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**PRELIMINARY RESULTS ON THE ORIGIN OF CHUM
SALMON HARVESTED INCIDENTALLY IN THE 1994 BERING
SEA TRAWL FISHERY DETERMINED BY GENETIC STOCK
IDENTIFICATION**

by

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PRELIMINARY RESULTS ON THE ORIGIN OF CHUM SALMON HARVESTED INCIDENTALLY IN THE 1994 BERING SEA TRAWL FISHERY DETERMINED BY GENETIC STOCK IDENTIFICATION

ABSTRACT

The Bering Sea trawl fishery in some years incidentally harvests large numbers of chum salmon, and is commonly referred to as bycatch. Due to declining spawning escapements of chum salmon to some Western Alaska areas, the stock origins of the chum salmon bycatch was seen as important to an evaluation of this fishery's effect on those stocks. Tagging studies have shown that chum salmon originating from throughout Asia and North America migrate through the eastern Bering Sea. A method for estimating stock composition in mixed-stock fisheries, referred to as genetic stock identification (GSI), has been used on the west coast of North America to evaluate stock contributions to salmon fisheries. Cooperative efforts between state and Federal agencies have led to the development of a comprehensive genetic baseline for Pacific Rim chum salmon stocks that allows GSI to be used to assess the stock contributions to fisheries such as the Bering Sea trawl fishery.

In 1994, the National Marine Fisheries Service, Auke Bay Laboratory, initiated a feasibility study on the use of GSI to determine the stock origins of the Bering Sea trawl fishery chum salmon bycatch. The objective of this first year of study was to determine whether the existing Observer program could provide tissue samples from the bycatch of sufficient quantity and quality for genetic analysis. The study was not designed to provide statistically valid samples of the total chum salmon bycatch.

Results from this first year determined that the Observer program can provide high quality samples for genetic analysis, and with proper sampling design, can provide enough samples to represent the total chum salmon bycatch. Stock composition estimates for the 1994 fishery samples we obtained were comprised of from 42% to 58% Asian stocks, from 20% to 35% Western Alaska stocks, and from 11% to 30% Southeast Alaska/British Columbia/Washington stocks. One small sample (N=47) of maturing fish showed a surprisingly large contribution of British Columbia stocks (53%).

Efforts are underway to obtain statistically valid sample sizes from the 1995 fishery that will truly represent the total chum salmon bycatch. We are also investigating the use of a larger genetic baseline (190 populations versus 77 populations) that may give more accurate composition estimates among Southeast Alaska, British Columbia, and Washington stocks.

INTRODUCTION

The Bering Sea trawl fishery for walleye pollock (*Theragra chalcogramma*) in some years incidentally harvests large numbers of chum salmon (*Oncorhynchus keta*). The incidental catch is commonly referred to as "bycatch." 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). The majority of chum salmon bycatch is taken in the "B" fishery. The incidental harvest of chum salmon became of concern when spawning escapements of chum salmon to several Western Alaska areas declined below historic levels (Eggers 1995), and the stock origins of the bycatch were seen as important to an evaluation of this fishery's effect on those stocks. The term stock and population will be used interchangeably and refers to "fish spawning in a particular lake or stream (or portion of) at a particular season, which fish to a substantial degree do not interbreed with any group spawning in a different place, or in the same place at a different season" (Ricker 1972, p. 28).

Tagging studies have shown that chum salmon originating from throughout Asia and North America migrate through the eastern Bering Sea (Aro et al. 1971; Aro 1972; Brannian 1984; Eggers et al. 1991; Eggers 1992; Meyer 1983). Although tagging studies demonstrated the presence of many stocks in the fishery, estimates of the contributions of these stocks from tagging would be unreliable given the level of tagging and the disproportionate tag recovery effort.

A method for estimating stock composition in mixed-stock fisheries, referred to as genetic stock identification (GSI), was developed in the 1970's, and has been used on the west coast of North America to evaluate stock contributions to salmon fisheries (Utter et al. 1974; Wishard 1980; Grant 1980; Okazaki 1981; Milner et al. 1981; Seeb et al. 1986; Seeb et al. 1990; Winans et al. 1989; Shaklee et al. 1990; Wilmot et al. 1992; Seeb et al. 1995). The method relies on genetic differences among stocks in relative frequencies of protein-coding genes detected by allozyme electrophoresis. The preferred statistical methodology for computing the stock composition is conditional maximum likelihood (Milner et al. 1981; Fournier et al. 1984; Millar 1987; Pella and Milner 1987; Smouse et al. 1990; Pella et al. 1994). GSI provides a means for assessing the stock composition of the Bering Sea trawl fishery bycatch of chum salmon.

Before GSI could be applied to the Bering Sea trawl fishery bycatch of Pacific Rim chum salmon, a genetic baseline from potentially contributing chum salmon stocks was needed. This database is now available due to cooperation between various state and Federal agencies (Kondzela et al. 1995; Phelps et al. 1995; Seeb et al. 1995; Wilmot et al. 1995; Winans et al. 1995). This database contains information for more than 200 populations of chum salmon throughout the Pacific Rim. Some collections have data on more than 60 loci. However, data for the complete range of chum salmon is currently limited to 20 loci. Previous studies found good geographical differentiation of allozyme frequencies among

chum salmon stocks that should provide good estimations of regional contributions to mixed stock fisheries. Seeb et al. (1995) recently estimated contributions from chum salmon stocks of major regions (Japan, Russia, Western Alaska, Fall Yukon, Alaska Peninsula/Kodiak/Chignik, Prince William Sound/Southeast Alaska, British Columbia, and Washington) to incidental catches in the South Unimak, Alaska, sockeye salmon fishery.

