auto ID differed from manual ID likely because some rare species were more likely to be identified using manual vetting. Overall, the bat community described by these data are consistent with our knowledge of bat species occurrence, however, there were some unexpected species detected on our transects.

Poster 10

THE USE OF BRIDGES AS DAY-ROOSTS BY BAT SPECIES IN EAST TEXAS Jayme E. Czap[1], Makani L. Fisher[1], and Richard D. Stevens[12] - [1]Department of Natural Resources Management, Texas Tech University; [2]Natural Science Research Laboratory, Museum of Texas Tech University (jczap@ttu.edu)

Understanding resource selection is critical for wildlife management, particularly for bats, whose roosting decisions strongly influence their distribution. Bats are increasingly reported using highway infrastructure such as bridges as both day- and night-roosts, suggesting that bridge design and placement may affect roost availability. However, the influence of bridge characteristics and surrounding habitat on bat roosting remains poorly understood. We investigated whether specific bridge attributes promote bat day-roosting during winter and summer. From 2023 to 2025, we surveyed approximately 550 randomly selected bridges across the piney woods and post-oak savannah ecoregions of east Texas. For each bridge, we recorded 10 variables describing bridge structure and underside habitat, as well as season, ecoregion, bat species presence or absence, and abundance. We used negative binomial generalized linear models to assess relationships between bat abundance and bridge and habitat characteristics. Although five bat species were observed using bridges, analyses focused on the three most prevalent: *Tadarida brasiliensis*, *Eptesicus fuscus*, and *Perimyotis subflavus*. Prestressed concrete box girder bridges and the piney woods ecoregion significantly and positively influenced roosting for all three species. Bridge length was positively related, and average height was negatively related to *E. fuscus* abundance in bridges. *P. subflavus* was also positively influenced by bridge width and length. *T. brasiliensis* used bridges significantly more during the summer months. Bridge width, elevation and U.S. highway road types had a positive correlation with *T. brasiliensis* roosting. However increased underside obstruction was negatively related to roosting within a bridge. Although bats used other bridge types, no significant associations were detected, highlighting the importance of box girder bridges for bat conservation. These findings provide practical guidance for transportation and conservation planning by identifying bridge designs that promote bat roosting.

Poster 11

SPATIAL VARIATION OF AN INSECTIVOROUS BAT ASSEMBLAGE IN RESPONSE TO LANDSCAPE HETEROGENEITY AND PREY AVAILABILITY IN THE RURAL LANDSCAPE OF LIMA-PERU, PACIFIC COASTAL DESERT Jorge Rivero[1] and Richard Stevens[1,2]
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Spatial heterogeneity is a driver of bat diversity and distribution, providing various suitable areas for roosting and foraging. Fourteen insectivorous species occur in rural areas in the Pacific coastal desert of

South America, yet it is unclear whether coexistence relies on habitat specialization or prey availability. The project's primary goal is to investigate how the insectivorous bat assemblage responds to landscape composition and prey availability in the rural zone of Lima. Specifically, an important aim is to predict the occurrence of threatened species (*Tomopeas ravus* and *Amorphochilus schnablii*) and identify potential roosting and foraging sites. Bat activity will be sampled through passive acoustic monitoring at 30 sites during the austral winter and summer across the rural zone of Lima to estimate species richness, composition, and occupancy. Nine covariates will be used for landscape characterization at each site: percentage of the four most dominant vegetation units of the Peruvian Map of Ecosystems (desert, agricultural zone, lomas, and Andean shrublands), normalized vegetation index, distance to urban zones, distance to water bodies, elevation, and slope. Insect biomass will be sampled as a proxy of prey availability. Expected outcomes include a comparative assessment to identify areas with high species richness and scale-dependent species-habitat associations based on landscape and prey composition. This project aims to enhance our understanding of coexistence within an assemblage of 14 insectivorous bat species, potentially leading to future studies on ecological niches and co-occurrence. From a conservation perspective, outcomes include the development of an acoustic monitoring protocol and a local map to predict occurrences for threatened and data-deficient bat species.

Poster 12

IMPACTS OF CAPTIVITY ON BONE DENSITY AND LOCOMOTION IN MEXICAN GRAY WOLVES (*CANIS LUPUS BAILEYI*)

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Captive management plays a vital role in endangered mammal conservation. However, long-term consequences of captivity are not fully understood. Cursorial, large home ranged carnivorans, such as gray wolves (*Canis lupus*), are particularly vulnerable to captive conditions. This study seeks to examine the impacts of captivity on bone density and locomotor morphology in the Mexican gray wolf (*Canis lupus baileyi*), a critically endangered subspecies with both captive and reintroduced wild populations. While prior research has documented cranial differences between captive and wild Mexican gray wolves, postcranial effects of captivity remain unexplored. This project will assess trabecular bone density in the humeri and femurs of 20 Mexican gray wolf specimens from the Museum of Southwestern Biology (MSB), divided between 10 captive and 10 wild individuals. Using microCT, trabecular bone volume fraction (BVF) will be quantified as an indicator for bone density. BVF will be calculated through calibrated mineral density comparisons using three-dimensional image analyses to ensure methodological robustness. We will then evaluate differences in mean BVF between captive and wild wolves, as well as between forelimb and hindlimb densities within individuals. We hypothesize that captive wolves will exhibit significantly reduced trabecular bone density relative to wild wolves, reflecting decreased mechanical loading. Additionally, we predict a greater reduction in forelimb bone density compared to hindlimbs, given previous studies of carnivoran locomotion. Results from this study will address a critical gap in understanding how captivity affects postcranial skeletal health in endangered canids. Findings will have direct implications for zoo management, captive breeding programs, and reintroduction efforts by informing potential enclosure design and enhanced welfare strategies. Ultimately, this research aims to improve the long-term survival and functional performance of Mexican gray wolves released back into the wild and contribute to the broader study of captivity's effects on carnivore morphology and locomotion.

