Designing a conservation strategy for the California leaf-nosed bat (*Macrotus californicus)*: a genetic approach

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Introduction

- Year round resident of the LCR

- Species of special concern in AZ, CA

- MSCP evaluation species

Introduction

- Evaluation species – currently not enough information to develop a conservation plan

- Develop a conservation plan for *Macrotus*
    - Incorporate historic (mtDNA) and recent (microsat) genetic data with observational data
    - Prioritize conservation efforts
    - Generate baseline data
    - Know what we are conserving

Goals

- Provide information regarding:
  - population structuring
  - effective population size
  - genetic diversity
  - phylogeographic history

- Possibly:
  - Identify movement patterns and site preferences
  - Identify differences between sexes

Phylogeographic Hypotheses

- Determine how the LCR populations fit into the broader genetic diversity of the species
  - Some Phylogeographic Hypotheses
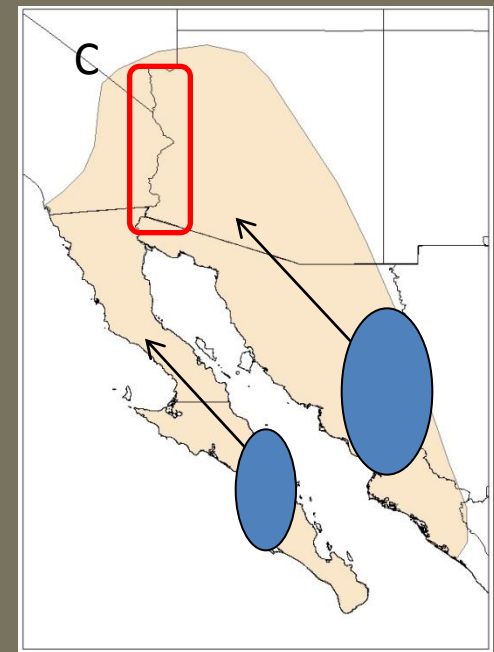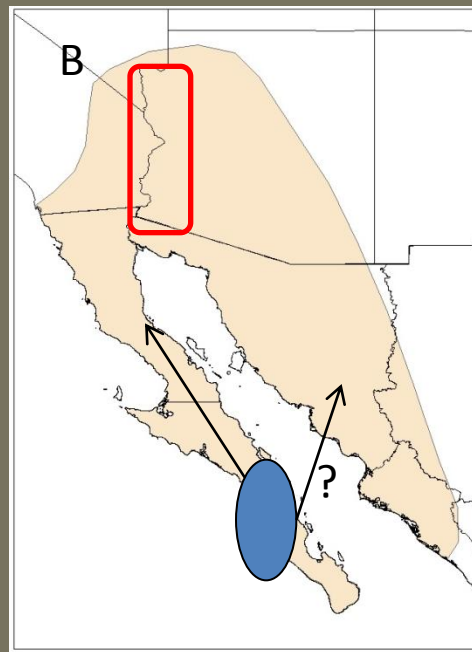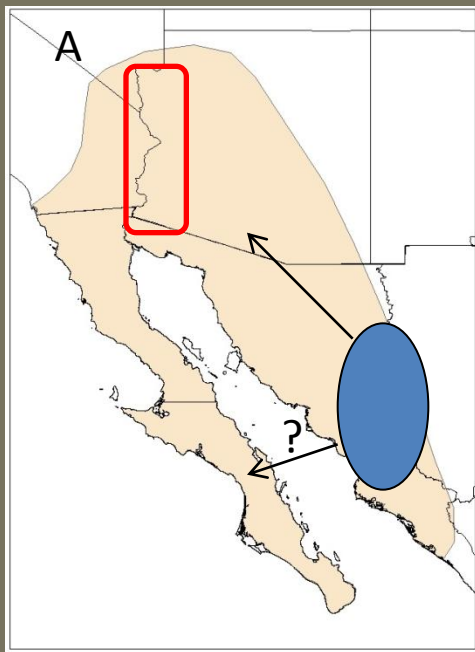
A and B both have single source populations, whereas C shows a scenario where two different populations diverged and have come back into contact around a barrier.

