

Conservation Status of *Peromyscus truei comanche* Based on a Landscape Genomic Assessment

Funding:

“Morphology, landscape genomics and effective population size of the Palo Duro Mouse, *Peromyscus truei comanche*,” awarded to PIs Joseph D. Manthey, Caleb D. Phillips, Robert D. Bradley from the Texas Parks and Wildlife Department and US Fish and Wildlife Service, \$282,585, 2021-2025.

Project Summary:

In 2021, Drs. Manthey, Phillips, and Bradley received funding from the Texas Parks and Wildlife Department and US Fish and Wildlife Service for a project entitled “Morphology, landscape genomics and effective population size of the Palo Duro Mouse, *Peromyscus truei comanche*” to determine the systematics and conservation status of the Palo Duro Deermouse. The subspecies *Peromyscus truei comanche* is endemic to the Texas Panhandle, and it occurs along the edges of the Llano Estacado escarpment, primarily in the Palo Duro and Caprock Canyons. Due to the semi-isolated nature of the Palo Duro and Caprock Canyons regions, the status of *P. t. comanche* has long been questioned. Of further interest is whether this population historically was connected to other populations of *P. truei* in eastern New Mexico, or rather, their affiliations lie with *P. truei* populations in northwestern Oklahoma.



The goals of this research project were to:

- Use state-of-the-art genomic research methods to evaluate differences in *P. t. comanche* relative to other subspecies of *P. truei* throughout the western U.S.
- Conduct fieldwork to determine population parameters of *P. t. comanche* in the Palo Duro and Caprock Canyon systems
- Use museum specimens for DNA and morphometric research to augment recently collected vouchers
- Conduct a sophisticated morphometric study to determine whether *P. t. comanche* differs in cranial and body size characteristics

Progress to date:

- First chromosome-level reference genome for the Palo Duro Deermouse, and in general for the species (*Peromyscus truei*).

- 72 genomes representing 10 subspecies across the entire distribution of *Peromyscus truei* were sequenced and evaluated (15 of *P. truei comanche* from the Palo Duro Canyon system). In addition, some closely related species belonging to the *Peromyscus truei* species group (*P. gratus*, *P. difficilis*, *P. nasutus*) were included for comparative purposes.
- Population level genomic analyses indicate that the Palo Duro Deermouse is genetically distinct from neighboring populations. The Great Plains potentially constitutes unsuitable habitat restricting gene flow between neighboring populations.
- 35 external and craniodental measurements were taken from 605 specimens across the entire distribution of *Peromyscus truei*, including 56 from Palo Duro Canyon.
- Multivariate analyses of morphometric measurements revealed that the Palo Duro Deermouse, *Peromyscus truei comanche*, is morphologically unique mainly because of a larger body and tail, but shorter ears, than in nearby populations.
- Genome-wide data and morphology support the recognition of the Palo Duro Deermouse, *Peromyscus truei comanche*, as an evolutionarily distinct unit, which ultimately clarifies its taxonomic status.
- Genomic health diagnostic analyses indicate that the population in Palo Duro Canyon (*P. t. comanche*) has lower overall genetic diversity and higher levels of inbreeding compared to nearby populations (e.g., New Mexico, Oklahoma). Despite this, the genetic load—a measure of deleterious mutations that could impact fitness—was not significantly different between populations.
- Together, these findings provide a foundation for future management decisions.
- Javier Colmenares-Pinzon (right) is using this research as the basis for his PhD dissertation, and he is currently developing at least one manuscript that will focus on this research.

