GENETIC IDENTIFICATION STUDY

ANNUAL PROGRESS REPORT, FY 81

by

George B. Milner

David J. Teel

and

Fred M. Utter

Bonneville Power Administration Contract
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Milner

Coastal Zone and Estuarine Studies Division
Northwest and Alaska Fisheries Center
National Marine Fisheries Service
National Oceanic and Atmospheric Administration
2725 Montlake Boulevard East
Seattle, Washington 98112

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I. Abstract

The genetic stock identification study began the development of a data base during FY81 for use in estimating the proportions of chinook salmon stocks of the Columbia River drainage in ocean fisheries. Genetic data were collected from 36 coastal stocks of chinook salmon in California, Oregon, Washington, British Columbia, and Alaska and from 9 stocks of the Columbia River drainage. These collections provide 1) a preliminary data base for those non-Columbia River stocks that may contribute to ocean fisheries in which Columbia River fish are harvested, and 2) the addition of data for new loci to the existing Columbia River data base. Evidences of genetic differences between Columbia and non-Columbia River stocks that would be useful in the analysis of ocean mixed fisheries were illustrated. Data collection is continuing and will result in a data base sufficient to perform mixed fishery analysis of ocean fisheries in FY82.

II. Objective of FY81 Work

The principal objective of the Genetic Identification Study during FY81 was to collect baseline genetic data from hatchery and wild stocks of chinook salmon in California, Oregon, Washington, British Columbia, and Alaska. This effort continues in FY82 and the resulting set of baseline data will be used to estimate the proportions of stocks of Columbia River chinook salmon stocks in an actual mixed stock fishery in the ocean. Emphasis of FY81 collections was on coastal hatchery stocks and both hatchery and wild stocks from within the Columbia River drainage.

A second objective of FY81 data collection was to refine and update the existing data base of Columbia River stocks to permit more precise

estimates of these stocks in Columbia River and ocean fisheries. The data base is broadened and strengthened with the inclusion of data for new genetic loci and the resampling of stocks which have had recent introductions of genes from other stocks.

III. Methods and Materials

Samples were collected, frozen on dry ice, and shipped to the Manchester Marine Experimental Station, Northwest & Alaska Fisheries Center, National Marine Fisheries Service. Samples of 50 to 100 individuals were collected from 10 hatchery and wild stocks of the Columbia River drainage and from 37 hatchery stocks of other Pacific Coast drainages (Table 1). Biochemical genetic data were collected for 14 protein systems representing 20 polymorphic loci (Table 2) by starch gel electrophoresis and histochemical staining as described in Utter et al. 1974 and Milner et al. 1980. Genetic data were put on computer tape and incorporated into existing data files.

The potential usefulness of the data base for estimating the contribution of Columbia River stocks in ocean fisheries was examined through a dendrogram constructed from genetic similarity values (Nei 1972) using the unweighted average linkage method (Sneath and Sokal 1973).[1/] Since similarity is the opposite of difference, the smaller the value at which a line connects two stocks in Figure 1, the greater the genetic difference between them, and the more likely they are to be separable in mixed stock fisheries.

[1/] This type of cluster analysis can better provide data regarding the general applicability of the method for detecting Columbia River populations in ocean samples than computer simulations which provide information only for a specified set of conditions. Thus cluster analysis has been used in place of simulations in this report.

Table 1.--Samples collected from chinook salmon stocks during FY81.

