

**Mixed Stock Analysis of Pacific Rim Chum Salmon
in the 1993 and 1994 South Alaska Peninsula June Fisheries
Using Allozyme and Mitochondrial DNA Data**

by

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ABSTRACT

Chum salmon populations from the Pacific Rim form mixed-stock aggregations during their ocean residency. In Alaska, migrating chum salmon are harvested incidentally in sockeye salmon fisheries during June in the areas of South Unimak Island and Shumagin Islands (South Alaska Peninsula). Numerous tagging studies have shown that these fish originate from throughout the Pacific Rim. A large genetic database for chum salmon using allozyme data has been developed over the last decade from populations around the Pacific Rim. This database can be used to provide information on migration routes and fishery composition. In this report, a baseline including 69 stock groupings representing the entire range of the species was evaluated for its ability to identify stock of origin in complex mixtures of Asian and North American chum salmon. It was then used to estimate the origin of 2,000 individuals caught in the Unimak Area of the South Alaska Peninsula during 1993 and 1994 using a maximum likelihood algorithm. The relative contributions of eight major regions (Japan, Northwest Alaska, Yukon River fall run, Alaska Peninsula and Kodiak Island, Southeast Alaska, British Columbia and Washington) were reported. Results indicated that northwest Alaska populations predominate in the fishery with estimates ranging from 0.52 to 0.62. Finally, a mitochondrial DNA (mtDNA) marker was assayed in 400 of the 1994 samples to provide an independent estimate of the Japanese component using the baseline of Park et al. (1993). The mtDNA (0.095) and allozyme (0.091) estimates were virtually identical for these 400 samples. Analysis of 1994 samples from the Shumagin Islands, continued monitoring of the South Alaska Peninsula June fishery, and continued expansion of the chum salmon baseline is planned. Continued collection of spawning populations from Russia and monitoring of Japanese hatchery populations is desirable.

INTRODUCTION

Chum salmon (*Oncorhynchus keta*) from North America and Asia migrate into the North Pacific Ocean, generally returning to their natal streams to spawn at age three, four or five. The salmon form aggregations composed of numerous stocks and species during their ocean residency and freshwater migrations. Identification of composite stocks in mixtures of chum salmon caught in international waters, in the U.S. Exclusive Economic Zone, and in the major river systems leading to spawning tributaries has been an ongoing challenge for fisheries biologists and management agencies throughout the Pacific Rim.

In Alaska, migrating chum salmon are harvested incidentally in sockeye salmon fisheries during June off the South Alaska Peninsula in the area of South Unimak Island and the Shumagin Islands. Numerous tagging studies (e.g. Gilbert and Rich 1925; Aro et al. 1971; Aro 1972; Meyer 1983; Eggers et al. 1991; Eggers 1992) have shown that significant numbers of chum salmon harvested are not of local origin. Tag recoveries have been reported not only from throughout Alaska, but also from Japan, Russia, British Columbia, and Puget Sound (Brannian 1984; Eggers et al. 1991; Eggers 1992).

Incidental catch of chum salmon in the sockeye fisheries may contribute to conservation and allocation problems in certain areas. Spawning escapements in some areas, such as Norton Sound, Kuskowim River, and fall Yukon River have been below historic levels in recent years (Eggers 1995). The potential impacts of the South Unimak June fisheries on these stocks of chum salmon cannot be adequately determined because of the lack

of geographic-specific data on stock composition of chum salmon caught as bycatch. Methods for identifying more specific geographic origins of chum salmon are needed.

Genetic stock identification or mixed stock analyses (MSA) using protein variation detected by allozyme electrophoresis was first applied to fisheries problems in the early 1970's (Utter et al. 1974) and has become an important part of many salmonid management programs (e. g. Wishard 1980; Milner et al. 1981; Utter et al. 1987; Kondzela et al. 1994; Phelps et al. 1994; Winans et al. 1994). It was recognized that underlying genetic differences could be extremely valuable to differentiate stocks in mixtures of Pacific salmon (e. g. Milner et al. 1981; Grant et al. 1980; Seeb et al. 1986; Seeb et al. 1990; Seeb et al. 1995; Winans et al. 1989; Wilmot et al. 1992), and a considerable statistical framework based on maximum likelihood estimates evolved to identify individual stocks within mixtures (Milner et al. 1981; Fournier et al., 1984; Millar 1987, 1990; Pella and Milner 1987; Smouse et al. 1990; Gomulkiewicz et al., 1990; Pella et al. 1994).

In this report we evaluate the performance of an updated allozyme database (Seeb et al. 1995) constructed from chum salmon around the Pacific Rim (Southeast Alaska, British Columbia: Kondzela et al. 1994; Asia: Wilmot et al. 1994, Winans et al. 1994; Washington, British Columbia: Phelps et al. 1994; Northwest Alaska: Seeb et al. 1995) and use it to estimate stock of origin of chum salmon caught in the South Alaska Peninsula June fishery during 1993-1994. Mitochondrial DNA ND5/ND6 *Ase I* haplotypes were assayed in a portion of the 1994 fishery samples to provide an independent estimate of the Japanese component using the mitochondrial DNA database of Park et al. (1993). Future studies will provide additional baseline information and continued monitoring of the fishery.

MATERIALS AND METHODS

Sample Collection

Mixed fishery samples were collected from tender deliveries from Southeast Unimak (Cape Lazaref to Ikatan Bay) and from Southwest Unimak (Cape Lutke) in 1993, with a sampling goal of 400 from each location for each fishing period (Figure 1). A total of 2,622 individual chum salmon were sampled from six open periods during the June 1993 fishery (Table 1). In 1994, sampling was expanded to include the Shumagin Islands. Additionally, the Southeast and Southwest Unimak fisheries were not distinguished, but were treated as a single site. A sample goal of 400 fish during each fishery opening at each site was established. Nearly 6,300 fish were collected in 1994 (Table 1). Tender deliveries were sampled at Peter Pan Seafoods, King Cove, Alaska, and Trident Seafoods, Sand Point, Alaska.

To estimate the stock composition of the incidental chum salmon catch, the fishery samples from 1993 and 1994 were subsampled. A sample size of 400 was established for each mixed fishery estimate. We stratified the 1993 fishery into two periods (June 13-20, June 22-29) and the 1994 fishery into three periods (June 17-20, June 21-25, June 26-30). June 20 was used as the delimiter for the first period for each year to allow comparison to previous tagging studies (Eggers et al. 1991; Eggers 1992). A total of 400 individuals for each period were randomly selected, proportional to the daily catch rate in each period (Table 2). Subsampling for 1993 was adjusted according to the varying catch rates between Southeast and Southwest Unimak areas.

Laboratory Methods

Allozyme analysis protocols used are described in Seeb (1994). We used the genetic nomenclature of the American Fisheries Society (Shaklee et al. 1990).

Mitochondrial DNA (mtDNA) was extracted from the 400 individuals analyzed for allozymes in the 1994 Period 2 subsample (June 21-June 25, 1994), and NADH dehydrogenase subunits 5 and 6 (ND5/ND6) were amplified (see Seeb et al. 1995 for protocols used). Polymorphisms were detected with *AseI*. Haplotype nomenclature follows that of Park et al. (1993) rather than Cronin et al. (1993); the haplotype designators B and C are interchanged between the two studies.

