

STUDY PERFORMANCE REPORT

State: Michigan

Project No.: F-81-R-5

Study No.: 230723

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, 2003 to September 30, 2004

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.

For Lake Sturgeon in Black Lake, we found evidence that previous management efforts to supplement the Black Lake population resulted in high levels of relatedness among progeny stocked. Individuals stocked during the 1980's will shortly make up approximately 50% of the adult spawning population, which possess a high risk of future inbreeding.

Walleye populations in Great Lakes waters of Michigan have recovered numerically, principally through extensive stocking efforts that continue today. We found evidence that past indiscriminant stocking without regard to basin of origin resulted in genetic homogenization of walleye stocks across formerly genetically structured populations. We found evidence for the existence of remnant stocks in impounded upstream areas.

Spawning populations of steelhead are increasingly composed of hatchery strains, including those produced by other agencies across the Lake Michigan basin. We have documented that introgression of hatchery strains has already occurred in the tributaries examined.

Coaster brook trout restoration is a primary goal in Lake Superior. We have found no evidence for introgression of hatchery brook trout into 6 Upper Peninsula tributaries to Lake Superior. Preliminary data suggests that migratory and resident brook trout are reproductively isolated.

Populations of northern musky have been maintained in inland Michigan waters primarily through supplementation. Interest is increasing in the use of Great Lakes musky. Preliminary

analyses suggest that northern and Great Lakes musky are highly differentiated genetically. Introgression of northern pike and northern musky has occurred.

Findings: Jobs 2, 3, 4, 5, 6, and 7 were scheduled for 2003-04, 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.—During the spring 2004 lake sturgeon spawning season we attempted to sample all adults spawning and sampled out-migrating larvae. We sampled 100 adults and 437 juvenile lake sturgeon. We saw evidence of males of a size consistent with cohorts from years of hatchery supplementation (1983, 1984, 1987) present in spawning aggregations within the Black River.

Historically, the spawning season consisted of multiple runs whereby individuals were seen to migrate multiple times from Black Lake into Black River and back again. Episodic migrations were believed to have been a response to fluctuations in water temperature and flow rate. This year, high water levels precluded estimation of the proportional contributions of all spawning runs to recruitment. Our sample size of juveniles represents the lowest number since juvenile studies were begun in 2001. It is unknown what effect if any high water and our lack of abilities to access the stream had to do with estimates of recruitment. However, we do have increasing support for earlier findings that suggest there is a relationship between spawning site used by adults and recruitment.

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. Such models have heretofore never been conducted on long-lived fish species. Population models are being used to simulate the effects of hatchery supplementation on inbreeding using Black Lake sturgeon data.

We are currently genotyping juveniles and adults to determine the extent to which hatchery-produced males contributed to recruitment.

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, Tittabawassee River, Saginaw Bay Reefs, Holloway Reservoir, Flint River, Clinton River, near-shore spawning areas in eastern Lake Erie and Lake Gogebic. The Gogebic population was added this year because it is believed that this population was established from reef-spawning fish from Saginaw Bay in Lake Huron. Walleye in Lake Gogebic have retained a reef-spawning life history. As such, the stock could be used for rehabilitation efforts in near-shore areas of the Great Lakes and in inland waters.

Previous findings (without Lake Gogebic) suggested that walleye populations spawning in tributaries of the Great Lakes could be partitioned into 3 genetic "clusters" based on genetic affinities established using pair-wise estimates of population similarity in allele frequency. One group was composed of spawners from the St. Mary's River and Little Bay de Noc. A second group was composed of populations from the Clinton River and eastern Lake Erie. A third group included the Flint River, Tittabawassee River, Saginaw Bay Reefs, and Muskegon River. Genetic affinities between the Muskegon River (a tributary to Lake Michigan) and walleye obtained from waters in and draining to Saginaw Bay in Lake Huron reveal the overwhelming influence of

previous stocking efforts in tributaries to Saginaw Bay that primarily utilized progeny from spawners from the Muskegon River.

