Conservation genetics of *Macrotus californicus* along the lower Colorado River

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Macrotus californicus

- *Phyllostomidae*
- Non hibernatory/migratory
- High philopatry
- Narrow thermoneutral zone
- Breeding
- Year round resident of the LCR
- MSCP evaluation species
- Species of special concern in AZ, CA

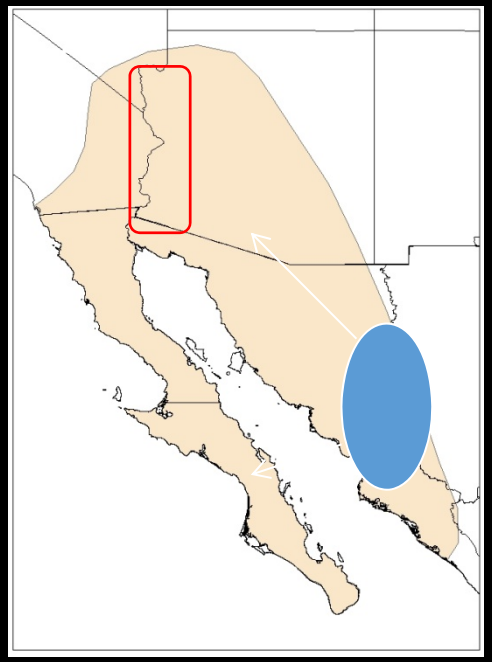
Objectives

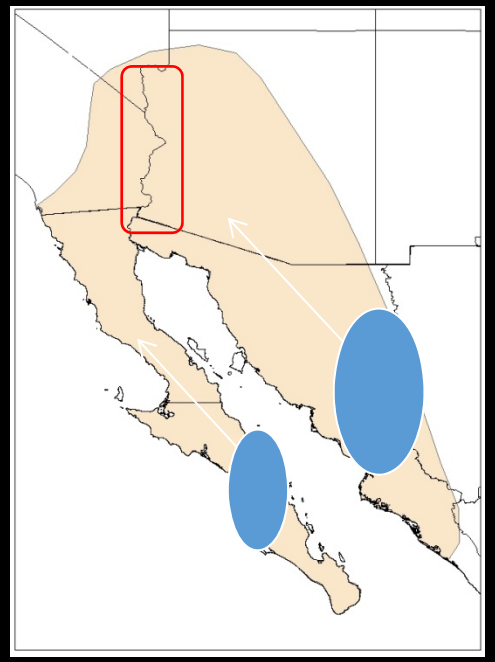
- Document genetic structuring of roost sites along the LCR
- Provide estimates for current and historic effective population size of the LCR population, including the timing of changes of population size.
- Provide information about the space use and foraging habitat requirements of *M. californicus* along the LCR

Hypotheses

- Mining efforts in the last 200 years has allowed *Macrotus* to expand North into areas previously unsuitable
- *Macrotus* have dispersed north using rivers as dispersal corridors.
- Due to the highly philopatric nature of *Macrotus*, there will be genetic structuring between LCR and Sonoran populations AND among LCR populations

- Determine how the LCR populations fit into the broader genetic diversity of the species
  - Some Phylogeographic Hypotheses