In 1994, the National Marine Fisheries Service (NMFS), Auke Bay Laboratory (ABL) was assigned the task of determining the feasibility of using GSI to estimate the regional stock contributions to samples from the chum salmon bycatch taken in the 1994 Bering Sea "B" season trawl fishery. One of the major questions to be addressed this first year was to determine if tissue samples of sufficient quantity and quality for allozyme analysis could be collected by the existing NMFS Observer Program. The study was not designed to obtain samples that were statistically valid representatives of the total chum bycatch.

MATERIALS AND METHODS

Baseline Data

The baseline in this analysis included the 69 population baseline constructed by ADF&G (Seeb et al. 1995) from data provided by various agencies: National Marine Fisheries Service (Kondzela et al. 1995; Winans et al. 1995); Washington Department of Fish and Wildlife (Phelps et al. 1995); and the U.S. Fish and Wildlife Service (Wilmot et al. 1995). In addition, eight new populations from two new areas in Asia, two from China and six from Russia were added, for a 77 population baseline. Twenty loci were available for each population. The rationale behind the construction of the Pacific Rim chum salmon baseline is thoroughly discussed in Seeb et al. (1995).

The baseline collections from China came from the Heilong (Amur) River and the Suifen River and were collected 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 name for their 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 from each fish, frozen and delivered to ABL for electrophoretic analysis.

Bycatch Sampling

Chum salmon bycatch samples from the Bering Sea "B" fishery were collected by personnel of the NMFS Observer Program. Sampling protocol this first year was not designed to provide a representative sample of the total chum salmon bycatch, but 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. The heads were packaged individually with catch information, frozen, and shipped to ABL. Tissue samples from the heads were taken, placed in individual tubes and frozen at -80°C until electrophoretic analysis.

Electrophoretic analysis followed procedures described by Aebersold et al. (1987) and Harris and Hopkins (1976), and we used the genetic nomenclature of the American Fisheries Society (Shaklee et al. 1990). A total of 62 loci was resolved, of which 20 are usable in the current Pacific Rim baseline. Details for standardizing allele mobility and allele pooling can be found in Seeb et al. (1995).

Statistical Procedures

The genetic structure of the baseline populations was described by calculating Cavalli-Sforza and Edwards (1967) chord distance among all 77 populations, and then constructing a dendrogram using the Unweighted Pair-Group Method with arithmetic averages (UPGMA) (Sneath and Sokal 1973).

A total of 457 chum salmon were sampled in 1994 from August 29 to October 8 (Fig. 1, Fig. 2) from five statistical areas in the Bering Sea [Areas 509 (N=8), 513 (N=24), 517 (N=316), 521 (N=91), and 541 (N=13)]. Of the 457 samples, 410 were from immature fish, and 47 were from maturing fish that were expected to spawn in the fall of 1994. Maturity was determined by the size of the fish and the condition of gonads. Four kinds of stock composition comparisons were performed: mature versus immature; east/west; time periods; and specific 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: August 29 to September 5 (N=319), September 6 to September 9 (N=51), and September 11 to October 8 (N=82).

Conditional maximum likelihood estimates (MLE) of stock composition of the mixed fishery samples were calculated using the GIRLS program of Masuda et al. (1991). Standard errors of stock composition estimates were determined by 500 bootstrap resamplings of baseline and mixture samples (Efron and Tibshirani 1986).

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 MLE's of regional composition were compared with the true contribution.

One further test to determine accuracy of composition estimates comprised 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 eight new populations from China and Russia to the UPGMA dendrogram (Fig. 3) had little effect on the basic geographic structure displayed in the dendrogram in Seeb et al. (1995). The populations from Sakhalin Island and Premor'ye clustered with the Japanese stocks. A group of outlier observations from Wallace H. Noerenberg (WHN) Hatchery, Prince William Sound; Peterson Lagoon, Alaska Peninsula; and Big Sukhoi Creek and Sturgeon River from Kodiak was shown in Seeb et al. (1995). Two of the eight additional populations joined these outliers: the Heilong (Amur) River from China and the Kalininka River from Sakhalin Island.

Mixture Analysis

We formed the same regional stock groups for reporting estimates as ADF&G used for the South Unimak fishery (Seeb et al. 1995). They were: Japan, Russia, Western Alaska (summer run), Yukon River (fall run), Alaska Peninsula/Kodiak/Chignik; Southeast Alaska/Prince William Sound, British Columbia, and Washington. In simulation studies where the true regional contributions were 100%, the MLE average estimates were >80% accurate. Estimates for the Southeast Alaska/Prince William Sound 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) in the immature fish group was estimated at 51% versus 32% in the maturing fish group; Western Alaskan component (including Western Alaska summer run, fall Yukon and Alaska Peninsula/Kodiak/Chignik) contributed 29% versus 12%; and the Southeast Alaska/Prince William Sound (PWS)/British Columbia/Washington State component, 20% versus 56%. British

Columbia origin fish were estimated to comprise 53% of the 56%.