Statistical Analyses

Construction of Pacific Rim Database

The baseline was created from 138 chum salmon populations (Figure 2) using 20 loci. Populations incorporated and their source are listed in Table 3. Populations not incorporated in the baseline due to missing data include: Tauy River, Magadan River, Avacha River, and Ossora River from Russia; Masuhoro, Shibetsu, Tokoro, and Yurrapu from Japan; and Canadian fall run from the Yukon River (see Wilmot et al. 1994; Winans et al. 1994). Fifteen loci were variable in most populations analyzed: *ALAT**, *mAAT-1**, *sAAT-1,2**, *mAH-3**, *ESTD**, *G3PDH-2**, *mIDHP-1**, *sIDHP-2**, *LDH-A1**, *sMDH-A1**, *sMDH-B1,2**, *mMEP-2**, *MPI**, *PEPB-1**, *PGDH**. Variation was regionally based for *GPI-B1,2**, *GPI-A**,

*LDH-B2**, *sMEP-1*, and *PEPA**.

Data have been standardized among laboratories through a series of coastwide information exchanges including distribution of mobility standards. Data were further standardized by recalculating allele frequencies at isoloci using a two locus model for data from Winans et al. (1994), Kondzela et al. (1994), and Wilmot et al. (1994) and pooling alleles (see Seeb et al. 1995 Appendix 1 for baseline allele frequencies). Pooling alleles may slightly erode the resolving power of MSA estimates, but it reduces the possibility of laboratory bias in the baseline data.

After standardization, data from nearly 200 populations were available for inclusion in the Pacific Rim data set. Trial analyses of South Unimak June fishery mixtures clearly indicated that populations from Southeast Alaska, British Columbia, and Washington were nearly absent. To reduce the number of stocks in the baseline and improve model performance, representative populations were chosen from Southeast Alaska, British Columbia, and Washington (Southeast Alaska, northern British Columbia: K. Hofmeister, Alaska Department of Fish and Game, Douglas, AK; southern British Columbia, Washington: S. R. Phelps, Washington Department of Fish and Wildlife, Olympia, WA, personal communication).

Further, heterogeneity among representative populations and adjacent populations was tested using G-Statistics (modified from Weir 1990). Populations were pooled if no heterogeneity was detected ($\alpha < 0.01$). A comprehensive hierarchical analysis was used to pool populations within regions in Northwest Alaska ($\alpha < 0.01$) (Seeb et al. 1995). Pooling populations allows greater precision for regional allele frequency estimates and improves

performance of the MSA model. Inclusion of populations with nearly identical genetic characteristics causes instability of estimates (Pella and Milner 1987).

Possible reporting regions for fishery estimates were selected using two methods. Cavalli-Sforza and Edwards chord distances (Cavalli-Sforza and Edwards 1967) among stocks were used for deriving a tree using Unweighted Pair-Group Method with Arithmetic Averaging (UPGMA, Sneath and Sokal 1973) and for multidimensional scaling analysis (MDS, Krzanowski and Marriott 1994). All computations were performed using *S-Plus* analytical software (Mathsoft, Inc., Seattle, WA.).

Mixed Fishery Analysis

Simulated mixtures were used to optimize potential reporting regions selected from the UPGMA and MDS analysis. Average mixture estimates were derived from 100 simulations, where reporting region comprised 100% of the mixture (N=400). In each simulation, new baseline and mixture genotypes were randomly generated from the baseline data using Hardy-Weinberg expectations, and each stock in the region contributed equally to the mixture. Reporting regions were enlarged until approximately 90% of the mixture allocated to the correct region.

Stock contributions of the mixed fishery samples were estimated via maximum likelihood (MLE) (Pella and Milner 1987; Masuda et al. 1991). A conjugate gradient searching algorithm using a square root transformation was employed (Pella et al. 1994). This algorithm provides good performance with large baselines and small stock differences (Pella et al. 1994). The precision (standard error) of the stock composition estimates were

estimated by a parametric bootstrap (Efron and Tibshirani 1986), where the observed multilocus genotype frequencies were assumed to be distributed multinomial as were the allele frequencies in the baseline. Used in this manner, the bootstrap accounts for sampling error in the mixture and in the baseline allele frequencies, but does not account for missing populations in the baseline.

One hundred bootstrap iterations were executed to provide estimates of standard error (Masuda et al. 1991). Genotypes were removed from the estimation procedure if their probability of occurring was zero. For these cases, the mixture estimates have an unknown group containing the percent of the mixture that was removed. Further, we deleted any individual missing data at \geq four loci. Individual population or stock estimates were first calculated, then summed into regional groupings (allocate-sum procedure, Wood et al. 1987).

Mitochondrial DNA was used to estimate the Japanese and pooled non-Japanese component to the Period 2 1994 fishery. Baseline mtDNA data were from Park et al. (1993), and the estimated mixture contribution was calculated following Adams and Ward (1973). Specifically, let p_1 and p_2 be the frequencies of the marker alleles in contributors 1 and 2, respectively, and p_m is the frequency in the mixture. Then the proportional contributions to the mixture are:

$$f_1 = \frac{p_m - p_2}{p_1 - p_2}, \quad (1)$$

where f_1 is the proportional contribution of the first contributor to the mixture and $(1-f_1)$ is the contribution of the second contributor.

RESULTS

Selection of Reporting Regions

The UPGMA phenogram (Figure 3) showed two distinct lineages of chum salmon: one composed of Asian and northwestern Alaskan populations; the second composed of North Peninsula, Gulf of Alaska, and Pacific Northwest populations. Within the Asian/Alaskan group, Japanese populations are distinctive, with Alaskan and Russian populations more similar to each other than either is to the Japanese populations. Two major groupings are present within the Peninsula/Gulf of Alaska group; North and South Peninsula populations cluster with southeastern Alaskan and British Columbian populations north of Nekite River, while British Columbian populations south of and including Nekite River are more similar to Washington.

The MDS is reflective of the UPGMA phenogram (Figure 4). Four non-overlapping stock groups are apparent: Japan, fall Yukon, Northwest Alaska summer, and Russia. Some overlap is observed among Peninsula/Kodiak and Southeast Alaska/PWS stocks.

Eight reporting regions for the MLE were selected based on the results from the UPGMA, MDS, and 100% simulations analysis: 1) Japan; 2) Russia; 3) Northwest Alaska summer (including Meshik River and Chunilna River); 4) fall Yukon; 5) Peninsula/Kodiak, 6) Southeast Alaska (including Prince William Sound-WHN population); 7) British Columbia; and 8) Washington. All reporting regions showed at least 90% accuracy with the exception of Southeast Alaska/PWS and British Columbia where accuracy dropped to 83% and 87%, respectively (Table 4).

Mixed Stock Analyses

Allozyme Results

MLEs were calculated for the samples collected from the South Unimak June fishery during 1993 and 1994 (Table 5, Fig. 5). The Northwest Alaska summer region was the predominant group in all the estimates; its contribution ranged from 0.721 in the second period in 1994 (1994-2) to 0.515 in 1994-1. The Japanese component was also fairly consistent ranging from a high of 0.169 in 1993-1 to a low of 0.091 in 1994-2. The Russian contribution showed a slightly greater variability ranging from a high of 0.189 in 1994-1 to a low of 0.057 in 1993-1. Alaska Peninsula to Kodiak populations were consistently present, ranging from 0.042 to 0.133. Fall Yukon River populations were likely absent, their estimated contribution statistically indistinguishable from 0.00. However, it should be noted that Canadian fall Yukon River populations were not included in the baseline. The Southeast Alaska/Prince William Sound, British Columbia, and Washington groups appeared to be consistently present at low levels.

