GENETIC ANALYSIS TO INFER THE ORIGIN OF MOUNTAIN WHITEFISH *PROSOPIUM WILLIAMSONI* IN THE BIG LOST RIVER

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We analyzed mountain whitefish (*Prosopium williamsoni*) from the Big Lost River and surrounding watersheds at 32 allozyme loci and four microsatellite loci. Populations analyzed from surrounding watersheds were from the Snake River above and below Shoshone Falls and from the Salmon River. Mountain whitefish from the Big Lost River appear to have entered the system via the upper Snake because the Big Lost River population shares allozyme and microsatellite alleles with the upper Snake populations but not with the Salmon River populations. The Big Lost River mountain whitefish population is characterized by an extreme lack of genetic variation; of the 32 allozyme loci analyzed, only one was variable. Heterozygosity at the four microsatellites was zero, greatly reduced from upper Snake populations, where the average heterozygosity at the same four loci was 0.294. Finally, mountain whitefish from the Big Lost River are highly genetically differentiated from surrounding populations. This fact is best demonstrated by fixation of a unique allele in the Big Lost River population at one of the microsatellite loci. We can infer from these data that genetic exchange has not occurred between whitefish in the Big Lost River and surrounding watersheds for a long time period. Genetic and morphological differences may warrant consideration of Big Lost River mountain whitefish as a separate subspecies.