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Contacts: Dr. Amy G. Vandergast
Phone: 619-225-6445
Email: avandergast@usgs.gov

San Diego Field Station, USGS Western Ecological Research Center, 4165 Spruance Road, Suite 200, San Diego, CA 92101-0812

Genetic Effects of Recent Habitat Fragmentation on the Mahogany Jerusalem Cricket

Habitat loss and fragmentation due to urbanization are the most pervasive threats to biodiversity in southern California. Loss of habitat and fragmentation can lower migration rates and genetic connectivity among remaining populations of native species, reducing genetic variability and increasing extinction risk. However, it may be difficult to separate the effects of recent urban fragmentation from the genetic signature of prehistoric fragmentation due to previous natural geological and climatic changes. To address theses changes, USGS scientists Drs. Amy Vandergast and Robert Fisher and colleagues at San Diego State University and California Academy of Sciences examined the population genetic structure of a flightless insect, the mahogany Jerusalem cricket. Their study is published in a recent issue of *Molecular Ecology*.

Management Implications:

- High levels of genetic connectivity were measured throughout the Santa Ana Mountains, emphasizing that this region has long contained a relatively intact swath of open and natural habitat.
- This analysis suggests that the Chino and Puente Hills are the center of ancestral genetic diversity in the mahogany Jerusalem cricket. If other species show concordant ancestry, then the area may be considered an important component of evolutionary diversity within the southern California ecoregion worthy of conservation.
- Land conservation efforts throughout this region should continue to focus on preserving and restoring large areas of intact habitat with maximum levels of connectivity.

Endemic to cismontane southern California and widespread throughout the region, the mahogany Jerusalem cricket is an ideal indicator species for monitoring the genetic effects of urban habitat fragmentation throughout southern California. Its relatively short generation time of two years may allow for the accumulation of detectable genetic changes on the timescale of widespread urbanization in southern California.

DNA sequences from genes located in mitochondria (cellular organelles that contain their own genome) were analyzed. Mitochondria are maternally inherited and their genes can be used to trace ancestry and estimate relatedness among populations. Analyses suggested that diversification of the mahogany Jerusalem cricket began during the Pleistocene. However, the levels of genetic divergence measured among populations correlated with contemporary urbanization, even after correcting for fragmentation caused by flooding from rising seas during the Pleistocene and early Holocene. Theoretical simulations confirmed that observed patterns of genetic divergence could be produced by recent urban fragmentation, using biologically reasonable assumptions about population sizes, generation time, and the rate at which mutations accumulate in mitochondrial genomes. Genetic variability within populations was positively correlated with current fragment size, but not prehistoric fragment size, suggesting that urban fragmentation has resulted in a loss of genetic variability in small fragments.

Loss of genetic connectivity and genetic variability can hinder a population's ability to adapt to ecological disturbances commonly associated with urbanization, such as habitat degradation, climatic changes, and introduced species. Consequently, these study results underscore the importance of preserving and restoring

landscape connectivity for long-term persistence of native species with low mobility and small ranges.

Vandergast, A. G., A. J. Bohonak, D. B. Weissman, and R. N. Fisher. 2007. Understanding the genetic effects of recent habitat fragmentation in the context of evolutionary history: phylogeography and landscape genetics of a southern California endemic Jerusalem cricket (Orthoptera: Stenopelmatidae: Stenopelmatus*). Molecular Ecology 16:977–992.*