Transitioning from microsatellites to SNP-based microhaplotypes in genetic monitoring programs: lessons from paired data spanning 20 years.

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Abstract

Many long-term genetic monitoring programs began before next-generation sequencing became widely available. Older programs can now transition to new marker systems usually consisting of 1000s of SNP loci, but there are still important questions about comparability, precision, and accuracy of key metrics estimated using SNPs. Ideally, transitioned programs should capitalize on new information without sacrificing continuity of inference across the time series. We combined existing microsatellite-based genetic monitoring information with SNP-based microhaplotypes obtained from archived samples of Rio Grande silvery minnow (Hybognathus amarus) across a 20-year time series to evaluate point estimates and trajectories of key genetic metrics. Demographic and genetic monitoring bracketed multiple collapses of the wild population, and included cases where captive-born repatriates comprised the majority of spawners in the wild. Even with smaller sample sizes, microhaplotypes yielded comparable and in some cases more precise estimates of variance genetic effective population size, multilocus heterozygosity and inbreeding compared to microsatellites because many more microhaplotype loci were available. Microhaplotypes also recorded shifts in allele frequencies associated with population bottlenecks. Trends in microhaplotype-based inbreeding metrics were associated with the fraction of hatchery-reared repatriates to the wild, and should be incorporated into future genomic monitoring. Although differences in accuracy and precision of some metrics were observed between marker types, biological inferences and management recommendations were consistent.