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Title: PHENOTYPIC COMPARISON OF HATCHERY AND WILD COHO SALMON (Oncorhynchus kisutch) IN OREGON, WASHINGTON, AND CALIFORNIA

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Phenotypic similarities of coho salmon (Oncorhynchus kisutch) stocks from Oregon, Washington, and California were compared using agglomerative and divisive cluster analyses. The phenotypic characters evaluated included the following: 1) the isozyme gene frequencies of transferrin and phosphoglucose isomerase; 2) the life history characters time of peak spawning and proportion of females in the population; and 3) the morphological characters scales in the lateral series, scales above the lateral line, anal rays, gill rakers, branchiostegal rays and vertebrae. Coho salmon stocks from similar environments were phenotypically similar. The groups of stocks found to be similar by the agglomerative cluster analysis were: 1) wild stocks from the northern Oregon coast; 2) wild stocks from the southern Oregon coast; 3) stocks from hatcheries using wild coho salmon for an egg source; 4) stocks from large stream systems;

and 5) hatchery stocks from the northern Oregon coast. There were three trends involved with the clustering patterns: 1) stocks that are geographically close tend to be phenotypically similar; 2) stocks from large stream systems were more similar to each other than to stocks from smaller stream systems, independent of geographic nearness; and 3) hatchery stocks were more similar to each other than to wild stocks, even those in their respective stream systems, and wild stocks were more similar to each other than to hatchery stocks, even those in their respective stream systems. These trends may be useful to fishery managers for selecting donor stocks from hatcheries for transplanting to stream systems or other hatcheries. Individual phenotypic characters were correlated with characters of the stream systems. Two agglomerative cluster analyses of the characters of the stocks and the characters of the stream system were used to determine whether stream types corresponded to phenotype-types. The clustering patterns of phenotypic characters of the stocks were not similar to the clustering found for characteristics of the stream systems from which the stocks came.

Phenotypic Comparison of Hatchery and Wild Coho Salmon (*Oncorhynchus kisutch*) in Oregon, Washington, and California

by

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PHENOTYPIC COMPARISON OF HATCHERY AND WILD COHO SALMON (*Oncorhynchus kisutch*) IN OREGON, WASHINGTON, AND CALIFORNIA

INTRODUCTION

An aspect of fisheries management more frequently discussed than utilized is the genetic differences among anadromous salmonids stocks (Simon and Larkin 1970). The tendency to return to native streams reduces gene flow among salmon populations and allows the individual stocks to adapt to the native stream systems. Stocks may be highly adapted to their native stream systems and mixing with other stocks or transplanting to other stream systems may have a negative effect on the rate of return or survival rate of the donor stock (Bams 1975 and Ritter 1976). If the survival rate of a salmon stock is related to how well it is adapted to its stream system, then an opportunity exists for fisheries managers to increase the survival of hatchery stocks that are transplanted to other stream systems. Hatchery stocks genetically similar to the native stock of the recipient stream should have a higher survival rate than stocks with lower similarities. Higher survival should be especially true during the first several generations until the transplanted stock adapts to the recipient environment. An additional advantage of using genetically similar stocks might be reduced introgression into wild stocks (Reisenbichler and McIntyre 1977).

A genetic description of each salmon stock would be beneficial to salmon management. These stock assessments could assist fishery managers in making decisions that would make efficient use of hatchery production and protect wild spawning stocks. Obviously at the present time determining the genetic similarity among stocks for the entire genome is not possible, but the similarity can be estimated by comparing genetically related characters. Characters exhibiting variation among stocks of anadromous salmonids include morphological characters (Ricker 1970), life history characters (Whitler 1966; Schaffer and Elson 1975) and enzyme gene frequencies (Allendorf 1973; Kristiansson 1975; May 1975).

The objective of this study is to characterize coho salmon (*Oncorhynchus kisutch*) stocks using gene frequencies, life history and morphological characters to help provide a basis for selecting donor stocks in Oregon hatchery programs. The stocks were selected so that comparisons could be made among geographical areas and stream types and between hatchery and wild stocks. A measure of genetic similarity was calculated and a cluster analysis was used to display the relationships among stocks. Factors affecting genetic similarity were hypothesized by determining common environmental parameters of the similar stocks.

Although this paper is primarily taxonomic in nature, the genetic characters were correlated with variables characteristic of the stream systems. Strong correlations do not prove a functional significance. They were included in this paper, however, because inferences and hypotheses can be developed from the correlations for future studies.

METHODS AND MATERIALS

Sampling

Ten characters were evaluated for 15 hatchery stocks and 12 wild stocks. Samples collected from hatcheries consisted of 75 to 100 juvenile coho salmon of the 1976 brood from 14 hatcheries in Washington, Oregon and California and nine hatcheries from Oregon for the 1977 brood year. Samples of 30 to 100 juvenile coho of the 1976 and 1977 brood were collected by electrofishing from 12 Oregon stream systems (see Tables 1-3 for names of hatcheries and stream systems). Because some hatcheries have utilized non-native egg sources and stream systems have been stocked with juvenile and adult coho salmon, very few pure native stocks remain. Hatchery stocks and tributaries of streams that have recently received a large supplement of a non-native stock were not used.

Morphological Characters

For each sample, fifteen carcasses were frozen so morphological counts could be made at a later date. Scales in the lateral series were counted by counting scales of the second row above the lateral line, starting with the anterior-most scale and terminating at the hypural plate. Scales above the lateral line were counted from the anterior insertion of the dorsal fin to the lateral line. Anal ray

Table 1. Means, standard errors and ranges for the morphological characters of the 1976 brood year hatchery samples of juvenile coho salmon (Oncorhynchus kisutch) and the hatchery water incubation temperatures for the first month of incubation. Sample sizes for the morphological characters was 15.

Stock		Scales in lateral series	Scales above lateral line	Anal rays	Gill rakers	Branchiostegals	Vertebrae	Incubation water temperature (°C)
WASHINGTON								
Quilcene River Hatchery	$\bar{x}$	126.93	28.13	14.07	22.33	27.87	64.40	7.3
	$S_{\bar{x}}$	.97	.38	.15	.19	.26	.13	
	range	116-132	25-30	13-15	21-23	26-30	64-65	
Quinault River Hatchery	$\bar{x}$	132.67	29.93	13.53	22.53	26.67	65.50	7 3
	$S_{\bar{x}}$	.48	.33	.16	.24	.21	.13	
	range	130-136	28-32	13-15	21-24	25-28	65-66	
OREGON								
Cascade Hatchery (Columbia River)	$\bar{x}$	133.07	28.20	14.00	22.20	27.27	66.80	6.9
	$S_{\bar{x}}$	.56	.40	.20	.35	.37	.22	
	range	128-135	26-32	12-15	20-25	25-29	66-68	
Big Creek Hatchery (Columbia River)	$\bar{x}$	132.67	28.80	14.31	22.87	26.07	65.80	7.4
	$S_{\bar{x}}$	.57	28	.13	.17	.30	.15	
	range	128-136	28-31	13-15	22-24	24-28	65-67	
Cowlitz Hatchery stock, Cascade Hatchery	$\bar{x}$	133.60	27.87	13.80	22.20	28.13	64.47	6.9
	$S_{\bar{x}}$	.63	.24	.14	.26	.24	.22	
	range	131-137	26-29	13-15	21-24	27-30	65-68	
Sandy River Hatchery (Columbia River)	$\bar{x}$	133.13	28.27	14.33	22.07	28.20	66.07	7.0
	$X_{\bar{x}}$	.72	.42	.13	34	.26	.21	
	range	128-137	24-30	14-15	20-25	26-30	65-67	
North Nehalem River Hatchery	$\bar{x}$	131.93	28.33	14.00	22.67	26.73	65.80	7.8
	$S_{\bar{x}}$	.64	.30	.14	.27	.32	.17	
	range	128-138	26-36	13-15	21-24	24-28	65-67	
Trask River Hatchery	$\bar{x}$	132.13	28.80	13.93	22.13	26.40	66.07	9.8
	$S_{\bar{x}}$	.48	.47	.12	.31	.32	.18	
	range	128-135	26-32	13-15	20-24	24-29	65-67	
Salmon River Hatchery	$\bar{x}$	129.40	27.00	13.60	22.13	25.40	64.93	6.2
	$S_{\bar{x}}$	.54	.59	.19	.24	.24	.30	
	range	125-132	23-33	13-15	21-24	24-27	62-66	

Table 1. (Continued)

Stock		Scales in lateral series	Scales above lateral line	Anal rays	Gill rakers	Branchiostegals	Vertebrae	Incubation water temperature (°C)
OREGON (Continued)								
Fall Creek Hatchery	$\bar{x}$	132.00	28.67	14.00	23.20	27.13	65.80	5.7
(Alsea River)	$S_{\bar{x}}$	.50	.29	.17	.20	.34	.17	
	range	129-135	27-31	13-15	22-25	25-29	65-67	
Umpqua Hatchery stock	$\bar{x}$	131.20	26.00	13.47	22.13	25.13	65.33	3.5
(Smith River), Cole	$S_{\bar{x}}$	.51	.34	.19	.22	.24	.23	
Rivers Hatchery	range	127-134	24-28	13-15	21-23	24-26	64-67	
CALIFORNIA								
Irongate Hatchery	$\bar{x}$	132.73	29.07	13.80	22.33	27.00	66.07	5.3
(Klamath River)	$S_{\bar{x}}$	.78	.18	.14	.25	.28	.30	
	range	129-138	28-30	13-15	21-24	25-28	64-68	
Trinity River Hatchery	$\bar{x}$	130.87	28.27	13.60	22 00	26.00	66.00	7.3
(Klamath River)	$S_{\bar{x}}$	.75	.64	.13	.31	.59	.14	
	range	126-137	24-33	13-14	19-23	20-28	65-67	
Mad River Hatchery	$\bar{x}$	129.20	25.27	13.40	20.93	23.47	65.60	8.5
	$S_{\bar{x}}$	.88	.37	.19	.33	.51	.31	
	range	121-134	22-27	12-15	19-23	20-27	63-68	

Table 2. Means, standard errors and ranges for morphological characters of the 1977 brood year hatchery samples of juvenile coho salmon (*Oncorhynchus kisutch*) and the hatchery water incubation temperatures for the first month of incubation. Sample size for the morphological characters was 15.

