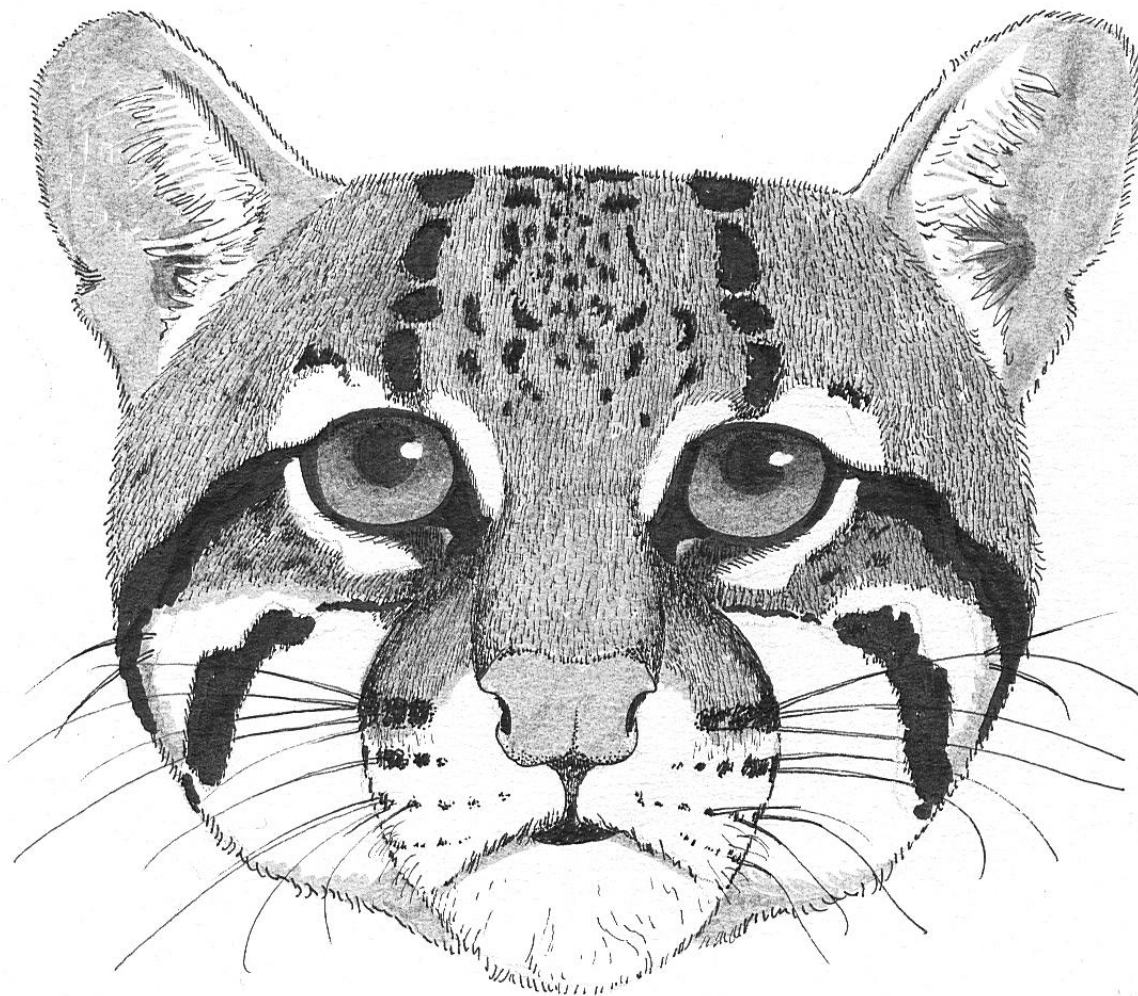


# TEXAS SOCIETY OF MAMMALOLOGISTS



**PROGRAM AND ABSTRACTS  
AND**

**NEWSLETTER**

28<sup>th</sup> Annual Meeting

26-28 February 2010

**Texas Tech University Center at Junction**

# Texas Society of Mammalogists

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Cover illustration of ocelot, *Leopardus pardalis*, by Terry Maxwell.

**Texas Society of Mammalogists**  
**28<sup>th</sup> Annual Meeting**  
**26-28 February 2010**

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## 2010 Program Schedule

### Friday, 26 February

3:00-7:30pm	Registration	Dining Hall
6:00pm	Dinner (serving line open 6:00-6:30pm)	Dining Hall
7:00pm	Announcements/Welcome Address TSM President Michael Tewes	Dining Hall
7:30pm	Poster Presentations	Dining Hall
8:30pm	Meeting of the Executive Committee	Academic Building

### Saturday, 27 February

7:00am	Breakfast and Registration (serving line open 7:00-7:30am)	Dining Hall
8:00am	Introduction and Announcements TSM President Michael Tewes	Packard Building

### PAPER SESSION -- Packard Building

**Chair: Dana Lee, Oklahoma State University**

*Papers 1 – 3 are in competition for the Rollin H. Baker Award.*

- 8:05 Paper 1 – **NUCLEAR DNA PHYLOGEOGRAPHY OF THE PALLID BAT (*ANTROZOUS PALLIDUS*)** Jeremy E. Wilkinson, Justin B. Lack, and Ronald A. Van Den Bussche, Department of Zoology, Oklahoma State University
- 8:20 Paper 2 – **THE GENETIC DIVERSITY OF STRIPED SKUNK (*MEPHITIS MEPHITIS*) POPULATIONS THROUGHOUT THE CENTRAL UNITED STATES** Kelly A. Smith and Michelle L. Haynie, University of Central Oklahoma
- 8:35 Paper 3 – **GENETIC CHARACTERIZATION AND NATURAL HOST RELATIONSHIPS OF MULESHOE VIRUS IN NORTH TEXAS AND WESTERN OKLAHOMA** Allie P. Clinton<sup>1</sup>, Robert D. Bradley<sup>1,2</sup>, Mary Louise Milazzo<sup>3</sup>, Charles F. Fulhorst<sup>3</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Museum of Texas Tech University, <sup>3</sup>Department of Pathology, University of Texas Medical Branch

*Papers 4 - 10 are in competition for the TSM Award.*

8:50 Paper 4 – **MOUNTAIN LION GENETIC STRUCTURE, GENE FLOW, AND GENETIC DIVERSITY IN TEXAS** Joseph D. Holbrook<sup>1</sup>, Randy W. DeYoung<sup>1</sup>, Michael E. Tewes<sup>1</sup>, and John H. Young<sup>2</sup>, <sup>1</sup>Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, <sup>2</sup>Texas Parks and Wildlife Department

9:05 **20 Minute Break**

**Chair: Michelle Haynie, University of Central Oklahoma**

9:25 Paper 5 – **PARAPHYLY AND SPECIATION WITHIN BULLDOG BATS (CHIROPTERA: NOCTILIONIDAE)** Faisal A. Anwarali Khan<sup>1</sup>, C. Miguel Pinto<sup>2</sup>, and Robert J. Baker<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Department of Mammalogy, American Museum of Natural History

9:40 Paper 6 – **IDENTIFYING THE CONFOUNDING FACTORS IN RESOLVING PHYLOGENETIC RELATIONSHIPS IN VESPERTILIONIDAE** Justin B. Lack and Ronald A. Van Den Bussche, Department of Zoology, Oklahoma State University

9:55 Paper 7 – **PHYLOGENETIC RELATIONSHIPS WITHIN THE NEOTOMINAE BASED ON COMBINED MITOCHONDRIAL AND NUCLEAR DATA SETS** Megan S. Corley<sup>1</sup>, Roy N. Platt<sup>2</sup>, Brian R. Amman<sup>3</sup>, and Robert D. Bradley<sup>1,4</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Department of Biological Sciences, Mississippi State University, <sup>3</sup>Centers for Disease Control, <sup>4</sup>Natural Sciences Research Laboratory, Museum of Texas Tech University

10:10 Paper 8 – **GENETIC VARIATION AND PHENOTYPIC EVOLUTION IN THE ANTILLEAN TREE BAT (*ARDOPS NICHOLLSI*)** Roxanne J. Larsen<sup>1</sup>, Peter A. Larsen<sup>1</sup>, Caleb D. Phillips<sup>1</sup>, Hugh H. Genoways<sup>2</sup>, Gary G. Kwiecinski<sup>3</sup>, Scott C. Pedersen<sup>4</sup>, and Robert J. Baker<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>University of Nebraska State Museum, <sup>3</sup>Biology Department, The University of Scranton, PA, <sup>4</sup>Department of Biology/Microbiology, South Dakota State University

10:25 **20 Minute Break**

**Chair: Adam Ferguson, Texas Tech University**

10:45 Paper 9 – **IS TRANSFERRIN-RECEPTOR 1 (TFR1) THE HOST RECEPTOR FOR NORTH AMERICAN ARENAVIRUSES?** Sheri B. Ayers<sup>1</sup> and Robert D. Bradley<sup>1,2</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Natural Sciences Research Laboratory, Museum of Texas Tech University

11:00 Paper 10 – **MOLECULAR EVIDENCE FOR HYBRIDIZATION BETWEEN *NEOTOMA MICROPUS* AND *N. FLORIDANA*** Matthew R. Mauldin<sup>1</sup>, J. Delton Hanson<sup>1</sup>, Robert J. Baker<sup>1,2</sup>, and Robert D. Bradley<sup>1,2</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Museum of Texas Tech University

*Papers 11 - 14 are in competition for the William B. Davis Award.*

- 11:15 Paper 11 – **PATTERNS OF DISTRIBUTION OF THE ENDEMIC MAMMALS IN ECUADOR** Juan P. Carrera-E. and Hugo Mantilla-Meluk, Department of Biological Sciences and the Museum of Texas Tech University
- 11:30 Paper 12 – **MODELING TRANSLOCATION OF OCELOT, *LEOPARDUS PARDALIS*, FROM MEXICO TO TEXAS** William C. Stasey, Michael E. Tewes, and Arturo Caso, Feline Research Center, Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville
- 11:45 Paper 13 – **SPECIES RICHNESS AND HABITAT HETEROGENEITY: ARE SPATIAL ANALYSES IMPORTANT?** J. Erin Fender<sup>1</sup>, Michael L. Kennedy<sup>2</sup>, Gary D. Schnell<sup>3</sup>, Cornelio Sánchez-Hernández<sup>4</sup>, María de Lourdes Romero-Almaraz<sup>5</sup>, Michael C. Wooten<sup>6</sup>, and Troy L. Best<sup>6</sup>, <sup>1</sup>Department of Wildlife and Fisheries Sciences, Texas A&M University, <sup>2</sup>Ecological Research Center and Department of Biology, The University of Memphis, <sup>3</sup>Sam Noble Oklahoma Museum of Natural History and Department of Zoology, University of Oklahoma, <sup>4</sup>Departamento de Zoología, Instituto de Biología, Universidad Nacional Autónoma de México, <sup>5</sup>Escuinapa No. 92 bis. Col. Pedregal de Santo Domingo, México, <sup>6</sup>Department of Biological Sciences, Auburn University
- 12:00 **Lunch** (serving line open 12:00-12:30pm)
- 1:15 **Group Photo** behind the Packard Building

### **PAPER SESSION – Packard Building**

**Chair: Caleb Phillips, Texas Tech University**

- 1:45 Paper 14 – **RESPONSE OF SMALL MAMMALS TO CHANGES IN PRECIPITATION AND FIRE IN SHORTGRASS PRAIRIE OF THE TEXAS PANHANDLE** Whitney J. Priesmeyer and Raymond S. Matlack, Life, Earth, and Environmental Science, West Texas A&M University

*Papers 15 - 20 are not competing for an award.*

- 2:00 Paper 15 – **A PREDICTIVE MODEL OF NON-VOLANT SMALL MAMMAL ASSEMBLAGES IN EASTERN PARAGUAY ATLANTIC FOREST REMNANTS** Noé de la Sancha and Richard Strauss, Department of Biological Sciences, Texas Tech University

- 2:15 Paper 16 – **PHYLOGEOGRAPHIC IMPLICATIONS OF HYBRIDIZATION BETWEEN THE MEXICAN GROUND SQUIRREL (*SPERMOPHILUS MEXICANUS*) AND THE THIRTEEN-LINED GROUND SQUIRREL (*S. TRIDECIMLINEATUS*)** Cody W. Thompson<sup>1</sup>, Frederick B. Stangl, Jr.<sup>2</sup>, and Robert D. Bradley<sup>1,3</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Biology Department, Midwestern State University, <sup>3</sup>Natural Science Research Laboratory, Museum of Texas Tech University
- 2:30 Paper 17 – **TAXONOMIC STATUS AND DISTRIBUTION OF THE *PEROMYSCUS BOYLI* GROUP (RODENTIA:CRICETIDAE)/ ESTADO TAXONÓMICO Y DISTRIBUCIÓN DEL GRUPO DE ESPECIES *PEROMYSUCS BOYLII* (RODENTIA:CRICETIDAE)** Nicté Ordóñez-Garza<sup>1</sup>, Ryan Duplechin<sup>1</sup>, Duke Rogers<sup>2</sup>, Elizabeth Arellano<sup>3</sup>, Francisco X. González-Cózat<sup>3</sup>, C. William Kilpatrick<sup>5</sup>, and Robert D. Bradley<sup>1,4</sup>, <sup>1</sup>Biological Sciences Department, Texas Tech University, <sup>2</sup>Department of Biology, Brigham Young University, <sup>3</sup>Centro de Educación ambiental y educación, Universidad Autónoma del Estado de Morelos, <sup>4</sup>Museum of Texas Tech University, Natural Research Laboratory, <sup>5</sup>Department of Biology, University of Vermont
- 2:45 Paper 18 – **MICROSATELLITE DATA OF *ARTIBEUS JAMAICENSIS* FROM THREE U.S. VIRGIN ISLANDS: IMPLICATIONS FOR EXPERIMENTAL DESIGN OF INTERISLAND MIGRATION** Julie A. Parlos<sup>1</sup>, Gary G. Kwiecinski<sup>2</sup> and Robert J. Baker<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Biology Department, University of Scranton
- 3:00 Paper 19 – **PATTERNS OF HANTAVIRUS SEROPREVALENCE IN WILD RODENTS FROM SOUTHEASTERN BRAZIL** Gilberto Sabino-Santos Jr<sup>1</sup>, Felipe Gonçalves Motta Maia<sup>1</sup>, Alex M. Machado<sup>1</sup>, Glauciane G. Figueiredo<sup>1</sup>, Jorge Salazar-Bravo<sup>2</sup> and Luiz Tadeu M. Figueiredo<sup>1</sup>, <sup>1</sup>University of Sao Paulo School of Medicine, Ribeirao Preto, Brazil, <sup>2</sup>Department of Biological Sciences, Texas Tech University
- 3:15 Paper 20 – **AN EVALUATION OF FECAL DNA PRESERVATION TECHNIQUES AND EFFECTS OF SAMPLE AGE AND DIET ON GENOTYPING SUCCESS** Michael Panasci<sup>1</sup>, Warren Ballard<sup>1</sup>, David Wester<sup>1</sup>, Stewart Breck<sup>2</sup>, David Rodriguez<sup>3</sup>, Llewellyn Densmore<sup>3</sup>, Robert Baker<sup>3</sup>, <sup>1</sup>Department of Natural Resources Management, Texas Tech University, <sup>2</sup>USDA, APHIS, Wildlife Services, National Wildlife Research Center, Fort Collins, CO, <sup>3</sup>Department of Biological Sciences, Texas Tech University

3:30 **15 Minute Break**

3:45pm

**Business Meeting**

All members, please attend!