The Gogebic Lake population was the most genetically diverged of all walleye stocks analyzed to date. This is interesting for several reasons. First, if the present genetic characteristics of Lake Gogebic walleye reflect characteristics of historical (pre-crash) reef-spawning walleye in Saginaw Bay, then there is minimal evidence of any genetic contributions of remnant Great Lakes stocks to restored populations draining into Saginaw Bay. Secondly, it is believed that the Lake Gogebic population was used to stock Little Bay de Noc in Northern Lake Michigan. Lack of genetic affinities between putative source and recipient release sites (Lake Gogebic and Little Bay de Noc, respectively), suggests that the walleye fishery in Northern Lake Michigan recovered based on recruitment from remnant stocks and not from stocking. The strong genetic affinities of the Little Bay de Noc population and the population from the St. Marys River supports this hypothesis.

Job 4. Title: Estimate the impacts of hatchery supplementation on naturalized steelhead populations. Estimate proportional contributions of different hatchery strains to the open water creel in Lake Michigan.—We estimate that approximately 25% of the hatchery steelhead spawning in Michigan tributaries to Lake Michigan were produced by other states across the basin. Eighteen percent of the hatchery fish were Ganaraska strain stocked by Wisconsin. Skamania (3%) and Chambers Creek (3%) strains also were found across all Michigan streams surveyed during 1998-1999. These strains are stocked by Wisconsin, Indiana, and Illinois. Most importantly, at the Little Manistee weir, which is the source of Michigan DNR steelhead gametes, we estimate that the proportion of hatchery steelhead to have increased 2% to 33%. Because only a fraction of the hatchery fish are marked, we estimate that a large fraction of the gametes taken annually are from unmarked hatchery fish that are mistaken for wild steelhead. Analyses of age structure and incidence of repeat spawning for hatchery fish of different strains and for wild steelhead are ongoing.

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.

The primary questions of this portion of the project focused on the extent of dispersal and establishment of stocked brook trout. As part of our current efforts, we have been conducting preliminary surveys of the fish community and habitat conditions in tributaries around the Keweenaw Peninsula (KP) and the eastern shore of northern Marquette County. Brook trout were sampled from 4 streams in each of 2 regions of Michigan's Upper Peninsula. Identification of stream resident and coaster phenotypes were based on diagnostic morphological traits. A fin clip biopsy was taken from the caudal fin for DNA analysis. Samples from each of the hatchery strains used for supplementation were provided by management agencies.

Genetic data in the form of multi-locus genotypes were being obtained for each individual based on microsatellite loci that are currently being used for brook trout in our lab in other projects. Summary measures of genetic similarity among populations are being used to quantitatively determine degree of reproductive isolation. Data show conclusively that resident populations of brook trout across streams in Michigan's Upper Peninsula are reproductively isolated based on

very high estimates of genetic divergence in allele frequency. We also found little evidence for introgression of hatchery brook trout of either coaster and resident forms.

We found evidence that that coaster and resident brook trout from the Salmon Trout River are reproductively isolated. Allele frequencies differ significantly between the fish of both life history forms. In addition, we found that the majority of young of the year sampled (YOY) had genetic affinities more closely allied with coaster than with resident brook trout suggesting higher rates of recruitment in coasters relative resident forms.

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.—Previously, we found that northern musky and Great Lakes musky are genetically distinct and could be easily identified using microsatellite loci. Based on genotypes and statistical assignment tests we were able to genotype individuals and assign them as either Northern or Great Lakes musky with very high accuracy.

Michigan DNR biologists provided samples of musky that were collected 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 above dams that lead to the Great Lakes, including on the Huron River, these fish could have plausibly been either form.

All individuals provided were genotyped and found to be northern musky (i.e., of hatchery origin). Implications of stocking genetically differentiated forms in close proximity to valued natural populations in the Great Lakes is of concern.

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

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