

The Origins of Chum Salmon Bycatch in the 1994 Bering Sea Trawl Fishery for Walleye Pollock Determined by Genetic Stock Identification

by Richard Wilmot

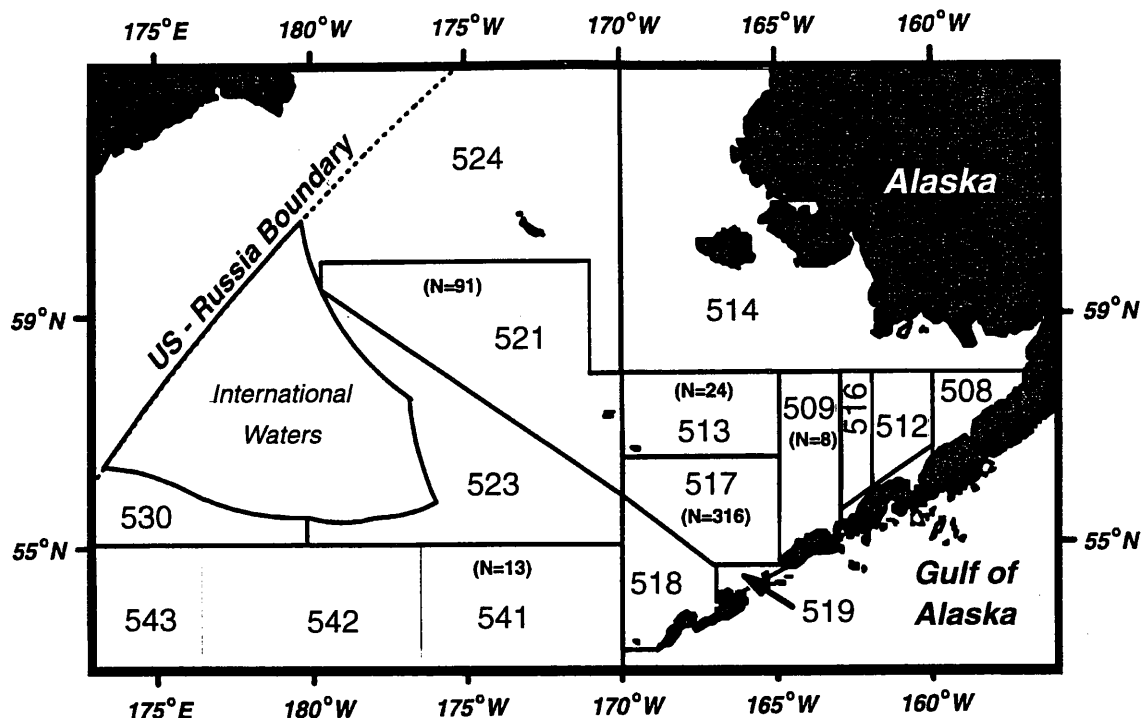


Figure 1. Statistical areas for the Bering Sea trawl fishery for walleye pollock. Sample sizes (N) taken from each area are listed in bold type.

INTRODUCTION

The Bering Sea trawl fishery for walleye pollock, *Theragra chalcogramma*, has incidentally harvested large numbers (200,000 in 1993) of chum salmon, *Oncorhynchus keta*, in recent years. The fishery takes place north of the Alaska Peninsula (Fig. 1) from January to March (the "A" fishery) and from late August to mid-October (the "B" fishery), with the majority of the incidental harvest (or bycatch) of chum salmon taken in the B fishery. This bycatch became a concern to western Alaska subsistence fishermen and the Alaska Department of Fish and Game (ADF&G) when spawning escapements of chum salmon in western Alaska rivers

declined below historic levels during the early 1990s. The stock origins of the chum salmon bycatch in the Bering Sea trawl fishery were viewed as potentially important elements in investigating the declining numbers of the western Alaska stocks and in determining whether the Bering Sea trawl fishery affected the decline.

Chum salmon have the widest natural distribution of all salmon species in the North Pacific Ocean. Tagging studies have shown that many stocks of chum salmon originating in Asia and North America migrate through the eastern Bering Sea; tagging studies, however, are not reliable for estimating the contributions of specific stocks to mixed-stock

fisheries such as the Bering Sea trawl fishery. Genetic stock identification (GSI) is a method for estimating stock composition in mixed-stock fisheries that has been used on the west coast of North America since the 1980s. The method relies on identifying genetic differences among stocks in the relative frequencies of protein-coding genes detected by allozyme electrophoresis. The preferred statistical methodology for computing the stock composition is conditional maximum likelihood.

