An Application of Polymerase Chain Reaction: Examination of Yellowtail Rockfish (Sebastes flavidus) Mitochondrial DNA

by

Kathleen McGauley

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ABSTRACT

The management of U.S. Pacific coast yellowtail rockfish, Sebastes flavidus, is of concern due to declining northern stocks, coastwide reductions in mean lengths, and changes in fishing patterns. Sound management of a fishery requires that the population structure be understood and that subpopulations, or stocks, if they exist, be identified and managed separately. The objective of this study was to use polymerase chain reaction (PCR) and mitochondrial DNA (mtDNA) analysis in an attempt to identify genetically discrete stocks of yellowtail rockfish along the Pacific Northwest coast.

The polymerase chain reaction was used to amplify a 1,600 base pair region of the mitochondrial ribosomal RNA genes from 74 yellowtail rockfish collected from three Pacific coast localities: Nootka Sound,Vancouver Island, British Columbia; Westport, Washington; and Cordell Bank, California. Intraspecific genetic variability was assayed by subjecting the amplified region to a restriction fragment length polymorphism (RFLP) analysis. The segment was digested with ten Type II restriction endonucleases, and the resulting fragment patterns were examined for polymorphisms. A total of 33 restriction sites allowed examination of 0.8% of the mtDNA molecule. Except for a single variant observed in the Westport Hha I digests, no variation was detected within or among the three yellowtail rockfish populations.

Results support an earlier allozyme study which concluded that Pacific coast yellowtail rockfish should be regarded as one genetically homogeneous group. Although size-at-age and tagging evidence suggest yellowtail assemblages may be wholly or partially isolated as adults, coastwide dispersal of pelagic larvae and juveniles may play a significant role in gene flow among populations.

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