Of the three time periods, the first period (August 29 to September 5) consisted of approximately 44% Asian component, 35% Western Alaska component, and 21% Southeast Alaska/PWS/British Columbia/Washington component. The second time period (September 6 to September 9) consisted of a 39% Asian component, 32% Western Alaskan component, and 28% Southeast Alaska/PWS/British Columbia/Washington component. Later in the season (September 11 to October 8) the percentage of the Asia component increased to 55%, the Western Alaskan component declined to 20%, and the Southeast Alaska/PWS/British Columbia/Washington component stayed relatively constant at 24%.

Area 517 consisted of 43% Asian, 28% Western Alaskan, and 30% Southeast Alaska/PWS/British Columbia/Washington components. Area 521 consisted of 58% Asian, 30% Western Alaskan, and 12% Southeast Alaska/PWS/British Columbia/Washington components. 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 Alaskan, and 27% Southeast Alaska/PWS/British Columbia/Washington components. Areas 521 and 541 were combined to form a western Bering Sea group that consisted of 66% Asian, 23% Western Alaskan, and 11% Southeast Alaska/PWS/British Columbia/Washington components. The pooled sample (N=457) consisted of 47% Asian, 29% Western Alaskan and 24% Southeast Alaska/PWS/British Columbia/Washington components.

The MLE's accurately tracked known additions to an actual mixture sample (Fig. 4). We used the maturing fish mixture sample (Table 2) since the MLE estimates 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 MLE's 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 among Pacific Rim chum salmon makes accurate stock identification at the regional level feasible as a management tool. This genetic differentiation has been amply described by Kondzela et al. (1995), Phelps et al. (1995), Wilmot et al. (1995), Winans et al. (1995), and summarized in Seeb et al. (1995). The addition of eight new populations to the baseline had little effect on the population

geographic structure shown in Seeb et al. (1995) for 69 populations. As expected, six of these 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 and the Heilong (Amur) River. According to our Russian source (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 started with a very small number of fish resulting in a "bottleneck" that probably changed gene frequencies substantially from that of the original wild stock. The samples from the Heilong River came from a spawning area nearly 1000 km upstream from the mouth. The genetic differences of these fish may be analogous to the situation in the Yukon River where upriver spawners differ substantially from lower river spawners (Wilmot et al. 1995).

Regional compositions of these Bering Sea chum salmon samples differ substantially from that found by Seeb et al. (1995) for the chum salmon bycatch in the South Unimak sockeye salmon fishery in 1993 and 1994. They 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 from 15% to 32%, and Southeast Alaska/PWS/British Columbia/Washington stocks comprised from 2% to 11%. In contrast, our samples consisted of 20% to 35% Western Alaskan stocks, from 42% to 58% Asian stocks, and from 11% to 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. The simulation studies showed, however, 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 trawl 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 (Dahlberg et al. 1994), and estimated annual returns to southern British Columbia over the last few years has exceeded five million per year (Pacific Salmon Commission Joint Chum Technical Committee Report 1994). The large percentage of maturing fish estimated to be from British Columbia would have to travel approximately 3000 km to their spawning rivers. Hartt (1966) has estimated migration speeds of chum salmon in the ocean at about 40 km/day, and that this rate increases the

closer they 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 will attempt to obtain samples that will be representative of the total chum salmon bycatch.

CONCLUSIONS

1. The genetic divergence among stocks of Pacific Rim chum salmon is very high, particularly among major regions (i.e. Japan, Russian, 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.
2. Sampling in the 1994 fishery were minimal and not designed to be representative samples of the total chum salmon bycatch, but designed to provide samples for a feasibility study. It would therefore, not be valid to extrapolate our results to the total bycatch. Only area 517, time period one (August 29 to September 05), and the immature group had sample sizes (without pooling) greater than 200. We have not conducted studies to determine how large the mixture sample size should be for statistically valid results. However, Shaklee (1991) in studies of the Columbia River spring chinook salmon baseline recommends a mixture sample size of at least 180 individuals. Marlowe and Busack (1995) conducted 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. Their results showed 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 requires sample sizes of 800 fish or more. Sampling in 1995 will take into consideration this requirement on sample size and attempt to collect samples in a manner that will be representative of the total chum salmon bycatch.
3. The complete Pacific Rim chum salmon baseline contains data for nearly 200 populations. We have conducted preliminary studies on the Bering Sea trawl chum salmon bycatch samples using a 190 population baseline. The increase from the 77

population baseline used in the current 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 components of the mixture samples. It does, however, effect the composition distribution among Southeast Alaska, British Columbia, and Washington State. In the majority of the samples, the MLE's for British Columbia decline and increase for Southeast Alaska and Washington State. We will be conducting further investigations into using this expanded baseline.

4. 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.

