

Desert Bighorn Sheep in the Trans-Pecos

Funding:

“Status of bighorn sheep in Texas: translocation history, disease risk potential, and establishment of archival tissue collection for range-wide disease surveillance,” awarded to PIs Warren Conway, Robert D. Bradley, Caleb D. Phillips from the Wild Sheep Foundation, \$50,000, 2016-2018.

“Funding for a PhD Student for Bighorn Research,” awarded to PIs Warren Conway, Robert D. Bradley, Caleb D. Phillips from the Texas Bighorn Society, \$160,000, 2016-2018.

Project Summary:

Desert Bighorn Sheep (*Ovis canadensis*) underwent a long period of decline beginning in the late 1800s, and culminated in the extinction of populations in the Trans-Pecos region of Texas that had been uniquely described as *O. c. texianus*. Beginning in the 1970s and continuing to present day, Texas Parks and Wildlife Department (TPWD) has undertaken a variety of efforts to reestablish populations of Desert Bighorn Sheep (DBS) on both private and public areas in the Trans-Pecos. These efforts have included multiple translocations and a captive breeding program. The programs were successful and resulted in at least 1,500 individuals of DBS being present across 11 different mountain ranges.



In 2016, Texas Tech University, in particular the NSRL, joined efforts with the Texas Bighorn Society and TPWD to develop methods for evaluating genetic diversity and to monitor disease. Recently, DBS populations have declined significantly, presumably as a result of pneumonia outbreaks, and it is crucial that genomic methods and state-of-the-art disease monitoring methods be developed to assist in the recovery of DBS.

The goals of this research project were to:

- Develop a genome-based study that allows for the collection of a variety of population genetic endpoints (relatedness, heterozygosity, inbreeding, fitness, etc.) that can be used to help assess the “genetic health” of DBS populations
- Develop a set of genomic markers that can be used for management purposes (selecting individuals for removal, translocation, or breeding purposes)
- Determine the historical genetic footprint of translocations to Texas
- Determine if there is a genetic association with susceptibility or resistance to pneumonia
- Determine if aoudad are involved in transmitting pneumonia to DBS

Progress to date:

- A living Genetic Database has been developed that is additive (new samples can be added in perpetuity) and can be reanalyzed in the future
- Genetic relationships were determined for over 100 individuals at Elephant Mountain Wildlife Management Area (WMA)
- The resolution of the data was sufficiently detailed to determine relatedness among individuals and even in some cases multi-generation pedigrees
- These data are now available for TPWD to use when considering future translocation events and other management decisions
- A new method (multi-locus sequencing) was improved that allows for better genotyping of pneumonia strains (*Mycoplasma ovipneumonia*)
- Hundreds of aoudad and DBS were screened to assess the frequency and geographic distribution of pneumonia-positive individuals
- Emily Wright based her PhD dissertation on these studies and has published extensively on DBS and aoudad. Below is a list of those publications.



Publications:

- Wright, Emily A., Rachael C. Wiedmeier, Emma K. Roberts, David R. Pipkin, II, Froylán Hernández, Joseph P. Bayouth, Warren C. Conway, and Robert D. Bradley. 2022. Distinct mtDNA lineages in free-ranging *Ammotragus* (aoudad) from the US indicate multiple introductions from northern Africa. *Ecology and Evolution*, 12:1-21.
- Wright, Emily A., and Robert D. Bradley. Genetic divergence and mtDNA lineages in six subspecies of aoudad. 2023. *Occasional Papers*, Museum of Texas Tech University, 387:1-11.
- Wright, Emily A., Robert D. Bradley, and Joseph D. Manthey. 2024. Translocations, rising populations, and phylogeographic consequences: Genomic implications for conservation of introduced aoudad (*Ammotragus lervia*) in the southwestern US. *Journal of Mammalogy* gyae078. <https://doi.org/10.1093/jmammal/gyae078>
- Wright, Emily A., Georgina G. Brugette, Kai F. Buckert, Frolán Hernández, J. Hunter Reed, Sara R. Wyckoff, Jace C. Taylor, Kezia R. Manlove, Caleb D. Phillips, and Robert D. Bradley. 2024. Multi-locus sequence typing indicates multiple strains of *Mycoplasma* in desert bighorn sheep and aoudad in Texas. *Journal of Wildlife Management*, 88:1-25.
- Wright, Emily A., Joseph D Manthey, Michael R Buchalski, Bonnie R McKinney, David A Ray, Caleb D Phillips, and Robert D Bradley. 2024. Genomic affinity following restoration of

a locally extirpated species: a case study of desert bighorn sheep in Texas. *Conservation Genetics*. <https://doi.org/10.1007/s10592-024-01635-5>.

Wright, Emily A., Michael R. Buchalski, and Robert D. Bradley. In press. Mitochondrial DNA indicates that extirpated *Ovis canadensis texianus* was a member of the desert bighorn complex. *Occasional Papers*, Museum of Texas Tech University.