In 1994, the National Marine Fisheries Service (NMFS) Auke Bay Laboratory (ABL) initiated a study to determine the feasibility of using GSI to estimate regional stock

contributions to the chum salmon bycatch taken in the 1994 Bering Sea B-season trawl fishery. One of the major questions to be addressed during the first year of the study was to determine if tissue samples of sufficient quantity and quality for allozyme analysis could be collected by the NMFS Fisheries Observer Program. Although the feasibility study was not conducted to obtain samples that were statistically valid representatives of the total chum bycatch, we believe the results of GSI of the bycatch samples are statistically valid for segments of the total bycatch with an adequate sample size ($N > 200$). Essentially, results of the ABL study in 1994 show that, given an adequate sample size that represents the total bycatch, we can determine areas of origin with great accuracy for the total bycatch.

MATERIALS AND METHODS

Baseline Data

Before GSI could be applied to the bycatch of chum salmon in the Bering Sea trawl fishery, a genetic baseline from potentially contributing chum salmon stocks was needed. The genetic data for the ABL analysis included a 69-population baseline constructed by the ADF&G for estimating contributions of chum salmon stocks from major regions to incidental catches in the South Unimak, Alaska, sockeye salmon fishery. Major geographic regions were Japan; Russia; western Alaska (summer run); Yukon River (fall run); Alaska Peninsula/Kodiak/Chignik; Prince William Sound (PWS)/Southeast Alaska; British Columbia; and Washington. The ABL study added 8 new populations, 2 from China and 6 from Russia, to the 69 populations to form a 77-population baseline. Data on 20 genetic loci common

to each population were available.

The collections from China came from the Heilong (Amur) River and the Suifen River and were collected in 1994 by personnel from the Heilongjiang Fisheries Research Institute, Chinese Academy of Fisheries Science, Harbin, People's Republic of China. The Heilong River is the Chinese portion of the Russian Amur River. The Suifen River flows south out of China and enters the Pacific Ocean just south of Vladivostok, Russia. The baseline collections from Russia were taken by personnel from the Institute of Marine Biology, Far East Branch of the Russian Academy of Science in Vladivostok. Three of the collections are from the southern end of Sakhalin Island (Naiba, Udarnitsa, and Kalininka Rivers), and three are from the Premor'ye region near Vladivostok (Avakumovka, Narva, and Ryzanovka Rivers). Tissue samples (eye, heart, liver, and muscle) were taken during 1994 from each fish and were frozen and delivered to the ABL for electrophoretic analysis.

Bycatch Sampling

Personnel from the Fisheries Observer Program collected chum salmon bycatch samples from the Bering Sea B fishery from 29 August to 8 October 1994. As mentioned previously, sampling protocol was designed to determine the feasibility of obtaining high quality samples through the Observer Program. Whole heads were removed so that muscle tissue, heart, and liver remained with the head. Heads were packaged individually with catch information and were frozen and shipped to the ABL. Tissue samples from the heads where taken, placed in individual tubes, and frozen at -80°C until electrophoretic

analysis could be conducted. Electrophoretic analysis followed standard procedure, using the genetic nomenclature of the American Fisheries Society.

Statistical Procedures

The genetic structure of the baseline populations was described by calculating Cavalli-Sforza and Edwards chord distance among all 77 populations and then constructing a dendrogram using the Unweighted Pair-Group Method with arithmetic averages (UP-GMA).

A total of 457 chum salmon were sampled from five North Pacific Fisheries Management Council statistical areas in the Bering Sea (Figs. 1 and 2): Areas 509 ($N=8$), 513 ($N=24$), 517 ($N=316$), 521 ($N=91$), and 541 ($N=13$). Five immature fish were received with unreadable tags and could not be assigned by area or time strata. They were, however, used in the pooled and immature/mature analyses. Of the 457 samples, 410 were from immature fish, and 47 were from maturing fish that were expected to spawn in fall 1994. Maturity was determined by the size of the fish and the condition of gonads. Four kinds of stock composition comparisons were performed: immaturity vs. maturity; eastern vs. western fishing area; sampling time periods; and sampling statistical areas. Only areas 517 and 521 had sufficient numbers of samples for independent analysis. Areas 521 and 541 were pooled ($N=104$) and areas 517, 509, and 513 were pooled ($N=348$) for an east/west comparison. We stratified the samples by three time periods: 29 August to 5 September ($N=319$), 6-9 September ($N=51$), and 11 September to 8 October ($N=82$). The distribution of the catch over time makes the choice of time periods for analysis difficult. The