MtDNA Results

A total of 362 individuals from the 1994 South Unimak June fishery (Period 2) were successfully assayed for fragment analysis of the ND5/ND6 region (Table 6). Two haplotypes (*B* and *C*) previously described by Park et al. (1993) were observed. In addition, a new haplotype (*D*) was observed in two fish. The majority of individuals (85.4%) expressed haplotype *C*; haplotype *B* was found in 14.1% of the individuals. Two major

chum salmon groups are identifiable: a Japanese and a pooled non-Japanese component which includes Russian populations. The estimated Japanese component for the Period 2 1994 (June 21-25) South Unimak June fishery was 0.095. This agrees very closely with the allozyme result of 0.091 for the same collection.

DISCUSSION

The significant genetic diversity among chum salmon populations (Kondzela et al. 1994; Phelps et al. 1994; Seeb et al. 1995; Winans et al. 1994; Wilmot et al. 1994) can be utilized as an accurate stock identification tool. In this study, we apply the MSA approach to the analysis of the South Unimak June fishery, a fishery likely composed of chum salmon originating from both the Asian and North American continents.

A basic requirement of MSA using genetic data is that all major contributing populations are represented in the baseline. To a large extent, this assumption can be met by the extensive genetic information provided in this study and in the recently published literature. We were unable to include the Canadian fall Yukon River populations reported in Wilmot et al. (1994) due to incomplete data, but these will be added in future analyses as data become available. In this study, their contribution must be inferred from the results for the United States fall Yukon populations. However, it should be noted some of these populations (i.e. Teslin and Kluane Rivers) represent a divergent lineage within the Yukon River, possibly of Southeast Alaska origin (Wilmot et al. 1994), and may not be adequately represented by other fall Yukon stocks.

In Asia, we also know that Russian populations may not be adequately surveyed. Key areas that were missing in this baseline are the Amur River and Sakhalin Island. This might explain the result that approximately 5% of each mixture sample contained genotypes not adequately explained by our baseline. Moreover, the Russian samples in the baseline possess the smallest sample sizes and may contain a high sampling error relative to other areas of the

Pacific Rim. New data from Russia are now available from the Amur River and Sakhalin Island (Dr. Richard Wilmot, National Marine Fisheries Service-Auke Bay, Juneau, Alaska, personal communication). However, continued sampling, especially of populations with high escapements, is recommended.

It would be worthwhile to resample hatchery stocks in Japan. Waples (1991) discusses the temporal instability of chinook salmon hatchery allele frequencies which may have ramifications for mixture analyses (see Phelps et al. 1994 and references therein). This trend has not been observed in recent chum salmon population surveys (Phelps et al. 1994; Winans et al. 1994; Seeb et al. 1995), possibly attributable to the large numbers of chum salmon that are used for broodstock (Phelps et al. 1994). However, since Japanese chum salmon are entirely represented in the baseline by hatchery populations, it is important to continue to assess stability of allele frequencies over time.

We took a conservative approach to identifying regional reporting units. Dividing the Northwest Alaska region into smaller groupings may be possible in the future as additional markers are identified. One such marker, *mAAT-2**, may be particularly useful, but was absent for Southeast Alaska, British Columbia, and Washington populations. Other larger regions may also lend themselves to subdivision in different applications. For example, Winans et al. (1994) reported seven identifiable groups of Russian and Japanese populations.

The use of DNA-level analyses (both mitochondrial and nuclear) in MSA of Pacific salmon has been extolled by many authors (Hallerman and Beckmann 1988; Cronin et al. 1993; Park et al. 1993; Taylor et al. 1994). The preponderance of studies published to date have described spawning populations, but have not included actual analyses of mixture

samples. The distribution of mtDNA haplotypes in chum salmon provide an ideal application.

Park et al. (1993) first described the high frequency of the mtDNA ND5/ND6 *B* haplotype from Japanese fish and suggested that this marker could be useful in stock identification studies. They surveyed 798 fish from Japan to Washington and reported that the frequency of *B* averaged 0.80 in Japan, but dropped precipitously in Russian populations to 0.13, and was absent in British Columbia and Washington populations. Cronin et al. (1993) also report data for this marker in a limited survey of 50 individuals originating from Northwest Alaska to Washington. They observed the *B* haplotype in only a single individual from the Yukon River (their C7 haplotype). Forty eight of their 50 individuals (0.96) expressed the C haplotype.

We chose to use the mtDNA marker to provide an independent estimate of the proportion of Japanese chum salmon in the Unimak area fishery during Period 2. Combining the allozyme and mtDNA into a single database was impossible due to the limited mtDNA baseline information. The two independent estimates for Period 2 in 1994 are statistically indistinguishable (0.091 and 0.095 for the allozyme and mtDNA, respectively).

Numerous potential applications of the genetic database exist. Studies of migration routes and timing of Pacific Rim chum salmon are clearly possible. Seeb and Seeb (1986) attempted to utilize MSA to identify the continent of origin of container-loads of chum salmon confiscated by the National Marine Fisheries Service. Their study was based on limited Asian data. Their estimates were likely biased, but they did indicate the presence of North American chum salmon within the samples. Winans et al. (1989) utilized an expanded database to estimate the origin of chum salmon intercepted in highseas drift net fisheries

targeting squid. Future applications include analysis of chum salmon intercepted in the Bering Sea trawl fisheries as the bycatch of chum salmon in this fishery has increased markedly in the last several years.

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Table 1. Genetic sampling for chum salmon from the South Unimak and Shumagin Islands June fisheries, 1993 and 1994, by Alaska Department of Fish and Game. Sampling was conducted at commercial catch processing facilities and by test fishing. The subsamples reported in this study were taken from the commercial catch collections only.

Year	Geographic Area	Catch (N)	Test (N)	Total (N)	Catch Subsample (N)
1993	Southwest Unimak (Cape Lutke)	940	0	940	800 ¹
	Southeast Unimak (Cape Lazaref to Ikatan Bay)	1,682	0	1,682	
	Total 1993	2,622	0	2,622	800
1994	Shumagin Islands	1,940	1,500 ²	3,440	0
	Southwest and Southeast Unimak (Cape Lutke, Cape Lazaref to Ikatan Bay)	2,150	700 ³	2,850	1,200
	Total 1994	4,090	2,200	6,290	1,200
All years	Total	6,712	2,200	8,912	2,000

¹ Both areas were pooled together, and then a subsample was drawn.

² Test fishing dates: June 9, 10, 13, 14

³ Test fishing dates: June 13, 14, 16, 17

Table 2. Daily catch and number of genetic samples collected during 1993 and 1994 South Unimak June fishery. Number of fish subsampled for mixed fishery analysis was proportional to daily catch. Subsampling for 1993 was adjusted for the varying catch rates between Southwest Unimak (L) and Southeast Unimak (U) areas. These areas were not distinguished during 1994 sampling.

Year	Period	Date	Daily Catch	% Total Catch	Genetic Samples	Subsample Goal	Subsample	% Mixture
1993	1	June 13	37,965	13%	319	52	U: 15 L: 37	13%
		June 15	45,075	16%	165	64	U: 64	16%
		June 16	43,503	15%	206	60	U: 60	15%
		June 17	38,717	14%	124	56	U: 21 L: 35	14%
		June 19	51,147	18%	370	72	U: 55 L: 17	18%
		June 20	67,705	24%	404	96	U: 28 L: 68	24%
		Total	284,112	100%	1,588	400	400	100%
		June 22	67,705	75%	509	297	U: 149 L: 148	74%
		June 26	3,313	3%	345	14	U: 14	4%
		June 27	12,674	13%	95	52	U: 52	13%
June 29	8,980	9%	85	37	U: 37	9%		
Total	97,829	100%	1,034	400	400	100%		
1994	1	June 17	46,792	34%	400	136	157	39%
		June 18	24,283	18%	110	72	82	20%
		June 19	47,745	35%	430	140	161	40%
		June 20*	17,957	13%	80	52	0	0%
		Total	136,777	100%	1,020		400	100%
		June 21*	9,983	9%	44	36	0	0%
		June 22	26,376	24%	206	96	112	28%
		June 23	34,438	31%	120	125	120	30%
		June 24	20,153	18%	100	73	85	21%
		June 25	19,482	18%	100	70	83	21%
Total	110,432	100%	570	400	400	100%		
1994	2	June 26	19,058	15%	100	60	100	25%
		June 27	42,525	34%	100	134	100	25%
		June 28	53,844	42%	140	170	140	35%
		June 29	9,549	8%	100	30	50	13%
		June 30*	1,985	2%	120	6	10	3%
		Total	126,961	100%	560	400	400	100%

*Genetic samples collected June 20 and June 21, 1994 were not usable due to improper shipping; tissues were missing from 70 of the samples collected on June 30.

