

STUDY FINAL REPORT

State: Michigan

Project No.: F-80-R-3

Study No.: 688

Title: Evaluation of alternative mechanisms underlying spatial genetic diversity of Lake Michigan steelhead: an assessment using molecular genetic markers

Period Covered: April 1, 1998 - September 30, 2002

Study Objectives: (1) To quantify the degree of genetic variation among naturalized populations of steelhead from drainages of Lake Michigan, (2) to estimate the effective breeding population size of summer and winter run hatchery strains used in supplementation programs in the state of Michigan, (3) to estimate the effective population size of naturalized populations in Michigan drainages, (4) to correlate inter-population differences in gene frequency with population differences in life history and morphology, (5) to utilize genetic data from naturalized and hatchery populations to test and explain current spatial patterns of genetic differentiation and to make predictions of future trends in levels of genetic diversity, (6) to assess the feasibility of using gene frequency data in Mixed Stock Analysis for open-water Lake Michigan steelhead sport fisheries.

Summary: Steelhead in the Lake Michigan are genetically diverse. The major source of diversity was attributed to variation among hatchery strains stocked by state agencies surrounding the basin. Variation also was documented among naturalized populations in drainages across the lower and upper peninsula of Michigan. We found no evidence for genetic differentiation among fall- and spring-run steelhead from the same drainage. Controlled matings that utilized gametes obtained from spawning adults at the Little Manistee weir were conducted to simulate different spawning practices utilized by Michigan and other state agencies across the Great Lakes Basin. We found that pooling gametes from multiple males and females and reuse of gametes from the same male resulted in significant increases in levels of relatedness among progeny and significantly reduced effective population size. Data revealed that the optimal breeding strategy to maintain levels of genetic diversity involved large numbers of contributing males and females and a one male to one female mating regime. We used scale samples from contemporary and historical sources to determine whether incidence of hatchery fish to spawning populations had increased over a two decade period, and if changes could be attributed to changes in stocking practices. Stocking of large hatchery pre-smolt steelhead has led to significant increases in the incidence of hatchery fish in spawning populations throughout Michigan. Hatchery strains include substantial numbers of fish from strains stocked in states other than Michigan. Long-term maintenance of genetic and phenotypic diversity of steelhead in Lake Michigan will be seriously compromised by present management practices.

Findings: This final report was prepared, including Jobs 1, 2, and 6, which were scheduled for 2001-02. All jobs are reported on below.

Job 1. Title: Use molecular genetic markers to characterize gene frequencies of each of several naturalized spawning steelhead from tributaries across the Lake Michigan basin.—Analyses focused on characterizations of spawning populations across the Lake Michigan Basin. Analyses include populations in close geographic proximity (i.e., within streams) and comparisons of steelhead from fall and spring runs within the same stream. Data were further used to examine the

potential effects of hatchery supplementation on the degree of spatial genetic structuring within and among three rivers in Michigan that support large naturalized runs of steelhead. Sampling included adults from tributaries within rivers that have historically been heavily stocked (Muskegon and Manistee Rivers) and a river that has received far lower levels of supplementation (the Pere Marquette River). Hierarchical analysis indicated there was little genetic differentiation among drainages or among spawning areas within drainages. Analyses of all pair-wise population relationships do suggest some degree of spatial genetic structuring, and all populations are highly differentiated from Skamania steelhead, a second strain widely planted in the basin.

We found no evidence for differences in allele frequency between adults in fall- and spring-runs within the same river system suggesting that steelhead entering a river in the fall are a random subset of the spring spawning population, even though the sex ratio of adults during the two periods differ. We did observe that for one river, genotypic frequencies of fall-run adults were not consistent with expectations based on population allele frequencies. Departures from expectation are likely due to the fact that the fall-run is composed of a mixture of adults that spawn in different tributaries.

All fall-run and spring-run Steelhead differed significantly in allele frequency from the Skamania strain of steelhead that have historically been widely stocked into the Pere Marquette, Muskegon and Manistee Rivers.

Detailed analyses are provided in the accompanying manuscript.

Bartron, M. P.W. DeHaan, and K.T. Scribner. Temporal and spatial genetic structure in Lake Michigan Steelhead (*Oncorhynchus mykiss*). J. Great Lakes Res. In review.

Job 2. Title: Determine whether the degree of population differentiation in genetic characteristics can be correlated to population differences in juvenile life history and to morphology.

