



NOAA Technical Memorandum NMFS-AFSC-271

Genetic Stock Composition Analysis of Chum Salmon Bycatch and Excluder Device Samples from the 2012 Bering Sea Walleye Pollock Trawl Fishery

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

U.S. DEPARTMENT OF COMMERCE
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ABSTRACT

A genetic analysis of chum salmon (*Oncorhynchus keta*) bycatch from the 2012 Bering Sea walleye pollock (*Gadus chalcogrammus*) trawl fishery was undertaken to determine the overall stock composition of the sample set. A genetic analysis of chum salmon collected during a test of a salmon excluder device was also conducted. Samples were genotyped for 11 microsatellite markers and results were estimated using the current chum salmon microsatellite baseline. In 2012, genetic samples were collected systematically as part of a special project that commenced in 2011 to reduce sample biases that exist in collections from previous years and have the potential to affect stock composition analysis results. One genetic sample was collected for every 31.5 chum salmon caught in the 98% 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 673 chum salmon bycatch samples collected throughout the 2012 Bering Sea trawl fishery, the North Asian stocks dominated the sample set (39%), with moderate contributions from East Asian (20%), Eastern Gulf of Alaska (GOA)/Pacific Northwest (PNW) (18%), and Western Alaska (14%) stocks, and smaller contributions from Upper/Middle Yukon River (7%) and Southwest Alaska (2%) stocks. The estimates for the 2012 chum salmon bycatch sample set differed from the mean of the 2005–2011 estimates for the two Asian regions, but not for the North American regions. The pattern of changes of regional stock contributions over three time periods in 2012 differed from previous years for some regions. There were some spatial differences in stock distribution (e.g., the East Asian stock contribution was higher in the central Bering Sea than in the southeastern Bering Sea). As with the bycatch samples, the salmon excluder device samples included fish from all geographic regions despite being collected at small spatial and temporal scales.

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INTRODUCTION

It is important to understand the stock composition of Pacific salmon (*Oncorhynchus spp.*) caught in Bering Sea groundfish fisheries because this area is a known feeding habitat for multiple brood years of chum salmon (*O. 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 (NPFMC 2012). This report includes genetic stock identification results for the chum salmon bycatch samples collected from the 2012 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.

Also included in this report are the results of a genetic stock identification analysis of chum salmon caught during a test of salmon excluder devices in late-summer/fall 2012 (Gauvin et al. 2013). These samples represent collections of relatively large numbers of chum salmon caught in individual trawl hauls. Results from the excluder device tests are important, as they provide chum salmon stock composition estimates on a smaller geographic and temporal scale than is usually possible with bycatch analyses.