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

Estimated Region	100% Simulations							
	Japan	Russia	Western Alaska (Summer run)	Fall Yukon	Peninsula/Kodiak/Chignik	SE Alaska/PWS	British Columbia	Washington
Japan	0.9440	0.0337	0.0082	0.0010	0.0056	0.0032	0.0017	0.0002
Russia	0.0266	0.9215	0.0265	0.0031	0.0254	0.0237	0.0107	0.0023
Western Alaska (Summer run)	0.0143	0.0376	0.9200	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	0.9219	0.0533	0.0255	0.0020
SE Alaska/PWS	0.0014	0.0048	0.0006	0.0002	0.0122	0.9210	0.0575	0.0033
British Columbia	0.0011	0.0043	0.0004	0.0002	0.0123	0.0748	0.9572	0.0522
Washington	0.0004	0.0009	0.0002	0.0001	0.0022	0.0176	0.0506	0.9396

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 06	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 508/513/517	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

STATISTICAL REPORTING AREAS OF THE BERING SEA/ALEUTIAN ISLANDS

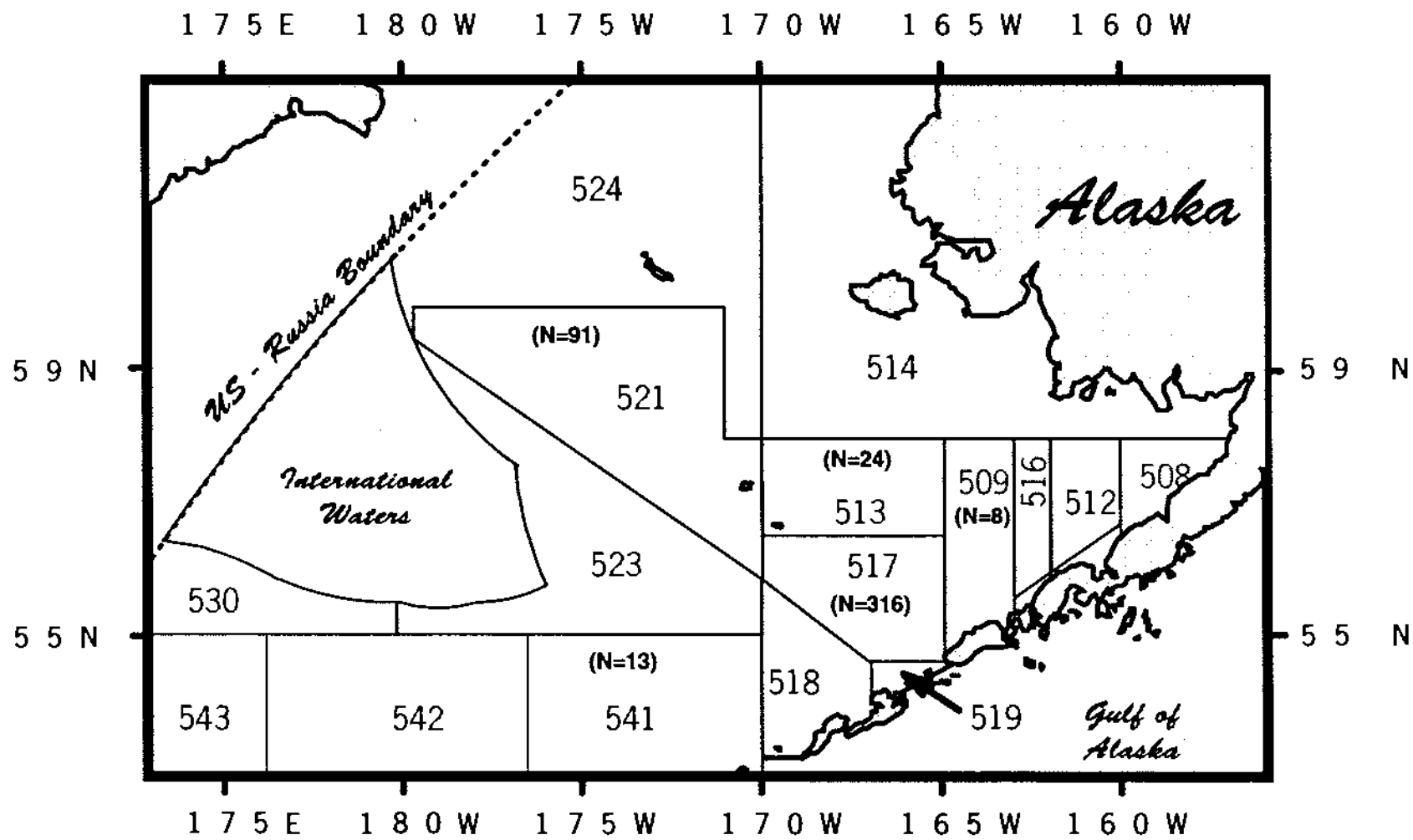


Figure 1.--Statistical areas for the Bering Sea trawl fishery. Sample sizes (N) taken from each area are listed in bold type.

