NOTEBOOK COPY

STATE OF WASHINGTON
DEPARTMENT OF FISH AND WILDLIFE
FISH MANAGEMENT - RESOURCE ASSESSMENT

4 May 1999

TO: Distribution list

FROM: Anne Marshall, Genetics AM

SUBJECT: **Genetic analyses of 1998 Skokomish River chinook samples**

Chinook salmon in the Skokomish River were sampled in 1998 in order to evaluate genetic characteristics, and assess their relationships with other chinook populations. Out-migrating juveniles were sampled during June in the South Fork Skokomish (n=32), and in the North Fork Skokomish (n=28) by WDFW staff. This represents the first genetic sample of naturally-spawned chinook from this basin. Adult spawners were sampled in October in the South Fork (n=14), North Fork (n=32) and in the mainstem (n=15), for a total of 61. This was the first time adults returning to the river were sampled genetically.

We assayed genetic characteristics by collecting data on allelic variation at 57 allozyme gene loci. These are loci that have shown genetic variation in chinook salmon studied from Alaska to California. We used our standard baseline sample electrophoretic protocol for analysis of muscle, heart, liver, and eye tissues. The final product of laboratory analysis was a multi-locus genotype for each chinook.

Allele frequencies at all loci were calculated from genotype data of each sample, and/or combinations of samples, and variable loci were tested for conformance to expected Hardy-Weinberg genotypic proportions. *G*-tests (log-likelihood ratio tests) of the homogeneity of allele frequencies were done with variable loci for pair-wise comparisons of Skokomish samples and other Puget Sound population samples. Allele frequencies for 42 loci were used to compute genetic distances among samples and examine genetic relationships through cluster analyses and three-dimensional scaling techniques. Information on other Puget Sound population samples used in comparative analyses is presented in Table 1.

Due to small sample sizes, and because they were of the same brood year (1997), juveniles collected from the South Fork and the North Fork Skokomish were combined for the first round of analyses. We found allelic variation at 22 loci in the combined juveniles, and at 24 loci in the 1998 adult spawners. In the juvenile sample, three loci had significant ($p<0.05$) deviations from Hardy-Weinberg expected genotypic proportions, while the adult sample had no significant test results. Although sampling error is a plausible explanation for the Hardy-Weinberg disequilibria in juveniles, it could also indicate a mixture of two populations, as two loci showed heterozygote deficiencies. This possibility was explored in subsequent analyses.

Given these results, I contacted the Coded-Wire Tag Recovery Laboratory for results on adipose-clipped chinook that were sampled for tags as well as genetic tissues. In the genetic sample of Skokomish spawners, ten chinook were ad-clipped and all had coded-wire tags. Origins of these chinook and other information are shown in Table 2. All were hatchery-origin fish from facilities in Hood Canal. Ageing by scales showed that seven of the ten had a scale pattern of one winter in fresh water with outmigration in the second year of life, which is associated with the rearing and release of yearlings at hatcheries. Upon reviewing scale ages of unmarked Skokomish spawners, I found 16 other fish with the yearling scale pattern (ages 3.2 and 4.2), seven from the North Fork, five from the South Fork, and four from the mainstem.

Thus, assuming all chinook with the yearling outmigration pattern were hatchery-origin, 43% of the adult genetic sample was composed of hatchery strays. The breakdown of hatchery strays by sampling location was 31% in the North Fork, 64% in the South Fork, and 47% in the mainstem. The relatively close genetic relationship between Skokomish natural spawners and Hoodsport Hatchery chinook is likely a result of spawning success by hatchery strays. It would be useful to know also if, and to what extent, wild fish contribute to hatchery broodstocks. Because allele frequencies were not homogenous between the total Skokomish sample and the Hoodsport Hatchery sample, it is reasonable to speculate that there may be a wild-origin component in the Skokomish that contributes to this genetic diversity. To address this possibility we would need to increase sample size of spawners that do not appear to be first generation hatchery-origin, and also analyze another sample of the Hoodsport broodstock. In the 11 years since the last Hoodsport sample, it is possible that allele frequencies may have changed somewhat due to changes in hatchery transfer practices.

This is only a brief summary of results and their interpretation. I will be glad to provide other details or clarifications as needed. Genetics Unit staff contributing to this analysis were Bruce Baker, Cherril Bowman, Bill Ingram, and Norm Switzler. Lynn Anderson supplied the code-wire tag information, and John Sneva did the scale pattern analysis.

Distribution list:

Thom Johnson, WDFW
Tim Flint, WDFW
Dan Collins, WDFW
Bruce Sanford, WDFW
Rich Eltrich, WDFW
Ed Jouper, WDFW
Derek Poon, NMFS
Jim Myers, NMFS
Chris Weller, PNPTC
Nick Lampsakis, PNPTC
Dave Herrera, Skokomish Tribe
Ken Currens, NWIFC

Figure 1. Dendrogram resulting from cluster analysis of pair-wise genetic distances among 15 South Puget Sound and Hood Canal chinook population samples. Populations are fall-run unless otherwise indicated. R=River, H=Hatchery, CR=Creek, SP=spring-run, SU=summer-run.