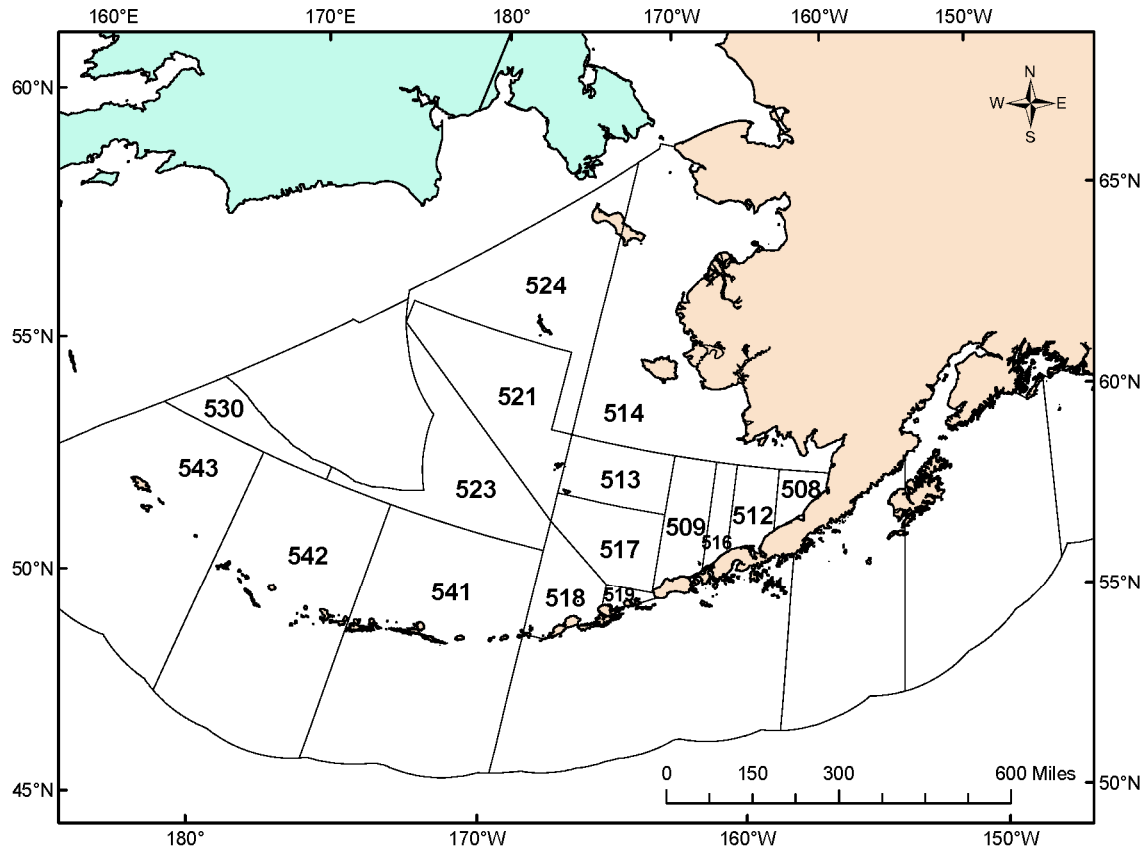


Figure 1. -- NMFS reporting areas associated with the Bering Sea-Aleutian Island groundfish fishery.

We present the stock composition estimates for the 2012 chum salmon bycatch samples collected from the Bering Sea. For additional background and methods, this report is intended to be supplemented with the chum salmon reports prepared previously for the 2005–2011 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, 2013). 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 2012 for the AFSC's Auke Bay Laboratories. Sampling was changed in 2011 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 (*Gadus chalcogrammus*) trawl fishery.

In 2012, an estimated 22,277 chum salmon were taken as bycatch in the pollock-directed midwater and bottom trawl fisheries, accounting for more than 91% of the total chum salmon bycatch taken in the Bering Sea groundfish fisheries (NMFS 2013). The remaining chum bycatch was taken in the Atka mackerel (*Pleurogrammus monopterygius*) fishery (4.7%) and other groundfish fisheries (3.7%). This is the fourth smallest non-Chinook salmon bycatch in the pollock fisheries between 1994 and 2011, less than 16% of the average of 142,537 fish, and about one-third the median of 71,612 (Fig. 2). The 2012 genetic samples were collected from the midwater trawl fishery during the B-season (June 11 to December 31) in North Pacific Fishery Management Council (NPMFC) statistical areas 509-524 (Fig. 1). Of the 22,266 chum salmon caught in this fishery, genetic samples were collected from 708 fish, which represents a sampling rate of one of every 31.5 chum salmon (or 3.2% of the midwater trawl chum salmon bycatch). This sampling rate is nearly identical to that in 2011, the first year representative sampling was implemented.

