GENETIC STOCK IDENTIFICATION OF SOUTHEAST ALASKA
CHINOOK SALMON FISHERY CATCHES

Final Report of the Alaska Department of Fish and Game to US Chinook Technical Committee

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EXECUTIVE SUMMARY

- Genetic stock identification (GSI) was used to estimate the origin of chinook salmon *Oncorhynchus tshawytscha* sampled from the Southeast Alaska (SEAK) summer troll fishery in 1998.
- Chinook salmon were sampled by observers onboard troll vessels. Muscle, liver, eye, and heart tissues were collected from 417 legal-size fish (≥28 inches total length) and 133 sublegal-size fish (<28 inches total length).
- Data for chinook salmon populations from Russia, Alaska, British Columbia, and the Pacific Northwest were added to the allozyme coastwide baseline by National Marine Fisheries Service, Alaska Department of Fish and Game, and Washington Department of Fish and Wildlife. The updated baseline comprised 254 populations with allele frequency data for 34 loci. A simulation study suggested that 44 fine-scale and 29 broader-scale population groups (reporting regions) could be identified in mixtures (Teel et al. 1999). We used the broader-scale reporting regions for the mixture analysis. Simulations patterned on mixture composition estimates of the 1997 SEAK fisheries derived from the Chinook Salmon Model of the Pacific Salmon Commission indicated that the baseline can provide accurate estimates of what is expected to appear in the fishery.
- We genotyped the fishery samples at 27 allozyme loci. The largest contributions to the legal samples were made by West Vancouver Island, Thompson River, Upper Columbia Summer and Fall/Snake Fall, and Mid and North Oregon Coastal. The largest contributions to the sublegal samples were Upper Columbia Summer and Fall/Snake Fall, Strait of Georgia, and Southern Southeast Alaska.
- The updated coastwide allozyme baseline for chinook salmon can be used to estimate the stock composition of the SEAK troll fishery if representative samples are obtained. This information can be used to compare and calibrate the chinook salmon model, and to obtain information on the migration patterns of chinook salmon stocks that are not coded-wire tagged through Southeast Alaska waters.

INTRODUCTION

Pre- and postseason estimates of relative abundance of chinook salmon *Oncorhynchus tshawytscha* stocks in the Southeast Alaska (SEAK) troll fishery are generated by the chinook salmon model of the Chinook Technical Committee (CTC) of the Pacific Salmon Commission (PSC). Discrepancies between age composition estimates in the SEAK troll fishery based on the chinook salmon model and estimates based on aging fish scales have been identified and indicate that the PSC model underestimates the abundance of spring-type stocks in the SEAK troll fishery. Development of stock identification methods based on genetic markers can potentially provide accurate information on wild spring-stock contributions. This information will provide independent stock-specific catch estimates to which the CTC model can be calibrated. Additionally, this information can be used over time as an independent feedback mechanism to validate the performance of the model.

Genetic stock identification (GSI) has been used extensively to estimate the stock contribution to Columbia River, coastal Washington, and Strait of Juan de Fuca fisheries of six major stock aggregates of chinook salmon: 1) California-Oregon; 2) Columbia River; 3) Washington Coast; 4) Puget Sound; 5) British Columbia: Fraser River; and 6) British Columbia: non-Fraser River (e.g. Marshall et al. 1991; Miller et al. 1993). The genetic baseline for the analyses of these fisheries was composed of allozyme data for 196 populations of chinook salmon ranging from the Sacramento River in California to the Stikine River in Alaska and British Columbia. These data have been standardized and combined into a coastwide baseline managed by the Northwest Fisheries Science Center (NWFSC) of the National Marine Fisheries Service (NMFS). Data were collected by NMFS, Washington Department of Fish and Wildlife (WDFW), and University of California, Davis; a large portion of the data can be found in Utter et al. (1989), Bartley et al. (1990), and Waples et al. (1993).

In 1992, the Alaska Department of Fish and Game (ADF&G) initiated a program to develop an up-to-date baseline for Alaska (Seeb et al. 1995). The project was designed to complement ongoing studies in southeast Alaska by the NMFS, Auke Bay Laboratory (ABL), by focusing on populations in western and southcentral Alaska and southeast Alaska hatchery stocks.

Our objective for this study was to estimate the relative contribution of genetic groups of chinook salmon sampled from the 1998 summer SEAK salmon troll fishery by: 1) standardizing allozyme data previously collected by ADF&G for chinook salmon in Alaska and contributing these data to the coastwide chinook salmon database maintained by NMFS, 2) sampling additional populations of chinook salmon in Alaska, 3) evaluating an expanded coastwide database for its ability to identify regional groups of chinook salmon in mixtures, and 4) using the updated baseline to estimate the origin of chinook salmon sampled from the fishery.

METHODS

Standardization of Alaskan Baseline Data

Allele frequency data were standardized at allozyme loci for 39 wild stock and 11 hatchery samples from western, southcentral, and southeastern Alaska (see Teel et al. 1999, attached as Appendix A, for list of populations). We ran variant alleles observed in these populations along with known standards for the following alleles: *mAAT-1*-100,*-77*, and **-104; sAAT-1,2*100* and **85*; *sAAT-3*100* and **90*; *sAAT-4*100,*130*, and **63; ADA-1*100* and **83*; *sAH*100* and **116*; *GPI-A*100* and **105*; *FDHG*100* and **143*; *sIDHP-1*100*, **83*, **129*, and **136*; *sIDHP-2*100* and **50*; *LDHB-2*100*; *mMDH-2*100* and **200*; *sMDHB-1,2*100* and **121*; *sMEP-1*100*; *sMEP-2*100*; and *MPI*100* and **109*. Horizontal starch gels were run according to the recommendations of laboratories contributing to the coastwide baseline (Table 1) and Crane et al. (1996). Alleles were pooled at some loci for data consistency among all coastwide samples, and populations sampled in multiple years were pooled if no significant allele frequency differences were observed ($P<0.05$) (Teel et al. 1999). We represented each Alaska hatchery strain sampled over multiple years by the mean frequency (Waples et al. 1990), following the treatment of other Pacific Northwest hatcheries in the baseline (D. J. Teel, NMFS, personal communication). These data were submitted to NMFS in June 1998 for inclusion in the coastwide database.

Expansion of Alaskan Database

Chinook salmon tissues (muscle, liver, heart, and eye) were collected from brood fish at egg takes at the following hatcheries in Southeast Alaska: Medvejie Hatchery (Andrew Creek source of brood stock), Hidden Falls Hatchery (Andrew Creek), Crystal Lake Hatchery (Andrew Creek), Whitman Lake Hatchery (Chickamin River), and Neets Bay Hatchery (Chickamin River). In addition, juvenile chinook salmon were sampled using minnow traps from Keta River, Andreafsky River, and Chena River. Sampling goals were N=100 for adults and N=150 for juveniles to maximize accuracy of allele frequency estimates (Allendorf and Phelps 1981).

Laboratory analyses followed Crane et al. (1996) using the general protocols outlined in Harris and Hopkinson (1976), May et al. (1979), Aebersold et al. (1987). We used the enzyme nomenclature of Shaklee et al. (1990).

Baseline Evaluation

Potential stock groups that could be identified in mixtures (reporting region) were identified in part from chinook salmon evolutionarily significant units (ESU) defined by the recent status review by NMFS (Myers et al. 1998) and by results from multidimensional scaling analyses of genetic distances and heterogeneity analyses of populations in the coastwide baseline.

Reporting regions were refined and tested using simulation studies. Simulations were performed using the Statistics Program for Analyzing Mixtures developed by ADF&G (SPAM 3.2, Debevec et al. submitted) based on the GIRLS (Masuda et al. 1991) and CONJA-S (Pella et al. 1996) algorithms. In each simulation, baseline and mixture genotypes were randomly generated from the baseline allele frequencies using Hardy-Weinberg expectations. Each simulated mixture (N=400) was composed 100% of the reporting region under study, with each population in the reporting region contributing equally to the mixture. Average estimates of mixture proportions were derived from 100 simulations. Reporting regions were judged acceptable for mixture analysis if approximately 90% of the mixture on average was allocated to the correct region.

We also performed simulations patterned on mixture estimates of the 1997 SEAK fisheries derived from the Chinook Salmon Model of the Pacific Salmon Commission (CTC 1997) to determine how well the baseline could estimate stock contributions that might occur in the actual fishery. For these simulations, the mixture estimates and 90% confidence intervals were calculated from 1000 resamplings.

Stock Composition of Chinook Salmon Sampled from the 1998 SEAK Summer Fishery

Chinook salmon were sampled from the 1998 fishery as a part of the project *Chinook Encounter Rates in the SEAK Troll Fishery* (Bloomquist et al. 1999). Observers on troll vessels collected muscle, liver, eye, and heart tissues from legal-size fish (≥28 inches total length) and sublegal-size fish (<28 inches total length). Chinook salmon were sampled regardless of gender, size, or adipose clip. Individual tissues from each fish were placed in a single plastic ziploc bag and stored on dry or wet ice on board the troll vessels. The GSI sample number was cross-referenced with data recorded by Bloomquist et al. (1999), including catch location and date, CWT information, length, maturity, gender, and age. Samples were transferred to dry ice in port and shipped to Anchorage. In Anchorage, variation at allozyme loci was assayed using coastwide recommendations (Table 1) and the protocols in Crane et al. (1996).

Stock contributions to the SEAK troll fishery samples were estimated via maximum likelihood using SPAM 3.2. Two separate estimates were provided, one for the legal chinook salmon and one for the sublegals. For each estimation procedure, genotypes were removed from the estimation procedure if their probability of occurring was zero. For these cases, the mixture estimates include an "unknown" group containing the percent of the mixture that is removed. Further, we deleted any individual missing data at five or more loci. Individual population or stock estimates were first calculated, then summed into reporting regions (allocate-sum procedure, Wood et al. 1987). All populations in the baseline were included in the analysis except those from Russia. Ninety percent confidence intervals for all regional contribution estimates were computed from 1000 bootstrap resamples of the baseline and mixture genotypes. For each resample, contribution estimates were generated for all populations and summed to the regional level. The 1000 estimates for a region were sorted from lowest to highest with the 51st and 950th values in the sequence taken respectively as the lower and upper bounds of the 90% confidence interval for that region.

RESULTS

Baseline Sample Collections

We assayed genetic variation at allozyme loci in six collections of chinook salmon: Medvejie Hatchery (Andrew Creek), Hidden Falls Hatchery (Andrew Creek), Crystal Lake Hatchery (Andrew Creek), Whitman Lake Hatchery (Chickamin River), and Andreafsky River. Variation was observed at 30 (Table 2) of the coastwide-approved loci (see Table 1) successfully resolved in all collections. We have sampled Hidden Falls Hatchery, Crystal Lake Hatchery, and Whitman Lake Hatchery in previous years. Allele frequency homogeneity was tested within hatcheries and among hatcheries using the same broodstock. Allele frequency heterogeneity was observed among Hidden Falls Hatchery broodyears 1993, 1994, and 1998 (G=131.24, df=60, *P*<0.001) and Whitman Lake broodyears 1992, 1994, and 1998 (G=114.83, df=66, *P*<0.001), but was not observed between Crystal Lake broodyears 1992 and 1998 (G=33.53, df=24, *P*=0.09). Allele frequency heterogeneity was observed between hatcheries using Andrew Creek as a brood source (Hidden Falls and Crystal Lake hatcheries, G=179.60, df=62, *P*<0.001) and between hatcheries using Chickamin River as a brood source (Whitman Lake and Little Port Walter hatcheries, G=284.29, df=33, *P*<0.001).

Baseline Evaluation

In addition to data submitted by ADF&G, the 1992 baseline was updated with new information from populations in the Pacific Northwest, British Columbia, and Russia (unpublished data, C. M. Guthrie III, NMFS-ABL, Juneau, AK; unpublished data, A. Marshall, WDFW, Olympia, WA; Teel et al. [in press]; unpublished data, D. Teel, NMFS-NWFSC, Conservation Biology Division, Seattle, WA; Utter et al. [1995]; unpublished data, N. Varnavskaya, Kamchatka Research Institute of Fisheries and Oceanography, Petropavlosk, Russia). Populations and loci included in the baseline and evaluation and designation of reporting regions for fishery analyses are described in Teel et al. (1999) (Appendix A, for locus list see also Table 1). Teel et al. (1999) found that 44 reporting regions could be successfully identified in mixtures using the updated coastwide baseline using the criterion of the mean estimate of 100 simulations approaching 90% (see Table 1 of Appendix A). These were termed "fine-scale" reporting regions, and are appropriate for use in local fisheries where not many stock groups are expected to contribute. Teel et al. (1999) also evaluated 29 "broad-scale" reporting regions which are more appropriate for more complex fisheries (Table 1 of Appendix A).

For the fishery analysis, we used the broad-scale reporting regions described in Teel et al. (1999). We repeated the simulations for these groups using the loci resolved in the mixture samples (see below) to confirm that these regions would be appropriate for this mixture analysis. The mean stock composition estimates for these groups did not change by more than 2.6%

(Lower Fraser) with the reduced set of loci, and the confidence intervals were only very slightly larger (Figure 1).

We also used these loci for the simulations imitating stock contributions to the 1997 SEAK fishery generated by the Chinook Salmon Model (Table 3a.). These simulations indicated that GSI should provide accurate estimates of stocks expected to appear in SEAK fisheries; for all reporting regions the expected value fell within the 90% confidence interval calculated from 1000 resamplings of the mixture and baseline (Table 3b.).