Table 3. Populations used to construct Pacific Rim chum salmon baseline and source of data. Numbers preceding population names correspond to sampling locations in Figure 2. Asterisks following population names from Southeast Alaska, British Columbia*, and Washington stocks indicate these populations are representative of their region.

Reporting Region	Pooled Population	Population	N	Data Source		
NW ALASKA SUMMER	Kotzebue Sound	Noatak River	(1) Sikusuilag Hatchery 1991	100	Seeb et al. 1995	
			(1) Sikusuilag Hatchery 1993	100	Seeb et al. 1995	
			(2) Noatak River 1991	100	Seeb et al. 1995	
			Total Noatak River	300		
		Kelly Lake	(3) Kelly Lake 1991	100	Seeb et al. 1995	
		Salmon River	(4) Salmon River 1991	106	Seeb et al. 1995	
		Norton Sound	Pilgrim River	(5) Pilgrim River 1994	90	Seeb et al. 1995
		Norton Sound		(6) Snake River 1992	47	Seeb et al. 1995
				(6) Snake River 1993	35	Seeb et al. 1995
				(7) Nome River 1991	27	Seeb et al. 1995
				(7) Nome River 1992	13	Seeb et al. 1995
				(7) Nome River 1993	53	Seeb et al. 1995
				(8) Kwiniuk River 1994	100	Seeb et al. 1995
				(9) Fish River 1994	100	Seeb et al. 1995
				(10) Unalakleet River 1992	100	Seeb et al. 1995
				Total Norton Sound:	475	
		Yukon River: Summer Run				
		Chena River	(20) Tanana/Chena River 1992	86	Seeb et al. 1995	
		Salcha River	(21) Tanana/Salcha River 1992	100	Seeb et al. 1995	
		Lower Yukon/Kuskokwim		(11) W. Fk. Andreafsky River 1993	100	Seeb et al. 1995
			(12) E. Fk. Andreafsky River 1993	100	Seeb et al. 1995	
			(13) Innoko River 1993	88	Seeb et al. 1995	
			(14) Anvik/Beaver Creek 1992	100	Seeb et al. 1995	
			(14) Anvik/Beaver Creek 1993	100	Seeb et al. 1995	
			(15) Anvik/Canyon Creek 1993	50	Seeb et al. 1995	
			(16) Anvik/Otter Creek 1992	100	Seeb et al. 1995	
			(17) Anvik/Swift River 1992	100	Seeb et al. 1995	
			(17) Anvik/Swift River 1993	100	Seeb et al. 1995	
			(18) Anvik/Yellow River 1992	100	Seeb et al. 1995	
		(19) Huslia River 1993	100	Seeb et al. 1995		
	Kuskokwim/Goodnews Bay		(27) Kwethluk River 1994	100	Seeb et al. 1995	
			(28) Tulukaak River 1993	100	Seeb et al. 1995	
			(29) Aniak River 1992	100	Seeb et al. 1995	

Table 3. Continued.

Reporting Region	Pooled Population	Population	N	Data Source	
NW ALASKA SUMMER		(30) Kogruluk River 1992	75	Seeb et al. 1995	
		(30) Kogruluk River 1993	50	Seeb et al. 1995	
		(31) Tatlawiksuk River 1994	100	Seeb et al. 1995	
		(32) 4th of July Creek 1994	100	Seeb et al. 1995	
		Total Lower Yukon/Kuskokwim:	1663		
		Kanektok/Goodnews/Togiak Rivers	(33) Kanektok River 1993	39	Seeb et al. 1995
			(34) Goodnews River 1991	100	Seeb et al. 1995
	Bristol Bay		(35) Togiak River 1993	100	Seeb et al. 1995
			(35) Togiak River 1994	100	Seeb et al. 1995
		Total Kanektok/Goodnews/Togiak Rivers:	339		
		Nushagak River	(36) Upper Nushagak River 1992	53	Seeb et al. 1995
			(36) Upper Nushagak River 1993	50	Seeb et al. 1995
			(37) Mulchatna River 1994	100	Seeb et al. 1995
			(38) Stuyahok River 1992	31	Seeb et al. 1995
			(38) Stuyahok River 1993	57	Seeb et al. 1995
		Total Nushagak River:	291		
		Naknek/Alagnak Rivers	(39) Alagnak River 1992	84	Seeb et al. 1995
			(40) Naknek/Big Creek 1993	80	Seeb et al. 1995
		Total Naknek/Alagnak Rivers	164		
		Egegik/Ugashik Bay	(41) Egegik Bay/King Salmon R./Whale Mountain Creek 1993	98	Seeb et al. 1995
			(42) Ugashik Bay/King Salmon R./Pumice Creek 1993	100	Seeb et al. 1995
				198	
		North Alaska Peninsula			
	Meshik River	(43a) Meshik/Plenty Bear Creek 1993	93	Seeb et al. 1995	
		(43b) Meshik/Braided Creek 1992	78	Seeb et al. 1995	
	Total Meshik River:	171			
	Cook Inlet				
	Chunilna Creek	(63) Susitna/Chunilna Creek 1993	87	Seeb et al. 1995	
FALL YUKON	Yukon River: Fall Run				
	Toklat River	(22) Toklat River 1991	60	Seeb et al. 1995	
		(22) Toklat River 1992	155	Seeb et al. 1995	
	Total Toklat River:	215			
		Tanana Fall Run	(23) Tanana River (mainstem) 1992	97	Seeb et al. 1995
			(23) Tanana River (mainstem) 1993	100	Seeb et al. 1995
			(24) Bluff Cabin Slough 1992	100	Seeb et al. 1995
			(25) Delta River 1991	100	Seeb et al. 1995
			(25) Delta River 1992	100	Seeb et al. 1995
		Total Tanana Fall Run:	497		

Table 3. Continued.

