Genetic Stock Composition Analysis of Chum Salmon Bycatch Samples from the 2011 Bering Sea Walleye Pollock Trawl Fishery

by C. M. Kondzela, C. T. Marvin, S. C. Vulstek, H. T. Nguyen, and J. R. Guyon

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ABSTRACT

A genetic analysis of samples from the chum salmon (Oncorhynchus keta) bycatch from the 2011 Bering Sea walleye pollock (*Theragra chalcogramma*) trawl fishery was undertaken to determine the overall stock composition of the sample set. Samples were genotyped for 11 microsatellite markers and results were estimated using the current chum salmon microsatellite baseline. In 2011, genetic samples were collected systematically as part of a special project to reduce sample biases that exist in collections from previous years that have the potential to affect stock composition analysis results. One genetic sample was collected for every 31.1 chum salmon caught in 97% of the midwater trawl fishery that was sampled. Evaluation of sampling based on time, location, and vessel indicated that the genetic samples were representative of the total bycatch. Based on the analysis of 1,472 chum salmon bycatch samples collected throughout the 2011 Bering Sea trawl fishery, the Eastern Gulf of Alaska (GOA)/Pacific Northwest (PNW) stocks dominated the sample set (38%), with moderate contributions from East Asian (17%), North Asian (18%), and Western Alaska (16%) stocks, and smaller contributions from Upper/Middle Yukon River (9%) stocks. The estimates for the 2011 chum salmon bycatch sample set differed from the 2005–2010 estimates, indicating a change in the consistency of the regional stock contributions across the previous 6 years, possibly due to the larger proportion of by catch caught later in the season and in the more southeastern NMFS reporting areas in 2011. There were significant spatial differences in stock distribution, with the Asian stocks dominating the central Bering Sea area and the Eastern GOA/PNW stocks dominating the southeastern Bering Sea. Analysis of temporal groupings revealed changes in stock composition during the course of the season with decreasing contribution of East Asia and Upper/Middle Yukon stocks and increasing contribution of Eastern GOA/PNW stocks over time.

CONTENTS

ABSTRACT	iii
CONTENTS	
INTRODUCTION	
SAMPLE DISTRIBUTION	3
GENETIC STOCK COMPOSITION	
COMPARISON WITH PREVIOUS ESTIMATES	
TEMPORAL STRATIFICATION	
SPATIAL STRATIFICATION	
SUMMARY	23
Sampling Issues	
Stock Composition Estimates	
Temporal and Spatial Effects on Stock Composition Estimates	24
Application of These Estimates	25
ACKNOWLEDGMENTS	
CITATIONS	
APPENDIX	31

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 2011 U.S. Bering Sea groundfish trawl fishery. National Marine Fisheries Service (NMFS) reporting areas associated with the groundfish fishery are shown in Figure 1 and are presented later to describe the spatial distribution of the chum salmon bycatch and genetic samples.

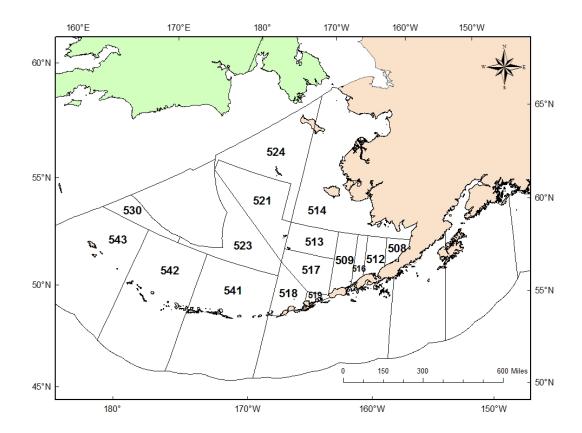


Figure 1. -- NMFS reporting areas associated with the Bering Sea-Aleutian Island groundfish fishery.

We present the stock composition estimates for the 2011 chum salmon bycatch samples collected from the Bering Sea. This report is divided into seven sections: Introduction, Sample Distribution, Genetic Stock Composition, Comparison with Previous Estimates, Temporal Stratification, Spatial Stratification, and Summary. For additional background and methods, this report is intended to be supplemented with the chum salmon reports prepared previously for the 2005–2010 Bering Sea trawl fisheries (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2011a,b; Gray et al. 2010; Kondzela et al. 2012). The chum salmon bycatch is designated as non-Chinook in the NMFS database and comprises over 99% of the non-Chinook category (NPFMC 2005).

