## **STUDY PERFORMANCE REPORT**

State: Michigan

Study No.: <u>230723</u>

Project No.: <u>F-81-R-6</u>

Title: Effects of exploitation and fisheries management on genetic diversity of fish stocks in inland and Great Lake waters of Michigan

## Period Covered: October 1, 2004 to September 30, 2005

- **Study Objectives:** (1) To use molecular markers and population genetics theory to investigate genetic stock relationships and status of indigenous fish species of importance in Michigan, (2) to estimate the effects of past and proposed management on population and meta-population levels of genetic diversity.
- **Summary:** Research is ongoing in each of several topical areas, all related to historical and contemporary factors affecting the genetic diversity of fisheries in Michigan waters. Studies involve numerous native species of economic importance that are intensively managed. This project seeks to provide information to better understand how recent management practices have impacted the genetic diversity of Michigan's fisheries. Review of available literature conclusively shows that historically, Michigan's fisheries were composed of taxonomically diverse fish assemblages. Most species were also genetically quite diverse as the result of admixture events whereby fishes that were geographically isolated into glacial refugia mixed following the retreat of glacial ice. All available literature suggests that humans have left an indelible, and mostly negative mark on the genetic architecture on Michigan's fishes. Management efforts have contributed to community and species declines in genetic diversity. Each job addresses issues of importance to fish species in Michigan.

Findings: Jobs 2–7 were scheduled for 2004-05, and progress is reported below.

Job 2. Title: Determine effects of hatchery supplementation on relatedness among adult lake sturgeon in Black Lake. Assess potential for future inbreeding. Estimate effective population size of the remnant Black Lake sturgeon population.—A total of 154 lake sturgeon (46 females and 108 males) were captured and tagged during the Black River spawning run in 2005. This is the largest number of fish captured since adult spawning surveys were initiated in 2001. Of the 46 females captured this year, 33 were untagged and 13 had been tagged during previous spawning runs. Of the 108 males captured this year, 45 were untagged and 63 had been previously tagged during spawning runs. Nearly half of all fish (49.4%) in the 2005 spawning run were recaptures. A large proportion of all adults (31%) have also been observed (recaptured) several times at the spawning grounds during the course of this study.

To date, 423 unique individuals (257 males, 166 females) have been captured during the spawning runs from 2001-2005. We have collected biological information including weight, total length, fork length, girth and sex from all individuals. We also recorded the PIT tag number from individuals that had been captured and marked during previous field seasons. Fin clips were taken from the tip of dorsal fin for genetic analysis. During 2005 the first adult sturgeon was captured on 05/03/05 and the last was captured on 05/25/05. At least four different spawning runs were observed in 2005. We saw evidence of males of a size consistent with cohorts from years of hatchery supplementation (<120 cm; 1983, 1984, 1987 cohorts) present in spawning aggregations

within the Black River (Figure. 1). Recruitment of related hatchery adults and periodicity of spawning will be a critical variable in future modeling efforts to determine the effects of longevity and spawning frequency on levels of inter-individual relatedness and inbreeding in the Black Lake population.

We have been collaborating with Dr. Daniel Hayes of the Department of Fisheries and Wildlife at Michigan State University. We have constructed individual-based models simulating the effects of population abundance on probabilities of population extinction and accrual of inbreeding. Data suggest that inbreeding will accrue at fairly low levels for adult populations of size >20 individuals (Figure 2). Population models are being used to simulate the effects of hatchery supplementation on inbreeding using Black Lake sturgeon data.

Job 3. Title: Estimate stock structure of walleye in Michigan waters of the Great Lakes. Determine the impacts of extensive transfers of walleye across drainages.–Walleye (N=502) from 10 populations were collected by Michigan DNR biologists and other cooperators. Sampling locales were surveyed during the spawning season and included the St. Mary's River, Little Bay de Noc, Muskegon River, Titabawasee River, Saginaw Bay Reefs, Holloway Reservoir, Flint River, Clinton River, near-shore spawning areas in eastern Lake Erie and Lake Gogebic. Analyses are ongoing to describe the relative relationships among stocks, and to interpret findings in the context of known patterns of movement and of stocking history.

