DISPERSAL AND INTROGRESSION OF NON-NATIVE RAINBOW TROUT GENES IN NATIVE WESTSLOPE CUTTHROAT TROUT POPULATION

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We used diagnostic microsatellite loci and Bayesian admixture analysis to describe the dispersal pattern of hybrids between native westslope cutthroat trout (*Oncorhynchus clarki lewisi*) and introduced rainbow trout in the North Fork Flathead River drainage, Montana. Hybridization was detected in 17 of 31 sites and the proportion of admixture and number of rainbow trout alleles within hybridized sites showed a significant negative correlation with fluvial distance from Abbot Creek, a suspected source of rainbow trout introgression in the drainage.Most (85%) of the rainbow trout alleles found among hybridized sites were present in Abbot Creek and several F1 individuals were detected in upstream sites lacking pure rainbow trout. Sites with low levels of admixture contained individuals classified as later-generation backcrosses. These findings suggest that straying from a downstream source population ultimately facilitates the spread of rainbow trout alleles in this drainage. Over time, this pattern of gene flow and introgression may lead to a loss of inter-population genetic diversity and local adaptation in native westslope cutthroat trout populations.