

Report to the North Pacific Fishery Management Council

**Genetic Stock Composition Analysis of Chum Salmon Bycatch Samples from the 2009
Bering Sea Trawl Fisheries**

Andrew Gray
Colby Marvin
Chris Kondzela
Tyler McCraney
Jeffrey R. Guyon, PhD

Auke Bay Laboratories
Alaska Fisheries Science Center
NOAA Fisheries
Ted Stevens Marine Research Institute
17109 Pt. Lena Loop Road
Juneau, AK 99801

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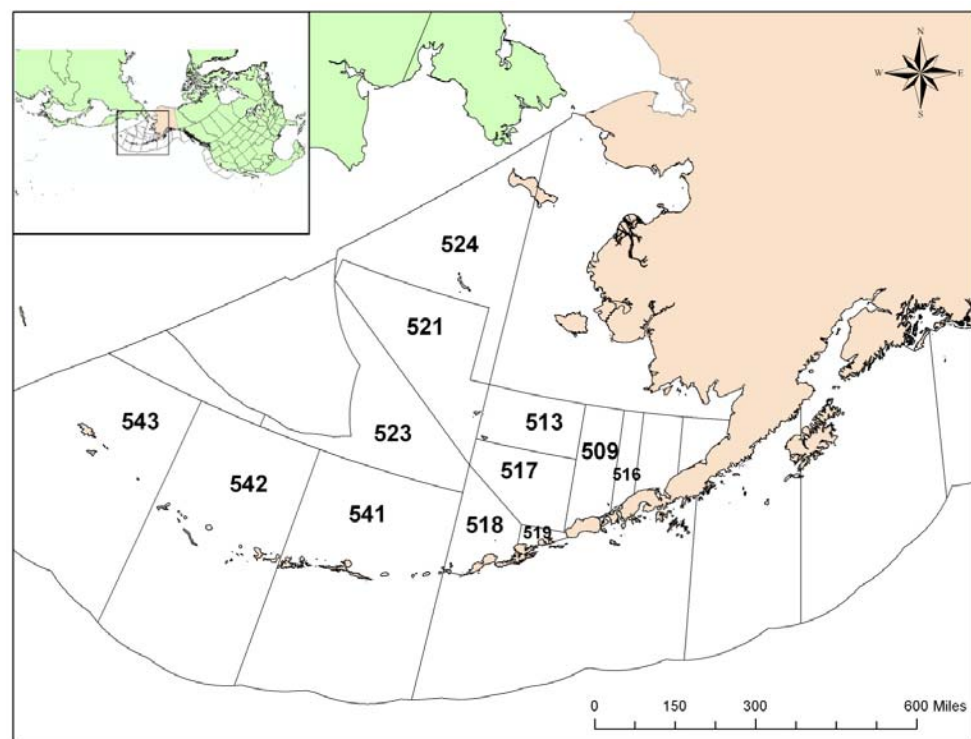
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Introduction

It is important to understand the stock composition of salmon caught in Bering Sea fisheries because this area is a known feeding habitat for multiple brood years of chum salmon (*Oncorhynchus keta*) from many different localities in North America and Asia. Determining the geographic origin of salmon caught in federally managed fisheries is essential to understanding whether management of federal fisheries could address conservation concerns. This report includes preliminary genetic stock identification results for a subset of chum salmon bycatch samples collected from the 2009 U.S. Bering Sea groundfish trawl fishery. The final analysis will be reported in a National Oceanic and Atmospheric Administration (NOAA) Technical Memorandum or other journal publication. National Marine Fisheries Service (NMFS) geographical statistical areas associated with the groundfish fishery are shown in Figure 1 and are used later in the report to describe the spatial distribution of the chum salmon bycatch and genetic samples.

Figure 1. Statistical areas associated with the Bering Sea Aleutian Island groundfish fishery.

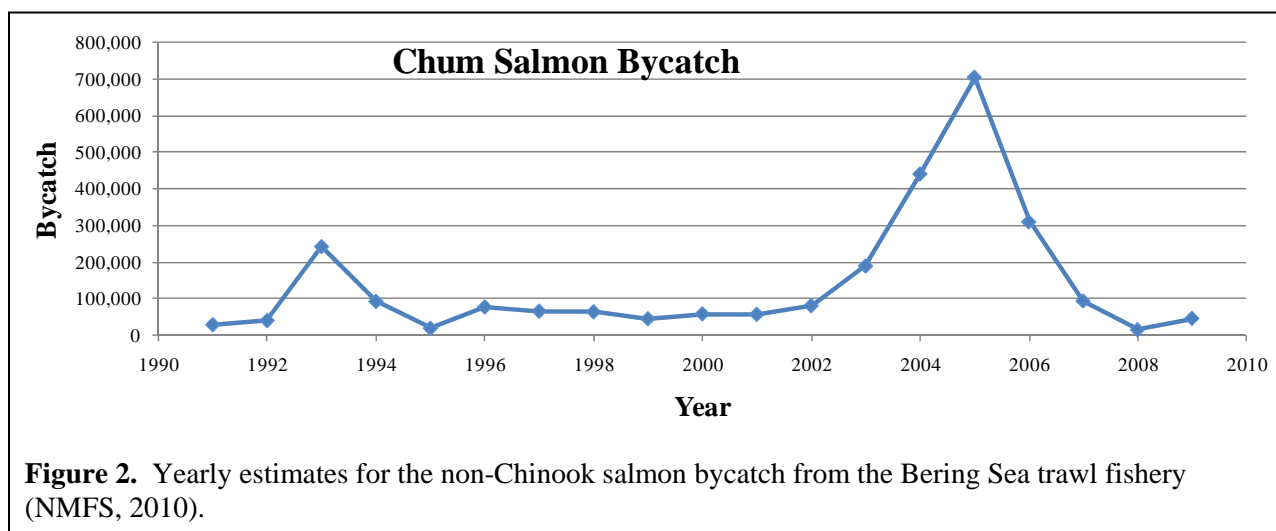


The goal of this report is to present a stock composition estimate for the 2009 chum salmon bycatch samples collected from the Bering Sea, but it is important to understand the limitations for making accurate estimates of the entire bycatch imposed by the sampling distribution and the genetic baseline. Hence, this report is divided into the following six sections: Introduction, Sample Distribution, Baseline Evaluation, Genetic Stock Composition, Comparison With Previous Estimates, and a Summary. For additional information regarding background and methodology, this report is intended to be supplemented with the chum salmon report prepared previously for the 2005 Bering Sea trawl fishery (Guyon et al., 2010). For the purpose of this report, the chum salmon genetic samples are designated as non-Chinook in the NMFS database since chum salmon comprise over 99.6% of the total non-Chinook bycatch (NPFMC, 2005).