Stock		Scales in lateral series	Scales above lateral line	Anal rays	Gill rakers	Branchiostegals	Vertebrae	Incubation water temperature (°C)
Bonneville Hatchery (Columbia River)	$\bar{x}$	133.33	26.73	13.93	22.53	27.00	65.80	5.4
	$S_{\bar{x}}$	.61	.27	.12	.29	.32	.15	
	range	129-138	25-29	13-15	21-25	25-29	65-67	
Big Creek Hatchery	$\bar{x}$	133.60	27.20	13.53	23.13	25.60	66.07	7.2
	$S_{\bar{x}}$	.46	.33	.13	.22	.24	.21	
	range	130-136	26-30	13-14	22-25	23-27	65-67	
Cowlitz Hatchery stock (Big Creek Hatchery)	$\bar{x}$	132.20	26.60	13.60	21.80	26.00	65.67	7.2
	$S_{\bar{x}}$	.40	.41	.13	.22	.34	.16	
	range	129-135	25-30	13-14	20-23	24-28	65-67	
North Nehalem Hatchery	$\bar{x}$	130.93	27.73	13.73	23.07	26.13	65.27	7.7
	$S_{\bar{x}}$	.42	.25	.15	.27	.29	.18	
	range	128-134	26-29	13-15	21-24	24-28	64-66	
Trask River Hatchery	$\bar{x}$	130.33	25.53	13.67	22.73	25.60	65.40	9.9
	$S_{\bar{x}}$	.42	.32	.13	.23	.32	.24	
	range	128-133	23-27	13-14	21-24	24-28	63.66	
Salmon River Hatchery	$\bar{x}$	130.53	26.80	13.67	22.40	26.27	65.53	7.8
	$S_{\bar{x}}$	.59	.28	.16	.16	.25	.19	
	range	127-135	25-29	13-14	22-24	25-29	64-66	
Fall Creek Hatchery (Alsea River)	$\bar{x}$	131.53	26.20	13.80	22.53	26.07	66.13	7.4
	$S_{\bar{x}}$	.68	.33	.17	.27	.23	.19	
	range	127-136	24-28	13-15	21-24	25-28	65-67	
Umpqua Hatchery stock (Smith River) Cole Rivers Hatchery	$\bar{x}$	129.07	26.40	13.40	21.47	25.87	65.40	8.6
	$S_{\bar{x}}$	.37	.32	.13	.17	.24	.13	
	range	126-131	24-29	13-14	21-23	24-28	65-66	
Cole Rivers Hatchery (Rogue River)	$\bar{x}$	130.33	26.20	13.80	22.20	26.20	65.20	8.6
	$S_{\bar{x}}$	.66	.33	.17	.30	.24	.26	
	range	125-134	24-28	13-15	20-24	25-28	64-67	

Table 3. Means, standard errors and ranges of morphological characters for 1977 brood year samples of wild juvenile coho salmon (Oncorhynchus kisutch).

Stream system	Sample size		Scales in the lateral series	Scale rows above lateral core	Anal fin rays	Gill rakers	Branchiostegals	Vertebrae
North Nehalem River	12	$\bar{x}$	132.25	27.75	13.58	23.25	26.75	65.50
		$S_{\bar{x}}$	.88	.33	.15	.37	.25	.26
		range	126-137	26-30	13-14	22-25	26-28	63-66
Nehalem River	12	$\bar{x}$	132.50	26.67	13.75	23.00	27.33	65.75
		$S_{\bar{x}}$	.77	.35	.13	.25	.22	.25
		range	127-136	25-29	13-14	22-24	26-28	64-67
Trask River	12	$\bar{x}$	131.17	26.50	14.00	22.92	26.58	65.83
		$S_{\bar{x}}$	.47	.31	.12	.31	.26	.11
		range	128-133	24-28	13-15	21-24	25-28	65-66
Nestucca River	12	$\bar{x}$	132.17	26.83	14.00	22.92	27.25	65.58
		$S_{\bar{x}}$	.68	.40	.12	.34	.28	.19
		range	128-136	25-29	13-15	21-25	26-29	65-67
Salmon River	12	$\bar{x}$	131.83	26.92	13.67	23.08	26.67	65.00
		$S_{\bar{x}}$	.61	.31	.14	.29	.19	.17
		range	128-135	24-28	13-14	22-25	26-28	64-66
Siletz River	12	$\bar{x}$	130.33	27.08	13.58	23.00	27.50	65.25
		$S_{\bar{x}}$	.61	.29	.15	.21	.23	.28
		range	128-135	26-29	13-14	22-24	26-29	63-67
Beaver Creek	12	$\bar{x}$	132.27	27.33	13.27	23.27	27.18	65.33
		$S_{\bar{x}}$	.49	.38	.20	.36	.30	.14
		range	130-135	25-29	12-14	21-25	26-29	65-66
Alsea River	12	$\bar{x}$	131.25	27.17	13.67	23.17	26.83	65.25
		$S_{\bar{x}}$	.37	.30	.19	.34	.30	.18
		range	129-134	26-29	12-14	21-25	26-28	64-66
Umpqua River	12	$\bar{x}$	131.75	26.83	13.25	22 92	27.00	65.83
		$S_{\bar{x}}$	.70	.40	.13	.19	.28	.27
		range	128-136	25-30	13-14	22-24	26-29	65-68

Table 3. (Continued)

Stream system	Sample size		Scales in the lateral series	Scale rows above lateral core	Anal fin rays	Gill rakers	Branchiostegals	Vertebrae
Tenmile Lakes	15	$\bar{x}$	131.73	26.20	13.47	22.53	26.60	65.73
		$S_{\bar{x}}$	.58	.28	.13	.19	.31	.25
		range	128-136	25-29	13-14	21-24	25-28	64-67
Coquille River	15	$\bar{x}$	131.67	26.27	13.27	22.40	26.47	65.93
		$S_{\bar{x}}$	.43	.43	.18	.19	.27	.21
		range	129-134	24-30	13-14	21-24	24-28	65-67
Rogue River	12	$\bar{x}$	132.75	26.58	14.00	22.50	26.92	65.42
		$S_{\bar{x}}$	.59	.26	.17	.31	.40	.15
		range	131-137	25-28	13-15	21-25	24-29	65-66

counts did not include the short rudimentary anterior rays, and branched rays were counted as one. The total number of gill rakers on the first gill arch was recorded. Alizarin red was used to highlight rudimentary gill rakers. The total number of branchiostegal rays from both sides was counted. Vertebral counts were made on X-ray plates including all of the last three upturned centra. Accuracy of morphological counts were checked by recounting two individuals from each sample. If errors were found, then additional individuals from that sample were recounted.

Electrophoresis

Blood was collected from the fish that were not saved for morphological counts by severing the caudal peduncle and collecting the blood in heparinized microhematocrit tubes that were then centrifuged and stored at -10°C. White muscle samples (1 cm^3) were removed from the anterior dorsal portion of the frozen carcasses, homogenated with 2-3 drops of water and then centrifuged to clear the supernatant. Only the blood serum and supernatant were used for electrophoresis.

The methodology for electrophoresis of transferrin and phosphoglucose isomerase followed the basic principles found in May (1975) with some modifications by Solazzi (1977). The gel and electrode buffers were described by Ridgway (1975). Four genotypes of transferrin (AA, AC, CC and BC) present in the serum samples were interpreted according to Utter *et al.* (1973). Transferrin was recorded as the frequency of the "A" allele since the "B" allele was present in very low numbers. The variant allele for the second locus of phosphoglucose isomerase was first observed in white muscle tissue by May (1975). This character was recorded as the frequency of the variant allele.

Life History

The life history characters I used were time of peak spawning and proportion of females in the adult population. The peak spawning times were estimated by interviewing district fish biologists and hatchery managers. These estimates could be verified in some cases with spawning ground survey records and hatchery records. The peak spawning times were stratified into five segments, 2 weeks long each. The proportions of adult females (3 year-olds) were estimated from hatchery records and spawning ground surveys. Jacks (2 year-old males) were not included.

Environmental Data

Stream characteristics include spawning distance, basin area, area and length of the estuary on the stream system, latitude, gradient, spring runoff and the presence or absence of other fish species and *Ceratamyxa shasta*. Spawning distances were measured from the mouth of the stream system to the upper limit of coho spawning which was estimated from Anadromous Fish Distribution Maps[1] and interviews with district fish biologists. The latitude for each stream system was measured at the mouth. Gradients were calculated from tidewater to the upper limit of coho spawning. Elevations, distances and lengths of estuaries were measured on United States Geographical Survey Quadrangle Maps. The areas of the stream systems and estuaries were obtained from sources cited in Table 4. The presence of a spring runoff from snow melt was determined by interviews with district biologists. The distributions of other fish species in Oregon stream systems were obtained from C. E. Bond (personal communication). The distribution of *Ceratamyxa shasta* was provided by J. E. Sanders (personal communications). The species and disease data were recorded in terms of either presence or absence.

