
EFFECTS OF TOPOLOGY, NUMBER AND LOCATION OF NODES, POPULATION DENSITY, AND STOCKING DURATION ON HYBRIDS? DISPERSAL ACROSS A NETWORK

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Hybridization between native cutthroat trout (*Oncorhynchus clarki* sp.) and introduced rainbow trout (*O. mykiss*) has been a topic of fisheries research for decades in the northern Rocky Mountains, USA. Several studies suggest that the likelihood of introgression at any location in a stream network is influenced by the distance between that location and the source of non-native genes, e.g., stocking locations or areas dominated by non-native or introgressed fish. The relationship between “distance to non-native source” and hybridization rates, however, is rarely quantified. Studies that attempt to quantify the relationship generally ignore the potential influence of stream network topology on gene movement. We have developed and applied an agent-based model that tracks the lineage and breeding location of individual fish over time, this simulating the movement of non-native genes among spawning locations within a stream network. The model considered both distances between spawning sites and network topology in determining non-natal spawning site selection by stocked and straying fish. Model results suggest that stream network topology has a strong influence on the relationship between “stream distance from genetic source” and “degree of hybridization” at spawning locations. However, the importance of topology varies depending on underlying model assumptions about, stocking duration, number and location of spawning grounds, population density, and spawning site fidelity, i.e., “straying rates,” within the river system.