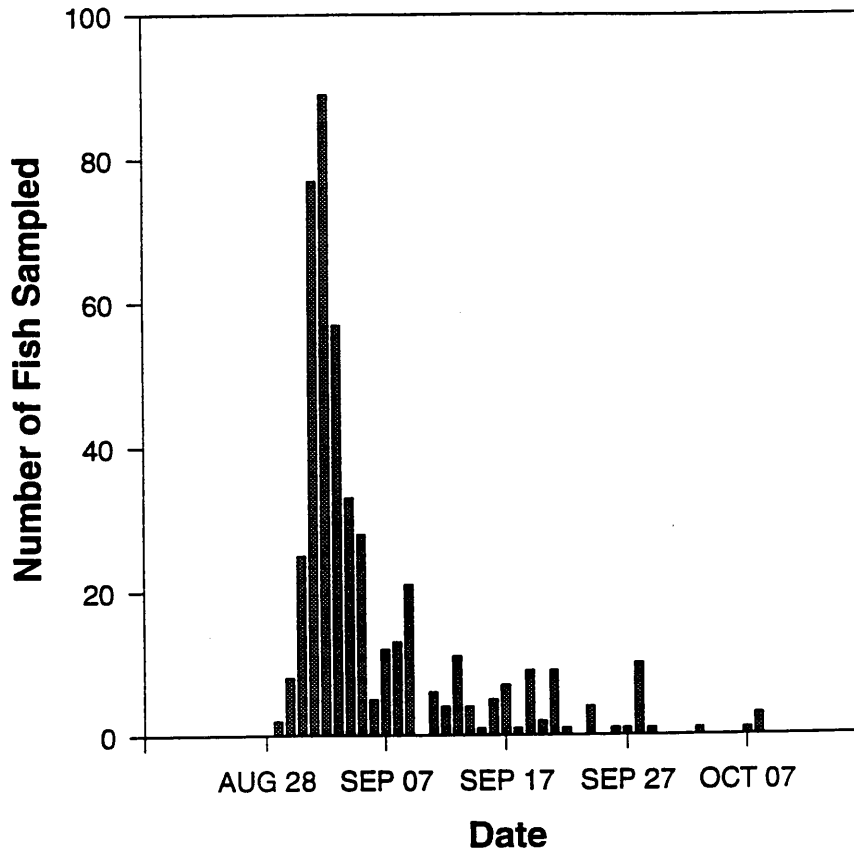


Figure 2. Number of chum salmon sampled by the NMFS Observer Program from the 1994 Bering Sea trawl B season from 29 August to 8 October.

majority of the catch is taken in the first time period. After the first week of September the catch numbers decline substantially (Fig. 2).

Conditional maximum likelihood estimates (MLE) of stock composition of the mixed fishery samples were calculated using the genotypic iteratively reweighted least squares (GIRLS) program. Standard errors of stock composition estimates were determined by 500 bootstrap resamplings of baseline and mixture samples. We conducted simulation studies to evaluate the reliability of stock composition estimates. Mixture samples composed of 100% of stocks from a given region in equal proportions were simulated from baseline allele frequencies. These hypothetical mixtures of

known composition were generated assuming Hardy-Weinberg equilibrium. The GIRLS program calculated the MLE of stock composition for each simulated sample, and the average MLEs of regional composition were compared with the true contribution. One further test to determine accuracy of composition estimates involved additions of incremental numbers of simulated fish from a region to a real mixture sample to determine how accurately the average composition estimates could track the changing composition of the altered sample. Genotypes of the added fish were generated from the baseline in the same manner as described for the simulation studies.