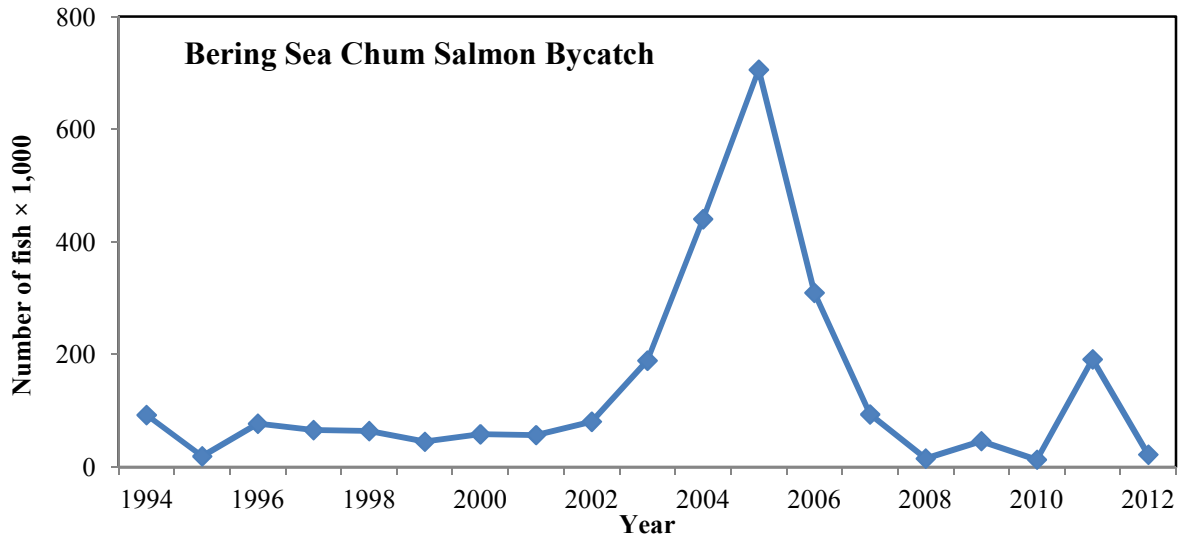


Figure 2. -- Yearly estimates for the non-Chinook salmon bycatch from the Bering Sea pollock directed trawl fisheries (NMFS 2013).

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 and with a chi-square test ($\chi^2 = 3.83$, 5 *d.f.*, $P = 0.575$). Temporal bias by statistical week ending on Sunday was minimal (Fig. 3) when samples were pooled across management areas and minor discrepancies may reflect differences in how bycatch and genetic sample dates were reported. 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.

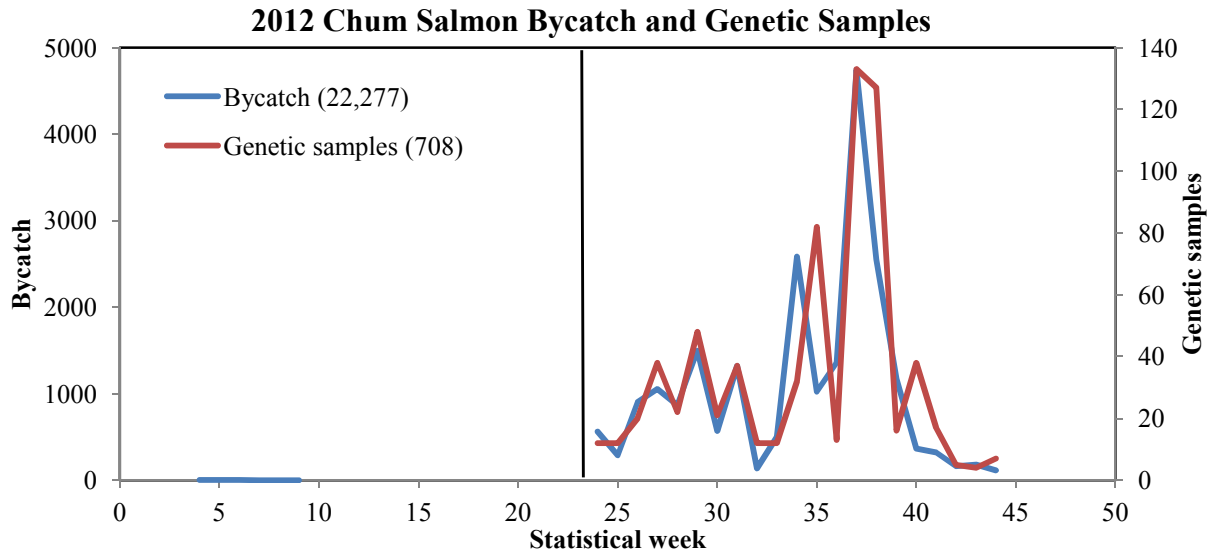


Figure 3. -- Number of Bering Sea chum salmon bycatch and genetic samples from 2012 by statistical week. Total numbers of chum salmon caught in the Bering Sea pollock midwater trawl fishery compared with the available 708 genetic samples collected and analyzed. Weeks 1-23 correspond to the groundfish “A” season, whereas weeks 24-45 correspond to the “B” season, the demarcation of which is a vertical line.