Sample Distribution

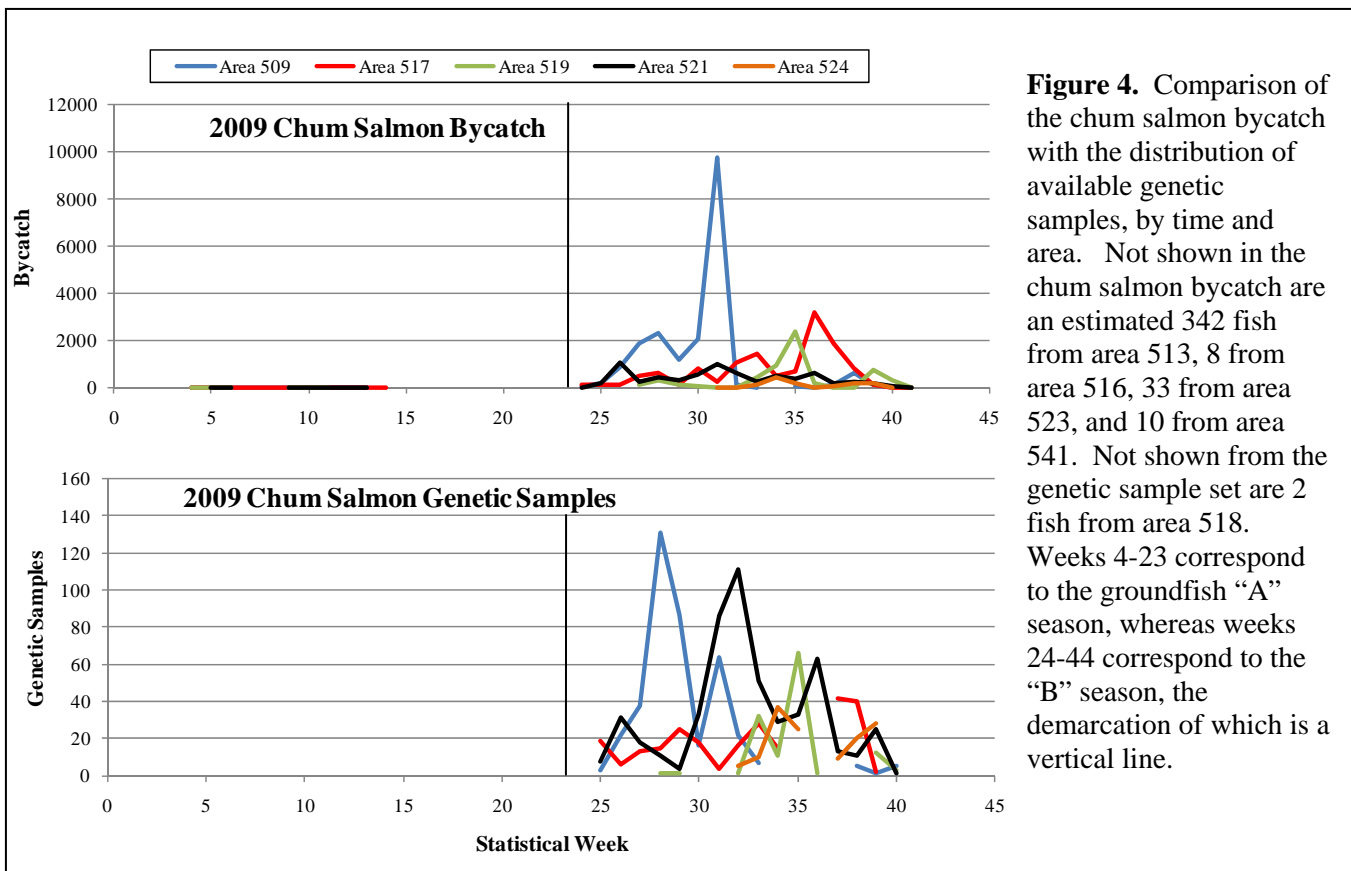
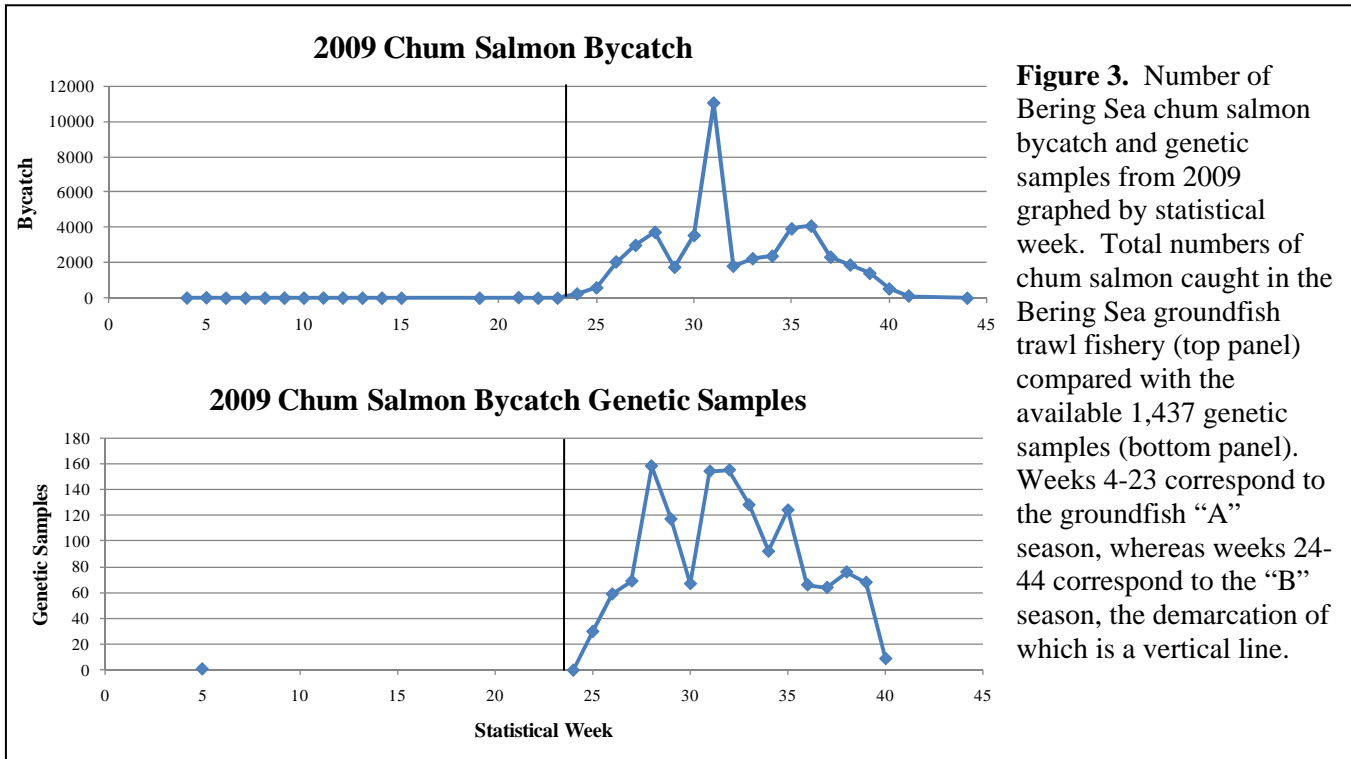
Genetic samples were collected by the Alaska Fisheries Science Center's (AFSC) North Pacific Observer Program in 2009 for the Auke Bay Laboratories as a Special Project (designated "Salmon Genetic Project"). As opposed to previous years when samples were collected opportunistically, genetic samples were collected in 2009 as part of the observer's species composition analysis. Axillary processes for genetic analysis and scales for ageing were collected throughout the season and stored in coin envelopes which were labeled, frozen and shipped to the Auke Bay Laboratories.