Packard Building

5:30-9:00pm	<b>Annual Banquet and Auction</b>	Dining Hall
5:30-6:30	Dinner (serving line open 5:30-6:00pm)	
5:30	Silent Auction opens for bidding	
6:30-7:00	Award Presentations	
7:00-8:00	Guest Speaker Address:	

**Dr. Marcella Kelly**

Department of Fisheries and Wildlife Sciences  
Virginia Tech University

***Wild Cats of Belize – Portraits of a Predator***

8:00-9:00	Live Auction (Silent Auction ends 10 minutes after Live Auction)	
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9:00pm-?	Socializing and Dancing	Dining Hall
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**Sunday, 28 February**

7:30am	Breakfast (serving line open 7:30-8:00am)	Dining Hall
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## Poster Presentation Abstracts

The following posters (1 - 6) are to be considered for the Vernon Bailey Award.

Poster 1

### **MOLECULAR SYSTEMATICS OF *GEOMYS* BASED ON DNA SEQUENCES FROM THE PROTEIN CODING THE ALCOHOL DEHYDROGENASE GENE (*ADH-1*)**

Erica Vargas<sup>1</sup>, Sheri B. Ayers<sup>1</sup>, and Robert D. Bradley<sup>1,2</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Natural Science Research Laboratory, Museum of Texas Tech University (erica.vargas@ttu.edu)

Phylogenetic relationships among members of the genus *Geomys* have been difficult to discern because of the conservation of morphological characters presumably as the result of their fossorial lifestyle. Early studies of chromosomes and allozymes generated a few phylogenetic hypotheses, but most were hindered by taxon sampling or a low resolving power of characters and data due to homoplastic events. In recent years, DNA sequence data has been obtained from two mitochondrial genes (12S rRNA and cytochrome-*b*) and one nuclear gene (*Rbp3*) and used to generate phylogenetic relationships for all members of the genus. In this study, we examine a second nuclear marker, the coding region of the alcohol dehydrogenase gene (*Adh-1*). Sequences for the *Adh-1* locus were analyzed independently and in combination with the other three genes (12S rRNA, *Cytb*, and *Rbp3*) using maximum likelihood and Bayesian methods. Although this study is preliminary – only nine species were examined – the data appears to be informative and supports many results from previous studies. However, more taxa or species of *Geomys* need to be further examined to have better resolution of the phylogenetic relationships.

Poster 2

### **SAM HOUSTON NATIONAL FOREST, TEXAS: TO NET OR NOT TO NET?**

Anica Debelica and Kenneth T. Wilkins, Department of Biology and Graduate School, Baylor University (Anica\_Debelica@baylor.edu)

Sam Houston National Forest (SHNF) comprises 65,978 ha of southeastern Texas “pineywoods”. Because of the presence of old tall trees and relatively mild climate, SHNF offers suitable habitat for multiple bat species throughout the year. A complex community (multiple species, presence of both males and females, adults and subadults) was expected to be present and to exhibit complex interactions (resource partitioning on multiple levels) due to different energetic needs and behavior of these subgroups. During summer 2009, we conducted a pilot study to determine if SHNF might be a suitable area for study of resource partitioning. We captured bats using a triple-high net, then processed them: identified to species, sexed, measured, and examined for reproductive state. Feces were collected for detailed dietary study. We also collected insects as reference for the dietary study and bat activity. We captured 114 individuals belonging to 8 species: 20 eastern red bats (*Lasiurus borealis*), 1 hoary bat (*L. cinereus*), 40 Seminole bats (*L. seminolus*), 13 big brown bats (*Eptesicus fuscus*), 28 evening bats (*Nycticeius humeralis*), 6 eastern pipistrelle bats (*Perimyotis subflavus*), 2 southeastern myotis bats (*Myotis austroriparius*), and 4 Mexican free-tailed bats (*Tadarida brasiliensis*). We observed variation in demographics of the bat community during the summer: a shift from a community dominated by pregnant/lactating females to a community dominated by males and non-reproductive subadults of both sexes, and differences in emergence times among species. Differences in community structure and emergence times suggest temporal partitioning of foraging areas. We anticipate that the

insect data will shed light on this phenomenon – presence of certain subgroups of bats might be directly related to insect community structure at various times.

Poster 3

### **BITE FORCE ANALYSIS OF FOREST INTERIOR INSECTIVOROUS BATS**

Juliana Senawi<sup>1,2</sup>, Bjorn Simers<sup>3</sup>, Daniela Schmieder<sup>4</sup>, and Tigga Kingston<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Institute for Environment and Development (LESTARI), Universiti Kebangsaan Malaysia, <sup>3</sup>Max Planck Institute for Ornithology, Germany, <sup>4</sup>Institute of Biological Sciences, University of Malaya (juliana.senawi@ttu.edu)

Malaysia's rainforests are home to the greatest diversity of bat species in the Old World with over 70 species recorded at a single location, Krau Wildlife Reserve, Pahang. This outstanding diversity is likely achieved through an intricate partitioning of the available resources within the habitat. In insectivorous bat assemblages, niche partitioning of food resources is effected in large part by physical and sensory access to the insect prey base. Differences in wing morphology and echolocation signal design among species influence access to particular foraging habitats and the ability to detect or capture prey within them. Differences in food processing capabilities, particularly bite force, may further mediate resource partitioning in species-rich assemblages. However, experimental data documenting biting ability (bite force) at the assemblage level are limited. Here, we examine the relationship between bite force and  $CM^3$  (tooth row as a measure of head size) and forearm length (as a measure of body size) in 20 species from three families of forest interior insectivorous bats from Krau Wildlife Reserve. There was a highly significant relationship between bite force and forearm length and  $CM^3$  at the assemblage level (i.e., across all species), and within families. The consequences of these findings for structuring mechanisms in species-rich monophagous assemblages are discussed.

Poster 4

### **EFFECT OF VEGETATION ALTERATION ON SMALL MAMMAL DIVERSITY IN CALLAHAN COUNTY, TEXAS**

Rachel Ames, Vania Arroyo, Lisa Medina, Lindsay Roach, and Joel G. Brant, Department of Biology, McMurry University (ames.rachel@students.mcm.edu)

Native habitats are increasingly transformed to suit human needs, often without consideration for the other species therein. Small mammals, particularly rodents, tend to be sensitive to habitat alterations, resulting in changes in faunal composition. We compared the rodent fauna of a 50-acre cleared pasture to that of a 50-acre native woodland. Rodents were sampled using 3500 trap-nights during the Fall of 2009. Several diversity indices (Berger-Parker dominance, Margalef's richness, Shannon's diversity, Simpson's diversity, and Simpson's evenness) were calculated in order to compare the rodent faunas of the altered and unaltered habitats. Of the six species encountered, only *Peromyscus leucopus* was found in both habitats. *Peromyscus attwateri* was the species primarily found in the wooded area and *Chaetodipus hispidus* was the species primarily found in the pasture area. In general, the altered and unaltered areas showed no significant difference in diversity. However, the unaltered woodland was significantly more dominated by a single species (*P. attwateri*) than the altered pasture. This result appears to fit the expectation of an increase in diversity following a disturbance event.

Poster 5

**MECHANISMS OF BOUNDARY RESPONSES IN SMALL MAMMALS —  
PRELIMINARY FINDINGS**

Nicholas S. Green and Kenneth T. Wilkins, Department of Biology, Baylor University  
(nick\_green@baylor.edu)

We report preliminary findings of a test of the recent resource-distribution model of edge responses in a small mammal community of the Texas blackland prairie. Hispid cotton rat (*Sigmodon hispidus*) abundance responded negatively to boundaries with non-prairie habitat, and showed weak positive correlation with grassy plant cover and moderate negative correlation with bare ground. North American deermouse (*Peromyscus maniculatus*) abundance did not respond to boundaries and was weakly correlated with bare ground and woody biomass. The weak cotton rat response to food abundance may indicate that other environmental cues drive both boundary responses and broader-scale habitat selection. Field sampling will be expanded in summer 2010 to include bioassays of energy availability to directly test these hypotheses.

Poster 6

**CHOERONYCTERINE BATS AS A MODEL TO STUDY THE EFFECT OF  
GLOBAL CLIMATE CHANGE AMONG MAMMALS**

Hugo Mantilla-Meluk and Robert J. Baker, Department of Biological Sciences, Texas Tech University (hugo.matilla@ttu.edu)

Mountain ecosystems have recently received considerable interest based on the understanding that climate change might have particularly serious irreversible impacts on these habitats. As a result of global warming, changes in the elevational ranges of mountain ecosystems have been observed and it is likely that the structure of highland mammalian assemblages is silently changing with the potential negative effect of extinction events among highland specialists due to the combination of habitat lost, competition, and niche displacement. Phyllostomid bats in the tribe Choeronycterina are considered highland specialists. The high geographic partitioning and ecological sensitivity documented for this group of bats made them a perfect model to study the effect of global warming on Neotropical highland ecosystems and to solve the fundamental question of: How can we determine to what extent the integrity of the “greater ecosystem” is being affected when the climate is changing? Herein, GIS and niche modeling were used to produce models of potential distribution for all choeronycterine species based on ecoregions inhabited by each taxon and their current minimum and maximum elevational ranges. Distribution models were used to analyze: 1) the geographic and ecological structure of choeronycterine’s diversity, particularly the effect of elevation on species richness and species composition, and 2) to generate predictive scenarios to understand the effect of climate changes on the geographic distribution of these highland specialists. Our predictive distributional scenarios were based on a warming elevational progression of 0.95°C/100 m for a 100 years’ time frame. Our models predicted a massive loss of suitable environments for choeronycterine bats of more than 65% in the current distribution of 8 of the 17 recognized choeronycterine species by 2110. Finally, geographic information systems also were applied to identify areas of priority of conservation for the most affected choeronycterine species.

The following posters (7 - 12) are to be considered for the Clyde Jones Award.

Poster 7

**SMALL MAMMAL BIODIVERSITY AND PHYLOGEOGRAPHY ACROSS THE KYRGYZ REPUBLIC**

R. M. Duplechin<sup>1</sup>, B. J. Briggs<sup>2</sup>, P. A. Larsen<sup>1</sup>, Cibele G. Sotero-Caio<sup>1</sup>, J. P. Carrera<sup>1</sup>, J. Hay<sup>2</sup>, R. Hewson<sup>3</sup>, A. T. Junushov<sup>4</sup>, O. N. Gavrilova<sup>5</sup>, I. Breininger<sup>5</sup>, C. J. Phillips<sup>1</sup>, and R. J. Baker<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Department of Microbiology and Witebsky Center for Microbial Pathogenesis and Immunology, University at Buffalo, New York, <sup>3</sup>Public Health Affairs, Centre for Applied Microbiology and Research, Health Protection Agency, UK, <sup>4</sup>Biotechnology Institute, National Academy of Sciences of the Kyrgyz Republic, <sup>5</sup>Republican Center of Quarantine and Especially Dangerous Infections, Ministry of Healthcare of the Kyrgyz Republic (ryan.duplechin@ttu.edu)

The Kyrgyz Republic (Kyrgyzstan) is a small mountainous country located just west of China in Central Asia. Relatively little is known about the evolutionary history, genetic diversity, or associated zoonotic viruses of the small mammal species distributed throughout Kyrgyzstan. Furthermore, it is likely that mammalian species diversity within the country is underestimated. With this in mind, we conducted two expeditions to Kyrgyzstan in 2007 and 2009 with the following objectives: 1) collect and prepare voucher specimens and tissues of small mammals representative of the country, 2) generate DNA sequence data from all specimens collected to provide a molecular identification and phylogenetic perspective of species diversity within the country, and 3) screen associated tissue samples for zoonotic diseases. To date, we have archived vouchers and associated tissues of approximately 370 specimens from 16 species of rodents and shrews. Our collecting efforts have been staged across the Western, Northern, and Eastern regions of the country, in and among a variety of elevations, habitats, and climates. Here we present phylogeographic data from 5 species of rodents and discuss the potential for unrecognized species within the genera *Alticola* and *Meriones*. In addition, our team reports the establishment of a reservoir species relationship for Tick-borne Encephalitis and the Himalayan field mouse *Apodemus pallipes*.

Poster 8

**MICROSATELLITE VARIATION IN FOREST AND GRASSLAND *PEROMYSCUS MANICULATUS***

Ruth Litwinowicz<sup>1</sup>, Scott E. Chirhart<sup>1</sup>, and Ira F. Greenbaum<sup>2</sup>, <sup>1</sup>Department of Biology, Centenary College of Louisiana, <sup>2</sup>Department of Biology, Texas A&M University (rlitwino@my.centenary.edu)

*Peromyscus maniculatus* has historically been divided into two major morphologic and ecologic types, each of which comprises numerous subspecies. Forest forms with long tails, large ears, and large hind feet range through the Appalachian Mountains from northern Georgia northward to Labrador, across the continent in Canadian forests, and southward through the Rocky Mountains and the mountains and coast of the Pacific Northwest. Grassland deer mice with short tails, small ears, and small hind feet generally occupy the prairies and grasslands of the continental interior and extend into the deserts of the western and southwestern United States. In areas where these forms meet, particularly in the northwestern and eastern portions of the range, they generally maintain morphological and ecological distinction. However, distributional complexities, inferences of intergradation in the north-central portion of the range, and the lack of data establishing discrete character differences have complicated resolution of the taxonomic and systematic status of these

forms. Initial mtDNA and chromosomal data, however, support the hypothesis that the central-grassland and eastern-forest deer mice represent separate phylogenetic lineages. To further evaluate the specific validity and evolutionary history of these two forms, we assessed sequence variation at the ND3/ND4L/ND4 region of the mtDNA and 9 dinucleotide microsatellite markers for 29 individuals from four localities of the eastern forest form and for 20 individuals from a single locality of the central grassland form. Neighbor-joining and Fitch-Margoliash analyses of three estimates of microsatellite genetic distance and Neighbor-joining and Parsimony analyses of the mtDNA data yielded entirely concordant results separating the forest from grassland deer mice. These and the previously reported mtDNA and chromosomal data support the hypothesis that northeastern *P. maniculatus* contains at least two species.

