Population monitoring and management

Temporal population genomics reveals evidence of load purging in small, isolated populations of conservation concern

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Small, isolated populations are susceptible to genomic erosion that can lead to declines in individual fitness and population productivity. Nevertheless, freshwater fishes are often found in small, isolated populations as exemplified by desert pupfishes (family Cyprinodontidae) that often exist in extreme isolation. Pupfishes in the Tularosa basin of New Mexico consist of two native populations (Malpais Spring and Salt Creek) as well as two non-native populations (Lost River and Mound Spring) that were established as refugia using founders from Salt Creek. The native populations diverged recently (~4500 years ago) due to genetic drift. We used whole genome sequences from 214 individual pupfish to monitor short-term evolutionary dynamics (~18 generations). By comparing geographic sites and temporal replicates, we monitored patterns of genomic diversity, inbreeding, load and adaptive potential of these endangered pupfishes. Heterozygosity was exceedingly low (~0.0001) and effective population sizes were consistently small (<1000). Nearly one-quarter of the typical genome was autozygous and estimates of genetic load indicate that purging was modest and negatively correlated with N_e. The native sites each harbour distinct gene pools on unique evolutionary trajectories. The refugia sites, which exhibited the lowest genomic diversity, could benefit from reciprocal gene flow with the native Salt Creek population.