For the fishery simulations, we combined the Lower Fraser, Mid and Upper Fraser, and Thompson River reporting regions into a "Fraser River" reporting region, and the central BC coastal, Nass, and Skeena into "central BC Coastal, Nass, and Skeena" reporting region to more closely follow the model stocks. We did 100 % simulations on these new reporting groups; the mean contribution estimate for Fraser River was 0.96 and for central BC coastal, Nass, and Skeena was 0.87. For the mixture analysis of the fishery samples we presented for the uncombined regions because combining regions did not result in an important change in estimation accuracy.

Stock Composition of Chinook Salmon Sampled From the 1998 SEAK Summer Fishery

Fishery Sample Collection

Sampling of legal chinook salmon was conducted during the two chinook salmon retention periods of the 1998 summer troll fishery, July 1-July 11 and August 20-September 21. Sublegal chinook salmon were collected during these two time periods and also from July 19-August 7, when chinook salmon retention was not allowed. Between July 1 and July 11, samples were collected from 7 troll vessels; between July 19 and August 7, samples were collected from 10 troll vessels; and between August 20 to September 21, samples were collected from 12 troll vessels.

Tissue samples were collected from 417 legal and 133 sublegal chinook salmon (Table 4). Equal numbers of legal chinook salmon were collected from each chinook salmon opening. Over 50% of the samples were taken in Northern Outside waters (Figure 2, Table 4). For the sublegal salmon, the majority of samples were collected during the second and third troll opening.

Stock Composition

We successfully resolved 27 of the 34 loci comprising the updated coastwide baseline (Table 1). We could not distinguish *sIDHP-1*129* and *142* from *sIDHP-2*127* and *mAAT-1*-77* and *mAAT-1*-100*; alleles at these loci were pooled in the baseline. The largest contributors to the legal samples were West Vancouver Island (0.17), Thompson River (0.15), Upper Columbia Summer and Fall/Snake Fall (0.14), and Mid and North Oregon Coastal (0.13) (Table 5). Lesser contributions were made by Puget Sound, Washington Coastal, Central British Columbia Coastal, and Southern Southeast Alaska. The largest contributors to the sublegal samples were Upper Columbia Summer and Fall/Snake Fall (0.22), Strait of Georgia (0.14), and Southern Southeast Alaska (0.13) (Table 5).

DISCUSSION

Baseline

The addition of allozyme data from Alaska by ADF&G and NMFS, ABL, to the coastwide baseline for chinook salmon allows the application of genetic stock identification techniques in fisheries where these stocks are likely to occur. Thirty collections representing coastal (Chickamin River, Harding River, Farragut River, King Salmon River, Chilkat River, and Situk River) and transboundary populations (Stikine River, Taku River, and Alsek River) have been added as well as samples from five hatcheries using four brood sources (Andrew Creek, Chickamin River, Unuk River, and King Salmon River) (Teel et al. 1999).

A baseline of genetic data for analyzing mixtures of chinook salmon from Southeast Alaska must include a representation of hatchery-produced chinook salmon strains. Recognizing their important contribution to the fisheries of Southeast Alaska, ADF&G analyzed samples of chinook salmon collected from hatcheries in Southeast Alaska (Seeb et al. 1995, Crane et al. 1996). Crane et al. (1996) showed that almost all strains descending from a common progenitor stock possess significantly different frequencies for at least one protein marker, and differed from their wild progenitor stocks as well. Furthermore, these frequencies were found to be temporally unstable, as expected with 'young' and frequently mixed hatchery strains (Waples and Teel 1990).

In this project, we continued sampling Southeast Alaska broodstocks. We continued to see allele frequency heterogeneity at Hidden Falls and Whitman Lake hatcheries, but did not see it at Crystal Lake hatchery. Crystal Lake is one of the older hatchery programs in the state, with few broodstock transfers into the hatchery. Waples (1990) suggested either representing hatcheries in a baseline for genetic stock identification by including data from each broodyear that may be present in the mixture or by representing a population by its mean frequency averaged over an entire generation.

For use in mixture analyses, we used the mean frequency of Alaska hatchery strains sampled over multiple years in the baseline. We used the 1998 hatchery collections from Southeast Alaska as a mixture to test the treatment of hatcheries in the baseline; the stock contribution estimate was 0.87, virtually identical to that of the 100% simulation study testing this region (0.89). Further, the majority of missallocation was to another Southeast Alaska region, Chilkat River. This confirmed that though temporal heterogeneity of allele frequencies exists in some Southeast Alaska hatchery stocks, allele frequency differences are not larger among multiple-year collections within a hatchery than among regions.

Russia and western and southcentral Alaska still remain the weak link in the Pacific Rim baseline for chinook salmon. Continued sampling effort in these areas is desirable for stock composition estimates for fishery samples taken from the Bering Sea and Gulf of Alaska.

Fishery Estimates

In the 1998 summer troll fishery, over 400 legal chinook salmon were collected, but the sample size for sublegal chinook salmon was comparatively small. Marlowe and Busack (1995), analyzing the 1992 chinook salmon baseline, suggested that sample sizes of greater than 200 are necessary for relatively precise stock contribution estimates. The sublegal sample size in this study was less than 200, and the 90% confidence intervals for the estimates are larger than those for the legal sample.

This project was intended to be a pilot study of the ability to assay protein markers from chinook salmon sampled from the troll catch and to test the ability of an updated chinook salmon baseline to identify stock groups in mixtures. However, the legal samples should not be considered representative of the fishery: an excess proportion of chinook salmon were from Southern Inside waters during the second chinook salmon fishery opening (Table 3). However, the stock composition estimates can be used to indicate presence/absence of chinook salmon stocks during the 1998 summer troll fishery. Chinook salmon from the Thompson River, West Vancouver Island, Upper Columbia Summer and Fall/Snake Fall, and Mid and North Oregon Coastal all contribute to the fishery.

Though sample size for sublegal chinook salmon was small, observer sampling effort was thought to be representative of the fishing effort (Bloomquist et al. 1999). Not unexpectedly, stock composition estimates for the two size classes of chinook salmon differed, with a higher proportion of sublegal fish originating from Upper Columbia Summer and Fall/Snake Fall, Strait of Georgia, and Southern Southeast Alaska. Fewer sublegal fish originated from West Vancouver Island. Interestingly, the estimates indicated that sublegal chinook salmon from the California Central Valley may be present in Southeast Alaska. Historic tagging information suggests that these stocks typically do not migrate farther north than Oregon (Myers et al. 1998; Healey 1991); however, five coded-wire tagged chinook salmon from this area have been recovered in Southeast Alaska waters in the past two decades (data were accessed through the ADF&G Coded-Wire Tag Database web site at http://tagotoweb.adfg.state.ak.us/).

CONCLUSION

We used genetic stock identification techniques and an extensive allozyme baseline for chinook salmon to estimate the origins of legal and sublegal chinook salmon collected from the 1998 SEAK summer troll fishery. Simulations of the baseline indicated that GSI should provide accurate estimates of stocks expected to appear in SEAK fisheries. Stock composition estimates indicated that most of the legal chinook salmon originated from West Vancouver Island, Thompson River, Upper Columbia Summer and Fall/Snake Fall, and Mid and North Oregon Coastal. Stock composition estimates for the sublegal chinook salmon were slightly different, with most fish originating from Upper Columbia Summer and Fall/Snake Fall, Strait of Georgia, and Southern Southeast Alaska.

These results indicate that GSI can successfully be used to estimate the stock composition of the SEAK troll fishery if representative samples are obtained. Further, information on the migration patterns of immature chinook salmon stocks that are not coded-wire tagged can be obtained.

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Table 1. Loci and alleles consistently scored among laboratories contributing to the coastwide baseline and the tissues and buffers used to resolve them.[1]

					Alleles							
Locus	Included in 1999 baseline	Resolved in fishery samples	Tissue	Buffer	1	2	3	4	5	6	7	8
*mAAT-1**	x	x	H,M	ACE6.8	-100	-77	-104					
*sAAT-1,2**	x	x	M	TBE	100	85	105					
*sAAT-3**	x	x	E	TBE	100	90	113					
*sAAT-4**	x		L	TBE	100	130	63					
*ADA-1**	x		E,M	TBE	100	83						
*ADA-2**	x		E,M	TBE	100	105						
*ADH**			L	TBE, ACE7	-100	-52	-170					
*mAH-1**			E,H	ACE6.8	100	65						
*mAH-3**			H,M	ACE6.8	100	126	74					
*mAH-4**			H,M	ACE6.8	100	119	112					
*sAH**	x	x	L	ACE7	100	86	116+108	69				
*ALAT**			M	TG	100	90						
*FDHG**	x	x	L	TBE	100	143						
*GAPDH-2**			H	ACEN7	100	22						
*GPI-A**	x	x	M	TBCLE	100	105	93					
*GPI-B2**	x	x	M	TBCLE	100	60/60						
*GPI-B2a**	x	x	M	TBCLE	100+60		135	24				
*GPIr**	x	x	M	TBCLE	100	***						
*GR**			E,M	TBCLE	100	85	110					
*bHEX**			L	TC4	100	60						
*IDDH-1**			L	TBCL	100	0						
*mIDHP-2**	x	x	E,M	ACE7	100	154						
*sIDHP-1**	x	x	M,E,L	ACE6.8	100		74	142		94	83	129
*sIDHP-2**	x	x	E,L	ACE6.8	100	127			50		83	
*LDH-B1**			H,E	TBCLE	100	48						
*LDH-B2**	x	x	L,E,M	TBCLE	100	112	134	71				
*LDH-C**	x	x	E	TBCLE	100	90+84						
*mMDH-2**	x	x	M	ACE6.8	100	200	-20					
*sMDH-A1,2**	x	x	M	ACE7	100	120	27	-45				
*sMDH-B1,2**	x	x	M	ACE7	100	121	70	83				

Table 1. Continued.

Locus	Included in 1999 baseline	Resolved in fishery samples	Tissue	Buffer	Alleles 1	2	3	4	5	6	7	8
*sMEP-1**	x	x	H,M	TC4	100	92	105					
*sMEP-2**	x	x	M,L	TC4	100	78/78						
*MPI**	x	x	E,L	TBE	100	109+113	95					
*PEPA**	x	x	E,M	TBE	100	90+86						
*PEPB-1**	x	x	E,M	TBCLE,TC4	100	130	-350	71				
*PEPD-2**	x		E,M	TBE	100	107						
*PEPLT**	x		E,M	TBE	100	110						
*PGDH**	x	x	E,L	ACE7	100	90	85					
*PGK-2**	x	x	E,M,L	ACE7	100	90	74					
*PGM-1**	x		H,M	TG	100	210						
*PGM-2**	x		L,M	TBCL	100	166	136					
*mSOD**			H,M	TBE	100	142	50					
*sSOD-1**	x	x	L,E,M	TBE	-100	-260	580	1260				
*TPI-3**	x	x	H,E,M	TG	100	96						
*TPI-4**	x	x	M,E	TBE	100	104						

[1] Tissues: H=heart, M=muscle, E=eye, L=Liver

Buffers: ACE6.8, 7 = amine-citric acid-EDTA buffer, pH 6.8 or 7, (Clayton and Tretiak 1972), "N" indicates modification with NAD (Harris and Hopkinson 1976); TBCLE = Tris-citric acid-EDTA gel buffer, lithium hydroxide-boric acid electrode buffer,pH 8.5 (Ridgway et al. 1970, Harris and Hopkinson 1976); TC4 = Tris-citric acid buffer, pH 5.95 (Schaal and Anderson 1974); TG = Tris-glycine buffer, pH 8.5 (Holmes and Masters 1970).

Allele descriptions: Numbers for alleles are relative mobilities, "+" indicates pooled alleles, "/" indicates loci where only homozygote phenotypes are scored, "***" indicates absence *of GPI-A/GPIB-1* heterodimer. *TPI-3** was added to baseline after the writing of Teel et al. (1999).

Table 2. Allele frequency estimates for chinook salmon populations sampled in 1998. Hatchery broodsources are listed. Adult fish were sampled unless otherwise noted.

