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Background:

The Flat-tailed Horned Lizard (Phrynosoma mcallii) is a species of special conservation concern in California, Arizona, and Mexico. Much of this lizards' range in the United States is found on public land including various military installations. From 1993 to 2011, P. mcallii was scrutinized for protection under the federal Endangered Species Act, but in a series of court cases, the U.S. Fish & Wildlife Service (USFWS) withdrew the proposed 1993 rule four times. In 1997, multiple state and federal agencies with populations of P. *mcallii* on their lands signed a voluntary Interagency Conservation Agreement (ICA) to implement the Flattailed Horned Lizard Rangewide Management Strategy (FTHL RMS). One of the major goals of the ICA is to "encourage and support research to promote conservation of [P. mcallii] and desert ecosystems" (FTHL RMS 8), specifically to "determine genetic variation among populations and effects of barriers." NAVFAC Southwest, NAF El Centro, and MCAS Yuma are three of the 13 federal and state agencies that are signatories to the RMS.

Objective:

The objectives of this study were to determine which populations of *P. mcallii* have the highest genetic diversity (heterozygosity), and how these levels compare to other benchmark species; to determine how many populations are there and how are they related to each other; to determine the main natural barriers to gene flow (migration) across the range of this species; and to determine how to incorporate patterns of genomic diversity and gene flow into predicting the effects of projects and other manageable impacts in the Colorado Desert region on long-term population viability.

Summary of Approach:

Thousands of nuclear loci were collected from across the genomes of 41 individuals across the range of this species using restriction-associated DNA sequencing. From these data we found that P. mcallii has unexpectedly high heterozygosity, possibly resulting from hybridization with neighboring species of horned lizards, or a very large ancestral population size. We analyzed these data with phylogenetic methods that indicate northwestern populations are nested within southeastern ones, and fixation index (FsT) values

indicate relatively high rates of historic migration between these populations. For Open Publication

Benefit:

This research enhances strategic planning and Department of Defense OFFICE OF PREPUBLICATION AND SECURITY REVIEW management of DoD's natural resources by developing a modern genetic fingerprint of extant FTHL populations. These results uncovered phylogenetic relationships, and historic corridors and barriers to gene flow that will help in protecting processes crucial to survival of the species into the foreseeable future. This information will aid resource managers at installations in assessing project level impacts to the species.

Accomplishments:

This study represents the first time genomic data were used to analyze the demographic history and population structure of Flat-tailed Horned Lizards. Prior efforts used orders of magnitude fewer informative markers in their genome, and the present study provides a much more thorough understanding of this species genetic diversity, and phylogeny. This information is crucial to managing the species in perpetuity so that unique haplotypes are protected and corridors to movements are identified and maintained. For example, we modeled estimated effective migration rates between local populations and effective diversity rates within populations, which confirmed that the Colorado River and Salton Sea constitute the main barriers on the landscape. Furthermore, the population on the Barry M. Goldwater Marine Corps Air Station also represents an effective diversity hotspot for this species. Given the numerous anthropogenic barriers that now fragment remaining populations, these data indicate that a land management strategy focused on maintaining connectivity between management areas may be most effective.

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