California

Spring chinook salmon

Feather River

Fall chinook salmon

Mokelumne River
Nimbus Hatchery
Feather River
Coleman (Battle Creek and late fall stocks)
Trinity River
Iron Gate

Oregon

Spring chinook salmon

Cole Rivers
Rock Creek
Cedar Creek
Trask River

Fall chinook salmon

Elk River (Elk and Chetco stocks)
Fall Creek
Salmon River
Cedar Creek
Trask River

Washington

Spring chinook salmon

Soleduck River

Summer chinook salmon

Skykomish River
Skagit River
Soleduck River

Table 1.--Continued

Fall chinook salmon

Green River
Naselle River
Hood Canal Hatchery
Elwha Spawning Channel
Quinault National Fish Hatchery
Queets River (wild)
Hoh River (wild)
Nemah River

British Columbia

Fall chinook salmon

Quinsam River
Robertson Creek
Capilano Hatchery
Puntledge Hatchery
Big Qualicum Hatchery

Alaska

Spring chinook salmon

Taku River (wild)

Columbia River

Spring chinook salmon

Winthrop National Fish Hatchery
Leavenworth National Fish Hatchery
Cowlitz Hatchery

Summer chinook slmon

Wells Hatchery
Wenatchee (wild)

Fall chinook salmon

Priest Rapids Hatchery
Ice Harbor Dam Interceptions
Bonneville Dam Interceptions
Spring Creek National Fish Hatchery

Table 2.--Protein systems and number of polymorphic loci for which data were collected.

Protein system	Nmber of polymorphic loci
Aconitase	1
Adenosine deaminase	1
Alcohol dehydrogenase	1
Aspartate aminotransferase	2
Glycylleucine dipeptidase	2
Isocitrate dehydrogenase	1
Lactate dehydrogenase	2
Leucylglycylglycine tripeptidase	1
Malate dehydrogenase	1
Phenylalanylproline dipeptidase	2
Phosphoglucomutase	1
Phosphoglucose isomerase	3
Phosphomannose isomerase	1
Tetrazolium oxidase	1

IV. Results of Study

Cluster Analysis

The data of the 1981 collections were added to the existing data base and the combined information was used to examine the genetic differentation of Columbia River from non-Columbia River stocks. The 52 stocks that are jointly analyzed in this report include data from 13 polymorphic loci.[2/] These samples have been analyzed for this report through a dendrogram (Figure 1 and Table 3) based on pairwise comparisons of genetic similarities over the 13 polymorphic loci for each of the samples. This rather simple graphic presentation is conservative, i.e., not all useful genetic differences are made obvious. Similarity values less than approximately 0.995 represent genetic differences that would be useful in mixed fishery analysis. However, useful genetic differences may or may not be present between stocks or groups of stocks having average similarities greater than approximately 0.995 in the dendrogram. Some examples of groupings from the dendrogram that are useful in evaluating our ability to estimate contributions of Columbia River stocks in ocean fisheries (group or stock numbers are given in parenthesis):

1) The Priest Rapids stock from the upper Columbia River has low genetic similarites to all California, Oregon, Alaska, other Columbia River stocks, and Coastal Washington stocks except for the Soleduck Spring run. Average similarities for Priest Rapid stocks to these stocks or groups range from 0.994 to 0.979.

2/ Complete data for all 20 of the polymorphic loci currently being surveyed and listed in Table 2, were not available for many of the stocks sampled prior to FY81.

