

Johnson, O.W., G.B. Milner and F.W. Waknitz. National Marine Fisheries Service, Coastal Zone and Estuarine Studies, 2725 Montlake Blvd. E., Seattle, WA 98112.

GENETIC CONSIDERATIONS IN THE STATUS REVIEW OF LOWER COLUMBIA RIVER COHO SALMON.

In June 1990, Oregon Trout, Oregon Natural Resources Council, Northwest Environmental Defense Center, American Rivers, and the Oregon and Idaho Chapters of the American Fisheries Society petitioned the National Marine Fisheries Service (NMFS) to list coho salmon (*Oncorhynchus kisutch*) in the lower Columbia River (LCR) as an endangered species. NMFS conducted a status review of existing information to determine whether LCR coho salmon qualify as a "species" as defined by the U.S. Endangered Species Act (ESA). NMFS' policy is that for a population to qualify as a species under the ESA, it must represent an evolutionary significant unit (ESU) of the biological species. An ESU is defined as a population that is reproductively isolated from other conspecific populations and represents an important component in the evolutionary legacy of the biological species. The status review of biological information on LCR coho salmon covered life history, historical and current abundance, history of hatchery stocks and outplantings, effects of parasitism and biochemical genetics.

The genetic portion of the status review considered morphological and electrophoretic studies of coho salmon from the Pacific Northwest. To help evaluate the population structure of LCR coho salmon, NMFS also collected some fish samples from LCR streams and hatcheries for allozyme analysis. This provided data for genetic characters (gene loci) from 16 populations. These data were compared with published and unpublished genetic data from a variety of sources.

No clear evidence was found of the continued existence of a distinct population of naturally spawning coho salmon in the LCR that would qualify as an ESU. However, indications of possible genetic differences between the LCR and Washington or Oregon coastal coho salmon were seen in some analyses. While NMFS did not recommend listing, the decision did not exclude the possibility that a population that would qualify for ESA protection still exists, only that there was inadequate evidence at the time to make such a recommendation. Studies to clarify the population structure of coho salmon in the LCR and nearby coastal regions are discussed.

Klein, D.B., H. Ono, C. O'Uigin, V. Vincek, and J. Klein. Department of Microbiology and Immunology, University of Miami School of Medicine, Miami, FL 33101 and Max-Planck-Institut für Biologie, Abteilung Immungenetik, 7400 Tübingen, Germany.

EXTENSIVE Mhc VARIABILITY IN AFRICAN CICHLID FISHES

The major histocompatibility complex, Mhc, is a cluster of genes controlling the immune response of vertebrates to parasites. In mammals, the functional Mhc loci are characterized by high polymorphism and the Mhc alleles often differ by more than a hundred nucleotide substitutions. A collection of alleles is passed on from species to species during speciation in a trans-species manner. These characteristics make the Mhc polymorphism an ideal tool for studying phylogenetic relationships in flock species. We have cloned and sequenced the expressed class II Mhc genes of one cichlid species and on the basis of the sequence have designed oligonucleotide primers which enabled us to sequence the most variable region of these genes from different species very rapidly by the polymerase chain reaction (PCR). We have thus far obtained 35 sequences of Mhc class II genes from 12 species of African cichlids. The results suggest that the founding populations from which the cichlids of the African lakes radiated were highly polymorphic at their Mhc loci and that during radiation, different Mhc alleles were distributed into different species. It should therefore be possible to trace cichlid phylogenetic lineages through their Mhc polymorphism.