

Chaparral Rodent Evolutionary Genetics

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OBJECTIVES: The primary objective of this research is to study genetic variation in two species of California chaparral rodents (the California pocket mouse: *Chaetodipus californicus*, and the California mouse: *Peromyscus californicus*) by analysis of both allozymes and mtDNA sequences from throughout their respective ranges. This project, when completed, will be a significant contribution to understanding the role of the Great Central Valley in increasing biotic diversity in California. David Wake's work with *Ensatina eschscholtzi*, and Brad Shaffer's work with *Ambystoma californiense* have both revealed the importance of the valley for creating/maintaining genetic diversity for taxa distributed around its periphery. Data from these two rodent species will complement those from the amphibians. Whereas *Ensatina* apparently has colonized California from the North, and *Ambystoma* has been an isolated resident of California for several million years, the two rodents seem to have colonized the region around the valley from the south (based both on current distribution and taxonomic affinities). This is not to imply that the distribution of chaparral habitat has remained static; it has certainly changed much since the Pliocene, and those changes have possibly left their mark on the genetic composition of these species.

Another very important aspect of this study is the direct comparison of genetic structure of two very different mice with nearly identical habitat requirements and distributions. Besides the obvious morphological and taxonomic differences (one is a heteromyid, the other a sigmodontine murid), the two species presumably differ in mating system. I say presumably because nothing is known about the mating system of *C. californicus*; if it is like the other members of its genus it is promiscuous, and males show a greater premating dispersal distance. *P. californicus*, on the other hand, is monogamous, and females disperse farther than males. This difference in behavior should result in different distributions of genetic variation in the nuclear (as revealed by allozymes) and the maternally inherited mitochondrial genomes. If this turns out to be the case, it will be the first time that mating system has been shown to have an effect on the distribution of genetic variation, and will have important implications for management of species with different mating systems.

Finally, the taxonomy of *C. californicus* is horribly confused. A careful application of modern molecular techniques will help to alleviate this problem.

DESIGN: This project will be conducted in two phases: 1) the field or specimen collection phase, and 2) the laboratory or data collection phase. The field phase will entail collecting trips to all portions of the range of both species to ensure the broadest possible representation of genetic variability. Seven of the eight subspecies of *C. californicus* currently recognized are found in California (I will not trap in Mexico). One of these subspecies (*C. c. dispar*) exists in two disjunct areas; thus there are eight separate "regional taxa" that are of interest. By sampling at a minimum of two localities within the distributions of these eight "regional taxa" of *C. californicus* (a total of 16 localities) the between population component of variation should be well covered for both species. For statistical reliability of the allozyme data, I will need to collect about 20 individuals of each species from each locality. For use as outgroup members, and to help complete my extensive genetic data on pocket mice, I will also be collecting a maximum of ten of each of the other species of *Peromyscus*, *Chaetodipus* and *Perognathus* I encounter. I will use Sherman live-traps to collect animals. Non-target species will be identified and released. Target species will be killed and prepared in the field; allozyme electrophoresis requires large amounts of fresh tissues, thus the need to kill the animals. Tissue samples will be frozen in liquid nitrogen, and returned to U.C. Davis for analysis. Voucher specimens of all collected animals will be prepared and deposited in a reputable museum (most likely the MVZ at U.C. Berkeley).

The laboratory phase will involve horizontal starch gel electrophoresis of tissue extracts and histochemical staining by standard techniques, and direct sequencing of Polymerase Chain Reaction (PCR) amplified mtDNA segments. Preliminary results indicate that a portion of the mitochondrial cytochrome-b gene is sufficiently variable to discern variability in these mice. I intend to sequence the entire cytochrome-b gene for this study. First I will sequence individual mice from the different collecting localities to get a first approximation of the variation. Using this sequence information and the sequence analysis software *Genejockey*, I can predict the banding pattern that would result from digestion of the PCR product with restriction enzymes. I can more rapidly and cheaply assess the genetic variation by restriction enzyme digestion than by sequencing. Restriction fragment patterns that do not fit any predicted pattern are new, and can then be sequenced.