Temperature data were obtained from hatchery records to help interpret the morphological data of the hatchery stocks. The average temperature for the first month of incubation was used, as previous studies indicate this time is a period during ontogeny when the morphological features may be most sensitive to the effects of temperature

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[1] Water Resources Board of Oregon.

Table 4. Environmental data for the stream systems sampled in this study.

STREAM SYSTEM	Spawning distance Km.	Latitude	Estuary area Hect.	Estuary length Km.	Gradient m/Km.	Runoff in Spring	Basin area sq. Km.
WASHINGTON							
Quilcene River	13	47.75	512[2]	3.2	19.7	yes	179[4]
Quinault River	92	47.33	64[2]	3.2	2.8	yes	1123[4]
OREGON							
Columbia River							
-Cascade-Bonneville Hatcheries	235	46.25	37,513[2]	236.5	0	yes	51,769[5]
-Cowlitz Hatchery stock	193	46.25	37,513[2]	109.4	.8	yes	6418[4]
-Big Cr Hatchery	60	46.25	37,513[2]	43.4	14.2	no	88[4]
-Sandy River Hatchery	270	46.25	37,513[2]	194.7	7.1	yes	1299[4]
North Nehalem River	45	45.68	1128[3]	11.3	18.6	no	233[2]
Nehalem River	195	45.68	1128[3]	24.1	52.4	no	2192[4]
Trask River	72	45.52	3480[3]	20.9	9.5	no	455[6]
Nestucca River	76	45.16	400[3]	12.9	7.7	no	657[4]
Salmon River	29	45.05	82[3]	6.4	13.0	no	194[7]
Siletz River	122	44.93	475[3]	37.0	3.4	no	797[4]
Beaver Creek	21	44.52	3[2]	3.2	24.3	no	31[2]
Alsea River	93	44.43	858[3]	19.3	3.2	no	1227[7]
Umpqua River	372	43.68	2285[3]	45.0	1.9	yes	11,801[7]
Smith River[1]	122	43.68	2285[3]	24.1	2.5	no	898[4]
Tenmile Lakes	24	43.57	1[2]	1.6	3.2	no	254[6]
Coquille River	138	43.11	308[3]	66.0	3.4	no	2738[7]
Rogue River	249	42.44	251[3]	6.4	1.9	yes	13,199[7]
CALIFORNIA							
Klamath River	293	41.58	200[2]	3.2	2.2	yes	31,314[8]
Trinity River	235	41.58	200[2]	3.2	2.4	yes	7383[8]
Mad River	72	40.95	200[2]	6.4	6.5	no	1255[8]

[1] Source of Umpqua Hatchery stock

[2] Provided by district biologists

[3] Gaumer et al. (1973)

[4] Pacific Northwest River Basins Commission (series)

[5] Personal estimate

[6] Water Resources Board of Oregon (1969)

[7] Wilsey and Ham Incorp. (1974)

[8] United States Geological Survey (1977)

(Tåning, 1952).

Statistics

Averages of the morphological counts, enzyme gene frequencies and proportion of females were calculated for each stock. I used analysis of variance to determine if significant differences existed among the stocks for each morphological character. All environmental data, except for latitude and the presence or absence of data were transformed to natural log to stabilize the variances and improve normality. The stock characters were standardized ($\bar{z} = 0,\ s^2 = 1$) for the cluster analysis using the formula:

$$z_{ij} = \frac{y_{ij} - \bar{y}_j}{s_j}$$

z_{ij} = standardized variable for the i^{th} stock and j^{th} character

y_{ij} = i^{th} stock average for the j^{th} character

$\bar{y}_j$ = average of j^{th} character for all stocks combined

s_j = standard deviation for the j^{th} character.

This standardization expresses the stock character as standard deviations from the character means, thus giving equal weight to each character.

I calculated correlation coefficients (Snedecor and Cochran 1967) between the stock characters and the environmental data using all stocks and between the morphological characters and the temperature data for hatchery stocks only. The levels of significance for the correlation coefficients were also calculated as described in Snedecor and Cochran (1967).

Two cluster analysis programs were used to demonstrate the similarities among stocks. One, a nonhierarchical divisive cluster analysis, minimizes the total sum of squares between observations and the cluster means (McIntire 1973). The other program is a hierarchical agglomerative cluster analysis developed by Keniston (1978). In the agglomerative method Euclidean distance was used as the dissimilarity measure and the clustering strategy was group average [see Sneath and Sokal (1973) or Clifford and Stephenson (1975) for terminology]. Both programs used standardized data. I used canonical variate analysis to investigate the relationships among the clusters from the agglomerative cluster analysis (Clifford and Stephenson 1975). All of the statistical analyses were calculated by a Control Data Corporation 3300 computer using the Statistical Interactive Programming System at the Oregon State University Computer Center.

RESULTS AND DISCUSSION

Morphological Characters

Analysis of variance on each of the morphological characters (Tables 1-3) indicated that significant differences ($\alpha = .01$) existed among the 35 samples, which consisted of wild and hatchery stocks from two brood years. Comparison of morphological characters for each stock between brood years were made for each of the hatcheries that were sampled both years of the study (Table 5). The similarity between brood years is not particularly high, especially for scale rows and branchiostegal ray counts.

Generally, morphological characters and water temperature during the incubation period of the eggs are correlated (Hubbs 1922; Taning 1952; Ricker 1959; Barlow 1961; Garside 1966; McCart and Anderson 1967; and Kwain 1975). I found that lateral series scale counts was the only morphological character that was significantly ($\alpha = .05$) correlated with the temperature of the hatchery water during incubation (Table 6). These results indicate that water temperature during incubation has a minimal effect on the morphological characters. Other factors that may affect morphological features include founder effect, random drift, selection and pleiotrophic effects from genes that may be affected by selection.

Of all the possible correlations between morphological

Table 5. Hatchery stocks in which differences in morphological characters occurred between the 1976 and 1977 brood years as determined by a two sample test. (*) indicates significant differences at $\alpha = .05$ and (**) indicates significant differences at $\alpha = .01$.

Hatchery	Lateral series scales	Scales above lateral line	Anal rays	Gill rakers	Branchiostegal rays	Vertebrae
Cascade-Bonnevile		**				**
Cowlitz stock		**			**	**
Big Creek		**	**			
North Nehalem River						
Trask River	**	**				*
Salmon River					*	*
Alsea River		**			*	
Umpqua River	**			*		

Table 6. Correlation coefficients between the morphological characters of the hatchery samples (Tables 1 and 2) and the hatchery water temperatures during incubation (Tables 1 and 2). The correlation coefficients are significant (α = .05) at r = .34.

Morphological character	Correlation coefficient
Lateral series scales	-.3412
Scales above lateral line	.0693
Anal rays	.0571
Gill rakers	-.0005
Branchiostegal rays	-.0209
Vertebrae	-.0880

characters and stream characteristics (Table 4) only vertebral number and estuary length and vertebral number and spawning distance had correlations coefficients greater than r = .50 (Table 7). The other possible correlations each accounted for less than 25% of the variation observed.

Life History Characters

Earlier peak spawning times (Table 8) are associated with the northern stream systems and those stream systems with large estuaries (Table 7). The correlation of peak spawning time with size of the estuary may be the result of the large number of samples from Columbia River hatcheries leading to biased interpretation of results. The stocks from the Columbia River have spawning times earlier than coastal stocks and the Columbia River has a large estuary. Petersen (1978) presented evidence for a genetic component of spawning time in steelhead trout (*Salmo gairdneri*). Selection for earlier spawning times through hatchery practices is a likely factor for the differences in spawning times between hatchery and wild stocks in the North Nehalem, Trask and Alsea rivers. The peak spawning times at the hatcheries using wild stocks for an egg source were similar to the peak spawning times of naturally spawning fish on their respective stream system.

The proportion of females (Table 8) appears to be lower in the

Table 7. Significant correlation coefficients between the characteristics of coho salmon (*Oncorhynchus kisutch*) stocks and the environmental characteristics of their respective stream systems. r=.28 at α=.05 and .37 at α=.01.

	Significant correlations for all stocks	
Stock characteristic	Environmental characteristic	Correlation
Scales in lateral series	Spawning distance	.418
Scales in lateral series	Estuary size	.341
Scales in lateral series	Estuary length	.430
Scales in lateral series	Gradient	-.368
Scale rows	Latitude	.360
Scale rows	Spring runoff	.315
Anal rays	Estuary size	.414
Anal rays	Latitude	.382
Gill rakers	Latitude	.346
Gill rakers	Basin area	-.353
Gill rakers	Spring runoff	-.319
Branchiostegals	Latitude	.431
Branchiostegals	Spring runoff	.381
Vertebrae	Estuary size	.350
Vertebrae	Basin area	.445
Vertebrae	Gradient	-.432
Vertebrae	Spawning distance	.549
Vertebrae	Estuary length	.533
Proportion of females	Latitude	-.426
Time return	Estuary size	-.613
Time return	Spring runoff	-.345
Time return	Estuary length	-.391
Time return	Latitude	-.702
Phosphoglucose Isomerase	Spring runoff	-.410
Transferrin	Estuary length	.326
Transferrin	Latitude	-.381
Transferrin	Spawning distance	.590
Transferrin	Basin area	.588
Transferrin	Spring runoff	.528
Transferrin	Gradient	-.596

Table 8. Proportion of females, time of peak spawning and gene frequency, 95% confidence interval and sample size of phosphoglucose isomerase variant of hatchery and wild coho salmon (Oncorhynchus kisutch) stocks. Years of data used to estimate proportion of females are in parenthesis.

