GENETIC ESTIMATES OF STOCK COMPOSITIONS OF 1983 CHINOOK SALMON, *ONCORHYNCHUS TSHAWYTSCHA*, HARVESTS OFF THE WASHINGTON COAST AND THE COLUMBIA RIVER

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ABSTRACT

Allele frequency data for 17 polymorphic protein coding loci from 88 populations of chinook salmon between British Columbia, Canada and California, U.S.A. were used to obtain maximum likelihood estimates of contributing populations to fisheries off the coast of Washington, U.S.A. Data were available for the commercial troll fishery of May 1982 and for commercial, Indian, and sport fisheries during spring and summer 1983. The estimated contributions of fall run fish returning to areas of the lower Columbia River (collectively called "tules") to the May troll fisheries were 76.5% in 1982 and 54.9% in 1983. In contrast, the estimated proportion of fall run fish destined for areas of the upper Columbia River (collectively called "upriver brights") was less than 5% in both years, although these runs are known to make substantial contributions to more northern fisheries of Canada and Alaska. A considerable difference for each year occurred in the estimated proportion of California fish (2.8% in 1982 and 18.7% in 1983).

Differences occurred among the fisheries and areas sampled in 1983. Larger estimates for Canadian and Puget Sound (Washington) fish occurred in fisheries of northern areas; the largest was 41% for the Indian fishery in the Strait of Juan de Fuca. A greater proportion of California fish in any particular area was taken in sport fisheries. The subset of tule populations returning to the Kalama and Cowlitz river drainages was harvested at a higher rate in sport than commercial fisheries. This study demonstrates the capabilities of the involved procedures for generating timely and reliable estimates of stock composition, and serves as a starting point for more detailed understandings of the oceanic distribution of chinook salmon populations.

Chinook salmon, *Oncorhynchus tshawytscha*, runs returning to Pacific drainages of the western United States are a major biological, recreational, and economic resource. Their importance persists in spite of the often excessive harvests, disruptions of habitats, and blockages of migratory routes that have occurred during the past century. The vitality of these runs continues to fluctuate under the influence of many factors. Conflicting demands of multiple user groups, including recreational, commercial, native American, and international fishing interests, tend to stress the overall resource. Water requirements for energy, irrigation, and human consumption often conflict with even minimal conditions for fish rearing, passage, and reproduction. Instabilities of nature in freshwater and marine environments also contribute substantially to fluctuations in growth, migration, and survival.

The management of this resource is further complicated by the ecological and genetic diversity of its individual populations. For instance, fish harvested off the Washington coast represent a complex and continually changing mixture of stocks destined for many areas (Fig. 1; see also Miller et al. 1983). Runs returning to the Columbia River illustrate this diversity; here freshwater entry extends from February through October, and upstream migration distances range from virtually nothing to many hundreds of miles.

The largest numbers of Columbia River chinook salmon return in the fall and consist of two distinct types. Fish of that segment of the run commonly called "brights" retain the silver color of ocean-caught salmon for extended periods following their freshwater entry and return primarily to areas above The Dalles Dam. Brights are largely maintained by natural reproduction with hatchery supplementation of some segments. Fish of the largest segment of the fall run are referred to as "tules"; they approach spawning condition rapidly as soon as, and often before, they enter fresh water. Tules return to areas below The Dalles Dam and are perpetuated almost entirely by hatcheries. Although both tules

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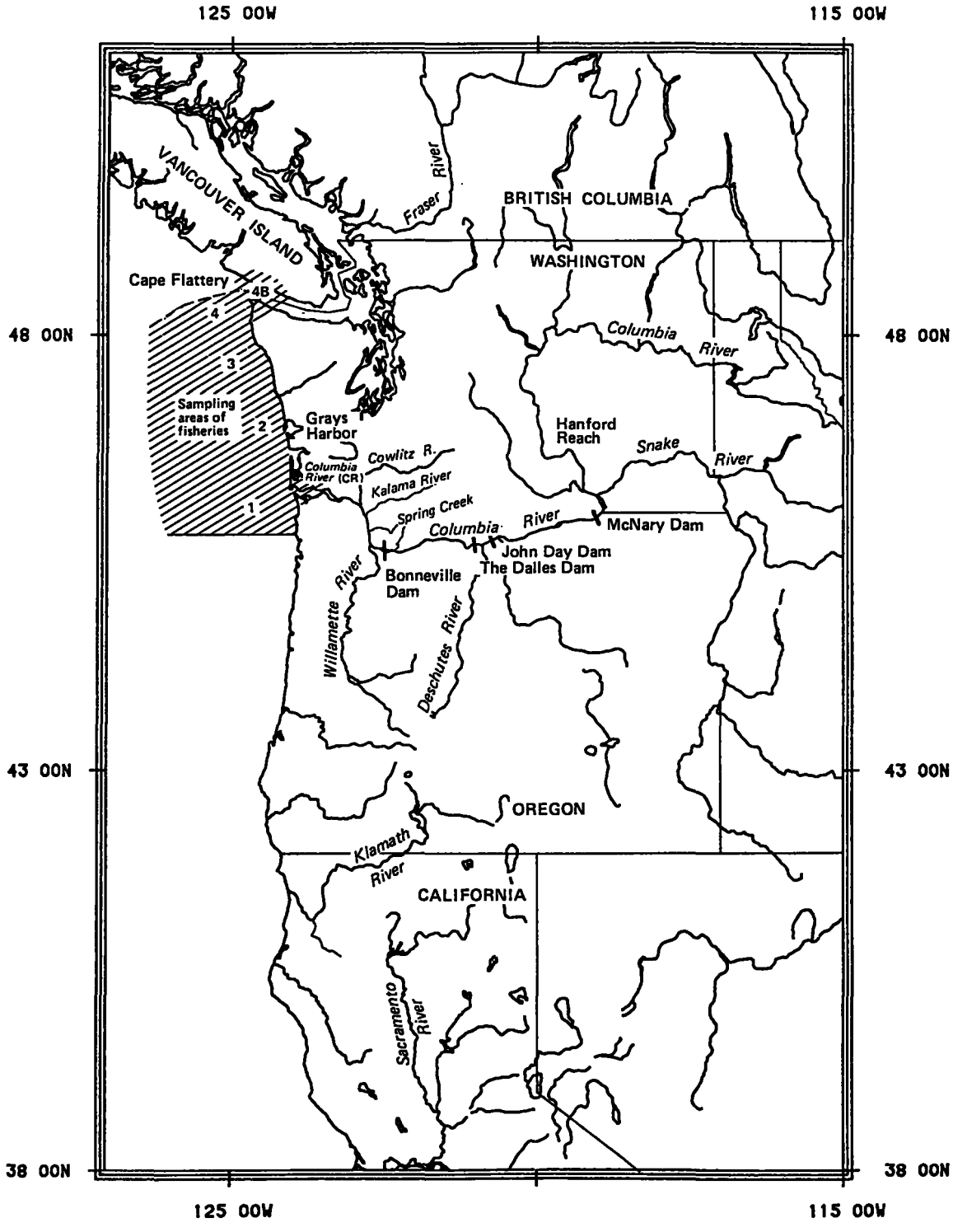