SAMPLE DISTRIBUTION

Genetic samples were collected from the salmon bycatch of the Bering Sea trawl fishery by the Alaska Fisheries Science Center's (AFSC) North Pacific Observer Program in 2011 for the AFSC's Auke Bay Laboratories. Sampling was changed from previous years to implement a systematic sampling protocol recommended by Pella and Geiger (2009). With a goal to sample approximately every 30th chum salmon, 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. All of the chum salmon genetic samples were collected from bycatch in the midwater walleye pollock (*Theragra chalcogramma*) trawl fishery.

In 2011, an estimated 191,441 chum salmon were incidentally taken as bycatch in the pollock-directed midwater and bottom trawl fisheries, accounting for more than 98% of the total chum salmon bycatch taken in the Bering Sea groundfish fisheries (NMFS 2012). This is the fourth largest non-Chinook salmon bycatch in the pollock fisheries between 1994 and 2010, ~37% more than the average of 139,660 fish, and nearly three times larger than the median of 65,988 (Fig. 2). The 2011 genetic samples were collected from the midwater trawl fishery in North Pacific Fishery Management Council statistical areas 509-524. Of the 189,537 chum salmon caught in this fishery, genetic samples were collected from 6,102 fish, which represents a sampling rate of one of every 31.1 chum salmon (or 3.2% of the midwater trawl chum salmon bycatch). Due to the large number of samples collected, the genetic analysis was based on a subsample of every fourth fish from the total genetic samples.

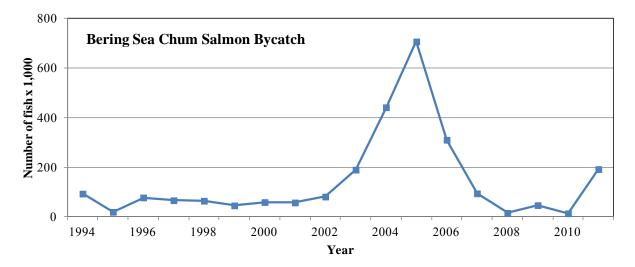


Figure 2. -- Yearly estimates for the non-Chinook salmon bycatch from the Bering Sea pollock directed trawl fisheries (NMFS 2012).

Biases and errors associated with past collections of genetic samples from the bycatch are well documented, and have the potential to affect stock composition estimates. The systematic sampling protocols recommended by Pella and Geiger (2009) were implemented in 2011 to reduce sampling error and bias, the efficacy of which was evaluated by visually comparing the genetic sample distributions with the overall bycatch estimates. Temporal bias by statistical week ending on Sunday was minimal (Fig. 3) when samples were pooled across management areas. Nearly all of the chum salmon bycatch occurred in the pollock "B" season (99.9%), where temporal biases were also minimal at finer spatial scales (Fig. 4). Due to the uncertainty of catch location for samples collected from shore-side deliveries in which the hauls were mixed, the NMFS reporting area of the entire catch of a fishing trip was identified as the area of the most abundant haul. For vessels that fished in multiple areas during a trip, the NMFS reporting area was identified as the area where the fishery target species was most abundant.

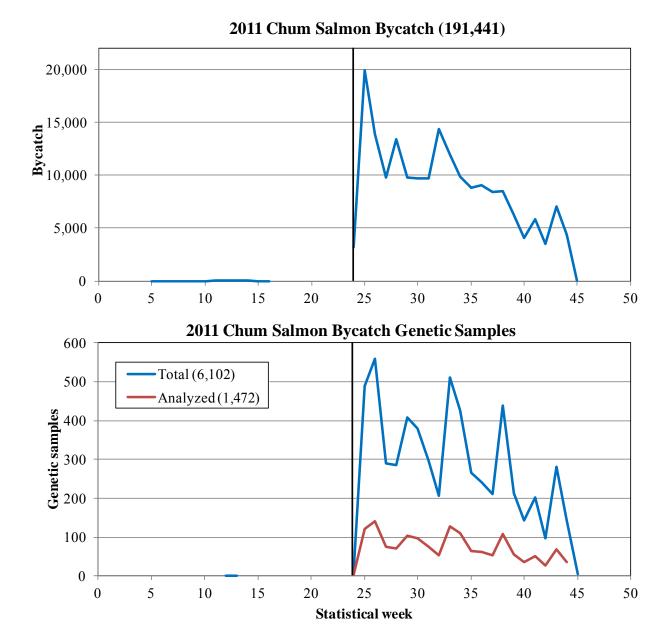


Figure 3. -- Number of Bering Sea chum salmon bycatch and genetic samples from 2011 by statistical week. Total numbers of chum salmon caught in the Bering Sea pollock midwater trawl fishery (top panel) compared with the available 6,102 and 1,472 genetic samples collected and analyzed, respectively (bottom panel). Weeks 3-23 correspond to the groundfish "A" season, whereas weeks 24-45 correspond to the "B" season, the demarcation of which is a vertical line.

