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*AMERICAMYSIS BAHIA: A NEW LABORATORY MODEL FOR CONSERVATION GENETICS IN CHANGING ENVIRONMENTS*

Levels of population genetic diversity are expected to play an important role in species persistence during periods of environmental change, yet our understanding of how to quantify relevant aspects of this diversity is not well developed. We are conducting a long-term study with the mysid shrimp *Americamysis bahia* to understand the relationship between genetic diversity and extinction risk. Here we present results from a unique experimental design that replicates distinct levels of genetic diversity in order to measure population viability in altered environments. We constructed laboratory populations with five levels of experimentally manipulated genetic diversity with a minimum of 10 replicates for each level. Half of each replicate population was exposed to a novel environment (low salinity) and half were maintained as controls. Populations were completely counted each week. Population growth rates in the permissive environment (controls) were inversely correlated with expected autozygosity. Populations with higher levels of genetic diversity do well in both permissive and stressful environments. While high diversity stressed populations were smaller than the control populations throughout the experiment, they showed an increase in relative population size as the experiment progressed, suggesting recovery after an early selective event. Populations with low genetic diversity have a diminished capacity to adapt to (and thrive in) an experimentally altered environment, indicating that the deleterious effects of reduced genetic diversity may only manifest themselves in degraded environments. A formal population viability analysis (PVA) using weekly census data confirms that long term extinction risk is low in permissive environments for all diversity levels and high in stressful environments for all but the highest genetic diversity levels. We also incorporate molecular markers and the statistics derived from them to determine the three-way predictive relationship between population fitness, 'true' genetic diversity, and estimators of this diversity derived using techniques from molecular ecology.

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