FIGURE 1.—Areas of baseline and mixed stock sampling.

and brights contribute to oceanic fisheries (Pacific Fishery Management Council 1981[3]) the persisting prime condition of brights makes them highly favored in river fisheries.

An ideal program for harvest management of chinook salmon would include the capability of identifying the abundance and distribution of distinct breeding groups (such as component stocks of the tule and bright runs of the Columbia River) in a particular fishery. This capability would permit adjustments of regulations to permit both protection of weaker stocks and more optimal harvest of abundant stocks, depending on their proportions in a fishery. Current information based primarily on data from coded wire tags provides a broad and general overview of hatchery stocks, but lacks details to impose differential harvest regulations adequately and does not yield information on wild populations. In addition, a sufficient number of tags must accumulate in the fishery or in terminal areas before any quantitative interpretation can be made concerning stock distribution. This requirement coupled with the lag time between field collection and tag decoding has precluded in-season regulatory adjustments based on relative stock strengths.

The ability to estimate component stocks in stock mixtures based on genetic profiles of contributing groups has recently been developed and applied (Grant et al. 1980; Fournier et al. 1984; Beacham et al. 1985; Pella and Milner 1987). Numerous estimates of stock mixtures of chinook salmon have been made using a genetic stock identification (GSI) procedure described by Milner et al. (1983). These applications (Miller et al. 1983; Milner et al. 1985) have substantially increased the ability to manage stock mixtures of chinook salmon.

The genetic procedures provide estimates of stock composition with greater detail and precision than has previously been possible when the following two conditions are met. First, known genetic differences (presently identifiable by electrophoretic methods, among other techniques) must exist among populations contributing to a particular stock mixture. Second, a data base of calculated genotypic frequencies (based on a sufficient number of genetic systems) must be developed for those populations that are likely to compose a fishery.

The GSI procedure obtains maximum likelihood estimates of stock composition using the genotypic frequencies of the data base and of the stock mixture. The GSI analysis of the May 1982 troll fishery off the Washington coast using a data base for California through British Columbia provided the most detailed analysis of an oceanic salmon fishery to date (Miller et al. 1983).

This paper follows a general description of the GSI and its application to stock mixtures of salmonids provided in Milner et al. (1985). Estimates of stock composition were obtained from samples collected from fisheries off the Washington coast during the spring and summer of 1983. A particular focus was given to the fall runs of the Columbia River because of the major contributions these runs have historically made to oceanic fisheries. This information is intended to provide managers and biologists with better insights into the life histories of chinook salmon populations in this area of intermingling, and to initiate a continuing record of this species' oceanic distribution and relative abundance.

MATERIALS AND METHODS

The procedures used in this study are outlined below. Many of the details required for specific application are necessarily omitted, but are available in the referenced sources.

Baseline Populations

Data were obtained from 88 collections taken from British Columbia through California and represented distinct breeding units in most cases (Table 1). Intact juveniles or samples of tissues (eye and liver were the tissues of interest in the present study) from adult fish were taken in the field and transported frozen (usually on dry ice) to the laboratory for further processing prior to electrophoresis.

Methods used for detection of electrophotetic variants followed procedures outlined in Utter et al. (1974) and May et al. (1979). The three buffer systems used included:

1) A Tris-boric acid-EDTA gel and tray buffer, pH 8.5 (Markert and Faulhaber 1965).

2) An amine citric acid gel and tray buffer, pH 6.5 (Clayton and Tretiak 1972).

3) A Tris-citric acid-lithium hydroxide-boric acid gel buffer, and a lithium hydroxide-boric acid tray buffer, pH 8.5 (Ridgway et al. 1970).

A system of nomenclature for locus and allelic designations followed Allendorf and Utter (1979).