The Gogebic Lake population was the most genetically diverged of all Michigan walleye stocks . Historical hatchery records indicated that Lake Gogebic walleye originated from reef-spawning walleye in Saginaw Bay. Based on the close genetic affinities of present Saginaw Bay and Saginaw Bay tributary populations to the Muskegon river population from the Lake Michigan basin, there is minimal evidence of any genetic contributions of remnant Lake Huron Great Lakes stocks to restored populations within or draining into Saginaw Bay.

The Lake Gogebic population is also genetically distinct from walleye populations in northern Lake Michigan (Little Bay de Noc) or the St. Mary's River. Records indicate that walleye from Lake Gogebic were used to stock Little Bay de Noc. Walleye from the Little Bay de Noc population are genetically more similar to walleye from the St. Mary's River than they are to the Lake Gogebic putative source population. These data suggest that hatchery plants from Lake Gogebic have not contributed demonstrably to recruitment in the Little Bay de Noc population.

## Job 4. Title: <u>Estimate the impacts of hatchery supplementation on naturalized steelhead</u> <u>populations. Estimate proportional contributions of different hatchery strains to the open</u> <u>water creel in Lake Michigan.</u>-

*Stocking Background:* An average of 1,718,945 steelhead were stocked annually into the Lake Michigan basin between 1996 to 2000. Across the entire lake basin, the Skamania strain accounts for the majority of steelhead stocked (41.3%), followed by the Michigan strain (37.4%), the Ganaraska strain (10.8%), and the Chambers Creek strain (10.4).

*Contributions of Hatchery and Wild Steelhead to the Creel:* Origin (hatchery strain or river) was identified for a total of 1,106 samples that had been collected from the 2001 Lake Michigan open water steelhead creel for all states bordering Lake Michigan (497 individuals were from Michigan, 420 individuals were obtained from Wisconsin, 135 from Indiana, and 54 from Illinois). Combining data from marked (strain identification via fin clips, maxillae clips, or combination thereof) and non-marked (strain identification via scale pattern analysis to determine origin, genetic markers used to identify strain) steelhead resulted in an overall estimated contribution of hatchery fish to the creel of 80.0% and natural reproduction of 20%.

*Creel Returns:* A total of 739 marked steelhead were present in the 2001 Lake Michigan steelhead creel sampled. All hatchery strains as identified via mark observations were present in the creels of each state. A portion of the marked creel was unable to be identified to a particular strain (n=71, 9.6%). Across the entire basin, the Skamania strain had the highest contribution to the overall creel (n=332, 44.9% of total marked creel). The Michigan strain contributed to 31.8% (n=235) of the creel. The Ganaraska (9.7%, n=72) and Chambers Creek strains (3.9%, n=29) were estimated to contribute the smallest numbers to the creel.

A total of 217 non-marked hatchery steelhead were present in the 2001 Lake Michigan creel. The Skamania strain contributed the largest amount to the non-marked portion of the creel (47.5%, n=103). The Michigan strain contributed to 22.2% of the non-marked creel (n=48), followed by Ganaraska and Chambers Creek strains (n=35, 16.1% and n=31, 14.3% respectively). With the exception of the absence of the Ganaraksa strain in the Illinois creel, all strains were observed in the creel of each state.

Combined results of marked and non-marked hatchery individuals to the creel indicated that each of the four strains stocked into the basin were present in the creel of each state. The Skamania strain was most abundant in the creel (39.3%) followed by Michigan strain (25.6%), Ganaraska strain (9.7%), and Chambers Creek strain (5.4%). Statistical differences in estimates of strain contribution were documented between marked and unmarked fish, presumably due to the differences in percentages of different strains routinely marked by different states.

Strain Distribution in Creel: Significant differences in the proportion of hatchery (all strains combined) and river contributions to the creel were observed among the states ( $X^2$ =16.2; P<0.001). Larger numbers of wild steelhead were caught by anglers in Michigan and Wisconsin that in Indiana and Illinios. Proportional contributions of each strain in the creel also differed significantly across states ( $X^2$ =45.4; P<0.001). Pair-wise comparisons of strain-specific contributions to each state's creel were significant (P<0.001) for all state-to-state comparisons except between Michigan and Wisconsin.

