

GENETIC VARIABILITY IN CUTTHROAT TROUT

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During the summer of 1976 an investigation into the nature of genetic variability in the cutthroat trout (Salmo clarki) was initiated. The results presented here are the product of only one summer's data, and will be subject to rigorous testing in the next two summers. This project has been supported in part by a New York Zoological Society Scholarship and a National Science Foundation Energy-Related Traineeship. I wish to thank Pete Hayden of Grand Teton National Park, Max Rollefson, Jon Erickson, and John Kiefling, of the Wyoming Game and Fish Commission, and John Varley and Ron Jones of the U.S. Fish and Wildlife Service for their cooperation in collection of cutthroat trout. I would also like to thank Drs. R. M. Kitchin, H. Bergman, and G. T. Baxter, of the Department of Zoology and Physiology, University of Wyoming for their help in organizing this research project.

Introduction

The family Salmonidae is composed of the trouts (*Salmo*), chars (*Salvelinus*) and salmon (*Oncorhynchus*), and whitefish (*Coregonus*). This entire family has been exploited to the extent that pure forms exist only in a few isolated areas. Grand Teton and Yellowstone National Parks provide such a pristine condition for the cutthroat trout.

One of the priorities of modern fish managers is to maintain and reestablish native fish. This study will provide data on the genetic structure of pristine salmonid populations. Fish managers should be able to use this data to evaluate reestablishment projects elsewhere, and to provide guidelines for picking brook stock for future culture and reestablishment programs. This data should also provide information valuable to managers regarding the integrity of distinct cutthroat trout populations in Northwest Wyoming.

Objectives

- A. Evaluate the hypothesis that exploitation has reduced the genetic variability in cutthroat trout populations.
- B. Evaluate the hypothesis that sympatry should result in disruptive selection causing differentiation of cutthroat trout gene pools.
- C. Determine if chromosome variation in cutthroat trout is a somatic phenomenon or a population based polymorphism.
- D. Determine, using Hardy-Weinberg genetic equilibrium, if the large and fine spotted cutthroats are interbreeding.

Methodology

Cutthroat trout were collected at five localities during the summer of 1976. Yellowstone cutthroats were collected from the Pelican Creek fish trap (a lake population $N=30$), and LeHardy's Rapids (a river population $N=30$). Large spotted Snake River cutthroats were collected on Dime Creek (a small tributary to the upper Snake River North of Jackson Lake $N=10$), and from the main body of the Snake River just below Jackson Lake ($N=30$). Fine spotted cutthroat trout were collected in the Black Tail Springs ($N=12$).

Cytogenetic analysis, which involves injection of colchicine, and an in-vivo incubation was completed on a limited number of specimens. (Dime Creek $N=5$, LeHardy's Rapids $N=6$, Pelican Creek $N=3$, Snake River $N=17$, Black Tail Springs $N=0$). Whole blood was taken from the remaining fish, via caudal vein puncture, and the fish returned to the water. Sera and hemolysate were separated and frozen in liquid nitrogen. Electrophoretic analysis is presently underway in Laramie, Wyoming at the University of Wyoming.

Preliminary Results

Chromosomal analysis has been completed on 27 individuals. The modal chromosome number for each population was 64, with 104 chromosome arms. This is in disagreement with Simon's earlier report of 64 chromosomes and 106 arms. Variation in chromosome number seems to be a prevalent phenomenon in cutthroat trout. The most perplexing situation is the considerable intra-individual variation. This variation may arise as the result of inversions, acrocentric fusions and fissions, and chromosome loss. It is the present opinion of the author that this variation is not surprising, and may be part of an underlying preadaptive mechanism for polyploidization, and gene duplication prevalent in salmonid fish. Because the numbers of fish from each population is at present low, it is too early to draw any conclusion about population polymorphisms. It is of interest that there are individuals in the Snake River whose modal chromosome is $2N=62$, with 104 arms, rather than $2N=64$, with 104 arms. This indicates that the possibility for an underlying population based polymorphism is good, and needs further study.

The electrophoretic analysis is at present underway. Staining and techniques have been worked out for tetrazolium oxidase, malate dehydrogenase, esterase, alpha-glycerolphosphate dehydrogenase, acetylcholinesterase, transferrin, and hemoglobin. No conclusions are yet available.

Future Studies

From the preliminary results it is obvious there is a need for additional study. Cytogenetic analysis should be performed on at least 15 to 20 individuals per population. This will provide a sufficient sample to detect a population polymorphism. Collection of an additional 30 electrophoretic samples per population should enlarge that portion of the study sufficiently. In addition to sera and hemolysate, muscle samples will be collected. Sera and hemolysate will be run fresh at JHBRS, and muscle frozen and analyzed in Laramie.