	*ALAT**			*mAAT-1**			*sAAT-1,2**		
Population	N	100	90	N	-100	-104	N	100	85
Hidden Falls Hatchery-Andrew Creek	99	0.944	0.056	99	0.985	0.015	99	0.995	0.005
Medvejie Hatchery-Andrew Creek	100	0.945	0.055	99	0.985	0.015	100	0.975	0.025
Crystal Lake Hatchery-Andrew Creek	96	0.938	0.063	98	0.975	0.026	100	0.998	0.003
Whitman Lake Hatchery-Chickamin River	99	0.919	0.081	100	0.990	0.010	100	0.983	0.018
Andreafsky River Juveniles	35	0.943	0.057	40	1.000	0.000	39	1.000	0.000
Chena River Juveniles	136	0.952	0.048	150	1.000	0.000	141	1.000	0.000

	*sAAT-3**			*sAAT-4**				*ADA-1**		
Population	N	100	90	N	100	130	63	N	100	83
Hidden Falls Hatchery-Andrew Creek	96	0.859	0.141	86	0.913	0.000	0.087	99	0.985	0.015
Medvejie Hatchery-Andrew Creek	95	0.879	0.121	96	0.839	0.026	0.135	97	0.949	0.052
Crystal Lake Hatchery-Andrew Creek	95	0.811	0.190	84	0.863	0.000	0.137	100	0.965	0.035
Whitman Lake Hatchery-Chickamin River	97	0.964	0.036	92	0.913	0.000	0.087	98	0.934	0.066
Andreafsky River Juveniles	40	0.775	0.225	39	0.949	0.000	0.051	40	0.913	0.088
Chena River Juveniles	150	0.570	0.430	149	0.990	0.000	0.010	150	0.997	0.003

	*ADA-2**		*sAH**			*GAPDH-2**			
Population	N	100	N	100	86	N	100	22	20
Hidden Falls Hatchery-Andrew Creek	99	1.000	100	0.970	0.030	99	1.000	0.000	0.000
Medvejie Hatchery-Andrew Creek	96	1.000	99	0.975	0.025	96	1.000	0.000	0.000
Crystal Lake Hatchery-Andrew Creek	100	1.000	98	0.939	0.061	97	1.000	0.000	0.000
Whitman Lake Hatchery-Chickamin River	98	1.000	100	0.860	0.140	97	0.943	0.052	0.005
Andreafsky River Juveniles	40	1.000	40	0.963	0.038	40	0.988	0.013	0.000
Chena River Juveniles	150	1.000	148	1.000	0.000	149	1.000	0.000	0.000

	*GPIA**				*GPIB-2**		*GPI-B2a**		*GPIr**	
Population	N	100	105	85	N	100	N	100	N	100
Hidden Falls Hatchery-Andrew Creek	99	0.955	0.040	0.005	99	1.000	99	1.000	99	1.000
Medvejie Hatchery-Andrew Creek	100	0.970	0.025	0.005	100	1.000	100	1.000	100	1.000
Crystal Lake Hatchery-Andrew Creek	100	0.960	0.040	0.000	100	1.000	100	1.000	100	1.000
Whitman Lake Hatchery-Chickamin River	98	0.964	0.036	0.000	99	1.000	99	1.000	99	1.000
Andreafsky River Juveniles	40	1.000	0.000	0.000	40	1.000	40	1.000	40	1.000
Chena River Juveniles	150	1.000	0.000	0.000	150	1.000	150	1.000	150	1.000

Table 2. Continued.

	*FDHG**			*IDDH-1**			*mIDHP-2**	
Population	N	100	143	N	100	0	N	100
Hidden Falls Hatchery-Andrew Creek	99	1.000	0.000	97	0.809	0.191	99	1.000
Medvejie Hatchery-Andrew Creek	100	0.995	0.005	98	0.781	0.219	100	1.000
Crystal Lake Hatchery-Andrew Creek	100	0.980	0.020	96	0.880	0.120	100	1.000
Whitman Lake Hatchery-Chickamin River	100	0.955	0.045	96	0.922	0.078	100	1.000
Andreafsky River Juveniles	40	1.000	0.000	40	0.975	0.025	40	1.000
Chena River Juveniles	146	1.000	0.000	148	0.980	0.020	150	1.000

	*sIDHP-1**				*sIDHP-2**				*LDHB-1**		
Population	N	100	74	94	N	100	127	50	N	100	48
Hidden Falls Hatchery-Andrew Creek	97	0.825	0.000	0.175	100	0.990	0.005	0.005	97	1.000	0.000
Medvejie Hatchery-Andrew Creek	97	0.830	0.000	0.170	100	0.985	0.000	0.015	100	1.000	0.000
Crystal Lake Hatchery-Andrew Creek	99	0.909	0.000	0.091	100	0.995	0.000	0.005	100	0.995	0.005
Whitman Lake Hatchery-Chickamin River	97	0.912	0.000	0.088	100	0.995	0.000	0.005	99	1.000	0.000
Andreafsky River Juveniles	40	0.988	0.013	0.000	40	0.988	0.000	0.013	40	1.000	0.000
Chena River Juveniles	150	1.000	0.000	0.000	147	0.997	0.000	0.003	150	1.000	0.000

	*LDHB-2**			*LDHC**		*mMDH-2**		
Population	N	100	71	N	100	N	100	200
Hidden Falls Hatchery-Andrew Creek	100	1.000	0.000	99	1.000	99	0.990	0.010
Medvejie Hatchery-Andrew Creek	100	1.000	0.000	96	1.000	100	1.000	0.000
Crystal Lake Hatchery-Andrew Creek	100	1.000	0.000	99	1.000	99	0.995	0.005
Whitman Lake Hatchery-Chickamin River	100	1.000	0.000	98	1.000	100	0.975	0.025
Andreafsky River Juveniles	40	1.000	0.000	40	1.000	40	0.963	0.038
Chena River Juveniles	150	0.987	0.013	131	1.000	150	1.000	0.000

	*sMDHA-1,2**			*sMDHB-1,2**					
Population	N	100	27	N	100	121	70	126	92
Hidden Falls Hatchery-Andrew Creek	99	1.000	0.000	99	0.992	0.000	0.008	0.000	0.000
Medvejie Hatchery-Andrew Creek	99	1.000	0.000	99	0.987	0.000	0.013	0.000	0.000
Crystal Lake Hatchery-Andrew Creek	99	1.000	0.000	100	0.995	0.000	0.005	0.000	0.000
Whitman Lake Hatchery-Chickamin River	100	1.000	0.000	100	0.960	0.000	0.040	0.000	0.000
Andreafsky River Juveniles	40	1.000	0.000	40	1.000	0.000	0.000	0.000	0.000
Chena River Juveniles	150	0.998	0.002	150	0.942	0.013	0.037	0.007	0.002

Table 2. Continued.

	*sMEP-1**				*sMEP-2**		
Population	N	100	92	86	N	100	78
Hidden Falls Hatchery-Andrew Creek	97	0.237	0.763	0.000	99	0.950	0.051
Medvejie Hatchery-Andrew Creek	99	0.338	0.662	0.000	100	0.910	0.090
Crystal Lake Hatchery-Andrew Creek	96	0.266	0.734	0.000	100	0.980	0.020
Whitman Lake Hatchery-Chickamin River	95	0.211	0.790	0.000	100	0.940	0.060
Andreafsky River Juveniles	40	0.063	0.938	0.000	38	0.816	0.184
Chena River Juveniles	149	0.000	0.997	0.003	150	0.713	0.287

	*MPI**					*PEPA**		
Population	N	100	109	95	85	N	100	90
Hidden Falls Hatchery-Andrew Creek	99	0.758	0.242	0.000	0.000	99	0.965	0.035
Medvejie Hatchery-Andrew Creek	95	0.753	0.242	0.005	0.000	100	0.970	0.030
Crystal Lake Hatchery-Andrew Creek	97	0.722	0.278	0.000	0.000	100	0.985	0.015
Whitman Lake Hatchery-Chickamin River	98	0.791	0.199	0.005	0.005	100	0.970	0.030
Andreafsky River Juveniles	39	0.923	0.077	0.000	0.000	40	0.988	0.013
Chena River Juveniles	147	0.993	0.007	0.000	0.000	149	0.956	0.044

	*PEPB-1**				*PEPD-2**			*PEPLT**		
Population	N	100	130	-350	N	100	107	N	100	110
Hidden Falls Hatchery-Andrew Creek	98	0.939	0.026	0.036	100	1.000	0.000	98	0.959	0.041
Medvejie Hatchery-Andrew Creek	99	0.944	0.025	0.030	99	1.000	0.000	100	0.965	0.035
Crystal Lake Hatchery-Andrew Creek	99	0.939	0.020	0.040	100	1.000	0.000	100	1.000	0.000
Whitman Lake Hatchery-Chickamin River	100	0.910	0.055	0.035	98	0.989	0.010	97	0.928	0.072
Andreafsky River Juveniles	40	0.900	0.100	0.000	40	1.000	0.000	39	0.987	0.013
Chena River Juveniles	149	0.705	0.295	0.000	140	1.000	0.000	150	1.000	0.000

	*PGDH**		*PGK-2**			*PGM-1**		*PGM-2**	
Population	N	100	N	100	90	N	100	N	100
Hidden Falls Hatchery-Andrew Creek	100	1.000	97	0.098	0.902	99	1.000	99	1.000
Medvejie Hatchery-Andrew Creek	100	1.000	100	0.095	0.905	99	1.000	100	1.000
Crystal Lake Hatchery-Andrew Creek	100	1.000	100	0.170	0.830	100	1.000	100	1.000
Whitman Lake Hatchery-Chickamin River	100	1.000	100	0.090	0.910	100	1.000	97	1.000
Andreafsky River Juveniles	40	1.000	39	0.000	1.000	40	1.000	40	1.000
Chena River Juveniles	150	1.000	149	0.000	1.000	150	1.000	150	1.000

Table 2. Continued.

Population	*mSOD** N	100	50	*sSOD-1** N	-100	-260	580	1260	*TPI-3** N	100	96
Hidden Falls Hatchery-Andrew Creek	98	1.000	0.000	97	0.918	0.067	0.016	0.000	99	0.965	0.035
Medvejie Hatchery-Andrew Creek	94	0.984	0.016	97	0.887	0.093	0.021	0.000	100	0.960	0.040
Crystal Lake Hatchery-Andrew Creek	100	0.985	0.015	100	0.945	0.035	0.020	0.000	100	0.955	0.045
Whitman Lake Hatchery-Chickamin River	100	1.000	0.000	100	0.810	0.165	0.020	0.005	99	0.965	0.035
Andreafsky River Juveniles	37	0.851	0.149	39	0.923	0.077	0.000	0.000	40	1.000	0.000
Chena River Juveniles	0			140	0.957	0.043	0.000	0.000	150	1.000	0.000

Population	*TPI-4** N	100	104
Hidden Falls Hatchery-Andrew Creek	99	1.000	0.000
Medvejie Hatchery-Andrew Creek	100	1.000	0.000
Crystal Lake Hatchery-Andrew Creek	100	1.000	0.000
Whitman Lake Hatchery-Chickamin River	100	1.000	0.000
Andreafsky River Juveniles	40	0.925	0.075
Chena River Juveniles	150	0.867	0.133

Table 3. Simulations of mixtures using estimates of stock composition from the 1997 SEAK fisheries. (a.) Simulation design from estimates from the 1997 Chinook Model Calibration (CTC 1997) and expected allocation to GSI reporting region. (b.) Mean GSI estimates calculated from 1000 resamplings of the mixture and baseline.

a. Simulation design

Chinook Salmon Model		GSI Simulation	
Model Stock	1997 Fishery Estimate	GSI Reporting Region	Expected
Oregon Coastal North Migr.	0.078	Mid and North Oregon Coastal	0.078
Lewis River Wild	0.002	Lower Columbia Spring and Fall	0.003
Fall Cowlitz Hatchery	0.001		
Spring Cowlitz Hatchery	0.000		
Spring Creek Hatchery	0.000		
Lower Bonneville Hatchery	0.000		
Willamette River Hatchery	0.007	Willamette	0.007
Columbia Upriver Bright	0.159	Upper Columbia Summer, Fall, Snake Fall	0.239
MidColumbia Brights	0.070		
Columbia Upriver Summer	0.010		
Snake River Fall	0.001		
Washington Coastal Wild	0.033	Washington Coastal	0.075
WA Coastal Hatchery	0.042		
Puget Sound Fingerling	0.001	Puget Sound	0.003
Skagit Summer/Fall	0.001		
Puget Sound Natural	0.000		
Nooksack Fall	0.000		
Stillaguamish Summer/Fall	0.000		
Snohomomish Summer/Fall	0.000		
Puget Sound Yearling	0.000		
Nooksack Spring	0.000		
Fraser	0.062	Lower Fraser And Mid and Upper Fraser AND Thompson River	0.063
Fraser Late	0.002		
Upper Georgia Strait	0.021	Strait of Georgia	0.029
Lower Georgia Strait	0.006		
Lower GS Hatchery	0.002		
WCVI Hatchery	0.185	WCVI	0.236
WCVI Wild	0.051		
North/Central BC	0.218	central BC Coastal AND Nass AND Skeena	0.218
Alaska South SE	0.049	Southern SE AK	0.049

Table 3. Continued.

b. Simulation results

	Expected	Mean Estimate	90% CI	
			Lower	Upper
Central Valley	0.000	0.004	0.000	0.018
California, S. Oregon coastal	0.000	0.019	0.000	0.051
Klamath	0.000	0.004	0.000	0.017
Mid and North Oregon Coastal	0.078	0.076	0.036	0.120
Lower Columbia Spring and Fall	0.003	0.012	0.000	0.039
Willamette	0.007	0.008	0.000	0.020
Mid and Upper Columbia, Snake Spring and Summer	0.000	0.004	0.000	0.015
Upper Columbia Summer, Fall, Snake Fall	0.239	0.220	0.165	0.276
Washington Coastal	0.075	0.061	0.016	0.109
Puget Sound	0.003	0.018	0.000	0.048
Fraser River	0.063	0.080	0.037	0.127
Strait of Georgia	0.029	0.035	0.007	0.071
WCVI	0.236	0.206	0.133	0.281
central BC coastal, Nass, and Skeena	0.218	0.180	0.116	0.248
AK/BC Transboundary	0.000	0.009	0.000	0.030
Southern SE AK	0.049	0.054	0.010	0.109
King Salmon River	0.000	0.001	0.000	0.007
Chilkat	0.000	0.006	0.000	0.025
Gulf of Alaksa	0.000	0.002	0.000	0.009
Susitna	0.000	0.001	0.000	0.004
Kodiak	0.000	0.000	0.000	0.002
AK Peninsula	0.000	0.001	0.000	0.007
Western AK	0.000	0.001	0.000	0.006
Upper Canadian Yukon	0.000	0.000	0.000	0.004

Table 4. Sampling results for collection of chinook salmon from the SEAK 1998 summer troll fishery. Samples from legal and sublegal chinook salmon were taken by observers working onboard troll vessels (Bloomquist et al. 1999). For legal chinook salmon, harvest information is included to indicate how well the genetics samples represent the fishery.

a. Legal salmon

Date	Quadrant	# Genetics Samples	Proportion of Genetics Samples	Proportion of Fishery
July 1-11	Northern Outside	106	0.254	0.438
	Northern Inside	34	0.082	0.140
	Southern Outside	69	0.165	0.136
	Southern Inside	0	0.000	0.030
	Total	209	0.501	0.743
Aug. 20-21 Sept.	Northern Outside	121	0.290	0.245
	Northern Inside	0	0.000	0.004
	Southern Outside	4	0.010	0.003
	Southern Inside	83	0.199	0.005
	Total	208	0.499	0.257

b. Sublegal Chinook Salmon

Date	Quadrant	# Genetics Samples
July 1-11	Northern Outside	2
	Northern Inside	2
	Southern Outside	2
	Southern Inside	0
	Total	6
July 19-7 Aug	Northern Outside	36
	Northern Inside	26
	Southern Outside	7
	Southern Inside	3
	Total	72
Aug. 20-21 Sept.	Northern Outside	34
	Northern Inside	4
	Southern Outside	0
	Southern Inside	17
	Total	55

Table 5. Contribution estimates of 28 stock groups of chinook salmon to legal and sublegal chinook salmon sampled from the 1998 SEAK summer troll fishery.

