STUDY PERFORMANCE REPORT

State: Michigan   **Project No:** F-80-R-2

Study No: 475   **Title:** Development and implementation of conservation genetic initiatives for Michigan inland and Great Lakes fisheries

Period Covered: October 1, 2000 to September 30, 2001

Study Objectives: (1) to develop genetic guidelines and policies governing broodstock and hatchery production and release for the Fisheries Broodstock Committee of the Michigan Department of Natural Resources, (2) to assess levels of genetic diversity in Lake Sturgeon and other threatened species in Michigan Great Lakes and inland waters and to assist in the implementation of genetics guidelines to aid in species restoration efforts, (3) to collect, analyze, and interpret demographic and genetic data bases for Great Lakes sport fisheries to assist in efforts to establish the extent of interaction of hatchery supplemented fisheries to natural reproduction, (4) to collect, analyze, and interpret demographic and genetic data bases for Great Lakes sport fisheries to assist in efforts to identify areas of endemism and of high genetic diversity which could serve as species conservation areas or management zones.

Summary: During the past year work has continued in areas related to assessments of the influences of hatchery and management practices on gene diversity of Great Lakes fish populations. Our focus during the past year has been on species that are spawned and reared by the Michigan Department of Natural Resources for release into waters of the Great Lakes. Species and strains included those retained as domestic broodstocks (Assinica and Iron River strains of brook trout and Marquette, Lewis Lake, and Lake Ontario strains of lake trout) and anadromous salmonid species (coho salmon, chinook salmon, and steelhead) that are collected and spawned during spawning migrations. Baseline genetic data including estimates of allele frequency and genetic diversities for fish of hatchery origin are being used with data from naturalized populations.

Job 6: Conduct surveys of genetic diversity in naturalized and supplemental salmonid fisheries. Continue background assessment to characterize levels of genetic variation

Findings: Work is continuing for steelhead. We have compiled information on annual stocking numbers of steelhead in the Lake Michigan basin by strain and by state agency. We have collated historical information on stocking numbers by strain for all Michigan drainages in Lake Michigan. We collected data on incidence of adult spawning steelhead using fin clips to identify strain of origin for a portion of spawning run in four Michigan Rivers where good sample sizes were available (Pere Marquette River (N=117), Little Manistee River (N=5294), Bear Creek (N=70) of the Manistee River, and the Platte River (N=79)]. Using scale pattern analysis (SPA: ratio 2:3) we identified the proportion of unclipped fish that were of hatchery origin to determine bias in counts of hatchery strays due to incomplete clipping. Using genetic markers, we estimated strain of origin of all fish determined to be of hatchery origin based on SPA using a likelihood-based assignment test.

Based on 5560 spawning adult steelhead examined 402 (7.2%) had fin clips and were classified as of hatchery origin. Using scale pattern analysis an additional 63 fish were identified as being of hatchery origin. Estimates of the proportion of spawning runs composed of fish of natural origin varied among streams [81.2% Pere Marquette, 92.5% Little Manistee, 67% Bear Creek, 70% Platte River]. The greatest bias between estimates of hatchery contributions to spawning populations based solely on fin clip and estimates that combined fin clips with SPA and genetic markers was for the Ganaraska and Chambers Creek strains. These two strains are marked with

maxillary clips that can also easily be caused by hooking or other natural source. Estimates of the proportion of spawning runs composed of hatchery fish reflect stocking levels for each stream. Return rates of spawning adults of hatchery origin did not reflect the magnitude of total basin-wide stocking levels (average annual numbers of juvenile steelhead stocked = 2,634,396). Neither were estimates of straying rate of each strain consistent with strain-specific stocking levels. Of over 2.6 million juveniles stock annually, 55.5% were Michigan strain steelhead. However, Michigan strain steelhead comprise 66.3% of strays into Michigan tributaries. Interestingly, of all hatchery strays documented, 3.0% were Ganaraska and 12.9% were Chambers Creek strains, which have not been stocked in Michigan waters.

We are analyzing historical data from archived scales (early 1980's) and contemporary samples (1998-99) of the same populations to examine the effects of hatchery supplementation. Specifically we focused on issues related to potential homogenization of genetic characteristics across drainages due to stocking of progeny for hatchery sources across multiple geographically dispersed naturalized populations. Data will be analyzed in the coming year for historical samples. Estimates of inter-drainage variance in allele frequency will be used to estimate the rate of introgression of hatchery fish into naturalized populations.

We are continuing to evaluate Michigan Department of Natural Resources domestic broodstocks of lake trout and brook trout. We received fin clips from adults of each species and strain during spawning activities of 2000. For lake trout across Lewis Lake, Lake Ontario and Marquette strains were characterized for 6 microsatellite loci. 248 brook trout across Assinica and Iron River strains, 292 fish were characterized for 6 microsatellite loci. Estimates of allele frequency, genetic diversity, and measures of degree of inter-individual relatedness were estimated for all individuals. Statistical analyses will be completed during the coming year. Data will be combined with data from previous years to develop a long-term monitoring strategy to ensure that newly established goals forwarded in the Broodstock Management Plan are being realized.

Species-specific difference in allele frequency will allow us to possibly detect inter-specific hybrids (i.e., F1 splakes) and to assess the degree to which F1 hybrids reproduce in the wild. Despite laboratory breeding studies to the contrary, it is widely assumed that splakes are infertile. Molecular genetics data collected this past year will allow us the means to unambiguously identify individuals of higher filial generations.

Job 7. Title: Genetic model for Lake Michigan salmonid fisheries. Use preliminary background data to begin to model future trends in genetic diversity of introduced and native salmonids.

Findings: We have developed two 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. The second model is written using the Statistical Analysis System (SAS). The model was created to allow varying contributions of two source populations whose allele frequencies were known for a suite of bi-parentally inherited loci. Source populations could be altered to reflect the genetic diversity observed in hatchery and naturalized populations. Results of preliminary simulations suggest that the net change in genetic diversity over time is dependent on relative contributions of each source populations and their relative diversities.

Prepared by: Kim T. Scribner
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