RESULTS

Baseline Data

The addition of the 8 new populations from China and Russia to the UPGMA dendrogram (Fig. 3) had little effect on the basic geographic structure displayed in the ADF&G dendrogram constructed for the original 69 populations of Pacific Rim chum salmon. The populations from Sakhalin Island and Premor'ye clustered with the Japanese stocks. A group of outlier observations from Wallace H. Noerenberg (WHN) Hatchery, PWS; Peterson Lagoon, Alaska Peninsula; and Big Sukhoi Creek and Sturgeon River from Kodiak was shown in the ADF&G study. Two of the eight additional populations joined these outliers: the Heilong (Amur) River from China

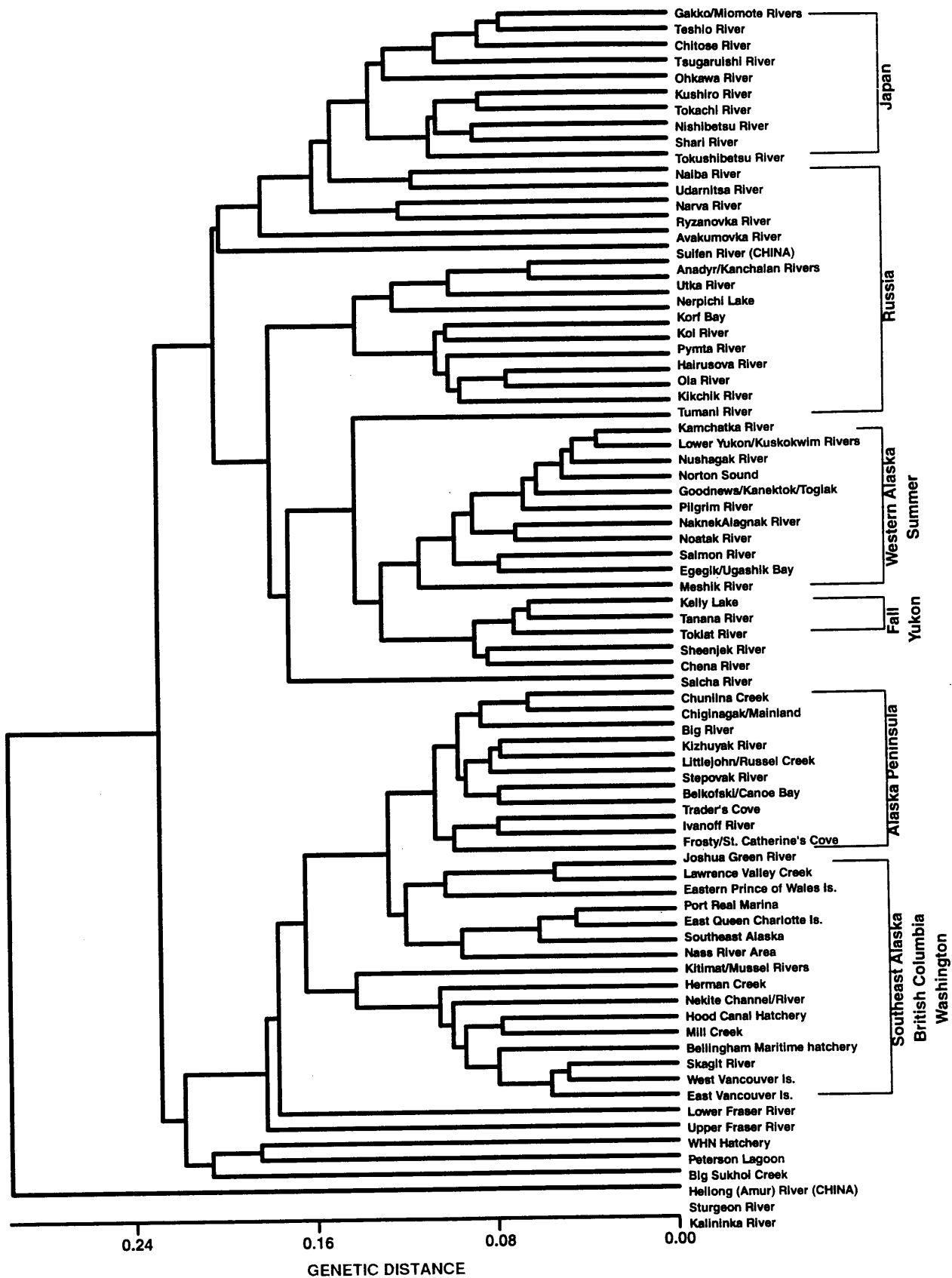


Figure 3. UPGMA clustering of Cavalli-Sforza and Edwards (1967) chord distance among 77 populations of Pacific Rim chum salmon.

and the Kalininka River from Sakhalin Island.