Predictions

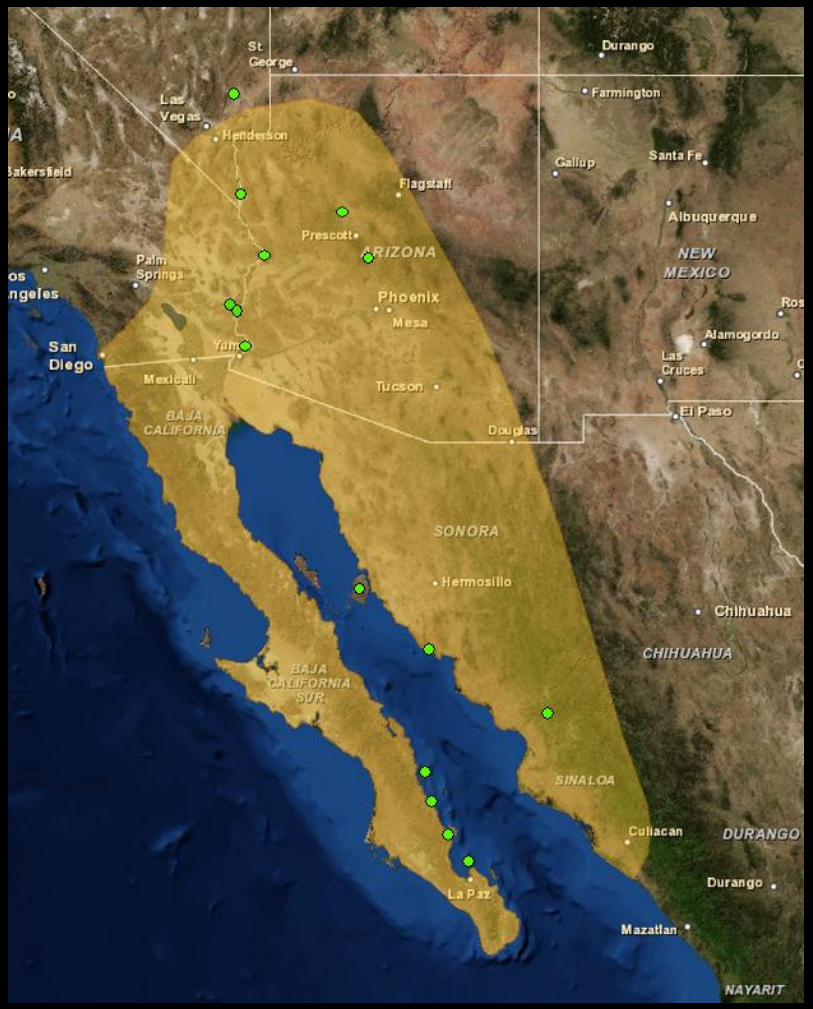
- Northern populations will have less diversity
  - In 200 years, would not have time to build a reasonable subset
  - Increased Fst between founder populations
- No unique alleles
  - Not enough time

Importance and Applications

- Know what we are conserving
- Inform conservation and management plans
  - Isolation, migration, fragmentation issues
- Optimize conserved genetic diversity per dollar spent
- Genetic Diversity ex: Florida Panthers, Tasmanian Devils
- MSCP evaluation

Study area, sampling localities

- 48 from 5 localities along LCR
- 11 samples from 4 localities in Baja
- 8 samples from 3 localities in Sonora
- 6 from 3 U.S. non-LCR



Sampling

- ≤ 15 samples from each cave at dusk along the LCR known to have *M. californicus*
- 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