[3]Pacific Fishery Management Council. 1981. Proposed plan for managing the 1981 salmon fisheries off the coast of California, Oregon, and Washington. Pacific Fishery Management Council, 526 S.W. Mill St., Portland, OR 97201.

TABLE 1.—Geographical area and stock group of the 88 baseline populations used in estimating composition of mixed stock fisheries.

Major geographical district, type of stock, and baseline population[1,2]	Stock group	Total no. examined
Columbia River Basin		
Tule (lower river fall run)	1	150
Spring Creek-Little White Salmon R.-Washougal R.	1a	—
Cowlitz R.-Kalama R.	1b	144
Upriver brights (fall run)	2	
Mid river		
Deschutes R.	2a	49
Priest Rapids-Hanford Reach	2b	249
Snake River		
Ice Harbor	2c	200
Other stocks	3	—
Lower river, fall run		
Lewis R., brights		50
Lower river, spring run		
Cowlitz R.,-Kalama R.		100
Lewis R.		50
Willamette R., spring run		
Eagle Creek-McKenzie R.		88
Hatcheries using stocks of upper river origin, (spring run)		
Little White Salmon*-Carson*-Leavenworth*		148
Mid-Columbia River, spring run		
Klickitat R.		50
Deschutes R., spring run		
Warmsprings*-Round Butte*		109
Upper Columbia River		
Winthrop, spring run		129
Wells Dam, summer run		50
Snake River, spring run		
Rapid R.-Valley Ck.		
Sawtooth Hatchery-Red R.		165
Snake River, summer run		
McCall Hatchery*-Johnson Ck.*		106
California	4	
Sacramento River, fall run		
Coleman (Battle CK.)-Nimbus-Upper Sacramento (late)		300
Feather River-Mokelumne		200
Sacramento River, spring run		
Feather River		50
Klamath River, fall run		
Iron Gate		99
Trinity R.		100
Klamath River, spring run		
Trinity R.		50
Oregon and Washington coast	5	
Oregon, fall run		
Chetco R.		100
Lobster Ck.		50
Elk R.		100
Sixes Estuary*		100
Oregon and Washington coast—*Continued*		
Oregon, fall run—*Continued*		
Coquille Estuary		115
Siuslaw Bay		82
Salmon R.		99
Nestucca R.-Alsea Bay-Siletz R.-Fall Ck.		346
Cedar Ck.*		100
Trask R.-Tillamook R.		188
Nehalem Estuary		141
Oregon, spring run		
Cole R.-Hoot Owl Ck.		163
Rock Ck.		100
Cedar Ck.		99
Trask R.		100
Washington, fall run		
Naselle R.		99
Humptulips R. (early)		50
Quinault R.		100
Queets R.		120
Hoh R.		100
Soleduck		50
Washington, summer run		
Soleduck R.*		100
Washington, spring run		
Soleduck R.		100
Puget Sound and British Columbia	6	
Puget Sound, fall run		
Elwha R.		100
Hood Canal*		98
Deschutes R.		150
Green R.-Samish R.		149
Puget Sound, summer run		
Skykomish R.		100
Skagit R.		100
Puget Sound, spring run		
N. Nooksack R.		50
S. Nooksack R.		50
British Columbia, fall run		
Qualicum*		85
Puntledge*		100
Quinsam*		97
Robertson Ck.		100
Capilano*		99
San Juan R.		50
British Columbia, summer run		
Fraser River		
Tete Jaune		38
Clearwater		45
Chilko R.*		49
Stuart R.*		50
Nechako R.		55
Babine R.*		39

[1]Populations joined by hyphens were not distinguishable based on significant differences of allelic frequencies, and were analyzed as single units.
[2]Asterisks (*) indicate stocks or stock groups excluded from final estimates based on preliminary estimates indicating a contribution of less than 30 fish to total catch of all fisheries sampled (see text).

Multiple loci for the same class of protein are numbered sequentially starting with the locus having the most cathodal activity. Alleles are designated numerically as the percentage of the mobility of the homomeric band of a protein encoded by a variant allele relative to the mobility of the homomeric protein band encoded by the common allele (which is designated 100).

Estimates of allele frequencies were obtained for 17 polymorphic loci from each population sampled. These loci, the conditions for their electrophoretic detection, and the numbers and relative electrophoretic mobilities of their variant allelic forms are outlined in Table 2. The allelic frequencies of these collections for these loci will be presented in a companion publication describing the genetic population

TABLE 2.—Polymorphic enzymes providing genetic information for baseline populations and stock mixtures. Tissue used were eye (E), and liver (L). Explanations for locus and allele designations and for buffers are given in text.