Stream system	LIFE HISTORY DATA						PHOSPHOGLUCOSE ISOMERASE								
	WILD			HATCHERY			WILD			HATCHERY					
							1977			1976			1977		
	Proportion of females [1]	Years	Time of peak spawning month day	Proportion of females	Years	Time of peak spawning	Frequency	95% CI	Sample size	Frequency	95% CI	Sample size	Frequency	95% CI	Sample size
WASHINGTON															
Quilcene Hatchery				.41	(1972-78)	10/15-10/30				0	-	36			
Quinault Hatchery				.37	(1973-75)	10/15-10/30				0	-	40			
OREGON															
Columbia River															
-Cascade-Bonneville Hatchery				.51	(1970,72-76)	11/1-11/15				0	-	40	0	-	60
-Cowlitz Hatchery stock				.50	(2)	11/1-11/15				0	-	40	0	-	60
-Big Creek Hatchery				.55	(1970-76)	11/1-11/15				0	-	40	0	-	40
-Sandy River Hatchery				.45	(1970-76)	11/1-11/15				0	-	40			
North Nehalem River	.43	(3)	12/1-12/15	.43	(1970-76)	11/1-11/15	.05	.08	19	.05	.04	44	.08	.04	60
Nehalem River	.43	(1949-69)	12/1-12/15				.11	.06	64						
Trask River	.33	(1949-69)	12/1-12/15	.43	(1970-76)	11/1-11/15	.06	.04	62	.08	.06	40	.20	.08	60
Nestucca River	.56	(1949-69)	12/1-12/15				.03	.04	59						
Salmon River	.46	(1975-77)	12/1-12/15	.46	(1975-77)	12/1-12/5	.01	.02	64	0	-	40	0	-	60
Siletz River	.54	(1949-69)	12/1-12/15												
Beaver Creek	.58	(1949-69)	12/15-12/31				0	-	32						
Alsea River	.53	(1949-69)	12/1-12/15	.42	(1970-76)	11/16-11/30	.01	.02	49	.05	.04	40	.15	.06	60
Umpqua River	.63	(1949-69)	12/1-12/15	.49	(1977-78)	12/1-12/15	0	-	41	0	-	40	0		60
Tenmile Lake	.65	(1954-74 except 59)	12/15-12/31				0	-	50						
Coquille River	.55	(1949-69)	12/1-12/15				.01	-	59						
Rogue River	.44	(3)	12/1-12/15	.44	(1974, 75, 77 and 78)	12/1-12/15	0	-	29				0		60
CALIFORNIA															
Klamath River															
-Irongate Hatchery				.53	(1969-78)	12/1-12/15				0		40			
-Trinity Hatchery				.53	(1966-78)	12/1-12/15				0		40			
Mad River				.62	(1971-78)	12/1-12/15				0		36			

[1] Three year old fish only

[2] Estimated by hatchery manager

[3] Estimated from hatchery data

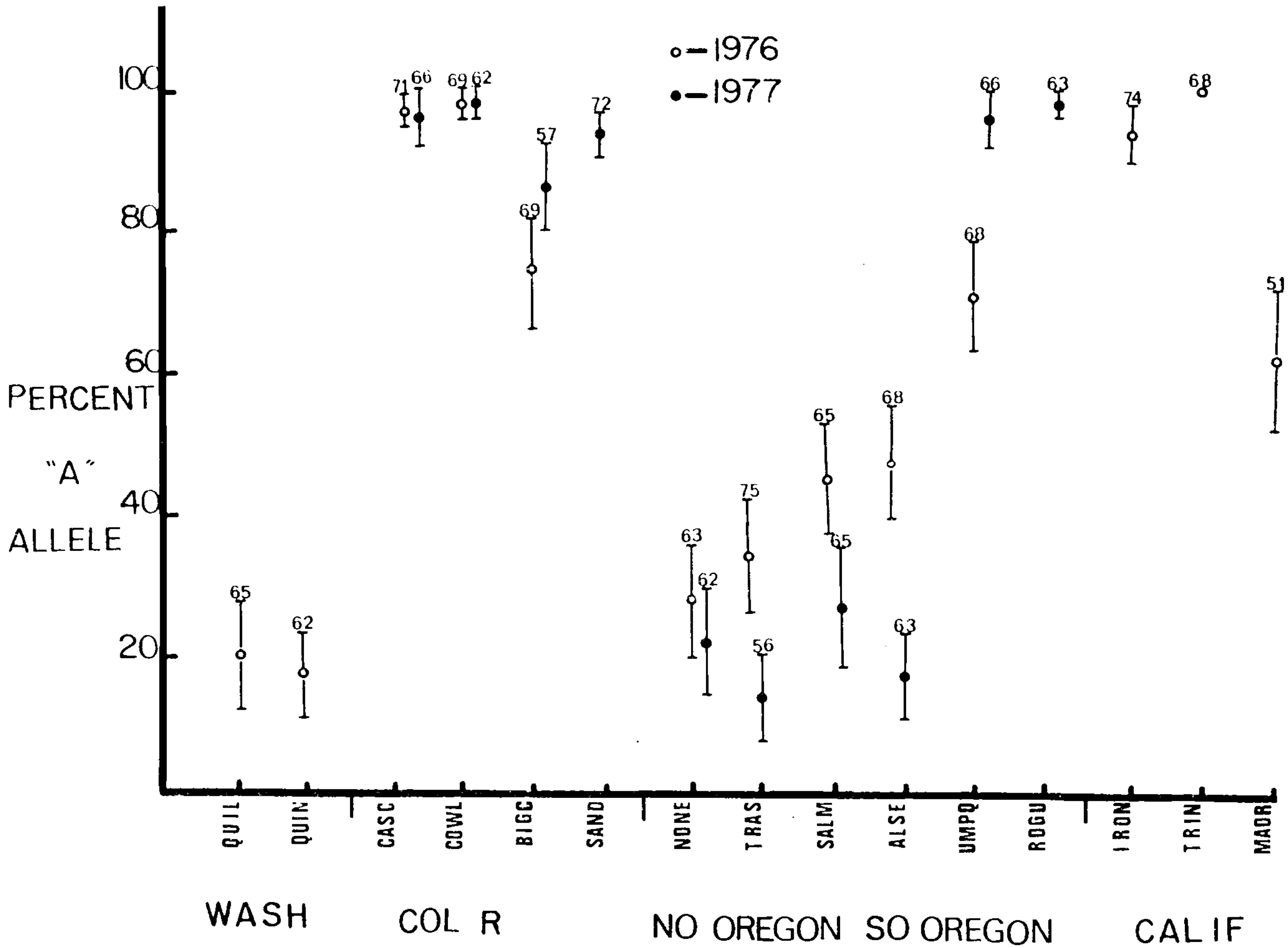
northern stream systems. I chose this character because I believed that it would be related to the proportion of jacks (males that mature at two years of age) in the population. A direct measure of the proportion of jacks can not be used because of the differences in body size between jacks and adults (three year olds). Body size affects the catch in gill net fisheries, retention in hatchery holding ponds, the recovery of carcasses on spawning ground surveys, and catch rate in sports fisheries. The effective sex ratio, including jacks, at the time of spawning should be close to 1:1 (Fisher 1930). If only three year old males and females are counted, then the proportion of females should be greater than .50, depending on how many jacks returned the previous year. This is not the case in stocks from the Quilcene, Quinault, Sandy, North Nehalem, Nehalem, Trask, Salmon, Alsea, Umpqua and Rogue rivers, all of which had a higher proportion of males. Nikolskii (1969) reviewed several possible causes for sex ratios departing from 1:1, however the reason for a high proportion of males in these stocks is not known.

Isozyme Gene Frequencies

Breeding studies by Utter *et al.* (1973) and May (1975) established that the electrophoretic expressions of transferrin and phosphoglucose isomerase (PGI) are genetically determined.