Poster 9

### **COMPARATIVE PHYLOGEOGRAPHY OF TWO SPECIES OF *PEROMYSCUS* IN OKLAHOMA, ARKANSAS, AND TEXAS**

Tiffany L. Cloud, Kimberly L. Koppari, Michelle L. Haynie, and Gregory M. Wilson,  
Department of Biology, University of Central Oklahoma (tcloud3@uco.edu)

Phylogeographic theory has been used to assess processes governing geographic distributions and population genetic structure for a diverse array of species. It combines multiple disciplines, such as ecology, molecular biology, biogeography, population genetics, and historic geography. Most of these studies have focused on intraspecific relationships of a single species over a broad geographic range using only data from mitochondrial markers. Few studies have compared gene genealogies from multiple, co-distributed species, and even fewer have incorporated nuclear markers. The white-footed mouse (*Peromyscus leucopus*) and the deer mouse (*P. maniculatus*) occur sympatrically throughout Oklahoma and adjacent states. Both of these species are considered habitat generalists and are distributed fairly continuously throughout their range. Although both species are more widespread ecologically compared to other species of mice in North America, *P. leucopus* prefers woody or brushy habitats, whereas *P. maniculatus* predominately resides in grass or prairie habitats. In order to investigate the contemporary and historic population genetic and phylogeographic structure of these co-distributed species, I am utilizing microsatellite data as well as DNA sequence data from the control region of the mitochondrial genome (mtDNA). I hypothesize that the population genetic structure of *P. leucopus* and *P. maniculatus* will exhibit similar population genetic structure throughout Oklahoma and adjacent states. By incorporating maternally-inherited (mtDNA sequence data) and bi-parentally inherited (microsatellites) markers, I will be able to better understand how each species has responded to both contemporary and historic factors which occurred both during and following the Pleistocene.

Poster 10

### **POPULATION GENETIC STRUCTURE OF *MYOTIS VELIFER* AS INFERED BY MITOCHONDRIAL SEQUENCE DATA IN NORTHWESTERN OKLAHOMA DURING WINTER MONTHS**

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The cave myotis, *Myotis velifer*, is an insectivorous bat which occurs in caves and man-made structures from Kansas southward through Mexico to Honduras. Individuals that comprise populations in Kansas and Texas appear to be permanent residents, hibernating in caves during the winter. Both sexes of the cave myotis hibernate in the same localities in the

winter, but disperse to separate maternity and bachelor roosting sites during the spring and summer. Previous studies conducted at caves in northwestern Oklahoma reported that cave myotis begin arriving in their hibernaculum in October and continued to increase in number until December when population densities reached a high. These studies also indicate that after December, densities of bats begin to decrease due to relocation of individuals to other cave localities for the remainder of the winter. The goal of our study is to examine if the movement patterns of *M. velifer* among cave localities in the late fall, winter, and early spring impacts the population genetic structure of bats within several caves in northwestern Oklahoma. Wing punches have been collected from 330 *M. velifer* from November 2007 to January 2009. To investigate population genetic structure among cave localities, we amplified the left domain of the control region of the mitochondrial genome (mtDNA). Preliminary results reveal high genetic diversity within each cave locality. In addition, there does not appear to be significant population genetic structure of *M. velifer* among caves in northwestern Oklahoma from late fall to early spring.

Poster 11

**FIVE NEW COUNTY RECORDS OF BATS (VESPERTILIONIDAE AND MOLOSSIDAE) IN TEXAS IDENTIFIED USING MOLECULAR AND MORPHOLOGICAL TECHNIQUES**

T. Marie Tipps<sup>1</sup>, Loren K. Ammerman<sup>1</sup>, and Bonny Mayes<sup>2</sup>, <sup>1</sup>Angelo State University, <sup>2</sup>Texas Department of Health (ttipps@angelo.edu)

Bats from around the state have been submitted to the Texas Department of Health to be tested for the rabies virus for many years. These specimens have been valuable as a source of information on bat distributions and numerous county records have been reported using these bats. In some cases, however, the bat carcasses are damaged such that diagnostic features are unrecognizable. To positively identify problematic material from 1996-2009, we sequenced the cytochrome-*b* mitochondrial gene and compared to sequences on GenBank using BLAST. A combination of molecular and morphological data confirmed the following county records: *Myotis yumanensis* from Tarrant County, *M. austroriparius* from Smith and Dallas counties, *M. californicus* from Hidalgo County, and *Nyctinomops macrotis* from Hockley County. All specimens were deposited into the Angelo State Natural History Collection. We conclude that molecular identification is a feasible technique for confirmation of species, even for bats that were submitted over a decade ago. However, unusual records of occurrence such as *M. yumanensis* in Tarrant County, although plausible, are not probable. Even with molecular confirmation of species identification, the absence of detailed locality information and lack of information on the circumstances associated with each specimen requires that records based on bats submitted to the Texas Department of Health be interpreted cautiously. Future captures could validate these records and change our understanding of bat distributions that are not evident today.

Poster 12

**PHYLOGENY, EVOLUTION, AND SYSTEMATICS OF THE SOUTH AMERICAN GENUS *MICROCAVIA* (RODENTIA: CAVIDAE)**

Harshad S. Mahadeshwar<sup>1</sup>, Jonathan L. Dunn<sup>2</sup>, and Jorge Salazar-Bravo<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Museum of Southwestern Biology, University of New Mexico (harshad.mahadeshwar@ttu.edu)

Along with guinea pigs, yellow-toothed caviies, and maras, mountain caviies (genus *Microcavia*) are a distinctive element of the South American mammal fauna. Species of mountain caviies play an important role on the ecology of several species and they are even

hunted by people for use as food. Currently, there are 3 extant species which is in contrast with a higher diversity back in the Pleistocene (at least five extinct species). Although the diversity of current forms is small, there is still disagreement as to the phylogenetic relationships among its species. Therefore, the goal of this study is to address the phylogenetic relationships among these 3 species based on a battery of nuclear and mitochondrial loci. Representatives of the 3 species of *Microcavia* (*M. niata*, *M. shiptoni*, and *M. australis*) and outgroups (*Cavia*, *Galea*, *Dolichotis*, *Kerodon* and *Hydrochoeris*) were used in our analyses. The nuclear loci including: exon of recombination activating gene 2 (RAG2, 444bp), exon #10 of the growth hormone receptor (GHR, 805bp), and the intron 7 of the Beta Fibrinogen (BFG, ca. 780bp). The mitochondrial loci included portions of the mitochondrial 12S mitochondrial ribosomal DNA (12SmtrDNA, 936bp) and the complete cytochrome b gene (CytB, 1140bp). These data was analyzed with BEST v2.3 (Bayesian Estimation of Species Trees) and a phylogeny of morphological data mapped on the species tree generated with these analyses. We discuss these results in light of the evolution of the Andes and the diversification of Caviid rodents.

*The following posters (13 - 14) are not competing for an award.*

Poster 13

**EVALUATION OF A *NEOTOMA MICROPUS*/*NEOTOMA FLORIDANA* HYBRID ZONE: TWENTY YEARS LATER**

Ethan B. Rowell and Michelle L. Haynie, Department of Biology, University of Central Oklahoma (erowell4@uco.edu)

The Southern Plains Woodrat (*Neotoma micropus*) and the Eastern Woodrat (*Neotoma floridana*) hybridize under natural conditions. An area just outside the town of Seiling, Oklahoma, provides a suitable environment in which these two species can produce hybridized individuals. Early hybridization studies on *N. micropus* and *N. floridana* have been done in this area using morphological data to identify hybrid individuals. Not until recently, with a study done by Bradley et al. (2007), have genetic markers been used to classify hybridization in the Seiling hybrid zone. Bradley et al. (2007) found a high degree of hybridization (26.2%) in samples collected in 1988, using restriction enzyme data. The aim of this current project is to re-evaluate the hybrid area near the town of Seiling, Oklahoma, and to determine any changes within the hybrid zone that may have occurred during the last 20 years. To do this, specimens of both *N. micropus* and *N. floridana* are being collected and analyzed using microsatellite markers.

Poster 14

**DISTRIBUTION OF THE MULE DEER (*ODOCOILEUS HEMIONUS*) IN OKLAHOMA: AN ANALYSIS OF HARVEST DATA**

Paul D. Wade and Brandon K. McDonald, Department of Biological Sciences, Cameron University (pwade@cableone.net)

The distribution of the mule deer (*Odocoileus hemionus*) in the southern Great Plains has been well documented. However, few specimen records exist for Oklahoma. The purpose of our study was to better estimate the current distribution of mule deer in Oklahoma. We surveyed eight years of harvest records (2001-2008) from 93 Oklahoma Department of Wildlife Conservation (ODWC) harvest regions in western Oklahoma. Mule deer were reported from 37 of the harvest regions (40%). Consistent harvest numbers among years for all regions indicate stable populations or steady immigration from permanent populations in the panhandle regions of Texas and Oklahoma. Abundance of mule deer

reports followed a west to east gradient, with the highest abundance in the western most regions. This gradient of abundance was associated with the distribution of optimal and marginal habitats for the species. Our results give an approximated range boundary and help to identify specific regions where future research efforts might add to our knowledge of the species.



## POSTERS AT-A-GLANCE

- 1 - MOLECULAR SYSTEMATICS OF *GEOMYS* BASED ON DNA SEQUENCES FROM THE PROTEIN CODING THE ALCOHOL DEHYDROGENASE GENE (*ADH-1*) Erica Vargas
- 2 - SAM HOUSTON NATIONAL FOREST, TEXAS: TO NET OR NOT TO NET? Anica Debelica
- 3 - BITE FORCE ANALYSIS OF FOREST INTERIOR INSECTIVOROUS BATS Juliana Senawi
- 4 - EFFECT OF VEGETATION ALTERATION ON SMALL MAMMAL DIVERSITY IN CALLAHAN COUNTY, TEXAS Rachel Ames
- 5 - MECHANISMS OF BOUNDARY RESPONSES IN SMALL MAMMALS — PRELIMINARY FINDINGS Nicholas S. Green
- 6 - CHOERONYCTERINE BATS AS A MODEL TO STUDY THE EFFECT OF GLOBAL CLIMATE CHANGE AMONG MAMMALS Hugo Mantilla-Meluk
- 7 - SMALL MAMMAL BIODIVERSITY AND PHYLOGEOGRAPHY ACROSS THE KYRGYZ REPUBLIC R. M. Duplechin
- 8 - MICROSATELLITE VARIATION IN FOREST AND GRASSLAND *PEROMYSCUS MANICULATUS* Ruth Litwinowicz
- 9 - COMPARATIVE PHYLOGEOGRAPHY OF TWO SPECIES OF *PEROMYSCUS* IN OKLAHOMA, ARKANSAS, AND TEXAS Tiffany L. Cloud
- 10 - POPULATION GENETIC STRUCTRE OF *MYOTIS VELIFER* AS INFERED BY MITOCHONDRIAL SEQUENCE DATA IN NORTHWESTERN OKLAHOMA DURING WINTER MONTHS K.L. Koppari
- 11 - FIVE NEW COUNTY RECORDS OF BATS (VESPRTLIONIDAE AND MOLOSSIDAE) IN TEXAS IDENTIFIED USING MOLECULAR AND MORPHOLOGICAL TECHNIQUES T. Marie Tipps
- 12 - PHYLOGENY, EVOLUTION, AND SYSTEMATICS OF THE SOUTH AMERICAN GENUS *MICROCAVIA* (RODENTIA: CAVIDAE) Harshad S.Mahadeshwar
- 13 - EVALUATION OF A *NEOTOMA MICROPUS/NEOTOMA FLORIDANA* HYBRID ZONE: TWENTY YEARS LATER Ethan B. Rowell
- 14 - DISTRIBUTION OF THE MULE DEER (*ODOCOILEUS HEMIONUS*) IN OKLAHOMA: AN ANALYSIS OF HARVEST DATA Paul D. Wade

## Oral Presentation Abstracts

### Paper 1 – **NUCLEAR DNA PHYLOGEOGRAPHY OF THE PALLID BAT (*ANTROZOUS PALLIDUS*)**

Jeremy E. Wilkinson, Justin B. Lack, and Ronald A. Van Den Bussche, Department of Zoology, Oklahoma State University (jeremy.wilkinson@okstate.edu)

Male-biased dispersal with female philopatry is a common pattern for many mammalian taxa. Due to the maternal inheritance of mtDNA, biparentally inherited nuclear markers are necessary to obtain correct estimates of population structure and gene flow. The pallid bat (*Antrozous pallidus*) exhibits a relatively continuous distribution across arid western North America, and a previous mtDNA study suggested little gene flow among populations and identified 3 distinct phylogroups. We examined population structure of *A. pallidus* using amplified fragment length polymorphism (AFLP) in 187 individuals from 29 localities across the distribution of the species. Eight primer pairs identified 797 polymorphic loci. All analyses indicated that populations in California and British Columbia were distinct from each other and all other populations. *A. pallidus* from the Baja peninsula were also distinct, but cluster analysis indicated gene flow has been occurring with more eastern populations. The pallid bat appears to be characterized by male-mediated dispersal and gene flow, while females are largely philopatric. The overall pattern is indicative of isolation by distance and does not support the presence of distinct phylogroups, suggesting significant gene flow has been occurring since populations diverged during Pliocene desert formation and mountain building.

### Paper 2 – **THE GENETIC DIVERSITY OF STRIPED SKUNK (*MEPHITIS MEPHITIS*) POPULATIONS THROUGHOUT THE CENTRAL UNITED STATES**

Kelly A. Smith and Michelle L. Haynie, University of Central Oklahoma (Ksmith96@uco.edu)

The striped skunk (*Mephitis mephitis*) is distributed throughout southern Canada, the United States and northern Mexico, and is one of the main vectors of the rabies virus. Skunks carry 3 known rabies variants: one in the south central United States, one in the north central United States, and one in California. Striped skunks have been the focus of several rabies investigations, but few genetic studies have been performed on this species and none have looked at the potential for genetic subspecies. The immediate goal of this project is to determine levels of genetic variation within striped skunk populations found in the geographic distribution of the south central strain of rabies in the United States. Currently, skunks are being sampled from OK, KS, NE, MO, TX, NM, ND, WY, and AZ. To determine levels of genetic variation, the D-loop portion of the control region of the maternally-inherited mitochondrial genome is being amplified. Preliminary data indicates two distinct haplotype groups among samples from Oklahoma, Kansas, New Mexico, and Texas. This research is only the third study of genetic variation within striped skunk populations and the first to be conducted over a wide geographic range (central United States).

Paper 3 – **GENETIC CHARACTERIZATION AND NATURAL HOST RELATIONSHIPS OF MULESHOE VIRUS IN NORTH TEXAS AND WESTERN OKLAHOMA**

Allie P. Clinton<sup>1</sup>, Robert D. Bradley<sup>1,2</sup>, Mary Louise Milazzo<sup>3</sup>, Charles F. Fulhorst<sup>3</sup>,  
<sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Museum of Texas Tech University, <sup>3</sup>Department of Pathology, University of Texas Medical Branch (allie.clinton@ttu.edu)

Hantavirus pulmonary syndrome (HPS) is a rodent-borne zoonosis caused by certain members of the virus family *Bunyaviridae*, genus *Hantavirus*. Specific members of the rodent family Cricetidae are the principal hosts of the hantaviruses known to cause HPS. The etiological agents of HPS in North America are Bayou virus (BAYV), Black Creek Canal virus (BCCV), Choclo virus (CHOV), New York virus (NYV), and Sin Nombre virus (SNV). Other hantaviruses native to North America include Muleshoe virus (MULV). Our knowledge of the natural hosts relationships of this virus is limited to the detection of MULV RNA in two hispid cotton rats (*Sigmodon hispidus*) captured in 1995 in northern Texas. The purpose of this study was to extend our knowledge of the natural host relationships of MULV and define better the phylogenetic relationship of MULV to other hantaviruses. Four hundred twenty-six (426) cricetid rodents and 50 heteromyid rodents were captured in the summer of 2009 at 2 localities in northern Texas and 3 localities in western Oklahoma. Antibodies (IgG) to a hantavirus were found in blood samples from hispid cotton rats captured in Texas and white-footed mice (*Peromyscus leucopus*), a southern plains woodrat (*Neotoma micropus*), and hispid cotton rats captured in Oklahoma. The results of assays for hantavirus RNA in tissues from the antibody-positive rodents will be presented.