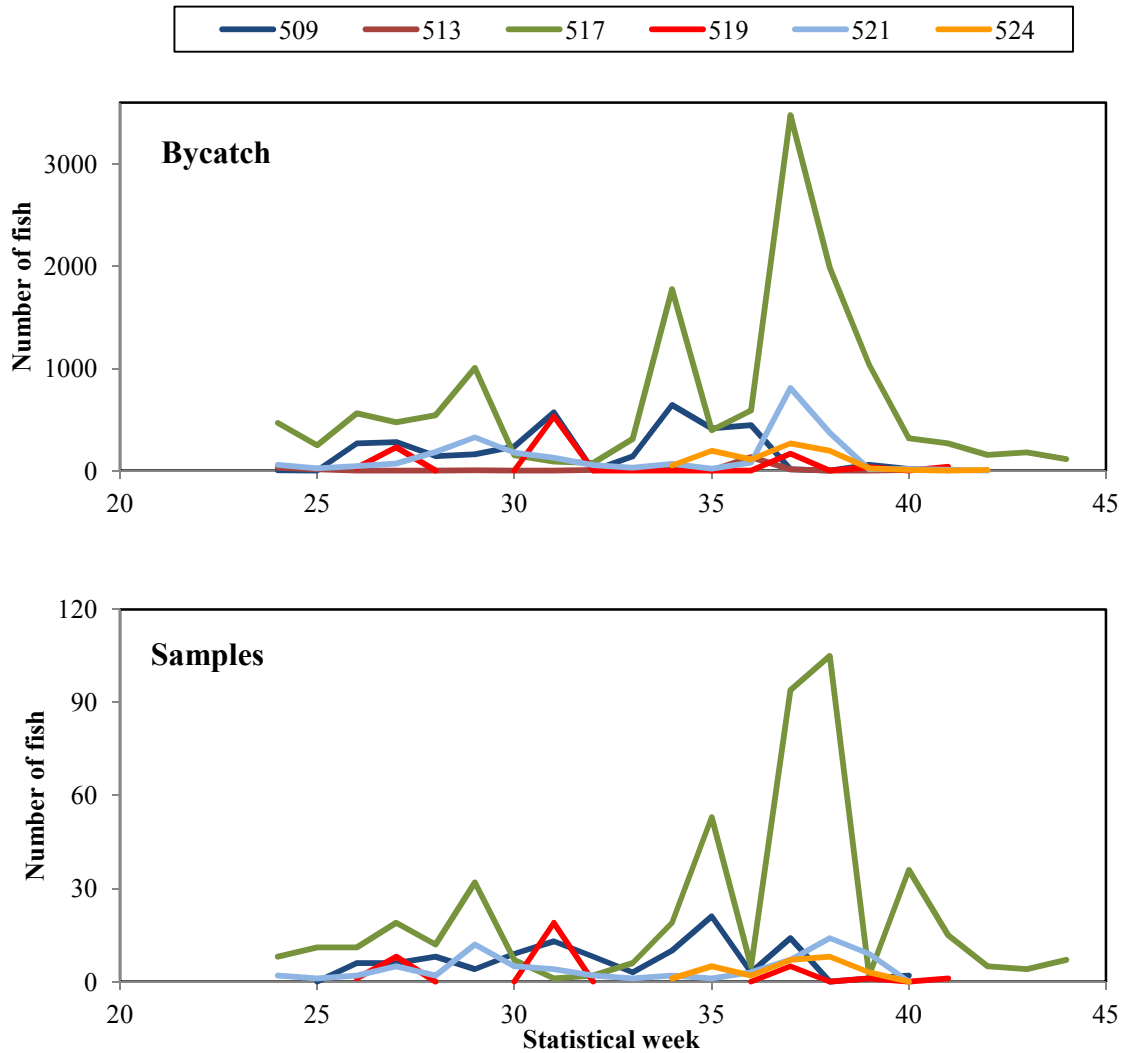


Figure 4. -- Number of Bering Sea chum salmon bycatch and analyzed genetic samples from the 2012 “B” season by statistical week and NMFS reporting area. Not shown in the analyzed genetic sample set are an estimated 13 fish from statistical area 513. NMFS reporting areas are designated in the legend.

