

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

FY16 Estimate	FY16 Actual Obligations	Cumulative Expenditures Through FY16	FY17 Approved Estimate	FY18 Proposed Estimate	FY19 Proposed Estimate	FY20 Proposed Estimate
\$40,000	\$39,374.35	\$157,220.76	\$0	\$0	\$0	\$0

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Start Date: FY11

Expected Duration: Closed in FY16

Long-Term Goal: Assess the population demographics and habitat use of the California leaf-nosed bat (*Macrotus californicus*)

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. 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 deoxyribonucleic acid (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 were sequenced, and these sequences were used to create haplotype networks and neighbor joining trees to explore diversity and relatedness among roosts. Microsatellite-enriched whole genome data for six individuals were received from the genome sequencing laboratory. The data were combined across the six individuals to identify possible population genetic patterns in the genetic samples from 91 individuals.

FY16 Accomplishments: Genetic analyses were completed. The cytochrome *b* mitochondrial sequences from 99 individuals from 17 localities along the LCR, the Southwestern United States, Baja California, and northern Mexico were used to create haplotype networks and neighbor joining trees to explore diversity and relatedness among roosts. There were 18 haplotypes identified across the range, with 5 haplotypes present in the samples taken from the LCR and 3 haplotypes unique to the river. Genotypic clustering analyses of 6 microsatellite loci across 87 individuals from 19 localities were conducted.

The results indicated that there are two genetic groups present in the species range, with none being unique to the LCR and surrounding areas, and low levels of genetic variation in the northern range of the species, which is typical of animals residing at an edge of a species' range or a recent range expansion.

FY17 Activities: The work task was closed in FY16.

Proposed FY18 Activities: The work task was closed in FY16.

Pertinent Reports: The *Genetic Characterization of *Macrotus californicus* Populations along the Lower Colorado River – 2016 Annual Report* is posted on the LCR MSCP Web site. The final report will also be posted upon completion.