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Genetic Variability of *Melampus bidentatus* in Connecticut Salt Marshes

Species sensitive to environmental stressors can show population declines when exposed to them. As an ecosystem begins to degrade, the biodiversity within the system may begin to decline, which can be signaled by a loss of genetic diversity within the populations of individual species. By evaluating the genetic diversity of such species, it is hoped that a better understanding of the genetic underpinnings of population maintenance can be obtained. The goal of this project was to assess genetic variation in localized populations of *Melampus bidentatus*, a small, pulmonate gastropod resident in salt marshes along the Atlantic coast. The species resides in the high marsh areas, and as such, is sensitive to changes in water level and related habitat conditions, as for example increased tidal inundation due to sea level rise. Specimens of *Melampus* were collected from marshes in Branford and Guilford, Connecticut. DNA was extracted from these specimens and the mitochondrial cytochrome oxidase subunit I (COI) gene sequenced. Analysis of the sequences showed 84 unique haplotypes out of 100 individuals, indicating a general lack of discernable population structure throughout the sampled marshes. A rarefaction analysis of the sequences suggested more sampling is required before further conclusions can be drawn regarding the genetic structure of *Melampus* populations in Connecticut. This study does, however, support previous research that suggests populations in the region have a very high degree of genetic diversity.