	Legal			Sublegal		
		90% CI			90% CI	
Reporting Region	Estimate	Lower	Upper	Estimate	Lower	Upper
Central Valley	0.000	0.000	0.016	0.025	0.000	0.072
California, Southern Oregon Coastal	0.006	0.000	0.032	0.000	0.000	0.008
Klamath River Basin	0.000	0.000	0.000	0.000	0.000	0.001
Mid and North Oregon Coastal	0.126	0.079	0.170	0.052	0.001	0.140
Lower Columbia River	0.006	0.000	0.061	0.041	0.000	0.136
Willamette River	0.000	0.000	0.009	0.033	0.000	0.068
Mid and Upper Columbia Spring, Snake River Spring and Summer	0.008	0.000	0.025	0.000	0.000	0.015
Upper Columbia Summer and Fall/Snake Fall	0.137	0.080	0.178	0.216	0.116	0.328
Washington Coastal	0.074	0.029	0.137	0.065	0.000	0.156
Puget Sound	0.027	0.008	0.084	0.037	0.000	0.153
Lower Fraser River	0.020	0.000	0.057	0.000	0.000	0.050
Thompson River	0.146	0.077	0.201	0.067	0.012	0.150
Mid and Upper Fraser	0.054	0.018	0.097	0.000	0.000	0.039
Strait of Georgia	0.060	0.021	0.109	0.143	0.063	0.239
West Vancouver Island	0.172	0.077	0.232	0.014	0.000	0.080
Central BC Coastal	0.063	0.021	0.113	0.016	0.000	0.068
Skeena River	0.001	0.000	0.035	0.011	0.000	0.110
Nass River	0.014	0.000	0.033	0.033	0.000	0.087
AK/BC Transboundary	0.005	0.000	0.032	0.059	0.000	0.098
Southern Southeast Alaska	0.048	0.007	0.087	0.133	0.038	0.245
King Salmon River	0.006	0.000	0.018	0.020	0.000	0.062
Chilkat River	0.000	0.000	0.006	0.000	0.000	0.000
Gulf of Alaska	0.009	0.000	0.030	0.022	0.000	0.073
Susitna River	0.012	0.000	0.021	0.000	0.000	0.000
Kodiak Island	0.000	0.000	0.012	0.000	0.000	0.000
Alaska Peninsula	0.000	0.000	0.005	0.000	0.000	0.000
Western Alaska	0.000	0.000	0.006	0.000	0.000	0.000
Canadian Yukon	0.000	0.000	0.000	0.000	0.000	0.006

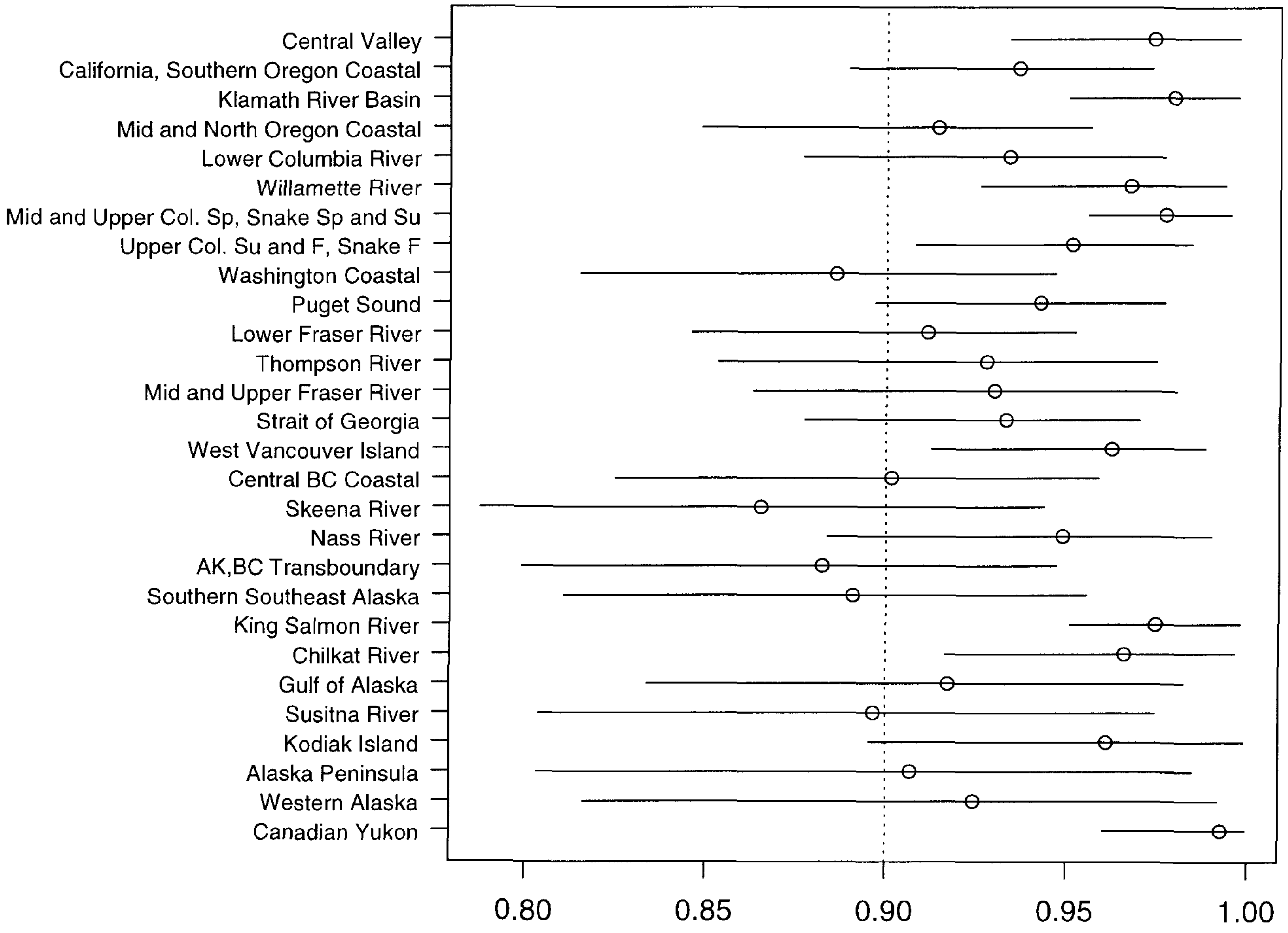

Figure 1. Simulation results of broader-scale reporting regions for chinook salmon using the 27 loci resolved in the 1998 SEAK troll samples.

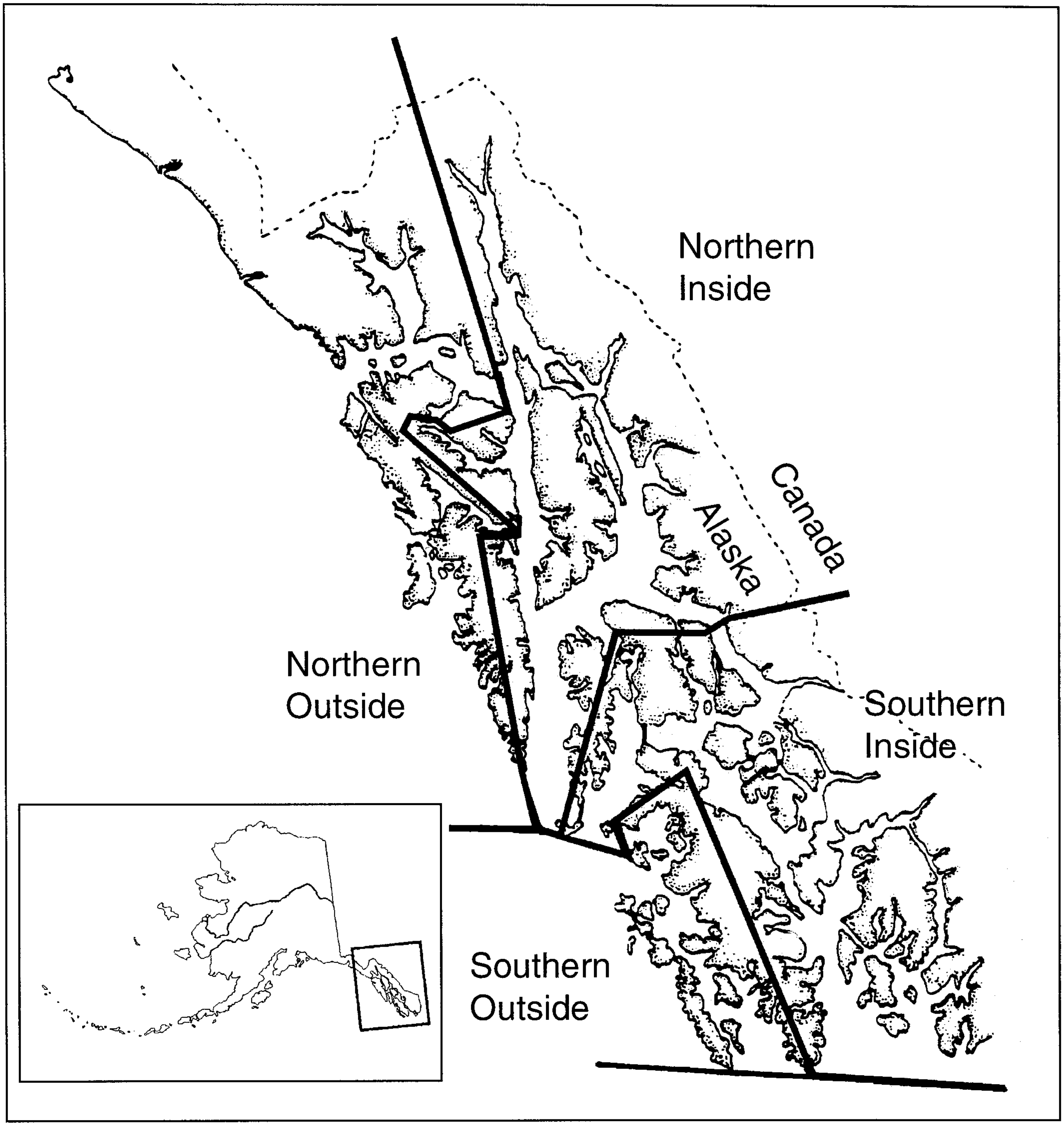

Figure 2. Quadrants comprising Southeast Alaska commercial fishing districts.

APPENDIX A.

NPAFC
Doc. 440
REV. _____

COMPREHENSIVE ALLOZYME DATABASE DISCRIMINATES CHINOOK SALMON AROUND THE PACIFIC RIM

by

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Background

The population genetics of chinook salmon have been studied throughout much of the species range in western North America using allozyme analyses (e.g., Gharrett et al. 1987; Utter et al. 1989; Beacham et al. 1989; Bartley et al. 1990; Utter et al. 1993), and the data have been utilized extensively in the stock identification of fisheries in the Pacific Northwest and along the California Coast (e.g. Utter et al. 1987). This information has also been used to delineate evolutionary significant units (ESUs) under the Endangered Species Act (ESA) for populations from the southern portion of the range (e.g. Meyers et al. 1998). Allozyme allele frequencies from numerous studies have been standardized and combined into a single comprehensive database, which is managed by the Northwest Fisheries Science Center (NWFSC) of the National Marine Fisheries Service (NMFS). Genetic studies utilizing DNA-level markers have also been applied to chinook salmon, but, in contrast to allozyme studies, differing techniques and differing loci have been utilized in various portions of the range. Efforts to standardize DNA data across the range of the species are only now beginning.

Previous versions of the allozyme database included nearly 200 populations ranging from the Sacramento River in California to the Stikine River in British Columbia. However, adequate coverage for Alaska and Russia had been lacking, so no Alaskan, Russian, or high-seas applications were possible. In recent years, the Alaska Department of Fish and Game (ADF&G) and the Auke Bay Laboratory (ABL) of NMFS initiated programs to update, enlarge, and standardize allozyme data from northern and western populations to develop a species-wide database (Seeb et al. 1995; Crane et al. 1996; Guthrie, NMFS/ABL, unpublished). Additional populations from British Columbia as well as other Pacific Northwest populations have recently become available (Utter et al. 1995; Teel et al. In press; Marshall, WDFW, unpublished). The Chinook Salmon Genetics Working Group met in Anchorage, Alaska, October 4-6, 1999, to finalize an enlarged database. This report documents the collaborative database constructed at that meeting and the results of simulations conducted to identify genetic groups that can be accurately and precisely identified in mixtures.

