



NOAA Technical Memorandum NMFS-AFSC-220

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J. R. Guyon

**U.S. DEPARTMENT OF COMMERCE**

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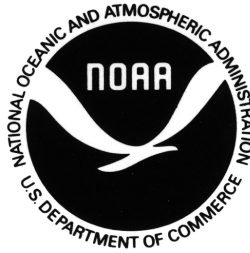
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J. R. Guyon

Alaska Fisheries Science Center  
Auke Bay Laboratories  
17109 Lena Point Loop Road  
Juneau, AK 99801  
*www.afsc.noaa.gov*

## **U.S. DEPARTMENT OF COMMERCE**

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**National Oceanic and Atmospheric Administration**

Jane Lubchenco, Under Secretary and Administrator

**National Marine Fisheries Service**

Eric C. Schwaab, Assistant Administrator for Fisheries

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## ABSTRACT

A genetic analysis of samples from the chum salmon (*Oncorhynchus keta*) bycatch of the 2006 Bering Sea walleye pollock (*Theragra chalcogramma*) trawl fishery was undertaken to determine the overall stock composition of the sample set. Samples were genotyped for eleven microsatellite markers and results were estimated using the current chum salmon microsatellite baseline. In 2006, genetic samples were collected opportunistically as part of a special project, but sample biases have the potential to affect stock composition analysis results. Consequently, stock composition estimates apply to the sample set and may not represent the entire chum salmon bycatch. Based on the analysis of 1,367 chum salmon bycatch samples collected throughout the 2006 Bering Sea trawl fishery, North Asian (31%), East Asian (29%), and Eastern Gulf of Alaska/Pacific Northwest (25%) stocks dominated the sample set with smaller contributions from Western Alaska (8%) and Upper/Middle Yukon River (6%) stocks. The estimates for the 2006 chum salmon bycatch sample set were similar to the 2005 and 2009 chum salmon bycatch estimates, suggesting consistency of the regional stock contributions across years. Analysis of temporal groupings within the groundfish “B” season revealed changes in stock composition during the course of the season with decreasing contribution of Upper/Middle Yukon stocks over time, but leaves unanswered whether these changes are due to temporal or spatial differences in the sample set.



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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 (Myers et al. 2007, Davis et al. 2009, Urawa et al. 2009). Determining the geographic origin of salmon caught in federally managed fisheries is essential to understanding the effects that fishing has on chum salmon stocks, especially those with conservation concerns. This report includes genetic stock identification results for the chum salmon bycatch samples collected from the 2006 U.S. Bering Sea groundfish trawl fishery. 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.

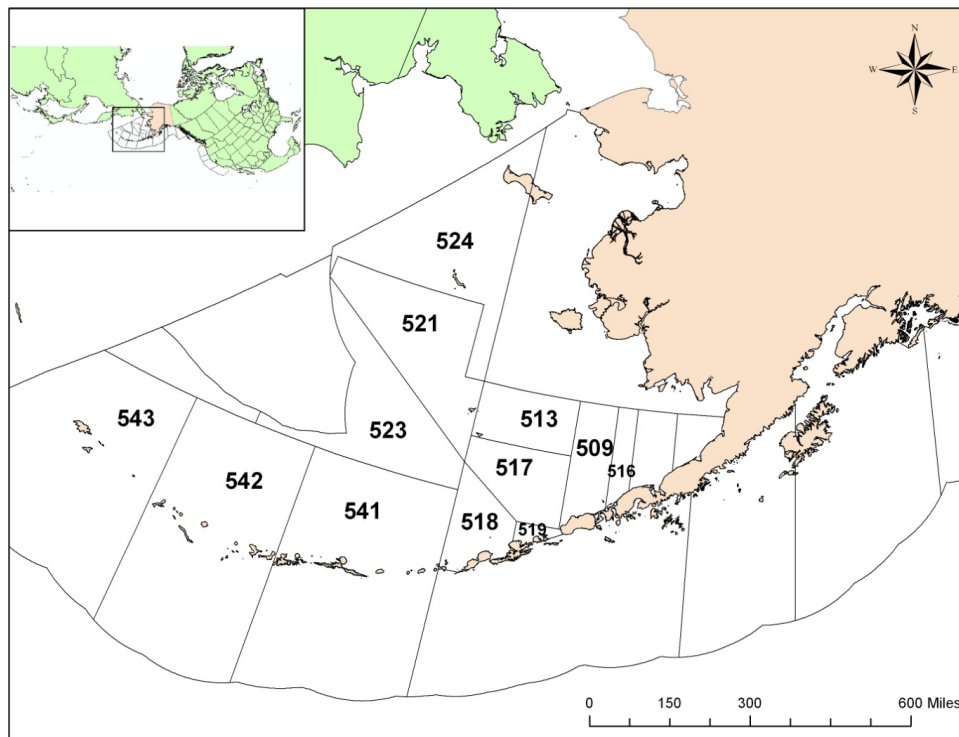


Figure 1. -- Statistical areas associated with the Bering Sea-Aleutian Island groundfish fishery.

This report presents a stock composition estimate for the 2006 chum salmon bycatch samples collected from the Bering Sea; however, it is important to recognize the limitations imposed by the sampling distribution and the genetic baseline. Hence, this report is divided into six sections: Introduction, Sample Distribution, Genetic Stock Composition, Comparison with Previous Estimates, Temporal Stratification of the Bycatch Samples, and Summary. For additional background and methods, this report is intended to be supplemented with the chum salmon reports prepared previously for the 2005 and 2009 Bering Sea trawl fisheries (Guyon et al. 2010, Gray et al. 2010). The chum salmon bycatch, designated as non-Chinook in the NMFS database, comprises 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 2006 for the Auke Bay Laboratories as part of a Special Project (designated "Salmon Genetic Project"). Axillary processes for genetic analysis and scales for ageing were collected throughout the season and stored in coin envelopes that were labeled, frozen, and shipped to the Auke Bay Laboratories.

In 2006, an estimated 325,185 chum salmon were incidentally taken as bycatch in the Bering Sea groundfish fisheries (NMFS 2010). This number is more than twice the average of 147,472 non-Chinook salmon taken as bycatch between 1994 and 2009 and 354% greater than the median of 71,612 (Fig. 2). The final genetic sample set for the 2006 chum salmon bycatch was 1,367 fish from statistical areas 509-541 which represented a sampling rate of 0.44% of the 309,359 chum salmon caught in those areas.

