

**Title:** Genetic Variability within Bull Trout (*Salvelinus confluentus*) populations in the Yakima River Basin

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Stream connectivity in the Yakima River basin has been fragmented by the construction of reservoirs with no fish passage. Bull trout (*Salvelinus confluentus*) exist in the basin in adfluvial and fluvial forms, as well as resident populations. The genetic structure of twelve spawning populations of bull trout was examined for this study, using six polymorphic microsatellite loci. Overall expected heterozygosities were low (0.2252-0.4544) and variability among populations was high ( $F_{ST} = 0.217$ ). Pairwise comparisons of genotype frequencies show gene flow between four fluvial populations with no migration barriers. In addition, one population from Rimrock reservoir had similar gene frequencies, possibly reflecting historical connectivity with fluvial populations. In the two reservoirs sampled that contained more than one population, each spawning stream was genetically distinct. These results show that without migration barriers, there is potential for gene flow, however there seem to be other factors contributing to levels of genetic exchange.