In 2009, an estimated 46,617 chum salmon were taken in the bycatch of the Bering Sea trawl fishery (NMFS, 2010). This number is 69% less than the average of 147,472 non-Chinook salmon taken in the bycatch between 1994-2009 and 36% less than the median of 71,612 during the same time period (Figure 2). The final genetic sample set for the 2009 chum bycatch was 1,437 fish corresponding to an overall sampling rate of 3.1%.



Potential biases associated with the collection of genetic samples from the bycatch are well documented, and have the potential to affect resulting stock composition estimates (Pella and Geiger, 2009). Methods to collect representative samples are now being reviewed by the Alaska Fisheries Science Center and, when implemented, will reduce biases and improve defensibility of overall stock composition estimates. Potential biases associated with the 2009 chum salmon bycatch sample set were evaluated by comparing the genetic sample distributions with the overall bycatch estimates. To evaluate temporal bias, bycatch estimates and genetic samples were graphed by statistical week (week ending on Sunday) and a visual comparison of the two distributions showed they were comparable (Figure 3).

To evaluate the sample spatial distribution, the chum salmon bycatch was compared with the bycatch samples by statistical area over time (Figure 4). Spatial and temporal sample biases can become more apparent at these higher resolution scales. For example, while high levels of both bycatch and genetic samples were available from statistical area 509, statistical area 521 was overrepresented in the genetic sample set. In addition, spatial bias may be further exacerbated by the uncertainty of catch location for samples collected from shoreside deliveries in which the hauls are mixed and the location of the catch was taken from the first haul of a fishing trip.



Baseline Evaluation

Baseline allele frequencies from the published chum salmon microsatellite baseline (Beacham et al., 2009a) were downloaded from the Fisheries and Oceans Canada (DFO) Molecular Genetics web page (http://www-sci.pac.dfo-mpo.gc.ca/mgl/data_e.htm) and a SPAM (ADFG, 2003) baseline file was created within Excel. While this baseline has been used to identify over 50 regional groupings of salmon (Beacham et al., 2009b), our analysis used 6 broad regional groupings to analyze the chum salmon bycatch to (1) ensure the most reliable estimates for this contentious issue and (2) ensure that enough samples from this diverse collection were from a particular region to positively identify it. Regional groupings were similar to that reported previously (Guyon et al., 2010), except (1) all of southeast Alaska, Prince William Sound, British Columbia, and Washington were grouped into one region and (2) 6 populations were moved from east Asia to north Asia (Naiba, Kalininka, Amur, Tym, Udarnitsa, Tugur_River). The resulting six regional groupings are shown in Figure 5 and individual populations from each region are identified in Appendix 1.

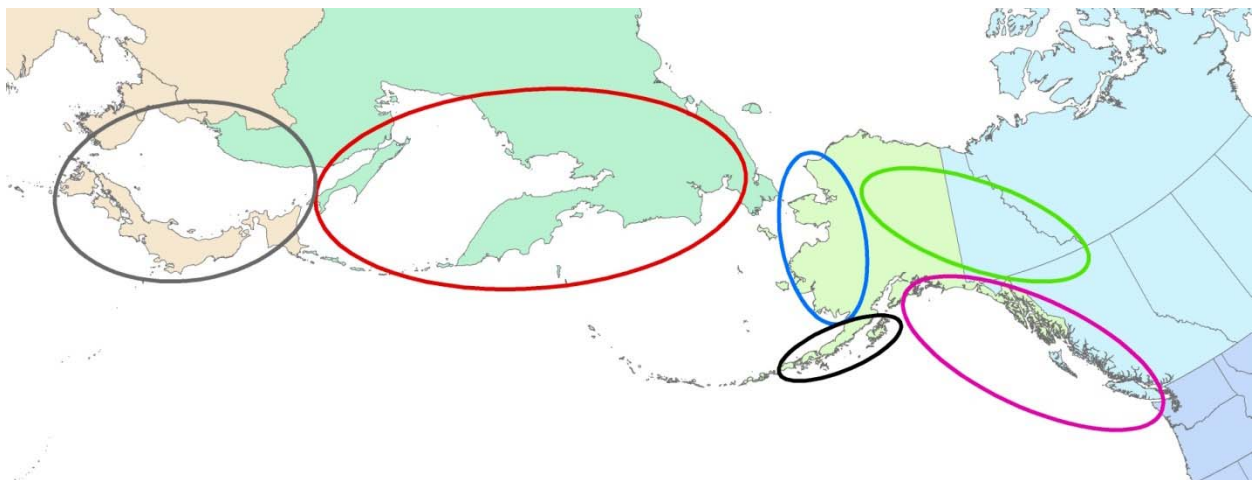


Figure 5. Six regional groupings of chum salmon populations used in the analysis including east Asia (grey), north Asia (red), coastal western Alaska (blue), upper/middle Yukon (green), southwest Alaska (black), and the Pacific Northwest (magenta).

The DFO baseline contains 381 populations of chum salmon assayed for 14 microsatellite markers (Beacham et al., 2009a). For our analysis, 11 markers were used: *Oki100*, *Omm1070*, *Omy1011*, *One101*, *One102*, *One104*, *One114*, *Ots103*, *Ots3*, *Ots68*, and *Ssa419*. *Oki2* and *One111* may be available in future analyses, pending optimization, while attempts to optimize the final locus, *Oke3*, have been unsuccessful. To evaluate the ability of the 11 loci to effectively separate the 6 regional groupings in mixed-stock analyses, 100% simulation studies were completed in which all samples of a hypothetical mixture were from one region and that mixture was re-evaluated against the baseline to determine the percentage reallocating back to the correct region. This analysis was completed in SPAM for all six regions (Table 1, top panel). East Asia, western Alaska, upper/middle Yukon, and the Pacific Northwest all allocated back to the correct region with 89-98% accuracy, whereas 85% correctly reallocated to the north Asia region and 82% correctly reallocated to the southwest Alaska region. In an effort to improve stock composition accuracy, the baseline was reevaluated with a subset of loci to increase resolution of the southwest Alaska region and the 100% simulation analyses were repeated (Table 1, bottom panel). With a suite of eight loci, the accuracies of estimates were improved with all simulations now at or above 87%. Based on these results, stock composition estimates are provided based on the allele frequencies for

all loci and for the suite of eight loci. Further analyses of marker characteristics are currently ongoing to determine effects of allele number and frequency.