Comparisons of estimates of proportions of each strain stocked to observed contributions to the creel reveal that for all states, anglers were catching strains in numbers significantly out of proportion to what was stocked by each state. Based on all individuals in the creel sample (marked and unmarked and assigned genetically to strain), we compared these observed proportions to those expected on the basis of proportions of each strain stocked by each state, assuming that the sport fishery of each state benefits solely on the basis of resources expended (and strains stocked) by management agencies within the state. We found that observed numbers of each strain in the creel sampled differed significant from expected in each state  $[X^2=309.9, 3df, P<0.001 (MI); X^2=236.1, 3 df, P<0.001 (WI); X^2=79.0, 3df, P<0.001 (IN); X^2=47.5, 3df, P<0.001 (IL)].$ 

Chi-square tests of temporal comparisons of strain-specific contribution among and within states indicated significant differences in strain distribution within Lake Michigan. Within each state, the proportional abundance of the four strains over the three time periods (April-May, June-July, and August-September) was significantly different. Comparisons of the distribution of each strain by state throughout the creel season also indicated that there were significant differences in the proportional abundance by strain in the creel of each state.

The proportional contributions of each of the four strains during the three time periods varied by state. For example, the Michigan strain was most abundant in the state of Michigan during April-May (37% of the Michigan strain in the creel in Michigan was caught during that time period) and August-September (35%). In Wisconsin, 48% of the Michigan strain was caught in both June-July and August-September. In Indiana, the 67% of the Michigan strain was caught during

April-May, and in Illinois, 43% of the Michigan strain was caught in August-September. The temporal abundance of the other strains in the lake fishery creel for each of the four states also varied. For each state, the Ganaraska strain was most abundant in the creel during June-July. Similar consistent trends in abundance in each state were not observed for any other strain.

Job 5. Title: Estimate levels of stock structure in Lake Superior coaster brook trout in and immediately surrounding the Salmon Trout River. Assess the efficacy of developing a coaster broodstock from this population.—The Salmon Trout River in the Upper Peninsula of Michigan represents the only known viable population of coaster brook trout along the south shore of the Lake Superior basin. Brook trout of both migratory and resident life history forms have been widely stocked across the basin. There is intense interest to ascertain whether stocking of different strains of resident and coaster brook trout has been successful, and what effects stocking has had on population relationships across the southern shores of the basin.

Brook trout were sampled from 9 streams in each of 2 regions of Michigan's upper peninsula. Streams sampled were selected because they supported wild self-sustaining brook trout except the Gratiot River which was selected because it is currently stocked with Nipigon coaster strain brook trout.

We sampled wild brook trout using electrofishing gear from all sampled streams. In addition, in the Salmon Trout River we collected fish with a trap that was used to monitor fish movement. Captured fish were measured and weighed and the adipose fin was clipped for genetic analysis. We also conducted genetic analysis on three hatchery brook trout strains that have been recently stocked in nearby streams and Lake Superior waters, including the Assinica strain, Nipigon strain, and Jumbo River strain.

Are Stocking Programs Contributing to the Recruitment of Brook Trout: We found little evidence to suggest that fish from the Assinica, Nipigon, or Jumbo River strains of brook trout were present in the streams surveyed. Levels of genetic differentiation between hatchery and wild strains was on average several times greater than between differences among wild populations.

*Genetic Relationships Among Stream Resident Populations in Michigan Tributaries to Lake Superior*: Wildlife stream-resident populations of brook trout are highly genetic differentiated, suggesting reproductive isolation. A significant portion of the variance in allele frequency was apportioned to region (populations from around the Kewanaw Peninsula and in a south-eastern region in the vicinity of Marquette) and among populations within region. There was no suggestion that population genetic affinities were correlated to geographic proximity. Within the Salmon Trout River there is evidence for down-stream migration from an isolated population segment above a waterfall.

*Relationships Between Resident and Migratory Life-History Forms*: Samples of coaster and stream resident brook trout differed significantly in allele frequency. These differences are comparatively smaller that among populations from different streams. Using assignment tests we were not able to accurately place individuals with the Salmon Trout River to one or the other life form. Thus, genetic markers will not be able to distinguish unknowns. Adults of known (or suspected) coaster phenotype will likely have to be spawned directly if a broodstock is to be developed.