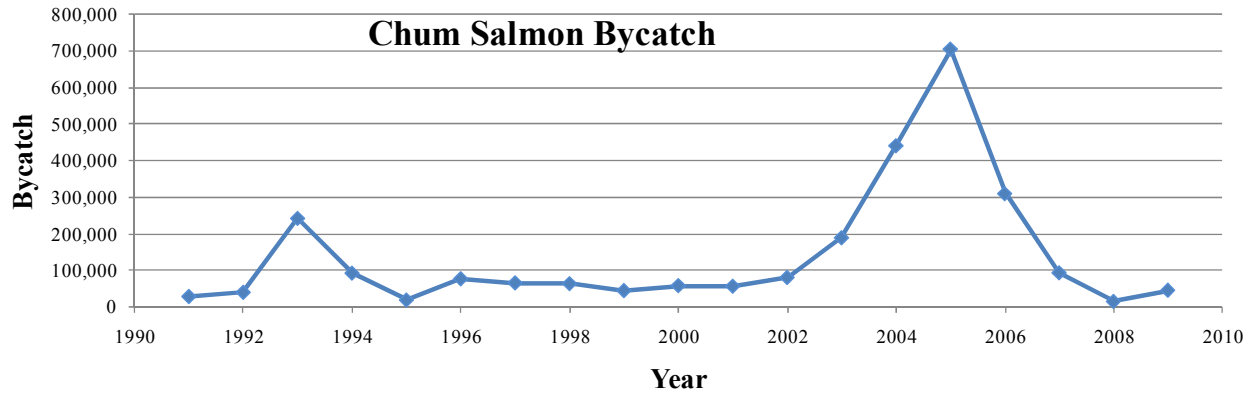


Figure 2. -- Yearly estimates for the non-Chinook salmon bycatch from the Bering Sea pollock trawl fishery (NMFS 2010).

Biases and errors associated with the collection of genetic samples from the bycatch are well documented, and have the potential to affect stock composition estimates (Pella and Geiger 2009). Methods to collect representative samples are being reviewed by the Alaska Fisheries Science Center, and when implemented, will reduce sampling error and bias. Potential biases associated with the successfully genotyped 2006 chum salmon bycatch sample set were evaluated by visually comparing the genetic sample distributions with the overall bycatch estimates. A visual comparison of the two distributions showed the sample set was weighted towards samples collected near the end of the pollock “B” season (Fig. 3). Temporal biases can become even more evident at finer spatial scales (Fig. 4). For example, statistical area 509 was underrepresented in the genetic sample set early in the groundfish “B” season (weeks 24-30), while statistical area 521 was overrepresented late (weeks 36-41). In addition, spatial bias may be further exacerbated by the uncertainty of catch location for samples collected from shoreside deliveries in which the hauls were mixed and the location of the entire catch of a fishing trip was identified as the location of the first haul.

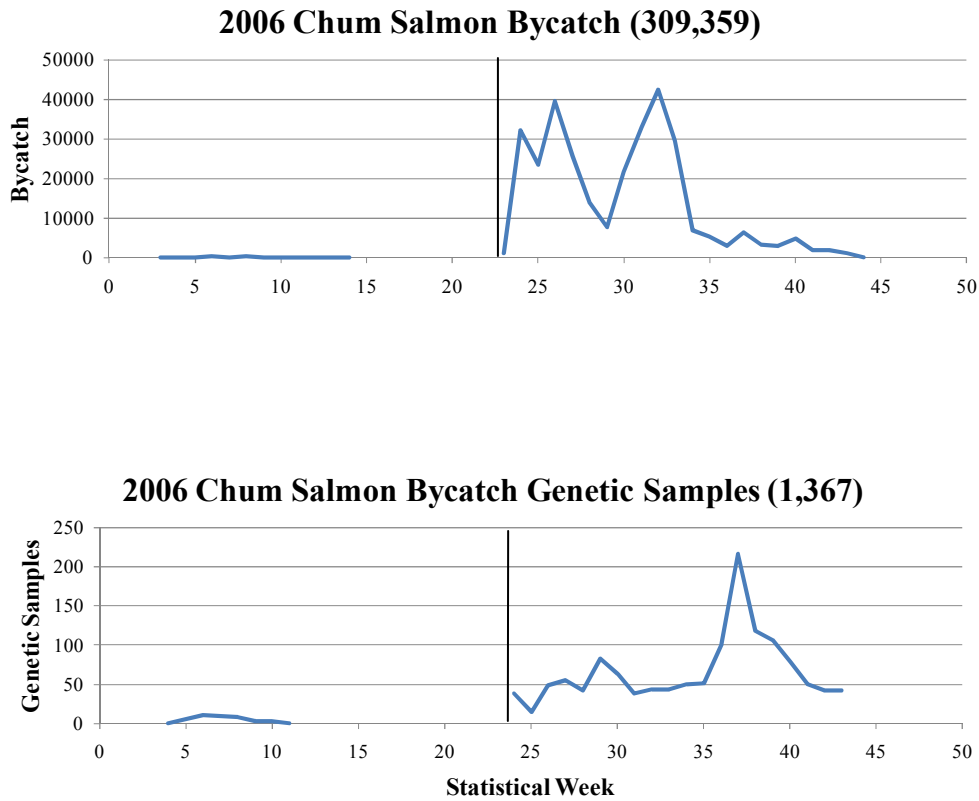


Figure 3. -- Number of Bering Sea chum salmon bycatch and genetic samples from 2006 by statistical week. Total numbers of chum salmon caught in the Bering Sea groundfish trawl fishery (top panel) in areas 509-541 compared with the available 1,367 genetic samples (bottom panel). Weeks 4-22 correspond to the groundfish “A” season, whereas weeks 23-44 correspond to the “B” season, the demarcation of which is a vertical line.