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 97.6% of the chum salmon bycatch (Fig. 5, top panel). All of the 90 vessels that participated in the midwater trawl fishery caught chum salmon. Catches from 74 vessels representing 97.6% of the total chum salmon bycatch were sampled, while the remainder of the bycatch, 2.4%, was caught by 16

vessels that were not sampled (Table 1). Half of the unsampled vessels caught fewer than 30 fish each and overall, fewer than 34 chum salmon on average were caught during the entire B-season on the unsampled vessels. The number of vessels that were undersampled was only slightly more than the number oversampled, an improvement over 2011 sampling by vessel. Of the bycatch that was sampled (Fig. 5, bottom panel), the mean sampling ratio of numbers of bycatch to numbers of genetic samples per vessel was 30.9 fish, which is very close to the protocol sampling goal of one genetic sample collected from every 30th chum salmon caught.

Table 1. -- Proportion of chum salmon bycatch not sampled, oversampled, or undersampled based on the expected sampling rate of every 30th chum salmon caught.

	Proportion
not sampled	0.024
oversampled	0.518
undersampled	0.458

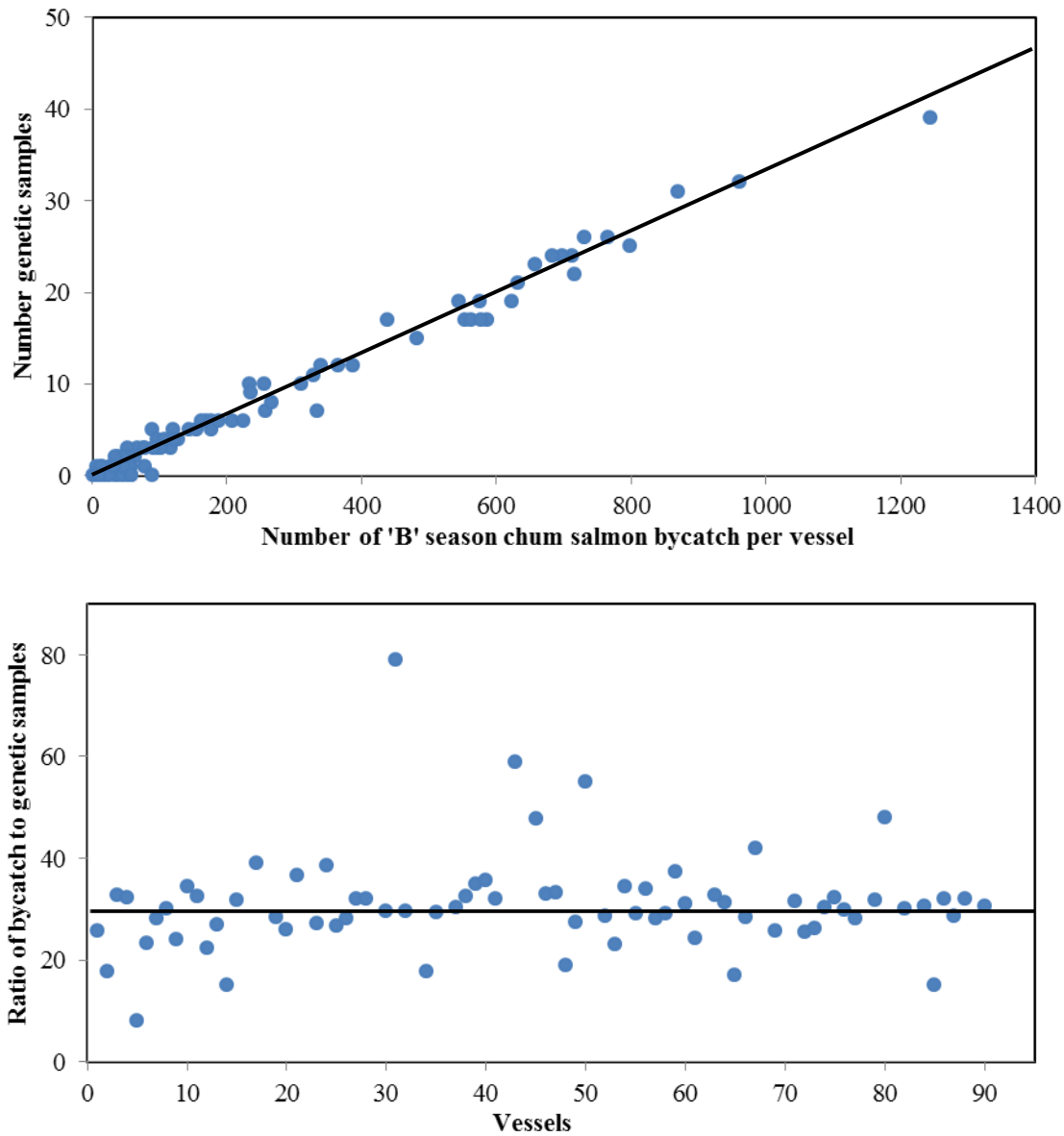


Figure 5. -- Bering Sea chum salmon bycatch and genetic samples from the 2012 pollock “B” season. Number of genetic samples collected from the total number of chum salmon bycatch from each of 90 vessels; black diagonal line represents the expected sampling rate (top panel). The ratio of total number of bycatch sampled to number of genetic samples collected per vessel for the 74 vessels sampled; black horizontal line represents the expected sampling ratio (bottom panel).

GENETIC STOCK COMPOSITION

DNA was extracted from the axillary processes of chum salmon for all but 1 of the 708 bycatch samples and all of the 307 samples from three salmon excluder device trawl hauls, while the remaining bycatch sample had DNA extracted from a pool of seven scales. 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), *Ots68* (Williamson et al. 2002), and *Ssa419* (Cairney et al. 2000). Thermal cycling for the amplification of DNA fragments with 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 (Applied Biosystems, Inc.). Genotypes were double-scored with GeneMapper 4.0 software (Applied Biosystems, Inc.) and exported to Excel (Microsoft, Inc.) spreadsheets.