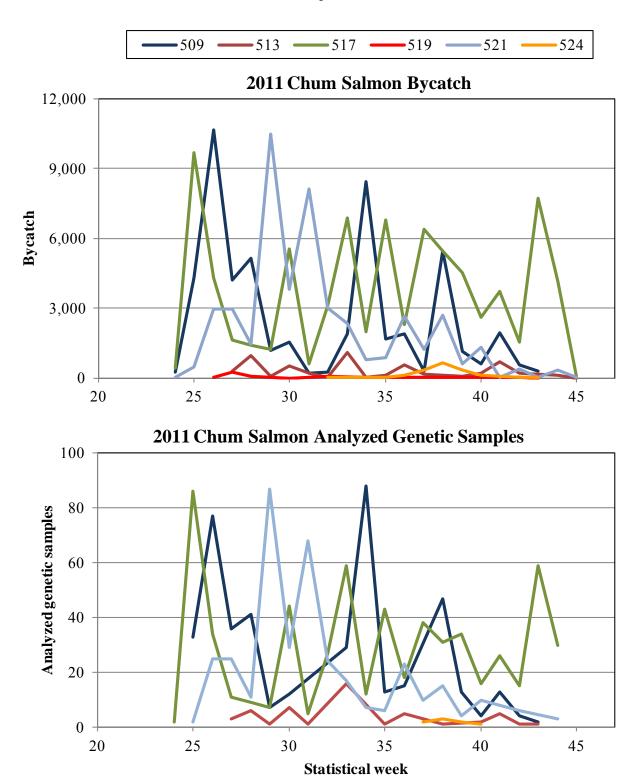
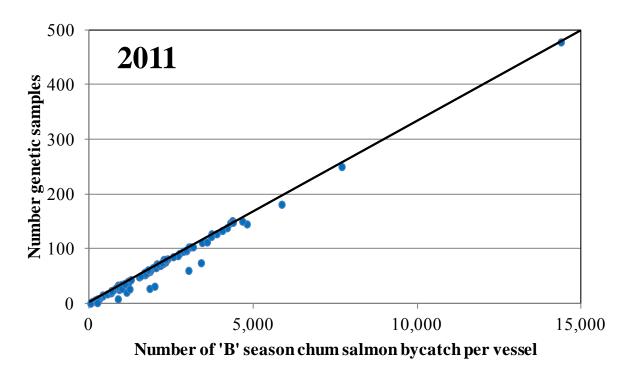


Figure 4. -- Number of Bering Sea chum salmon bycatch and analyzed genetic samples from the 2011 "B" season by statistical week and NMFS reporting area. Not shown in the chum salmon bycatch are an estimated 33 fish from statistical area 514, 56 fish from area 516, and 4 fish from area 523. One fish from area 519 for statistical week 32 is not shown for the analyzed genetic sample set. NMFS reporting areas are designated in the legend.

The systematic collecting protocol was also evaluated by comparing the total number of chum salmon caught on each vessel to the number of genetic samples collected from each vessel. During the "B" season, a subset of genetic samples was collected from 97% of the chum salmon bycatch (Fig. 5, top panel). All of the 90 vessels that participated in the midwater trawl fishery caught chum salmon. The entire catch from 82 vessels and part of the catch from 8 vessels, representing 93% and 4% of the total chum salmon bycatch, respectively, was sampled.

Approximately twice as many vessels were undersampled, and by a wider margin, than vessels that were oversampled. Of the bycatch that was sampled (Fig. 5, bottom panel), the sampling ratio of numbers of bycatch to numbers of genetic samples per vessel ranged from 23 to 39 fish, with a mean of 30.3 fish, which is very close to the protocol sampling goal of one genetic sample collected from every 30th chum salmon caught.



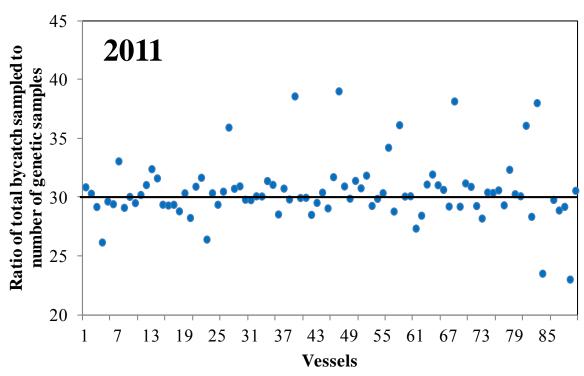


Figure 5. -- Bering Sea chum salmon bycatch and genetic samples from the 2011 pollock "B" season. Number of genetic samples collected from the total number of chum salmon bycatch from each of 90 vessels; black diagonal line represents the expected sampling rate (top panel). The ratio of total number of bycatch sampled to number of genetic samples collected per vessel (excluding one vessel that caught fewer than 30 chum salmon); black horizontal line represents the expected sampling ratio (bottom panel).

