

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

FY14 Estimate	FY14 Actual Obligations	Cumulative Expenditures Through FY14	FY15 Approved Estimate	FY16 Proposed Estimate	FY17 Proposed Estimate	FY18 Proposed Estimate
\$50,000	\$57,873.82	\$83,294.29	\$25,000	\$40,000	\$0	\$0

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Start Date: FY11

Expected Duration: FY16

Long-Term Goal: Assess the population demographics and habitat use of an LCR MSCP evaluation species, the California leaf-nosed bat

Conservation Measures: CLNB1 and CLNB2

Location: Reaches 3–5

Purpose: To investigate the genetic variation in California leaf-nosed bats at roost sites along the 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 in 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 collected from bats netted at restoration sites will be contributed from that 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 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 various population analyses, including the connectivity of the species' populations and level of rarity, and demographic parameters to be estimated such as population size, previous population expansion or contraction, and dispersal between 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 were gathered, 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.

FY14 Accomplishments: The majority of the sampling effort has been completed. A total of 99 samples from the LCR and other areas within the species' range have been collected. In FY14, samples from two localities away from the LCR, Picacho Peak and the Sawtooth Mountains, were collected to fill gaps in the range of California leaf-nosed bats in Arizona. In addition, representative samples were submitted for Next-Gen sequencing to identify specific genetic markers that will best contribute to the full-scale analysis of the genetic diversity and relatedness among roosts.

FY15 Activities: Additional samples will be collected or obtained from other researchers in order to make comparative assessments on the relative uniqueness and diversity of California leaf-nosed bat colonies along the LCR. Next-Gen sequencing will be completed, and genetic analyses of all the samples will begin.

Proposed FY16 Activities: Genetic analyses and the analysis of the population demographics and habitat use of California leaf-nosed bats based on the genetic results will be completed.

Pertinent Reports: A report titled *Genetic Characterization of *Macrotus californicus* Populations along the Lower Colorado River—2010 Annual Report* is available on the LCR MSCP Web site. The research design is available upon request.