

Refined California Bighorn Sheep Taxonomy Project Goals (Feb 2019)

The objective of this project is to provide genetic analysis to inform management of “California” bighorn, given the long history of translocations and founder effects for those populations.

Specifically, we wish to provide data and analysis to help managers determine whether they should:

- I) Preserve existing genetic structure and make no additional effort to increase or maintain genetic diversity beyond existing management practices (business as usual?);
- II) Or, preserve distinction between “California” and “Rocky Mountain” populations, but encourage more genetic mixing across “California” populations to preserve identified diversity within that potential lineage and increase genetic diversity for populations showing signs of inbreeding/very low diversity (*identify thresholds*)
- III) Allow, or work harder to prevent, mixing between “California” and “Rocky Mountain” origin populations

We have identified the following prospective goals (*we need to not take on too much in the first crack at this, but it seemed good to capture a range of goals*):

- 1) Develop a genome-wide and range-wide genetic dataset and protocol for generating additional data that can be used flexibly to address questions ranging from phylogenetics, inbreeding depression, characterizing fitness-related genetic variation, and demographics
 - a. Should be repeatable and publically available
- 2) Determine whether “California” bighorn (CAB) are a distinct lineage, or are part of the variation within the Rocky Mountain bighorn (RMB) lineage
 - a. Establish clear criteria!
 - b. Determine whether differences between CAB, RMB populations represents selection deep historical differentiation, or simply drift resulting from the two having been managed separately for a few generations?
- 3) Identify potential *thresholds* of genetic diversity below which intervention may be warranted
 - a. Estimate inbreeding depression (much better estimates are possible with genomic data!) in a subset of reintroduced CAB populations and assess correlation with other indices of genetic diversity (e.g., existing microsatellite or SNP data, to make it easier to act on existing data)
 - b. Ultimately, make it possible to link these estimates to existing or future demographic data
- 4) Estimate what proportion of genetic variation exists in native versus reintroduced range of CAB

- a. For instance, what proportion of variation was captured in the reintroductions at local, state, national scale, compared to what remains in native range?
 - b. Assess adaptive genetic variation, e.g., MHC alleles
 - i. Determine whether differences between CAB, RMB populations seen in previous work with neutral markers extends to differences in genes/alleles for adaptive traits
 - c. Suggest strategies to maintain as much of the diversity remaining as possible
- 5) Determine whether reintroduced CAB in U.S. exhibit an adaptive mismatch with their current habitat
- a. Need to develop methods to consider this piece. Focus on genes for horn development, body size, etc?
 - b. Explore genetic consequences in mixed populations (CAB & RMB in same location)- Examples from North Dakota, Washington, Oregon, other states? (intentional and accidental mixing)
- 6) Clarify phylogenetic position of historical samples from OR, WA, ID (what used to be there). This might be a spinoff project.