Database Construction

Shaklee and Phelps (1990) outlined several criteria that should guide the creation of a database for use in genetic stock identification (GSI). One is that genotype data for large numbers of individuals and loci are best summarized as allele frequencies or allele counts, because they can be used to view population genetic structure and to estimate population components in mixed-stock samples. Limitations on sampling restrict the accuracy and utility of accurately estimating the frequencies of multilocus genotypes. The baseline must also include all spawning stocks that potentially contribute to a mixed-stock fishery. Since not all stocks may be genetically distinct from one another, genetic data for these stocks can be 1) dropped, especially for minor populations that are unlikely to contribute to a fishery, 2) pooled with genetically similar stocks connected by gene flow, or 3) increased to provide for greater levels of genetic discrimination. At least some of the baseline populations should be sampled annually to determine the extent of temporal stability of allele frequencies. When frequencies are stable, they can be pooled to represent a spawning stock. Once baseline population data are available, simulations should be performed to determined levels of accuracy and precision that the baseline can provide in making estimates of mixed-stock components. These procedures have been followed in compiling the database reported here.

Populations included in the baseline ranged from northern California, USA, to Kamchatka, Russia (Appendix 1). Sample sizes for the majority of populations included in the database exceeded 80 individuals. Given the expected number of alleles per locus, allele frequency estimates are highly accurate. Populations were selected for inclusion in the baseline if they were consistently scored for a common set of 33 characters: *mAAT-1*; sAAT-1,2*; sAAT-3*; sAAT-4*; ADA-1*; ADA-2*; sAH*; FDHG*; GPIA*; GPIB-2*; GPIB-2a*; GPIr*; mIDHP-2*;sIDHP-1*;sIDHP-2*; LDHB-2*; LDHC*; mMDH-2*; sMDHA-1,2*; sMDHB-1,2*; sMEP-1*; sMEP-2*; MPI*; PEPA*; PEPB-1*; PEPD-2*; PEPLT*; PGDH*; PGK-2*; PGM-1*; PGM-2*; sSOD-1*; TPI-4**. Alleles were pooled at the following loci for data consistency, *sAH*116/108, PEPA*86/90, LDHC*84/90*, and *MPI*113/109*. The Russian populations, Voroskaia and Kamchatka rivers, lacked data at 13 and five loci, respectively. Simulations on these populations were conducted separately on a reduced set of loci. Data from samples collected in more than a single year at a location were pooled following the recommendations of Waples (1990) to counter the effects of drift and sampling error.

Database Evaluation

Potential reporting groups for fishery analyses were identified from chinook salmon ESUs defined by the recent status review by NMFS (Myers et al. 1998), by multidimensional scaling analyses of genetic distances, and by heterogeneity analyses among populations. Potential reporting groups were evaluated further using simulation studies. Simulations were performed using the Statistics Program for Analyzing Mixtures developed by ADF&G (SPAM ver. 3.2, ADF&G 1997) based on the GIRLS (Masuda et al. 1991) and CONJA-S (Pella et al. 1996) algorithms. In each simulation, baseline and mixture genotypes were randomly generated from the baseline allele frequencies using Hardy-Weinberg expectations. Each simulated mixture (N=400) was composed 100% of the reporting group under study, with each population in the reporting group contributing equally to the mixture. Average estimates of mixture proportions were derived from 100 simulations. Individual population estimates were first calculated, then summed into reporting groups (allocate-sum procedure). Reporting groups were enlarged until approximately 90% of the mixture on average was allocated to the correct reporting group. We tested fine- to broader-scale groupings with the same methods.

Results and Recommendations

The heterogeneity and multidimensional scaling analyses revealed considerable divergence at allozyme loci across the range of the species. We report both fine-scale and broad-scale reporting groups (Table 1, Figures 1a, b and 2). Simulation analyses supported 29 broad-scale reporting regions as well as 44 fine-scale reporting groups using the criteria of 90% correct allocation in a 100% simulation. Broad-scale reporting groups are recommended for mixtures estimated to contain fish from a large number of genetic groups. Fine-scale reporting groups are more appropriate for mixtures estimated to originate from a smaller number of genetic groups. The reporting groups can be easily modified for specific applications by individual investigators.

The allozyme database is now comprehensive, with representation from the majority of known lineages and populations. Finer scale reporting groups would likely be possible for southcentral and western Alaska with inclusion of additional populations and baseline data from these areas. Completed datasets from Russian populations would enhance analyses of mixtures that potentially include fish originating in Asia. A variety of applications are now possible throughout the species' range including both near-shore and high-seas mixtures of chinook salmon in all life history stages.

Table 1. Reporting regions for chinook salmon. Populations numbers are listed in Appendix 1.

Fine Scale	Population Numbers	Broad Scale	Population Numbers
Central Valley	1-6	Central Valley	1-6
California Coastal	7-16	California, Southern Oregon Coastal	7-16,23-31
Southern Oregon, North California Coastal	23-28		
Rogue River	29-31		
Klamath River Basin	17-22	Klamath River Basin	17-22
Mid Oregon Coastal	32-42	Mid and North Oregon Coastal	32-49
North Oregon Coastal	43-49		
Willamette River	56-62	Willamette River	56-62
Lower Columbia Spring	50,52,54	Lower Columbia River	50-55,63,64
Lower Columbia Fall	51,53,55,63		
Spring Creek/Big Creek Hatcheries	64		
Mid and Upper Columbia Spring	65-79	Mid and Upper Columbia Spring, Snake River Spring and Summer	65-79,94-109
Snake River Spring and Summer	94-109		
Upper Columbia Summer and Fall	80-83,85,87-92	Upper Columbia Summer and Fall and Snake Fall	80-93
Lyons Ferry, Deschutes, Marion Drain Fall	84,86,93		
Washington Coastal	110-120	Washington Coastal	110-120
South Puget Sound	132-143	Puget Sound	121-143
North Puget Sound	121-131		
Lower Fraser River	144,145	Lower Fraser River	144,145
Lower Thompson River	146-150	Thompson River	146-159
South Thompson River	151-155		
North Thompson River	156-159		
Mid Fraser River	160-167	Mid and Upper Fraser River	160-175
Upper Fraser River	168-175		
Lower Strait of Georgia	176-181	Strait of Georgia	176-183
Upper Strait of Georgia	182,183		
West Vancouver Island	184-186	West Vancouver Island	184-186
Central BC Coastal	187-189	Central BC Coastal	187-189
Lower Skeena River	190,191	Skeena River	190-197
Upper Skeena River	192-197		

Fine Scale	Population Numbers	Broad Scale	Population Numbers
Nass River	198,199	Nass River	198,199
Alaska/BC Transboundary	200,207,210-215	Alaska/BC Transboundary	200,207,210-215
Southern Southeast Alaska	201-206,208,220-227	Southern Southeast Alaska	201-206,208,220-227
King Salmon River	209,228	King Salmon River	209,228
Chilkat River	216,217,229	Chilkat River	216,217,229
Alsek River	218	Gulf of Alaska	218,219,230-233
Situk River	219		
Copper River, Kenai Peninsula	230-233		
Susitna River	234-237	Susitna River	234-237
Kodiak Island	238,239	Kodiak Island	238,239
Alaska Peninsula	240,241	Alaska Peninsula	240,241
Western Alaska	242-250,252	Western Alaska	242-250,252
Canadian Yukon	251	Canadian Yukon	251
Russia[1]	253,254	Russia[1]	253,254

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[1] Reduced set of loci only. Loci excluded: *sAAT-3*; sAAT-4*; ADA-2*; FDHG*; GPIA*; GPIB-2*; GPIB-2a*; GPIr*; sIDHP-1*; sIDHP-2*; LDHB-2*; LDHC*; sMEP-1*; PEPB-1*; PEPLT*.*

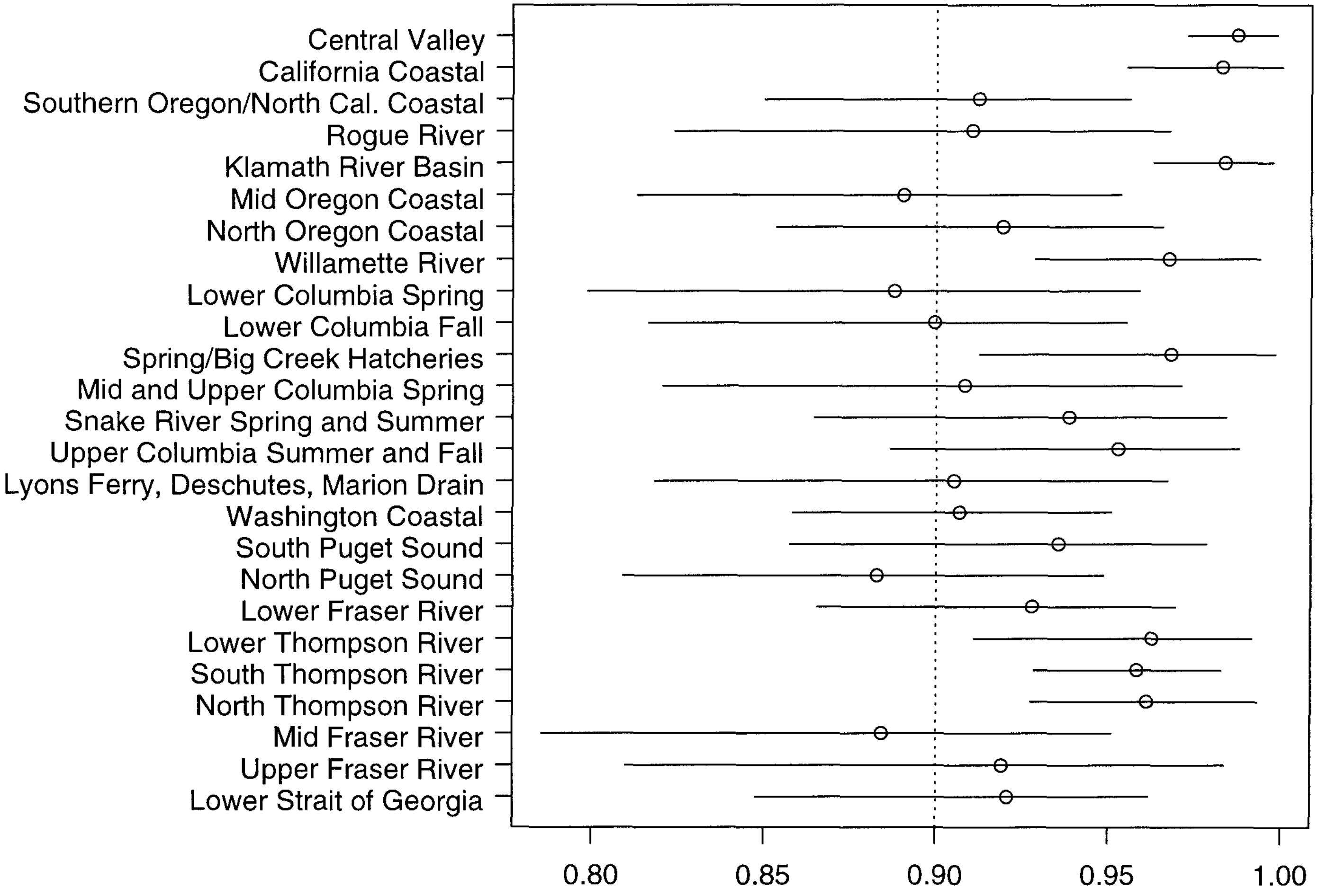

Figure 1a. Simulation results for fine-scale reporting groups for chinook salmon from the southern portion of the range. Point estimates and 90% bootstrap confidence intervals are given.