GENETIC STOCK COMPOSITION

DNA was extracted from the axillary processes for all but 13 of the 1,525 of chum salmon samples genetically analyzed. Those 13 fish had DNA extracted from a pool of 4-8 scales per sample. DNA extraction 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), *Otsg68* (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.).

A total of 1,525 samples from the 2011 chum salmon bycatch were analyzed, of which 1,472 samples were successfully genotyped for 8 or more of the 11 loci. No duplicate genotypes were detected with GENALEX (Peakall and Smouse 2006). 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). The remaining 1,472 samples had genetic information for an average of 10.82 loci (out of 11). There were 1,276 samples with data for all 11 loci, 140 with 10 loci, 41 with 9 loci, and 15 with 8 loci. There were six alleles observed in eight individuals that were not present in the chum salmon baseline; those alleles and the associated

haplotype were removed from further analysis. Of the 13 fish whose DNA was extracted from scales, we saw evidence of cross-contamination (more than two peaks in the Genemapper software) within only one sample, which was removed from subsequent analyses.

Quality control of genotyping was examined by plating DNA from the bottom row of each the 16 elution plates onto two 96-well plates for a total of 192 samples that were then processed for genotyping as described above. Genotypes from the quality control dataset were then compared to the genotypes of the original dataset. Overall, the genotyping error was low; there were a total of 22 differences in allele calls across 11 loci, which represented an overall error rate of 0.56% (22/3,936, where 3,936 is the number of alleles with unquestionable scores obtained from the original and quality control datasets). There were few differences in allele calls between the two datasets; only one locus (*Omm1070*) had differences higher than 1% (Table 1).

Table 1. -- Number of allele differences by locus between the original and quality control datasets for samples with non-questionable genotypes.

	Number alleles	Number allele	
Locus	compared	differences	% differences
Oki100	356	3	0.84
Omm1070	346	6	1.73
Omy1011	346	1	0.29
One101	342	3	0.88
One102	342	2	0.58
One104	374	0	0
One114	374	2	0.53
Ots 103	378	2	0.53
Ots3	362	1	0.28
OtsG68	366	2	0.55
Ssa419	350	0	0

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,c). Genotypes from converted mixtures were then exported from Excel as text files, and C++ programs were used to format the data into mixture files compatible with SPAM and BAYES software. Stock compositions were determined by comparing mixture genotypes with allele frequencies from 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 the Eastern Gulf of Alaska/Pacific Northwest (Prince William Sound to Washington State). A listing of the individual populations grouped by region is shown in the Appendix.

As with previous chum bycatch analyses (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010; Gray et al. 2011a,b; Kondzela et al. 2012), stock composition analysis for the 2011 chum bycatch samples was performed with previously published maximum-likelihood (SPAM 3.7 software; ADF&G 2003) and Bayesian (BAYES software; Pella and Masuda 2001) procedures. Because the maximum-likelihood estimates were in close agreement with the Bayesian estimates, the maximum-likelihood estimates are not shown. The Bayesian method uses an algorithm to produce stock composition estimates and can account for missing alleles in the baseline (Pella and Masuda 2001). BAYES stock composition estimates based on data from all 11 loci were derived for the six regional groupings (Table 2). For each 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 40,000 with the first 20,000 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 1.02 or less (Table 2), conveying strong convergence to a single posterior distribution (Pella and Masuda 2001).

Table 2. --Regional BAYES stock composition estimates for 1,472 chum salmon samples from the bycatch of the 2011 Bering Sea pollock midwater trawl fishery. BAYES estimates used information from all 11 loci. BAYES mean estimates are provided with standard deviations (SD), 95% credible intervals, median estimate, and the associated Gelman and Rubin shrink statistic.

BAYES Region	Mean	SD	2.5%	Median	97.5%	Shrink
East Asia	0.173	0.011	0.153	0.173	0.194	1.00
North Asia	0.184	0.013	0.158	0.184	0.210	1.00
Western Alaska	0.162	0.013	0.138	0.162	0.188	1.01
Upper/Middle Yukon	0.089	0.010	0.070	0.089	0.108	1.02
Southwest Alaska	0.015	0.005	0.007	0.014	0.026	1.01
Eastern GOA/PNW	0.378	0.014	0.351	0.378	0.405	1.00

COMPARISON WITH PREVIOUS ESTIMATES

The stock composition results from the analysis of the 2011 chum salmon bycatch samples differed somewhat from previous estimates (Fig. 6). The primary difference in 2011 appears to be the higher contribution from the Eastern GOA/PNW and lower contributions from East and North Asia in comparisons across years. Contributions in 2011 from Western Alaska are similar to the 1994, 1995, 2005 – 2010 average, and the contributions from the Upper/Middle Yukon and Southwest Alaska were below 10%, as in other years. Caution must be used in comparisons across years because there are differences in where and when genetic bycatch samples were collected each year.

