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# Conservation genomics of the Mexican Wolf

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Title:

Conservation Genomics of the Endangered Mexican Wolf

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Abstract:

The Mexican wolf (*Canis lupus baileyi*) was extirpated from the southwestern US and Mexico by 1980. During this time, however, a certified (McBride) and 2 additional (Aragón and Ghost Ranch) captive breeding programs were established. The three independent lineages are descended from three, two, and two individuals, respectively. Over time, the small number of founders for each captive lineage resulted in a high level of inbreeding. To mitigate this, the three captive wolf lineages were merged in 1995. The merger led to an increase in fitness traits, known as genetic rescue, in cross-lineage wolves. In 1998, Mexican wolves were reintroduced into Arizona and New Mexico. Currently, the free-ranging wolf population numbers approximately 50 individuals. Previous genetic studies using up to 20 microsatellites have measured levels of relatedness and genetic variation among wolves. Despite these studies, numerous concerns remain, including: the purity of founders (whether or not they have mixed with domestic dogs or coyotes in the past), the extent of inbreeding in the captive and wild populations, and the current distribution of genetic variation from the founders. We are examining these concerns using genomic technologies developed for the domestic dog. We are analyzing ~90 Mexican wolves for more than 173,000 SNPs (single nucleotide polymorphisms). We will use our results to improve the design of the captive breeding and reintroduction programs, in addition to investigating questions regarding more ancestral evolutionary processes. This presentation will highlight the basic methodologies of the project and provide some preliminary results.