Enzyme (enzyme commission no.)	Locus designation (variante alleles)	Tissue	Buffer
Aconitate hydratase (4.2.1.3)	Ah-4(69,86,108,116)	L	2
Adenosine deaminase (3.5.4.4)	Ada-1(83)	E	1
Aspartate aminotransferase (2.6.1.1)	Aat-3(90)	E	1
Dipeptidase (glycyl-L-leucine) (3.4.13.11)	Dpep-1(90)	E,L	1
Glucose-6-phosphate isomerase (5.3.1.9)	Gpi-3 (93,105)	E,L	3
Glutathione reductase (1.6.4.2)	Gr-1(85)	E,L	1
Hydroxyacylglutathione hydrolase (3.1.2.6)	Hagh(140)	L	1
Isocitrate dehydrogenase (1.1.1.42)	Idh-3,4(50,74,127,142)	E,L	2
Lactate dehydrogenase (1.1.1.27)	Ldh-4(71,134)	E,L	3
	Ldh-5(70,90)	E	1
Malate dehydrogenase (1.1.1.37)	Mdh-1,2(27,-45,146)	E,L	2
	Mdh-3,4(70,83,121)	E,L	2
Mannose-6-phosphate isomerase (5.3.1.8)	Mpi(95,109,113)	E,L	1
Phosphoglucomutase (5.4.2.2)	Pgm-1(-70,-84)	E,L	2
Phosphoglycerate kinase (2.7.2.3)	Pgk-2(90)	E,L	2
Superoxide dismutase (1.15.1.1)	Sod-1(-260,560,1250)	L	1
Tripeptide aminopeptidase (L-leucylglycylglycine) (3.4.11.4)	Tapep(45,130)	E,L	3

structure of North American chinook salmon stocks. The general locations of baseline samples and mixed fisheries are outlined in Figure 1.

The data base of six major groupings used to analyze the ocean fisheries was derived from the data of the 88 collections as follows: 1) Contingency tests were used to combine data for populations lacking significant allelic differences, thus reducing the number of groups to 65. 2) GSI estimates were made from weighted (by catch) samples of genotypic data from each fishery; based on this information, those groups estimated by maximum likelihood (see below and Milner et al. 1983[4]) to contribute less than 0.034% (30 fish) to the total catch of all fisheries sampled were eliminated. This brought the number of groups down to 50. 3) Estimates made for each of the 50 groups were combined into the six major groupings of Table 1 to permit a particular focus on tule and upriver bright stocks in the Columbia River.

Estimates of the composition of the 1 September gill net fishery in the Columbia River were obtained for each of the 11 Columbia River fall run collections and combined as indicated in Table 1.

Population Mixtures

Almost all of the ocean sampling was done at port of landing. Eye fluid, the only tissue, was collected in tubes placed on chipped ice, stored in various freezers, and shipped weekly in a portable freezer to the laboratory where storage was at -90°C until preparation for electrophoresis. The September gill net fishery was sampled for livers only. Samples obtained by Washington Department of Fisheries (WDF) personnel from fish buyers in Ilwaco and Chinook, WA, and Astoria, OR, were collected and shipped on dry ice, and electrophoresis was carried out immediately following their arrival.

Electrophoretic data were collected only for those polymorphic loci that were expressed in the collected tissues:

[4]Milner, G. B., D. J. Teel, and F. M. Utter. 1983. Genetic stock identification study. Unpubl. rep., 66 p. Northwest and Alaska Fisheries Center, National Marine Fisheries Service, NOAA, 2725 Montlake Blvd. E., Seattle, WA 98112. (Final Report of Research to Bonneville Power Administration, Agreement DE-A179-82BP28044M001.)

eye — Aat-3; Ada-1; Dpep-1; Gpi-3; Gr-1; Idh-3,4; Ldh-4; Ldh-5; Tapep; Mdh-1,2; Mdh-3,4; Pgm-1; Pgk-2; Mpi.

liver — Ah-4; Dpep-1; Hagh; Gpi-3; Gr-1; Idh-3,4; Tapep; Ldh-4; Mdh-1,2; Mdh-3,4; Pgm-1; Pgk-2; Mpi; Sod-1 (Table 2).

Mixed Fishery Analysis

Maximum likelihood estimates of proportionate contributions of baseline populations to different population mixtures were obtained by the procedures described in Milner et al. (fn. 4). Through an iterative procedure (the EM algorithm, Dempster et al. 1977), the estimates are obtained using the frequencies of genotypes in the mixtures and in the baseline populations. Standard deviations of indiviual and pooled estimates were based on an asymptotic variance as described in Milner et al. (fn. 4). These variances were found to be consistently higher than empirically derived variances within the sample sizes of the present study (Milner et al. fn. 4). The geographic range of mixed fisheries sampled in this study was from the Strait of Juan de Fuca southward through the mouth of the Columbia River to the northern coast of Oregon (Fig. 1).

TABLE 3.—Estimated proportions of stock groups and subgroups in fisheries of 1983.