Paper 4 – **MOUNTAIN LION GENETIC STRUCTURE, GENE FLOW, AND GENETIC DIVERSITY IN TEXAS**

Joseph D. Holbrook<sup>1</sup>, Randy W. DeYoung<sup>1</sup>, Michael E. Tewes<sup>1</sup>, and John H. Young<sup>2</sup>,  
<sup>1</sup>Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville, <sup>2</sup> Texas Parks and Wildlife Department (joseph.holbrook@students.tamuk.edu)

Mountain lion (*Puma concolor*) demographic and genetic information in Texas is sparse, hindering the development of management strategies. A comprehensive management plan for mountain lions in Texas would consider genetically distinct management units as well as the genetic and demographic properties of the management units. Our objectives were to genetically identify mountain lion subpopulations across the Texas landscape, quantify the differentiation among subpopulations, and estimate genetic diversity within each subpopulation. We sampled 176 mountain lions during 1995-2009 throughout West and South Texas and genotyped the samples at 12 microsatellite DNA loci. We characterized genetic structure and diversity based on fixation indices ( $F_{IS}$ ,  $F_{ST}$ ), Bayesian clustering, and genetic diversity ( $H_E$ ) indices. We observed a positive  $F_{IS}$  (global  $F_{IS} = 0.039$ ,  $SE = 0.026$ ) and  $F_{ST}$  (global  $F_{ST} = 0.111$ ,  $SE = 0.016$ ), suggesting population subdivision within and throughout West and South Texas. Results from the Bayesian clustering algorithm and pairwise  $F_{ST}$  indicated 3 differentiated subpopulations, 2 subpopulations in West Texas (W. TX#1 – W. TX#2, pairwise  $F_{ST} = 0.064$ ) and 1 subpopulation in South Texas (S. TX – W. TX#1, pairwise  $F_{ST} = 0.159$ ; S. TX – W. TX#2, pairwise  $F_{ST} = 0.221$ ). All subpopulations exhibited moderate levels of genetic diversity ( $H_E = 0.357 - 0.538$ ) relative to an averaged sample of North American mountain lions. Our findings indicate strong genetic differentiation between West Texas and South Texas, and suggest restricted gene flow among all subpopulations. The 2 subpopulations identified in West Texas exhibited substantial spatial overlap, and we speculate West Texas might be functioning as a

population contact zone. Therefore, population boundaries of mountain lions in West Texas may extend beyond state borders. We are collecting additional samples to substantiate this hypothesis.

#### Paper 5 – **PARAPHYLY AND SPECIATION WITHIN BULLDOG BATS (CHIROPTERA: NOCTILIONIDAE)**

Faisal A. Anwarali Khan<sup>1</sup>, C. Miguel Pinto<sup>2</sup>, and Robert J. Baker<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Department of Mammalogy, American Museum of Natural History (faisal.anwarali@ttu.edu)

Assessing species' boundaries or phylogroups using multifaceted approaches from independent genetic markers would be an appropriate method to identify independent evolutionary units. Under this framework, intrageneric relationship and species limits within Bulldog bats, genus *Noctilio*, with an emphasis on *Noctilio albiventris*, were explored using 4 datasets: cytochrome-*b* (*cyt-b*), cytochrome c oxidase-I (COI), Amplified Fragment Length Polymorphisms (AFLPs), and morphology. We genetically analyzed 51 samples of *Noctilio* from two currently recognized species: *N. albiventris* and *N. leporinus*. In *cyt-b* and COI gene phylogenetic analyses, *N. albiventris* form a paraphyletic clade, containing the gigantic species *N. leporinus*. Moreover, 5 monophyletic clades were documented, 4 associated with *N. albiventris* with > 5% genetic distance and a single clade for *N. leporinus*. Clades within *N. albiventris* are morphologically indistinguishable but they mostly have different geographic distributions, matching with all the recognized subspecies in *N. albiventris*: *N. a. minor*, *N. a. affinis*, *N. a. albiventris*, and *N. a. cabrerai*. Although we recovered all the clades from mitochondrial DNA in AFLP analysis (nuclear DNA), there are two individuals from different clades that were positioned differently. These individuals are from Guyana. These localities lie in the periphery of the geographic range of subspecies suggesting that these sites may represent a contact zone with gene flow between different maternal lineages. Genetic divergences in the mitochondrial genes (>5%) that are congruent with geographic distribution, and the paraphyly of *N. albiventris* (sensu lato) suggest that currently recognized subspecies within *N. albiventris* should be recognized at the specific level.

#### Paper 6 – **IDENTIFYING THE CONFOUNDING FACTORS IN RESOLVING PHYLOGENETIC RELATIONSHIPS IN VESPERTILIONIDAE**

Justin B. Lack and Ronald A. Van Den Bussche, Department of Zoology, Oklahoma State University (justin.lack@okstate.edu)

Resolving phylogenetic relationships within Vespertilionidae have been difficult, with large datasets (>100 taxa, >7 kilobases) resolving some portions of the phylogeny, but leaving intertribal relationships within the Vespertilioninae unresolved. As a result, the evolutionary history of the most speciose chiropteran family is largely unknown. The presence of short internodes followed by long terminal branches relative to other chiropteran phylogenies suggests evolutionary rates of DNA substitution and lineage diversification may be inhibiting phylogenetic resolution. To test this hypothesis, we obtained sequences of the mtDNA 12s rRNA, tRNA<sup>VAL</sup>, and 16s rRNA as well as the nuclear exon RAG2, resulting in over 3 kilobases of digenomic DNA sequence data for representatives of all subfamilies and tribes within Vespertilionidae and Phyllostomidae, a family of bats of similar age (~30 mya) as Vespertilionidae. Analyses revealed substitution rates for Vespertilionidae were significantly higher than Phyllostomidae, with the majority of fast-evolving lineages found within Vespertilioninae. Cladogenesis analyses characterized the vespertilionid radiation as one compressed toward the root, with a rapid initial diversification, while the phyllostomid diversification was much more gradual. We suggest ecological differences between tropical

and temperate environments may have influenced diversification rates for Vespertilionidae and Phyllostomidae.

**Paper 7 – PHYLOGENETIC RELATIONSHIPS WITHIN THE NEOTOMINAE BASED ON COMBINED MITOCHONDRIAL AND NUCLEAR DATA SETS**

Megan S. Corley<sup>1</sup>, Roy N. Platt<sup>2</sup>, Brian R. Amman<sup>3</sup>, and Robert D. Bradley<sup>1,4</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Department of Biological Sciences, Mississippi State University, <sup>3</sup>Centers for Disease Control, <sup>4</sup>Natural Sciences Research Laboratory, Museum of Texas Tech University (megan.corley@ttu.edu)

Phylogenetic relationships and taxonomy of the North American neotomine-peromyscine rodents have been controversial for many years. There have been various arguments regarding the number of tribes within this speciose group of rodents as well as the relationships of genera in each tribe. The goal of this study is to use molecular data to address the issue of how many tribes should be recognized within the subfamily Neotominae. Most studies provided support for 4 tribes: Baiomyini, Neotomini, Peromyscini, and Tylomyini, some have suggested the placement of *Ochrotomys* into a separate tribe, Ochrotomyini, whereas others have used Reithrodontomyini to represent the “old” Peromyscini. More recently, 5 tribes, Baiomyini, Neotomini, Ochrotomyini, Peromyscini, and Reithrodontomyini, have been recognized based on molecular data. Additionally, the controversial relationships of genera within each tribe have contributed to the various taxonomic arrangements. Combined mitochondrial and nuclear DNA sequences of 19 genera of neotomine-peromyscine rodents, including the cytochrome *b* gene, intron 7 of the  $\beta$ -fibrinogen gene, exon 6 of the dentin matrix protein 1 gene, intron 2 of the alcohol dehydrogenase gene, exon 1 of the interphotoreceptor retinoid-binding protein gene, and exon 10 of the growth hormone receptor gene were analyzed to create a phylogeny. Our preliminary data suggests that there may be 5 to 6 tribes that should be recognized within this subfamily of rodents.

**Paper 8 – GENETIC VARIATION AND PHENOTYPIC EVOLUTION IN THE ANTILLEAN TREE BAT (*ARDOPS NICHOLLSI*)**

Roxanne J. Larsen<sup>1</sup>, Peter A. Larsen<sup>1</sup>, Caleb D. Phillips<sup>1</sup>, Hugh H. Genoways<sup>2</sup>, Gary G. Kwiecinski<sup>3</sup>, Scott C. Pedersen<sup>4</sup>, and Robert J. Baker<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>University of Nebraska State Museum, <sup>3</sup>Biology Department, University of Scranton, PA, <sup>4</sup>Department of Biology/Microbiology, South Dakota State University (roxy.larsen@ttu.edu)

Intraspecific phenotypic variation is a product of many forces and mechanisms, involving genetics and the environment. To better understand the processes underlying the tempo of phenotypic evolution in allopatry, we analyzed multiple molecular datasets from *Ardops nichollsi*, a recently evolved species of phyllostomid bat (i.e., the most recent common ancestor of the genus occurred ~ 1.8 million years ago). Despite its recent origin in the family Phyllostomidae, the only member of this monotypic genus is comprised of five subspecies: *A. n. montserratensis*, *A. n. annectens*, *A. n. nichollsi*, *A. n. koopmani* and *A. n. luciae*. Previous work has suggested the subspecies of this Caribbean endemic vary in size with respect to the islands they inhabit. Our initial phylogenetic analysis indicates a distinct separation between the northern and southern subspecies. Thus, the objectives of the current study are: 1) to test the morphological taxonomic arrangement against molecular datasets, 2) to compare and contrast mitochondrial and nuclear datasets, and 3) to examine the processes

underlying evolution and subspeciation in an insular endemic. In the future, we will use morphometric, genetic and environmental datasets to elucidate important evolutionary questions regarding the tempo of phenotypic evolution in allopatric island populations.

#### Paper 9 – **IS TRANSFERRIN-RECEPTOR 1 (TfR1) THE HOST RECEPTOR FOR NORTH AMERICAN ARENAVIRUSES?**

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Arenaviruses are rodent-borne RNA viruses associated with hemorrhagic fevers in humans. North American arenaviruses, hosted mostly by woodrats (genus *Neotoma*), are important zoonoses in the southwest United States and northern Mexico. Although there is often a specific association between a single principal host and a single arenavirus, multiple species of woodrats as well as the California deer mouse (*Peromyscus californicus*) have been shown to acquire the virus through interactions with a principal host, and some woodrats are known to host multiple arenaviruses. Recently, the transferrin-receptor 1 gene (TfR1) was identified as the cellular receptor used by South American clade B arenaviruses, with all host species possessing a tyrosine at residue 211 and amino acid residues 208-212 of the human TfR1 gene being implicated as a determinant of host specificity. The North American arenaviruses are most closely related to clade B viruses and therefore may use the same receptor. To test this hypothesis, DNA sequences from the TfR1 genes were obtained from 14 species representing virus-positive individuals, virus-negative individuals from host species, and species not known to carry an arenavirus. Sequence data suggests that all woodrats as well as *P. californicus* are highly conserved at residues 208-212, regardless of the viral status of the woodrat. Additionally, although all host species were characterized by Tyr211, this did not appear to be strictly correlated with arenavirus infection as this was present in species which are not known to carry arenaviruses. These results suggest that although amino acids 208-212 may be important for arenavirus entry, North American arenaviruses may not use the same mechanism of cell recognition and entry used by clade B viruses, and other ecological or genetic factors may play a role.

#### Paper 10 – **MOLECULAR EVIDENCE FOR HYBRIDIZATION BETWEEN NEOTOMA MICROPUS AND N. FLORIDANA**

Matthew R. Mauldin<sup>1</sup>, J. Delton Hanson<sup>1</sup>, Robert J. Baker<sup>1,2</sup>, and Robert D. Bradley<sup>1,2</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Museum of Texas Tech University (matt.mauldin@ttu.edu)

One hundred three individual woodrats were collected from a putative hybrid zone between *Neotoma floridana* and *N. micropus*. Three genetic markers, 1 mitochondrial (Cytochrome-*b* gene) and 2 nuclear (Alcohol Dehydrogenase, and Beta Fibrinogen) were used to develop a composite genotype for each individual to ascertain genetic identification of specimens and for detection of hybridization. Composite genotypes indicated 13 individuals were identified as parental *N. micropus*, 85 as hybrids, and 5 as parental *N. floridana*. The genetic data revealed a high frequency of hybridization (83%) and that hybrids were formed by bidirectional matings of the 2 parental types as well as matings involving hybrid individuals. Given the high frequency of hybrid individuals it would appear that hybrids are “superior” to parental types and that the hybrid zone is being maintained by either the Hybrid-Superiority Model or the Hybrid-Equilibrium Model.

## Paper 11 – PATTERNS OF DISTRIBUTION OF THE ENDEMIC MAMMALS IN ECUADOR

Juan P. Carrera-E. and Hugo Mantilla-Meluk, Department of Biological Sciences and the Museum of Texas Tech University (juan.p.carrera@ttu.edu)

Ecuador is categorized as one of the megadiverse countries showing high level of endemism for several taxa. The most recent checklist of mammals recognized 382 species including 38 endemics. In spite of their importance, no formal analysis has been conducted on the historical and geographic determinants that explain endemic species distribution inside the Ecuadorian territory. The main goal for this study was to identify the geographic affinities among Ecuadorian endemic mammalian records and to analyze the spatial relationship between endemic sampling localities and the National System of Protected Areas (SNAP). We analyzed public and museum records collected from 1859-2004, housed in 24 museums abroad. Endemic records were georeferenced and mapped. A polygon layer representing eight bioregions in Ecuador was used to determine the ecogeographic origin of the samples. To verify the spatial relationship between endemic records and conservation areas, a polygon layer representing SNAP, was overlaid using ArcGIS 9.3. Of the 23,000 mammalian records analyzed, we recovered 409 endemic records, containing only 265 with confirmed localities in our samples. The majority of our endemic records were located in the Andean region; a sample bias is suggested by the presence of 99 records in areas surrounding Quito. The majority of endemic species are rodents and most of the records come from the highlands. Surprisingly, with the exception of Galapagos, only 5 records were collected inside National Protected Areas. In general, these results position the whole country as a main hotspot for studying and conserving endemic species.