The 1994-1995 chum salmon bycatch estimates were produced with allozyme data (Wilmot et al. 1998), whereas the 2005 (Guyon et al. 2010), 2006 (Marvin et al. 2011), 2007 (Gray et al. 2011a), 2008 (Gray et al. 2011b), 2009 (Gray et al. 2010), 2010 (Kondzela et al. 2012), and 2011 (this report) chum salmon bycatch sample estimates were derived from DNA-based 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. The effect of the bycatch on chum salmon populations is influenced by the overall size of the bycatch; the large variation in total chum salmon bycatch in 1994, 1995, 2005 – 2010 (Fig. 2) is reflected in the high standard errors of the mean number of bycatch by region when stock composition estimates are extrapolated to the total bycatch from the Bering Sea groundfish fisheries (Fig. 6, lower panel). It is worth noting that for the first time, in 2011 the genetic samples were collected systematically from the bycatch, resulting in the numerical extrapolations being relatively free of sample bias. The location and timing of collections from other years was not always representative of the entire bycatch within a given year.

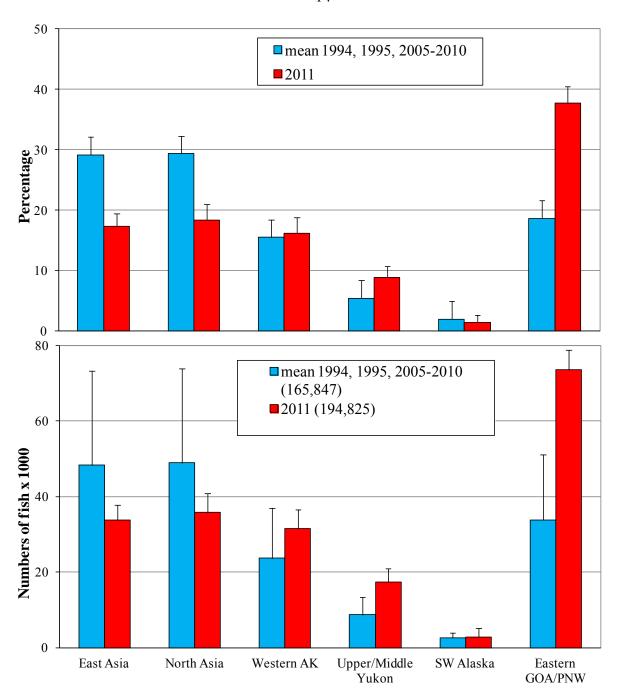


Figure 6. -- Comparison of the 2011 Bering Sea chum salmon bycatch with the mean stock composition estimates of available genetic samples from 1994, 1995, and 2005 – 2010. Percentages in top panel; numbers of fish in bottom panel, which for comparison purposes across years are based on the total chum salmon bycatch in all groundfish fisheries. Standard errors of the mean estimates are shown for the combined years; 95% BAYES credible intervals are shown for the 2011 analysis. Error bars are based on only the mixed-stock analyses and do not include errors associated with the overall annual bycatch size estimation or potential biases in sample distribution. Total chum salmon bycatch from the Bering Sea groundfish fisheries is shown in parentheses in the bottom figure legend; 1994-2010 are estimates and 2011 is a census.

TEMPORAL STRATIFICATION

An understanding of the temporal distribution of the chum salmon bycatch is important. For example, if the samples are randomly distributed or represent a distribution that can be described mathematically, temporally biased estimates could be adjusted with respect to the overall bycatch rate. With the systematic sampling approach used in 2011, the temporal estimates should accurately reflect the total bycatch stock contributions present within each time period. Likewise, if the bycatch stock distribution changes consistently over time, the bycatch could be managed in a manner to minimize effects on critical stocks.

As with the 2005–2010 analyses, the 2011 sample set was temporally split into three "B" season time periods: early, middle, and late (Table 3, Fig. 7). Stock composition analyses for 2011 and similar temporal strata of the average 2005–2010 chum salmon bycatch sample sets are included for comparison purposes (Fig. 8). Results from this analysis should be used cautiously because spatial differences exist in the time-stratified sample sets and these differences are known to affect the stock composition estimates.

Table 3. -- Temporal groupings from the 2011 "B" season chum salmon bycatch genetic sample sets.