Of the 708 bycatch and the 307 salmon excluder device samples analyzed, 673 bycatch samples and all excluder samples were successfully genotyped for 8 or more of the 11 loci (Table 2). No duplicate genotypes were detected with GenAlEx 6.5 (Peakall and Smouse 2006, 2012). The remaining 673 bycatch samples and the excluder samples had genetic information for an average of 10.8 loci (out of 11). There were two alleles observed in one individual that were not present in the chum salmon baseline; those alleles and the associated haplotypes were removed from further analysis. Of the one fish whose DNA was extracted from scales, we saw no evidence of cross-contamination (more than two peaks at multiple loci in the GeneMapper 4.0 software).

Table 2. -- Number of genetic samples successfully genotyped for chum salmon from the 2012 excluder device and bycatch chum salmon samples.

Number loci	Excluder	Bycatch
11	269	593
10	31	58
9	4	13
8	3	9
<8	0	35

Quality control of sample handling and genotyping was examined by plating DNA from the eight samples in the first (left-most) column of each of the 11 elution plates (bycatch and excluder) onto one 96-well plate for a total of 88 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 (Table 3). Overall, the genotyping error was low and very similar to the error rate in the 2011 dataset; there were a total of nine differences in allele calls across 11 loci, which represented an overall discrepancy rate of 0.55% (9/1,644, where 1,644 is the number of alleles with unquestionable scores obtained from the original and quality control datasets).

Table 3. -- Number of allele differences by locus between the original and quality control datasets for samples with non-questionable genotypes.

Locus	Number alleles compared	Number allele differences	Percent difference
<i>Oki100</i>	150	1	0.67
<i>Omm1070</i>	148	2	1.35
<i>Omy1011</i>	144	1	0.69
<i>One101</i>	154	1	0.65
<i>One102</i>	150	2	1.33
<i>One104</i>	150	0	0
<i>One114</i>	150	0	0
<i>Ots103</i>	156	1	0.64
<i>Ots3</i>	150	0	0
<i>OtsG68</i>	152	1	0.66
<i>Ssa419</i>	140	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. 2008; Beacham et al. 2009b). Genotypes from converted mixtures were then exported from Excel as text files, and C++ or FORTRAN 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 (Fig. 6). The regional groupings were selected based on principal coordinate and simulation analyses as described in Guyon et al. (2010). A listing of the individual populations grouped by region is provided in the Appendix.