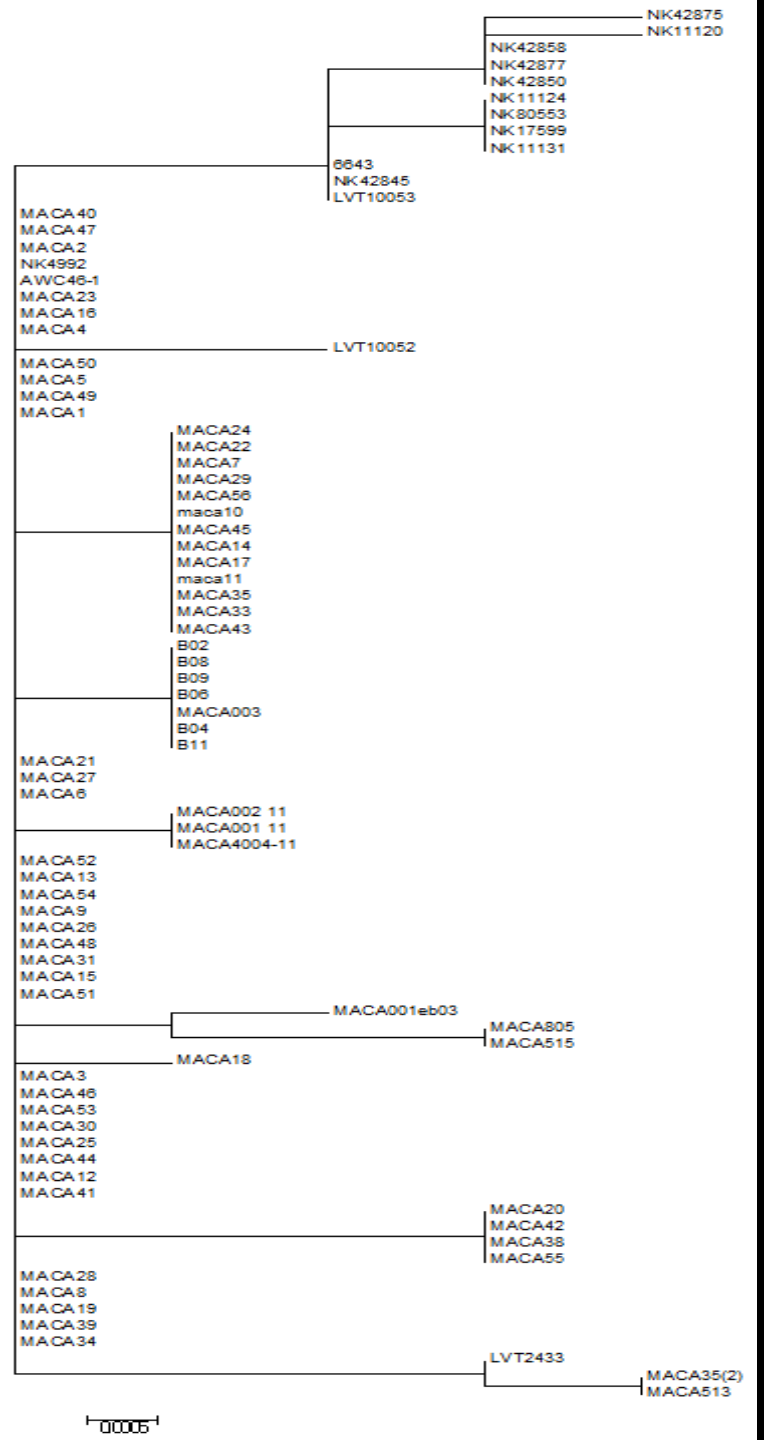
Sequencing

- ~1000 base pairs of CO3 mitochondrial gene region
- Additionally, looking into highly variable microsatellites or other high-throughput genomic DNA sequencing

Analysis

- Fst: Population differentiation due to genetic structure
  - Range from 0 (no genetic differentiation) to 1 (fixation of alternative alleles)
  - 0 – 0.5 = little differentiation, >0.25 large differentation
- Θ: Unbiased estimator of Fst that corrects for error associated with incomplete sampling of populations
- Ψ: Gives directionality of gene transfer
- Phylogenetic trees/networks
- Bayesian Skyline plots
- AMOVA

- Programs used: Arleqiun, MEGA, STRUCTURE (assignment tests)