Time period	Weeks	Dates	Number samples
Early	24-29	June 12 – July 23	503
Middle	30-34	July 24 – August 27	446
Late	35-44	August 28 – November 5	522

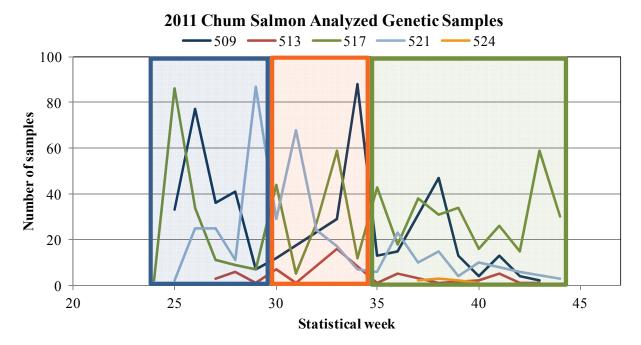


Figure 7. -- Analyzed genetic samples from the 2011 "B" season chum salmon bycatch identified by early (blue), middle (brown), and late (green) temporal groupings. NMFS reporting areas are designated in the legend.

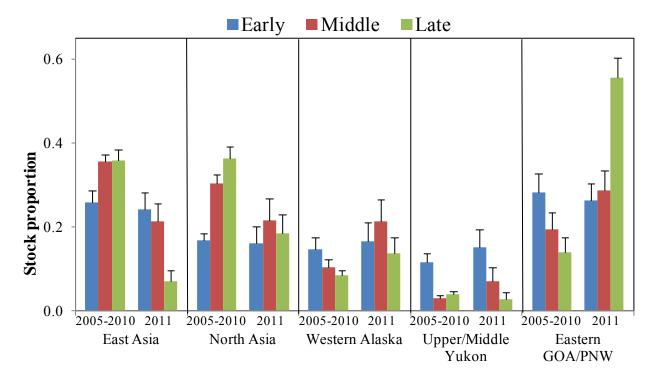


Figure 8. -- BAYES stock composition estimates for the early, middle, and late periods (defined in Table 3) from the 2005–2010 (mean) and 2011 chum salmon bycatch. Standard errors of the mean estimates are shown for the combined years; 95% BAYES credible intervals are shown for the 2011 analysis. Not shown is the Southwest Alaska region for which estimates never exceeded 5.6%.

BAYES stock composition estimates were made as described previously for each of the three temporal strata for. Gelman and Rubin shrink statistics were in all cases below 1.02 and suggested strong convergence to a single posterior distribution. The stock composition estimates of the 2011 genetic samples differed across the three time periods (Fig. 8). Within 2011, the contribution of fish from East Asia and Upper/Middle Yukon decreased over the three time periods and was significantly lower in the third time period (Weeks 35-44). The North Asia and Western Alaska contribution was highest in the middle time period (Weeks 30-34). The prevalence of fish from the Eastern GOA/PNW was similar in the first two time periods, but nearly doubled in the latest period (Weeks 35-44) and resulted in the highest proportion observed for any region across the 7-year time period.

In addition, some differences were observed in the pattern of 2011 within-season temporal stock contributions from the trends reported previously with the 2005–2010 chum salmon bycatch samples (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2011a,b; Gray et al. 2010; Kondzela et al. 2012). The decrease in contribution from East Asia and the nearly uniform contribution from North Asia across the three time periods in 2011 differs from the pattern more typical of these regions in previous years, a result of the unusually high proportion of GOA/PNW fish in the late mixture. Whereas the Upper/Middle Yukon contribution was highest in the early part of the season (Weeks 24-29) as in other years, the very high contribution from the Eastern GOA/PNW in the latest period (Weeks 35-44) had not been reported previously. The higher contribution from the Eastern GOA/PNW in the latest period may be due to the prevalence of samples from the southeastern Bering Sea areas 509 and 517 during the late part of the "B" season. This demonstrates that stock composition of the chum salmon bycatch changes during the course of the season, and how the temporal changes are interrelated to the spatial differences is addressed below.

SPATIAL STRATIFICATION

An understanding of the spatial distribution of the chum salmon bycatch is also important for the same reasons and concerns described for temporal stratification. In 2011, for the first time, the AFSC's North Pacific Observer Program undertook a complete census of chum salmon bycatch from the Bering Sea trawl fisheries. More than half of the chum salmon bycatch was counted and sampled at shoreside facilities where catches were offloaded from vessels that theoretically can participate in multiple fishery management areas on a particular cruise before an offload. For vessels that fished in multiple NMFS reporting areas during a trip, the area was identified as the area where most of the fishery target species were caught.