Sampling of juvenile and spawning adult steelhead for analyses of phenotypic and life history traits was carried out in several Lake Michigan tributaries. The life history traits were inferred from scale pattern analysis of adults spawning in spring. Efforts were made to sample the beginning, middle, and end of each spawning run. The traits included: age at maturity, smolt age, stream growth, lake growth, percent repeat spawning, percent jacks, and sex ratio. For some populations, ancillary data were available on age composition of the smolt run and stream survival. Data were checked for normality and heterogeneity of variance. Percentage data were log-transformed. Individual traits were compared among populations using Analysis of Variance (ANOVA) or Kruskal Wallis tests. River populations were compared using multivariate analysis of variance (MANOVA). Tests were considered significant at $\alpha=0.05$.

There was little variation in life history traits among Lake Michigan Steelhead runs (D. Swank and E. Rutherford, unpubl. data). There was no evidence for significant differences in any of the life history traits among central and southern Lake Michigan tributaries. The Black River population in Mackinaw County in Michigan's Upper Peninsula appeared to be different from other populations in smolt age (more age 3 smolts in the Black River than in other drainages in the basin) and percent jacks (percentages in the Black River were significantly higher than in other drainages in the basin).

Joint variation in genetic and life history traits of all river populations will be analyzed using MANOVA and classification techniques.

Job 3. Title: Determine the effective population size of steelhead spawning in each of several drainages of Lake Michigan.

We focused our efforts on analyses of hatchery gamete-take

strategies and the effects of hatchery practices and stocking strategies on over-all estimates of effective population size. Specific details are provided in an accompanying manuscript.

Bartron, M., and K.T. Scribner. Genetic evaluations of alternative hatchery mating strategies. Conservation Genetics. in prep.

Job 4. Title: Estimate the effective breeding population sizes of summer and winter hatchery stocks, and estimate short- and long-term trends of genetic diversity.—See results under Job 3. Based on past and present state mating strategies we formulated projections for overall levels of diversity and potential for changes given estimates of total numbers of males and females spawned and stocked. Details are provide in an accompanying manuscript.

Bartron, M., and K.T. Scribner. Genetic evaluations of alternative hatchery mating strategies. Conservation Genetics. in prep.

Job 5. Title: Assess the feasibility of using Mixed Stock Analysis (MSA) for open water steelhead fisheries in Lake Michigan.—Results are described in two attached manuscripts that describe the estimates of accuracy and precision in strain-specific assignment. We further summarized stocking data and straying data to estimate strain-specific straying rates for streams across several Michigan streams in the Lake Michigan Basin.

Bartron, M. and K.T. Scribner. 2003. Temporal comparisons of genetic diversity in Lake Michigan steelhead, *Oncorhynchus mykiss*, populations: effects of hatchery supplementation. Environmental Biology of Fishes. In press.

Bartron, M. D.R. Swank, E. Rutherford, and K.T. Scribner. Methodological bias in estimates of strain composition and straying rates of hatchery-produced steelhead in Lake Michigan tributaries. North American Journal of Fisheries Management. In review.

Job 6: To assemble results of genetic characterizations of naturalized and supplemented stocks into a predictive model of present and future levels of genetic diversity for steelhead in the Lake Michigan Basin.—We have developed several computer programs that create population mixtures of individuals produced under different breeding conditions (e.g., hatchery mating schemes). One program is written in Visual Basic. This program is based on user-defined input for population allele frequency and degree of coancestry (as would be developed in release hatchery juveniles). Simulated individuals can interbreed or not. Simulations can be prepared over a series of generations to track changes in population gene frequencies and gene diversity. A second program is also developed in Visual Basic. This program allow user-specific input about different breeding and stocking strategies and the effects on overall genetic diversity, how diversity is partitioned, and on effective population size. This program is designed to integrate with existing data bases on location-specific stocking and on gamete-take practices.

Two additional programs, also written in Visual Basic are designed to utilize genetic data to assign individuals to population of origin on the basis of genotype and the likelihood of observing the genotype in each of a series of putative populations of origin. One program (MLE) provides estimates of confidence in individual assignment decisions using Bayesian formulations. The second program (GA) utilizes a Genetic Algorithm to select optimal multi-locus combinations that maximize classification accuracy.

Prepared by: Kim T. Scribner and Meredith L. Bartron

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