Developing Tools for Endangered Salt Marsh Harvest Mouse Conservation: Genetic Identification of Species and Population Variation using Functional Loci

Anastasia G. Ennis*, Romberg Tiburon Center, Biology Department, San Francisco State University, age@mail.sfsu.edu
C. Sarah Cohen, Romberg Tiburon Center, Biology Department, San Francisco State University, sarahcoh@sfsu.edu

The salt marsh harvest mouse (*Reithrodontomys raviventris*) is endemic to diked and tidal marshes of the San Francisco Bay Estuary and is endangered due to habitat limitation and disruption. Because the fate of *R. raviventris* is so closely tied to that of its habitat, its response to wetland management and restoration programs may be used as an indicator of ecosystem health. Conservation planning for *R. raviventris* is challenging because there are no data pertaining to current population sizes, gene flow, or selective pressures for this species. In addition, morphological species identification is problematic between the endangered species and another native and common *Reithrodontomys* species. This study addresses these challenges by genetically identifying sampled mice to species, characterizing genetic variation in populations across the range of *R. raviventris*, and examining genetic variation related to pathogens and habitat destruction. We are currently developing a more robust genetic protocol for species identification using 96 samples collected to date from a total of 10 populations in Suisun, San Pablo, and South San Francisco Bays. Thus far, we have sequenced 36 samples at the mitochondrial cytochrome b locus, confirming morphological species identity for 18, identifying 15 unknown, and correcting the identity of 3 individuals. Assessing genetic variation at functional loci contributes to our understanding of how endangered organisms adapt to a rapidly changing environment. In particular, adaptive immune system variation is frequently characterized in endangered species to assess the potential of limited populations to respond to disease. We have isolated the first functional genetic locus from *R. raviventris*, an adaptive immune system gene in the major histocompatibility complex (MHC, Class II DRB). Population studies using these loci will be used to estimate abundance, population connectivity, and selection, enabling effective management of *R. raviventris* genetic diversity as mandated by state and federal regulations.

Keywords: Reithrodontomys, genetic, species identification, MHC, habitat fragmentation, endangered, mice, population

Poster topic: Population Estimation and Viability