## Paper 12 – MODELING TRANSLOCATION OF OCELOT, *LEOPARDUS PARDALIS*, FROM MEXICO TO TEXAS

William C. Stasey, Michael E. Tewes, and Arturo Caso, Feline Research Center, Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville (wcstasey@hotmail.com)

Extant ocelot (*Leopardus pardalis*) populations in the United States of America (U.S.) are vulnerable to extinction. Currently, there are only two known geographically isolated populations in the U.S., both occurring in extreme southern Texas located at Laguna Atascosa National Wildlife Refuge and a private ranch in Willacy County. The Ocelot Translocation Working Group has determined that translocation of ocelots into the Texas populations will be necessary to prevent local extinction in the U.S. Using remote sensing cameras we estimated the size of a potential source ocelot population in the Sierra Tamaulipas, Tamaulipas, Mexico. We evaluated translocation scenarios of moving ocelots from Mexico into Texas using program VORTEX population viability analysis software. We estimated the minimum viable population size necessary to support annual removal of 4 female ocelot for 10 years.

## Paper 13 – SPECIES RICHNESS AND HABITAT HETEROGENEITY: ARE SPATIAL ANALYSES IMPORTANT?

J. Erin Fender<sup>1</sup>, Michael L. Kennedy<sup>2</sup>, Gary D. Schnell<sup>3</sup>, Cornelio Sánchez-Hernández<sup>4</sup>, María de Lourdes Romero-Almaraz<sup>5</sup>, Michael C. Wooten<sup>6</sup>, and Troy L. Best<sup>6</sup>, <sup>1</sup>Department of Wildlife and Fisheries Sciences, Texas A&M University, <sup>2</sup>Ecological Research Center and Department of Biology, The University of Memphis, <sup>3</sup>Sam Noble Oklahoma Museum of Natural History and Department of Zoology, University of Oklahoma, <sup>4</sup>Departamento de

Zoología, Instituto de Biología, Universidad Nacional Autónoma de México, <sup>5</sup>Escuinapa No. 92 bis. Col. Pedregal de Santo Domingo, C.P. 04360, México, D.F., México, <sup>6</sup>Department of Biological Sciences, Auburn University (erinfender@tamu.edu)

The prediction that habitat heterogeneity and species richness of small mammals are associated was tested at three spatial scales (0.04-ha, 0.25-ha, and 1-ha) in the tropical dry-forest region of Colima, Mexico. This location, within the Mesoamerican biodiversity hotspot, was sampled during winters of 2003-2007. Sampling was conducted (in total) on 25 trapping grids. Each grid was established with an arboreal and ground-level trap at all trapping stations using a 10m x 10m design at each level, which resulted in 200 traps per grid. Five grids were trapped annually for an average of 7 nights during each sampling session. Collectively, there were 40,000 trap-nights (1 trap night = 1 trap set for 1 night). Species richness at each spatial scale was examined in relation to 14 vertical or horizontal structure-based indicators of the heterogeneity of habitats recorded at each trap site. Data were examined using non-parametric multiplicative regression (NPMR). In total, 17 species were found within the region studied. The best fitting NPMR model ( $xR^2 = 0.5131$ ) occurred at the 1-ha scale. This model showed that species richness was greatest when there was moderate vegetation in the lower strata of habitats and when percent bare ground was near 0.0%. Also, inverse relationships with the average distance to nearest tree and percent of dead wood on the ground were observed with species richness. Results verified spatial scale as a factor in understanding the relationships between habitat heterogeneity and species richness.

#### **Paper 14 – RESPONSE OF SMALL MAMMALS TO CHANGES IN PRECIPITATION AND FIRE IN SHORTGRASS PRAIRIE OF THE TEXAS PANHANDLE**

Whitney J. Priesmeyer and Raymond S. Matlack, Life, Earth, and Environmental Science, West Texas A&M University (wjpriesmeyer1@buffs.wtamu.edu)

Cross Bar Cooperative Management Area (CMA) is a 4,856 ha shortgrass prairie that has been heavily invaded by mesquite and cholla because of previous land management, and is similar to much of the private land between the Canadian River Breaks. We began sampling the small mammals at Cross Bar in 2004 as part of an inventory in association with a large-scale, replicated study of the influence of fire and fire frequency on small mammals in shortgrass prairie. The research site was organized using a randomized block design consisting of 9 separate units. These units are composed of 3 replicates of 3 fire treatments; 2-3 fire frequency, 4-6 year fire frequency, and >10 year fire frequency, each with 2, 15-station sampling transects within each replicate. We captured 835 individuals of 15 species of small mammals during 17,010 trap nights. Overall, capture success averaged 4.91 individuals/100 trap nights and reached a maximum of 12.80 individuals/100 trap nights following a period of heavy precipitation in fall 2005. Richness peaked in spring 2008 also following a prolonged wet period. The Cross Bar CMA is semi-arid and continental, and is classified as having low and irregularly distributed precipitation of about 35-48 cm per year. Similar to other arid environments, the small mammal community on the Cross Bar CMA appears to respond strongly to changes in precipitation. Abundance and biomass of all small mammals was positively correlated to the amount of precipitation recorded during the previous growing season regardless burning treatments. However, several species appeared to show a response to burn treatment which was noticeable only during the years of highest precipitation.



Paper 15 – **A PREDICTIVE MODEL OF NON-VOLANT SMALL MAMMAL ASSEMBLAGES IN EASTERN PARAGUAY ATLANTIC FOREST REMNANTS**  
Noé de la Sancha and Richard Strauss, Department of Biological Sciences, Texas Tech University (delasancha@msn.com)

The Atlantic Forest (AF) of South America, extending from northeastern Brazil to eastern Paraguay, is the second most diverse forest system in that continent, which has experience dramatic deforestation throughout its extent. Few studies have focused on Paraguayan taxa where deforestation is a new phenomenon. In this study, 19 Brazilian studies on non-volant small mammals, were used to develop a predictive model for number of species expected to be found in eastern Paraguay remnants using 2008 GIS data. Bi-variable statistical functions based on relationships between forest patch size, trapping effort, and number of species was developed to predict number of species. We compared linear vs quadratic models using an improvement-of-fit test which allowed us to assess validity of our quadratic model. Species richness was calculated for 46,435 forest patches varying from 0.1ha to 95,758ha. Initial forest patch sizes were reduced in intervals from 5%-75% and expected number of species were recalculate. Species estimates did not change between initial and reduced fragments when smaller than 670ha. Fragments between 14,000ha and 22,700ha showed the highest number of spp. Larger forest remnants showed initial species declines, but increase of number of species with increased deforestation. This study suggests that intermediately disturbed forest systems harbor more species than either a highly fragmented remnant or “pristine” forest. This type of study is valuable for future management of Paraguayan forests.

Paper 16 - **PHYLOGEOGRAPHIC IMPLICATIONS OF HYBRIDIZATION BETWEEN THE MEXICAN GROUND SQUIRREL (*SPERMOPHILUS MEXICANUS*) AND THE THIRTEEN-LINED GROUND SQUIRREL (*S. TRIDECIMLINEATUS*)**

Cody W. Thompson<sup>1</sup>, Frederick B. Stangl, Jr.<sup>2</sup>, and Robert D. Bradley<sup>1,3</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Biology Department, Midwestern State University, <sup>3</sup>Natural Science Research Laboratory, Museum of Texas Tech University (cody.thompson@ttu.edu)

The Mexican ground squirrel (*Spermophilus mexicanus*) and the thirteen-lined squirrel (*S. tridecemlineatus*) are reported to come in contact in areas ranging from southeastern New Mexico to the Texas Panhandle. Morphological identifications and verification of hybridization through laboratory crosses of parental-types has confirmed the potential for hybridization in the southeastern portion of the Texas Panhandle. However, recently analyzed cytochrome-*b* data has indicated a common mitochondrial genome among populations of *S. mexicanus* and *S. tridecemlineatus* found within Texas. Furthermore, genetic distances indicate deep divergence between these Texas animals and their respective populations of *S. mexicanus* and *S. tridecemlineatus* south and north of this region. This introgression and divergence suggests an ancient hybridization event, which has led to interspecific phylogeographic structuring between both species. In addition, intraspecific phylogeographic structuring does appear within all populations of *S. mexicanus* but is limited within *S. tridecemlineatus*, possibly due to incomplete sampling of all populations (subspecies). Therefore, populations outside of the hybrid zone may have been affected by events leading to the isolation and subsequent dispersal of populations during the hybridization event. To further understand these relationships, this study will

focus on the interspecific and intraspecific phylogeographic relationships between these species. Additional mitochondrial and nuclear data are being collected to further evaluate these relationships.

**Paper 17 - TAXONOMIC STATUS AND DISTRIBUTION OF THE *PEROMYSCUS BOYLI* GROUP (RODENTIA:CRICETIDAE) / ESTADO TAXONÓMICO Y DISTRIBUCIÓN DEL GRUPO DE ESPECIES *PEROMYSUCS BOYLII* (RODENTIA:CRICETIDAE)**

Nicté Ordóñez-Garza<sup>1</sup>, Ryan Duplechin<sup>1</sup>, Duke Rogers<sup>2</sup>, Elizabeth Arellano<sup>3</sup>, Francisco X. González-Cózatl<sup>3</sup>, C. William Kilpatrick<sup>5</sup>, and Robert D. Bradley<sup>1,4</sup>, <sup>1</sup>Biological Sciences Department, Texas Tech University, <sup>2</sup>Department of Biology, Brigham Young University, <sup>3</sup>Centro de Educación ambiental y educación, Universidad Autónoma del Estado de Morelos, <sup>4</sup>Museum of Texas Tech University, Natural Research Laboratory, <sup>5</sup>Department of Biology, University of Vermont (nicte.ordonez-garza@ttu.edu)

The genus *Peromyscus*, with approximately 56 species, is distributed widely throughout North and Central America arranged into 13 species groups. The *P. boylii* species group, with eight recognized species, is one of the most systematically complex in terms of defining phylogenetic relationships among members and delimiting species. Members of this group are distributed in Mexico, Southern US, and Central America. Since Osgood (1909) revision, this species group has been expanded to include several additional species. Most additions have been the result of more refined morphological analyses, availability of allozyme and karyotypic, and more recently, the advent of DNA sequence data. Currently, it is hypothesized that as many as four undescribed species may be present within this group.

**Paper 18 - MICROSATELLITE DATA OF *ARTIBEUS JAMAICENSIS* FROM THREE U.S. VIRGIN ISLANDS: IMPLICATIONS FOR EXPERIMENTAL DESIGN OF INTERISLAND MIGRATION**

Julie A. Parlos<sup>1</sup>, Gary G. Kwiecinski<sup>2</sup> and Robert J. Baker<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup> Biology Department, University of Scranton (julie.parlos@ttu.edu)

*Artibeus jamaicensis* (Chiroptera: Phyllostomatidae: Stenodermatinae) is a wide-ranging frugivorous bat, inhabiting Central America, the Caribbean Islands, and South America west of the Andes. The subspecies *A. j. jamaicensis* is found throughout the Lesser Antilles and part of the Greater Antilles. To address questions regarding the migration of this species among the U.S. Virgin Islands specimens were collected from the three islands. Microsatellites developed in *A. jamaicensis* were amplified among collected specimens. The programs used to evaluate these data suggest that these islands are not genetically distinct. Individuals on the island of St. Croix are more similar to one another, and the other two islands contain a mix of individuals representing two genetic populations. Migration appears to be unidirectional, from St. Croix, with minimal migration between St. Thomas and St. John. Based on small sample sizes, the genetic variation observed can be explained as sampling error resulting from migration among and between the islands rather than local adaptation. Future directions include increasing sampling size, geographic sampling and identifying rare alleles to contribute to our understanding of the migratory patterns among the Caribbean islands as well as whether observed genetic similarities are the result of common ancestry.

Paper 19 - **PATTERNS OF HANTAVIRUS SEROPREVALENCE IN WILD RODENTS FROM SOUTHEASTERN BRAZIL**

Gilberto Sabino-Santos Jr<sup>1</sup>, Felipe Gonçalves Motta Maia<sup>1</sup>, Alex M. Machado<sup>1</sup>, Glauciane G. Figueiredo<sup>1</sup>, Jorge Salazar-Bravo<sup>2</sup> and Luiz Tadeu M. Figueiredo<sup>1</sup>, <sup>1</sup>University of Sao Paulo School of Medicine, Ribeirao Preto, Brazil, <sup>2</sup>Department of Biological Sciences, Texas Tech University (sabinogsj@usp.br)

Hantaviruses are a group of rodent-borne pathogens (family *Bunyaviridae*; Genus *Hantavirus*) that represent emerging threats to human health. It is thought that the main route of transmission occurs via inhalation of viral particles through the respiratory tract, or by direct contact with blood or saliva. Hantaviruses in South America are associated with rodent hosts of the family *Cricetidae* (subfamily *Sigmodontinae*). The aim in this study was to relate characteristics of rodents: age and sex, influencing its hantavirus infections. Rodents were live-trapped in 2 grids of 100 Sherman's traps each, placed at 10-m intervals, for 2–3 consecutive nights. Grids were separated by at least 800 m to represent individual populations. Captured rodents had blood collected by retro-orbital sinus. IgG antibodies to hantavirus were detected by indirect ELISA using as antigen a nucleocapside recombinant protein for Araraquara Hantavirus. These mark-recapture mammals consisted of *Necromys lasiurus*, *Akodon sp.*, *Calomys tener*, *Mus musculus*, *Oligoryzomys nigripes*, *Scapteromys tumidus*, *Gracilinanus agilis*, *Oxymycterus judex*, *Oryzomys sp.*, and *Rhipidomys sp.* Hantavirus antibodies were noted in *Necromys lasiurus* (23), *Akodon sp.* (3), *Calomys tener* (1), and *Rhipidomys sp.* (1) throughout the study period. About 38% of the captured rodents were *Necromys lasiurus* and among them, 10% were seropositive to Hantavirus. This rodent has been previously recognized as a reservoir of Araraquara Hantavirus. An insignificant sex-ratio difference, with more males than females, was observed on the sites of capture. 291 juveniles including 3 seropositivities (1.0% positivity), 94 sub-adults including 7 seropositivities (7.4%), and 207 adults (8.7% positivity) were captured. This data suggests that age classes in rodents, more than gender, may be a risk factor for Hantavirus infection. Further studies are necessary in order to understand the dynamics of rodent populations and of the species that become infected with Hantavirus in this region.

Paper 20 - **AN EVALUATION OF FECAL DNA PRESERVATION TECHNIQUES AND EFFECTS OF SAMPLE AGE AND DIET ON GENOTYPING SUCCESS**

Michael Panasci<sup>1</sup>, Warren Ballard<sup>1</sup>, David Wester<sup>1</sup>, Stewart Breck<sup>2</sup>, David Rodriguez<sup>3</sup>, Llewellyn Densmore<sup>3</sup>, Robert Baker<sup>3</sup>. <sup>1</sup>Department of Natural Resources Management, Texas Tech University, <sup>2</sup>USDA, APHIS, Wildlife Services, National Wildlife Research Center, Fort Collins, CO, <sup>3</sup>Department of Biological Sciences, Texas Tech University (michael.panasci@ttu.edu)

Although biologists increasingly utilize fecal DNA, optimal collection protocols are not yet established. We evaluated 3 factors that influence microsatellite genotyping of fecal DNA extracted from coyote (*Canis latrans*) scats: age, preservative, and diet content. We used the multiple tubes approach to generate consensus genotypes and recorded errors in replicate amplifications. Samples were subjected to 3 age and 3 preservation treatments. Ethanol and DET buffer performed similarly, and both were superior to lysis buffer. Samples collected at 5 and 10 days yielded poorer quality DNA than samples collected on day 1. We tested the influence of diet by using scats consisting of insect, mammalian, or juniper (*Juniperus spp.*) remains. Scats comprised of juniper were most reliably genotyped when preserved in DET buffer. Mammal-based scats were most reliable when stored in EtOH. Scats comprised of insects did not differ between preservatives. We recommend the collection of scats < 5 days old, ethanol preservation for scats of obligate carnivores, and

DET buffer preservation for animals with plant-derived diets. Our study provides important methodology for studies utilizing fecal DNA analyses.