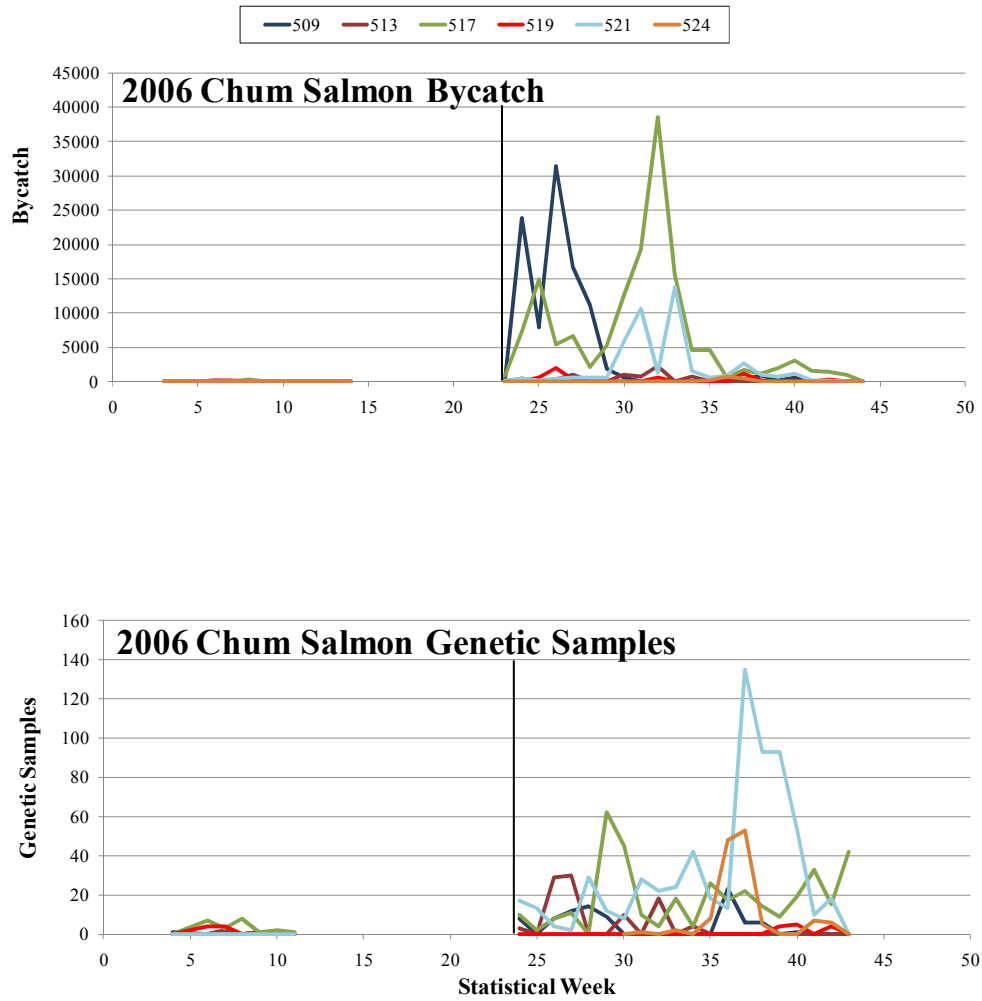


Figure 4. -- Comparison of the chum salmon bycatch with the distribution of available genetic samples, by time and area. Not shown in the chum salmon bycatch are an estimated 1,656 fish from area 514, 2,089 from area 523, and 1 from area 541. All samples in the genetic sample set are shown. Weeks 4-22 correspond to the groundfish “A” season, whereas weeks 23-44 correspond to the “B” season, the demarcation of which is a vertical line. NMFS statistical areas are designated in the legend.

## 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. 2009a), *Omm1070* (Rexroad et al. 2001), *Omy1011* (Spies et al. 2005), *One101*, *One102*, *One104*, *One114* (Olsen et al. 2000), *Ots103* (Nelson and Beacham, 1999), *Ots3* (Greig and Banks 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 by 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 1,536 samples from the 2006 chum salmon bycatch were analyzed, of which 1,369 samples were successfully genotyped for 8 or more of the 11 loci and analyzed in GENALEX (Peakall and Smouse 2006) for data integrity. Previous simulation analyses have demonstrated that a set of 8 selected loci can provide similar levels of stock resolution as the entire set of 11 loci (Gray et al. 2010); this is also supported by results reported in the literature for other loci sets (Beacham et al. 2009b). From this analysis, two duplicate samples (individuals with identical genotypes) were detected and one of each was removed. The remaining 1,367 samples had genetic information for an average of 10.32 loci (out of 11). There were 747 samples with data for all 11 loci, 392 with 10 loci, 145 with 9 loci, and 83 with 8 loci. There

were nine individual allele calls observed that were not present in the chum salmon baseline; those alleles and the associated haplotype were changed to “no calls” for the analysis.

For the mixture files, allele designations were converted to match those in the Fisheries and Oceans Canada (DFO) chum salmon microsatellite baseline (Beacham et al. 2009b, Beacham et al. 2009c). 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 compositions were determined using both maximum likelihood and Bayesian approaches by comparing mixture genotypes with reference baseline populations. As described previously (Gray et al. 2010), baseline populations were grouped into the following six regions: East Asia, North Asia, Western Alaska, Upper/Middle Yukon, Southwest Alaska, and Eastern Gulf of Alaska/Pacific Northwest (Prince William Sound to Washington State). A listing of populations grouped by region is presented in the Appendix.

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 by using all available 11 loci in the mixture (Table 1, 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 stock composition analyses were completed for a chain length of 10,000 with the first 5,000 deleted during the burn-in

phase. Convergence of the chains to posterior distributions of stock proportions was determined with Gelman and Rubin shrink statistics, which were all 1.03 or less (Table 1, top panel), conveying convergence to a single posterior distribution (Pella and Masuda 2001).

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 (ADF&G 2003). SPAM estimates were performed both with and without Bayesian modeling of baseline allele frequencies, a feature introduced in version 3.7 of the software. The BAYES estimate was best approximated by the SPAM estimate for 11 loci using the Bayesian model of baseline allele frequency distributions with the Pella-Masuda baseline posterior estimates. This suggests that rare alleles may be an issue with the unmodified SPAM estimate. In addition, two SPAM estimates for each method were provided, one with all 11 and another with 8 loci for comparison purposes (Table 1). The eight loci included *Oki100*, *One101*, *One104*, *Ots103*, *Ots3*, *Ots68*, *Omy1011*, and *Ssa419*; the rationale for their selection was described previously (Gray et al. 2010). Convergence was monitored with the “Percent of Maximum” value, which exceeded the 90% guaranteed percent achievement of the maximal likelihood for all SPAM estimates. Stock composition estimates for the two sets of loci were nearly identical (Table 1, middle table, see overlapping SPAM 90% nonsymmetric bootstrap confidence intervals), although the SPAM estimates derived from the 8 loci set were generally closer to the BAYES and SPAM-PM estimates for all 11 loci. This suggests that rare alleles in loci *Omm1070*, *One102*, and *One114*, the 3 loci excluded from the 8 loci set, could be affecting the 11 loci SPAM maximum likelihood estimate. Overall, these results suggest that the BAYES analysis is likely the best method for determining stock composition of the chum salmon bycatch using the entire marker set.