Fishery class[1]	area[2]	month[3]	Stock group (Estimated contribution and in parentheses standard deviation)									Number in sample [fishery]
			1a	1b	2a	2b	2c	3	4	5	6	
C	1	5	0.350	0.130	0.009	0.010	0.008	0.147	0.049	0.092	0.202	1,243
			(0.022)	(0.020)	(0.042)	(0.036)	(0.038)	(0.034)	(0.052)	(0.079)	(0.037)	[10,870]
	2		0.393	0.228	0.010	0.001	0.002	0.100	0.019	0.080	0.187	2,050
			(0.044)	(0.047)	(0.052)	(0.021)	(0.069)	(0.041)	(0.101)	(0.101)	(0.055)	[23,780]
	3		0.456	0.054	0.022	0.004	0.009	0.168	0.124	0.042	0.122	319
			(0.183)	(0.187)	(0.488)	(0.282)	(0.523)	(0.314)	(0.471)	(0.873)	(0.449)	[1,600]
	4		0.375	0.054	0.007	0.003	0.004	0.133	0.189	0.081	0.153	600
			(0.076)	(0.111)	(0.212)	(0.112)	(0.255)	(0.098)	(0.385)	(0.430)	(0.226)	[4,062]
	1-4		0.362	0.187	0.013	0.001	0.004	0.121	0.047	0.079	0.187	3,475
			(0.002)	(0.003)	(0.005)	(0.007)	(0.009)	(0.007)	(0.010)	(0.007)	(0.004)	[40,314]
	2	7	0.515	0.156	0.014	0.001	0.011	0.123	0.035	0.047	0.101	1,044
			(0.068)	(0.073)	(0.180)	(0.120)	(0.195)	(0.090)	(0.296)	(0.263)	(0.114)	[4,965]
	3		0.225	0.214	0.032	0.000	0.012	0.069	0.115	0.191	0.142	784
			(0.060)	(0.104)	(0.161)	(0.105)	(0.166)	(0.140)	(0.109)	(0.287)	(0.162)	[3,511]
	4		0.341	0.078	0.016	0.013	0.016	0.101	0.160	0.148	0.126	1,243
			(0.045)	(0.066)	(0.111)	(0.071)	(0.123)	(0.075)	(0.093)	(0.195)	(0.099)	[5,739]
	2-4		0.353	0.143	0.019	0.007	0.026	0.111	0.087	0.133	0.121	2,989
			(0.032)	(0.039)	(0.074)	(0.037)	(0.069)	(0.047)	(0.046)	(0.104)	(0.060)	[14,214]
	1-4	5-7	0.366	0.187	0.014	0.001	0.006	0.101	0.056	0.090	0.181	4,701
			(0.001)	(0.001)	(0.004)	(0.003)	(0.005)	(0.003)	(0.005)	(0.006)	(0.003)	[54,527]
I	3-4		0.298	0.197	0.021	0.002	0.019	0.163	0.126	0.061	0.114	462
			(0.113)	(0.129)	(0.391)	(0.246)	(0.304)	(0.149)	(0.161)	(0.622)	(0.261)	[3,923]
	4a		0.357	0.054	0.003	0.002	0.003	0.076	0.409	0.022	0.082	428
			(0.095)	(0.125)	(0.477)	(0.226)	(0.277)	(0.166)	(0.426)	(0.663)	(0.358)	[2,283]
	3-4a		0.330	0.115	0.012	0.003	0.008	0.171	0.221	0.032	0.109	731
			(0.064)	(0.082)	(0.259)	(0.130)	(0.243)	(0.098)	(0.448)	(0.409)	(0.202)	[6,206]
S	1-2	6	0.218	0.158	0.011	0.000	0.015	0.085	0.014	0.099	0.399	1,633
			(0.045)	(0.060)	(0.128)	(0.076)	(0.124)	(0.093)	(0.147)	(0.177)	(0.092)	[13,232]
	1	6-7	0.202	0.266	0.017	0.001	0.010	0.125	0.029	0.079	0.271	1,530
			(0.007)	(0.010)	(0.028)	(0.016)	(0.024)	(0.018)	(0.032)	(0.063)	(0.024)	[9,581]
	2		0.294	0.215	0.005	0.000	0.006	0.099	0.037	0.114	0.228	1,760
			(0.008)	(0.017)	(0.031)	(0.013)	(0.033)	(0.024)	(0.044)	(0.047)	(0.015)	[15,522]
	1-2		0.247	0.263	0.008	0.000	0.009	0.122	0.046	0.107	0.198	2,846
			(0.006)	(0.007)	(0.014)	(0.007)	(0.016)	(0.010)	(0.018)	(0.023)	(0.007)	[25,103]
		7-8	0.326	0.217	0.014	0.000	0.011	0.048	0.069	0.070	0.232	368
			(0.165)	(0.238)	(0.849)	(0.780)	(0.563)	(0.548)	(0.981)	(1.58)	(0.747)	[2,483]
		8-9	0.240	0.228	0.009	0.047	0.040	0.057	0.088	0.137	0.155	739
			(0.076)	(0.110)	(0.304)	(0.205)	(0.251)	(0.146)	(0.435)	(0.517)	(0.206)	[6,066]
		5-9	0.251	0.211	0.007	0.001	0.013	0.118	0.044	0.096	0.259	5,315
			(0.001)	(0.002)	(0.004)	(0.003)	(0.005)	(0.003)	(0.008)	(0.007)	(0.003)	[46,884]
C	CR	9	0.780	0.146	0.011	0.052	0.007	0.004	—	—	—	2,040
			(<0.001)	(0.001)	(0.001)	(<0.001)	(<0.001)	(<0.001)				[15,668]

[1]C = commercial, I = Indian, S = Sport.

[2]Areas are as indicated in Figure 1.

[3]In sport fishery, dates for month are 6 = 5-29 – 6-17, 7 = 6-18 – 7-29, 9 = 8-16 – 9-11; in Columbia River commercial fishery 9 = 9-1 only.

DISTRIBUTIONS OF STOCK GROUPS IN OCEAN FISHERIES

Estimated contributions to different fisheries by the two tule and three upriver bright subgroups, and by the four other geographic groupings, are listed in Table 3. Some of the major features of Table 3 are graphically projected in Figure 2. A stock structure that varies with regard to both time and area is evident.

Some consistency over time is seen in comparisons of the May and July commercial troll catches in sampling areas 2 and 4. Notable features in sampling area 2 include the overall predominance of the tule stocks and a minimal contribution of Puget Sound and Canadian fish. Sampling area 4 has a smaller tule contribution and a substantially larger proportion of Puget Sound and Canadian fish.