Reporting Region	Pooled Population	Population	N	Data Source	
FALL YUKON		(26) Sheenjek River 1992	100	Seeb et al. 1995	
	Sheenjek River	(26) Sheenjek River 1993	64	Seeb et al. 1995	
		Total Sheenjek River:	164		
PENINSULA/KODIAK	North Alaska Peninsula				
	Lawrence Valley Creek	(44) Lawrence Valley Creek 1992	100	Seeb et al. 1995	
	Joshua Green River	(45) Joshua Green River 1992	80	Seeb et al. 1995	
	Frosty/St. Catherine's Cove		(46) Frosty Creek 1992	100	Seeb et al. 1995
			(47) St. Catherine's Cove 1992	80	Seeb et al. 1995
			Total Frosty/St. Catherine's Cove	180	
	Trader's Cove Creek	(48) Traders Cove Creek 1992	100	Seeb et al. 1995	
	Peterson Lagoon	(49) Peterson Lagoon 1992	86	Seeb et al. 1995	
	South Alaska Peninsula				
	Littlejohn/Russell Creek		(50) Little John Lagoon 1992	87	Seeb et al. 1995
			(51) Russell Creek 1993	100	Seeb et al. 1995
			Total Littlejohn/Russell Creek:	187	
	Belkofski/Canoe Bay		(52) Belkofski River 1992	87	Seeb et al. 1995
			(53) Canoe Bay 1992	100	Seeb et al. 1995
			Total Belkofski/Canoe Bay:	187	
	Stepovak River	(54) Stepovak River 1993	100	Seeb et al. 1995	
	Chignik				
	Ivanoff River	(55) Ivanoff River 1993	94	Seeb et al. 1995	
	Chiginagak/Mainland	(56) Chiginagak River 1993	75	Seeb et al. 1995	
	Mainland District		(57) Wide Bay/Kilagvik River 1993	100	Seeb et al. 1995
		(58) Algogshak River 1993	95	Seeb et al. 1995	
		Total Chiginagak/Mainland	270		
Big River	(59) Hallo Bay/Big River 1993	100	Seeb et al. 1995		
Kodiak					
Big Sukhoi Creek	(60) Sukhoi Lagoon/Big Sukhoi Creek 1992	100	Seeb et al. 1995		
Sturgeon River	(61) Sturgeon Lagoon/Sturgeon River 1992	71	Seeb et al. 1995		
Kizhuyak River	(62) Kizhuyak River 1992	88	Seeb et al. 1995		

Table 3. Continued.

Reporting Region	Pooled Population	Population	N	Data Source
SE ALASKA/PWS	Prince William Sound			
	WHN Hatchery	(64) WHN Hatchery 1992	92	Seeb et al. 1995
	Lynn Canal			
	Herman Creek	(65) Herman Creek 1987	100	Kondzela et al. 1994
		(65) Herman Creek 1990	59	Kondzela et al. 1994
		Total Herman Creek:	159	
	Southeast Alaska			
		(66) Fish Creek 1986*	100	Kondzela et al. 1994
		(66) Fish Creek 1987*	50	Kondzela et al. 1994
		(66) Fish Creek 1988 (early)*	100	Kondzela et al. 1994
		(66) Fish Creek 1988 (late)*	52	Kondzela et al. 1994
		(66) Tombstone River 1986	98	Kondzela et al. 1994
		(66) Marten River 1986	105	Kondzela et al. 1994
		(67) Keta River 1986*	101	Kondzela et al. 1994
		(67) Blossom River 1986	101	Kondzela et al. 1994
		(67) Wilson River 1986	103	Kondzela et al. 1994
		(68) Harding River 1986*	95	Kondzela et al. 1994
		Total Southeast Alaska:	905	
	Prince of Whales Island			
	Port Real Marina	(69) Port Real Marina 1986*	100	Kondzela et al. 1994
		(69) Port Real Marina 1988*	48	Kondzela et al. 1994
		Total Port Real Marina:	148	
	Eastern Prince of Whales Island			
	(70) Kugel Creek 1986	104	Kondzela et al. 1994	
	(70) Disappearance Creek 1986*	100	Kondzela et al. 1994	
	(70) Disappearance Creek 1988*	100	Kondzela et al. 1994	
	(70) Lagoon Creek 1986	102	Kondzela et al. 1994	
	(70) Old Tom Creek 1986	100	Kondzela et al. 1994	
	(70) Old Tom Creek 1988	53	Kondzela et al. 1994	
	(70) Cabin Creek 1986	103	Kondzela et al. 1994	
	Total Eastern Prince of Whales Island:	662		
BRITISH COLUMBIA	British Columbia			
	Eastern Queen Charlotte Islands			
		(71) Pallant Creek 1988*	100	Kondzela et al. 1994
		(71) Lagoon Creek 1989	83	Kondzela et al. 1994
		(71) Sedgewick Creek 1989	74	Kondzela et al. 1994
		(71) Bag Harbor Creek 1989	89	Kondzela et al. 1994
		(71) Surprise Creek 1989	85	Kondzela et al. 1994
		Total Eastern Queen Charlotte Islands	431	
	Nass River Area			
		(72) Kshwan River 1988	88	Kondzela et al. 1994
		(72) Kitsault River 1988	95	Kondzela et al. 1994
	(72) Stago Creek 1988*	75	Kondzela et al. 1994	
	(72) Stago Creek 1989*	53	Kondzela et al. 1994	

Table 3. Continued.

Reporting Region	Pooled Population	Population	N	Data Source	
BRITISH COLUMBIA		Total Nass River Area	311		
	Kitimat/Mussel River	(73) Kitimat River 1988*	92	Kondzela et al. 1994	
		(73) Kitimat River 1989*	100	Kondzela et al. 1994	
		(73) Mussel River 1989	100	Kondzela et al. 1994	
		Total Kitimat/Mussel River:	292		
	Nekite Channel/River	(74) Nekite Channel 1989	100	Kondzela et al. 1994	
		(74) Nekite River 1989	97	Kondzela et al. 1994	
		Total Nekite Channel/River	197		
	East Vancouver Island	(75) Puntledge Hatchery	100	Phelps et al. 1994	
		(75) Big Qualicum Hatchery*	200	Phelps et al. 1994	
		(75) Little Qualicum	100	Phelps et al. 1994	
		(75) Nanaimo River	100	Phelps et al. 1994	
		(75) Chemainus River	100	Phelps et al. 1994	
		(75) Cowichan River	100	Phelps et al. 1994	
		(75) Goldstream River	100	Phelps et al. 1994	
	Total E. Vancouver Island:	800			
	West Vancouver Island	(76) Nitinat River and Hatchery*	380	Phelps et al. 1994	
		(76) Nahmint River	100	Phelps et al. 1994	
		(76) Sarita River	127	Phelps et al. 1994	
		Total W. Vancouver Island:	607		
Lower Fraser River	(77) Alouette River	100	Phelps et al. 1994		
	(77) Stave River	100	Phelps et al. 1994		
	(77) Chilliwack - Vedder Hatchery	100	Phelps et al. 1994		
	(77) Chehalis Hatchery*	100	Phelps et al. 1994		
	Total Lower Fraser River	400			
Upper Fraser River	(78) Chehalis at Harrison Hatchery*	100	Phelps et al. 1994		
	(78) Weaver River	100	Phelps et al. 1994		
	(78) Harrison River	100	Phelps et al. 1994		
	(78) Squakum Creek	100	Phelps et al. 1994		
	(78) Wahleach Creek	100	Phelps et al. 1994		
	Total Upper Fraser River	500			
WASHINGTON	Puget Sound				
		Skagit River	(79) Illabot Creek	98	Phelps et al. 1994
			(79) Dan Creek*	153	Phelps et al. 1994
	Total Skagit River:	251			
	Bellingham Maritime Hatchery	(80) Bellingham Maritime Hatchery	100	Phelps et al. 1994	
	Mill Creek	(81) Mill Creek	179	Phelps et al. 1994	

Table 3. Continued.

