

*Captive Breeding Protocols and Their Impact on Genetic Diversity in White-footed Mice (*Peromyscus leucopus*): Implications for Threatened and Endangered Species*

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Captive breeding protocols used in zoos often are aimed at increasing population sizes and retaining genetic diversity of endangered species. However, captive breeding causes genetic adaptation to captivity that can lead to an overall decrease in genetic diversity and reduce chances of a successful reintroduction to the wild. In this study, we assess how 3 different breeding protocols—random mating, preferential breeding of individuals with the lowest mean kinship scores, and selection for docility—affect the variability of mitochondrial DNA in white-footed mice (*Peromyscus leucopus*). We used mice that were captured from the wild but were mated for up to 20 generations using one of the aforementioned breeding protocols. Using animals from generations 0, 6, and 19, as well as the wild source population, we sequenced the mitochondrial D-loop in 2 replicate populations representing each of the 3 breeding protocols. Initial sequences indicate there is genetic variation at this mitochondrial locus, and further sequencing will allow us to quantify the genetic diversity maintained under each breeding protocol. These results will increase our understanding of the decline in genetic diversity due to adaptation to captivity. Thus, our results will have direct relevance for the maintenance and growth of zoo populations of critically endangered species.