Table 1. -- Regional SPAM and BAYES stock composition estimates for 1,367 chum salmon samples from the bycatch of the 2006 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. SPAM estimates were performed without (designated “SPAM”) and with the Bayesian model of baseline allele frequency distributions by using Pella-Masuda baseline posterior estimates (designated “SPAM – PM”). 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 upper and lower confidence intervals for the SPAM estimates were determined by the analysis of 500 bootstrap 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>	<b>0.285</b>	0.013	0.260	0.285	0.311	1.00
<i>North Asia</i>	<b>0.306</b>	0.016	0.275	0.306	0.337	1.01
<i>Western Alaska</i>	<b>0.084</b>	0.010	0.065	0.084	0.105	1.01
<i>Upper/Middle Yukon</i>	<b>0.060</b>	0.008	0.045	0.059	0.075	1.03
<i>Southwest Alaska</i>	<b>0.013</b>	0.006	0.003	0.013	0.025	1.03
<i>Eastern GOA/PNW</i>	<b>0.252</b>	0.014	0.226	0.252	0.280	1.01

**SPAM**

<u>Region</u>	<u>11 Loci</u>				<u>8 Loci</u>			
	<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>	<b>0.262</b>	0.012	0.243	0.284	<b>0.271</b>	0.013	0.251	0.293
<i>North Asia</i>	<b>0.271</b>	0.014	0.251	0.299	<b>0.280</b>	0.016	0.261	0.313
<i>Western Alaska</i>	<b>0.108</b>	0.010	0.090	0.123	<b>0.092</b>	0.011	0.071	0.108
<i>Upper/Middle Yukon</i>	<b>0.056</b>	0.007	0.046	0.068	<b>0.059</b>	0.007	0.047	0.072
<i>Southwest Alaska</i>	<b>0.019</b>	0.005	0.010	0.026	<b>0.021</b>	0.005	0.011	0.028
<i>Eastern GOA/PNW</i>	<b>0.275</b>	0.013	0.253	0.294	<b>0.274</b>	0.014	0.247	0.292
<i>Unknown</i>	<b>0.009</b>				<b>0.003</b>			

**SPAM - PM**

<u>Region</u>	<u>11 Loci</u>				<u>8 Loci</u>			
	<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>	<b>0.285</b>	0.013	0.264	0.307	<b>0.291</b>	0.014	0.269	0.314
<i>North Asia</i>	<b>0.277</b>	0.015	0.262	0.311	<b>0.272</b>	0.016	0.256	0.309
<i>Western Alaska</i>	<b>0.087</b>	0.011	0.068	0.104	<b>0.083</b>	0.012	0.063	0.102
<i>Upper/Middle Yukon</i>	<b>0.062</b>	0.008	0.048	0.073	<b>0.065</b>	0.008	0.049	0.076
<i>Southwest Alaska</i>	<b>0.020</b>	0.005	0.010	0.027	<b>0.023</b>	0.006	0.012	0.031
<i>Eastern GOA/PNW</i>	<b>0.268</b>	0.013	0.241	0.286	<b>0.267</b>	0.014	0.238	0.284
<i>Unknown</i>	<b>0.001</b>				<b>0.000</b>			

## COMPARISON WITH PREVIOUS ESTIMATES

The stock composition results from the analysis of the 2006 chum salmon bycatch samples were similar to previous estimates (Fig. 5), although differences within individual regions were apparent between years. 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), 2006 (this report), and 2009 (Gray et al. 2010) chum salmon bycatch estimates were derived from DNA-based

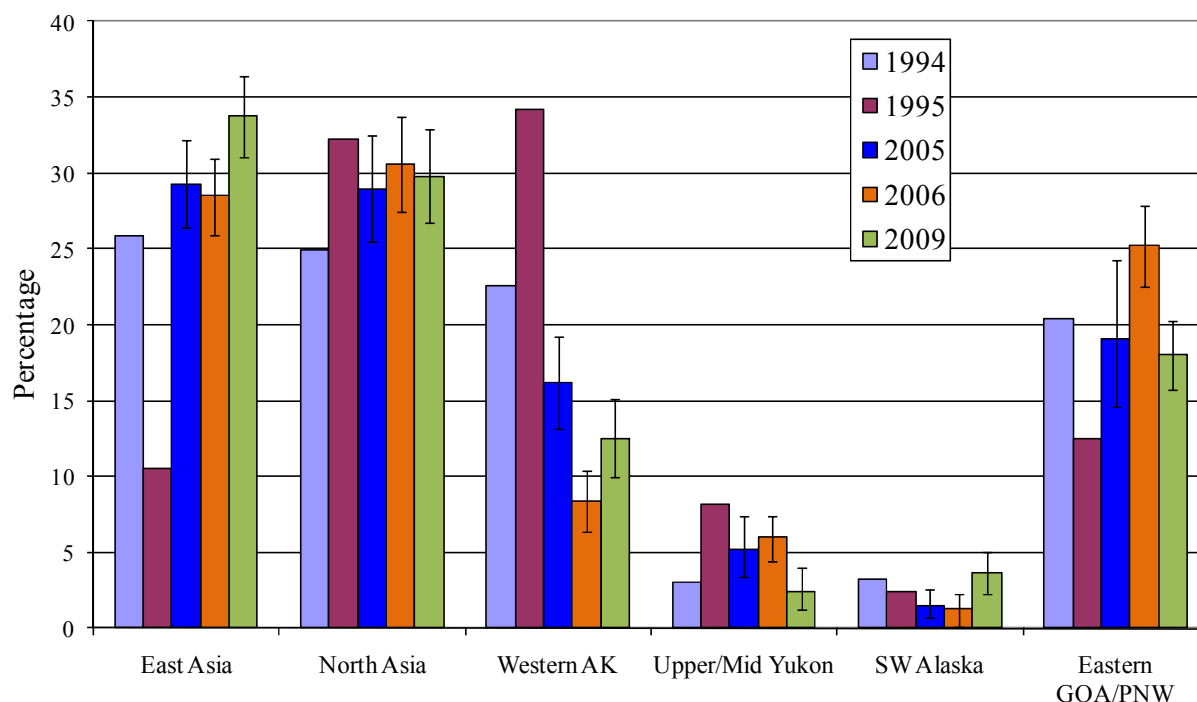


Figure 5. -- Comparison of yearly stock composition estimates of available genetic samples from the Bering Sea chum salmon bycatch. The 1994-1995 estimates were derived with allozyme loci, and the 2005, 2006 and 2009 estimates were produced with DNA-based loci. 95% BAYES credible intervals are shown for the DNA-based analyses.

microsatellite loci. The allozyme (77 populations) and microsatellite DNA (381 populations) baselines have data from many of the same populations and have similar regional groupings.

#### TEMPORAL STRATIFICATION OF THE BYCATCH SAMPLES

As reported previously for the 2005 chum salmon bycatch samples, there was a shift in the regional contributions of the 2006 chum salmon composition (sample estimate) over time, with Western Alaska stocks more dominant in the early sampling and Asian fish more dominant in the later sampling period. The relatively large number of 2006 chum salmon bycatch samples (1,367) allowed the temporal splitting of the sample set into three “B” season time segments: early, middle, and late peak with sample sizes as indicated in Table 2. Sample analyses for similar temporal strata of the 2005 (Guyon et al. 2010) and 2009 year chum salmon bycatch sample sets are included for comparison purposes (Table 2). Results from this analysis should be used cautiously because sample spatial differences are apparent in the time stratified sample sets (Fig. 6) and these biases could affect the stock composition estimates.