Mixture Analysis

We formed the same regional stock groups as the ADF&G used for the South Unimak fishery (Japan, Russia, western Alaska (summer run), Yukon River (fall run), Alaska Peninsula/Kodiak/Chignik, Southeast Alaska/PWS, British Columbia, and Washington). In simulation studies where the true regional contributions were 100%, the MLE average estimates were more than 80% accurate. Estimates for the Southeast Alaska/PWS region were least accurate (82%), and the estimate for the Yukon River fall run the most accurate (96%) (Table 1).

Estimates of the origins of immature and maturing fish were substantially different (Table 2). The Asian component (Japan and Russia) of the immature fish group was estimated at 51% compared to 32% of the mature group; the western Alaska component (including western Alaska summer run, Yukon River fall run, and Alaska Peninsula/Kodiak/Chignik) of the immature group was an estimated 29% compared to 12% of the mature group; and the Southeast Alaska/PWS/British Columbia/Washington state component of the immature group was 20% compared to 56% of the mature group. British Columbia origin fish were estimated to comprise 53% of the 56%.

In comparing the three sampling periods, the composition of fish sampled during the first period (29 August to 5 September) was approximately 44% Asian stocks, 35% western Alaska stocks, and 21% Southeast Alaska/PWS/British Columbia/Washington stocks. During the second time period (6 September to 9 September) the

composition of fish sampled was 39% Asian stocks, 32% western Alaska stocks, and 28% Southeast Alaska/PWS/British Columbia/Washington stocks. In the third period (11 September to 8 October) the percentage of Asian stocks increased to 55%, the percentage of western Alaska stocks declined to 20%, and the percentage of Southeast Alaska/PWS/British Columbia/Washington stocks stayed relatively constant at 24%.

Area 517 consisted of 43% Asian, 28% western Alaska, and 30% Southeast Alaska/PWS/British Columbia/Washington stocks. Area 521 consisted of 58% Asian, 30% western Alaska, and 12% Southeast Alaska/PWS/British Columbia/Washington stocks. Areas 509, 513, and 517 were combined to form an eastern Bering Sea group that is located close to the Alaska Peninsula and the mouth of Bristol Bay. This group consisted of 42% Asian, 29% western Alaska, and 27% Southeast Alaska/PWS/British Columbia/Washington stocks. Areas 521 and 541 were combined to form a western Bering Sea group that consisted of 66% Asian, 23% western Alaska, and 11% Southeast Alaska/PWS/British Columbia/Washington stocks. The pooled sample (N=457) consisted of 47% Asian, 29% western Alaska and 24% Southeast Alaska/PWS/British Columbia/Washington stocks.

The MLEs accurately tracked known additions to an actual mixture sample (Fig. 4). We used the maturing fish mixture sample (Table 2) because the MLEs indicated a high percentage of British Columbia fish. We added known numbers of simulated British Columbia fish to the observed mixture sample (equivalent to altering British Columbia percentages

from 53% to 88%) and known numbers of simulated Washington fish (equivalent to altering the percentage of British Columbia fish from 53% to 16%). We then plotted the estimated proportion against the known, altered proportion. Average MLEs were within 1% of the true proportions when British Columbia fish were added, and within 5% when Washington fish were added.

DISCUSSION

The significant geographical differentiation in gene frequencies among Pacific Rim chum salmon populations makes accurate stock identification at the regional level feasible as a management tool. The addition of 8 new populations to the baseline had little effect on the population geographic structure shown in the ADF&G study of 69 chum salmon populations. As expected, six of the new populations clustered between the Japanese and northerly Russian populations; Sakhalin Island and Premor'ye are located near Japan and represent an area where summer-run chum salmon typical of northern Russia overlap with fall-run chum salmon typical of Japan. Two of the eight stocks were outliers: Kalininka River on Sakhalin Island and the Heilong (Amur) River. According to Dr. Vladimir Efremov, Institute of Marine Biology, Far East Branch Russian Academy of Sciences, Vladivostok, Kalininka chum salmon are now the result of hatchery operations that probably substantially changed gene frequencies from those of the original, wild stock. The samples from the Heilong River came from a spawning area nearly 1,000 km upstream from the river mouth. The genetic differences of these fish may be analogous to the situation in the Yukon River where

Table 1. Mean estimated proportion for 500 simulations where each region comprises 100% of the mixture (N=300). Cells in bold are the correct allocations and should equal 1.0000.