**Texas Society of Mammalogists  
28<sup>th</sup> Annual Business Meeting  
Texas Tech University Center  
27 February 2010**

**AGENDA**

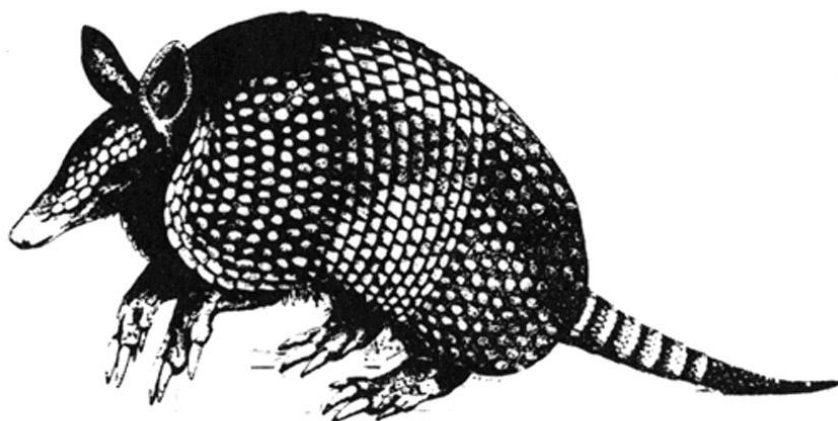
1. Approval of the Minutes of the 2009 Business Meeting
2. Report of Secretary-Treasurer, Loren Ammerman
3. Report of Permanent Secretary, Lisa Bradley
4. Report of Editor, Russell Pfau
5. Reports of Committees
  - a. Committee for Honorary Members, Phil Sudman
  - b. Committee on Conservation, Cathy Early
  - c. Student Honoraria, Terry Maxwell
  - d. Government Liaison Committee, John Young
  - e. Auction Committee, Joel Brant
6. Election of President-Elect
7. Election of Permanent Secretary
8. New Business
  - a. Selection of site for 2011 Annual Meeting
  - b. Other New Business
9. Closing Remarks of TSM President, Michael Tewes

**Texas Society of Mammalogists  
Treasurer's Report for Calendar Year 2009  
Submitted by Loren K. Ammerman, Secretary-Treasurer**

Income and expenses of TSM for the 2009 calendar year are shown below. The checking account for TSM is held at Citibank. Our investment fund with Security Global Investors has changed its name to Rydex/SGL. The checking account balance as of the first of the year was \$3,154.48. Total income in 2009 was \$13,000.54 and total expenses were \$9,677.42. The checking account had \$2,820.60 at the end of 2009. Our investment fund earned \$18,180.08 in 2009. The net gain in total assets for 2009 was \$21,350.54.

Checking Account Balance as of 25 December 2008	\$3,154.48
Security Benefit Group Investment Account balance 1 January 2009	\$25,309.84
<b>Total TSM assets as of 1 January 2009</b>	<b>\$28,464.32</b>
<b>2009 Income</b>	
2009 Annual Meeting income (registration, meals and lodging fees)	\$7,997.00
Membership Dues	\$238.00
T-shirts	\$800.00
Auction Income	\$2,889.00
Contributions/Patron memberships	\$926.00
Meeting photos and artwork of Past-Presidents	\$6.00
Collected donation for new screen	\$132.18
Checking account interest	\$12.36
Total income	\$13,000.54
<b>2009 Expenses</b>	
2009 Annual Meeting Expenses to TTU Center	\$6,166.00
Program copy charges	\$247.98
Student Awards	\$650.00
T-shirt charges (Gandy Ink)	\$674.95
Entertainment - DJ	\$550.00
Refreshments/Beverages	\$286.86
Speaker Honorarium	\$250.00
Deposit for TTU Center for 2010 meeting	\$617.00
Supplies (badges, certificates, print cartridge)	\$64.94
Reimbursement - meeting registration	\$82.00
GKG.net charges for domain name and hosting web page (1 year)	\$67.49
Checking account service charge	\$10.20
Total expenses	\$9,667.42
<u>Transfer from checking to mutual fund - July 2009</u>	\$3,667.00
2009 meeting auction income (\$2889) + patron memberships (\$778)	
Checking Account Balance 25 December 2009	\$2,820.60
Security Benefit Group Investment Account balance 31 December 2009	\$46,994.26
<b>Total TSM assets as of 31 December 2009</b>	<b>\$49,814.86</b>

# **Texas Society of Mammalogists**



**Newsletter**

**2010**

**The 28<sup>th</sup> Annual Meeting**

# Patron Membership

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Members are encouraged to consider becoming Patrons of the Society by donating \$100 (or more) to support the Society's student paper awards. A list of Patron members is published on the website and in the program. Regular Patron membership is achieved with a donation of \$100. Members who exceed \$100 in donations to the Society's student awards fund will receive a certificate recognizing their total donation level as follows: \$125, Ocelot Level; \$250, Bobcat Level; \$500, Puma Level; \$1000, Jaguar Level. Members can upgrade at any time, and all donations are cumulative. There is no time limit or minimum contribution requirement as a member works toward the next level. Donation levels are confidential.

# Minutes of the 2009 Business Meeting

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Texas Society of Mammalogists  
Annual Business Meeting  
Texas Tech University Center  
Junction, Texas  
21 February 2009

The meeting was called to order at 3:25 p.m. by President David Ribble in the Packard Building of the Texas Tech University Center at Junction. The minutes of the 2008 Annual Business Meeting as written in the 2009 annual meeting program for the Texas Society of Mammalogists (TSM) were approved.

## **Officers' Reports**

Secretary-Treasurer Loren Ammerman, summarized the Treasurer's Report for 2008 as printed in the 2009 meeting program.

Total assets at the end of 2008 were \$28,464.32. The checking account balance as of 1 January 2008 was \$7,974.21. Total income in 2008 was \$14,071.50 and total expenses were \$9,609.23 for 2008. The checking account ended the year with a balance of \$3,154.48. Due to the general economic downturn, the Security Fund lost \$10,627.13 in 2008. We invested income from the auction, patron memberships, \$2,000 from checking account, and contributions to the Rollin H. Baker memorial fund in June 2008 (\$6,161.00). Earlier in the year (February 2008) contributions from the 2007 meeting were also invested. Transfers from checking to the mutual fund totaled \$9,282 in 2008 and the account balance was \$25,309.84 at the end of that year.

The treasurer's report was approved.

Permanent Secretary Lisa Bradley told the membership that she receives items for the TSM archives to be deposited at Texas Tech University and she has been taking photos throughout the meeting for historical purposes. She also announced that the 25<sup>th</sup> anniversary publication "History of the Texas Society of Mammalogists" by Robert J. Baker, Clyde Jones, Robert E. Martin, and Lisa C. Bradley (Vol. 52, Special Publications of the Museum, Texas Tech University) is available. New members should see her to get a copy, or a pdf is available on the TSM website.

President Ribble and Permanent Secretary Bradley reported for Newsletter Editor Russell Pfau that the newsletter is printed with the program this year and we will continue to use this format. The program/newsletter will be posted on the website. He also announced that the Executive Committee approved the purchase of a domain name for the TSM website in the next year.



## **Reports of Committees**

Phil Sudman reported for the Committee for Honorary Members that there were no new nominations to bring forward. The membership should contact a member of the executive committee or himself to nominate honorary members. Honorary members are listed on the inside cover of the program. John Bickham will receive his award for contributions to the science of mammalogy at the banquet tonight.

Cathy Early, Chair of the Conservation Committee, reported on the progress of the proposed sale of the Christmas Mountains (Brewster County). Currently the land is not up for sale and it appears that Big Bend National Park will be involved in determining the future of this land donated to the state by the Mellon Foundation in 1991. She will keep the membership informed. Additionally, the Conservation Committee will work to update the document on the website that lists potential funding sources. Early introduced John Young (Texas Parks and Wildlife Department, TPWD) who made a plea for input from the society on the revisions to the list of Texas threatened and endangered mammal species. Early closed the report by asking for members that are interested to see her about serving on this committee.

The Committee for Student Honoraria gave their report at the banquet. President-Elect Michael Tewes announced winners of the presentation awards after the banquet dinner. Each award winner received a certificate signed by TSM President Ribble and a cash prize (\$150 for the Packard Award and \$100 for all others). Tewes thanked the committee members for their assistance with the judging process.

The award winners for oral presentations were:

1. Rollin H. Baker Award — Wes Brashear (Angelo State University)
2. TSM Award — Dana Lee (Angelo State University)
3. William B. Davis Award — Noe de la Sancha (Texas Tech University)
4. Robert L. Packard Award — Justin Lack (Oklahoma State University)

Poster presentation award winners were:

1. Clyde Jones Award — Eric Howell (Texas Tech University)
2. Vernon Bailey Award — Thomas Pettit (Baylor University)

John Young (TPWD) reported for the *ad hoc* Government Liaison Committee. He notified members that he would keep the membership informed of potential policy changes that would be relevant to mammalogists in the upcoming legislative session.

Joel Brant, on behalf of the *ad hoc* Auction Committee, thanked the membership for their support of the auction last year and their help raising \$3,461. There are 50 items this year for the silent and live auction. He thanked the members of the committee for their work throughout the year (Marcy Revelez, Adam Ferguson, Mandy Husak, Mike Husak, Robert Bradley, and Meredith Hamilton). If any new members are interested in serving, they should contact Joel.

## **Election of Officers**

President Ribble announced that the Executive Committee had nominated Terry Maxwell from Angelo State University for President-Elect. The floor was opened for additional nominations. There were none. Maxwell was elected by acclamation.

President Ribble announced that the Executive Committee had nominated Loren Ammerman from Angelo State University to continue as Secretary-Treasurer. The floor was opened for additional nominations. There were none. Ammerman was elected by acclamation.

President Ribble announced that the Executive Committee had nominated Russell Pfau from Tarleton State University for Newsletter Editor. The floor was opened for additional nominations. There were none. Pfau was elected by acclamation.

## **New Business**

The first item of New Business was the selection of a site for the 2010 meeting. It was moved and seconded to hold the meeting at TTU Center. Motion was approved and the dates of the meeting as originally discussed (February 12-14) had to be changed due to scheduling conflicts. The next meeting will be 26-28 February 2010.

Lisa Bradley presented the changes to the By-laws that were approved by the Executive Committee. The changes were summarized for the membership. The modifications were made to reflect technological changes (e-mail distribution, web mastering) and the actual duties performed. The membership approved the changes to the By-laws.

Loren Ammerman summarized membership statistics for TSM. There were 115 people registered for the 2009 meeting and 121 paid memberships. There are 9 states and 29 different institutions represented by our members. There were 37 new applications for membership this year. Ammerman asked the membership to recognize (anonymously) four new patron members of TSM.

Ammerman thanked those people that helped with the meeting duties this year. Lisa Bradley produced the meeting program, Jason Strickland arranged the beverages, Richard Dolman was responsible for the audiovisual support, Dana Lee printed nametags, Robbie Heischman, Marie Tipps, and Will Hernandez helped at the registration table and the poster session. Mike Dixon helped with T-shirt orders, registration, and general record keeping.

President Ribble announced the establishment of an ad hoc Committee on Mammal Records that will be chaired by Robert Dowler. Dowler proposed that this committee would be established to examine important records that are submitted to the membership in formats other than voucher specimens (mainly photographs of large and medium-sized mammals). The committee would confirm or reject the records and mammalogists would benefit from this new knowledge. The potential problem with the proposed role of the committee was discussed (volume of photos, compromising the methods currently in place for validating records). Robert Baker was opposed to having TSM be associated with a practice that might damage the reputation of the society. Ribble emphasized that this committee would be temporary to evaluate the feasibility and value of this endeavor. Dowler concluded by asking members to send photographic records to him and that he would report back to the membership next year.

John Young questioned the membership about the best way for field biologists to find out about potentially dangerous disease outbreaks in the state (such as plague, rabies). He announced that a National Park Service employee had recently died of plague and other TPWD biologists were recently exposed when conducting rodent work. Although the Texas Department of Health or the Centers for Disease Control (CDC) might have information on these outbreaks, the question was how could members find out where disease outbreaks are to protect themselves? Darin Carroll and Serena Reeder (CDC) mentioned that the website ProMed (<http://www.promedmail.org/>) has up-to-date information on infectious diseases. Anyone can sign up for e-mail updates (digests) or can search the archives. There are other links that the TSM members might benefit from as well (on plague, rabies, Hanta virus).

John Young is working with TPWD to establish a Mammal Specimen policy that would outline the procedures to follow when important specimens (such as black bears) are discovered. He requested contact information from collections that would be interested in receiving specimens or responding to calls about important road-kills.

Michelle Haynie announced that there is a new tenure track position opening at University of Central Oklahoma.

President Ribble closed the meeting by thanking Lisa Bradley and Loren Ammerman for their work on behalf of the society. The meeting was adjourned at 4:15 pm.

Respectfully submitted,  
Loren K. Ammerman  
Secretary-Treasurer

## Abilene Christian University

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Department of Biology, Box 27868, Abilene Christian University, Abilene, Texas 79699

### **Tom Lee**

Phone: 325-674-2574  
Fax: 325-674-2009  
Email: leet@acu.edu

#### Research Interests, Projects, and Grants:

Abilene Christian University Math/Science, Research Grant and Grant from the dean of Arts and Sciences for the summer of 2010.

#### Undergraduate Students and Their Research:

Joel Thompson and Hannah Rainer are working on the mammals of Taylor County Texas. Working with us is Dr. Joel Brant.

#### Additional Information:

Tyler Cochran and Emily Wilkinson have graduated and are now working for Dr. Bob Dowler at Angelo State on their masters.

## Angelo State University

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Department of Biology, Angelo State University, San Angelo, TX 76909

### **Loren K. Ammerman**

Phone: 325-486-6643  
Email: loren.ammerman@angelo.edu  
Web page URL: [http://www.angelo.edu/dept/biology/faculty\\_staff/lorenkammerman.html](http://www.angelo.edu/dept/biology/faculty_staff/lorenkammerman.html)

#### Research Interests, Projects, and Grants:

I am interested in working with students to use molecular data to reconstruct evolutionary relationships of organisms and to investigate species boundaries. Projects on bonneted bats (*Eumops*) and *Myotis* species are currently underway. The lab has been funded by an ASU grant to investigate molecular systematics of the family Molossidae and this project is close to completion.

I am also interested in community structure and the ecology of bats, especially in Big Bend National Park and the Lower Canyons of the Rio Grande. This summer will be the fourth year to monitor the colony size of *Leptonycteris nivalis* in Emory Cave using thermal infrared imaging techniques. Recently funding was obtained to work on developing collaborative teaching/research programs with colleagues in Malaysia (in collaboration with Robert Baker).