Table 1. Results from simulation studies in which 100% of a hypothetical mixture of 400 fish was derived from one region (columns) and reallocated back to the region (rows) with SPAM software. The fraction of fish from each region is designated.

Results based on all 11 loci

Region	<i>E. Asia</i>	<i>N. Asia</i>	<i>W. AK</i>	<i>U. Yukon</i>	<i>SW AK</i>	<i>PNW</i>
<i>East Asia</i>	0.886	0.028	0.002	0.001	0.008	0.001
<i>North Asia</i>	0.026	0.851	0.010	0.002	0.054	0.008
<i>Western Alaska</i>	0.005	0.049	0.960	0.059	0.040	0.002
<i>Upper/Middle Yukon</i>	0.000	0.002	0.010	0.934	0.001	0.000
<i>Southwest Alaska</i>	0.001	0.007	0.004	0.000	0.819	0.003
<i>Pacific Northwest</i>	0.011	0.043	0.010	0.002	0.071	0.977

Results based on 8 loci (*Oki100*, *One101*, *One104*, *Ots103*, *Ots3*, *Ots68*, *Omy1011*, *Ssa419*)

Region	<i>E. Asia</i>	<i>N. Asia</i>	<i>W. AK</i>	<i>U. Yukon</i>	<i>SW AK</i>	<i>PNW</i>
<i>East Asia</i>	0.946	0.023	0.002	0.001	0.006	0.001
<i>North Asia</i>	0.020	0.885	0.011	0.002	0.040	0.008
<i>Western Alaska</i>	0.004	0.035	0.955	0.045	0.033	0.002
<i>Upper/Middle Yukon</i>	0.000	0.002	0.014	0.951	0.001	0.000
<i>Southwest Alaska</i>	0.001	0.008	0.005	0.001	0.866	0.004
<i>Pacific Northwest</i>	0.007	0.037	0.011	0.001	0.051	0.983

Genetic Stock Composition

DNA was extracted from the axillary processes of the chum salmon bycatch genetic samples and microsatellite genotyping was performed as described previously (Guyon et al., 2010). Briefly, samples were genotyped for the following 11 microsatellite loci *Oki100* (Beacham et al., 2009c), *Omm1070* (Rexroad et al., 2001), *Omy1011* (Spies et al., 2005), *One101*, *One102*, *One104*, *One114* (Olsen et al., 2000), *Ots103* (Nelson and Beacham, 1999), *Ots3* (Banks et al., 1999), *Ots68* (Williamson et al., 2002), and *Ssa419* (Cairney et al., 2000). Thermal cycling for the amplification of DNA fragments with the polymerase chain reaction (PCR) was performed on a dual 384-well GeneAmp PCR System 9700 (Applied Biosystems, Inc.). Samples from the PCR reactions were diluted into 96-well plates for analysis with a 16-capillary, 36 cm array on the ABI 3130xl Genetic Analyzer. Genotypes were double-scored with GeneMapper 4.0 software (Applied Biosystems, Inc.) and exported to Excel spreadsheets (Microsoft, Inc.) for further analysis.

A total of 1,563 samples from the 2009 chum salmon bycatch were analyzed, of which 1,442 samples were successfully genotyped for 8 or more of the 11 loci and analyzed in GenAEx (Peakall and Smouse, 2006) for data integrity. Two duplicate samples (individuals) were removed. In addition, 3 of the remaining 1,440 samples (individuals) were removed due to an unusual excess of homozygotes (between 7 and 10 of the 11 loci were homozygous or not scored). Internal observations have suggested that unusually high homozygosity rates can potentially result from poor DNA quality, although it is unlikely that the affected 3 samples would impact the resulting stock composition estimates. The remaining 1,437 samples used in this analysis had genetic information for an average of 10.77 loci (out of 11). There were 1,226 samples with data for all 11 loci, 123 with 10 loci, 50 with 9 loci, and 38 with 8 loci. There were only 13 individual allele calls which referenced alleles not present in the chum salmon baseline; those alleles were pooled with a baseline allele nearest in size.

To generate the BAYES baseline, a program was written in C to convert the allele frequencies from the SPAM format into allele counts for the BAYES format. For the mixture files, allele designations were converted to match those in the baseline. Genotypes from converted mixtures were then exported from Excel as text files, and C programs were used to format the data into both SPAM and BAYES mixture files. Stock composition analysis was performed with both the SPAM and BAYES software by using previously published procedures (ADFG, 2003; Pella and Masuda, 2001). BAYES software uses a Bayesian algorithm to produce stock composition estimates and can account for missing alleles in the baseline (Pella and Masuda, 2001). BAYES stock composition estimates were derived using all available 11 loci in the mixture (Table 2, top panel). For each BAYES analysis, six Monte Carlo chains starting at disparate values of stock proportions were configured such that 95% of the stocks came from one designated region with weights equally distributed among the stocks of that region. The remaining 5% was equally distributed among remaining stocks from all other regions. For all estimates, a flat prior of 0.002625 (calculated as 1/381) was used for all 381 populations. The analyses were completed for a chain length of 10,000 with the first 5,000 deleted during the burn-in phase when determining overall stock compositions. Convergence of the chains to posterior distributions of stock proportions was determined with Gelman and Rubin shrink statistics, which were all 1.07 or less (Table 2, top panel) conveying strong convergence to a single posterior distribution (Pella and Masuda, 2001).

Table 2. Regional SPAM and BAYES stock composition estimates for 1,437 chum salmon samples from the bycatch of the 2009 season Bering Sea groundfish trawl fishery. BAYES estimates utilized information from all 11 loci whereas SPAM estimates were derived from both 11 and 8 informative loci. The BAYES mean estimates are provided with standard deviations (SD), 95% credible intervals, median estimate, and the associated Gelman and Rubin shrink statistic. Standard deviations and 90% nonsymmetric confidence intervals for the SPAM estimates were determined by the analysis of 500 bootstrapping resamplings of the mixture.

BAYES

<u>Region</u>	<u>Mean</u>	<u>SD</u>	<u>2.5%</u>	<u>Median</u>	<u>97.5%</u>	<u>Shrink</u>
<i>East Asia</i>	0.338	0.014	0.311	0.338	0.364	1.00
<i>North Asia</i>	0.298	0.016	0.267	0.298	0.329	1.00
<i>Western Alaska</i>	0.125	0.013	0.100	0.125	0.151	1.04
<i>Upper/Middle Yukon</i>	0.024	0.007	0.012	0.024	0.040	1.07
<i>Southwest Alaska</i>	0.036	0.007	0.023	0.035	0.050	1.00
<i>Pacific Northwest</i>	0.180	0.012	0.157	0.179	0.203	1.01