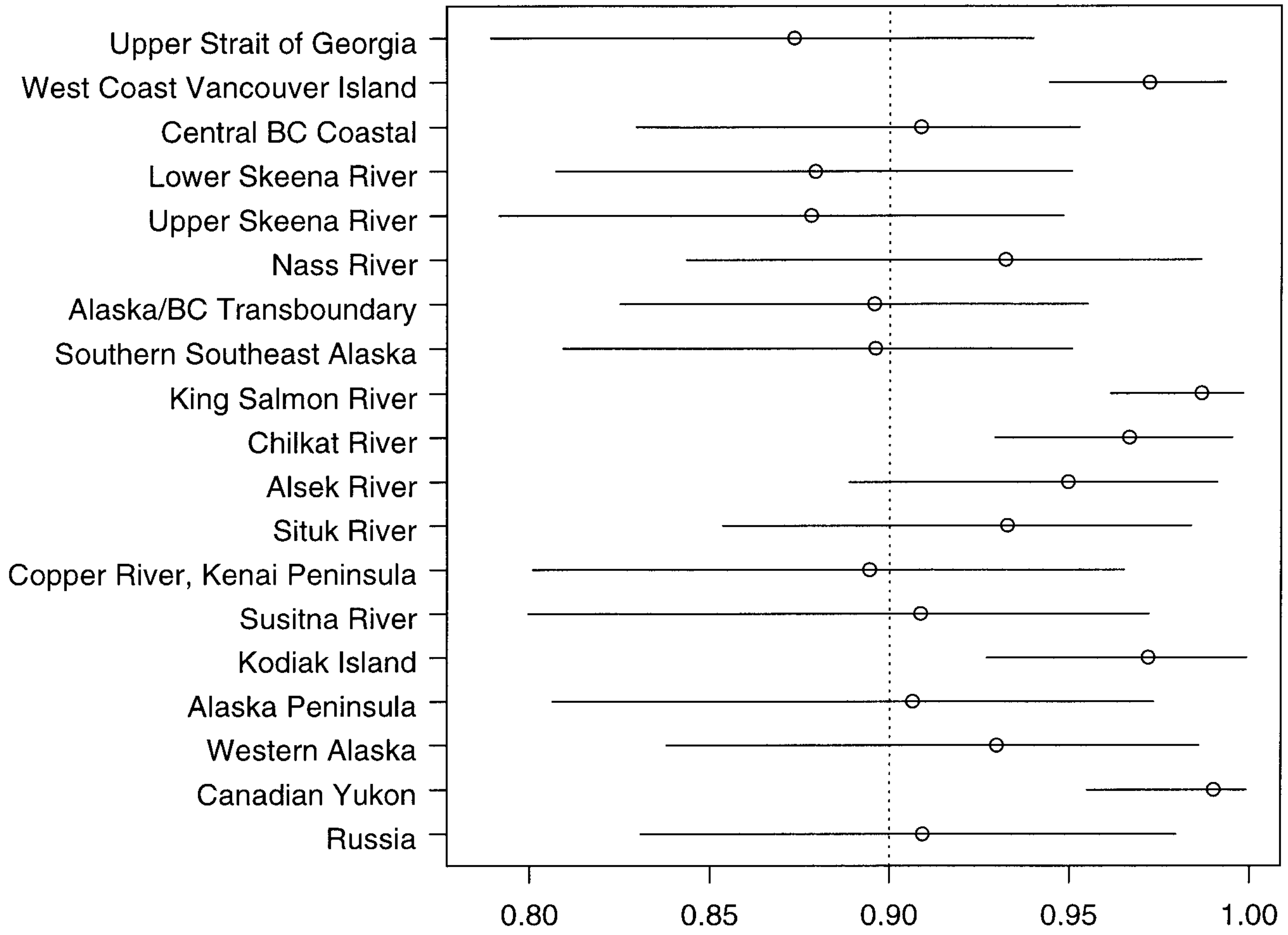

Figure 1b. Simulation results for fine-scale reporting groups for chinook salmon from the northern portion of the range. Point estimates and 90% bootstrap confidence intervals are given.

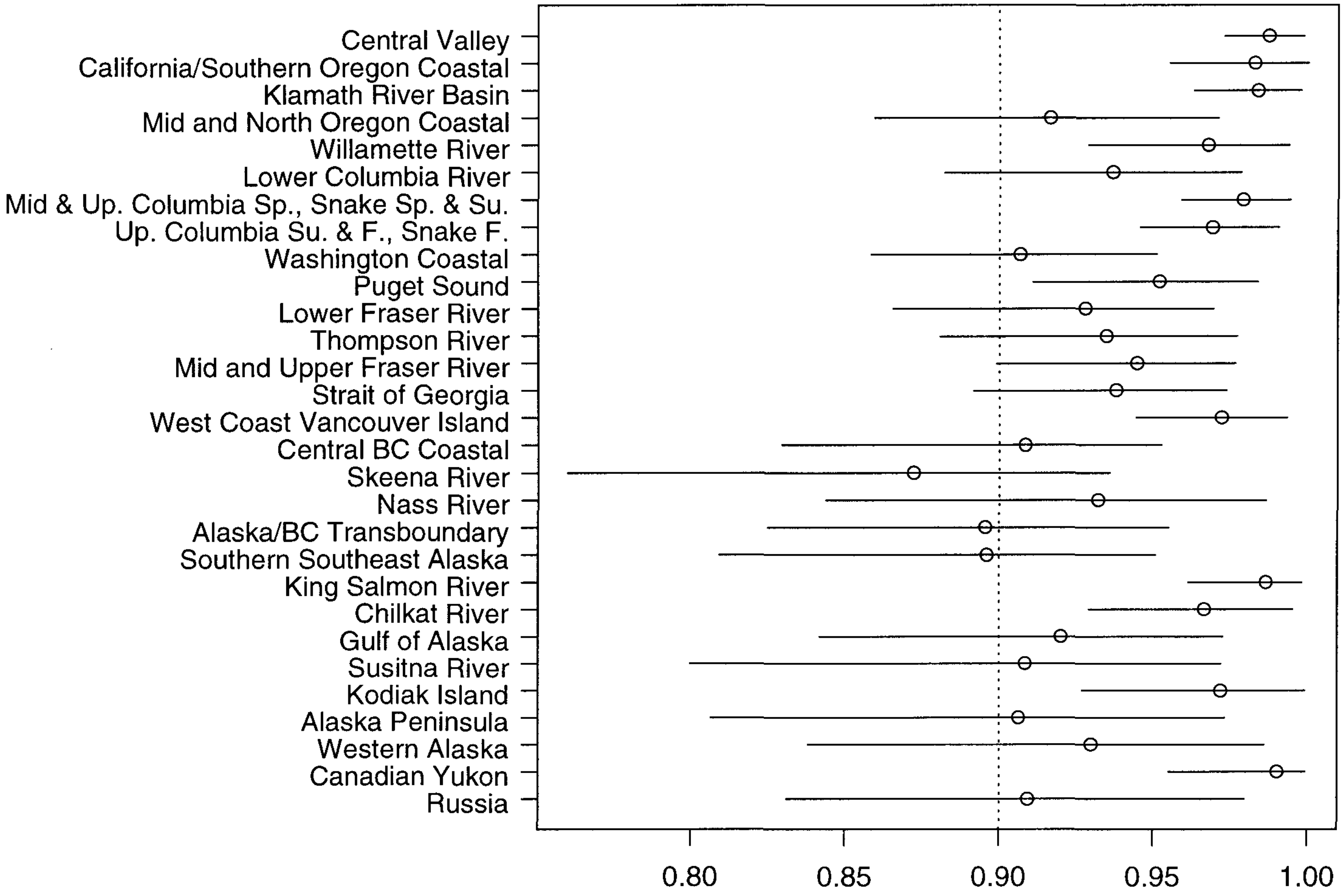

Figure 2. Simulation results for broad-scale reporting groups for chinook salmon. Point estimates and 90% bootstrap confidence intervals are given.

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Appendix 1. Location and collection details for each population of chinook salmon included in the database. Population numbers are also given.

Geographic Area	Pop Number	Sample Number[1]	Source	Run Time	Total N	Sample Numbers (if combined)[1]	N (if combined)	Brood or Return Years	Sample Years	Age	Comments
Sacramento and San Joaquin rivers	1	C0030	Mokelumne and Nimbus Hatcheries	fall	350	S0169, S0179, S0180, D0034	100, 100, 50, 100	80, 80, 83, 87	81, 81, 84, 88	J, J, J, J	S0169 from Mokelumne H., others from Nimbus H.
	2	D0036	Merced Hatchery	fall	100			87	88	J	
	3	C0031	Feather Hatchery	fall	300	S0076, S0078, D0035	100, 100, 100	80, 83, 87	81, 84, 88	J, J, J	
	4	C0090	Feather Hatchery	spring	244	S0077, S0079, W88AV	50, 94, 100	80, 83, 88	81, 84, 88	J, J, A	
	5	C0032	Coleman Hatchery	fall	200	S0040, D0020	100, 100	80, 86	81, 87	J, J	
	6	D0015	Upper Sacramento River	winter	94			86	87	J	
California Coast	7	C0033	Mattole River	fall	150	S0153, D0008	50, 100	83, 86	84, 87	J, J	
	8	D0022	Van Duzen River	fall	100			86	87	J	
	9	D0016	Salmon Creek	fall	96			86	87	J	
	10	D0011	Redwood Creek	fall	93			86	87	J	
	11	D0024	Benbow Creek	fall	99			86	87	J	
	12	D0004	Hollow Tree Creek	fall	100			86	87	J	
	13	D0023	Mid Fork Eel River	fall	95			86	87	J	
	14	C0034	Mad River Hatchery	fall	149	S0151, D0007	50, 99	83, 86	84, 87	J, J	
	15	D0010	North Fork Mad River	fall	61			86	87	J	
	16	C0035	Redwood Creek	fall	195	D0012, D0013	100, 95	86, 86	87, 87	J, J	
Klamath River Basin	17	C0036	Iron Gate Hatchery	fall	247	S0101, S0100, D0006	99, 50, 98	80, 83, 86	81, 84, 87	J, J, J	
	18	C0196	Trinity Hatchery	fall	370	S0285, S0283, D0021, S1138	100, 50, 120, 100	80, 83, 86, 97	81, 84, 87, 98	J, J, J, J	

Geographic Area	Pop Number	Sample Number[1]	Source	Run Time	Total N	Sample Numbers (if combined)[1]	N (if combined)	Brood or Return Years	Sample Years	Age	Comments
	19	C0197	Trinity Hatchery	spring	250	S0284, S0286, S1139	50, 100, 100	81, 83, 97	82, 84, 98	J, J, J	
	20	C0038	Salmon and Scott Rivers	fall	198	S0234, D0017	100, 98	83, 86	84, 87	J, J	S0234 is Scott, D0017 is Salmon
	21	C0039	Shasta River and Bogus Creek	fall	259	S0239, D0019, D0002	31, 100, 128	83, 86, 86	84, 87, 87	J, J, J	D0002 is Bogus Cr., others are Shasta
	22	D0018	South Fork Trinity River	fall	100			86	87	J	
South Oregon and North California Coasts	23	C0040	Rowdy Creek Hatchery	fall	112	S0249, D0014	50, 62	83, 86	84, 87	J, J	
	24	D0009	Mid fork Smith River	fall	99			86	87	J	
	25	C0189	Winchuck River	fall	170	S0315, S1015	50, 120	84, 94	84, 95	A, J	
	26	C0176	Chetco River	fall	343	S0029, S0030, D0025, S1069	100, 93, 100, 50	80, 83, 87, 95	81, 84, 88, 96	J, J, J, J	
	27	C0181	Pistol River	fall	200	S0193, S1014	100, 100	83, 94	84, 95	J, J	
	28	S1013	Hunter Creek	fall	100			94	95	J	
	29	C0177	Cole Rivers Hatchery	spring	263	S0036, S0039, S1009	113, 50, 100	80, 84, 94	81, 85, 95	J, J, J	
	30	C0043	Applegate River	fall	181	S0007, D0027	81, 100	83, 87	84, 88	J, J	
	31	D0033	Rogue River at Gold Hill	fall	100			87	88	J	
Mid and North Oregon Coast	32	S1068	Euchre Creek	fall	57			95	96	J	
	33	C0179	Elk River and Elk River Hatchery	fall	400	S0069, S0068, D0026, S1012	100, 100, 100, 100	80, 84, 87, 94	81, 85, 88, 95	J, J, J, J	S1012 is from Elk River, others are from Elk River Hatchery
	34	C0184	Sixes River	fall	268	S0246, S0245, S1011	100, 50, 118	80, 82, 94	81, 83, 95	J, J, J	
	35	D0030	South Fork Coquille River	fall	100			87	88	J	
	36	C0200	Coquille River and Bandon Hatchery	fall	224	S0043, S0042, S1010, S1019	115, 50, 28, 31	80, 82, 94, 95	81, 83, 95, 95	J, J, J, A	S0443 and S0042 are from Coquille Estuary, others from Bandon Hatchery
	37	D0031	Millicoma River	fall	100			87	88	J	

Geographic Area	Pop Number	Sample Number[1]	Source	Run Time	Total N	Sample Numbers (if combined)[1]	N (if combined)	Brood or Return Years	Sample Years	Age	Comments
	38	D0032	Morgan Creek Hatchery	fall	100			87	88	J	
	39	S1018	Noble Creek Hatchery	fall	100			95	95	A	
	40	C0182	Rock Creek Hatchery	spring	300	S0217, S0218, S1008	100, 100, 100	80, 84, 94	81, 85, 95	J, J, J	
	41	S1007	Rock Creek Hatchery	fall	100			94	95	J	
	42	S1129	West Fork Smith River (Umpqua Basin)	fall	80			97	98	J	
	43	C0183	Siuslaw River	fall	160	S0268, S0267, S1020	82, 34, 44	80, 82, 95	81, 83, 96	J, J, J	
	44	C0174	Alsea River	fall	181	S0005, S0004, S1017	94, 50, 37	80, 82, 95	81, 83, 95	J, J, A	
	45	C0049	Fall Creek Hatchery	fall	300	S0075, S0074, D0029	100, 100, 100	80, 84, 87	81, 85, 88	J, J, J	
	46	C0195	Siletz River	fall	184	S0243, S0242, S1016, S1097	92, 50, 25, 17	80, 82, 95, 97	81, 83, 95, 97	J, J, A, A	
	47	C0198	Trask Hatchery	spring	300	S0282, S0280, S1092	100, 100, 100	80, 84, 96	81, 85, 97	J, J, J	
	48	C0199	Trask Hatchery	fall	400	S0281, S0279, W87BI, S1093	100, 100, 100, 100	80, 84, 87, 96	81, 85, 87, 97	J, J, A, J	
	49	S1072	Nehalem River	summer	53			96	96	A	
Lower Columbia River	50	C0172	Cowlitz Hatchery	spring	152	S0053, W87QA	50, 102	82, 87	82, 87	A, A	
	51	C0093	Cowlitz Hatchery	fall	198	S0049, S0045, W88QZ	49, 50, 99	81, 81, 88	81, 82, 88	A, J, A	
	52	C0130	Kalama Hatchery	spring	159	S0113, W90BK	50, 109	82, 87	82, 87	A, A	
	53	C0102	Kalama Hatchery	fall	199	S0116, W88AB, W89BG	50, 49, 100	81, 88, 89	82, 88, 89	J, A, A	
	54	W88XF	Lewis Hatchery	spring	135			88	88	A	