#### Graduate Students and Their Research:

- Jason Strickland – Phylogeographic variation in the cottonmouth, *Agkistrodon piscivorous*, in Texas using nuclear AFLP markers and venom protein profiles (MS thesis project, Fall 2009-present)
- Richard Dolman – Molecular systematics of the genus *Nyctinomops* (Carr Research Scholar, MS thesis project, graduated August 2009 and now enrolled in the PhD program at Oklahoma State University)
- Dana Lee – Taxonomic status of *Sylvilagus robustus* as revealed by amplified fragment length polymorphisms (Carr Research Scholar, MS thesis project, graduated May 2009 and now enrolled in the PhD program at Oklahoma State University)

#### Undergraduate Students and Their Research:

- Sarah Bartlett – Multi-gene phylogeny of *Eumops* species (undergraduate research project, Spring 2010)
- Candace Frerich— Genotyping isolates of the Bovine Viral Diarrheal Virus using DNA sequence of the 5' UTR (undergraduate research project, Fall 2009-present, Internship with Texas Vet Labs, San Angelo, TX)
- Marie Tipps — A molecular approach to the phylogenetic position of *Cheiromeles* (Chiroptera: Molossidae) (Carr Research Scholar 2009-2010, undergraduate)

#### Additional Information:

A second edition of the book “Bats of Texas” is underway with coauthors David J. Schmidly and Christine L. Hice. It is to be published by Texas A&M Press. We are interested in including your recent publications on distribution or life history characteristics. Please contact one of us.

The Angelo State Natural History Collection has almost 14,000 mammal specimens and tissues from approximately 7500. The ASNHC databases are available for searching at <http://www.angelo.edu/dept/biology/asnhc/>

Contact Loren Ammerman or Robert Dowler if you have any questions about the collection.

### **Robert C. Dowler**

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#### Research Interests, Projects, and Grants:

My current research in Texas continues on the ecology of medium-sized carnivores. I recently received funding from the Davidson Foundation and Angelo State University for a radio-telemetry study of ringtails (*Bassariscus astutus*) and hog-nosed skunks (*Conepatus leuconotus*). This year my graduate students will be investigating the use of GPS radio-collars for studying skunks. With Terry Maxwell and Adam Ferguson, I am finishing a study on patterns of road-killed mammals over a 100-mile route near San Angelo. In addition to these projects I am working on a book entitled the Skunks of Texas with coauthors Jerry Drago and Adam Ferguson. For that project we are seeking any records of specimens of skunks from Texas, as well as visual or photo records, especially of the less common species of spotted skunks, hog-nosed skunks, or hooded skunks. I am also interested in the

conservation biology of Galapagos rodents, collaborating with a colleague at the Brookfield Zoo in Chicago and with Cody Edwards at George Mason University.

Graduate Students and Their Research:

I currently have one graduate student completing his thesis. Andrew Tiedt is in the analysis phase of his project on denning ecology of ringtails (*Bassariscus astutus*). I have three new graduate students who are beginning their thesis research this year. Tyler Cochran is currently planning to work on a comparison of activity patterns between striped skunks (*Mephitis mephitis*) and hog-nosed skunks (*Conepatus leuconotus*). Eric Pomposelli will be studying maternal den site selection and use for hog-nosed skunks. Emily Wilkinson will study maternal den site selection and use for striped skunks. Emily is also doing an independent study of quill distribution and density on porcupines (*Erethizon dorsatum*).

Undergraduate Students and Their Research:

Wes Brashear is completing his undergraduate study of seasonal den site selection and home range in hog-nosed skunks. He plans to begin the M.S. program at Angelo State University after completing his B. S. in Biology this May. Reagan Noland is studying mammal records from owl pellets in west-central Texas.

## Baylor University

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### **Kenneth T. Wilkins**

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Research Interests, Projects, and Grants:

Our projects generally relate to ecology and distribution of small mammals (primarily, rodents and bats) at the population and community levels. Recent funding is from the Nature Conservancy of Texas, Texas Parks & Wildlife Department, American Museum of Natural History (Theodore Roosevelt Fund), and assorted private foundations.

Graduate Students and Their Research:

With a recent graduation, the mammalogy group now includes 4 graduate students. Brianna Kirchner graduated with the MS. in Environmental Biology in May 2009; her thesis examined effects of fire on the small-mammal community in a native tallgrass prairie. Brianna is now teaching science at Waco High School. Tommy Pettit's dissertation research relates to use of vertical and horizontal edges by bats in montane forest communities; he has concluded his field work in the Rocky Mountains of Utah and has shifted data collection to the pineywoods of eastern Texas. Anica Debelica has conducted the first field season for her dissertation research which is related to roosting and foraging ecology in the bat community of eastern Texas pineywoods. Nick Green has concluded the first field season in his dissertation study of effects of degree of habitat contrast on the small-mammal community in Texas tallgrass prairies at Clymer Meadow and Leonhardt Prairie, properties of the Nature Conservancy of Texas. Li Han is developing a dissertation project on urban ecology of small mammals.

Undergraduate Students and Their Research:

Two undergraduate Honors students, Rachel Rotondi and Christina Skrovanek, are conducting their Honors thesis projects on bat ecology in connection with Anica Debelica's dissertation research.

Recent publications:

- J.W. Hermanson & K.T. Wilkins. 2008. Growth and development of two species of bats in a shared maternity roost. *Cells, Tissues and Organs*, 187:24-34.
- N.S. Green & K.T. Wilkins. Continuing range expansion of the northern pygmy mouse (*Baiomys taylori*) in northeastern Texas. In press, *The Southwestern Naturalist*, Spring 2010.
- A. Debelica & M. L. Thies. 2009. Atlas and key to the hair of terrestrial Texas mammals. Special Publications of the Museum of Texas Tech University, Number 55.

Recent presentations:

- Plasticity of Mexican free-tailed bat (*Tadarida brasiliensis*) echolocation in different clutter types. Poster: Texas Society of Mammalogists, Junction, February. T. Pettit and K.T. Wilkins. Winner of Vernon Bailey Award.
- Biogeographical patterns in the small mammal faunas of eastern and central Texas. Poster: Texas Society of Mammalogists, Junction, February. H. Li, N. Green & K.T. Wilkins.
- Resource partitioning in a forest-dwelling bat community in eastern Texas: preliminary findings. Poster: North American Symposium on Bat Research, Portland, OR, November. Anica Debelica & K.T. Wilkins.
- New method for quantifying physical clutter in forest edges. North American Symposium on Bat Research, Portland, OR, November. Tommy Pettit & K.T. Wilkins.

## California Baptist University

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### **Art Cleveland**

Dean of Research and Sponsored Programs

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Research Interests, Projects, and Grants: I continue to have success in acquiring federal and private funds for the university, especially in new programs in engineering and nursing. The mammals I deal with most these days are in the halls of congress. However, my fun in 2009 was two reviews for the JM. I am finishing a review of the Mammals of India and trying to finish two other manuscripts on China mammal species by this summer. I continue to enjoy serving as associate editor for mammalian ecology for the Western North American Naturalist.

Additional Information: Vicki and I have grandchild number six as of last November, Constance Elizabeth Cleveland. We are continuing to enjoy certain aspects of living near LA and the ski slopes and beaches in southern California. However, we do desire to return to Texas soon...to be closer to Junction, of course.

# Centenary College of Louisiana

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## **Scott Chirhart**

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### Research Interests, Projects, and Grants:

Evolutionary Biology, including: Evolutionary/Population Genetics, Vertebrate Speciation and Systematics, Molecular Variation Undergraduate

### Undergraduate Students and Their Research:

Ruth Litwinowicz-Research: Implications of mitochondrial and nuclear variation in a deer mouse species endemic to North Eastern U.S. Region

# McMurry University

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Department of Biology, McMurry University, Abilene, TX 79697

## **Joel G. Brant**

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### Research Interests, Projects, and Grants

My research interests are primarily concerned with the natural history of mammals, particularly in Texas and the Chihuahuan Desert. I am currently setting up a research program for myself and selected undergraduates that will focus on the natural history & ecology of mammals in the southern Rolling Plains, northern Edwards Plateau, and northeastern Chihuahuan Desert. My current projects include a survey of the mammals of the Southern Rolling Plains, specifically Taylor County & surrounding areas (with Tom Lee); a monitoring & management project for black capped vireos (*Vireo atricapilla*) in Taylor County; an examination of the ecological distribution of *Scalopus aquaticus* in Texas; & continued morphometric studies of *Perognathus flavus* & *merriami*.

# Oklahoma State University

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Department of Zoology and Collection of Vertebrates, Oklahoma State University, Stillwater, OK 74078

## **Karen McBee**

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### Research Interests, Projects, and Grants:

My research interests focus on two different aspects of the role that environmental stressors play in altering the genetic structure of populations. My lab uses several genetic techniques to investigate relationships between exposure to environmental pollutants and induction of genetic damage in wildlife species and to explore how induced genetic damage may translate into long term population demographic effects.

### Graduate Students and Their Research:

Kimberly Hays is working on her Ph.D. She is investigating genetic effects in rodents and turtles resulting from interactions among lead, zinc, and cadmium contaminants at Tar Creek Superfund Site.

### Undergraduate Students and Their Research:

Alesia Hallmark is a Wentz Scholar who is investigating use of PIXIMUS instrumentation to assess difference in bone density in *Tadarida brasiliensis* collected over a 50 year period from Vickery Cave, Oklahoma.

# Purdue University

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## **John W. Bickham**

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### Research Interests, Projects, and Grants:

Systematics, phylogenetics, phylogeography, conservation, ecotoxicology. Currently my lab is involved in genetic studies of Steller sea lions, bowhead whales, and bats with emphasis directed toward the afore mentioned disciplines.

### Graduate Students and Their Research:

Geoff Laban- Ecotoxicology: Evaluating sublethal effects of present and potential contaminants and other environmental stressors by developing molecular biomarkers of exposure and effects to these environmental contaminants, specifically silver nanoparticles on the growth and development of the Fathead Minnow.



## Undergraduate Students

Taylor Thompson, Heather Downing, Nick Storey

### Research Scientists:

John Patton (jcpatton@purdue.edu): Evolutionary processes using mtDNA, X- and Y-chromosome loci as contrasted to autosomal loci. This design allows the determination of the contribution of males and females, respectively, in the evolutionary history of a species. Autosomal loci involved include those under selection (MHC and Toll genes) as well as loci thought to primarily evolve in a near neutral fashion. Current primary emphasis is description of patterns of reticulate evolution in mammals utilizing these genetic tools.

# Tarleton State University

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Department of Biological Sciences, Tarleton State University, Stephenville, TX 76402

## **Allan D. Nelson**

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### Research Interests, Projects, and Grants:

My research interests are in the areas of floristics of the West Cross Timbers and Coastal Plain of Texas as well as the Ouachita Mountains of Oklahoma. I am interested in rare and endangered plants of Texas and Oklahoma. I am also interested in using vegetative ecology to examine habitat of rare animals. I have recently submitted a section six grant proposal asking for funds to carry out a status survey for the Texas kangaroo rat (*Dipodomys elator*).

### Graduate Students and Their Research:

- Paige Cowley- Flora of Hunewell Ranch
- Kelly Freeman- Characterization of black-capped vireo habitat in the West Cross Timbers

## **Russell S. Pfau**

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### Research Interests, Projects, and Grants:

- Development of microsatellite markers for the cotton rat (*Sigmodon hispidus*).
- Determination of genetic structure among populations (lake and estuary) of the mud crab (*Rhithropanopeus harrisi*) using mitochondrial DNA sequencing.
- DNA sequencing (mtDNA and Y chromosome loci) and AFLP analysis of cotton rats to map the geographical location of the hybrid zone between eastern and western lineages of this species in the United States.

- Analysis of a hybrid zone between the shrews *Blarina hylophaga* and *Blarina brevicauda* using AFLP, mtDNA, and Y-chromosome analyses. This study is in collaboration with Cody Thompson (Texas Tech) and Dr. Elmer Fink (Fort Hays State University).
- Design and testing of PCR primers to amplify a gene involved in sperm-egg recognition in the cotton rat.
- Population genetics of the Texas mouse (*Peromyscus attwateri*) across its geographic distribution.
- Population genetics of the pocket gopher (*Geomys breviceps*) across its geographic distribution (in collaboration with Phil Sudman).

Undergraduate Students and Their Research:

- Jordan Sparkman is finalizing the development of microsatellite markers for *Sigmodon hispidus*.
- Beth Colvin is sequencing mtDNA of *Sigmodon hispidus* to map location of the hybrid zone between eastern and western lineages of this species.

**Philip D. Sudman**

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Research Interests, Projects, and Grants:

Current projects include systematic studies of pocket gophers working with graduate students here at Tarleton as well as the University of North Texas and Fort Hays State University. I also have a student working on white-eyed and black-capped vireo genetics, looking specifically at sex ratios of hatchlings, and extra-pair mating. This research is being conducted at Ft. Hood.

Graduate Students:

- David Davis – Sex ratio and extra-pair mating in vireos.
- Ashley Hyatt – Development of microsatellite primers for *Geomys*.

## Texas A&M University-Kingsville

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Texas A&M University-Kingsville, 700 University Blvd., MSC 228, Kingsville, Texas 78363

**Scott E. Henke**

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Research Interests, Projects, and Grants:

- *Babesia bovis* and *B. bigemina* in white-tailed deer and nilgai from northern Mexico and southern Texas.

- Feral swine interactions with domestic swine: potential for disease transmission.
- Habitat selection and genetics of Maritime pocket gophers.
- Susceptibility of wildlife to aflatoxin.
- Home range and time budgets of urban squirrels.
- *Baylisascaris procyonis* in Texas
- Striped skunk movements along the urban and suburban interface: potential for rabies transmission

## Texas A&M University-College Station

Department of Wildlife and Fisheries Sciences, Texas Cooperative Wildlife Collection, Texas A&M, College Station, TX 77843

### Jessica Light

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#### Research Interests, Projects, and Grants:

My research program is focused broadly in evolutionary biology. I am especially interested in studying systematics, phylogeography, population genetics, and coevolutionary associations between distantly related organisms, particularly mammals and their parasites.

#### Graduate Students and Their Research:

- Erin Fender is a first year PhD student. Erin recently obtained her Master's degree from the University of Memphis and is she interested in evolutionary ecology
- Sarah Welborn is a first year Master's student. Sarah is interested in molecular phylogeography and ecology

#### Undergraduate Students and Their Research:

- John Andersen is using mitochondrial data to investigate phylogeography of *Chaetodipus hispidus*
- Marcy Ostroff is examining the phylogeography of *Baiomys taylori* using mitochondrial data

# Texas Tech University

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Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

## **Robert J. Baker**

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### Research Interests, Projects and Grants:

Robert J. Baker is in his 42<sup>nd</sup> year as a faculty member at Texas Tech University. He has no plans to retire in the immediate future, but would like to finish up a lot of projects that he has started over the last 42 years. Interests include: the Genetic Species concept, Phyllostomid bats, and the effects of the Chernobyl environment on mammals.

