Impact of historical climate change on the genetic structure of the Great Basin Pocket Mouse, Perognathus parvus

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**Introduction**

The dynamics of genetic patterns, such as genetic differentiation within and between populations and the geographic distribution of genetic lineages, are often influenced by historical events (such as climate changes) that have substantially impacted regional biodiversity (the study of phylogeography; Avise, 2000). The magnitude of genetic differentiation among populations is often increased if suitable habitat is reduced, because there is restricted migration among populations. When migration is restricted, the populations may become genetically differentiated from conspecific populations or, over time, may become independent lineages that follow distinctive evolutionary trajectories (Stebbins, 1951; Novis & Beles, 1989; Thomas et al., 1989). In particular, glacial cycles often result in expansion and contraction of suitable habitat for organisms, which we might predict leads to a similar expansion and contraction of organismal populations. Understanding the impact of past glacial-interglacial cycles (Figure 1), and thus climate changes, on species and species assemblages can help us understand what we may expect from current and future climate change trends.

The Great Basin and Columbia Plateau (Figure 2) comprise the middle to northern portions of Nevada, and these regions have been greatly impacted by Pleistocene climatic cycles (Thompson, 1990). Since the Last Glacial Maximum (ca. 10,000 years before present), the Great Basin and habitats have expanded while more geostationary areas, such as shrub-steppe habitats (Figure 3), have contracted. This has likely affected the distributions of resident species such as the Great Basin Pocket Mouse, *Perognathus parvus*. *Perognathus parvus*, an indicator species for shrub-steppe habitat, is abundant and relatively easy to sample, which makes it an ideal taxon to test the influence of past climate changes on evolutionary dynamics of lineages in the Great Basin and Columbia Plateau shrub-steppe habitats. For these reasons, I will evaluate the genetic structure within and among *P. parvus* populations throughout the Great Basin and Columbia Plateau.

**Methods**

I will sequence several genes from 183 previously collected *Perognathus parvus* tissues that have been deposited in the Las Vegas Tissue collection from throughout the range of *P. parvus* (Figure 2). To sequence DNA, I am doing DNA extractions (Figure 4). Polymerase Chain Reaction (PCR) (Figure 5), and cycle-sequencing. I will sequence four total genes so that we can identify both recent and older divergences: two relatively fast-evolving mitochondrial genes, Cytochrome b and Control Region; rapidly evolving nuclear Amplified Fragment Length Polymorphisms (AFLPs); and a slower evolving nuclear gene (Rag-1).

I will subsequently implement valuable phylogeographic inference methods, such as molecular dating of divergence events and phylogenetic tree and haplotype network construction. Use of these methods will allow me to infer the genetic dynamics and patterns that have occurred in response to historical climate changes.

**Hypotheses**

I will test the hypothesis that the climate during the last glacial cycle resulted in isolated refuge throughout the Great Basin and Columbia Plateau for *Perognathus parvus*. Leading to geographically structured genetic diversity. I hypothesize that the increasing aridity of the Great Basin and Columbia Plateau since the last glacial maximum resulted in increased fragmentation of suitable habitat, that will be reflected in the genetic structure of *P. parvus* populations. I further hypothesize that ad expansion of the Great Basin and Columbia Plateau since the last Glacial Maximum has caused rapid expansion of *P. parvus* populations, resulting in low genetic diversity between populations that expanded from the same refuge.

**References**


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