Table 2. -- Temporal groupings from the 2005, 2006, and 2009 chum salmon bycatch genetic sample sets for which temporal information was available and which samples fell between those sample collection dates.

<b>Year</b>	<b>Weeks</b>	<b>Dates</b>	<b>Number of samples</b>
2005	Wk 24-28	11 June - 6 July	356
	Wk 29-34	12 July - 18 August	205
	Wk 35-40	23 August - 29 September	461
2006	Wk 24-29	11 June –22 July	283
	Wk 30-34	23 July –26 August	240
	Wk 35-43	27 August –28 October	807
2009	Wk 24-29	12 June - 17 July	433
	Wk 30-34	19 July - 22 August	596
	Wk 35-40	23 August - 3 October	407

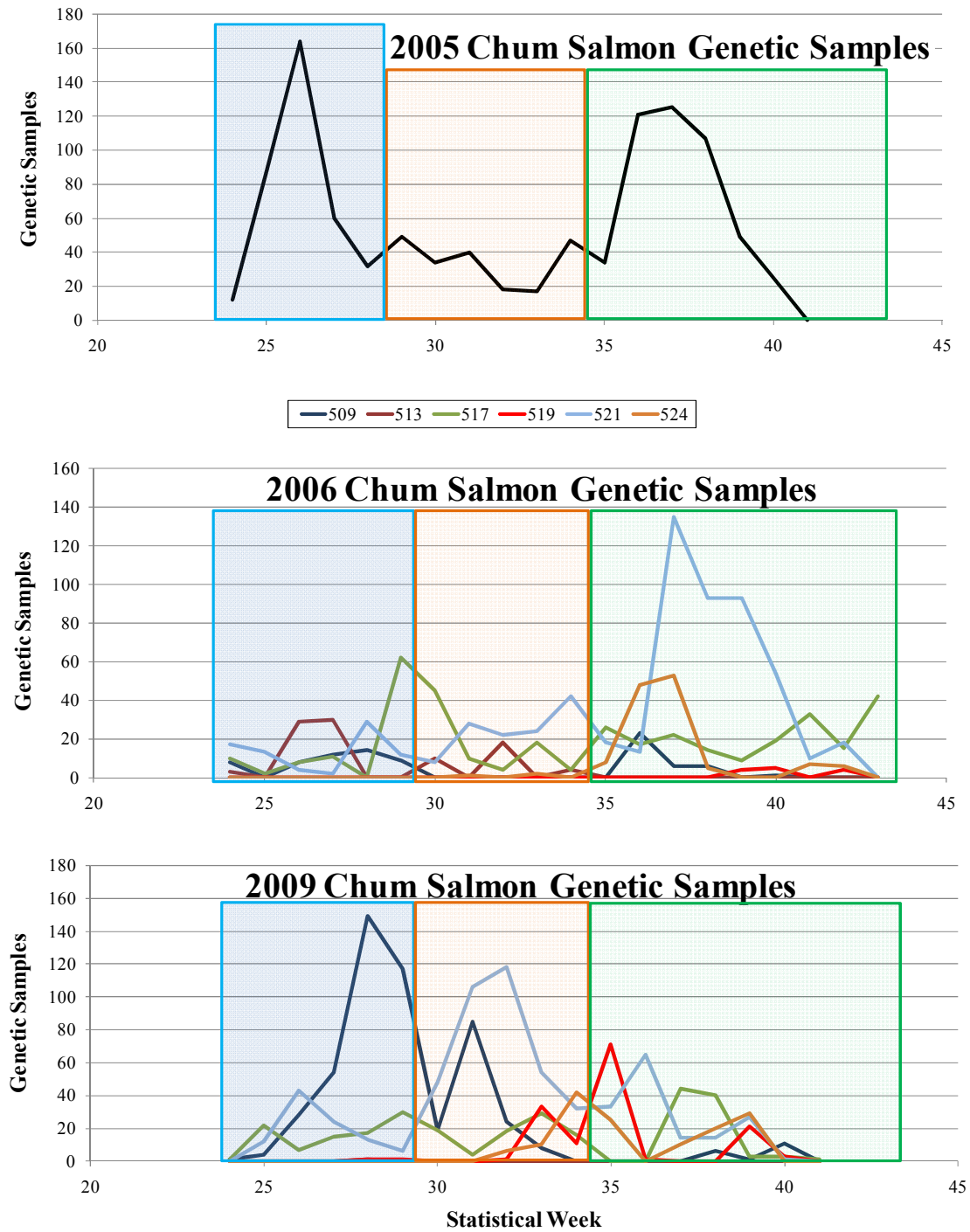


Figure 6. -- Genetic samples from the 2005, 2006 and 2009 chum salmon bycatch identified by early (blue), middle (brown), and late (green) temporal groupings. Samples from the 2005 chum salmon bycatch were collected differently than in 2006 or 2009 and were not grouped by NMFS statistical area, nor do they represent the cumulative catch (Guyon et al. 2010). NMFS statistical areas are designated in the legend.