Reporting Region	Pooled Population	Population	N	Data Source
WASHINGTON	Hood Canal Hatchery	(82) Hood Canal Hatchery	450	Phelps et al. 1994
JAPAN	Honshu			
	Gakko/Miomote Rivers	(83) Gakko River 1989 (84) Miomote River 1989 Total Gakko/Miomote Rivers	39 100 139	Winans et al. 1994 Winans et al. 1994
	Tsugaruishi River	(85) Tsugaruishi River 1989	100	Winans et al. 1994
	Ohkawa River	(86) Ohkawa River 1989	100	Winans et al. 1994
	Hokkaido			
	Teshio River	(87) Teshio River 1987	97	Winans et al. 1994
	Chitose River	(88) Chitose River 1989 (88) Chitose River 1990 Total Chitose River:	100 80 180	Winans et al. 1994 Winans et al. 1994
	Tokachi River	(89) Tokachi River 1989 (89) Tokachi River 1990 Total Tokachi River	100 80 180	Winans et al. 1994 Winans et al. 1994
	Kushiro River	(90) Kushiro River 1989	100	Winans et al. 1994
	Nishibetsu River	(91) Nishibetsu River 1989	100	Winans et al. 1994
	Shari River	(92) Shari River 1989	100	Winans et al. 1994
	Tokusibetsu River	(93) Tokushibetsu River 1994	42	Winans et al. 1994
RUSSIA	Northern Russia			
	Anadyr/Kanchalan Rivers	(94) Anadyr River 1991 (94) Anadyr River 1991 (95) Kanchalan River 1991 Total Anadyr/Kanchalan Rivers:	104 80 79 263	Winans et al. 1994 Wilmot et al. 1994 Wilmot et al. 1994
	Korf Bay	(96) Korf Bay 1991	18	Winans et al. 1994
	Kamchatka Peninsula			
	Nerpichi Lake	(97) Nerpichi Lake	40	Winans et al. 1994
	Kamchatka River	(98) Kamchatka River 1990 (98) Kamchatka River 1991 Total Kamchatka River:	80 40 120	Winans et al. 1994 Winans et al. 1994
	Utka River	(99) Utka River 1991	79	Winans et al. 1994

Table 3. Continued.

Reporting Region	Pooled Population	Population	N	Data Source	
RUSSIA	Kikchik River	(100) Kikchik River 1991	40	Winans et al. 1994	
	Pymta River	(101) Pymta River 1990	80	Winans et al. 1994	
		(101) Pymta River 1991	79	Winans et al. 1994	
		Total Pymta River	159		
	Kol River	(102) Kol River 1990	93	Winans et al. 1994	
	Hairusova River	(103) Hairusova River 1990	154	Winans et al. 1994	
	Southern Russia				
	Tumani River	(104) Tumani River 1991	66	Winans et al. 1994	
	Ola River	(105) Ola River 1990	80	Winans et al. 1994	
		(105) Ola River 1991	80	Winans et al. 1994	
Total Ola River:		160			

*Klownik River was selected as a representative stock. Due to missing loci, this population was not included. The next most southerly population, Nekite River, was used instead. The closest population to the north of Klownik River was a representative stock.

Table 4. Mean estimated contribution for 100 simulations where each region comprises 100% of the mixture (N=400)¹. Shaded cells are correct allocations and should equal 1.000.

Estimated Region	100% Simulation							
	Japan	Russia	NW Alaska Summer	Fall Yukon	Peninsula/Kodiak	SE Alaska/PWS	British Columbia	Washington
Japan	0.966	0.007	0.009	0.001	0.006	0.003	0.002	0.000
Russia	0.007	0.924	0.015	0.001	0.016	0.014	0.007	0.000
NW Alaska Summer	0.015	0.031	0.944	0.035	0.007	0.004	0.001	0.000
Fall Yukon	0.002	0.002	0.027	0.962	0.000	0.001	0.000	0.000
Peninsula/Kodiak	0.007	0.025	0.004	0.001	0.949	0.058	0.021	0.002
SE Alaska/PWS	0.002	0.005	0.000	0.000	0.009	0.831	0.052	0.004
British Columbia	0.001	0.005	0.001	0.000	0.011	0.075	0.869	0.042
Washington	0.000	0.001	0.000	0.000	0.002	0.013	0.046	0.951
Total	1.000	1.000	1.000	1.000	1.000	0.999	0.998	0.999

¹Mean estimates not summing to 1.000 are caused by randomly generated genotypes that cannot be explained by a randomly generated baseline.

Table 5. Estimated contributions of Pacific Rim chum salmon to the South Unimak June fishery in 1993 and 1994. Standard deviations were computed by a parametric bootstrap.

Year	Sample	Date	N	Japan		Russia		Northwest Alaska Summer		Fall Yukon	
				Estimate	S.D.	Estimate	S.D.	Estimate	S.D.	Estimate	S.D.
1993	1	June 13-20	399	0.169	0.046	0.057	0.072	0.621	0.101	0.000	0.011
	2	June 22 -29	398	0.147	0.043	0.066	0.074	0.569	0.101	0.009	0.007
1994	1	June 17-20	395	0.131	0.041	0.189	0.065	0.515	0.091	0.000	0.001
	2	June 21-25	396	0.091	0.031	0.064	0.086	0.721	0.104	0.000	0.000
	3	June 26-30	398	0.157	0.039	0.152	0.071	0.544	0.076	0.021	0.016

Year	Sample	Date	N	Alaska Peninsula to Kodiak		Prince William Sd and SE Alaska		British Columbia		Washington		Unknown
				Estimate	S.D.	Estimate	S.D.	Estimate	S.D.	Estimate	S.D.	
1993	1	June 13-20	399	0.042	0.028	0.064	0.048	0.035	0.018	0.009	0.010	0.003
	2	June 22 -29	398	0.133	0.046	0.045	0.022	0.031	0.013	0.000	0.007	0.000
1994	1	June 17-20	395	0.075	0.045	0.025	0.013	0.040	0.023	0.022	0.017	0.003
	2	June 21-25	396	0.104	0.050	0.017	0.006	0.002	0.007	0.000	0.006	0.000
	3	June 26-30	398	0.053	0.044	0.039	0.006	0.030	0.021	0.000	0.005	0.005

Table 6. Haplotype frequencies of *AseI* polymorphisms from the ND5/ND6 region of chum salmon mtDNA. a. Results from chum salmon sampled in the 1994 South Unimak June fishery. Fragment lengths in base pairs are given. b. Frequencies from spawning populations are from Park et al. (1993). Results from the South Unimak, Period 2, 1994 fishery are shown. Estimated Japanese component from allozyme data are from Table 5.

a.

Haplotype	Fragment Size (BP)	Observed (N)	Haplotype Frequency
A	1400, 1000		0.000
B	900, 750, 500, 250	51	0.141
C	1400, 750, 250	309	0.854
D	1650, 750	2	0.005
Total		362	1.000

b.

Source	N	Haplotype Frequencies		Estimated Japanese Component	
		A,C,D	B	mtDNA	Allozyme
Spawning populations					
Japan	254	0.20	0.80		
Other					
Russia	153	0.87	0.13		
NW Alaska	132	0.93	0.07		
British Columbia, Washington	259	1.00	0.00		
Mean (other)	544	0.93	0.07		
Fishery sampling					
Unimak, 1994-Period 2	365	0.86	0.14	0.095	0.091