SPAM

<u>Region</u>	11 Loci				8 Loci			
	<u>Estimate</u>	<u>SD</u>	<u>Lower</u>	<u>Upper</u>	<u>Estimate</u>	<u>SD</u>	<u>Lower</u>	<u>Upper</u>
<i>East Asia</i>	0.299	0.013	0.278	0.319	0.304	0.013	0.283	0.325
<i>North Asia</i>	0.265	0.015	0.245	0.294	0.288	0.016	0.265	0.316
<i>Western Alaska</i>	0.149	0.012	0.129	0.168	0.135	0.012	0.119	0.158
<i>Upper/Middle Yukon</i>	0.025	0.005	0.017	0.033	0.024	0.005	0.012	0.029
<i>Southwest Alaska</i>	0.035	0.006	0.023	0.044	0.039	0.007	0.027	0.049
<i>Pacific Northwest</i>	0.199	0.012	0.175	0.213	0.198	0.012	0.175	0.215
<i>Unknown</i>	0.029				0.013			

In contrast to the BAYES analysis, the SPAM software uses a maximum likelihood approach in which the mixture genotypes are compared directly with the baseline. Although Version 3.7 of the

SPAM software allows Bayesian modeling of baseline allele frequencies, these options were not utilized for the stock composition analyses. By comparing if there was a difference between the SPAM (which does not account for rare alleles) and BAYES (which can account for rare alleles) estimates, it was possible to determine if rare alleles could be adversely influencing the resulting stock composition estimates. Two SPAM estimates were provided using the maximum likelihood approach, one with all 11 and another with 8 loci for comparison purposes (Table 2, bottom panel). Convergence of the SPAM estimates was monitored with the “Percent of Maximum” value which was determined to be 92.2 for the 11 loci analysis and 90.3 for the 8 loci analysis, both exceeding the 90% guaranteed percent achievement of the maximal likelihood. While stock composition estimates for the two sets of loci were nearly identical (Table 2, bottom table, see overlapping 90% nonsymmetric bootstrap confidence intervals), it was interesting to note that the SPAM estimates derived from the 8 loci were closer to the BAYES estimates. In general, these 8 loci had lower numbers of alleles than the 3 unused loci, although the mechanism of this result is still under investigation.

Comparison With Previous Estimates

The stock composition results from the analysis of the 2009 chum salmon bycatch samples are in general agreement with previous estimates (Figure 6), particularly with the 2005 season. The primary difference in the stock composition of the chum salmon bycatch appears to be the higher contribution from east Asia and lower contribution from western Alaska in more recent years. However, caution must be used in comparisons across years as there are differences in where and when genetic bycatch samples were collected from year-to-year. The 1994-1995 chum bycatch estimates were produced with allozyme data (Wilmot et al. 1998), whereas the 2005 (Guyon et al. 2010) and 2009 chum salmon bycatch estimates were derived from DNA based microsatellite loci. The allozyme and microsatellite DNA baselines have data from many of the same populations, but there is some non-overlap.

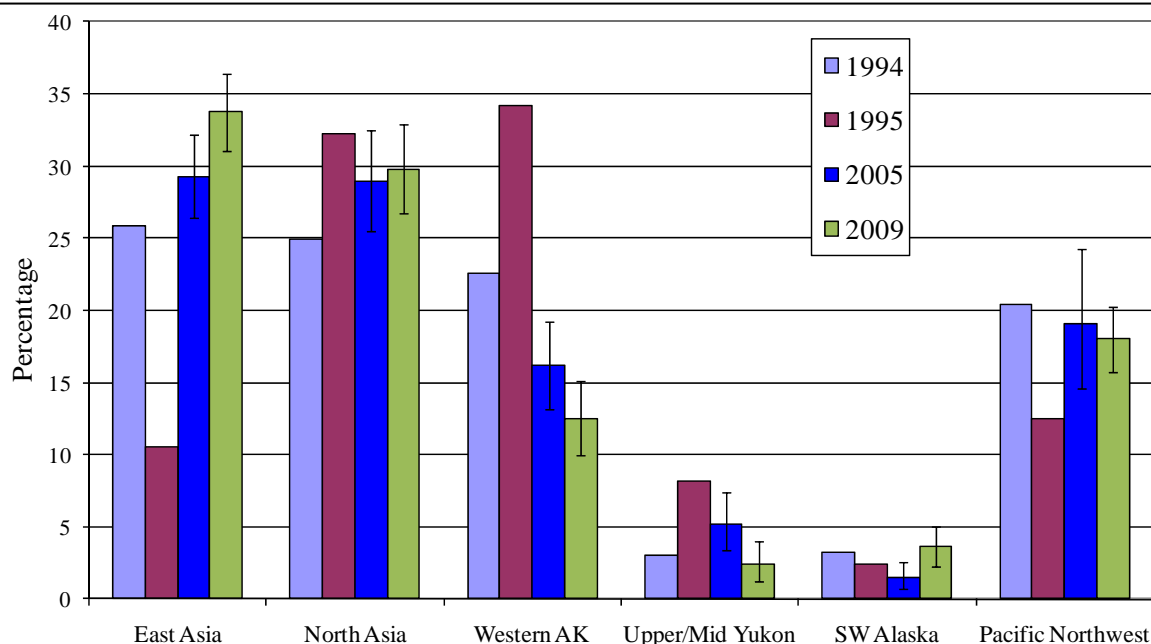


Figure 6. Comparison of yearly stock composition estimates of available genetic samples from the Bering Sea chum salmon bycatch. The 1994-1995 estimates were derived with allozyme loci, and the 2005 and 2009 estimates were produced with DNA based loci. 95% BAYES confidence intervals are shown for the DNA-based analyses.

Summary

Communities in western Alaska and elsewhere are dependent on salmon for subsistence and commercial purposes. Decreasing salmon returns to western Alaska have caused hardships in these communities. Salmon-dependent communities have expressed concern regarding the numbers of salmon caught as bycatch in the Bering Sea pollock fishery. Stock composition estimates of the salmon bycatch are needed for pollock and salmon fishery managers to understand whether the pollock fisheries may be impacting salmon returns. While stock composition estimates were developed for available 2009 chum salmon bycatch sample set, work remains before unbiased estimates of the entire bycatch can be produced. This report provides a stock composition analysis of a set of 1,437 individuals sampled from the 2009 chum salmon bycatch. The limitations and results of this analysis are summarized below.

Sampling issues:

We highlight the inherent spatial and temporal biases in the 2009 sample set (Figures 3 and 4), which may limit the application of the genetic sample stock composition estimate to the entire 2009 chum salmon bycatch. Through a collaboration with the Alaska Department of Fish and Game, Auke Bay Laboratories is also currently investigating methods for mitigating the effects of bias in a different salmon bycatch sample set. Methods developed through that collaboration may be applicable in future analyses of the chum salmon bycatch.

With regard to improved sampling protocols, NMFS recently published a proposed rule and notice of availability for Amendment 91 to the Fishery Management Plan for Groundfish of the Bering Sea and Aleutian Islands Management Area (75 FR 14016, March 23, 2010). If approved, this rule would require that all salmon bycatch taken in the Bering Sea pollock fishery be sorted by species and counted to ensure compliance with the salmon bycatch caps for the pollock fishery. This may provide additional opportunity for observers to provide representative sampling of the salmon bycatch for genetic analysis, and improve the capability to characterize the origin of salmon taken as bycatch in the Bering Sea pollock fishery.