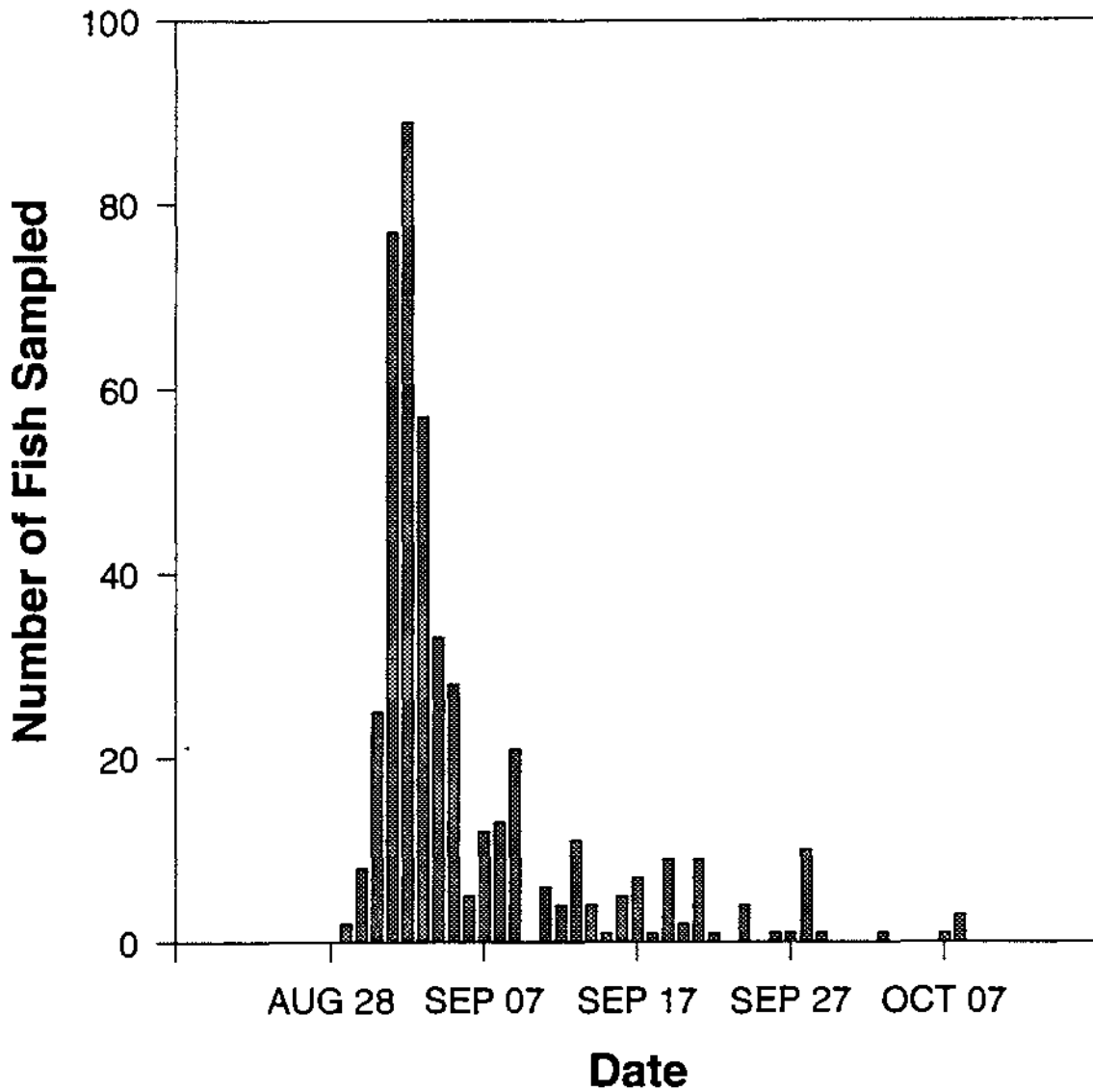


Figure 2.--Number of chum salmon sampled by the NMFS Observer program from the 1994 Bering Sea trawl "B" season by day, August 29 to October 8.

