A NEW BIOCHEMICAL GENETIC TECHNIQUE TO EXAMINE HYBRIDIZATION AMONG WESTSLOPE CUTTHROAT, YELLOWSTONE CUTTHROAT, AND RAINBOW TROUT

John Powell and Robb Leary, Division of Biological Sciences, 32 Campus Drive, University of Montana, Missoula, MT 59812, john.powell@umontana.edu

Hybridization is a large threat to the continued existence of native cutthroat trout (*Oncorhynchus clarkii*). Considerable effort has been spent identifying and attempting to conserve non-hybridized native cutthroat trout populations. Previously, Montana Fish, Wildlife, and Parks used a procedure examining fragments of nuclear DNA located between transposable elements (PINE analysis) to determine whether or not populations were hybridized and to what extent. A problem with this technique was that the markers used were inherited in a dominant/recessive fashion making identification of all genotypes not possible which from a statistical aspect weakens the power of the data. We developed a procedure that examines codominant insertion/deletion (indel) events as well as microsatellite markers that distinguish among westslope cutthroat (*O. c. lewisi*), Yellowstone cutthroat (*O. c. bouvieri*), and rainbow trout (*O. mykiss*). The codominant nature of these markers allows for the direct determination of all genotypes and estimates of allele frequencies in samples which greatly increases the power of the data. Furthermore, the new procedure requires only two independent polymerase chain reactions which reduces the amount of effort required to collect the data. This technique, therefore, is far superior to the previously used PINE analysis.