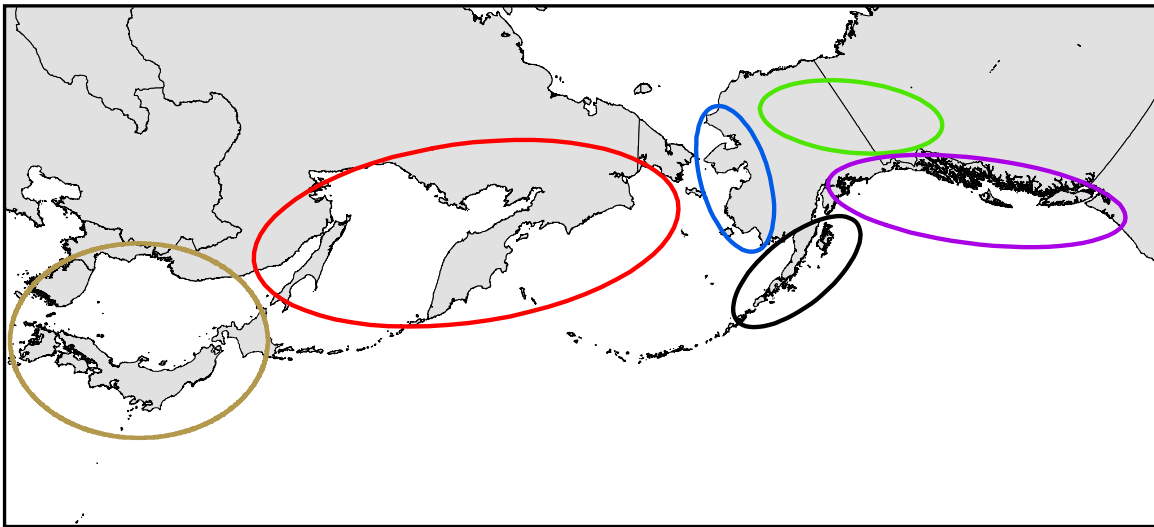


Figure 6. -- Six regional groupings of baseline chum salmon populations used in this report were: East Asia (brown), North Asia (red), Western Alaska (blue), Upper/Middle Yukon (green), Southwest Alaska (black), and the Eastern Gulf of Alaska/Pacific Northwest (purple).

As with previous chum salmon bycatch analyses (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010; Gray et al. 2011a,b; Kondzela et al. 2012, 2013), stock composition analysis for the 2012 chum salmon 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 4). 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 100,000 with the first 50,000 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 1.01 or less (Table 4), conveying strong convergence to a single posterior distribution (Gelman and Rubin 1992; Pella and Masuda 2001).

Table 4. --Regional BAYES stock composition estimates for 673 chum salmon samples from the bycatch of the 2012 Bering Sea pollock midwater trawl fishery. 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
<i>East Asia</i>	0.203	0.017	0.171	0.203	0.237	1.00
<i>North Asia</i>	0.389	0.024	0.344	0.389	0.436	1.00
<i>Western Alaska</i>	0.138	0.019	0.102	0.137	0.176	1.00
<i>Upper/Middle Yukon</i>	0.074	0.014	0.048	0.073	0.104	1.01
<i>Southwest Alaska</i>	0.020	0.009	0.004	0.019	0.040	1.01
<i>Eastern GOA/PNW</i>	0.176	0.017	0.143	0.176	0.211	1.00

COMPARISON WITH PREVIOUS ESTIMATES

The stock composition results from the analysis of the 2012 chum salmon bycatch samples differed somewhat from previous estimates (Fig. 7). The estimated contribution from North Asia is significantly higher, whereas the contribution from East Asia is significantly lower in comparisons across years. Contributions in 2012 from Western Alaska are similar to the 1994, 1995, 2005–2011 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 2005-2012 chum salmon bycatch sample estimates were derived from DNA-based microsatellite loci (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010, 2011a,b; Kondzela et al. 2012, 2013). 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, 2005–2011 (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. 7, lower panel). Beginning 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 earlier years was not always representative of the entire bycatch within a given year.