Although comparisons of the sport and commercial fisheries are limited by somewhat different sampling areas, a greater proportion of California fish is taken in the sport fisheries. This is seen particularly in the early fishery. More intense sampling in area 1 may account for some of the early differences, but the data of Table 3 suggest a persistent trend even in common times and sampling areas.

The Indian troll fishery provided the only information from sampling area 4B. The most distinctive feature of this fishery was the high proportion (41%) of the Puget Sound and Canadian group. This figure was more than double the estimated contribution of this group in any other fishery.

The ocean fisheries off the Washington coast are notable for the usually negligible representation of upriver bright stocks. The highest estimated contribution (9.6%) occurred in the sport fishery of 16 August-11 September which was the largest fishery sampled. The timing and distribution of upriver bright fish will be considered in greater detail below.

Estimated distributions for the May 1982 and 1983 troll fisheries were compared (Table 4), reveal-

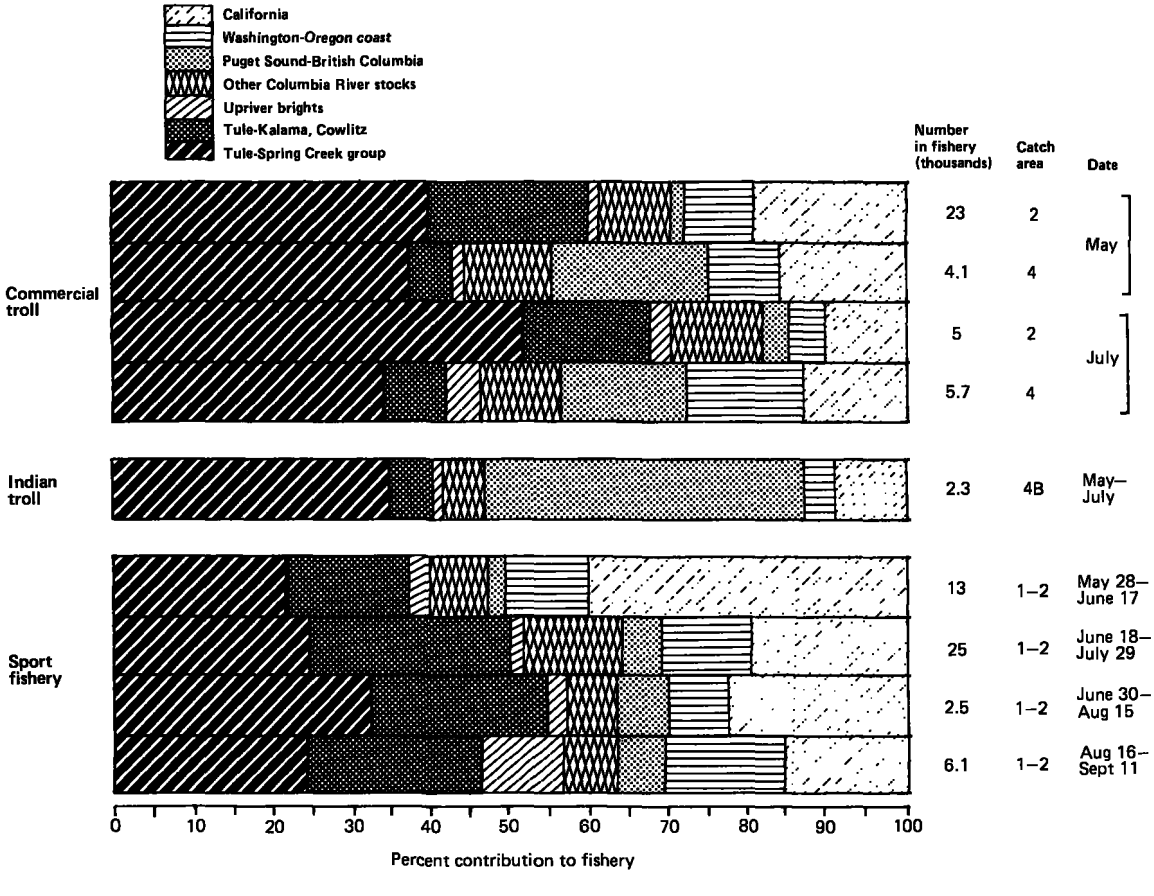

FIGURE 2.—Estimated contributions of seven stock groups in different ocean fisheries.

TABLE 4.—Comparisons of estimated percentage stock group contributions to May troll fisheries of 1982 and 1983 within sampling areas 1 and 4 and 1 through 4.

	Percentage catch estimated from sampling area					
	1		4		1 through 4	
Stock group	1982 (1,414)[2]	1983 (1,243)	1982 (448)	1983 (600)	1982[1] (2,504)	1983 (3,475)
Columbia River						
Tule	78.2	48.2	45.6	42.9	76.5	54.9
Upriver bright	4.0	2.7	8.8	1.0	4.3	1.8
All groups	88.9	65.6	56.8	57.6	90.9	69.5
California	5.3	20.2	4.4	15.3	2.8	18.3
Oregon-Washington coast	3.8	9.2	9.7	8.1	2.9	7.9
Puget Sound-Canada	1.9	4.9	29.2	18.9	3.4	4.7

[1]Data from Miller et al. 1983.
[2]Values in parentheses designate number of fish sampled.

ing considerable dissimilarity as well as some consistency. A much larger proportion of tules and a correspondingly smaller contribution of California fish was seen in 1982 in sampling areas 1 through 4.