The 2011 genetic samples were spatially split into two areas: the southeastern Bering Sea (reporting areas 509, 513, 517; n = 1,090 samples) and the central Bering Sea (reporting areas 521, 524; n = 381 samples). The single sample from area 519 was not included. BAYES stock composition estimates were made as described previously for each of the two spatial strata. Gelman and Rubin shrink statistics were 1.02 or less for both datasets and suggested strong convergence to a single posterior distribution. The stock composition estimates differed between the spatial strata (Fig. 9). Nearly three-quarters of the chum salmon bycatch in the more southeastern areas (509, 513, and 517) was of North American origin, with the highest proportion from the Eastern GOA/PNW region. In the central Bering Sea, in areas 521 and 524, chum salmon from Asia were dominant (~60%).

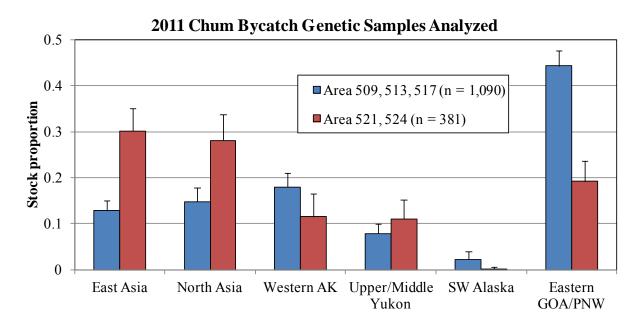


Figure 9. -- BAYES stock composition estimates and 95% credible intervals for the 2011 chum salmon bycatch genetic samples from the NMFS reporting areas of the central (521, 524) and southeastern (509, 513, 517) Bering Sea (Fig. 1).

To better understand the bycatch stock distribution across time and space, the 2011 sample set was split into the NMFS reporting areas and each of the reporting area datasets was

split into three time periods (Table 4). Samples from areas 513, 519, and 524 were not included due to small sample sizes in those areas.

Table 4. -- Spatial and temporal groupings from the 2011 chum salmon bycatch genetic sample sets across three time periods (Table 3) for the reporting areas with the most samples.

Reporting area	Time period	Number of samples
509	early	194
509	middle	129
509	late	111
517	early	149
517	middle	147
517	late	310
521	early	150
521	middle	145
521	late	77

BAYES stock composition estimates were made for each of the spatial and temporal strata as described above, with the exception that the stock composition analyses were completed for a chain length of 10,000 with the first 5,000 deleted during the burn-in phase. Gelman and Rubin shrink statistics were in all cases below 1.10. The stock distribution changed across the time periods, with some of the changes consistent in all three NMFS reporting areas (Fig. 10). In general, the contribution from East Asia decreased over time, whereas the contribution from North Asia increased over time. There was a small increase followed by a small decrease in the proportion from Western Alaska over time. The contribution from Western Alaska in area 521 was about half that in the more southeastern areas across all time periods. In all three reporting areas, the chum salmon bycatch from the Upper/Middle Yukon decreased over the time periods and by September, fish from that region appear to have migrated out of that part of the Bering Sea open to the trawl fisheries. The contribution from Southwest Alaska was negligible in all three areas and time periods. In all three areas, the Eastern GOA/PNW contribution increased

over the time periods, most notably in areas 517 and 521 in the late period. It should be noted that the numbers of fish from a region within a given area may not change over time, but the proportion will change if fish from other regions move into or out of the area.

The similarity of stock distributions among the areas and time periods may be due, at least in part, to vessels fishing near area boundaries. For example, the southern corner of area 521 shares the northwestern edge of area 517. Latitude and longitude information was not available for many samples, so the location of the bycatch samples within each area is unknown. In addition, more than half of the total bycatch was sampled from shoreside deliveries in which vessels may have fished in multiple areas--for each cruise, the NMFS reporting area was identified as the area most of the fishery target species were caught. Thus, for an unknown proportion of the chum salmon bycatch samples, the area designation may not be correct.