Poster 13

MULTI-SPECIES ASSESSMENT OF WILDLIFE–VEHICLE COLLISIONS USING BOBCATS AND SYMPATRIC WILDLIFE TO INFORM OCELOT CONSERVATION IN SOUTH TEXAS

Rupesh Maharjan[1], Sean Kiernan[1], Jack Towson[1], Elizabeth Grunwald[1], Thomas Langschied[1], Spencer Ferguson[1], Thomas J. Yamashita[2], John H. Young Jr.[3], Emma Brookover[1], and Michael E. Tewes[1] - [1]Texas A&M University-Kingsville, Caesar Kleberg Wildlife Research Institute; [2]Colorado State University; [3]Environmental Affairs Division, Texas Department of Transportation (rupesh.maharjan@students.tamuk.edu)

Globally, road networks have been expanding rapidly and are expected to increase further in the coming years. With more than 6.7 million km of roads available for public use, the United States benefits from a fast and efficient transportation network that facilitates the movement of people and goods across long distances. However, the same linear infrastructure can act as a physical barrier in wildlife movement resulting in habitat fragmentation. For wide-ranging meso-carnivores like ocelot (*Leopardus pardalis*) and bobcat (*Lynx rufus*), habitat fragmentation often increases the risk of wildlife-vehicle collisions that may lead to population level endangerment like it has with the ocelot. Because bobcats share similar movement patterns and habitat preferences with ocelots at south Texas, they are often used as a surrogate species to study and predict the impacts of roads on the more elusive ocelots. Building on this approach, we aim to describe the spatio-temporal distribution of wildlife-vehicle collisions along two South Texas highways by identifying potential roadkill hotspots and evaluating the environmental and road-related factors that contribute to collision risk. We will conduct wildlife road mortality survey along a section of US Highway 77 and Farm-to-Market Road 1847 once a week and record the spatial and temporal data of a roadkill. By identifying the key spatial, temporal, and environmental drivers of wildlife-vehicle collisions, this study will provide a foundation for predicting high-risk zones and informing the strategic placement of wildlife crossing structures, ultimately enhancing landscape connectivity and reducing mortality for bobcats, ocelot, and other sympatric species from vehicle collisions.

Poster 14

UNDERSTANDING DIEL ACTIVITY PATTERNS IN WILD BOAR (*SUS SCROFA*) INVASION SUCCESS: BEHAVIORAL PLASTICITY VERSUS CONSERVED TEMPORAL TRAITS

Namrata Bhandari and Iván Castro-Arellano **-** Department of Biology, Texas State University (lzy18@txstate.edu)

The wild boar *(Sus scrofa)* is among the most successful invasive mammals worldwide occupying a broad range of habitats across native and introduced ranges. Diel activity patterns (DAPs) likely play a significant role in their success, it remains unclear whether their global expansion is driven by high behavioral plasticity or evolutionarily conserved temporal traits. This study explores this dynamic through the lens of intraspecific diel temporal niche conservatism (Intra-DTNC): the tendency of populations to retain consistent activity patterns over time. We hypothesize that invasive wild boar populations exhibit significantly weaker Intra-DTNC than native populations, reflecting high plasticity to optimize foraging and avoid threats in novel environments. We further predict that nocturnality increases in response to higher maximum temperatures and closer proximity to human settlements, although habitat heterogeneity may mitigate these shifts by providing protective cover. To test these hypotheses, we will utilize time-stamped camera trap data from global repositories across continents. We aim to quantify Intra-DTNC using the ROSARIO randomization algorithm and analyze the influence of ambient temperature, human proximity, and habitat heterogeneity on nocturnality using generalized linear mixed models (GLMMs). By contrasting these patterns with the DAPs of related taxa, including peccaries, Asian and African suiformes, this study will provide the first macroecological test of temporal niche conservatism in an invasive mammal. These insights are critical for understanding behavioral shifts that facilitate the exploitation of novel environments and developing targeted management strategies in human-dominated landscapes.

Poster 15

CHARACTERIZATION OF *MYOCPLASMA* COMMUNITIES IN AOUDAD (*AMMOTRAGUS LERVIA*) POPULATIONS ACROSS TEXAS

Brendan Amman **-** Department of Biology, Texas Tech University (bamman@ttu.edu)

Outbreaks of pneumonia in desert bighorn sheep (*Ovis canadensis mexicanus/nelsoni*) in the Trans-Pecos ecoregion of Texas are thought to be a major contributor to population declines over the last decade. Recent detection of *Mycoplasma ovipneumoniae* in a nonnative ungulate, aoudad (*Ammotragus lervia*), from the Trans-Pecos ecoregion, suggests that aoudad may serve as a potential reservoir for pneumonia and a potential source of disease for desert bighorn sheep populations. Recent data suggest that in addition to competition for resources, the probability of disease transmission increases as aoudad and bighorn sheep populations interact more frequently. Further, aoudad do not seem to be affected by pneumonia and may have developed resistance mechanisms similar to those seen in domestic sheep and goats which allows them to serve as hosts without being dramatically impacted themselves. The objectives of this study are to explore the ecology, distribution, and frequency of *Mycoplasma* in aoudad in Texas using a DNA sequencing method called multi-locus sequence typing (MLST) and to characterize *Mycoplasma* strain type or species in aoudad and determine if there is a correlation between *Mycoplasma* strain type, geographic location, and aoudad haplogroup. To date, 46 individuals have been typed using the MLST method. Preliminary results have identified three strains of *Mycoplasma* which occur across five geographically separated localities in Texas. In addition, efforts are being developed to detect *Mycoplasma* in fecal samples.