Estimated Region	100% Simulations							
	Japan	Russia	NW Alaska	Fall Yukon	Peninsula/Kodiak/Chignik	SE Alaska/PWS	British Columbia	Washington
Japan	0.9446	0.0337	0.0082	0.0010	0.0056	0.0032	0.0017	0.0002
Russia	0.0266	0.8921	0.0265	0.0031	0.0254	0.0237	0.0107	0.0023
NW Alaska	0.0143	0.0376	0.9205	0.0374	0.0062	0.0052	0.0017	0.0001
Fall Yukon	0.0035	0.0023	0.0368	0.9573	0.0013	0.0011	0.0005	0.0000
Peninsula/Kodiak/Chignik	0.0080	0.0242	0.0066	0.0007	0.9348	0.0533	0.0255	0.0020
SE Alaska/PWS	0.0014	0.0048	0.0006	0.0002	0.0122	0.8211	0.0575	0.0033
British Columbia	0.0011	0.0043	0.0004	0.0002	0.0123	0.0748	0.8517	0.0522
Washington	0.0004	0.0009	0.0002	0.0001	0.0022	0.0176	0.0506	0.9399

Table 2.—Estimated regional proportions of Pacific Rim chum salmon in the 1994 Bering Sea Trawl Fishery. Standard deviations were calculated from 500 bootstraps of the mixture and baseline samples.

Sample	N	Japan		Russia		Western Alaska		Fall Yukon	
		Estimate	S.D.	Estimate	S.D.	Estimate	S.D.	Estimate	S.D.
Immature	410	0.2593	0.0361	0.2485	0.0453	0.2260	0.0502	0.0301	0.0279
Maturing	47	0.3245	0.0932	0.0000	0.0450	0.0630	0.0518	0.0567	0.0546
Aug 29 - Sep 05	319	0.2545	0.0403	0.1806	0.0452	0.2617	0.0526	0.0192	0.0257
Sep 06 - Sep 09	51	0.1511	0.0767	0.2428	0.1082	0.2648	0.1035	0.0251	0.0658
Sep 11 - Oct 08	82	0.3092	0.0754	0.2452	0.0830	0.0929	0.0738	0.1104	0.0522
Area 517	316	0.2421	0.0403	0.1844	0.0491	0.2358	0.0487	0.0146	0.0250
Area 521	91	0.3668	0.0807	0.2101	0.0769	0.2258	0.0862	0.0472	0.0486
Areas 521/541	104	0.4021	0.0710	0.2597	0.0768	0.1686	0.0791	0.0393	0.0412
Areas 509/513/517	348	0.2324	0.0376	0.1882	0.0452	0.2224	0.0521	0.0372	0.0300
Pooled	457	0.2670	0.0343	0.2022	0.0406	0.2227	0.0486	0.0357	0.0276

Sample	N	Alaska Peninsula/ Kodiak/Chignik		Southeast AK/PWS		British Columbia		Washington	
		Estimate	S.D.	Estimate	S.D.	Estimate	S.D.	Estimate	S.D.
Immature	410	0.0322	0.0255	0.0545	0.0320	0.1034	0.0362	0.0462	0.0288
Maturing	47	0.0000	0.0247	0.0000	0.0044	0.5324	0.1369	0.0234	0.1084
Aug 29 - Sep 05	319	0.0717	0.0328	0.0212	0.0317	0.1671	0.0413	0.0240	0.0294
Sep 06 - Sep 09	51	0.0312	0.0695	0.0538	0.0722	0.1179	0.0895	0.1132	0.0700
Sep 11 - Oct 08	82	0.0000	0.0195	0.0000	0.0344	0.1051	0.0579	0.1373	0.0618
Area 517	316	0.0277	0.0288	0.0594	0.0381	0.1601	0.0503	0.0759	0.0446
Area 521	91	0.0265	0.0365	0.0006	0.0245	0.1079	0.0444	0.0151	0.0185
Areas 521/541	104	0.0207	0.0308	0.0012	0.0220	0.0960	0.0387	0.0124	0.0167
Areas 509/513/517	348	0.0268	0.0267	0.0547	0.0364	0.1502	0.0489	0.0880	0.0447
Pooled	457	0.0303	0.0237	0.0428	0.0289	0.1438	0.0377	0.0555	0.0313