The comparisons of estimates within sampling areas 1 and 4 differed between both sampling areas and years. For each year, estimates within sampling area 1 were similar to the estimates based on the total sample. Estimates from sampling area 4 were consistent with those of the total sample but with a larger proportion of California fish estimated in 1983 and substantially larger Puget Sound-Canadian stock group and smaller tule estimates. These observations are consistent with the location of sampling area 4 at the southern point of entry for most of the populations destined for Puget Sound and British Columbia, and are reinforced by the high proportion of fish estimated for this stock group in sampling area 4B.

The much higher total harvest of the 1982 May troll fishery (73,196; Miller et al. 1983) than in the same fishery for 1983 (40,312) accentuates the difference in numbers of tules taken (approximately 56,000 vs. 22,700).

The numbers of tule group fish returning to the mouth of the Columbia River and to hatcheries (i.e., spawning escapement) were also much lower in 1983 (Washington Department of Fisheries 1984[5]) and were insufficient to fulfill hatchery requirements. This contrast was attributed to a climatological phenomenon termed "El Niño" that affected the oceanic distribution and survival of many species beginning in 1983 (Mysak 1986).

[5]Washington Department of Fisheries. 1984. Status of fall chinook stocks in the northern Oregon through Vancouver Island ocean fishing areas. Unpubl. rep., 35 p. Department of Salmon Harvest Management, Washington Department of Fisheries, 115 General Administration Building, Olympia, WA 98504.

DISTRIBUTION AND RELATIVE CONTRIBUTIONS OF TULES AND UPRIVER BRIGHTS

The actual and potential value of tule and upriver bright runs in the sampling areas of this study warrant a more detailed focus on the abundance of these stocks and their subgroups. The great value of tule stocks in ocean fisheries off the Washington coast has been demonstrated from these and other data (e.g., Miller et al. 1983). Although a similar value for upriver brights in either oceanic or river harvests is not yet apparent, it is premature to assign a lesser value to these runs because of geographic and temporal limitations of sampling. Indeed, data from coded wire tags (Table 5) indicate a distinctly different oceanic distribution of tules and upriver brights. Over half of the recoveries of the tagged fish from the tule stock (Spring Creek) were harvested off the Washington coast. However, only about 5% of the tagged fish from upriver bright stocks were recovered in this area, with over 90% harvested in waters of Alaska and British Columbia.

The substantially increased contribution of upriver brights in the late sport fishery (Table 3, Fig. 2) is consistent with a late migratory surge of these fish. Clearly, based on distributions indicated through tag data in Table 5, the upriver brights contribute heavily to fisheries in areas north of those sampled in this study. However, they were estimated at sizable numbers only very late in this study presumably enroute through the areas sampled to their spawning grounds.

The tules and upriver brights have been considered as unit populations to this point. The subgroup data indicate considerable heterogeneity within both groups with regard to time, area, and fishery. Comparisons of the two tule subgroups (Table 3, Fig. 2) indicate a considerable difference

TABLE 5.—Summary of distribution of oceanic coded wire tag recoveries (N) of 1975 brood year fall chinook salmon from the Snake River, and Priest Rapids and Spring Creek hatcheries.

Source and type of stock	Sample size	Recovery area: Alaska	Canada (B.C.)	Washington	Oregon	Total no. fish
Snake River[1] (upriver bright)	N	176	272	21	11	480
	%	36.7	56.7	4.3	2.3	
Priest Rapids[2] (upriver bright)	N	1,314	1,597	171	13	3,095
	%	42.4	51.9	5.4	0.3	
Spring Creek[2] (tule)	N	0	984	1,319	147	2,450
	%	0	40.2	53.8	6.0	

[1]Data from L. Gilbreath, Northwest and Alaska Fisheries Center, Seattle WA 98112, pers. commun. September 1984.
[2]Data obtained from Pacific Marine Fisheries Commission in 1983.

in their relative frequencies. In both May and July, the proportion of the Cowlitz-Kalama subgroup (group 1b) to the overall tule contribution in the commercial fisheries was considerably higher in sampling area 2 (average 30%) than in sampling area 4 (average 16%). The proportion of this subgroup was highest in the sport fisheries, approaching equality (46%) with the Spring Creek subgroup (1a) in the overall data set and predominating in the June-July fisheries (52%). The Spring Creek subgroup strongly predominated in the tule catch of the river fishery of 1 September (84%, Table 3).

The relative contributions of the three upriver bright subgroups vary considerably in the ocean fisheries (Table 3, Fig. 3). The most notable feature is the absence or negligible contribution of the Priest Rapids subgroup (2b) in all but the last ocean fishery that was sampled, where this subgroup contributes a substantial proportion (49%) of the total estimated upriver bright harvest. This finding was unexpected because this subgroup is by far the largest contributor to the overall upriver bright production (Pattillo and McIsaac 1982). The data of the 1 September river fishery are more consistent with expectations, with 83% of the upriver bright catch estimated to be from the Priest Rapids subgroup. The low estimated contribution of this subgroup to ocean fisheries cannot be explained by the large standard deviations accompanying most estimates because the more precise pooled estimates (Table 3) also indicate a small Priest Rapids contribution.

