

STUDY PERFORMANCE REPORT

State: Michigan

Project No.: F-53-R-13

Study No.: 471

Title: Chinook salmon population dynamics in Michigan's waters of the Great Lakes

Period Covered: April 1, 1996 to March 31, 1997

Study Objectives: (1) To assemble the volumes of data collected on all life stages of chinook salmon (*Oncorhynchus tshawytscha*) since the inception of the salmon program in Michigan; (2) to capture these data into computerized databases to allow for a) management and update of such data, b) analysis, c) development of predictive capabilities for future management of chinook salmon, and d) easier dissemination of these data to other interested researchers; (3) to develop information and mathematical models from these data which will allow managers to predict, with some predetermined level of certainty, the outcome of various management strategies on chinook salmon; and (4) to begin the process of a holistic approach to the management of the Great Lakes through the development of mathematical models to predict, with some predetermined level of certainty, the outcome of various management scenarios on the Great Lakes' ecosystem.

Summary: Work on Study 471 has thus far focused on Objectives 1 and 2 -- assembling statewide data on chinook salmon and capturing these data into computerized databases (Jobs 1, 3, 6, 8, and 10). Michigan Department of Natural Resources (MDNR) personnel at Platte River State Fish Hatchery, Wolf Lake State Fish Hatchery, and Thompson State Fish Hatchery helped in assimilating the many pieces of information and data currently stored at each hatchery concerning all aspects of chinook salmon production, egg-take operations, and fish distribution from hatcheries to stocking sites (Jobs 1, 3, and 8). These individuals were informed of the project and its goals, and input was solicited from them during visits to each facility. Available historical data were copied, collated, organized, and entered into computer databases.

Due to personnel changes and difficulty in pulling together widely separate sources of data, comparatively little effort has been expended in data analysis and synthesis. During the coming year (1997-98), effort will shift to focus more in this direction (Jobs 2, 4, 5, 7, 9, and 11). An amended study design has been submitted to reflect this change in focus.

Job 2. Title: Analyze chinook salmon hatchery culturing techniques data.

Findings: No work on this job was accomplished during 1996-97. Analysis will begin when all hatchery data has been compiled.

Job 4. Title: Analyze data for stocking and release techniques of chinook.

Findings: No work on this job was accomplished during 1996-97. Analysis will begin when all stocking data has been compiled.

Job 9. Title: Analyze data on chinook salmon egg-take operations.

Findings: Work on this job was completed as part of Julie Weeder's Masters of Science thesis at Michigan State University. A summary of work not previously presented in performance reports is given here; more detailed information will be presented in Weeder (1997).

Genetic drift has caused a loss of genetic diversity in managed salmonid populations (Gharrett and Thomason 1987, Quinn et al. 1996). In order to address the possibility of such a genetic loss in Lake Michigan chinook salmon, we used protein electrophoresis to determine whether this population shows evidence of genetic drift. Three methods were employed; 1) we compared the allelic frequencies of Lake Michigan and Green River populations, 2) we calculated the genetic distance between these two populations, and 3) we calculated the mean effective population size (N_e) of the Lake Michigan population.

First, we tested whether there has been genetic change in the chinook population since their Great Lakes introduction by testing the null hypothesis that the allelic variability of Lake Michigan and Green River chinook salmon is not significantly different. Significant differences would indicate a gain or loss of variability since 1967. We hypothesized that Lake Michigan and Green River chinook salmon would have similar genetic profiles. These two populations showed nearly identical mean numbers of alleles per locus (2.47 and 2.50, respectively); however, only 83 % of the loci variable in Green River fish were also variable in Lake Michigan fish. Specifically, three loci were fixed in Lake Michigan stocks, two of which were strongly polymorphic in Green River stocks. In general, alleles that were rare in the Green River population (e.g., GPI-B2* - *60) tended to be lost in the Lake Michigan population, while alleles that were more common in the former (e.g., sSOD-1* - *-100, sSOD-1* - *-260, and sSOD-1* - *-580) were retained more often in the latter.

Next, we calculated the genetic distance between the two populations. The statistic 'D' measures the extent of gene differences between two populations. There was detectable genetic distance ($D = 0.00082$) between Lake Michigan chinook salmon and their source population from the Green River (Figure 1), and this distance is weak evidence against our hypothesis of similar genetic profiles for Lake Michigan and Green River populations. We included fish from the Cowlitz hatchery, a Columbia River strain near the Toutle River, for comparison and to determine how closely related they are to Lake Michigan fish. As expected, the distance between the Green River and Lake Michigan fish is much less than that between the Cowlitz hatchery and Green River fish ($D = 0.03098$), which come from historically isolated drainages (Figure 1). This phenogram confirms that Great Lakes chinook salmon are more closely related to the Puget Sound-derived strain than to Columbia River-derived fish.