Evaluation of the baseline:

A chum salmon microsatellite DNA baseline developed by Dr. Beacham at the Fisheries and Oceans Canada was selected for this analysis and is the only publicly available baseline with known populations across the entire Pacific Rim (Beacham et al., 2009a). Genotype information from 11 loci provided discriminatory power to strongly identify the 6 stock distributions used in this analysis. These groupings were similar to regional groupings used in previous analyses using allozyme markers, thereby enabling comparison of the resulting estimates over time. A suite of eight loci selected to improve stock composition results for the southwest Alaska region showed improved accuracies in simulation analyses, although resulting stock composition estimates from this limited data set did not differ substantially from those produced using all 11 loci.

Stock composition estimates:

Overall, the genetic samples collected from the chum salmon bycatch were predominantly from Asian stocks (64%) although substantial contributions were also from western Alaska (13%) and the Pacific Northwest (18%). These are in general agreement with previous estimates; however, there appeared to be a higher contribution from east Asia and lower contribution from western Alaska in more recent years. Given the differences in where and when genetic bycatch samples were collected from year-to-year, caution must be used in comparisons across years. In addition, potential biases in the genetic sample set can adversely affect the stock composition estimates; therefore, estimates derived from these samples should be viewed as estimates of the sample set rather than estimates of the entire chum salmon bycatch.

Application of these estimates:

The extent to which any salmon stock is impacted by the bycatch of the Bering Sea trawl fishery is dependent on many factors including (1) the overall size of the bycatch, (2) the age of the salmon caught in the bycatch, (3) the age of the returning salmon, and (4) the total escapement of the affected stocks taking into account lag time for maturity and returning to the river. As such, a higher stock composition estimate one year does not necessarily infer greater impact than a smaller estimate the next. Efforts to better understand these relationships and their impacts are the subject of a NPRB proposal from Drs. Criddle and Adkison for which Auke Bay Laboratories is collaborating.

Acknowledgements

DNA was purified by Hanhvan Nguyen (NMFS). The baseline used for these analyses was obtained through a web portal sponsored by Fisheries and Oceans Canada and developed in the Molecular Genetics Laboratory with genetic loci identified in a number of laboratories. This document has been peer reviewed by internal and external reviewers.

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Appendices

Appendix 1. Chum salmon populations in the DFO microsatellite baseline with the regional designations used in the analyses of this report.

DFO Number	Population Name	Region Number	Region
41	Abashiri	1	East Asia
215	Avakumovka	1	East Asia
40	Chitose	1	East Asia
315	Gakko_River	1	East Asia
292	Hayatsuki	1	East Asia
44	Horonai	1	East Asia
252	Kawabukuro	1	East Asia
313	Koizumi_River	1	East Asia
300	Kushiro	1	East Asia
37	Miomote	1	East Asia
391	Namdae_R	1	East Asia
231	Narva	1	East Asia
298	Nishibetsu	1	East Asia
293	Ohkawa	1	East Asia
297	Orikasa	1	East Asia
214	Ryazanovka	1	East Asia
312	Sakari_River	1	East Asia
311	Shari_River	1	East Asia
36	Shibetsu	1	East Asia
299	Shikiu	1	East Asia
253	Shiriuchi	1	East Asia
310	Shizunai	1	East Asia
217	Suifen	1	East Asia
35	Teshio	1	East Asia
39	Tokachi	1	East Asia
38	Tokoro	1	East Asia
314	Tokushibetsu	1	East Asia
291	Toshibetsu	1	East Asia
296	Tsugaruishi	1	East Asia
316	Uono_River	1	East Asia
309	Yurappu	1	East Asia
218	Amur	2	North Asia
207	Anadyr	2	North Asia
384	Apuka_River	2	North Asia
382	Bolshaya	2	North Asia
380	Dranka	2	North Asia
223	Hairusova	2	North Asia
378	Ivashka	2	North Asia
213	Kalininka	2	North Asia
225	Kamchatka	2	North Asia
219	Kanchalan	2	North Asia
379	Karaga	2	North Asia
294	Kikchik	2	North Asia

DFO Number	Population Name	Region Number	Region
209	Kol_	2	North Asia
233	Magadan	2	North Asia
211	Naiba	2	North Asia
295	Nerpichi	2	North Asia
381	Okhota	2	North Asia
212	Oklan	2	North Asia
222	Ola_	2	North Asia
386	Olutorsky_Bay	2	North Asia
228	Ossora	2	North Asia
224	Penzhina	2	North Asia
385	Plotnikova_R	2	North Asia
221	Pymta	2	North Asia
220	Tauy	2	North Asia
383	Tugur_River	2	North Asia
226	Tym_	2	North Asia
230	Udarnitsa	2	North Asia
290	Utka_River	2	North Asia
208	Vorovskaya	2	North Asia
387	Zhypanova	2	North Asia
348	Agiapuk	3	Western Alaska
376	Alagnak	3	Western Alaska
3	Andreafsky	3	Western Alaska
357	Aniak	3	Western Alaska
301	Anvik	3	Western Alaska
80	Chulinak	3	Western Alaska
347	Eldorado	3	Western Alaska
358	George	3	Western Alaska
307	Gisasa	3	Western Alaska
371	Goodnews	3	Western Alaska
288	Henshaw_Creek	3	Western Alaska
339	Imnachuk	3	Western Alaska
361	Kanektok	3	Western Alaska
362	Kasigluk	3	Western Alaska
328	Kelly_Lake	3	Western Alaska
340	Kobuk	3	Western Alaska
343	Koyuk	3	Western Alaska
363	Kwethluk	3	Western Alaska
336	Kwiniuk_River	3	Western Alaska
303	Melozitna	3	Western Alaska
373	Mulchatna	3	Western Alaska
372	Naknek	3	Western Alaska
330	Niukluk	3	Western Alaska
329	Noatak	3	Western Alaska
345	Nome	3	Western Alaska
302	Nulato	3	Western Alaska
374	Nunsatuk	3	Western Alaska
13	Peel_River	3	Western Alaska
322	Pikmiktalik	3	Western Alaska
331	Pilgrim_River	3	Western Alaska

