

ABSTRACT

We used 14 microsatellite loci to examine population structure in humpback whitefish (*Coregonus pidschian*) from 10 locations in five regions of Alaska: Arctic, Kotzebue Sound, Yukon River, Kuskokwim River, southcentral Alaska. The results revealed significant population structure at broad (across Alaska) and fine (within the Yukon River) scales that is organized spatially at three hierarchical levels. In order of descending relative diversity these three levels are: Alaska (Arctic, western Alaska, southcentral Alaska); western Alaska (Kotzebue Sound, Yukon River, Kuskokwim River); Yukon River (Koyukuk River/mainstem at Rapids, Tanana River). These results support a conservation strategy that recognizes three spatially distinct major population groups (Arctic, western Alaska, southcentral Alaska) as the primary source of diversity but also recognizes significant population structure occurs at medium and fine-scales like western Alaska and the Yukon River. We also developed a genetic tool for identification of whitefish species in Alaska using a step-wise restriction-fragment length polymorphism assay of the cytochrome oxidase subunit I gene of mtDNA. This assay provides identification of six species and one species pair.

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Key Words: Whitefish, humpback whitefish, species marker, Alaska, RFLP, microsatellites, genetics.