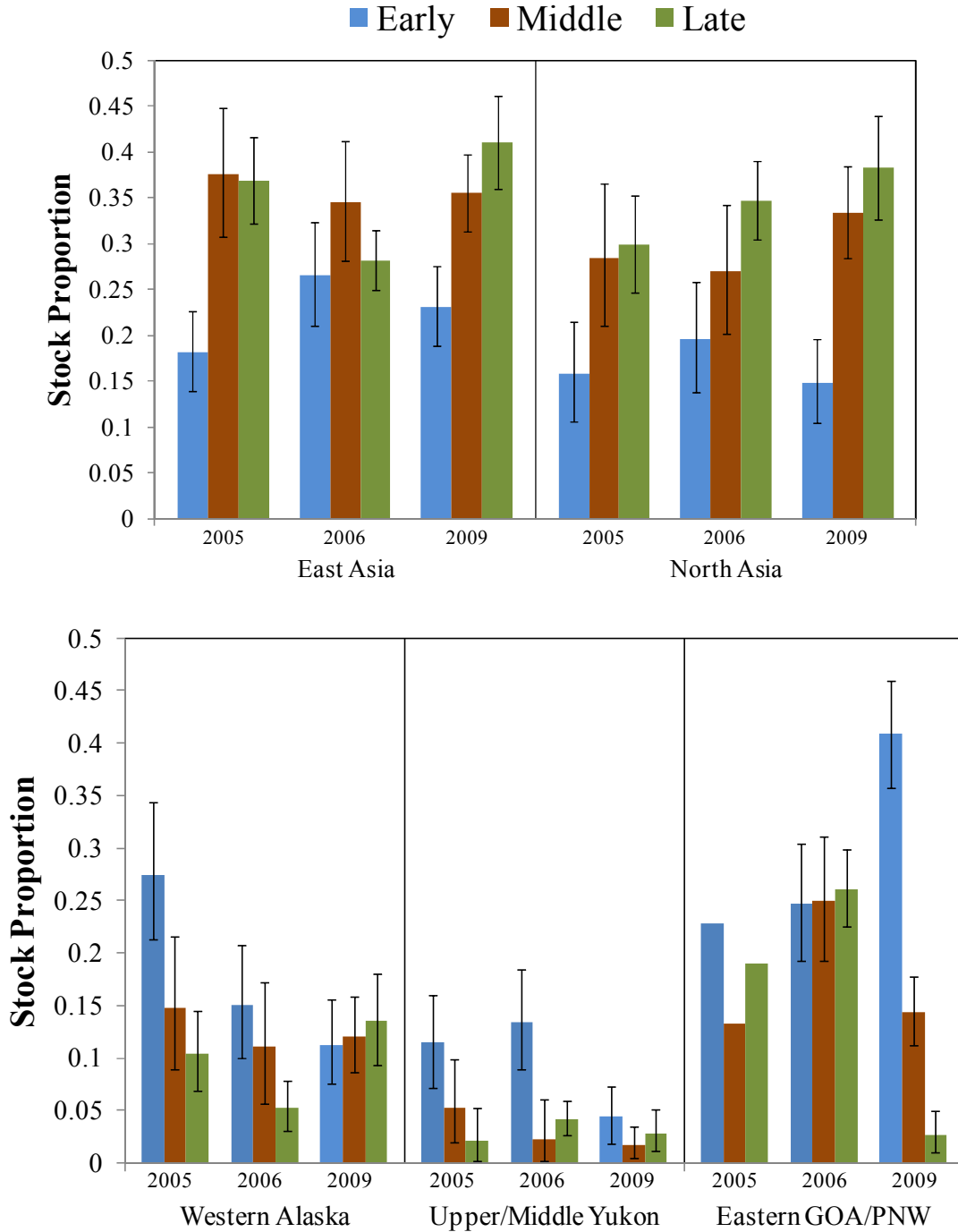


Figure 7. -- BAYES stock composition estimates and 95% credible intervals for the early, middle, and late periods (defined in Table 2) from the 2005, 2006, and 2009 chum salmon bycatch. The 95% credible intervals for the 2005 Eastern GOA/PNW grouping are not shown because this region represents a sum of the SE Alaska/N. BC, Skeena, and BC/Washington groupings used in the 2005 analysis (Guyon et al. 2010). Not shown is the SW Alaska region for which estimates never exceeded 5.6%.

Both BAYES and SPAM stock composition estimates were made for each of the three temporal strata for each year. All BAYES stock composition estimates were performed using six Monte Carlo chains starting at disparate starting values of stock proportions and flat prior. Gelman and Rubin shrink statistics were calculated and in all cases were below 1.10, suggesting strong convergence to a single posterior distribution. The SPAM and BAYES estimates were very similar (SPAM results not shown); however, stock composition estimates differed between time periods (Fig. 7). For example, fish from Western Alaska and the Upper/Middle Yukon were more prevalent in the early part of the season (Weeks 24-29) than the later (Weeks 35-43), whereas the inverse relationship was apparent for stocks from Asia (Fig. 7). Relatively small sample sets can bias the stock composition estimates, but the overall trends were repeatable across years and were also observed for chum salmon bycatch samples analyzed from the 1994-1995 years (Wilmot et al. 1998). In 2009, the lack of change seen for the Western Alaska and Upper/Middle Yukon groupings was offset by a large decrease in contribution of fish from the Eastern GOA/PNW Region (Prince William Sound to Washington) (Fig. 7), an observation which may be due to improved sampling protocols implemented in 2009. This demonstrates that stock compositions of the chum salmon bycatch change during the course of the season, but leaves unanswered whether these changes are due to temporal or spatial differences in the sample sets.

## SUMMARY

Stock composition estimates of the salmon bycatch in the Bering Sea groundfish fisheries are needed for fishery managers to understand the impact of these fisheries on salmon populations, particularly those in western Alaska. This report provides a stock composition

analysis of a set of 1,367 individuals sampled from the 2006 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 2006 sample set (Figs. 3 and 4), which may limit the application of the genetic sample stock composition estimate to the entire 2006 chum salmon bycatch. NMFS recently published regulations implementing Amendment 91 to the Fishery Management Plan for Groundfish of the Bering Sea and Aleutian Islands Management Area (75 FR 53026, August 30, 2010) which requires that all salmon taken as bycatch 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 samples from 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.

#### Stock Composition Estimates

Overall, the genetic samples collected from the chum salmon bycatch were predominantly from Asian stocks (59%) although substantial contributions were also from Western Alaska (8.4%), Upper/Middle Yukon (6%), and Eastern GOA/PNW (25%). These stock proportions are similar to previous estimates; however, there appeared to be a higher contribution from East Asia and a 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 making comparisons across years.

### Temporal Effects on Stock Composition Estimates

A temporal analysis was completed to determine whether stock compositions differed across the fishing season. This was limited to a time-stratified analysis of the bycatch from the pollock “B” season, a time when the majority of chum salmon are intercepted. As in 2005, 2006, and 2009, North American derived chum salmon were more predominant in the early part of the bycatch sampling effort for the groundfish “B” season; Asian fish dominated in the middle and late sampling times. Stock composition estimates differed in a consistent manner between years, suggesting temporal stratification of chum salmon stocks in the Bering Sea and/or changes in sampling or fishing locations.

### 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 in another year.

### ACKNOWLEDGMENTS

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 was peer reviewed by AFSC and external reviewers for which we are especially grateful.



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## APPENDIX

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

DFO number	Population name	Region number	Region
219	Kanchalan	2	North Asia
379	Karaga	2	North Asia
294	Kikchik	2	North Asia
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

DFO number	Population name	Region number	Region
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
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