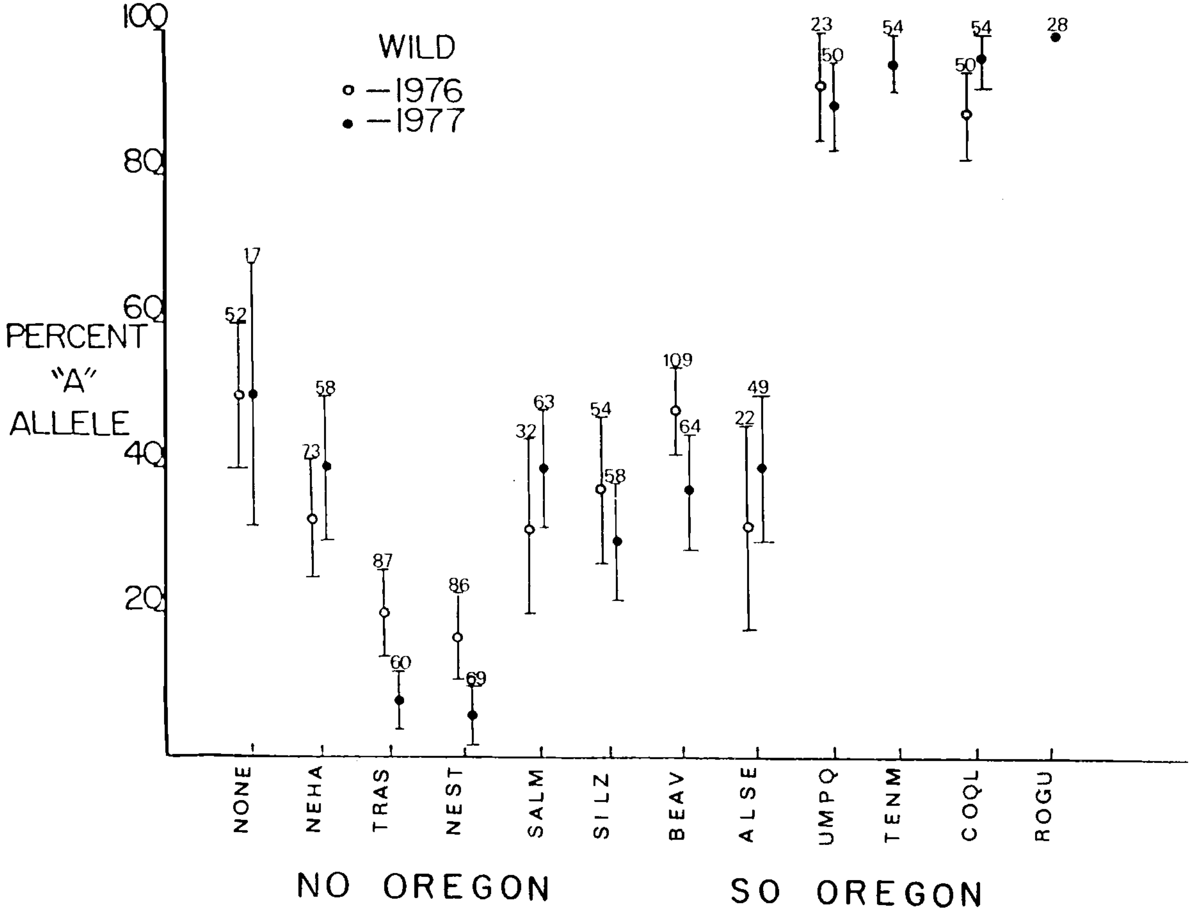
The transferrin gene frequencies in Figures 1 and 2 are

Figure 1. Transferrin gene frequencies of hatchery coho salmon (*Oncorhynchus kisutch*). Samples are arranged from north to south. Bars represent 95% confidence intervals and the sample sizes are above the bars. Location codes are in Figure 5.



o—1976
•—1977
100
80
60
40
20
PERCENT
"A"
ALLELE
71
66
69
62
57
69
72
66
63
74
68
68
51
65
68
75
63
65
62
56
63
65
62
QUIL
QUIN
CASC
COWL
BIGC
SAND
NONE
TRAS
SALM
ALSE
UMPQ
ROGU
IRON
TRIN
MADR
WASH
COL R
NO OREGON
SO OREGON
CALIF

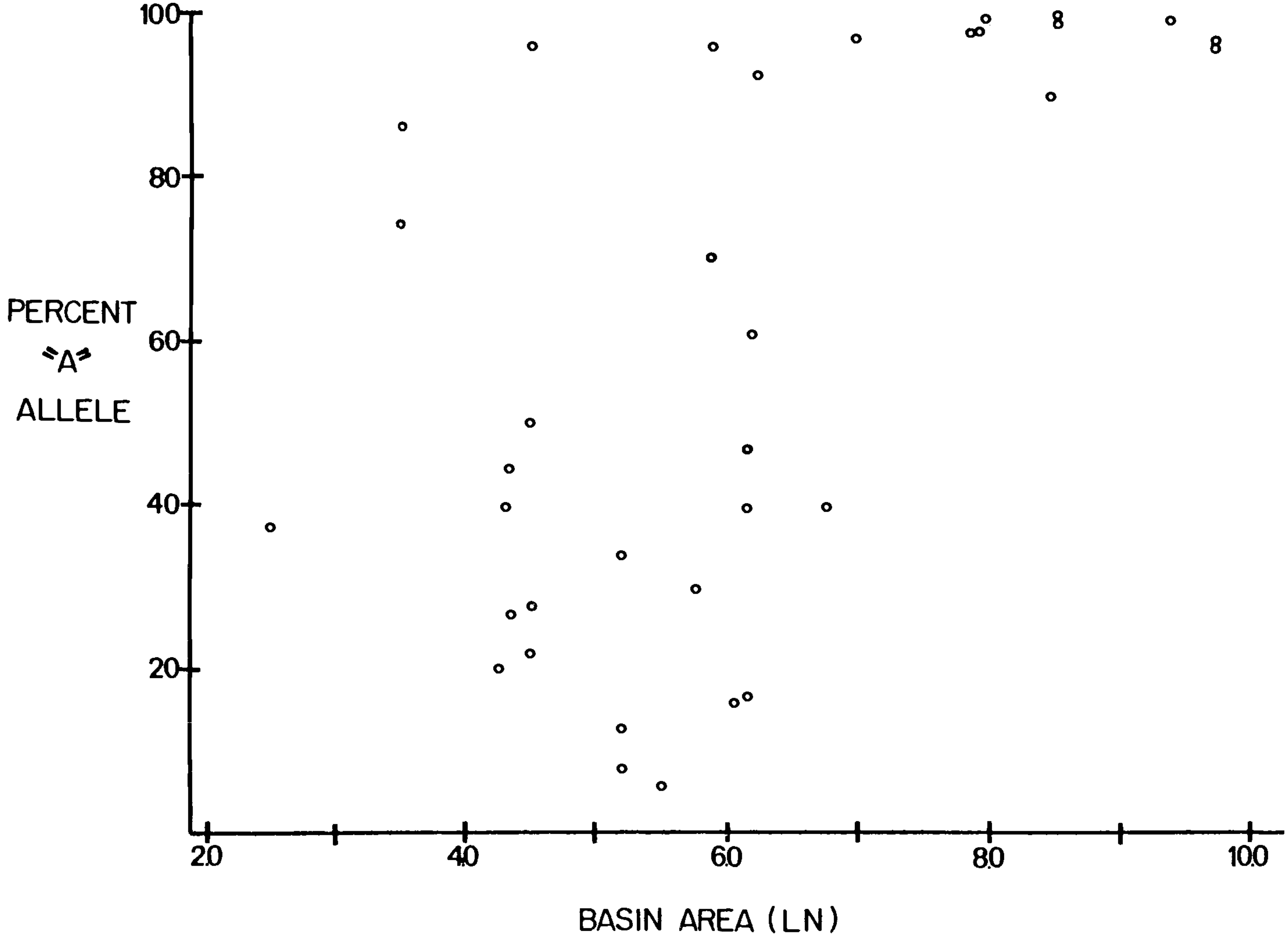
Figure 2. Transferrin gene frequencies of wild coho salmon (*Oncorhynchus kisutch*) stocks for 1976 and 1977 brood years. Stocks are arranged from north to south. Bars represent 95% confidence intervals and the sample sizes are above the bars. Location codes are in Figure 5.


WILD
○ —1976
● —1977
100
80
60
40
20
PERCENT "A" ALLELE
52
17
73
58
87
60
86
69
32
63
54
58
109
64
22
49
23
50
54
50
54
28
NONE
NEHA
TRAS
NEST
SALM
SILZ
BEAV
ALSE
UMPQ
TENM
COQL
ROGU
NO OREGON
SO OREGON

arranged in north to south order. These gene frequencies correlated significantly with six of the stream characters (Table 4). The best model from stepwise multiple regression explained only 68% of the variation in Figure 1. Analyzing the relationships of the "A" allele frequencies with basin area (Figure 3) and latitude (Figure 4) explains the variation better than the stepwise regression model. These correlations show that the stocks from large stream systems and the southernmost stream systems have high frequencies of the "A" allele. Stocks from smaller stream systems or northern stream systems are highly variable. Combining these two relationships helps explain the pattern of transferrin gene frequencies. Stocks from large stream systems have high frequencies of the "A" allele regardless of latitudinal position and the southern stocks also have high "A" allele frequecies regardless of stream size. Stocks from smaller stream systems on the northern Oregon coast and Washington have higher frequencies of the "C" allele.