### Graduate Students and their Research:

- Faisal Ali Anwarali Khan is a second year PhD student. His education before coming to Texas Tech University was in Universiti Malaysia Sarawak. Then, he completed his Master's degree at Dr. Baker's lab in March 2008. His Master's degree was concerned with the degree to which Borneo is isolated from Peninsula Malaysia as reflected in the genetics of bats. He is interested in the systematic and phylogeography studies that contribute towards the conservation effort in South East Asian mammals. Museum of Texas Tech University Occasional Paper 281 reports the results of his Malaysian field work in 2006. Current projects include the systematic of Southeast Asian bats of the genera *Kerivoula*, and *Hipposideros*. [faisal.anwarali@ttu.edu](mailto:faisal.anwarali@ttu.edu)
- Cibele Sotero-Caio is a second year PhD student. She obtained her Master's degree in March 2008 from Universidad Federal de Pernambuco, Recife – Brazil, where she developed a comparative chromosomal study among vampire bat species using chromosome painting. Her research interests include karyotypic evolution, as well as the use of cytogenetic approaches to the understanding of evolution, biogeography and systematics of mammals, with emphasis on bat species. Her current projects are the investigation of distributional patterns of repetitive sequences and single copy genes in bat chromosomes, as well as the use of chromosome paintings to assess karyotypic evolution on bat and rodent species. She is also working on the description of karyotypes of mammals from Kyrgystan, Ecuador, Panama, and Malasia. [cibele.caio@ttu.edu](mailto:cibele.caio@ttu.edu)
- Peter Larsen is a fifth year PhD student. His research interests include speciation, phylogeography, and systematics of Neotropical and Palearctic mammals. He is currently investigating i) a potential hybrid speciation event in Caribbean populations of fruit-eating bats (genus *Artibeus*) and ii) an ecologically driven speciation event in Central American populations of *Artibeus lituratus*. His dissertation is entitled: "Speciation, Hybridization, and the Bateson-Dobzhansky-Muller model: an analysis of a recent radiation of New World leaf-nosed bats". [peter.larsen@ttu.edu](mailto:peter.larsen@ttu.edu)
- Roxy Larsen is a third year PhD student. Her dissertation will focus on the biogeography of Lesser Antillean bats, specifically the genera *Myotis* and *Ardops*. Her current projects include origins and diversification of Caribbean *Myotis* and phenotypic variation in *Ardops nichollsi*. Last fall she received the Michelle C. Knapp Memorial Scholarship. [roxy.larsen@ttu.edu](mailto:roxy.larsen@ttu.edu)

- Hugo Mantilla-Meluk is a sixth year PhD student. His research interests include speciation, phylogeography, and systematics of Neotropical mammals. Current projects include systematics and phylogeography of Neotropical bats of the genera *Anoura*, *Lonchophylla*, *Uroderma*, *Desmodus*, and *Histiotus*, the primate genera *Lagothrix* and *Cebus*, and the carnivore genus *Mustela*. In his work Hugo applied innovative approaches such as molecular analysis and Geographic Information modeling in combination with classical morphological analysis to elucidate modes of mammalian speciation in the Neotropics. Hugo is part of the UICN group of experts on mammals, the group of experts of Highland Mammals of Colombia, and the group of experts Wild-life management of the Chocoan Mammals. His dissertation is entitled: "Computer modeling applied to the study of Phyllostomid bat speciation". Hugo is also in charge of a program of cooperation between Texas Tech and Colombian institutions. hugo.mantilla@ttu.edu
- M. Raquel Marchán-Rivadeneira is a second year PhD student, co-advised by Dr. Richard E. Strauss. Her work is focused on using morphometric analyses based on size and shape to discriminate and diagnose populations of small mammals, mainly of neotropical bats. In addition, she is using levels of fluctuating asymmetry as a biological monitor of environmental stress in the populations of *Myodes glareolus* from Chernobyl, Ukraine. Currently, she is a Visitor Scholar at the University of Michigan. raquel.marchan@ttu.edu
- Molly McDonough is a first year Ph.D. student beginning in August 2009. She published her first paper in October 2008, "Speciation within bonneted bats (Genus *Eumops*): the complexity of morphological, mitochondrial, and nuclear datasets in systematics" in the *Journal of Mammalogy*. molly.mcdonough@ttu.edu
- Julie Parlos is a second year Ph.D. student. Her dissertation projects include evaluating karyotypic, mitochondrial (cytochrome-b), and morphological congruence among multiple species of *Lonchophylla* and evaluating congruence of phylogenies generated using mitochondrial (cytochrome-b), AFLP and microsatellite data among *Dermanura*. She obtained research awards from TAS and TTUAB for her proposal on *Dermanura*. Her research interests include investigating both inter- and intraspecific variation among various genera of bats. Other projects include investigating intraspecific variation among Caribbean *Artibeus* and investigating interspecific differences among *Myotis*. julie.parlos@ttu.edu
- Lizette Siles Mendoza is a second year Ph.D. student. She received her Bachelor's degree from Universidad Mayor de San Simon (Bolivia) and has worked extensively in conservation projects across Bolivia. Her interests focus on the conservation, systematics and distribution of Bolivian bats and to learn molecular techniques that could be used to elucidate the taxonomic status of some Neotropical bats that occur in Bolivia. Her current research is on the systematics of bats of the genera *Micronycteris*. liz.siles-mendoza@ttu.edu
- Caleb Phillips (Post-doc) - Molecular evolution, phylogeography, systematics, evolution of adaptive differences, and genomics.
- Vicki Swier accepted a job with the U.S. Fish and Wildlife Service on March 2009. She is currently the Wildlife Refuge Specialist at Wichita Mountains Wildlife Refuge near Indianola, OK. Her publication, "Patterns of Chromosomal Evolution in *Sigmodon*, Evidence from Whole Chromosome Paints", was published in *Cytogenetics and Genome Research* in July 2009. vicki\_swier@fws.gov

## **Robert D. Bradley**

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### Research Interests, Projects, And Grants:

My research interests include: systematic relationships, molecular evolution, and natural history of mammals, particularly in geomyoid and cricetid rodents; examination of hybrid zones between genetically distinct taxa, including isolating mechanisms and the dynamics of genetic introgression; examination of the origin and evolution of rodent-borne viruses, especially in the use of rodent phylogenies and genetic structure to predict the transmission and evolution of viruses; modeling predictions associated with epidemiology; growth and utilization of natural history collections, especially those pertaining to mammals.

- Systematics of the genus *Peromyscus*.
- Systematics and phylogenetic studies of *Peromyscus boylii* species group.
- Phylogenetic relationships of Neotomine and Reithrodontine rodents.
- Study of hybridization between two species of *Neotoma*.
- Systematics and phylogenetic studies of the genus *Neotoma*.
- Systematics and phylogenetic studies of the genus *Geomys*.
- Ecology of emerging hanta- and arenaviruses in the southwestern US.
- Role of the transferrin receptor in binding arenaviruses.

### Graduate Students And Their Research:

- Cody W. Thompson (PhD student) is in his 3rd year. Dissertation topic to be determined.
- Ryan Duplechin (PhD student) is in his 1st year. Ryan was an undergraduate at TTU and worked in Dr. Robert Baker's laboratory for several months.
- Sheri B. Westerman (MS student) is in her 3rd year. Research topic involves determining if the transferrin receptor in *Neotoma* is associated with binding arenaviruses.
- Nicté Ordóñez-García (PhD student) is in her 2nd year. Research topic probably will involve aspect of the systematics of *Peromyscus*.
- Kathy MacDonald (PhD student, Co-chaired with Dr. Richard Strauss) is in her 4th year. Research topic will involve modeling biological and genetic parameters involved in the association of *Catarina arenavirus* with *Neotoma*.
- Matt Mauldin (MS student) is in his 2nd year. Thesis topic to be determined.
- Megan Corley (MS student) is in her 2nd year. Thesis topic to be determined.

#### Graduated Students:

- R. Neal Platt (MS student) graduated in December 2008. Thesis topic involved - Multigene approach in examining phylogenetic relationships of Neotomine-Reithrodontine rodents. Neal is pursuing his PhD with Dr. David Ray at Mississippi State University.

#### Undergraduate Students And Their Research:

Several other undergraduate students (2 HHMI Undergraduate Fellows) are involved in various research projects in the Laboratory.

- Allie Clinton - is isolating and characterizing the Muleshoe hantavirus.
- Erica Vargas - is producing a phylogeny of *Geomys* using the coding region of the alcohol dehydrogenase gene.

#### Additional Information:

I teach Mammalogy at the Texas Tech University Center at Junction during May (referred to as the Intersession Semester). This is an excellent opportunity to receive credit at the Graduate or Undergraduate level. I also teach "Field Methods" for the Museum of TTU during the summer.

## Trinity University

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### **David O. Ribble**

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#### Research Interests, Projects, and Grants:

I am interested in the evolutionary ecology of small mammals, primarily *Peromyscus* and elephant-shrews. My research in recent years has ranged from studies of social organization to mating behavior to thermal ecology. We are also starting some new research with mathematics funded through a Math-Biology NSF grant.

#### Undergraduate Students and Their Research:

- Laney Redus – Conservation Genetics of Dama Gazelles.
- Sultana Peffley and Jonathan Segal - Paternity in Round-eared Elephant-shrews (*Macroscelides proboscideus*).
- Richard Simpson and Samuel Keller – Changing Mammal Distributions in Central Texas

# University of Central Oklahoma

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## **Michelle L. Haynie**

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### Research Interests, Projects, and Grants:

My research interests lie in population genetics and molecular systematics. Currently, I have students examining genetic diversity in *Mephitis mephitis* populations in the central United States, a *Neotoma micropus/N. floridana* hybrid zone in Oklahoma, and *Onychomys leucogaster* in southern Texas. I also am collaborating with colleagues at UCO to examine genetic diversity in a population of eastern collared lizards in Oklahoma and Sonoran mud turtles in Arizona and New Mexico. Funding for this research has been provided by the Office of Research and Grants at UCO. I recently was awarded a NSF-MRI grant for acquisition of an automated DNA sequencer for the Department of Biology at UCO. I am a Co-PI on a collaborative NSF grant submitted to the Ecology of Infectious Diseases program.

### Undergraduate Students and Their Research:

- Kelly A. Smith – Genetic variation in striped skunk (*Mephitis mephitis*) populations in the central United States
- Ethan B. Rowell – Genetic variation in a *Neotoma micropus/N. floridana* hybrid zone in Oklahoma

### Graduate Students and Their Research:

- Michelle Gerlosky – Genetic variation in a population *Onychomys leucogaster* from southern Texas

### Additional Information:

I am in the process of writing the “Mammals of Oklahoma” with Bill Caire, Lynda Loucks, and Marcy Revelez.



# University of New Mexico

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## **Christine L. Hice**

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### Research Interests, Projects, and Grants:

Conservation and natural history of mammals in the southwest, particularly Texas, New Mexico, and Mexico. Natural history and ecology of neotropical mammals.

Current projects include:

- Second edition of *The Bats of Texas*, with Loren Ammerman and David Schmidly as co-authors.
- Small mammal trapping on Galveston Island to assess the impact of Hurricane Ike on the mammal community, with David Schmidly
- Revised edition of *The Mammals of Texas*, with David Schmidly as co-author
- Archival natural history of New Mexico: project uses national archives, particularly from the US Biological Survey, to assess changes in land use, habitat, etc. over the past 100 years in New Mexico, with David Schmidly

## **David J. Schmidly**

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### Research Interests, Projects, and Grants:

Conservation and natural history of mammals in the southwest, particularly Texas, New Mexico, and Mexico.

Current projects include:

- Second edition of *The Bats of Texas*, with Loren Ammerman and Chris Hice as co-authors.
- Small mammal trapping on Galveston Island to assess the impact of Hurricane Ike on the mammal community, with Chris Hice
- Revised edition of *The Mammals of Texas*, with Chris Hice as co-author
- Archival natural history of New Mexico: project uses national archives, particularly from the US Biological Survey, to assess changes in land use, habitat, etc. over the past 100 years in New Mexico, with Chris Hice

# University of Texas

The University of Texas at Austin, Texas Natural Science Center, 2400 Trinity St. Austin, TX 78705

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Paleo Lab: <http://www.utexas.edu/tmm/paleo/index.html>

DigiMorph: <http://www.digimorph.org/about/pamelaowen.phtml>

### Research Interests, Projects, and Grants:

- Evolutionary history of American badgers (Taxidiinae)
- Morphology, evolution and systematics of Carnivora
- Late Cenozoic mammalian faunas
- Natural science education and outreach

### Additional Information:

Public education and outreach have been my focus the past few years. I have been a co-leader of TNSC's Evolution Professional Development programs and this year I am teaching a set of workshops for secondary science teachers called Basic Bones & Bites: An Introduction to Mammalian Skeletal and Dental Anatomy. I continue to provide annual mammalogy training for the Capital Area Chapter of the Texas Master Naturalists and serve as Associate Editor (Fossil Record section) for Mammalian Species.

## STUDENT AWARDS

**The Texas Society of Mammalogists annually recognizes student presenters for excellence in research and presentation abilities by granting the following awards. These awards are made possible by the generous donations of the Society's members and by fundraising activities.**

Robert L Packard Award – The Robert L. Packard Award was first awarded in 1985 for the best student presentation. In 1990, when the TSM Award was established, the Packard Award was designated for the best presentation in classical mammalogy. Since 1998, the Packard Award has been designated for the Best Overall oral presentation. Currently, this award includes an honorarium of \$150. The award was named in honor of Robert L. Packard (1928-1979), the founder of the Texas Society of Mammalogists.

TSM Award – This award was established in 1990 and is awarded to the student with the best oral presentation in studies pertaining to mammalian cytology, evolution, and systematics. This award includes an honorarium of \$100.

William B. Davis Award – This award was established in 1998 and is granted to the student with the best oral presentation in classical mammalogy at the organismal level. This award includes an honorarium of \$100. The award is named in honor of William B. Davis (1902-1995), a leading mammalogist in Texas and the first Head of the Department of Wildlife and Fisheries Sciences at Texas A&M University. Davis authored or co-authored five editions of "Mammals of Texas" (1947, 1960, 1966, 1974, 1994).

Rollin H. Baker Award – This award was established in 2002 for the best overall oral presentation by an undergraduate student. This award includes an honorarium of \$100. The award was established in honor of Rollin H. Baker (1916-2007), president of the Society in 1984-85 and an active member of TSM from 1984 until his death in 2007.

Vernon Bailey Award – This award was established in 2004 for best poster presentation in classical mammalogy at the organismal level. This award includes an honorarium of \$100. The award was named for Vernon Bailey (1864-1942), Chief Field Naturalist and Senior Biologist for the Department of Agriculture's Bureau of Biological Survey from 1897 to 1933. Bailey conducted the first and most complete biological survey of Texas, from 1889 to 1905.

Clyde Jones Award – This award was established in 2004 for best poster presentation in studies pertaining to mammalian cytology, evolution, and systematics. This award includes an honorarium of \$100. The award was named in honor of Clyde Jones, who is currently Horn Professor Emeritus at Texas Tech University. Jones has been an active member of TSM since its inception in 1983 and was President of the Society in 1987-88.