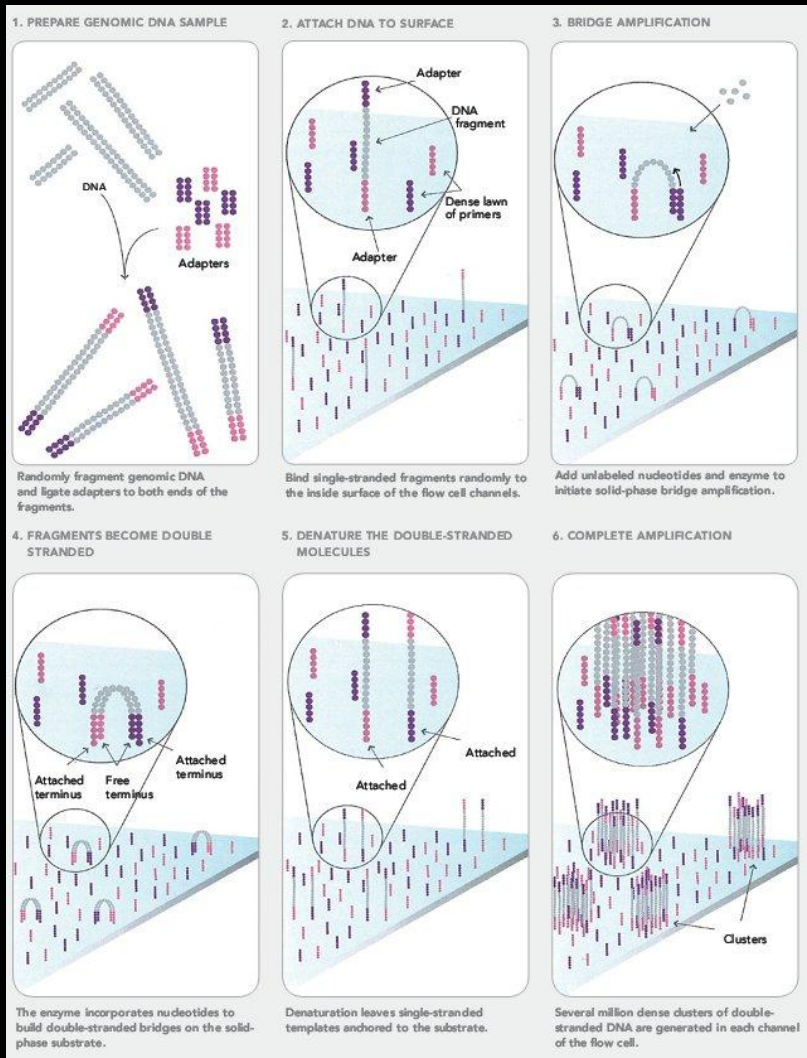
MtDNA tree

- Gene flow between LCR + Baja
- Gene flow between Sonora + LCR

Future work, timeline

- Next-gen sequencing
  - Illumina, Pyrosequencing
  - RAD-seq, microsatellites

- 2014: Finish collecting, select next-gen sequencing method/company, begin analysis
- 2015: Complete analysis, write final report/thesis



Conservation genomics

- More markers = more accurate!
- Non-model organisms!
  - Recent demographic events
  - Genetic Variation
  - Population Structure
  - Fecal analysis
  - Identifying conservation units
  - Disease susceptibility
    - Tasmanian Devil, Florida Panther et al.
  - QTL mapping
    - The role of natural selection at the genome level, and the identification of loci associated with fitness, including local adaptation, inbreeding depression, or disease susceptibility, can also be dissected by implementing quantitative trait loci (QTL) analyses

Discussion

- Preliminary mtDNA results suggest gene flow between LCR, Baja, and Sonora
  - Not enough sampling localities
- Combining data from traditional survey methods with data from genetic analysis
  - Banding data
  - Climate modeling
- How best to apply knowledge gained to *Macrotus* and other MSCP species

Help us help *Macrotus*!

- Need tissue samples from SE Arizona, S California, mainland Mexico and the Baja peninsula

- If I haven't already bothered you, and you know where you can find ^, come talk to me after the presentation!

Acknowledgements

- Pat Brown
- Brett Riddle
- Allen Calvert
- Ronnie Mixan +AZGFD
- UNLV systematics discussion group

Gene Flow/Population Structuring

Historical gene flow can be inferred from population genetic structure (e.g. from Fst). Greater genetic differentiation implies lower gene flow and vice versa.

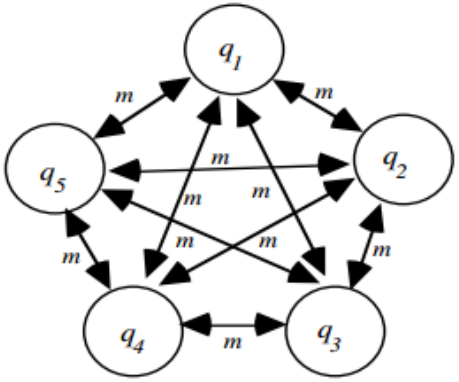
Statistical methods exist to relate genetic distance estimates to a parameter called Nm, which is the average number of immigrants per generation.

Wright's Fst $\quad Fst = \dfrac{1}{4Nm + 1}$

WRIGHT'S ISLAND MODEL

Sewell Wright (1931) imagined an ancestral population that was broken up into an array of partially isolated demes, each of effective size N. In the absence of selection, genetic differentiation among subpopulations results from an equilibrium between genetic drift (a function of N) and gene flow (m). At equilibrium, and for small values of m, F_{ST} is related to gene flow in the following way:

$$F_{ST} \approx \frac{1}{4Nm + 1}$$



Discussion

- The availability of genomic data increases the statistical power to tease apart changes in genetic variation and allele frequencies due to demography versus selection
- Conservation biologists frequently seek to estimate the spatial scale of gene flow to examine historical and contemporary population connectivity
- Wright's fixation index (F_{ST}): a measure of population differentiation that is due to genetic structure; it measures the fraction of the total genetic variation that is distributed among subpopulations relative to the total population