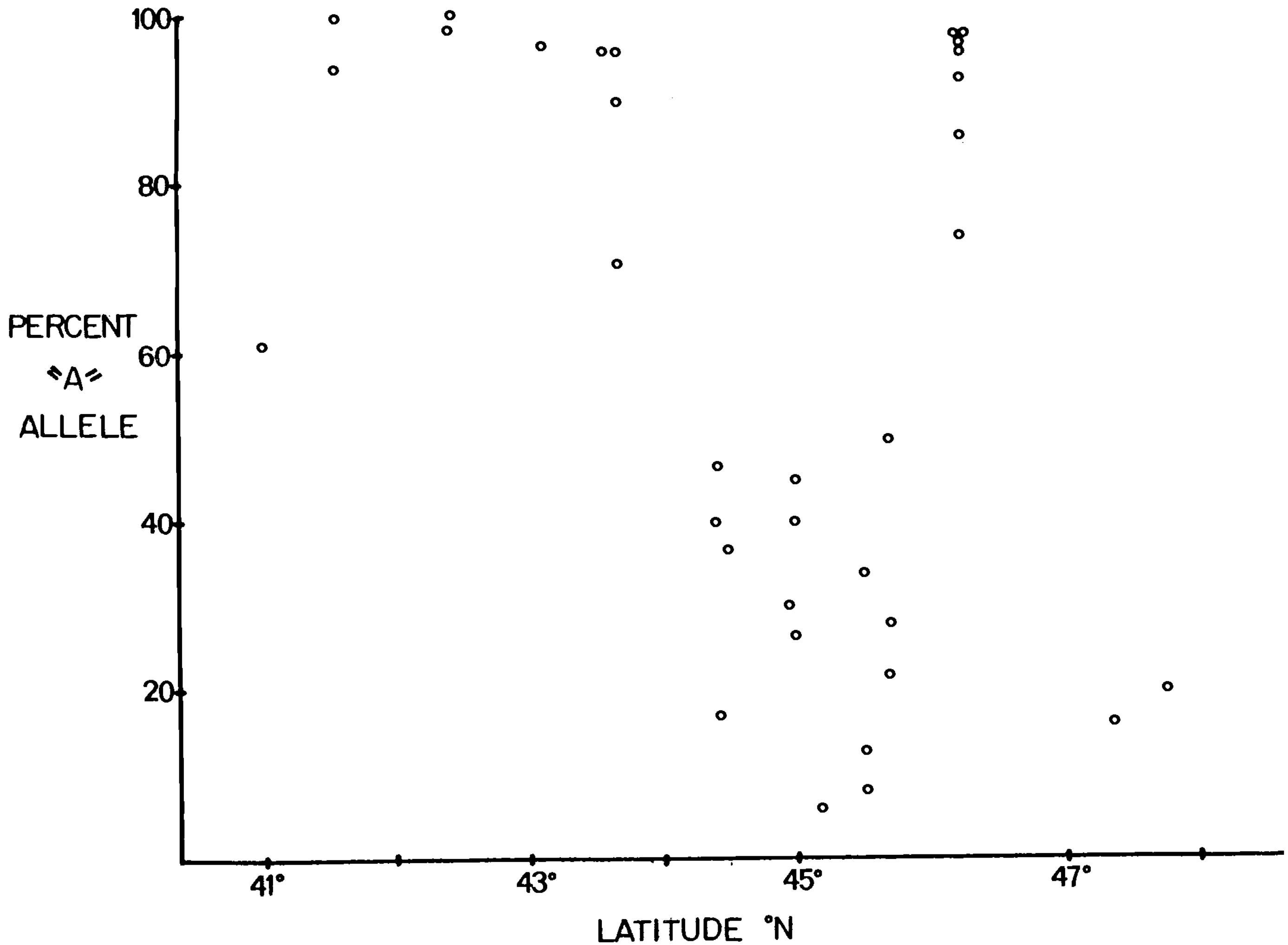
The factors causing the patterns of transferrin gene frequencies in coho salmon stocks are not known. However, Utter _et al._ (1978) suggested that the frequencies may be influenced by bacteriostatic properties of the different transferrin alleles. Genotypes of transferrin had differential mortality when exposed to bacterial kidney disease in studies by Suzumoto _et al._ (1977) and Winter _et al._ (1979) and to vibriosis, cold water disease and furunculosis in a study by

Figure 3. Transferrin gene frequencies for wild and hatchery coho salmon (*Oncorhynchus kisutch*) stocks from basins with different areas (natural log).



100
80
60
40
20
PERCENT
"A"
ALLELE
2.0
4.0
6.0
8.0
10.0
BASIN AREA (LN)

Figure 4. Transferrin gene frequencies for wild and hatchery coho salmon (*Oncorhynchus kisutch*) stocks from different latitudes.


PERCENT
"A"
ALLELE
100
80
60
40
20
41°
43°
45°
47°
LATITUDE °N

Pratschner (1978). Trasnferrin genotypes were also related to both differences in juvenile growth rates and propensity to return as jacks (McIntyre and Johnson 1977). Diseases, life history characteristics and other factors may play a role in maintaining the patterns of transferrin gene frequencies.

Another interesting finding with transferrin gene frequencies involves the variation between the two brood years studied for hatchery and wild stocks. There is good agreement between the two year classes of Oregon coast wild stock despite some small sample sizes (Figure 2). The heterogeneity between year classes is greater for the Oregon coast hatchery stocks (Figure 1). The gene frequencies of hatchery stocks may have been altered by importing stocks with different gene frequencies or by disease epizootics. If transferrin genotypes have different resistances to diseases and if epizootics are more severe because of the higher densities of fish found in hatcheries, then the transferrin gene frequency of a given year class could be altered without affecting the other two year classes.

The PGI variant (Table 8) was only present in the samples from Oregon stocks, particularly those from the northern Oregon coast. May (1975) reported this variant in Washington stocks.

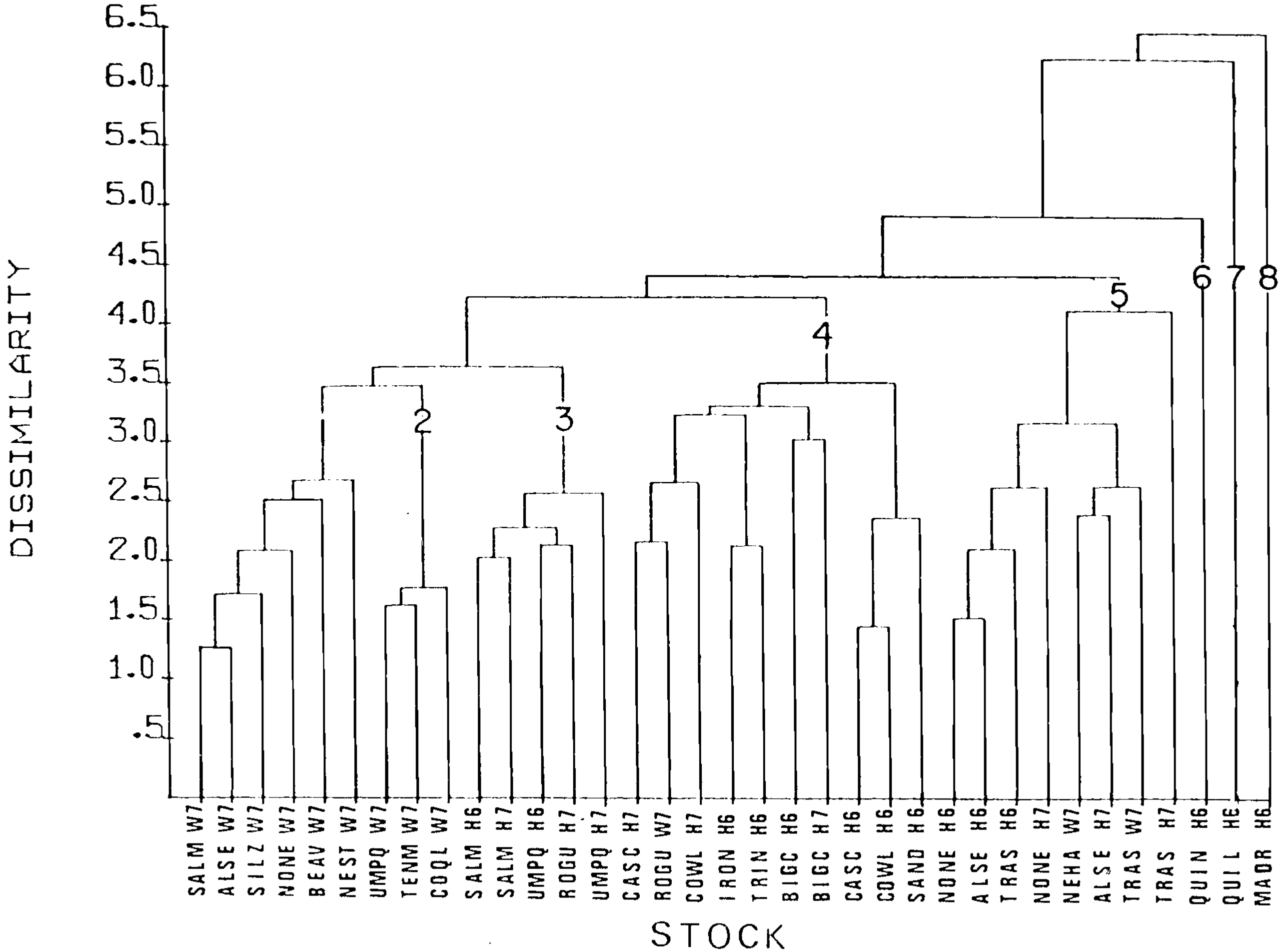
Similarity of Stocks

The groups of stocks of coho salmon found to be most similar by the agglomerative cluster analysis were composed of: northern Oregon coast wild stocks (cluster no. 1), southern Oregon coast wild stocks (cluster no. 2), stocks from hatcheries that used wild stocks for the egg source (cluster no. 3), stocks from large river systems (cluster no. 4), hatchery stocks and two wild stocks from the northern Oregon coast (cluster no. 5), and three individual hatchery stocks from California and Washington (clusters no. 6-8) (Figure 5).

