

Historical Bioaccumulation of Methyl Mercury in Tidal Wetlands of San Francisco Bay, California

Steven Schwarzbach, USGS WERC, steven_schwarzbach@usgs.gov

Josh Ackerman, USGS, jackerman@usgs.gov

Collin Eagles-Smith, USGS, ceaglesmith@usgs.gov

Mike Cassaza, USGS, mcassaza@usgs.org

Julie Yee, USGS, julie_yee@usgs.gov

David Krabbenhoft, USGS, dpkrabbe@usgs.gov

Alan Heyvaert, Desert Research Institute, alan.heyvaert@dri.edu

Thuy-Vy Bui, USGS, tbui@usgs.gov

John Takekawa, Audubon Society, jtakekawa@audubon.org

San Francisco Bay, California is today considered a mercury-impaired watershed. Elevated concentrations of mercury are found in water and sediment as well as fish and estuarine birds. Sources of mercury to the watershed since 1845 include sediment-associated mercury from mercury mining, mercury losses from gold amalgamation activities in mines of the Sierra Nevada, aerial deposition of mercury from global and regional emissions to air, and the direct discharge of mercury to Bay waters associated with the urbanization and industrialization of the estuary. We assessed historical trends in mercury bioaccumulation by measuring mercury concentrations in feathers of the endangered California Ridgway's rail (formerly California Clapper Rail) using museum specimens. San Francisco Bay differed from findings in other ecosystem studies by showing extreme historic contamination with significant declines in mercury from the 19th to 21st century. Despite the decline, rails in San Francisco Bay continue to have six times higher mercury concentrations than congeneric counterparts in southern California estuaries. We developed a structural equation model to attribute variation in historical bioaccumulation to sources of mercury. Our final model indicated that mining in New Almaden Mining District explained 69% of the historical variance in mercury concentration in rail feathers in the South Bay and 53% of the variance in the Central Bay. We did not find a statistically significant connection between urban development or aerial deposition patterns and rail mercury concentrations, but urbanization and California-wide mercury mining explained 93% of the variation of mercury flux into Lake Tahoe. We estimated the toxicological consequences of extreme mercury exposure to rails from known correlations between feather and blood mercury concentrations, and concluded that mercury poisoning was likely a contributor to the population decline of the California Ridgway's rail, especially in the southernmost reaches of the Bay.

Keywords: Methyl Mercury, Feathers, Sediment, Structural Equation Model, Clapper Rail, wetland

Poster Topic: At Risk Tidal Marsh Species

Characterizing Functional Genetic Variation in the Salt Marsh Harvest Mouse, *Reithrodontomys raviventris*

Anastasia G. Ennis*, Romberg Tiburon Center for Environmental Studies, San Francisco State University, age@mail.sfsu.edu

C. Sarah Cohen, Romberg Tiburon Center for Environmental Studies, 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. Conservation planning for *R. raviventris* is challenging because there are few 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 and characterizing functional genetic variation in populations across the range of *R. raviventris*. Using the mitochondrial cytochrome b locus, we have identified 124 *R. raviventris* individuals out of 167 samples collected from a total of 12 sites in Suisun, San Pablo, and South San Francisco Bays. 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 adaptive immune system locus from *R. raviventris* in the major histocompatibility complex (MHC, Class II DRB). Preliminary findings indicate low genetic variation at this locus. This may indicate limited adaptive potential of populations, raising concern for the future of this species. Population studies using these loci will be used to estimate effective population size, population connectivity, and selection, enabling effective management of *R. raviventris* genetic diversity as mandated by state and federal regulations.

Keywords: endangered species, conservation genetics, immunogenetics, habitat fragmentation

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