Finally, we estimated the impacts of genetic drift using effective population size (N_e), a population genetics parameter. Using a variation of Waples' (1989) "temporal method" as the basis for our estimate of N_e , we compared two contemporaneous populations, the planted population and its population of origin, to estimate the effects of drift based on allele frequency change between the two samples. The mean effective number of breeders per year from 1967-95

was less than or equal to 415. The more N_e differs from the actual number of breeders in a population, the more drift is implicated. As 415 is likely much less than the number of mature breeding chinook salmon in Lake Michigan, the effects of genetic drift on this population have been significant.

We concluded that Lake Michigan chinook salmon show the effects of genetic drift (reduced genetic variability) upon comparison to their source stock. There are several factors in the Michigan chinook salmon program that could have caused such a change. First, genetic bottlenecks early in the program could have resulted in founder effects which reduced the genetic variability of the first Michigan generations (Nei et al. 1975). Second, chinook salmon breeding practices that are expected to erode a population's genetic variability, including use of a skewed sex ratio and high variance in female reproductive success (Gall 1987, Simon et al. 1986), have consistently been used in Michigan's chinook salmon program. Although we cannot determine the relative impacts of genetic bottlenecks versus breeding practices, and founder effects from historical events cannot be directly mitigated, *current* causes of diversity loss should be identified and their impacts reduced. We recommend that every effort be made to increase the number of males contributing to breeding in order to equalize the sex ratio in the chinook salmon fertilization system. Even modest improvements can give genetic benefits, and may not appreciably decrease the efficiency of breeding operations. In addition, a one-time experiment is needed wherein individual broods remain isolated throughout the rearing program and their success is tracked in order to quantify the extent of variance in brood success. If this variance is high, the culling of broods with particularly high survival rates could be an easy-to-implement and effective method of reducing this variance and thus increasing the number of broods contributing to the pool of fish eventually stocked.

Job 10. Title: Compile sport data (catch, effort, and biological information), and assimilate with coded-wire tag and diet studies.

Findings: Compilation of sport angling data for the years 1993-96 -- including catch rates and average size of chinook salmon harvested -- is ongoing but has not yet been completed. Data from 1980-92 was compiled previously and presented in the 1992-93 performance report. Compilation of data from Studies 463 (chinook salmon diet) and 464 (coded-wire tag) and 485 (chinook salmon assessment) are in various stages of completion.

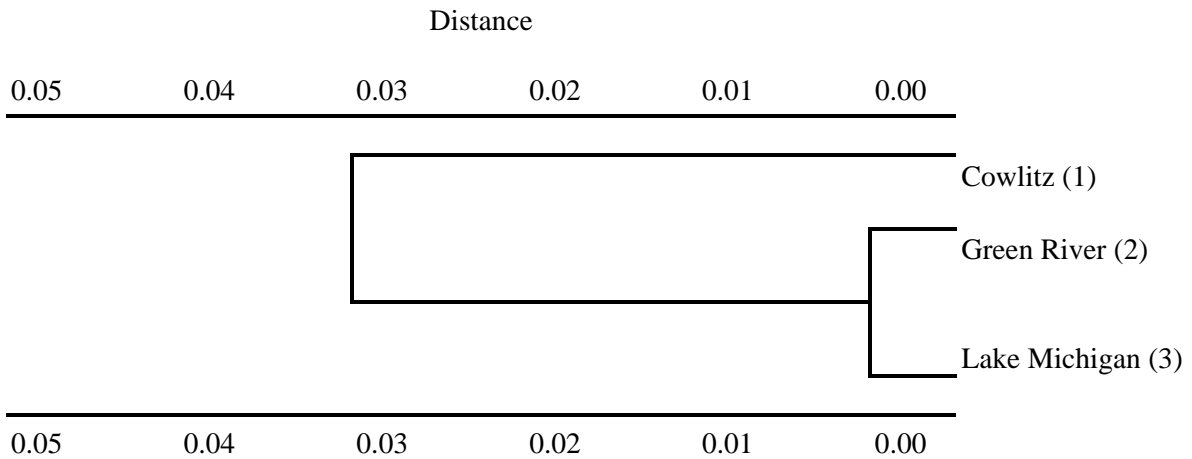
Job 11. Title: Analyze sport data.

Findings: No work was accomplished on this job during 1996-97. A synthesis of data from Studies 427, 463, 464, and 485 will be completed once all data has been collected.

Literature Cited:

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Population or cluster numbers joined		Clustering level	Cycle
2	3	0.00082	1
1	2	0.03098	2

Figure 1.—Genetic distance between Washington (1 and 2) and Lake Michigan (3) chinook salmon populations.