MANAGEMENT CONSIDERATIONS

The difference in relative proportions of the two tule groups, based largely on class of fishery and

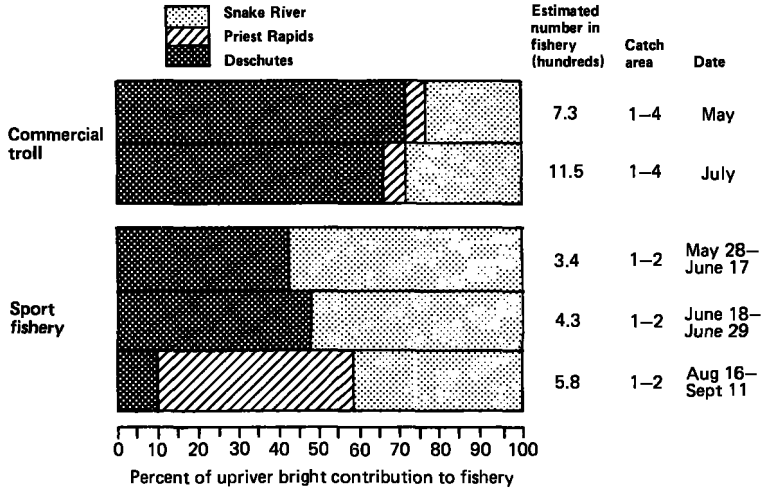

FIGURE 3.—Estimated proportions of three upriver bright stocks to different ocean fisheries.

area, has implications for management. The higher representation of the Cowlitz-Kalama subgroup in the sport fisheries than in the troll fisheries of common times and areas suggests a greater susceptibility of this subgroup to sport harvests. In addition, the relative abundance of the Cowlitz-Kalama subgroup compared with the Spring Creek subgroup was higher in more southern areas for both commercial and sport fisheries. If these trends continue to be observed, different management strategies could be applied for these groups when warranted.

The low estimates of the Priest Rapids subgroup of upriver brights relative to the two less abundant subgroups suggest different oceanic distributions of these subgroups. However, the coded wire tagging data (Table 5) indicate that at least the Snake River and Priest Rapids subgroups are harvested much more intensely in areas to the north of those sampled in this study (no tagging data were available for the Deschutes subgroup). Any attempts to identify and protect the weaker subgroups within the sampling areas of this study would be futile unless similar efforts could be applied to these much larger catches in more northern areas.

A general occurrence of larger proportions of Puget Sound and Canadian fish in the northern sampling areas is suggested by the similar observations for 2 consecutive years and by the particularly high estimates for these fish in area 4B. Since 1983, more detailed GSI estimates from area 4B have, in fact, been used by the WDF to monitor and regulate chinook salmon fisheries in the Strait of Juan de Fuca and Puget Sound areas.

Preliminary results from the September gill net fishery in the lower Columbia River (based on a subsampling of 500 fish) were available on the day following the collection of the samples. This potential for rapid turnaround time increases the value of the GSI as a management tool by permitting in-season regulatory adjustments. Such information would allow greater harvest of a healthy stock while continuing to provide for maximum protection of a depressed stock. For example, in years when bright fish are expected to return in great abundance and tules in low abundance, the GSI method could be used to monitor extended fall gill net fisheries to time the entry of tules. When ratios of tules to brights became unfavorable, fisheries could be curtailed.

It is important to emphasize the arbitrary nature of many of this study's groupings, which were necessary to provide a manageable basis for reporting. A focus on the tule and upriver bright contributions was appropriate because of the extensive baseline data from the Columbia River drainage, the dominance of the tule runs in ocean fisheries, and the distinct oceanic distributions of the tule and upriver bright groups. However, a similar focus on other groupings (e.g., Columbia River spring runs or wild and hatchery stocks of the Oregon coast) is equally feasible, and could easily provide a basis for more detailed information on the distributions of individual populations within such groups.

The completeness and the reliability of the sets of baseline data that are used affects the accuracy of GSI estimates. This study's focus on the contribution of Columbia River populations to stock mixtures in ocean areas adjacent to the mouth of the Columbia River was appropriate for the sets of baseline data that were used. Most estimates were obtained through a data base that included most of the major contributing groups within the Columbia River and allele frequency data from 17 polymorphic loci. These same baseline data can be used over successive years, providing the allele frequencies remain stable among year classes and over succeeding generations. Such stability has been observed for some loci and populations of anadromous salmonids (e.g., Utter et al. 1980; Grant et al. 1980; Altukhov 1981).

This temptation to regard the present baseline data as a static entity should nevertheless be resisted for a number of reasons. Gene flow, genetic drift, and selection could modify allelic frequencies over extended time periods; thus, periodic updating of previously sampled populations is desirable. Temporal changes in allele frequencies of chinook salmon have been reported (Carl and Healey 1984; Kristiansson and McIntyre 1976). The extensive stock transplantations of chinook salmon within the Columbia River make the possibility of gene flow particularly likely for the focal populations of this study. Hatchery populations perpetuated by limited numbers of breeders are particularly susceptible to allele frequency changes through genetic drift (Allendorf and Ryman 1987). Previously unsampled baseline populations should be added, particularly in areas where limited sampling has occurred, to increase the accuracy and broaden the usable range of analyses. The discriminatory powers of GSI analyses are substantially increased as new variable loci are added (see Milner et al. fn. 4). The continuing search for additional markers requires collection of electrophoretic data from previously sampled populations for each new variable locus that is found.

Increasing application of procedures used in this study seems virtually inevitable in view of the per-

sistent need to understand the composition of stock mixtures of salmonids (and other structured groups) better. The obvious management potential of such uses is matched by increased understanding of population structuring and of migratory behavior that will emerge as information accumulates.

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