Effective population size estimates

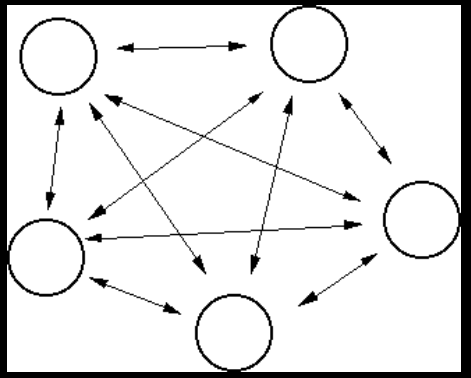
- Sewall Wright introduced the theory of effective population size (Ne)
- Ne = The number of individuals in a population that contribute to offspring in the following generation
- Coalescent based genetic analysis can infer effective population size
- Why is this important?

- Conservation Genetics
- Genetic Diversity / inbreeding depression examples
- Population Genetics / Phylogeography
- Population structure
- Gene Flow
- Effective population size
- Evolutionarily Significant Unit

Next-gen possibilities

- Conservation questions that can be asked
  - Gene flow (examples)
  - Poo analysis
  - Look to Javier’s paper

Dispersal patterns

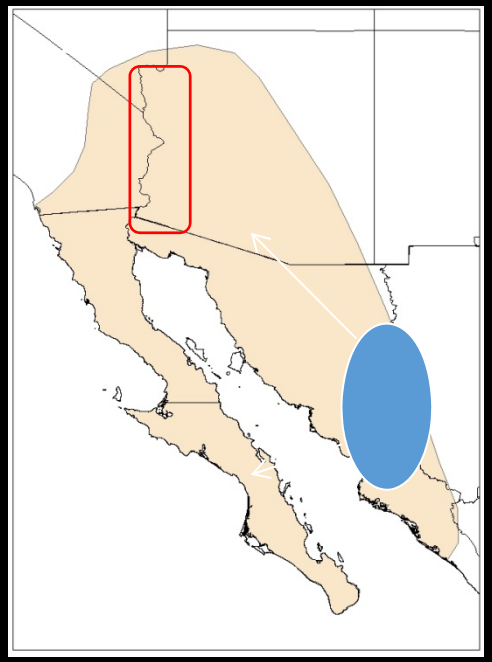


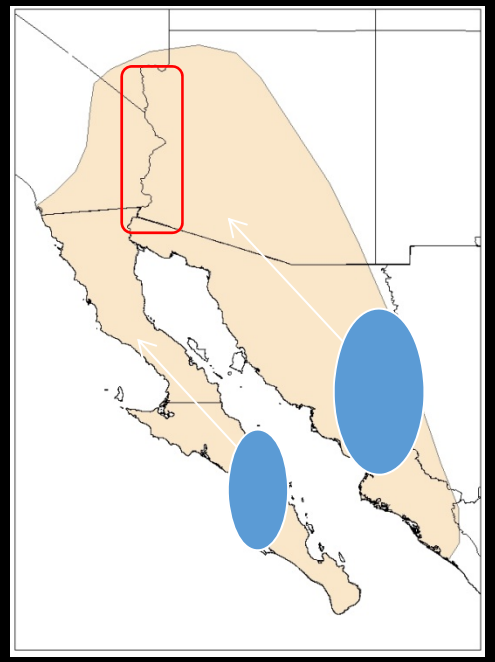
- Dispersal models
  - Continent-Island model: gene flow from large “continent” population to smaller “island” populations
  - Stepping Stone: Many small populations, sequential gene flow among populations, migration between
  - Isolation By Distance: Genetic differentiation is correlated with geographic distance
- Do *Macrotus* utilize rivers as dispersal corridors?
  - Sequential dispersal along rivers
  - What signals would I expect were this the case?
  - Remove words, add pictures

Fst results

Hypotheses

- Mining efforts in the last 200 years has allowed Macrotus to expand into areas previously unsuitable
  - Some scenarios





A and B both have single source population, whereas C shows a scenario where two different populations diverged and have come back into contact around a barrier.

Importance and Applications

- Population Genetics / Phylogeography
- Conservation Genetics
- Gene flow, population structuring
  -Maternity, Winter roosts
- Roost Assignment
- Effective population size
- Genetic Diversity ex: Florida Panthers
- MSCP evaluation