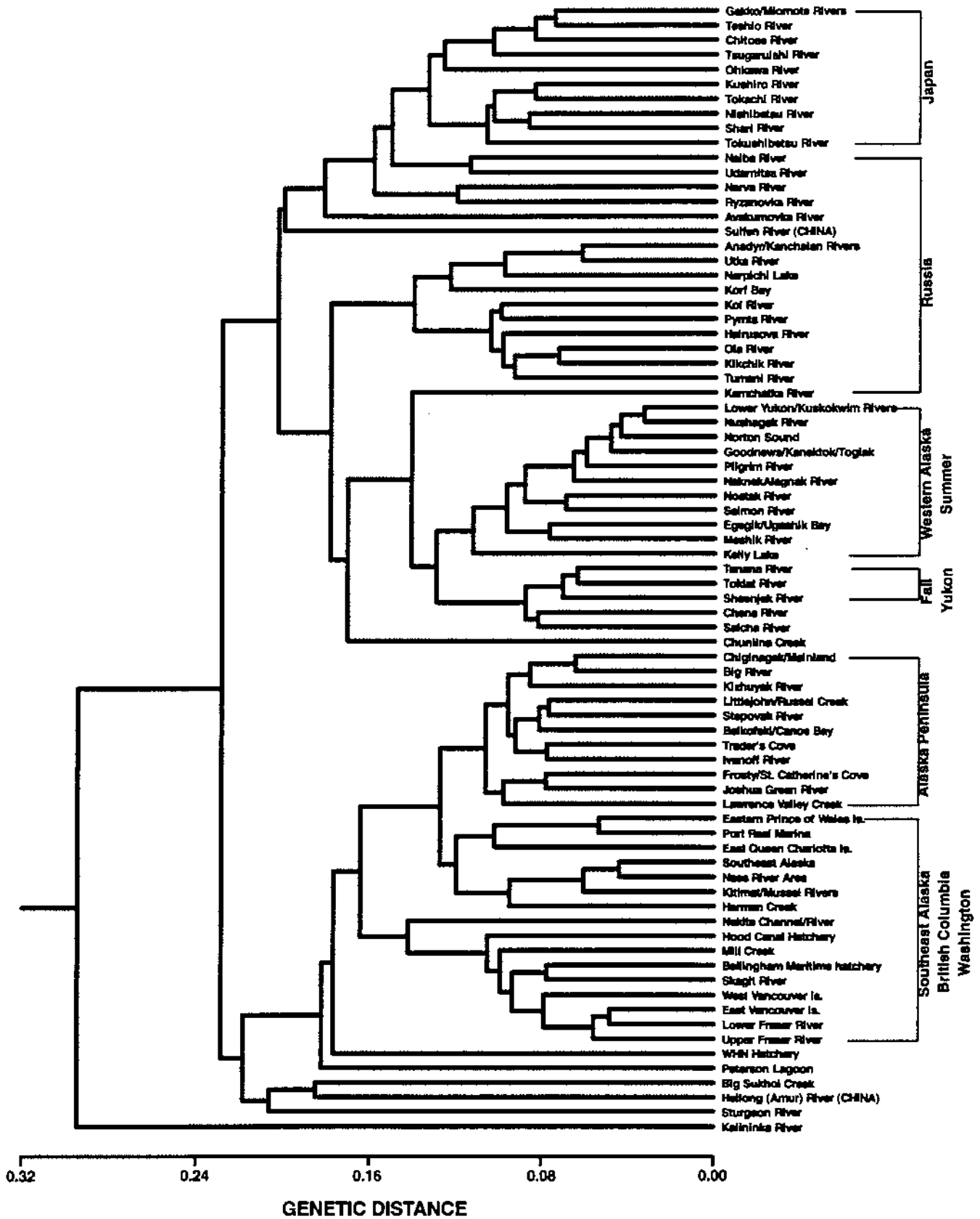


Figure 3.--UPGMA clustering of Cavalli-Sforza and Edwards (1967) chord distance among 77 populations of Pacific Rim chum salmon.

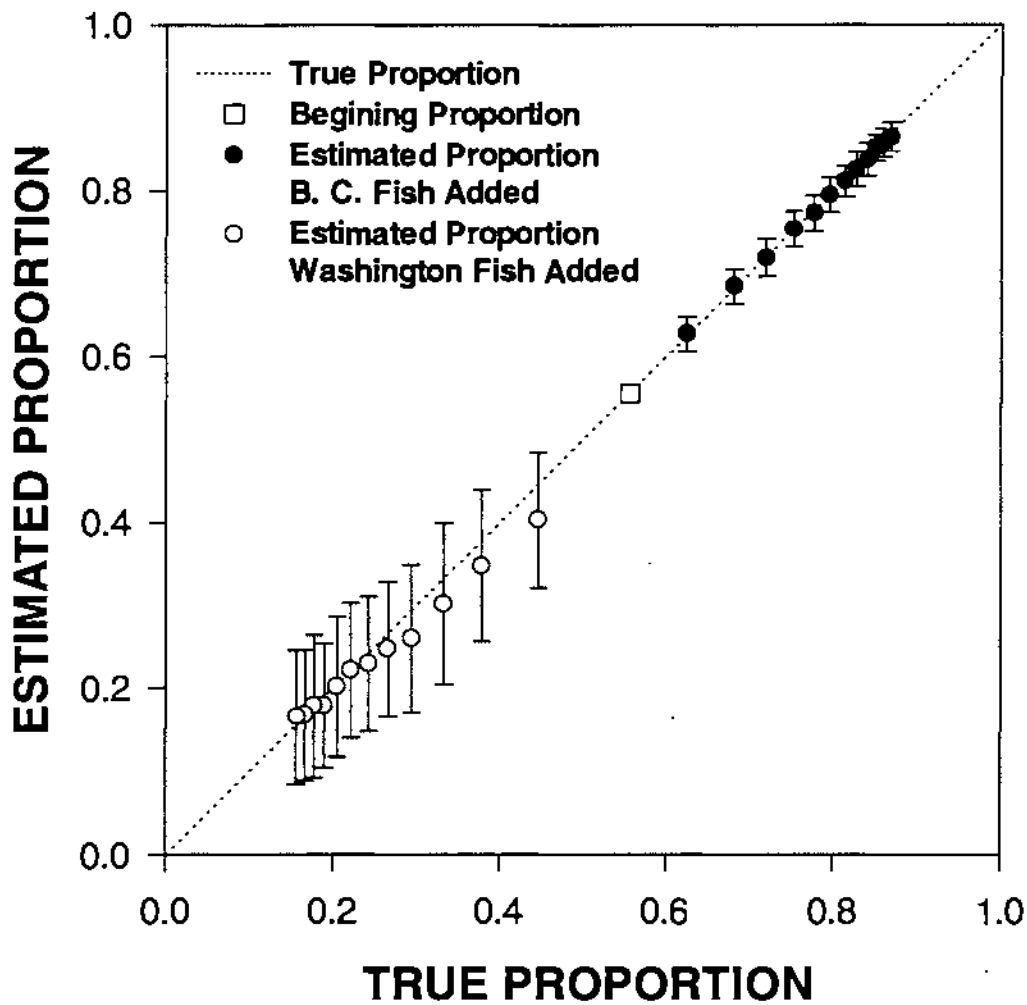


Figure 4.--Results of simulation tests to determine the accuracy of the MLE to follow additions of known numbers of British Columbia fish to an actual mixture sample. The dotted line represents 100% accuracy and the black circles represent the calculated proportion when British Columbia fish are added,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

Appendix I. Allelic frequencies at 20 loci for populations of chum salmon from China and Russia. Alleles are designated by their mobility relative to the most common allele (100).