It is important to realize that cluster analysis programs do not prove that discrete clusters exist in the multivariate data. A clustering strategy will cluster continuous multivariate data where no discrete groups exist. Canonical variate analysis produces canonical variables that project multidimensional data onto axes, separating the data as much as possible. Plotting the canonical variables against each other displays the relationships among clusters in two dimensional space. Analysis of the two dimensional plots can help determine the relationships among the clusters and the discreteness of the clusters.

Of the five larger clusters, only clusters no. 1 and no. 5 (Figure 5) were continuous in three dimensional space. The other clusters were discrete. Canonical variate analysis on the five larger clusters produced three canonical variables that were significant ($\alpha = .05$). When the three significant canonical variables were plotted against each other, only clusters no. 1 and 5 were not completely

Figure 5. Dendrogram of the agglomerative cluster analysis for all stocks of wild and hatchery coho salmon (Oncorhynchus kisutch) of two brood years, 1976 and 1977. Euclidean distance was the dissimilarity measure and group average was the clustering strategy. Codes are as follows: H6, hatchery stock of the 1976 brood year; H7, hatchery stock of the 1977 brood year; and W7, wild stock from the 1977 brood year. Location codes are: ALSE, Alsea River; BEAV, Beaver Creek; BIGC, Big Creek; CASC, Cascade and Bonneville hatcheries (Columbia River); COQL, Coquille River; COWL, Cowlitz hatchery stock (Columbia River); IRON, Irongate Hatchery (Klamath River); MADR, Mad River; NEHA, Nehalem River; NEST, Nestucca River; NONE, North Nehalem River; QUIL, Quilcene Hatchery; QUIN, Quinault Hatchery; ROGU, Rogue River; SALM, Salmon River; SAND, Sandy River; SILZ, Siletz River; TENM, Tenmile Lakes; TRAS, Trask River; TRIN, Trinity River; and UMPQ, Umpqua River.


DISSIMILARITY
6.5
6.0
5.5
5.0
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
.5
2
3
4
5
6
7
8
SALM W7
ALSE W7
SILZ W7
NONE W7
BEAV W7
NEST W7
UMPQ W7
TENM W7
COQL W7
SALM H6
SALM H7
UMPQ H6
ROGU H7
UMPQ H7
CASC H7
ROGU W7
COWL H7
IRON H6
TRIN H6
BIGC H6
BIGC H7
CASC H6
COWL H6
SAND H6
NONE H6
ALSE H6
TRAS H6
NONE H7
NEHA W7
ALSE H7
TRAS W7
TRAS H7
QUIN H6
QUIL H6
MADR H6
STOCK

separate in three dimensional space. These two clusters consisted of wild stocks from the northern Oregon coast and hatchery stocks of the northern Oregon coast.

Some of the variation within each cluster was reduced because the averages of each morphological character were used to characterize each stock in the canonical variate analysis. Reducing the variation makes it easier for the canonical variate analysis to discriminate between the clusters; however, the results of the analysis of variance indicated that significant differences exist among the stocks for each morphological character.

The results of the agglomerative and divisive cluster analysis were similar. At the 13 cluster level of the divisive cluster analysis (Table 9), all but two of the clusters were identical to clusters from the agglomerative cluster analysis dendrogram. The results of the cluster analyses should be interpreted cautiously because they are based on ten characteristics, a low number compared to the total number of genetically related characteristics possible. If other characteristics were used, then the results could vary. Thus, I did not emphasize the exact order or the levels of dissimilarity at which any two clusters joined together. Instead, I observed general trends in the clustering patterns.

Three general trends are present in the clustering patterns of the dendrogram. First, the stocks from the larger stream systems

Table 9. Clusters of coho salmon (Oncorhynchus kisutch) stocks at the 13 cluster level of the divisive cluster analysis. "Wild" denotes wild stocks.

Cluster No.	Divisive Cluster Analysis Stock	Brood Year
1	Cascade Hatchery	1976
	Cowlitz Hatchery	1976
	Sandy Hatchery	1976
2	Salmon River Hatchery	1976
	Salmon River Hatchery	1977
	Rogue River Hatchery	1977
	Umpqua River Hatchery	1976
	Umpqua River Hatchery	1977
3	North Nehalem wild	1977
	Nestucca River wild	1977
	Salmon River wild	1977
	Siletz River wild	1977
	Beaver Creek wild	1977
	Alsea River wild	1977
4	Quilcene Hatchery	1976
5	Nehalem River wild	1977
	Trask River wild	1977
6	Mad River Hatchery	1976
7	North Nehalem Hatchery	1976
	North Nehalem Hatchery	1977
	Trask Hatchery	1976
	Alsea Hatchery	1976
8	Umpqua River wild	1977
	Tenmile Lake wild	1977
	Coquille River wild	1977
9	Trask Hatchery	1977
	Alsea Hatchery	1977
10	Quinault Hatchery	1977
11	Bonneville Hatchery	1977
	Cowlitz Hatchery	1977
	Rogue wild stock	1977
12	Irongate Hatchery	1976
	Trinity Hatchery	1976
13	Big Creek Hatchery	1976
	Big Creek Hatchery	1977

(Columbia, Rogue and Klamath rivers) are more similar to each other than to the stocks from smaller streams. The only exceptions to this trend are the Umpqua River stocks and the Rogue Hatchery stock. The Rogue and Umpqua hatchery stocks are in the cluster with other hatcheries that used wild stocks as the egg source. The Umpqua wild stock clustered with the other southern Oregon coast wild stocks.

Geographical clustering was the second trend observed in the dendrogram. Three stocks from Washington and California had low similarities to the Oregon stocks. The Oregon wild stocks clustered into two groups, northern and southern coastal stocks.

The third trend was for hatchery stocks to cluster with each other and wild stocks to cluster with each other. One of the clusters were composed entirely of wild stocks from the northern Oregon coast and another cluster had all but one of the northern Oregon coast hatchery stocks in addition to two wild stocks from the northern Oregon coast. The hatchery stock that was not in this cluster (no. 5) was from the Salmon River, a hatchery program that uses wild coho salmon for its egg source. Both brood years of this stock were in the cluster of hatcheries that use wild stocks as an egg source. The rest of the northern Oregon coast hatcheries use returning hatchery reared adults for egg sources. The two wild stocks in this cluster are from the Trask and Nehalem rivers. They are also similar to the other wild stocks; however, because of the mechanics of the group average clustering strategy, they both clustered, with the hatchery stocks first. The average Euclidean distance between the Nehalem wild stock and the other wild stocks is actually lower than the average distance between the Nehalem wild stock and the hatchery stocks of cluster no. 5. The close relationships of the stocks on clusters no. 1 and 5 was apparent in the results of the canonical variate analysis. These are the two clusters that were continuous.

The three trends in the clustering pattern indicate that coho salmon stocks from similar environments have similar phenotypes. These trends can provide some guidance for the transfer of coho salmon stocks. The trends of geographical clustering indicates that the phenotypic or perhaps genetic similarity between stocks will probably decrease as the distance between stocks increases. McIntyre (1976) showed a strong negative correlation for the distance between stream systems and the genetic similarity of the steelhead trout stocks in those stream systems. If a similar relationship between phenotype and distance exists among coho salmon stocks, then a lower survival rate would be expected as the distance that the stock is transferred from its native stream is increased. The crucial question from the management standpoint, assuming the relationships I found are real, is how far can stocks be transferred before decreasing survival rate and the increasing genetic impact on the native stocks reduces the practicality of the hatchery supplementation.

The difference between stocks from large and small stream systems illustrates a problem in basing stock transfers primarily on geographical distance. Stocks from large stream systems are more similar to stocks in distant large stream systems than to stocks from small stream systems that are geographically close. Other environmental variables may also differ, affecting the phenotypes of geographically close stocks. Characteristics such as time of peak spawning or transferrin genotype may be closely related to flow and temperature regimes or diseases present in the stream systems. These characteristics and others not included in this study all must play a role in choosing stocks for transfer to other stream systems.

The third trend of hatchery and wild stocks diverging toward different phenotypes presents a problem to managers who must choose the best stock for transfer to other stream systems. The separate clustering of hatchery and wild stocks suggests that the hatchery stocks have become less similar to wild stocks, even those that are on the same drainage. Studies with steelhead trout indicate that hatchery fish survive better in the hatchery ponds while wild fish have higher survival in the stream systems (Reisenbichler and McIntyre 1977). The lower similarity of hatchery stocks with wild stocks may play a role in reducing the survival of hatchery reared coho when they are released into a stream system.

Similarity of Stream Systems and Wild Stocks

If coho salmon have similar phenotypes in similar environments, then one could possibly relate phenotypes of stocks with descriptions of their stream basins. Comparison of an agglomerative cluster analysis of wild stocks (Figure 6) with a cluster analysis of stream system characters (Figure 7) indicated that they were not as similar as I had expected. Some differences were expected because the stream character (Tables 4 and 10) are not necessarily related to taxonomic characters used in this study.

Conclusion

Coho salmon stocks from similar enviornments appear to have similar phenotypes. The results of the cluster analysis indicate that: stocks that are geographically close are similar, stocks from large stream systems are similar to each other, stocks from coastal stream systems are similar to each other, hatchery stocks are similar to other hatchery stocks and wild stocks are similar to other wild stocks. This information may be useful to fishery managers for selecting donor stocks from hatcheries for transplanting to stream systems or other hatcheries. The results of a cluster analysis of coho salmon stocks and a cluster analysis of the stream systems were not similar.