DFO number	Population name	Region number	Region
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	Eastern GOA/PNW
69	Ahta_____	6	Eastern GOA/PNW
155	Ain_	6	Eastern GOA/PNW
183	Algard	6	Eastern GOA/PNW
58	Alouette	6	Eastern GOA/PNW
325	Alouette_North	6	Eastern GOA/PNW
270	Andesite_Cr	6	Eastern GOA/PNW
428	Arnoup_Cr	6	Eastern GOA/PNW
153	Ashlulm	6	Eastern GOA/PNW
156	Awun	6	Eastern GOA/PNW
133	Bag_Harbour	6	Eastern GOA/PNW
164	Barnard	6	Eastern GOA/PNW
16	Bella_Bell	6	Eastern GOA/PNW
79	Bella_Coola	6	Eastern GOA/PNW
49	Big_Qual	6	Eastern GOA/PNW
201	Big_Quilcene	6	Eastern GOA/PNW
281	Bish_Cr	6	Eastern GOA/PNW
198	Bitter_Creek	6	Eastern GOA/PNW
103	Blackrock_Creek	6	Eastern GOA/PNW
390	Blaney_Creek	6	Eastern GOA/PNW
138	Botany_Creek	6	Eastern GOA/PNW
264	Buck_Channel	6	Eastern GOA/PNW
169	Bullock_Chann	6	Eastern GOA/PNW
61	Campbell_River	6	Eastern GOA/PNW
323	Carroll	6	Eastern GOA/PNW
78	Cascade	6	Eastern GOA/PNW
76	Cayeghle	6	Eastern GOA/PNW
42	Cheakamus	6	Eastern GOA/PNW
398	Cheenis_Lake	6	Eastern GOA/PNW
51	Chehalis	6	Eastern GOA/PNW
19	Chemainus	6	Eastern GOA/PNW
47	Chilliwack	6	Eastern GOA/PNW
392	Chilqua_Creek	6	Eastern GOA/PNW
117	Chuckwalla	6	Eastern GOA/PNW
139	Clapp_Basin	6	Eastern GOA/PNW
107	Clatse_Creek	6	Eastern GOA/PNW



DFO number	Population name	Region number	Region
118	Clyak	6	Eastern GOA/PNW
62	Cold_Creek	6	Eastern GOA/PNW
77	Colonial	6	Eastern GOA/PNW
353	Constantine	6	Eastern GOA/PNW
168	Cooper_Inlet	6	Eastern GOA/PNW
197	County_Line	6	Eastern GOA/PNW
12	Cowichan	6	Eastern GOA/PNW
414	Crag_Cr	6	Eastern GOA/PNW
161	Dak_	6	Eastern GOA/PNW
259	Dana_Creek	6	Eastern GOA/PNW
123	Date_Creek	6	Eastern GOA/PNW
250	Dawson_Inlet	6	Eastern GOA/PNW
91	Dean_River	6	Eastern GOA/PNW
261	Deena	6	Eastern GOA/PNW
170	Deer_Pass	6	Eastern GOA/PNW
46	Demamiel	6	Eastern GOA/PNW
210	Dipac_Hatchery	6	Eastern GOA/PNW
319	Disappearance	6	Eastern GOA/PNW
269	Dog-tag	6	Eastern GOA/PNW
177	Draney	6	Eastern GOA/PNW
114	Duthie_Creek	6	Eastern GOA/PNW
427	East_Arm	6	Eastern GOA/PNW
266	Eestall_River	6	Eastern GOA/PNW
94	Elcho_Creek	6	Eastern GOA/PNW
193	Ellsworth_Cr	6	Eastern GOA/PNW
203	Elwha	6	Eastern GOA/PNW
276	Ensheshese	6	Eastern GOA/PNW
263	Fairfax_Inlet	6	Eastern GOA/PNW
32	Fish_Creek	6	Eastern GOA/PNW
429	Flux_Cr	6	Eastern GOA/PNW
102	Foch_Creek	6	Eastern GOA/PNW
179	Frenchman	6	Eastern GOA/PNW
227	Gambier	6	Eastern GOA/PNW
96	Gill_Creek	6	Eastern GOA/PNW
166	Gilttoyee	6	Eastern GOA/PNW
145	Glendale	6	Eastern GOA/PNW
135	Gold_Harbour	6	Eastern GOA/PNW
11	Goldstream	6	Eastern GOA/PNW
66	Goodspeed_River	6	Eastern GOA/PNW
136	Government	6	Eastern GOA/PNW
205	Grant_Creek	6	Eastern GOA/PNW
100	Green_River	6	Eastern GOA/PNW
450	GreenRrHatchery	6	Eastern GOA/PNW
237	Greens	6	Eastern GOA/PNW
141	Harrison	6	Eastern GOA/PNW

DFO number	Population name	Region number	Region
438	Harrison_late	6	Eastern GOA/PNW
64	Hathaway_Creek	6	Eastern GOA/PNW
234	Herman_Creek	6	Eastern GOA/PNW
17	Heydon_Cre	6	Eastern GOA/PNW
407	Hicks_Cr	6	Eastern GOA/PNW
400	Homathko	6	Eastern GOA/PNW
411	Honna	6	Eastern GOA/PNW
204	Hoodsport	6	Eastern GOA/PNW
185	Hooknose	6	Eastern GOA/PNW
406	Hopedale_Cr	6	Eastern GOA/PNW
412	Hutton_Head	6	Eastern GOA/PNW
278	Illiance	6	Eastern GOA/PNW
152	Inch_Creek	6	Eastern GOA/PNW
146	Indian_River	6	Eastern GOA/PNW
92	Jenny_Bay	6	Eastern GOA/PNW
115	Kainet_River	6	Eastern GOA/PNW
144	Kakweiken	6	Eastern GOA/PNW
268	Kalum	6	Eastern GOA/PNW
395	Kanaka_Cr	6	Eastern GOA/PNW
402	Kano_Inlet_Cr	6	Eastern GOA/PNW
162	Kateen	6	Eastern GOA/PNW
389	Kawkawa	6	Eastern GOA/PNW
95	Kemano	6	Eastern GOA/PNW
192	Kennedy_Creek	6	Eastern GOA/PNW
238	Kennell	6	Eastern GOA/PNW
351	Keta_Creek	6	Eastern GOA/PNW
101	Khutze_River	6	Eastern GOA/PNW
126	Khutzeymateen	6	Eastern GOA/PNW
282	Kiltuish	6	Eastern GOA/PNW
93	Kimsquit	6	Eastern GOA/PNW
187	Kimsquit_Bay	6	Eastern GOA/PNW
419	Kincolith	6	Eastern GOA/PNW
273	Kispiox	6	Eastern GOA/PNW
106	Kitasoo	6	Eastern GOA/PNW
99	Kitimat_River	6	Eastern GOA/PNW
275	Kitsault_Riv	6	Eastern GOA/PNW
163	Kitwanga	6	Eastern GOA/PNW
271	Kleanza_Cr	6	Eastern GOA/PNW
437	Klewnuggit_Cr	6	Eastern GOA/PNW
21	Klinaklini	6	Eastern GOA/PNW
418	Ksedin	6	Eastern GOA/PNW
125	Kshwan	6	Eastern GOA/PNW
423	Kumealon	6	Eastern GOA/PNW
112	Kwakusdis_River	6	Eastern GOA/PNW
436	Kxngeal_Cr	6	Eastern GOA/PNW