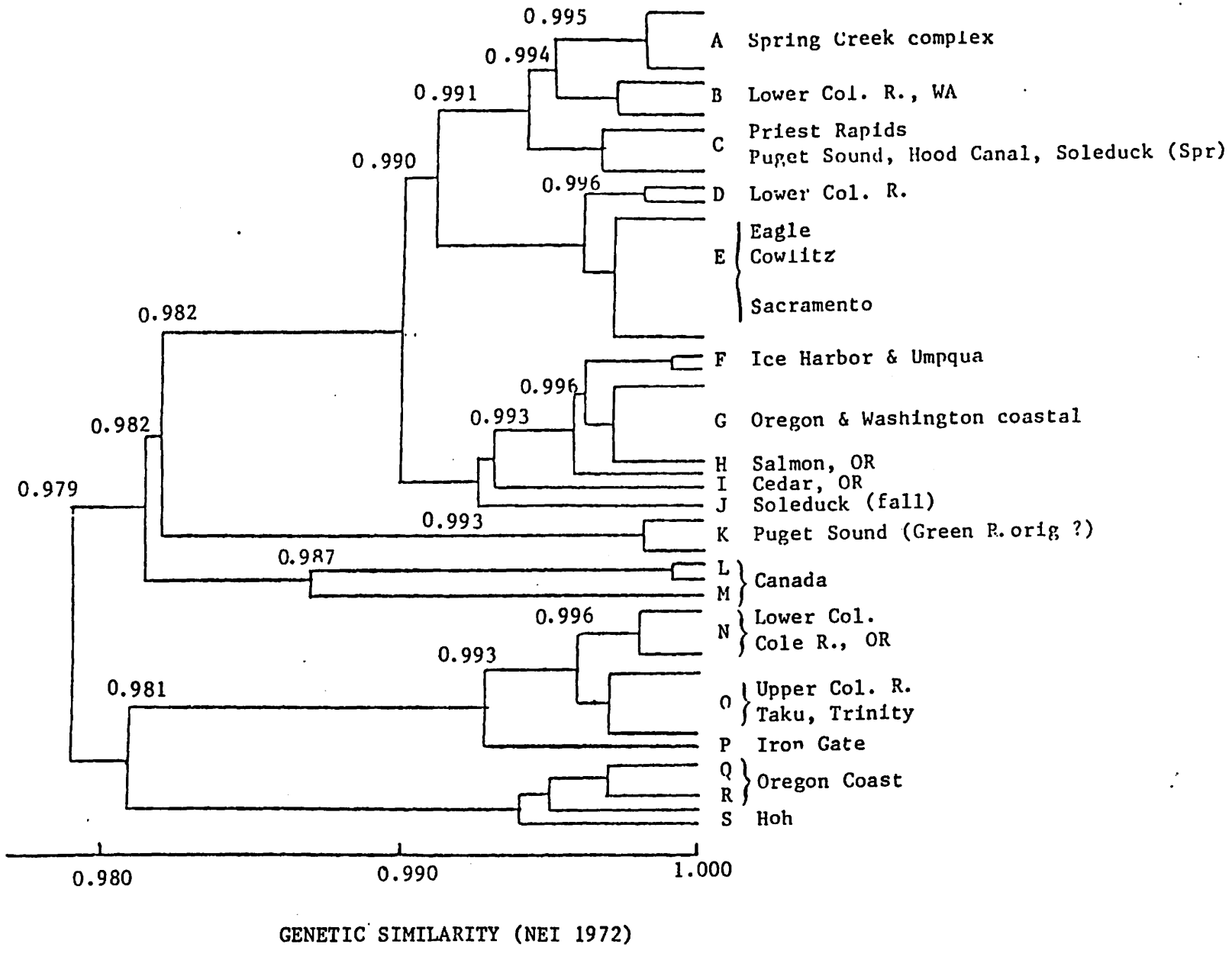

Figure 1.--Dendrogram based on genetic similarities of 13 loci for 52 stocks of chinook salmon. The lowest order stocks and groups of stocks (greater than 0.995 similarity) are given letter designations for cross reference to Table 3.

2) The Ice Harbor stock from the Snake River has low genetic similarities to all California and Canadian stocks, Alaska, other Columbia River stocks, and Oregon stocks except those in Group G. Average similarities range from 0.996 to 0.979 for these comparisons.

3) The Spring Creek complex of the Columbia River has average maximum similarity of 0.995 to all other stocks and groups, i.e., it is genetically quite different. The above comparisons, as well as others that are left for the interested reader, and the dendrogram as a whole show that strong genetic differences that are useful for mixed fishery analysis exist not only within the Columbia and Snake River complex, but also between this complex and many non-Columbia River stocks.

New Systems

A result of FY81 data collection that deserves specific mention was the electrophoretic resolution of the proteins aconitase and adenosine deaminase. The genetic basis of aconitase variation in liver and adenosine deaminase in heart, muscle, and eye were confirmed with inheritance crosses. Each protein system provided a new polymorphic locus for use in differentiating stocks of chinook salmon.