Figure 6. Dendrogram of the agglomerative cluster analysis for wild coho salmon (*Oncorhynchus kisutch*) stocks with a Euclidean distance dissimilarity measure and group average clustering strategy. Location codes are in Figure 5.

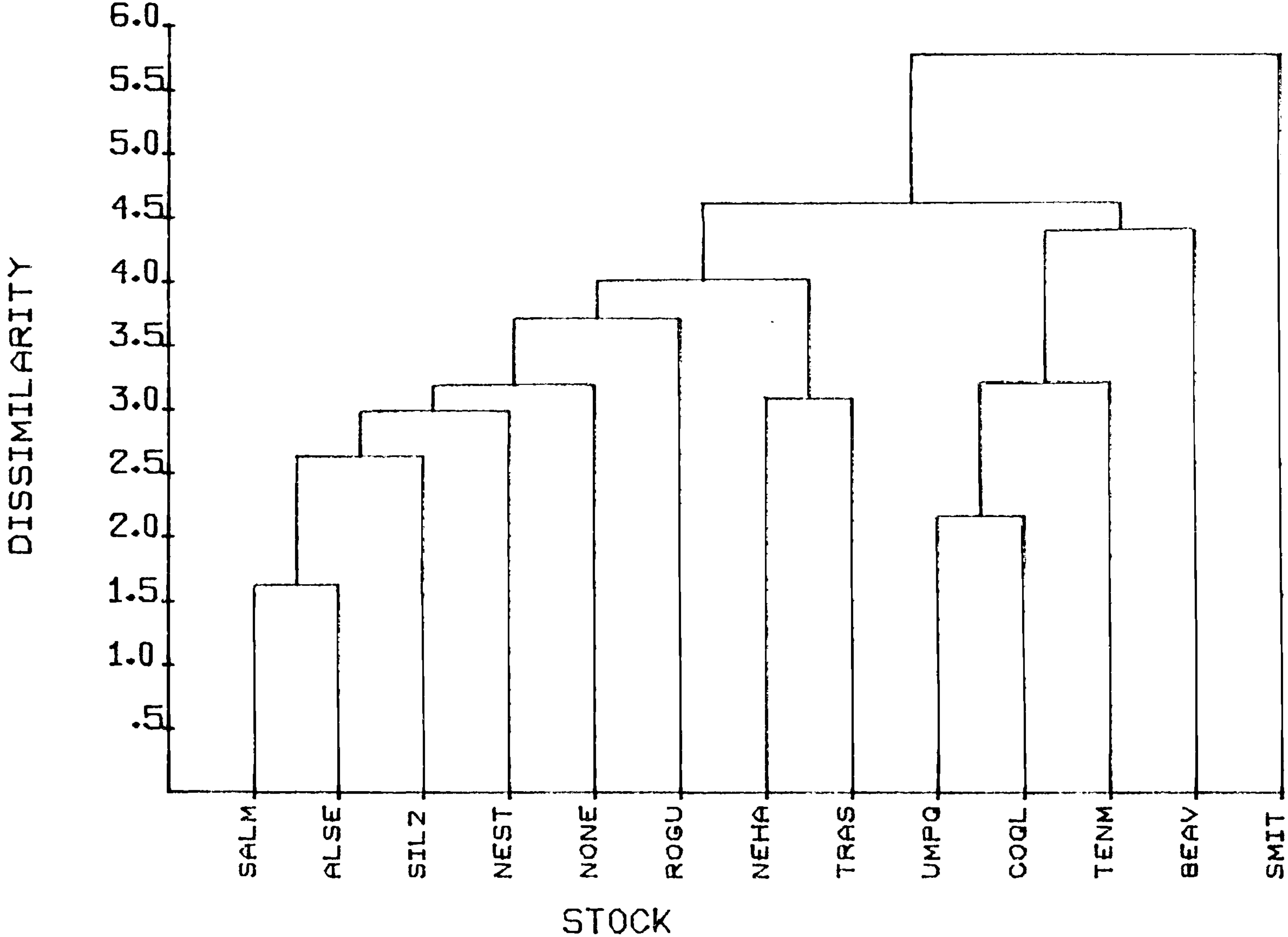

DISSIMILARITY
6.0
5.5
5.0
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
.5
SALM
ALSE
SIL2
NEST
NONE
ROGU
NEHA
TRAS
UMPQ
COQL
TENM
BEAV
SMIT
STOCK

Figure 7. Dendrogram of the agglomerative cluster analysis for stream systems with a Euclidean distance measure and group average clustering strategy. Location codes are in Figure 5.

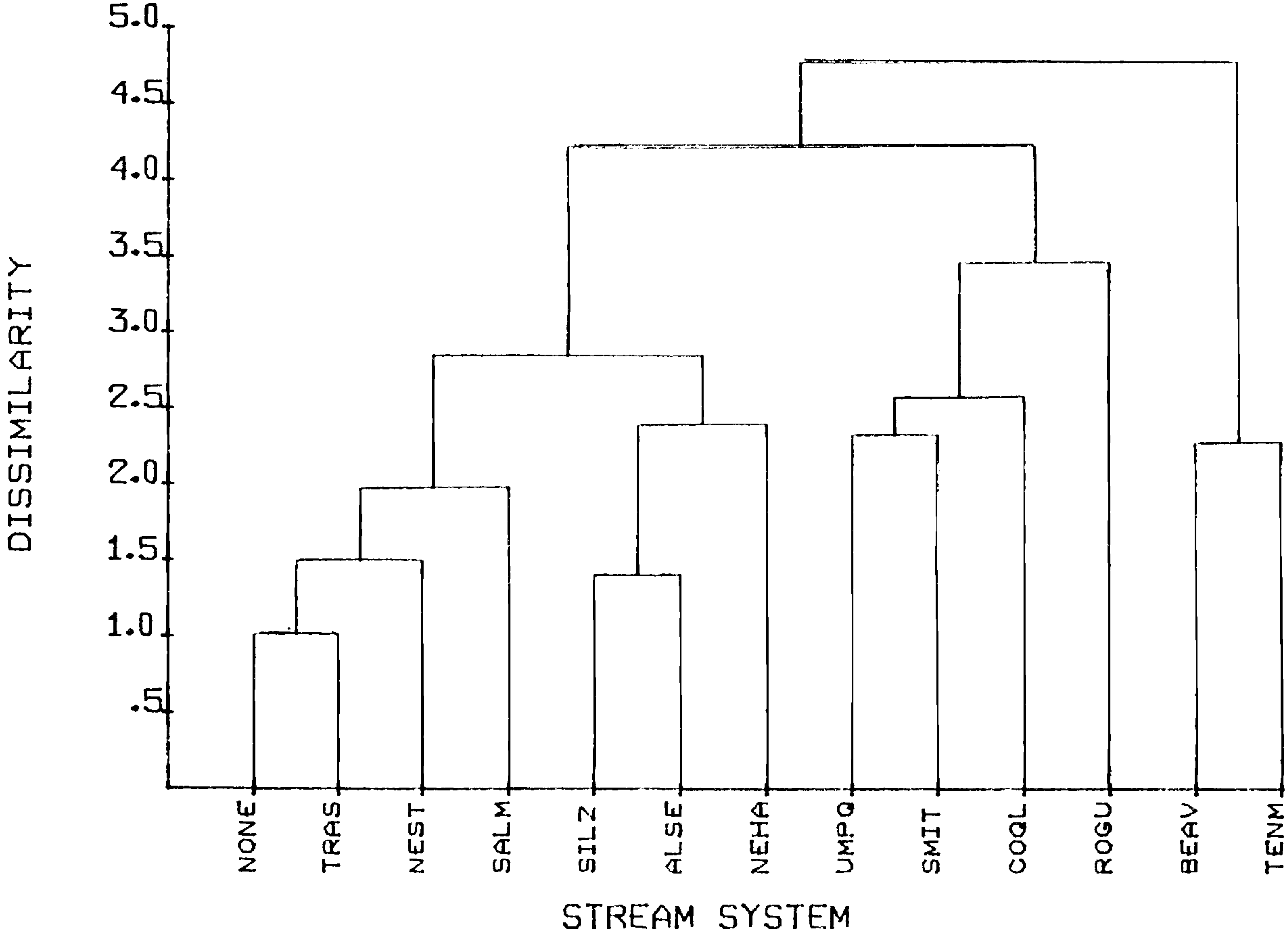

DISSIMILARITY
5.0
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
.5
NONE
TRAS
NEST
SALM
SILZ
ALSE
NEHA
UMPQ
SMIT
COQL
ROGU
BEAV
TENM
STREAM SYSTEM

Table 10. Species and disease (*Ceratamyxa shasta*) present in the stream systems of the wild juvenile coho salmon (*Oncorhynchus kisutch*) samples. An x = presence.

Stream systems	Carp	Oregon chub	Squawfish	Redside Shiner	*Catostomus* sp.	Speckled dace	Striped bass	Brown bull-head	Largemouth bass	*Ceratamyxa shasta*
North Nehalem River										
Nehalem River					X				X	
Trask River										
Nestucca River						X				
Salmon River										
Siletz River						X		X		
Beaver Creek						X				
Alsea River						X				
Smith River		X	X	X	X		X	X		
Umpqua River		X	X	X	X	X	X	X		
Tenmile Lake						X		X	X	
Coquille River					X	X	X	X		
Rogue River	X			X	X		X	X		X

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