## Job 6. Title: Estimate rates of loss of genetic diversity in northern musky. Estimate degree of introgression between stocked musky and northern pike. Determine relationships between northern musky and Great Lakes musky to assist in developing a comprehensive Esocid hatchery management plan.–

Analyses of Potential Northern Pike-Musky Hybrids: During one year survival of musky with the Michigan hatchery system was low and the DNR had musky sent from the Iowa hatchery system.

A portion of the progeny from the Iowa fish were retained in ponds at the Wolf Lake hatchery. When 18 of these large fish were removed a year later and stocked into one of the broodstock lakes, biologists noted a different pattern of vermiculation on the fish. It was believed that some or all the fish were northern pike/musky hybrids (or "tiger musky"). We were asked to genotype the fish to determine whether they were hybrids.

We obtained northern pike from Gun and Gull Lakes in Michigan. We genotyped the northern pike for the a suite of microsatellite loci we have historically used for musky in Michigan. We found that musky and northern had species-specific alleles at each locus. Thus, we could unambiguously determine if a fish was a hybrid. We found that of 18 suspected hybrids, 17 were tiger musky (hybrids) and 1 was a northern musky.

We analyzed several putative hybrids from lakes where gametes we historically taken taken. One lake (Gun) had what was believed to be hybrids. This was of concern because it is an important northern pike source. There is no suspected musky natural reproduction occurring, and musky had not been stocked into the lake for some time. We were given 3 samples to test from Gun Lake. Two samples were northern pike and a third sample was a hybrid. We also found that allele frequencies differed significantly between Gun and Gull Lakes.

Potential Introgression Between Northern and Great Lakes Musky: Previously, based on baseline samples from Lake St. Clair (N=69) and Thornapple (N=67), we found that Great Lakes musky and Northern musky were genetically distinct and could be easily identified using microsatellite loci. Based on genotypes and statistical assignment tests we were are able to genotype individuals and assign individual fish as either Northern or Great Lakes musky with very high accuracy (99.3% correct classification).

Over a 2 year period, musky were collected by Michigan DNR biologists below a dam on the Huron River in Southeastern Michigan. Fish were within the Lake Erie drainage and had access to the Great Lakes. Based on morphology, the fish did not appear to be Great Lakes musky. Given that Northern musky had been routinely stocked in reservoirs about dams that lead to the Great Lakes, including on the Huron River, these fish could have plausibly been either subspecies.

In 2003 21 musky were sampled below the dam and all were determined to be northern musky (i.e., of hatchery origin). In 2004 18 musky were sampled and 16 or 18 were found to be northern musky while 2 were Great Lakes musky. Over both years the mean level of statistical confidence in individual assignments was 0.983. Implications of stocking genetically differentiated forms in close proximity to valued natural populations in the Great Lakes is of concern. We are working with DNR biologists to collect additional samples of musky from drainages with connectivity to the Great Lakes and where hatchery supplementation of northern musky has occurred.

Job 7. Title: <u>Prepare annual report and as appropriate communicate program results in the</u> <u>form of peer-reviewed publications, reports, popular articles, and presentations.</u>–Findings from the first years activities are communicated in this document and to Michigan DNR and regional fisheries biologists via oral communications at meetings, professional meetings, and written reports.

Prepared by: <u>Kim T. Scribner</u> Date: <u>September 30, 2005</u>

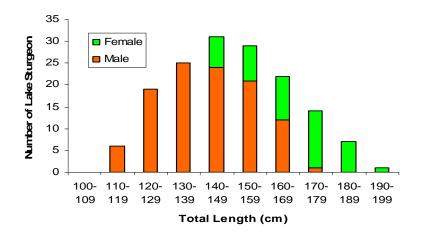


Figure 1.-Length-frequency histogram for adults captured at the spawning sites in 2005.

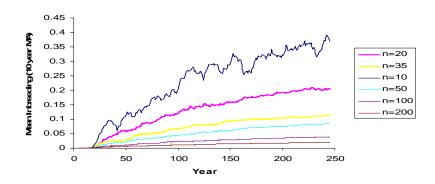


Figure 2.–Results of individual-based model that estimates the expected population levels of inbreeding over time for adult populations of different size.