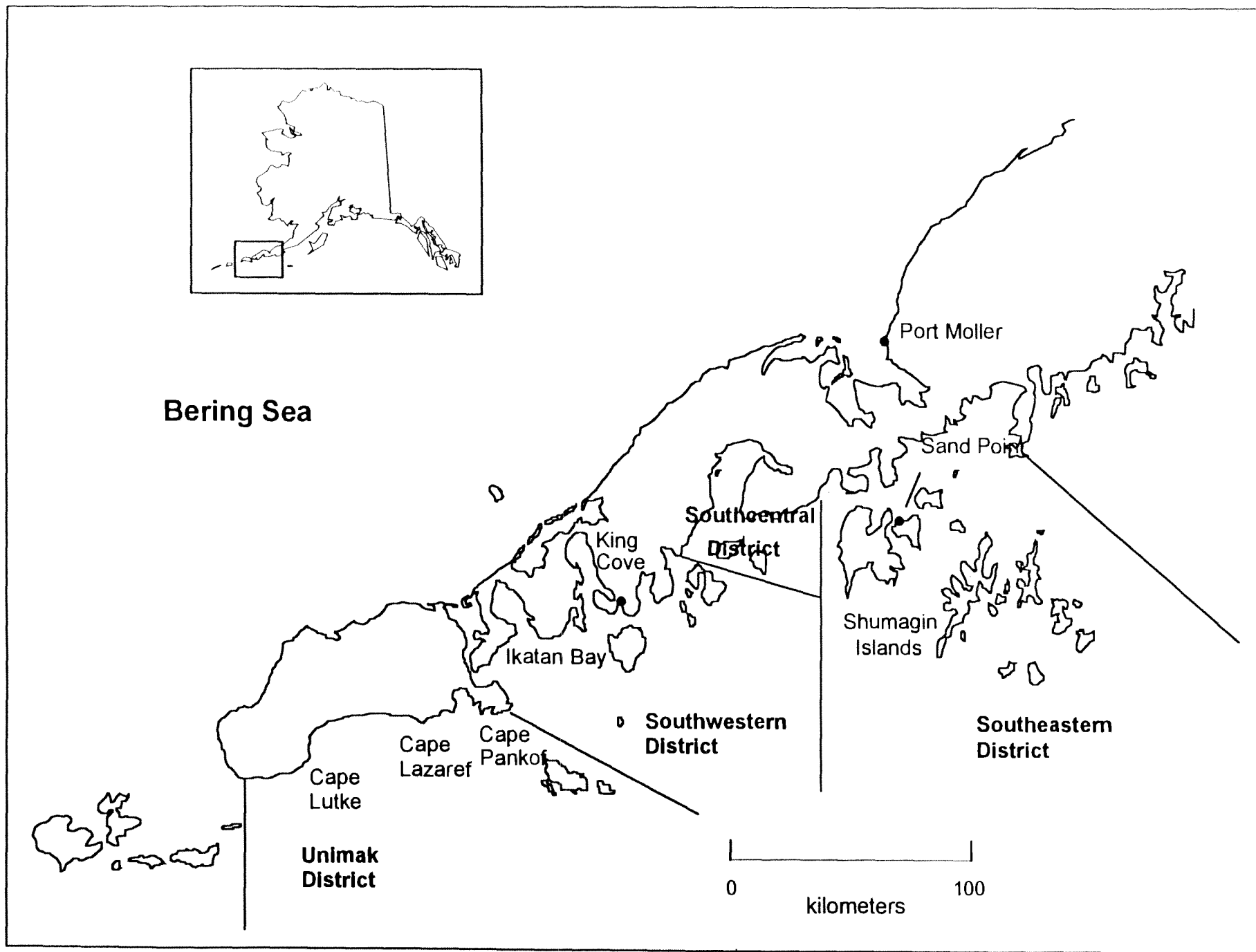


Figure 1. Map of south Alaska Peninsula fishery management districts.

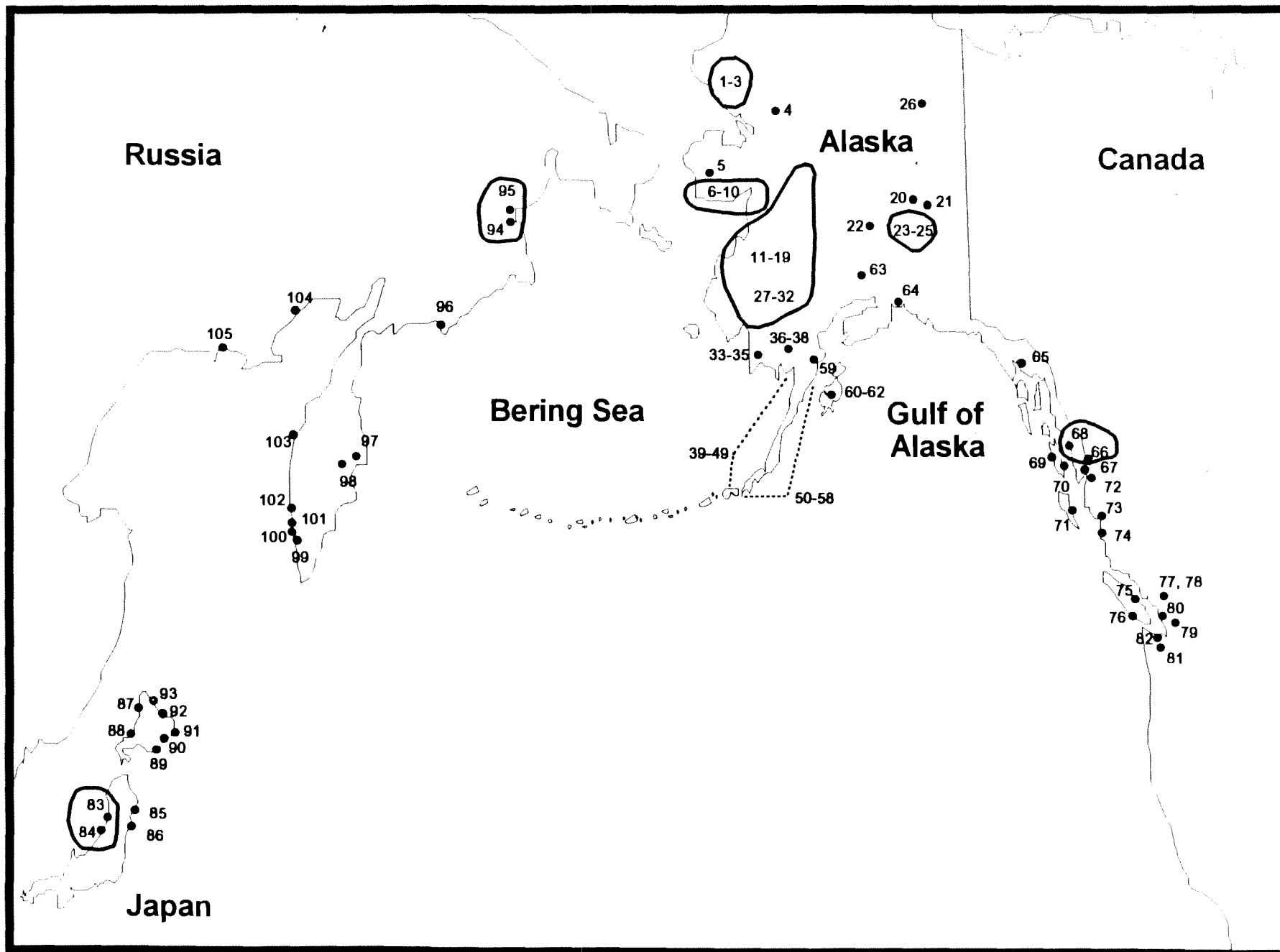


Figure 2. Sampling locations of chum salmon populations included in Pacific Rim baseline. Population numbers correspond to numbers in Table 3.

