
GENETIC VARIATION, ANCESTRY AND POPULATION STRUCTURE IN NATIVE ARCTIC GRAYLING IN THE UPPER MISSOURI RIVER

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Arctic grayling (*Thymallus arcticus*) were thought to be historically widespread in the Missouri River system in Montana and Wyoming, but have been reduced to a handful of remnant populations since Euro-American colonization. Conservation efforts have focused primarily on protecting the fluvial population in the Big Hole River, and re-establishing fluvial populations elsewhere. Widespread historical stocking of exogenous grayling has created some uncertainty about the origin of extant populations and the composition of native gene pools. Additionally, declines in native populations may have reduced the genetic template for adaptation and recovery. Effective conservation would benefit from a better understanding of genetic ancestries, and whether bottlenecks have substantially altered genetic diversity of remnant populations. Consequently, we conducted a population-level genetic analysis of native and introduced grayling from 18 locations. We genotyped 730 grayling at 10 microsatellite loci and used these data to identify population groupings, genetic variation within and among groups, and evaluate evidence for population bottlenecks. We found significant divergence among native populations from the Big Hole River, Madison River, and Red Rock lakes. The Big Hole population had greater heterozygosity and allelic diversity than the Madison and Red Rock populations, both of which showed some evidence of recent bottlenecks. Most introduced populations traced their ancestry to the adfluvial Red Rock lakes population, and we did not find strong evidence that stocking of hatchery grayling homogenized native gene pools. Geographic patterns of genetic variation among native Missouri River grayling were consistent with differentiated local populations historically connected by occasional gene flow.