More on hypotheses

- Northern portion of range is likely very recent
  - Coincident with mining
- Alternatively
  - Migrated
 - Underwent a natural history change with mining

Methods

Sampling

- ≤ 15 samples from each cave at dusk along the LCR known to have *M. californicus* during winter (and possibly during breeding)

- 2 mm biopsy punch or liver from voucher specimens

- Tissue from museum specimens will be obtained to include representatives of the species from outside the LCR as an out group
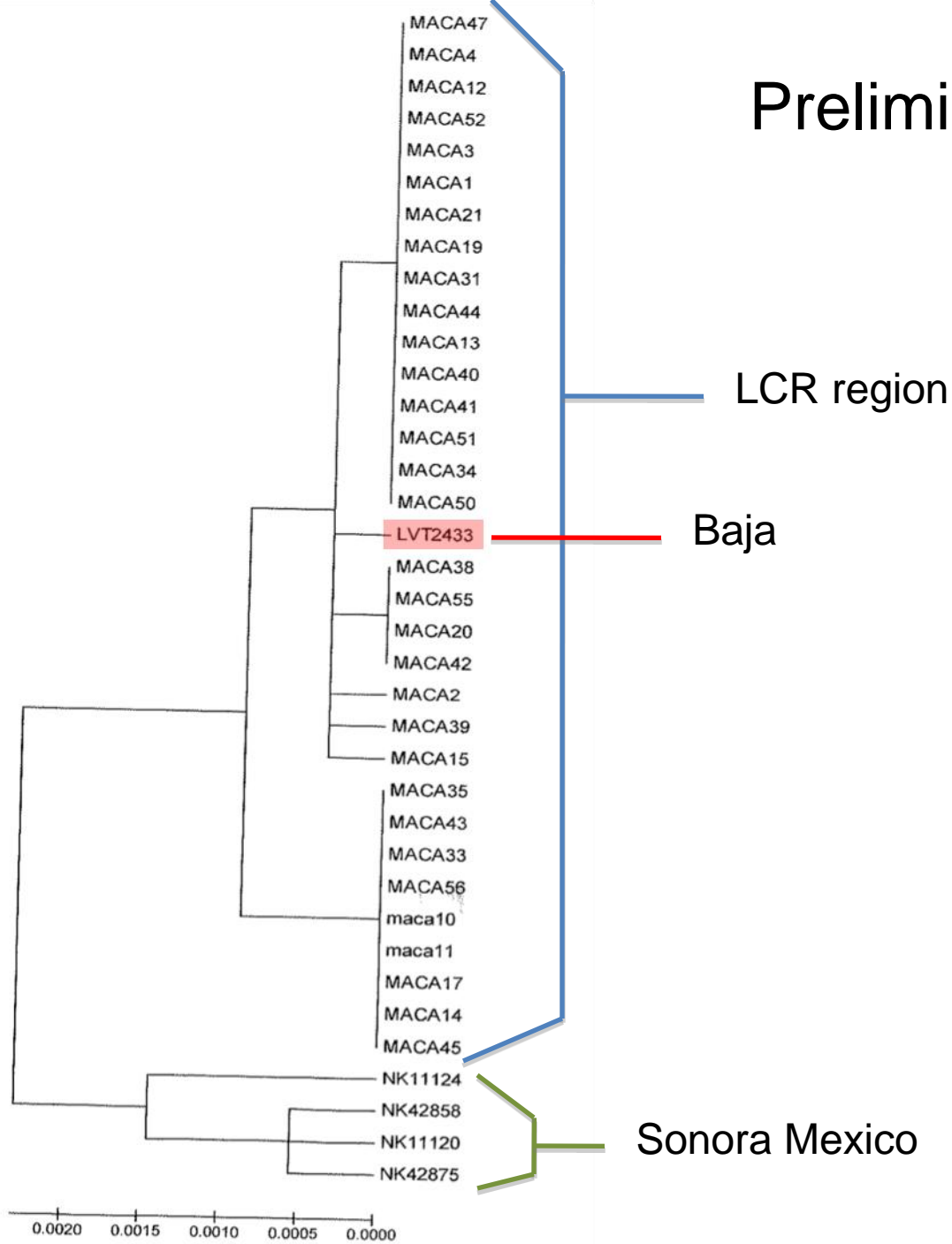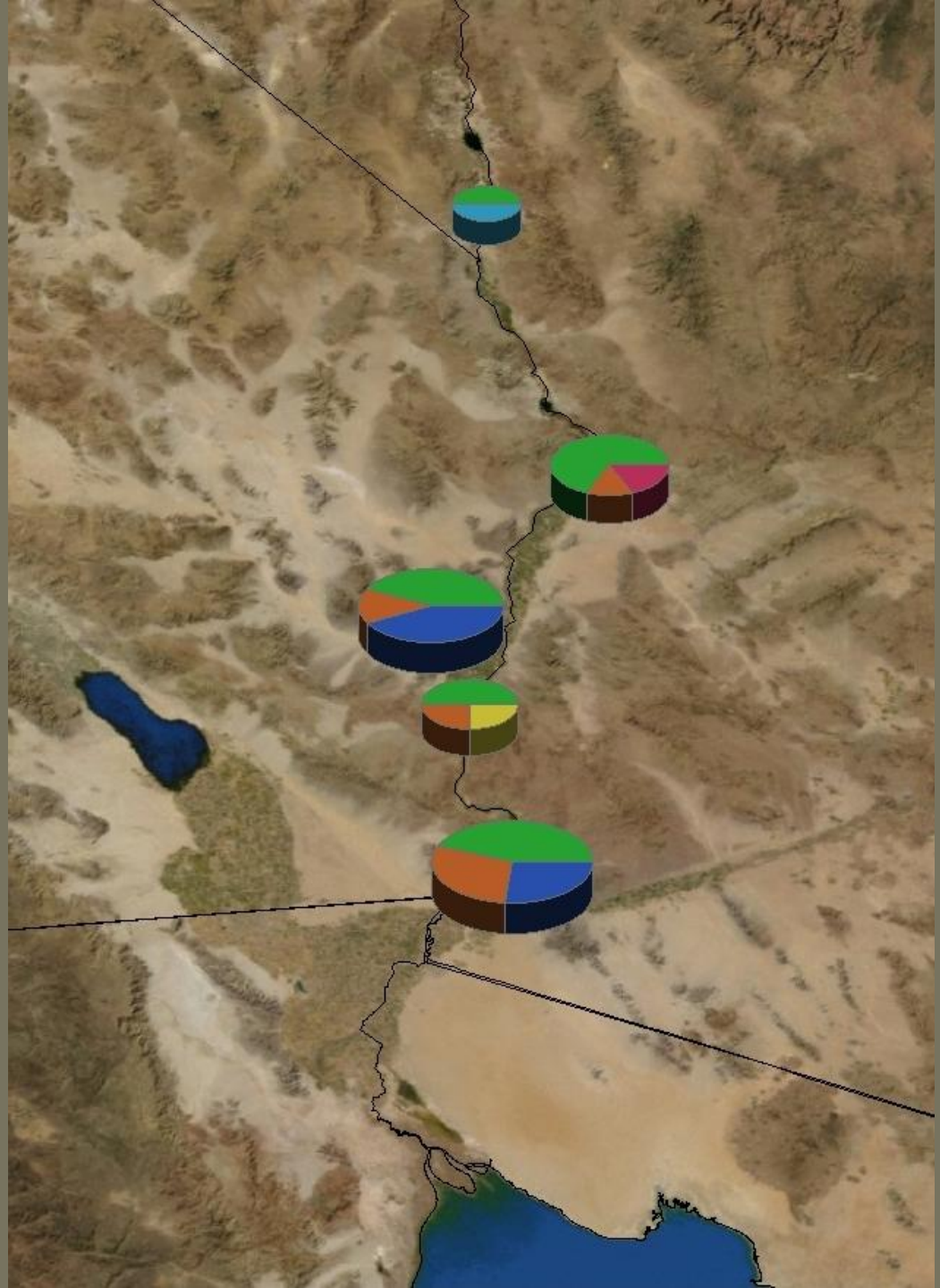
Range
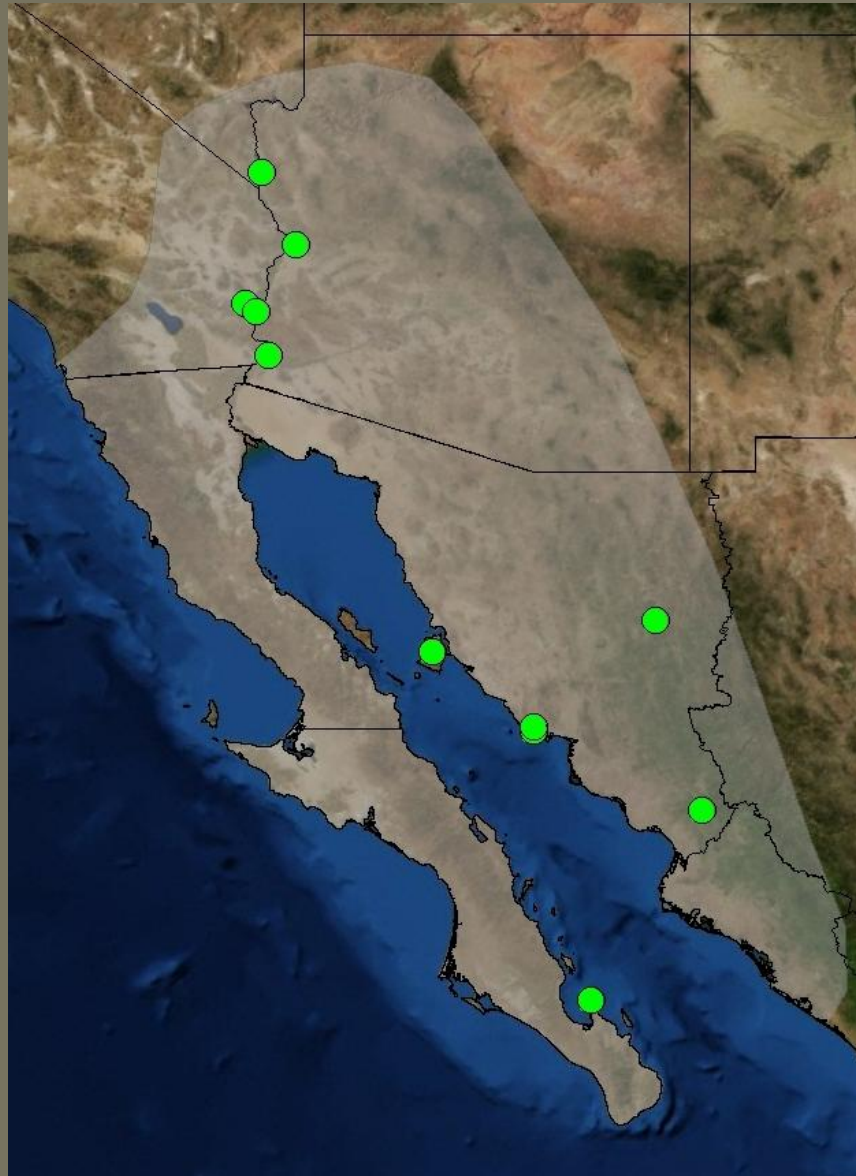
Sequencing/Analysis

- ~1000 Base pairs of the cytb for phylogeographic analysis

- 38 individuals so far

- Phylogenetic tree

Preliminary Results

LCR region

Baja

Sonora Mexico

- Pie size relative to # of individuals per locality
- Each color = unique haplotype
- We have diversity!

Discussion

- Future Directions
  - Finish mtDNA
  - More sampling in AZ, CA, MX?
  - Microsatellites
  - Estimate population size
  - Population structuring
  - Gene flow

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