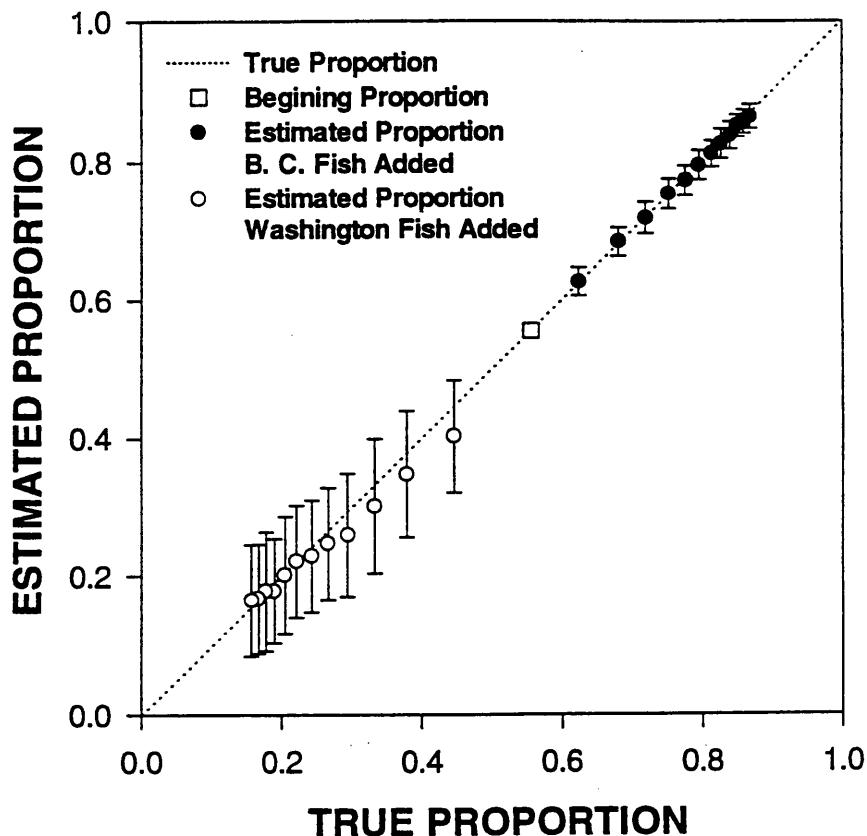


Figure 4. Results of simulation tests to determine the accuracy of the MLE to follow additions of known numbers of British Columbia fish to an actual mixture sample. The 45° dotted line represents 100% accuracy and the black circles represent the calculated proportion when British Columbia fish are added, and the open circles represent the calculated proportion when Washington fish are added. Error bars are one standard deviation derived from 100 bootstrap resamplings.

upriver spawners differ substantially from lower river spawners.

Regional compositions of the 1994 Bering Sea chum salmon bycatch samples differ substantially from those found by the ADF&G for the chum salmon bycatch in the South Unimak sockeye salmon fishery in 1993 and 1994. The ADF&G study found western Alaska (including fall-run Yukon River and Peninsula/Kodiak/Chignik) stocks dominated the catch from a low of 59% to a high of 83%; Asian stocks comprised 15%-32%, and Southeast Alaska/PWS/British Columbia/Washington stocks comprised 2%-11%. In contrast, our samples consisted of 20%-35% western Alaska stocks, 42%-58%

Asian stocks, and 11%-30% (excluding the maturing fish) Southeast Alaska/PWS/British Columbia/Washington stocks. The large contribution (53%, S.E.=14%) of British Columbia stocks to the maturing fish group was unexpected. Given the small mixture sample size (N=47), these results should be regarded cautiously. However, the simulation studies showed that the contribution of the British Columbia stock group could be reliably estimated when the mixture sample size was increased so composition was altered.

The differences in composition between the South Unimak fishery and the Bering Sea trawl fishery could be the result of both

seasonal timing and geography. The South Unimak fishery takes place in June, south of the Alaska Peninsula. The Bering Sea B fishery takes place from late August to early October, north of the Alaska Peninsula when most western Alaska chum salmon spawners would be in the rivers.

