

Work Task C43: Population Demographics and Habitat Use of the California Leaf-Nosed Bat, a Genetic Evaluation

FY15 Estimate	FY15 Actual Obligations	Cumulative Expenditures Through FY15	FY16 Approved Estimate	FY17 Proposed Estimate	FY18 Proposed Estimate	FY19 Proposed Estimate
\$25,000	\$24,984.19	\$110,099.63	\$40,000	\$0	\$0	\$0

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Start Date: FY11

Expected Duration: FY16

Long-Term Goal: Assess the population demographics and habitat use of the California leaf-nosed bat

Conservation Measures: CLNB1 and CLNB2

Location: Reaches 3–5

Purpose: The purpose of this work task is to investigate the genetic variation in California leaf-nosed bats at roost sites along the lower Colorado River (LCR) to inform program managers about the connectivity of the species' populations and level of rarity. This will include an analysis of the genetic history of California leaf-nosed bats along the LCR watershed and adjacent areas, including geographic structuring, evolutionary history, and other population demographic parameters.

Connections with Other Work Tasks (Past and Future): A portion of the roost site data and tissue samples analyzed were collected under Work Tasks D9 and F4.

Project Description: The genetics of California leaf-nosed bats along the LCR will be described. Genetic samples from each of the known roost sites near the LCR and from individuals captured during system-wide monitoring will be collected, and DNA sequencing and microsatellite analyses will be performed. This will document the genetic structuring of bats at roost sites and allow for various population analyses, including the connectivity of the species' populations and level of rarity, as well as demographic parameters to be estimated such as population size, previous population expansion or contraction, and dispersal among roosts, which may suggest which roost sites or areas along the river the bats netted at LCR MSCP conservation areas are coming from.

Previous Activities: Genetic samples and mitochondrial sequencing for samples collected prior to FY12 were conducted under Work Task G3. Additional samples were collected at roosts. A total of 917 base pairs of the mitochondrial cytochrome B gene have been sequenced, and these sequences were used to create haplotype networks and neighbor joining trees to explore diversity and relatedness among roosts.

FY15 Accomplishments: Microsatellite-enriched whole genome data for six individuals were received from the genome sequencing laboratory. The data were combined across the six individuals to allow for filtering and selection of an informative microsatellite dataset that will be used to identify possible population genetic patterns in the genetic samples from 91 individuals.

FY16 Activities: Next-Gen genetic data will be filtered down to an informative microsatellite dataset, and the analysis of population demographics of California leaf-nosed bats based on the genetic results will be completed. The final report will be written, which can be used to guide future management actions for California leaf-nosed bats along the LCR.

Proposed FY17 Activities: The work task will be closed FY16.

Pertinent Reports: A report titled *Genetic Characterization of *Macrotus californicus* Populations along the Lower Colorado River – 2010 Annual Report* is posted on the LCR MSCP Web site. The annual reports will also be posted upon completion.