## Work Task C43: Population Demographics and Habitat Use of the California Leaf-Nosed Bat

FY09 Estimates	FY09 Actual	Cumulative Accomplishment Through FY09	FY10 Approved Estimate	FY11 Proposed Estimate	FY12 Proposed Estimate	FY13 Proposed Estimate
\$0	\$0	\$0	\$0	\$20,000	\$60,000	\$40,000

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Start Date: FY11

**Expected Duration:** FY13

**Long-term Goal:** Determine the population demographics and habitat use of an LCR MSCP evaluation species, the California leaf-nosed bat (*Macrotus californicus*).

**Conservation Measures:** CLNB1, CLNB2

**Location:** Reaches 3-5

**Purpose:** This work task is being initiated to evaluate the status of *M. californicus* along the LCR. This research is designed to determine the population history of *M. californicus* along the LCR, including geographic structuring, evolutionary history, and other population demographic parameters, using modern molecular techniques. This study is also designed to determine the distribution of genetic variation in *M. californicus* roost sites and identify where individuals from different roosts are foraging. This will allow a better understanding of how far individuals are willing to travel to forage (currently assumed to be only 5 miles) and what constitutes appropriate habitat. Doing so will provide important information for use in developing future conservation efforts for this species.

Connections with Other Work Tasks (past and future): Data on roost site location and samples collected from Conservation Areas will come from surveys conducted under D9. This data will also incorporate work from F4 by identifying nightly movement patterns from the different roosts to the various conservation areas, and possibly pinpointing foraging sites that are preferred. Initial study design and collection of genetic samples in FY10 will be conducted under G3.

**Project Description:** Genetic samples taken from bats from each of the known roost sites near the LCR and from individuals captured during regular system and post-restoration monitoring will be collected, and DNA sequencing and microsatellite analyses will be performed. This will document the genetic structure of roost sites and allow various population demographic parameters to be estimated. These parameters include

population size, previous population expansion or contraction, and dispersal between roosts. Individuals collected during restoration site monitoring will be assigned to the most likely roost site based on their unique genetic signature. Distance from roosts to restoration sites and other pertinent habitat information will be determined using GIS.

**Previous Activities:** This is a new start in FY11.

**FY09 Accomplishments:** This is a new start in FY11.

**FY10 Activities:** Study design and initial genetic sampling from individuals will begin at roost locations and conservation areas under G3.

**Proposed FY11 Activities:** A protocol will be developed for microsatellite analysis. Sequencing candidate genes will begin and preliminary genetic data will be generated. Collection of genetic samples will continue from conservation areas. Distance to the nearest roost will be determined from known conservation areas, and what roost bats are most likely coming from will be determined.

**Pertinent Reports:** A summary of results will be posted on the LCR MSCP Web site. The study design is available upon request.