DFO number	Population name	Region number	Region
127	Lachmach	6	Eastern GOA/PNW
262	Lagins	6	Eastern GOA/PNW
131	Lagoon_Inlet	6	Eastern GOA/PNW
448	LagoonCr	6	Eastern GOA/PNW
167	Lard	6	Eastern GOA/PNW
160	Little_Goose	6	Eastern GOA/PNW
50	Little_Qua	6	Eastern GOA/PNW
413	Lizard_Cr	6	Eastern GOA/PNW
119	Lockhart-Gordon	6	Eastern GOA/PNW
176	Lower_Lillooet	6	Eastern GOA/PNW
137	Mace_Creek	6	Eastern GOA/PNW
242	Mackenzie_Sound	6	Eastern GOA/PNW
116	MacNair_Creek	6	Eastern GOA/PNW
55	Mamquam	6	Eastern GOA/PNW
121	Markle_Inlet_Cr	6	Eastern GOA/PNW
27	Martin_Riv	6	Eastern GOA/PNW
338	Mashiter_Creek	6	Eastern GOA/PNW
109	McLoughin_Creek	6	Eastern GOA/PNW
178	Milton	6	Eastern GOA/PNW
194	Minter_Cr	6	Eastern GOA/PNW
254	Mountain_Cr	6	Eastern GOA/PNW
111	Mussel_River	6	Eastern GOA/PNW
157	Naden	6	Eastern GOA/PNW
337	Nahmint_River	6	Eastern GOA/PNW
444	Nakut_Su	6	Eastern GOA/PNW
14	Nanaimo	6	Eastern GOA/PNW
122	Nangeese	6	Eastern GOA/PNW
422	Nass_River	6	Eastern GOA/PNW
399	Necleetsconnay	6	Eastern GOA/PNW
113	Neekas_Creek	6	Eastern GOA/PNW
321	Neets_Bay_early	6	Eastern GOA/PNW
320	Neets_Bay_late	6	Eastern GOA/PNW
173	Nekite	6	Eastern GOA/PNW
104	Nias_Creek	6	Eastern GOA/PNW
143	Nimpkish	6	Eastern GOA/PNW
53	Nitinat	6	Eastern GOA/PNW
191	Nooksack	6	Eastern GOA/PNW
186	Nooseseck	6	Eastern GOA/PNW
318	NorrishWorth	6	Eastern GOA/PNW
159	North_Arm	6	Eastern GOA/PNW
377	Olsen_Creek	6	Eastern GOA/PNW
184	Orford	6	Eastern GOA/PNW
287	Pa-aat_River	6	Eastern GOA/PNW
260	Pacofi	6	Eastern GOA/PNW
56	Pallant	6	Eastern GOA/PNW

DFO number	Population name	Region number	Region
65	Pegattum_Creek	6	Eastern GOA/PNW
48	Puntledge	6	Eastern GOA/PNW
98	Quaal_River	6	Eastern GOA/PNW
147	Quap	6	Eastern GOA/PNW
108	Quartcha_Creek	6	Eastern GOA/PNW
199	Quinault	6	Eastern GOA/PNW
110	Roscoe_Creek	6	Eastern GOA/PNW
397	Salmon_Bay	6	Eastern GOA/PNW
195	Salmon_Cr	6	Eastern GOA/PNW
134	Salmon_River	6	Eastern GOA/PNW
200	Satsop	6	Eastern GOA/PNW
236	Sawmill	6	Eastern GOA/PNW
410	Seal_Inlet_Cr	6	Eastern GOA/PNW
158	Security	6	Eastern GOA/PNW
130	Sedgewick	6	Eastern GOA/PNW
393	Serpentine_R	6	Eastern GOA/PNW
317	Shovelnose_Cr	6	Eastern GOA/PNW
249	Shustnini	6	Eastern GOA/PNW
206	Siberia_Creek	6	Eastern GOA/PNW
25	Silverdale	6	Eastern GOA/PNW
196	Skagit	6	Eastern GOA/PNW
274	Skeena	6	Eastern GOA/PNW
171	Skowquiltz	6	Eastern GOA/PNW
447	SkykomishRiv	6	Eastern GOA/PNW
132	Slatechuck_Cre	6	Eastern GOA/PNW
43	Sliammon	6	Eastern GOA/PNW
15	Smith_Cree	6	Eastern GOA/PNW
54	Snootli	6	Eastern GOA/PNW
180	Southgate	6	Eastern GOA/PNW
26	Squakum	6	Eastern GOA/PNW
142	Squamish	6	Eastern GOA/PNW
128	Stagoo	6	Eastern GOA/PNW
265	Stanley	6	Eastern GOA/PNW
52	Stave	6	Eastern GOA/PNW
396	Stawamus	6	Eastern GOA/PNW
409	Steel_Cr	6	Eastern GOA/PNW
424	Stewart_Cr	6	Eastern GOA/PNW
416	Stumaun_Cr	6	Eastern GOA/PNW
327	Sugsaw	6	Eastern GOA/PNW
324	Surprise	6	Eastern GOA/PNW
75	Taaltz	6	Eastern GOA/PNW
30	Taku	6	Eastern GOA/PNW
18	Takwahoni	6	Eastern GOA/PNW
251	Tarundl_Creek	6	Eastern GOA/PNW
149	Theodosia	6	Eastern GOA/PNW

DFO number	Population name	Region number	Region
22	Thorsen	6	Eastern GOA/PNW
129	Toon	6	Eastern GOA/PNW
279	Tseax	6	Eastern GOA/PNW
202	Tulalip	6	Eastern GOA/PNW
97	Turn_Creek	6	Eastern GOA/PNW
430	Turtle_Cr	6	Eastern GOA/PNW
247	Tuskwa	6	Eastern GOA/PNW
165	Tyler	6	Eastern GOA/PNW
33	Tzoonie	6	Eastern GOA/PNW
124	Upper_Kitsumkal	6	Eastern GOA/PNW
140	Vedder	6	Eastern GOA/PNW
70	Viner_Sound	6	Eastern GOA/PNW
45	Wahleach	6	Eastern GOA/PNW
172	Walkum	6	Eastern GOA/PNW
73	Waump	6	Eastern GOA/PNW
232	Wells_Bridge	6	Eastern GOA/PNW
352	Wells_River	6	Eastern GOA/PNW
105	West_Arm_Creek	6	Eastern GOA/PNW
267	Whitebottom_Cr	6	Eastern GOA/PNW
326	Widgeon_Slough	6	Eastern GOA/PNW
277	Wilauks_Cr	6	Eastern GOA/PNW
120	Wilson_Creek	6	Eastern GOA/PNW
401	Worth_Creek	6	Eastern GOA/PNW
60	Wortley_Creek	6	Eastern GOA/PNW
248	Yellow_Bluff	6	Eastern GOA/PNW
434	Zymagotitz	6	Eastern GOA/PNW



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