DFO Number	Population Name	Region Number	Region
346	Shaktoolik	3	Western Alaska
341	Snake	3	Western Alaska
368	Stuyahok_River	3	Western Alaska
375	Togiak	3	Western Alaska
154	Tozitna	3	Western Alaska
342	Unalakleet	3	Western Alaska
344	Ungalik	3	Western Alaska
8	Big_Creek	4	Upper/Middle Yukon
89	Big_Salt	4	Upper/Middle Yukon
86	Black_River	4	Upper/Middle Yukon
87	Chandalar	4	Upper/Middle Yukon
28	Chandindu	4	Upper/Middle Yukon
82	Cheena	4	Upper/Middle Yukon
81	Delta	4	Upper/Middle Yukon
7	Donjek	4	Upper/Middle Yukon
5	Fishing_Br	4	Upper/Middle Yukon
88	Jim_River	4	Upper/Middle Yukon
85	Kantishna	4	Upper/Middle Yukon
2	Kluane	4	Upper/Middle Yukon
59	Kluane_Lake	4	Upper/Middle Yukon
181	Koyukuk_late	4	Upper/Middle Yukon
90	Koyukuk_south	4	Upper/Middle Yukon
10	Minto	4	Upper/Middle Yukon
6	Pelly	4	Upper/Middle Yukon
439	Porcupine	4	Upper/Middle Yukon
83	Salcha	4	Upper/Middle Yukon
4	Sheenjek	4	Upper/Middle Yukon
1	Tatchun	4	Upper/Middle Yukon
9	Teslin	4	Upper/Middle Yukon
84	Toklat	4	Upper/Middle Yukon
360	Alagoshak	5	Southwest Alaska
333	American_River	5	Southwest Alaska
366	Big_River	5	Southwest Alaska
354	Coleman_Creek	5	Southwest Alaska
355	Delta_Creek	5	Southwest Alaska
359	Egegik	5	Southwest Alaska
332	Frosty_Creek	5	Southwest Alaska
365	Gertrude_Creek	5	Southwest Alaska
370	Joshua_Green	5	Southwest Alaska
364	Meshik	5	Southwest Alaska
283	Moller_Bay	5	Southwest Alaska
369	Pumice_Creek	5	Southwest Alaska
367	Stepovak_Bay	5	Southwest Alaska
335	Sturgeon	5	Southwest Alaska
350	Uganik	5	Southwest Alaska
334	Volcano_Bay	5	Southwest Alaska
356	Westward_Creek	5	Southwest Alaska
239	Ahnuhati	6	Pacific Northwest
69	Ahta_____	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
155	Ain_	6	Pacific Northwest
183	Algard	6	Pacific Northwest
58	Alouette	6	Pacific Northwest
325	Alouette_North	6	Pacific Northwest
270	Andesite_Cr	6	Pacific Northwest
428	Arnoup_Cr	6	Pacific Northwest
153	Ashlulm	6	Pacific Northwest
156	Awun	6	Pacific Northwest
133	Bag_Harbour	6	Pacific Northwest
164	Barnard	6	Pacific Northwest
16	Bella_Bell	6	Pacific Northwest
79	Bella_Coola	6	Pacific Northwest
49	Big_Qual	6	Pacific Northwest
201	Big_Quilcene	6	Pacific Northwest
281	Bish_Cr	6	Pacific Northwest
198	Bitter_Creek	6	Pacific Northwest
103	Blackrock_Creek	6	Pacific Northwest
390	Blaney_Creek	6	Pacific Northwest
138	Botany_Creek	6	Pacific Northwest
264	Buck_Channel	6	Pacific Northwest
169	Bullock_Chann	6	Pacific Northwest
61	Campbell_River	6	Pacific Northwest
323	Carroll	6	Pacific Northwest
78	Cascade	6	Pacific Northwest
76	Cayeghle	6	Pacific Northwest
42	Cheakamus	6	Pacific Northwest
398	Cheenis_Lake	6	Pacific Northwest
51	Chehalis	6	Pacific Northwest
19	Chemainus	6	Pacific Northwest
47	Chilliwack	6	Pacific Northwest
392	Chilqua_Creek	6	Pacific Northwest
117	Chuckwalla	6	Pacific Northwest
139	Clapp_Basin	6	Pacific Northwest
107	Clatse_Creek	6	Pacific Northwest
118	Clyak	6	Pacific Northwest
62	Cold_Creek	6	Pacific Northwest
77	Colonial	6	Pacific Northwest
353	Constantine	6	Pacific Northwest
168	Cooper_Inlet	6	Pacific Northwest
197	County_Line	6	Pacific Northwest
12	Cowichan	6	Pacific Northwest
414	Crag_Cr	6	Pacific Northwest
161	Dak_	6	Pacific Northwest
259	Dana_Creek	6	Pacific Northwest
123	Date_Creek	6	Pacific Northwest
250	Dawson_Inlet	6	Pacific Northwest
91	Dean_River	6	Pacific Northwest
261	Deena	6	Pacific Northwest
170	Deer_Pass	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
46	Demamiel	6	Pacific Northwest
210	Dipac_Hatchery	6	Pacific Northwest
319	Disappearance	6	Pacific Northwest
269	Dog-tag	6	Pacific Northwest
177	Draney	6	Pacific Northwest
114	Duthie_Creek	6	Pacific Northwest
427	East_Arm	6	Pacific Northwest
266	Ecstall_River	6	Pacific Northwest
94	Elcho_Creek	6	Pacific Northwest
193	Ellsworth_Cr	6	Pacific Northwest
203	Elwha	6	Pacific Northwest
276	Ensheshese	6	Pacific Northwest
263	Fairfax_Inlet	6	Pacific Northwest
32	Fish_Creek	6	Pacific Northwest
429	Flux_Cr	6	Pacific Northwest
102	Foch_Creek	6	Pacific Northwest
179	Frenchman	6	Pacific Northwest
227	Gambier	6	Pacific Northwest
96	Gill_Creek	6	Pacific Northwest
166	Gilttoyee	6	Pacific Northwest
145	Glendale	6	Pacific Northwest
135	Gold_Harbour	6	Pacific Northwest
11	Goldstream	6	Pacific Northwest
66	Goodspeed_River	6	Pacific Northwest
136	Government	6	Pacific Northwest
205	Grant_Creek	6	Pacific Northwest
100	Green_River	6	Pacific Northwest
450	GreenRrHatchery	6	Pacific Northwest
237	Greens	6	Pacific Northwest
141	Harrison	6	Pacific Northwest
438	Harrison_late	6	Pacific Northwest
64	Hathaway_Creek	6	Pacific Northwest
234	Herman_Creek	6	Pacific Northwest
17	Heydon_Cre	6	Pacific Northwest
407	Hicks_Cr	6	Pacific Northwest
400	Homathko	6	Pacific Northwest
411	Honna	6	Pacific Northwest
204	Hoodsport	6	Pacific Northwest
185	Hooknose	6	Pacific Northwest
406	Hopedale_Cr	6	Pacific Northwest
412	Hutton_Head	6	Pacific Northwest
278	Illiance	6	Pacific Northwest
152	Inch_Creek	6	Pacific Northwest
146	Indian_River	6	Pacific Northwest
92	Jenny_Bay	6	Pacific Northwest
115	Kainet_River	6	Pacific Northwest
144	Kakweiken	6	Pacific Northwest