Tagging information supports the presence of British Columbia fish in the area of the Bering Sea trawl fishery. Four coded-wire tagged fish from British Columbia have been caught in this fishery since 1986, and estimated annual returns to southern British Columbia over the last few years have exceeded 5 million per year according to the 1994 Pacific Salmon Commission Joint Chum Techni-

cal Committee Report. The large percentage of maturing fish estimated to be from British Columbia would have to travel approximately 3,000 km to their spawning rivers. The migration speed of chum salmon in the ocean is calculated to be about 40 km/day, increasing the closer the fish get to their spawning rivers. Many of the British Columbia chum salmon spawn in November and December. These fish would have sufficient time to migrate from the Bering Sea in August and September to their spawning rivers in southern British Columbia in November and December (approximately 75 days).

The results presented in this preliminary study show that the collection methods used by the NMFS Observer Program can provide high quality samples suitable for allozyme and GSI analysis. Sampling procedures were not designed to obtain representative collections of the 1994 B season chum salmon bycatch, and the results may not be a valid reflection of the true stock contributions to the total catch. Sampling in the 1995 B season was designed to obtain samples representative of the total chum salmon bycatch.

CONCLUSIONS

The quality of the samples obtained by the 1994 Observer Program from the Bering Sea trawl fishery was outstanding, and the same methods should be used in the future. However, sampling effort was minimal and was not designed to be representative of the total chum salmon bycatch. Only area 517, time period one (29 August to 5 September), and the immature group had sample sizes (without pooling) greater than

200. Simulation studies conducted by the Washington Department of Fish and Wildlife (WDFW) of the Columbia River spring chinook salmon baseline recommended a mixture sample size of at least 180 individuals. Other WDFW studies on the chinook salmon baseline covering from California to southern British Columbia and mixed fishery samples from the Washington coast and Strait of Juan de Fuca troll fisheries show that for stocks which contribute at rates of 5%-6% or greater, fishery samples of 200 fish are probably sufficient; stocks or stock groupings that contribute 2% or less to the fishery require sample sizes of 800 fish or more. Sampling for the ABL study in 1995 took into consideration this requirement on sample size and attempted to collect samples in a manner that is representative of the total chum salmon bycatch.

The genetic divergence among stocks of Pacific Rim chum salmon is very high, particularly among major regions (i.e., Japan, Russia, western Alaska, Southeast Alaska, British Columbia, and Washington). This gives us a high degree of confidence in composition estimates based on these major regions. Below the regional level, estimates must be viewed very cautiously. The fall run of chum salmon into the Yukon River is an exception because of their substantial genetic separation.

The complete Pacific Rim chum salmon baseline, developed since the 1980s by cooperating international, state, and Federal agencies, currently contains data for nearly 200 chum salmon populations, with data common to 20 loci in 190 populations. Members of the ABL have conducted preliminary studies on the Bering Sea

trawl chum salmon bycatch samples using this 190-population baseline. The increase from the 77-population baseline used in this recent analysis comes from additional populations from Southeast Alaska, British Columbia, and Washington State. This expanded baseline has little effect on composition estimates for the Asian and western Alaska stocks of the mixture samples. It does, however, affect the composition distribution among Southeast Alaska, British Columbia, and Washington State. In the majority of the samples, the MLEs for British Columbia stocks decline, and the MLEs for Southeast Alaska and Washington State stocks increase. Because this expanded baseline contains a preponderance of stocks from southern British Columbia and Washington State, there is concern that the results could be skewed towards those two regions. Substantial simulation studies will be necessary to determine whether this bias exists in the 190-population baseline.

Analysis of the 1995 chum salmon bycatch is under way. Both the quality and quantity of samples are excellent. In fact, based on preliminary catch figures, we have a sample size of nearly 10% of the total chum salmon bycatch. This should allow us to make an accurate estimate of the origins by major region.

This article is based on a report titled "Preliminary Results on the Origin of Chum Salmon Harvested Incidentally in the 1994 Bering Sea Trawl Fishery Determined by Genetic Stock Identification" by Richard Wilmot, Christime Kondzela, Charles Guthrie, and Michele Masuda of the Auke Bay Laboratory.