Geographic Area	Pop Number	Sample Number[1]	Source	Run Time	Total N	Sample Numbers (if combined)[1]	N (if combined)	Brood or Return Years	Sample Years	Age	Comments
	55	W90CZ	Lewis River	fall	120			90	90	A	
Willamette River	56	C0087	Mckenzie and Dexter Hatcheries	spring	248	S0157, W87AJ, W88QP	38, 100, 110	82, 87, 88	82, 87, 88	A, A, A	W87AJ is from Dexter Hatchery, others from Mckenzie Hatchery
	57	S1098	Mckenzie River	spring	100						
	58	S1135	North Santiam River	spring	99			97	98	J	
	59	W88AD	Clackamas Hatchery	spring	100			88	88	A	
	60	S1091	North Fork Clackamas River	spring	80			96	97	J	
	61	W90CK	Marion Forks Hatchery	spring	100			90	90	A	
	62	S1099	Sandy River	spring	93			96	97	J	
	63	P90DA	Sandy River	fall	140	WDFW	54, -, -	90, 91, 92	90, 91, 92	A, A, A	
	64	C0129	Spring Creek and Big Creek Hatcheries	fall	454	S0012, S0261, W87AL, W90CL, W90CM	50, 50, 104, 150, 100	81, 81, 87, 90, 90	82, 82, 87, 90, 90	J, J, A, A, A	S0012 and W90CM from Big Cr Hatchery, others from Spring Cr Hatchery
Mid and Upper	65	C0103	Carson Hatchery	spring	250	S0021, W89AT, W89AR	50, 100, 100	82, 89, 89	82, 89, 89	A, A, A	W89AT is Carson stock collected at Klickitat Hatchery
Columbia River spring	66	C90BF	Klickitat River	spring	261	WDFW	-, -, -, -	90, 91, 92, 93	90, 91, 92, 93	A, A, A, A	
	67	C0088	Warm Springs Hatchery and River	spring	210	S0295, S0403, S0410	50, 80, 80	82, 87, 87	82, 87, 87	A, A, A	S0410 is from Warm Springs River, others from W.S. Hatchery
	68	C0136	Round Butte Hatchery	spring	159	S0224, W90BO	59, 100	82, 90	82, 90	A, A	
	69	P90BY	North Fork John Day River	spring	85	WDFW	-, -, -	90, 91, 92	90, 91, 92	A, A, A	
	70	C0139	Yakima and Cle Elum Rivers	spring	401	W86QC, W89AX, W89AY, W90BR	40, 100, 100, 161	86, 89, 89, 90	86, 89, 89, 90	A, A, A, A	W89AX is from Cle Elum R, others from Yakima R
	71	C0141	American River	spring	226	W86QD, W89AG, W90BA	55, 80, 91	86, 89, 90	86, 89, 90	A, A, A	
	72	C0142	Naches, Little Naches, and Bumping Rivers	spring	251	W89AC, W89AI, W89AV, W90BH, W90BI, W90BJ	59, 33, 40, 66, 32, 21	89, 89, 89, 90, 90, 90	89, 89, 89, 90, 90, 90	A, A, A, A, A, A	W89AI and W90BI from Bumping R, others from Naches R

Geographic Area	Pop Number	Sample Number[1]	Source	Run Time	Total N	Sample Numbers (if combined)[1]	N (if combined)	Brood or Return Years	Sample Years	Age	Comments
	73	C0201	Leavenworth Hatchery	spring	250	S0135, W86DD, W91EZ	50, 100, 100	82, 86, 91	82, 86, 91	A, A, A	
	74	C89WW	White River	spring	137	WDFW	-, -, -	89, 91, 92	89, 91, 92	A, A, A	
	75	C89ZZ	Nason River	spring	122	WDFW	-, -, -	89, 92, 93	89, 92, 93	A, A, A	
	76	C89AZ	Chiwawa River	spring	247	WDFW	-, -, -, -, -, -	89, 90,91, 92, 93, 94	89, 90, 91, 92, 93, 94	A, A, A, A, A, A	
	77	W93EA	Methow River	spring	93			93	93	A	
	78	C93DZ	Chewack River	spring	151	WDFW	-, -	92, 93	92, 93	A, A	
	79	C93EB	Twisp River	spring	107	WDFW	-, -	92, 93	92, 93	A, A	
Mid and Upper Columbia River summer and fall	80	T91FJ	Klickitat River	summer	324	WDFW	-, -, -, -	91, 92, 93, 94	91, 92, 93, 94	A, A, A, A	
	81	T91FK	Klickitat River	fall	250	WDFW	-, -, -, -	91, 92, 93, 94	91, 92, 93, 94	A, A, A, A	
	82	C0131	Bonneville Hatchery	fall	200	W90AE, W90DB	100, 100	89, 90	89, 90	J, A	
	83	C0132	Little White Salmon Hatchery	fall	200	W90AC, W90DC	100, 100	89, 90	89, 90	J, A	
	84	C0178	Deschutes River	fall	179	S0058, S0057, P90DD, P90DD,(P90DD)	49, 54, 38, 29, 9	82, 84, 90, 91, 92	82, 85, 90, 91, 92	A, J, A, A, A	
	85	W90DF	Yakima River	fall	109			90	90	A	
	86	C0140	Marion Drain	fall	153	W89BX, W90DG	101, 52	89, 90	89, 90	A, A	
	87	C0137	Hanford Reach	fall	258	S0313, S0291, W90DH	44, 115, 99	82, 82, 90	82, 82, 90	A, A, A	
	88	C0138	Priest Rapids Hatchery	fall	400	S0195, W86NN, W87BS, W90DN	100, 100, 100, 100	80, 86, 87, 90	81, 86, 87, 90	J, A, A, A	
	89	C92FK	Wells Hatchery	summer	202	WDFW	-, -	91, 92	91, 92	A, A	
	90	C0143	Wenatchee River	summer	350	S0312, W88AC, W89BI, W90CX	50, 100, 100, 100	84, 88, 89, 90	85, 88, 89, 90	J, A, A, A	
	91	C93ED	Similkameen River	summer	206	WDFW	-, -, -	91, 92, 93	91, 92, 93	A, A, A	

Geographic Area	Pop Number	Sample Number[1]	Source	Run Time	Total N	Sample Numbers (if combined)[1]	N (if combined)	Brood or Return Years	Sample Years	Age	Comments
	92	C92FL	Methow River	summer	59	WDFW	-, -	92, 93	92, 93	A, A	
Snake River	93	C0144	Lyons Ferry Hatchery	fall	399	S0150, W86OO, W87BR, W90DI	100, 100, 99, 100	84, 86, 87, 90	85, 86, 87, 90	J, A, A, A	
	94	C0145	Tucannon Hatchery	spring	758	S0287, W86QQ, W87CC, W86QF, W87AC, W88BA, W88QA, W89AA, W90AU, W90DW	100, 102, 100, 99, 85, 100, 100, 65, 108, 100	83, 84, 85, 86, 87, 86, 88, 89, 90, 90	85, 86, 87, 86, 87, 88 88, 89, 90, 90	J, J, J, A, A, J, A, A, J, J	
	95	C0111	Rapid River	spring	293	S0214, S0213, S0211, S0541	43, 50, 100, 100	81, 81, 84, 88	82, 82, 85, 90	J, J, J, J	
	96	S0618	Lookingglass Hatchery	spring	100			90	91	J	
	97	S0580	Minam River	spring	100			89	90	J	
	98	C0146	Lostine River	spring	297	S0504, S0569, S0685	100, 99, 98	88, 89, 90	89, 90, 91	J, J, J	
	99	S0571	Catherine Creek	spring	100			89	90	J	
	100	C0148	McCall Hatchery	summer	350	S0154, S0516, S0555, S0665	50, 100, 100, 100	81, 88, 89, 90	82, 89, 90, 91	J, J, J, J	
	101	C0149	Secesh River	summer	254	S0502, S0557, S0674	94, 80, 80	88, 89, 90	89, 90, 91	J, J, J	
	102	C0150	Johnson Creek	summer	316	S0105, S0499, S0556, S0668	56, 100, 80, 80	81, 88, 89, 90	82, 89, 90, 91	J, J, J, J	
	103	C0151	Marsh Creek	spring	259	S0498, S0560, S0666	100, 80, 79	88, 89, 90	89, 90, 91	J, J, J	
	104	C0147	Sawtooth Hatchery	spring	350	S0233, S0517, S0558, S0667	50, 100, 100, 100	81, 88, 89, 90	82, 89, 90, 91	J, J, J, J	S0233 is from Sawtooth River, others from Sawtooth Hatchery
	105	C0152	Valley Creek	spring	279	S0501, S0559, S0669	100, 99, 80	88, 89, 90	89, 90, 91	J, J, J	
	106	S0671	Upper Salmon River at Blaine Bridge	spring	60			88	89	J	
	107	S0670	Upper Salmon River at Frenchman Creek	spring	60			90	91	J	

Geographic Area	Pop Number	Sample Number[1]	Source	Run Time	Total N	Sample Numbers (if combined)[1]	N (if combined)	Brood or Return Years	Sample Years	Age	Comments
	108	S0500	Upper Salmon River at Sawtooth	spring	100			90	91	J	
	109	C0153	Imnaha River and Hatchery	spring	480	S0505, S0542, S0570, S0619, S0684	100, 100, 80, 100, 100	88, 88, 89, 89, 90	89, 90, 90, 91, 91	J, J, J, J, J	S0542 and S0619 are from Imnaha Hatchery, others are from Imnaha River
Washington Coast	110	C0155	Naselle Hatchery	fall	448	W87AZ, W88QY, W89AW, W90CN	100, 149, 99, 100	87, 88, 89, 90	87, 88, 89, 90	A, A, A, A	
	111	C90CU	Wynoochee River and Hatchery	fall	209	WDFW	-, -	90, 93	90, 93	A, A	
	112	C90CT	Wishkah River	fall	96	WDFW	-, -	90, 93	90, 93	A, A	
	113	W93FI	East Fork Satsop River	fall	102			93	93	A	
	114	C90CO	Skookumchuck River	spring	74	WDFW	-, -, -, -	90, 91, 92, 93, 94	90, 91, 92, 93, 94	A, A, A, A	
	115	W90CS	Humptulips Hatchery	fall	103			90	90	A	
	116	C0126	Quinault Hatchery	fall	200	S0203, W90CQ	100, 100	80, 90	81, 90	J, A	
	117	C0127	Queets River	fall	190	S0200, W90DS	120, 70	80, 90	81, 90	J, A	
	118	C0128	Hoh River	fall	176	S0087, S0086, W90DR	50, 50, 76	80, 81, 90	81, 82, 90	J, J, A	
	119	C0156	Sol Duc	spring	264	S0401, W88QW, W90BQ	40, 123, 101	87, 88, 90	87, 88, 90	A, A, A	
Strait of Juan de Fuca	120	W93FD	Hoko River	fall	80			93	93	A	
	121	C91EJ	Elwha River	fall	200	WDFW	-, -	88, 90	88, 90	A, A	
Puget Sound	122	C0180	North Fork Nooksack Hatchery and River	spring	255	W85CC, W88QK, W93EW	54, 109, 92	85, 88, 93	85, 88, 93	A, A, A	W88QK is from North Fork Nooksack River, others are from NF Nooksack Hatchery
	123	W93EI	South Fork Nooksack River	spring	51			93	93	A	
	124	W90BD	Skagit Hatchery	spring	92			90	90	A	
	125	W87GG	Skagit River	fall	69			87	87	A	
	126	W86BB	Sauk River	summer	74			86	86	A	
	127	C0158	Suiattle River	spring	543	W85AA, W86QG, W87AA, W88AA, W89AE, W90BB	77, 114, 49, 113, 95, 95, 100, 92	85, 86, 87, 88, 89, 90	85, 86, 87, 88, 89, 90	A, A, A, A, A, A	

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	128	C0187	Sauk River	spring	147	W86AA, W94EL	100, 47	86, 94	86, 94	A, A	
	129	C93EZ	Cascade River	spring	84	WDFW	-, -	93, 94	93, 94	A, A	
	130	C0188	Skagit River	summer	284	W86GG, C94DV, (C94DV)	100, 184	86, 94, 95	86, 94, 95	A, A, A	
	131	C0099	North Fork Stilliguamish River	summer	106	W87AK, W88QN	70, 36	87, 88	87, 88	A, A	
	132	C0116	Skykomish River	summer	235	W87AM, W88AE, W89BC	54, 105, 76	87, 88, 89	87, 88, 89	A, A, A	
	133	C0101	Bridal Veil Creek	summer	87	W87QR, W88BP	5, 82	87, 88	87, 88	A, A	
	134	W87BE	Skykomish Hatchery	fall	106			87	87	A	
	135	W89BD	Wallace River	fall	82			89	89	A	
	136	C0117	Sultan River	fall	95	W87BL, W88QO, W89BE	18, 26, 51	87, 88, 89	87, 88, 89	A, A, A	
	137	W88AF	Snoqualmie River	fall	101			88	88	A	
	138	C0157	Green River Hatchery	fall	398	S0084, W87AS, W88QG, W90CJ	99, 100, 100, 99	80, 87, 88, 90	81, 87, 88, 90	J, A, A, A	
	139	C92ES	Puyallup Hatchery	fall	150	WDFW	-, -	92, 93	92, 93	A, A	
	140	C92EP	White River Hatchery	spring	400	WDFW	-, -	92, 93	92, 93	A, A	
	141	C92ER	South Prairie Creek	fall	86	WDFW	-, -	92, 93	92, 93	A, A	
	142	C0055	Deschutes Hatchery	fall	250	S0056, W87AY	150, 100	80, 87	80, 87	J, A	
	143	C0066	Hoodsport Hatchery	fall	248	S0088, W88QU	98, 150	80, 88	81, 88	J, A	
Lower Fraser River	144	C0160	Chehalis Hatchery and Harrison River	fall	440	W88EC, W89CO, W89CB, W90EI	100, 150, 100, 90	88, 89, 89, 90	88, 89, 89, 90	A, A, A, A	W89CB is from Harrison River, others are from Chehalis Hatchery
	145	C0159	Chilliwack Hatchery	fall	87	W89CP, W90EJ	51, 36	89, 90	89, 90	A, A	
Lower Thompson River	146	S0374	Spius Creek	spring	158			86	87	J	
	147	S0375	Nicola River	summer	196			86	87	J	
	148	C0070	Coldwater River	spring	202	S0035, S0372	42, 160	82, 86	82, 87	A, J	
	149	S0376	Bonaparte River	spring	120			86	87	J	