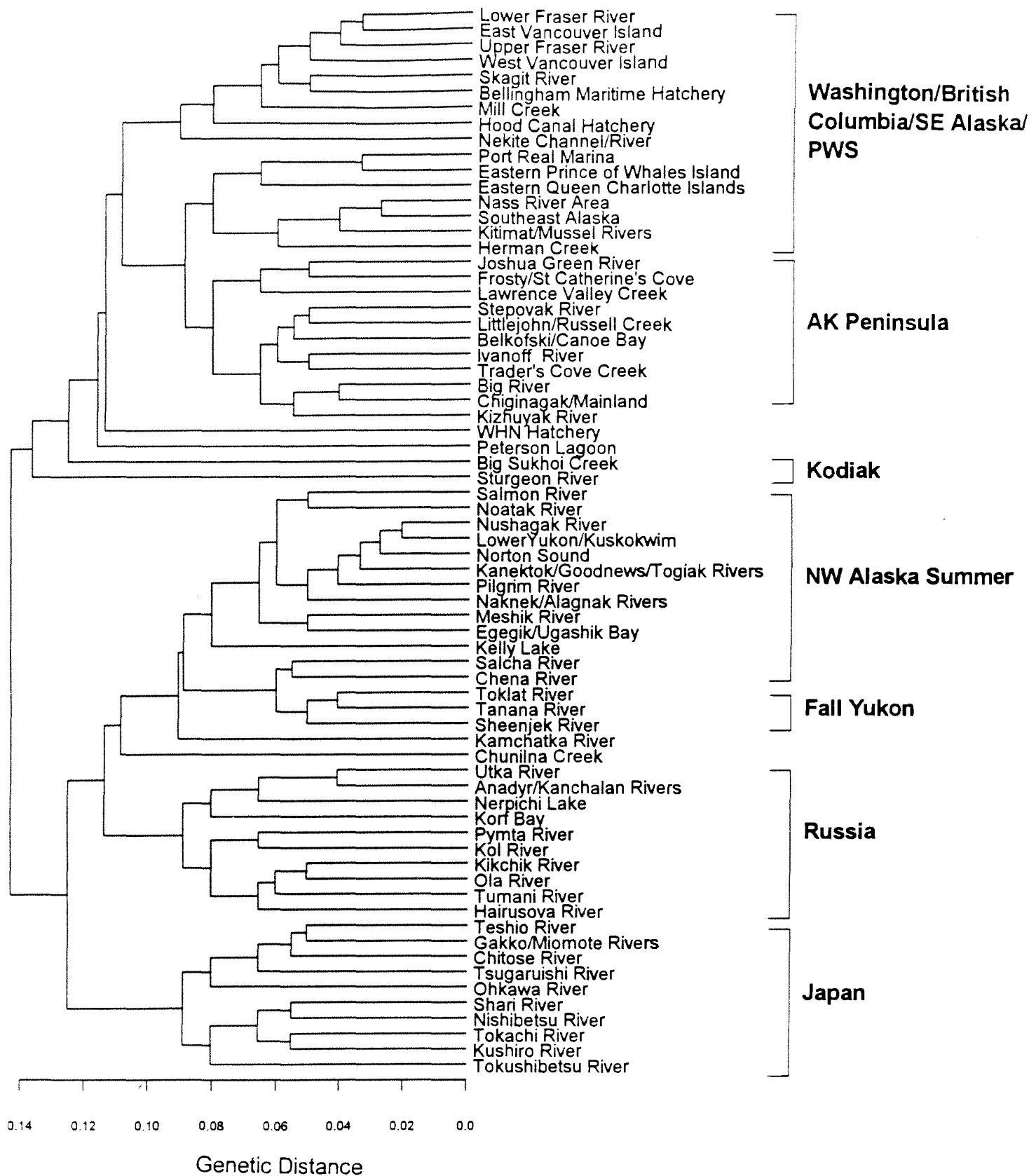


Figure 3. UPGMA phenogram showing genetic relationships among stock groupings of chum salmon around the Pacific Rim. Cavalli-Sforza and Edwards distances (1967) used to construct the tree are calculated from allele frequencies of the 20 loci used in the mixture model.



Figure 4. Multidimensional scaling plot of Pacific Rim chum salmon. Japan, Russia, NW Alaska Summer, and Fall Yukon chum salmon are clearly defined groups.

Chum Salmon Contributions South Unimak Fishery

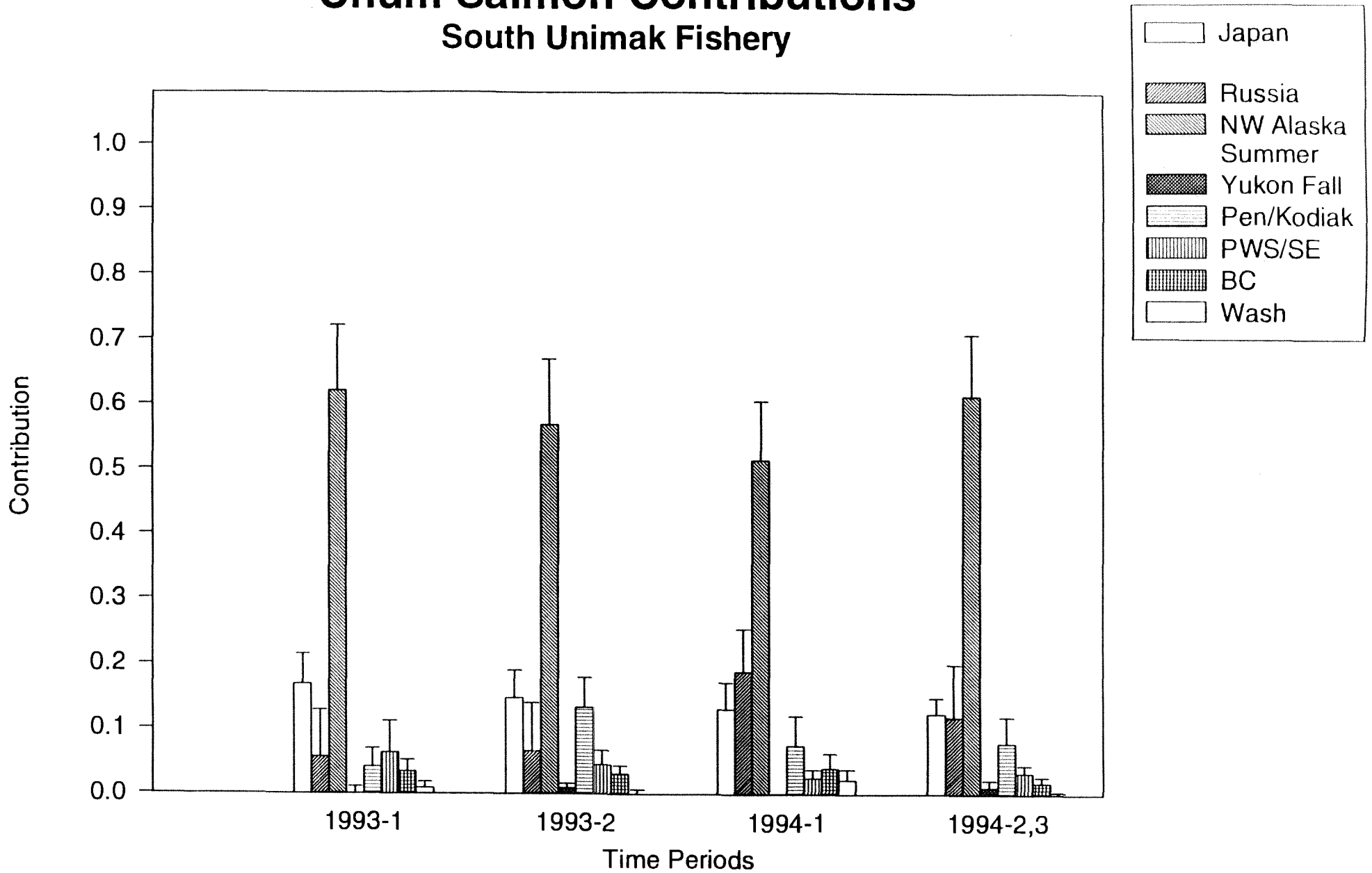


Figure 5. Estimated regional contributions of chum salmon to the South Unimak June fishery, 1993-1994. Standard errors are shown.