Population	N	<i>sAAT-1,2*</i>				N	<i>mAAT-1*</i>		
		100	120	65	95		-100	-120	-70
CHINA									
Heilong River (Amur)	46	0.962	0.039	0.000	0.000	46	0.924	0.000	0.076
Suifen River	25	0.980	0.020	0.000	0.000	25	1.000	0.000	0.000
RUSSIA - PREMOR'YE									
Avakumovka River	35	0.964	0.007	0.000	0.029	35	1.000	0.000	0.000
Narva River	18	0.958	0.042	0.000	0.000	18	1.000	0.000	0.000
Ryzanovka River	51	0.990	0.010	0.000	0.000	51	1.000	0.000	0.000
RUSSIA - SAKHALIN ISLAND									
Kalininka River	49	0.954	0.046	0.000	0.000	49	1.000	0.000	0.000
Naiba River	61	0.934	0.066	0.000	0.000	61	0.975	0.016	0.008
Udarnitsa River	98	0.944	0.056	0.000	0.000	98	0.985	0.000	0.015

Population	N	<i>mAH-3*</i>		N	<i>ALAT*</i>		
		100	124		100	93	78
CHINA							
Heilong River (Amur)	43	0.907	0.093	39	0.500	0.500	0.000
Suifen River	23	0.587	0.413	24	1.000	0.000	0.000
RUSSIA - PREMOR'YE							
Avakumovka River	23	0.457	0.544	34	0.838	0.162	0.000
Narva River	17	0.206	0.794	18	0.750	0.250	0.000
Ryzanovka River	28	0.411	0.589	50	0.750	0.250	0.000
RUSSIA - SAKHALIN ISLAND							
Kalininka River	35	0.571	0.429	48	0.521	0.479	0.000
Naiba River	30	0.717	0.283	60	0.750	0.233	0.017
Udamitsa River	42	0.595	0.405	96	0.672	0.328	0.000

Population	N	<i>ESTD*</i>			N	<i>G3PDH-2*</i>	
		100	91	110		100	90
CHINA							
Heilong River (Amur)	46	0.989	0.011	0.000	44	0.761	0.239
Suifen River	25	0.860	0.140	0.000	23	0.848	0.152
RUSSIA - PREMOR'YE							
Avakumovka River	35	0.729	0.271	0.000	34	0.868	0.132
Narva River	18	0.472	0.528	0.000	18	0.972	0.028
Ryzanovka River	51	0.657	0.343	0.000	50	0.940	0.060
RUSSIA - SAKHALIN ISLAND							
Kalininka River	49	0.153	0.847	0.000	49	0.786	0.214
Naiba River	61	0.762	0.238	0.000	61	0.820	0.180
Udamitsa River	98	0.551	0.449	0.000	98	0.903	0.097

Population	N	<i>GPI-B1,2*</i>			N	<i>GPI-A*</i>		
		100	145	40		100	95	105
CHINA								
Heilong River (Amur)	40	1.000	0.000	0.000	46	1.000	0.000	0.000
Suifen River	24	1.000	0.000	0.000	25	1.000	0.000	0.000
RUSSIA - PREMOR'YE								
Avakumovka River	35	0.993	0.007	0.000	34	1.000	0.000	0.000
Narva River	18	1.000	0.000	0.000	18	0.972	0.028	0.000
Ryzanovka River	51	0.995	0.005	0.000	51	0.971	0.029	0.000
RUSSIA - SAKHALIN ISLAND								
Kalininka River	49	1.000	0.000	0.000	49	1.000	0.000	0.000
Naiba River	55	1.000	0.000	0.000	61	1.000	0.000	0.000
Udamitsa River	98	1.000	0.000	0.000	97	1.000	0.000	0.000

Appendix I. (Continued)

Population	N	<i>mIDHP-1*</i>				
		100	60	140	20	85
CHINA						
Heilong River (Amur)	40	0.675	0.325	0.000	0.000	0.000
Suifen River	24	0.813	0.188	0.000	0.000	0.000
RUSSIA - PREMOR'YE						
Avakumovka River	35	0.871	0.129	0.000	0.000	0.000
Narva River	18	0.917	0.083	0.000	0.000	0.000
Ryzanovka River	51	0.882	0.118	0.000	0.000	0.000
RUSSIA - SAKHALIN ISLAND						
Kalininka River	48	0.875	0.125	0.000	0.000	0.000
Naiba River	60	0.875	0.125	0.000	0.000	0.000
Udamitsa River	96	0.839	0.162	0.000	0.000	0.000

Population	N	<i>sIDHP-2*</i>							
		100	35	85	25	20	110	28	45
CHINA									
Heilong River (Amur)	47	0.457	0.404	0.085	0.053	0.000	0.000	0.000	0.000
Suifen River	24	0.688	0.313	0.000	0.000	0.000	0.000	0.000	0.000
RUSSIA - PREMOR'YE									
Avakumovka River	30	0.583	0.183	0.000	0.000	0.000	0.233	0.000	0.000
Narva River	18	0.528	0.389	0.000	0.056	0.000	0.028	0.000	0.000
Ryzanovka River	47	0.553	0.245	0.000	0.138	0.000	0.064	0.000	0.000
RUSSIA - SAKHALIN ISLAND									
Kalininka River	27	0.593	0.296	0.000	0.037	0.000	0.074	0.000	0.000
Naiba River	20	0.650	0.250	0.075	0.000	0.000	0.025	0.000	0.000
Udamitsa River	53	0.585	0.255	0.047	0.066	0.000	0.047	0.000	0.000