The importance of increasing the number of polymorphic loci used in the genetic method for stock identification was previously demonstrated by computer simulation (Milner et al. 1980). This simulation showed the effectiveness of added polymorphic loci in the detection of genetic differences between stocks, and consequently in increasing the precision with which stock contributions can be estimated in mixed fisheries. Estimates of a given level of precision can therefore be obtained with a smaller sample from the mixture, or a more precise estimate with the same sample size.

Table 3.--Time of return and general location of chinook salmon stocks used in the genetic similarity analysis. Letter designations are for cross reference to Figure 1.

Stock or group letter designation	Stock	Time of return	Area
A.	Bonneville	Fall	Columbia River
	Little White Salmon	Fall	Columbia River
	Spring Creek	Fall	Columbia River
	Willard	Fall	Columbia River
B.	Toutle	Fall	Columbia River
	Kalama	Fall	Columbia River
	North Fork Lewis	Spring	Columbia River
C.	Priest Rapids	Fall	Columbia River
	Skykomish	Summer	Puget Sound
	Hoodsport	Fall	Puget Sound
	Soleduck	Spring	Washington Coast
D.	McKenzie	Fall	Columbia River
	Kalama	Spring	Columbia River
E.	Eagle Creek	Spring	Columbia River
	Cowlitz	Spring	Columbia River
	Mokelumne (Sacramento R.)	Fall	Sacramento River
	Nimbus "	Fall	Sacramento River
	Feather "	Fall	Sacramento River
	Feather "	Spring	Sacramento River
	Coleman "	Fall	Sacramento River
F.	Ice Harbor Dam	Fall	Columbia River
	Rock Creek (Umpqua)	Spring	Oregon Coast
G.	Chetco	Fall	Oregon Coast
	Elk	Fall	Oregon Coast
	Elwha	Fall	Washington Coast
	Queets	Fall	Washington Coast
	Quinault	Fall	Washington Coast
	Naselle	Fall	Washington Coast
H.	Salmon	Fall	Oregon Coast
I.	Cedar Creek (Nestucca)	Spring	Oregon Coast
J.	Soleduck	Summer	Washington Coast

Table 3.--Continued.

Stock or group letter designation	Stock	Time of return	Area
K.	Green river	Fall	Puget Sound
	Deschutes	Fall	Puget Sound
	Skagit	Summer	Puget Sound
L.	Big Qualicum	Fall	British Columbia
	Capilano	Fall	British Columbia
M.	Puntledge	Fall	British Columbia
N.	North Fork Lewis	Fall	Columbia River
	Round Butte	Summer	Columbia River
	Carson	Spring	Columbia River
	Cole River (Rogue R.)	Spring	Oregon Coast
O.	Capehorn, mid-Fork Salmon*	Summer	Columbia River
	Beaver Creek, mid-Fork Salmon*	Summer	Columbia River
	South Fork Salmon*	Summer	Columbia River
	Taku	Spring	Alaska Coast
P.	Iron Gate (Kalamath)	Fall	California Coast
	Trinity "	Fall	California Coast
Q.	Fall Creek	Fall	Oregon Coast
	Cedar Creek (Nestucca)	Fall	Oregon Coast
	Trask	Spring	Oregon Coast
R.	Trask	Fall	Oregon Coast
S.	Hoh	Fall	Washington Coast

* Denotes wild stock.

V. Summary and Conclusions

Project goals for FY81 were met through the initiation of a non-Columbia River data base to contrast with an extensive data base from the Columbia River. Sufficient population differences were identified beyond the Columbia River to ensure that the genetic method for stock identification can be a powerful tool for discriminating Columbia River fish in oceanic mixed fisheries. In addition, new variable genetic systems were identified that will further enhance the overall discriminatory powers of the method. Management agencies are urged to apply the method in view of its unique capabilities for providing timely estimates of both wild and hatchery contributions to mixed stock fisheries.

VI. Major Equipment Purchases During FY81

So-low chilling cabinet, $2,850.00. Heat systems ultrasonics sonicator, $1,830.00.

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