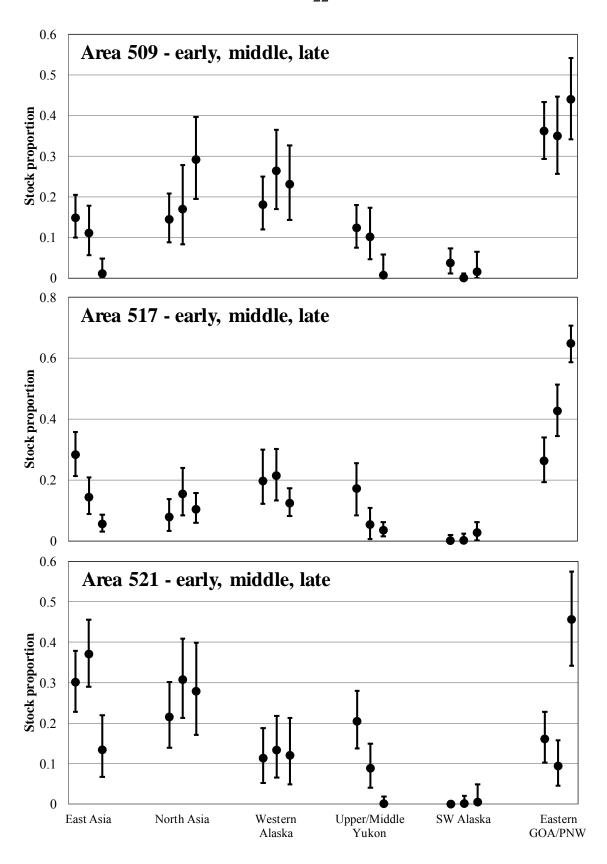


Figure 10. -- BAYES stock composition estimates and 95% credible intervals for the NMFS reporting areas 509, 517, and 521 for the early, middle, and late time periods (Table 4) from the 2011 chum salmon bycatch genetic samples.

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 1,472 individuals sampled from the 2011 chum salmon bycatch. The limitations and results of this analysis are summarized below.

Sampling Issues

We highlight the reduced spatial and temporal biases in the 2011 sample set (Figs. 3 and 4) that were inherent in collections from previous years. Reduction of those biases improves the application of the 2011 genetic sample stock composition estimate to the entire chum salmon bycatch. Implementation of Amendment 91 to the fishery management plan for groundfish of the Bering Sea and Aleutian Islands Management Area (75 FR 53026, August 30, 2010) 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 new regulation led to the collection of representative samples from 97% of the chum salmon bycatch for genetic analysis (Fig. 5), and improved 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 2011 bycatch of Bering Sea chum salmon were predominantly from Eastern GOA/PNW stocks (38%) although substantial contributions were also from Western Alaska (16%), Upper/Middle Yukon (9%), East Asia (17%), and North Asia (18%). These stock proportions differ from estimates from previous years, particularly the

higher proportion from the Eastern GOA/PNW and the lower proportion from Asia. Although samples in 2011 were collected representatively from the bycatch, there were differences in where and when genetic bycatch samples were collected from previous years, so that caution must be used in making year-to-year comparisons.

Temporal and Spatial 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, when the majority of chum salmon are intercepted. In 2011, unlike in most other years, the Eastern GOA/PNW fish contribution was predominant across all three sampling periods and increased throughout the season to dominate the late sampling period. For the most part, stock composition estimates changed across the three sampling periods in a manner unlike that observed across previous years, suggesting a shift in the temporal stratification of chum salmon stocks in the Bering Sea, changes in sampling or fishing locations, or both.

A spatial analysis was completed to determine whether stock compositions differed between two broad areas of the Bering Sea where most of the chum salmon bycatch occurred in 2011: the central Bering Sea, represented by NMFS reporting areas 524 and 521, and the southeastern Bering Sea, represented by areas 509, 513, and 517. The majority of chum salmon bycatch in the central Bering Sea was from Asia, whereas most of bycatch in the southeastern Bering Sea was from North America, principally from the Eastern GOA/PNW region (Fig. 9).

An examination of stock estimates on both spatial and temporal strata suggests that although there were some differences in stock distribution across areas or time periods, there were also consistent temporal changes in stock distribution within areas (Fig. 10). For example, the Upper/Middle Yukon and East Asia contributions decrease, and the Eastern GOA/PNW and

North Asia contributions increase over time in all three reporting areas. These changes across time regardless of area may tie in with the observation that the larger chum salmon leave early from the fishery (e.g., mature summer-run Yukon River chum salmon) and the smaller fish arrive later into the fishery (Myers et al. 2009, Stram and Ianelli 2009).

Application of These Estimates

The extent to which any salmon stock is impacted as the bycatch in 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 imply greater impact than a smaller estimate in another year.

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APPENDIX

Appendix -- 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	$\frac{1}{2}$	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
-	-	-	

DFO number	Population name	Region number	Region
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
370	Joshua Green	5	Southwest Alaska
364	Meshik	5	Southwest Alaska
283	Moller Bay	5	Southwest Alaska
369	Pumice Creek	5	Southwest Alaska
307	I diffice_Cicck	J	Douthwest Alaska

DFO number	Population name	Region number	Region
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
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

DFO number	Population name	Region number	Region
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	Ecstall 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
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

DFO number	Population name	Region number	Region
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
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

DFO number	Population name	Region number	Region
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 5 =	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
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

DFO number	Population name	Region number	Region
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
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

DFO number	Population name	Region number	Region
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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