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	150	S0373	Deadman River	spring	120			86	87	J	
South Thompson River	151	S0385	Adams River	summer	102			87	87	A	
	152	C0071	Salmon River and Hatchery	summer	500	S0333, S0393, S0429	180, 160, 160	84, 86, 87	85, 87, 88	J, J, J	
	153	C0084	Eagle River and Hatchery	summer	460	S0061, S0392, S0431	180, 120, 160	84, 86, 87	85, 87, 88	J, J, J	
	154	S0394	Lower Shuswap River	summer	120			86	87	J	
	155	S0371	Middle Shuswap River	summer	160			86	87	J	
North Thompson River	156	C0085	Clearwater Hatchery and Horseshoe River	summer	342	S0034, S0334, S0390	45, 177, 120	82, 84, 86	82, 85, 87	A, J, J	S0390 is from Horseshoe River, others from Clearwater Hatchery and River
	157	S0391	White Horse Bluff	summer	120			86	87	J	
	158	S0370	Finn Creek	summer	160			86	87	J	
	159	S0389	North Thompson River	summer	185			86	87	J	
Mid Fraser River	160	S0387	Chilcotin River	spring	120			86	88	J	
	161	C0086	Chilko River	spring	267	S0031, S0369, W88EJ	49, 120, 98	82, 86, 88	82, 87, 88	A, J, A	
	162	C0120	Quesnel Hatchery and River	spring	716	S0201, S0202, S0365, S0366, S0430, W88EI, W90AF	100, 80, 80, 80, 120, 100, 156	84, 84, 86, 86, 87, 88, 89	85, 85, 87, 87, 88, 88, 89	J, J, J, J, J, A, J	
	163	S0367	Lower Cariboo River	spring	160			86	87	J	
	164	C0022	Upper Cariboo River	spring	180	S0339, S0368	100, 80	84, 86	85, 87	J, J	
	165	C0072	Cottonwood River	spring	220	S0340, S0362	100, 120	84, 86	85, 87	J, J	
	166	C0073	Blackwater River	spring	334	S0341, S0363	174, 160	84, 86	85, 87	J, J	
	167	C0074	Baezaeko River	spring	300	S0342, S0361	180, 120	84, 86	85, 87	J, J	
Upper Fraser River	168	C0075	Willow River	spring	256	S0343, S0388	140, 116	84, 86	85, 87	J, J	
	169	C0076	Bowron River	spring	270	S0016, S0360	150, 120	84, 86	85, 87	J, J	
	170	S0378	Slim Creek	spring	140			86	87	J	

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	171	S0382	Walker Creek	spring	120			86	87	J	
	172	S0383	Morkill River	spring	120			86	87	J	
	173	S0381	Horsey River	spring	160			86	87	J	
	174	S0384	Swift Creek	spring	120			87	87	A	
	175	C0068	Fraser River at Tete Jaune	spring	137	S0271, W88EH	38, 99	82, 88	82, 88	A, A	
Southern British Columbia	176	C0185	Tenderfoot Hatchery	summer	435	S0265, W88EK, C91DG, C91DG	150, 88, -, -	84, 88, 91, 92	85, 88, 91, 92	J, A, A, A	
	177	W91DP	Bute Inlet	fall	109			91	91	A	
	178	C0161	Cowichan Hatchery	fall	484	W88EA, W89CN, W90EH	171, 200, 113	88, 89, 90	88, 89, 90	A, A, A	
	179	C0162	Nanaimo Hatchery	fall	241	S0349, W88ED, W89CM, W90EG	100, 70, 31, 40	84, 88, 89, 90	85, 88, 89, 90	J, A, A, A	
	180	C0163	Nanaimo Lake	summer	104	W89CL, W90EF	82, 22	89, 90	89, 90	A, A	
	181	C0164	Big Qualicum Hatchery	fall	537	S0013, S0350, W88EG, W89CQ, W90ED	85, 100, 152, 100, 100	80, 84, 88, 89, 90	81, 85, 88, 89, 90	J, J, A, A, A	
	182	W91DH	Puntledge Hatchery	summer	60			91	91	A	
	183	C0165	Quinsam Hatchery	fall	643	S0204, S0351, W88EF, W89CR, W90EC	97, 97, 150, 149, 150	81, 84, 88, 89, 90	81, 85, 88, 89, 90	A, J, A, A, A	
	184	C0166	Robertson Creek Hatchery	fall	300	S0216, S0356, S0698	100, 100, 100	81, 84, 91	81, 85, 91	A, J, A	
	185	C91FP	Kennedy River	fall	150	WDFW	-, -	91, 92	91, 92	A, A	
	186	C0202	Sucwoa and Conuma Rivers	fall	180	S0353, S0355, W92EC	40, 40, 100	84, 84, 92	85, 85, 92	J, J, A	S0353 is from Sucwoa R, others are from Conuma R
Central Coast British Columbia	187	C0167	Wannock River	fall	180	S0452, S0699	80, 100	88, 91	88, 91	A, A	
	188	C0079	Kitimat river	summer	190	S0119, S0425	90, 100	84, 88	85, 88	J, A	

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	189	C0168	Atnarko River	spring	329	S0009, S0593, S0694	150, 80, 99	84, 90, 91	85, 90, 91	J, A, A	
Skeena River	190	C0192	Kitsumkalum River	summer	338	S0442, S0521, S0688, S0689, S1036, S1086	40, 60,111, 70, 25, 32	88, 89, 91, 91, 95, 96	88, 89, 91, 91, 95, 96	A, A, A, A, A, A	
	191	S0687	Cedar River	spring	100			91	91	A	
	192	S0690	Kitwanga River	spring	111			91	91	A	
	193	C0203	Bulkley River	spring	272	S0470, S0691, S1056	80, 112, 80	88, 91, 95	89, 91, 95	J, A, A	
	194	C0194	Morice River	spring	176	S0692, S1042, S1087	100, 50, 26	91, 95, 96	91, 95, 96	A, A, A	
	195	C0190	Kispiox River	spring	105	S0471, S1035	80, 25	88, 95	89, 95	J, A	
	196	C0191	Babine River	spring	313	S0008, S0454, S1044, S1085	39, 74, 50, 150	82, 88, 95, 96	82, 88, 95, 96	A, A, A, A	
	197	C0193	Bear River	spring	243	S0693, W88FF, S1037	118, 100, 25	88, 91, 95	88, 91, 95	A, A, A	
Nass River	198	C0082	Cranberry River	spring	93	S0419, S0472	33, 60	88, 89	88, 89	A, A	
	199	S0453	Damdochax River	spring	75			88	88	A	
Southeast Alaska	200	C0220	Little Tahltan River	spring	328	A89TH,W90EV, A90TH,A91TH	101,100,50, 77	89,90,90 ,91	89,90,90,9 1	A,A,A,A	
	201	C0204	Chickamin River		151	A89CH, A90CH	100, 51	89, 90	89, 90	A	
	202	A89CL	Clear Creek		33			89	89	A	
	203	A88CC	Cripple Creek		121			88	88	A	
	204	A89GE	Gene's Lake Creek		67			89	89	A	
	205	A89HA	Harding River		45			89	89	A	
	206	C0205	North Arm Creek and Andrews Creek		168	A89NR, A89AN	18, 150	89, 89	89, 89	A, A	
	207	A93SH	Shakes Creek		29			93	93	A	
	208	C0207	Farragut River		186	A89FA, f0015, f0016, f0017	8, 38, 55, 85	89, 92, 93, 93	89, 93, 93, 94	A, J, A, J	

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	209	C0221	King Salmon River		100	A88KS, A89KS, A90KS,F0019	37, 31, 18,14	88, 89, 90,92	88, 89, 90,92	A, A, A,A	
	210	C0209	Nakina River		198	A89NA, A90NA	104, 94	89, 90	89, 90	A, A	
	211	C0210	Kowatua Creek		190	A89KO, A90KO	95, 95	89, 90	89, 90	A, A	
	212	C0211	Tatsatua Creek		228	A89LT, A90LT	112, 116	89, 90	89, 90	A, A	
	213	A90DU	Dudidontu River		28			90	90	A	
	214	A89TS	Tseta River		81			89	89	A	
	215	C0212	Upper Nahlin River		129	A89UN, A90UN	81, 48	89, 90	89, 90	A, A	
	216	C0213	Big Boulder Creek		73	A91BB, f0021, f0022	27, 21, 25	91, 92, 93	91, 92, 93	A, A, A	
	217	C0219	Tahini River		162	A89TA, A90TA, A91TA,F0025	26, 48, 19,69	89, 90, 91,92	89, 90, 91,92	A, A, A,A	
	218	C0215	Klukshu River		250	A89KL, A90KL, A91KL	105, 100, 45	89, 90, 91	89, 90, 91	A, A, A	
	219	C0216	Situk River		174	A90SI, A91SI, A92SI	31, 65, 78	90, 91, 92	90, 91, 92	A, A, A	
	220	F0001	Chickamin River LPW		100			93	93	A	Hatchery: Little Port Walter Hatchery, Chickamin Strain
	221	F0004	Chickamin River WHL		155	F0002, F0003	100, 55	92, 94	92, 94	A, A	Hatchery: Whitman Lake Hatchery, Chickamin strain
	222	F0005	Chickamin River		150			94	95	J	
	223	F0008	Unuk River DMT		153	F0006, F0007	100, 53	92, 94	92, 94	A, A	Hatchery: Deer Mountain Hatchery, Unuk strain
	224	F0009	Unuk River LPW		100			93	93	A	Hatchery: Little Port Walter Hatchery, Unuk strain
	225	F0010	Unuk River		150			93	94	J	
	226	F0011	Andrew Creek CRL		100			92	92	A	Hatchery: Crystal Lake Hatchery, Andrew strain

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	227	F0014	Andrew Creek HFL		210	F0012, F0013	60, 150	94, 93	94, 94	A, J	Hatchery: Hidden Falls Hatchery, Andrew strain
	228	F0020	King Salmon River LPW		100			93	93	A	Hatchery: Little Port Walter Hatchery, King Salmon strain
	229	F0024	Kelsall River		45			92	92	A	
Copper River	230	F0026	Klutina River		23			91	91	A	
	231	F0027	Gulkana River		94			93	94	J	
	232	F0028	Kasilof River CCR		87			92	92	A	Hatchery: Crooked Creek Hatchery, Kasilof strain
Kenai River	233	F0029	Kenai River		150			92	93	J	
Susitna River	234	F0030	Talachulitna Creek		53			95	95	A	
	235	F0031	Deception Creek		103			91	91	A	
	236	F0032	Moose Creek Deshka		51			95	95	A	
	237	F0033	Prairie Creek		52			95	95	A	
Kodiak Island	238	F0034	Karluk River		67			93	93	A	
	239	F0035	Ayakulik River		100			93	93	A	
South Peninsula	240	F0036	Chignik River		47			95	95	A	
North Peninsula	241	F0037	Nelson Lagoon		150			94	95	J	
Bristol Bay	242	F0038	Naknek River		100			95	95	A	
	243	F0041	Stuyahok River		87	F0039, F0040	36, 51	93, 94	93, 94	A, A	
	244	F0044	Nushagak River		153	F0042, F0043	53, 100	93, 94	93, 94	A, A	
	245	F0047	Togiak River		163	F0045, F0046	63, 100	93, 94	93, 94	A, A	
Goodnews River	246	F0048	Goodnews River		40			93	93	A	
Kanektok River	247	F0051	Kanektok River		78	F0049, F0050	31, 47	92, 93	92, 93	A, A	
Kuskokwim River	248	F0052	Tuluksak River		50			93	93	A	
	249	F0055	Kogrukluk River		100	F0053, F0054	50, 50	92, 93	92, 93	A, A	
	250	F0056	Stony River		100			94	94	A	

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Yukon River, Canada	251	F0058	Stony Creek		185			91	92	J	
Norton Sound	252	F0061	Unalakleet River		95	F0059, F0060	24, 71	92, 93	92, 93	A, A	
Russia	253	C0217	Kamchatka River		121	A92KM, A95KM	71, 50	92, 95	92, 95	A, A	
	254	C0218	Voroskaia River		55	A92VO, A95VO	40, 15	92, 95	92, 95	A, A	

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[1] First letter in sample number indicates collecting laboratory, and codes are as follows: (D) University of California, Davis; (S) Northwest Fisheries Science Center, National Marine Fisheries Service, Seattle, WA; (W) Washington Department of Fish and Wildlife, Olympia, Washington, (A) Auke Bay Laboratory, National Marine Fisheries Service, Juneau, AK; (F) Alaska Department of Fish and Game, Anchorage, AK. (C) indicates that the sample is a pooled sample.

OFFICE OF EQUAL OPPORTUNITY (OEO) STATEMENT