

Statewide Genomic Assessment of Texas Pocket Gophers

Funding:

“Population and conservation status of Texas pocket gophers (*Geomys* and *Thomomys*) in Texas with a focus on the subspecific status of *Thomomys bottae* via population genomic tools”, awarded to PIs David A. Ray, Richard D. Stevens, Robert D. Bradley from the Texas Parks and Wildlife Department, \$118,608, 2016-2019.

Project Summary:

Assessing the systematic and conservation status of pocket gophers in Texas has been a challenge, to say the least. Beginning with Vernon Bailey in the early 1900s, attempts to resolve and explain the biological diversity of pocket gophers has taken the time of many Texas mammalogists. W. B. Davis later spent many years tackling this issue, resulting in the description of several new gopher taxa. The discovery of new scientific information and need for systematic revision continues into modern times, with no fewer than 18 publications appearing in the last 25 years. Given the morphometric conservation between pocket gopher species, presumably as a result of adaptations to soil types, and given the isolated nature and distribution of pocket gophers, new methodologies often produce new interpretations in the data. Recent studies of pocket gophers have employed state-of-the-art genomic methods in an attempt to develop new systematic hypotheses and conservation interpretations for the three genera and at least 71 taxa (species and subspecies) occurring in Texas.



The three main goals of this project were to:

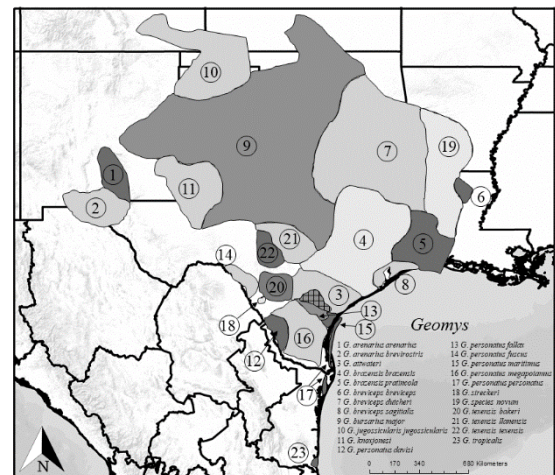
- Collect specimens from the type or near-type localities for each nominal subspecies and species of gopher occurring in Texas. As part of this collection, tissue samples were obtained and archived for genetic studies.
- Prepare an all-encompassing systematic review and taxonomic interpretation for Texas pocket gophers
- Use state-of-the-art methods to generate genome-level sequences from tissues obtained during this study. In a few cases where tissues were unavailable, skin clips were obtained from previously-collected specimens.
- Produce distribution models based on abiotic factors such as elevation, precipitation, and soil type.

Progress and conclusions:

The results of this study are featured in two major publications. The first involved a broad systematic reevaluation of the three Texas genera (*Cratogeomys*, *Geomys*, and *Thomomys*) that incorporated mitochondrial DNA sequences obtained from the cytochrome-b gene, a commonly

used dataset for addressing mammalian taxonomy. The second study used genomic methodologies to produce a genome-wide interpretation of pocket gopher systematics.

- A phylogenetic study was conducted based on a cytochrome-b dataset containing 66 sequences for *Cratogeomys*, 163 for *Geomys*, and 81 for *Thomomys*.
- Further, findings from previous morphometric, allozymic, karyotypic, and DNA studies were combined with the mtDNA sequence data to assemble the broadest possible dataset for providing a taxonomic synthesis of each genus.
- In the mtDNA study, 22 taxonomic names were evaluated for *Cratogeomys*, 25 for *Geomys*, and 24 for *Thomomys*. For *Cratogeomys* occurring in Texas and immediate surrounding areas, 1 species and 13 subspecies were proposed; for *Geomys* occurring in Texas and immediate surrounding areas, 12 species and 18 subspecies were proposed; and for *Thomomys* occurring in Texas and immediate surrounding areas, 4 species and 22 subspecies were proposed. Forty-three original names were synonymized, elevated to species, or otherwise reassigned, and two new taxonomic entities (*Geomys brazensis* and *G. sp. novum*) were identified.
- Distribution maps were developed for each taxon of the 3 genera.
- Efforts suggest that at least two subspecies, *Geomys personatus fuscus* of Fort Clark in Kinney County and *Thomomys bottae baileyi* of Sierra Blanca in Hudspeth County, could be extinct.
- Two other *T. bottae* subspecies, *spatiosus* (Brewster County) and *pervarius* (Presidio County), appear to be quite rare.
- A genome-level study was generated using a subset of the cytochrome-b endeavor. We used ddRAD-seq methods to generate 80,000 single nucleotide polymorphisms (SNPs), for addressing systematic boundaries within the 3 pocket gopher genera. These data agreed with current taxonomic hypotheses regarding *Geomys*; however, for *Cratogeomys*, there was some discordance between SNP-based trees and the cytochrome-b tree. Additionally, many *T. bottae* groups present similar genetic patterns that do not merit finer designation, suggesting a more conservative classification of *T. bottae* in Texas and southeastern New Mexico.



Publications:

Bradley, R. D., et al. (14 additional authors). 2023. Genetic identification of Pocket Gophers (Genera *Cratogeomys*, *Geomys*, and *Thomomys*) in Texas and surrounding areas. Special Publications, Museum of Texas Tech University 78:1–120.

Halsey, M. K., E. K. Roberts, E. A. Wright, T. J. Soniat, L. L. Lindsey, D. Moreno-Santillan, R. M. Pitts, L. M. Dávalos, R. D. Bradley, R. D. Stevens, and D. A. Ray. Accepted. Newly

assembled pocket gopher genomes can facilitate conservation management of biodiversity. *Journal of Mammalogy*.