Population	N	<i>LDH-A1*</i>			N	<i>LDH-B2*</i>		
		100	50	110		100	120	60
CHINA								
Heilong River (Amur)	38	1.000	0.000	0.000	48	1.000	0.000	0.000
Suifen River	24	0.917	0.021	0.063	25	1.000	0.000	0.000
RUSSIA - PREMOR'YE								
Avakumovka River	35	0.871	0.071	0.057	35	1.000	0.000	0.000
Narva River	18	0.972	0.028	0.000	18	1.000	0.000	0.000
Ryzanovka River	50	0.930	0.040	0.030	51	1.000	0.000	0.000
RUSSIA - SAKHALIN ISLAND								
Kalininka River	48	0.969	0.031	0.000	49	1.000	0.000	0.000
Naiba River	61	0.943	0.057	0.000	61	1.000	0.000	0.000
Udamitsa River	98	0.954	0.046	0.000	98	1.000	0.000	0.000

Population	N	<i>sMDH-A1*</i>			N	<i>sMDH-B1,2*</i>			
		100	200	400		100	72	50	130
CHINA									
Heilong River (Amur)	48	0.906	0.094	0.000	46	1.000	0.000	0.000	0.000
Suifen River	24	0.750	0.250	0.000	25	1.000	0.000	0.000	0.000
RUSSIA - PREMOR'YE									
Avakumovka River	35	0.871	0.129	0.000	35	0.957	0.014	0.000	0.029
Narva River	18	0.889	0.111	0.000	18	0.958	0.028	0.014	0.000
Ryzanovka River	50	0.750	0.250	0.000	51	0.990	0.010	0.000	0.000
RUSSIA - SAKHALIN ISLAND									
Kalininka River	49	1.000	0.000	0.000	49	0.857	0.015	0.122	0.005
Naiba River	35	0.929	0.071	0.000	61	0.967	0.004	0.004	0.025
Udamitsa River	95	0.916	0.084	0.000	98	0.929	0.010	0.046	0.015

Appendix 1. (Continued)

Population	<i>mMEP-2*</i>			<i>sMEP-1*</i>		
	N	100	122	N	100	90
CHINA						
Heilong River (Amur)	40	0.950	0.050	40.000	1.000	0.000
Suifen River	24	0.833	0.167	24.000	1.000	0.000
RUSSIA - PREMOR'YE						
Avakumovka River	35	0.857	0.143	35.000	1.000	0.000
Narva River	18	0.889	0.111	18.000	1.000	0.000
Ryzanovka River	51	0.922	0.078	51.000	0.990	0.010
RUSSIA - SAKHALIN ISLAND						
Kalininka River	48	0.896	0.104	48.000	1.000	0.000
Naiba River	60	0.825	0.175	60.000	1.000	0.000
Udamitsa River	97	0.881	0.119	98.000	1.000	0.000

Population	<i>MPI*</i>				<i>PEPA*</i>				
	N	100	94	110	80	N	100	90	113
CHINA									
Heilong River (Amur)	44	0.875	0.125	0.000	0.000	44	1.000	0.000	0.000
Suifen River	23	1.000	0.000	0.000	0.000	23	1.000	0.000	0.000
RUSSIA - PREMOR'YE									
Avakumovka River	34	0.941	0.059	0.000	0.000	34	1.000	0.000	0.000
Narva River	18	1.000	0.000	0.000	0.000	18	1.000	0.000	0.000
Ryzanovka River	49	1.000	0.000	0.000	0.000	50	1.000	0.000	0.000
RUSSIA - SAKHALIN ISLAND									
Kalininka River	49	1.000	0.000	0.000	0.000	49	1.000	0.000	0.000
Naiba River	61	0.975	0.025	0.000	0.000	61	1.000	0.000	0.000
Udamitsa River	98	0.980	0.020	0.000	0.000	98	1.000	0.000	0.000

Population	<i>PEP-B1*</i>					
	N	-100	-146	-126	-127	-72
CHINA						
Heilong River (Amur)	47	0.968	0.032	0.000	0.000	0.000
Suifen River	24	0.854	0.000	0.146	0.000	0.000
RUSSIA - PREMOR'YE						
Avakumovka River	34	0.750	0.044	0.206	0.000	0.000
Narva River	18	0.861	0.000	0.139	0.000	0.000
Ryzanovka River	51	0.745	0.020	0.235	0.000	0.000
RUSSIA - SAKHALIN ISLAND						
Kalininka River	49	0.469	0.092	0.439	0.000	0.000
Naiba River	61	0.795	0.025	0.180	0.000	0.000
Udamitsa River	96	0.719	0.057	0.224	0.000	0.000

Population	<i>PGDH*</i>				
	N	100	88	106	95
CHINA					
Heilong River (Amur)	48	0.969	0.031	0.000	0.000
Suifen River	25	1.000	0.000	0.000	0.000
RUSSIA - PREMOR'YE					
Avakumovka River	35	0.986	0.014	0.000	0.000
Narva River	18	0.972	0.028	0.000	0.000
Ryzanovka River	51	0.961	0.039	0.000	0.000
RUSSIA - SAKHALIN ISLAND					
Kalininka River	49	1.000	0.000	0.000	0.000
Naiba River	61	0.967	0.033	0.000	0.000
Udamitsa River	98	0.995	0.005	0.000	0.000