268	Kalum	6	Pacific Northwest
395	Kanaka_Cr	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
402	Kano_Inlet_Cr	6	Pacific Northwest
162	Kateen	6	Pacific Northwest
389	Kawkawa	6	Pacific Northwest
95	Kemano	6	Pacific Northwest
192	Kennedy_Creek	6	Pacific Northwest
238	Kennell	6	Pacific Northwest
351	Keta_Creek	6	Pacific Northwest
101	Khutze_River	6	Pacific Northwest
126	Khutzeymateen	6	Pacific Northwest
282	Kiltuish	6	Pacific Northwest
93	Kimsquit	6	Pacific Northwest
187	Kimsquit_Bay	6	Pacific Northwest
419	Kincolith	6	Pacific Northwest
273	Kispiox	6	Pacific Northwest
106	Kitasoo	6	Pacific Northwest
99	Kitimat_River	6	Pacific Northwest
275	Kitsault_Riv	6	Pacific Northwest
163	Kitwanga	6	Pacific Northwest
271	Kleanza_Cr	6	Pacific Northwest
437	Klewnuggit_Cr	6	Pacific Northwest
21	Klinaklini	6	Pacific Northwest
418	Ksedin	6	Pacific Northwest
125	Kshwan	6	Pacific Northwest
423	Kumealon	6	Pacific Northwest
112	Kwakusdis_River	6	Pacific Northwest
436	Kxngeal_Cr	6	Pacific Northwest
127	Lachmach	6	Pacific Northwest
262	Lagins	6	Pacific Northwest
131	Lagoon_Inlet	6	Pacific Northwest
448	LagoonCr	6	Pacific Northwest
167	Lard	6	Pacific Northwest
160	Little_Goose	6	Pacific Northwest
50	Little_Qua	6	Pacific Northwest
413	Lizard_Cr	6	Pacific Northwest
119	Lockhart-Gordon	6	Pacific Northwest
176	Lower_Lillooet	6	Pacific Northwest
137	Mace_Creek	6	Pacific Northwest
242	Mackenzie_Sound	6	Pacific Northwest
116	MacNair_Creek	6	Pacific Northwest
55	Mamquam	6	Pacific Northwest
121	Markle_Inlet_Cr	6	Pacific Northwest
27	Martin_Riv	6	Pacific Northwest
338	Mashiter_Creek	6	Pacific Northwest
109	McLoughin_Creek	6	Pacific Northwest
178	Milton	6	Pacific Northwest
194	Minter_Cr	6	Pacific Northwest
254	Mountain_Cr	6	Pacific Northwest
111	Mussel_River	6	Pacific Northwest
157	Naden	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
337	Nahmint_River	6	Pacific Northwest
444	Nakut_Su	6	Pacific Northwest
14	Nanaimo	6	Pacific Northwest
122	Nangeese	6	Pacific Northwest
422	Nass_River	6	Pacific Northwest
399	Necleetsconnay	6	Pacific Northwest
113	Neekas_Creek	6	Pacific Northwest
321	Neets_Bay_early	6	Pacific Northwest
320	Neets_Bay_late	6	Pacific Northwest
173	Nekite	6	Pacific Northwest
104	Nias_Creek	6	Pacific Northwest
143	Nimkish	6	Pacific Northwest
53	Nitinat	6	Pacific Northwest
191	Nooksack	6	Pacific Northwest
186	Nooseseck	6	Pacific Northwest
318	NorrishWorth	6	Pacific Northwest
159	North_Arm	6	Pacific Northwest
377	Olsen_Creek	6	Pacific Northwest
184	Orford	6	Pacific Northwest
287	Pa-aat_River	6	Pacific Northwest
260	Pacofi	6	Pacific Northwest
56	Pallant	6	Pacific Northwest
65	Pegattum_Creek	6	Pacific Northwest
48	Puntledge	6	Pacific Northwest
98	Quaal_River	6	Pacific Northwest
147	Quap	6	Pacific Northwest
108	Quartcha_Creek	6	Pacific Northwest
199	Quinault	6	Pacific Northwest
110	Roscoe_Creek	6	Pacific Northwest
397	Salmon_Bay	6	Pacific Northwest
195	Salmon_Cr	6	Pacific Northwest
134	Salmon_River	6	Pacific Northwest
200	Satsop	6	Pacific Northwest
236	Sawmill	6	Pacific Northwest
410	Seal_Inlet_Cr	6	Pacific Northwest
158	Security	6	Pacific Northwest
130	Sedgewick	6	Pacific Northwest
393	Serpentine_R	6	Pacific Northwest
317	Shovelnose_Cr	6	Pacific Northwest
249	Shustnini	6	Pacific Northwest
206	Siberia_Creek	6	Pacific Northwest
25	Silverdale	6	Pacific Northwest
196	Skagit	6	Pacific Northwest
274	Skeena	6	Pacific Northwest
171	Skowquiltz	6	Pacific Northwest
447	SkykomishRiv	6	Pacific Northwest
132	Slatechuck_Cre	6	Pacific Northwest
43	Sliammon	6	Pacific Northwest
15	Smith_Cree	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
54	Snootli	6	Pacific Northwest
180	Southgate	6	Pacific Northwest
26	Squakum	6	Pacific Northwest
142	Squamish	6	Pacific Northwest
128	Stagoo	6	Pacific Northwest
265	Stanley	6	Pacific Northwest
52	Stave	6	Pacific Northwest
396	Stawamus	6	Pacific Northwest
409	Steel_Cr	6	Pacific Northwest
424	Stewart_Cr	6	Pacific Northwest
416	Stumaun_Cr	6	Pacific Northwest
327	Sugsaw	6	Pacific Northwest
324	Surprise	6	Pacific Northwest
75	Taaltz	6	Pacific Northwest
30	Taku	6	Pacific Northwest
18	Takwahoni	6	Pacific Northwest
251	Tarundl_Creek	6	Pacific Northwest
149	Theodosia	6	Pacific Northwest
22	Thorsen	6	Pacific Northwest
129	Toon	6	Pacific Northwest
279	Tseax	6	Pacific Northwest
202	Tulalip	6	Pacific Northwest
97	Turn_Creek	6	Pacific Northwest
430	Turtle_Cr	6	Pacific Northwest
247	Tuskwa	6	Pacific Northwest
165	Tyler	6	Pacific Northwest
33	Tzoonie	6	Pacific Northwest
124	Upper_Kitsumkal	6	Pacific Northwest
140	Vedder	6	Pacific Northwest
70	Viner_Sound	6	Pacific Northwest
45	Wahleach	6	Pacific Northwest
172	Walkum	6	Pacific Northwest
73	Waump	6	Pacific Northwest
232	Wells_Bridge	6	Pacific Northwest
352	Wells_River	6	Pacific Northwest
105	West_Arm_Creek	6	Pacific Northwest
267	Whitebottom_Cr	6	Pacific Northwest
326	Widgeon_Slough	6	Pacific Northwest
277	Wilauks_Cr	6	Pacific Northwest
120	Wilson_Creek	6	Pacific Northwest
401	Worth_Creek	6	Pacific Northwest
60	Wortley_Creek	6	Pacific Northwest
248	Yellow_Bluff	6	Pacific Northwest
434	Zymagotitz	6	Pacific Northwest