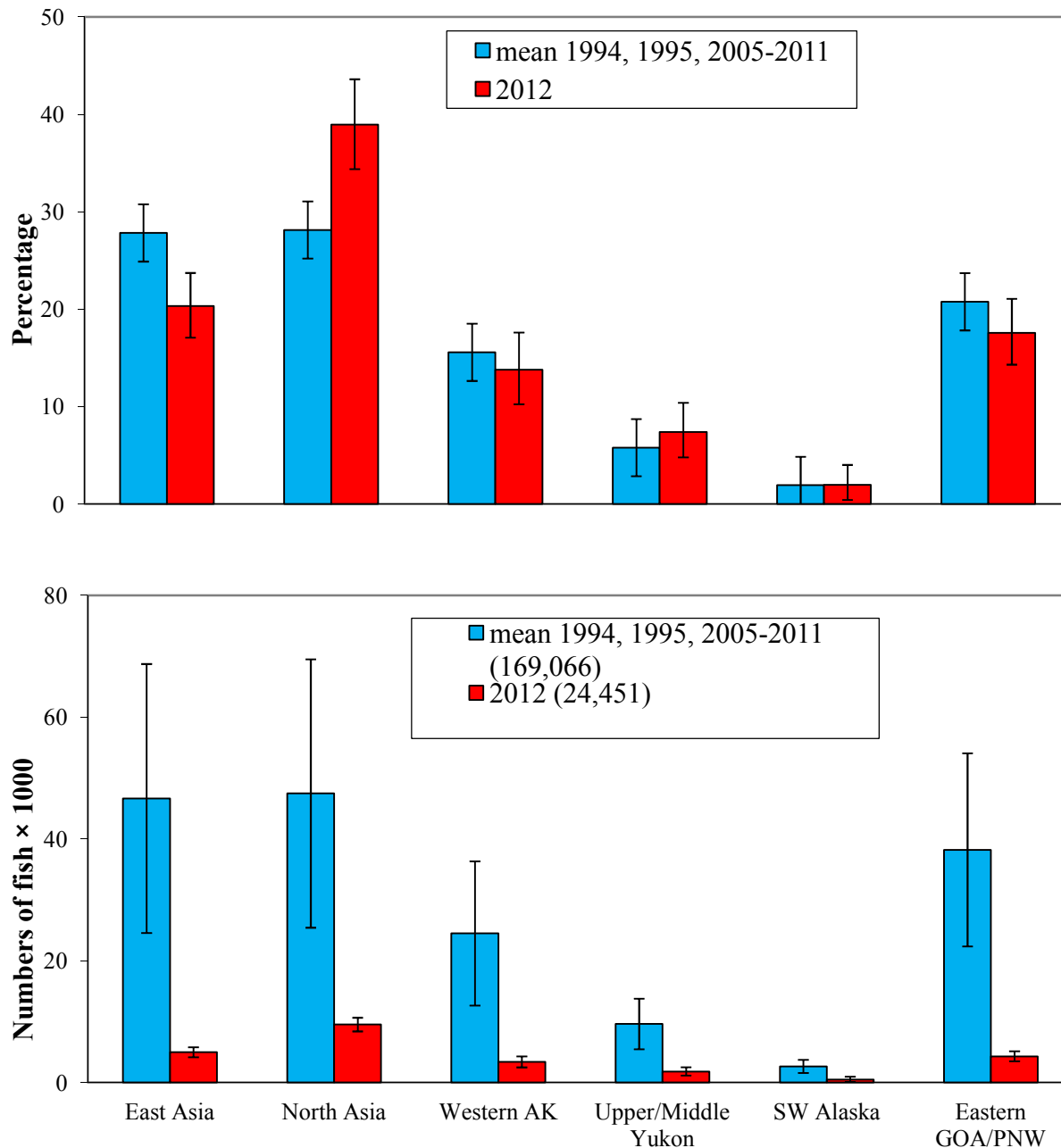


Figure 7. -- Comparison of the 2012 Bering Sea chum salmon bycatch with the mean stock composition estimates of available genetic samples from 1994, 1995, and 2005–2011. Percentages in top panel; numbers of fish in bottom panel, which for comparison purposes across years are based on the total chum salmon 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 2012 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 2011–2012 are censuses.

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 since 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, it may be possible to manage the bycatch in a manner that minimizes effects on critical stocks.

As with the 2005–2011 analyses, the 2012 sample set was temporally split into three “B” season time periods: early, middle, and late (Table 5, Fig. 8). Stock composition analyses for 2012 and similar temporal strata of the average 2005–2011 chum salmon bycatch sample sets are included for comparison purposes (Fig. 9). 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 5. -- Temporal groupings from the 2012 “B” season chum salmon bycatch genetic sample sets.

Time period	Weeks	Dates	Number of samples
Early	24-29	June 11 – July 21	148
Middle	30-34	July 22 – August 25	106
Late	35-44	August 26 – November 3	419

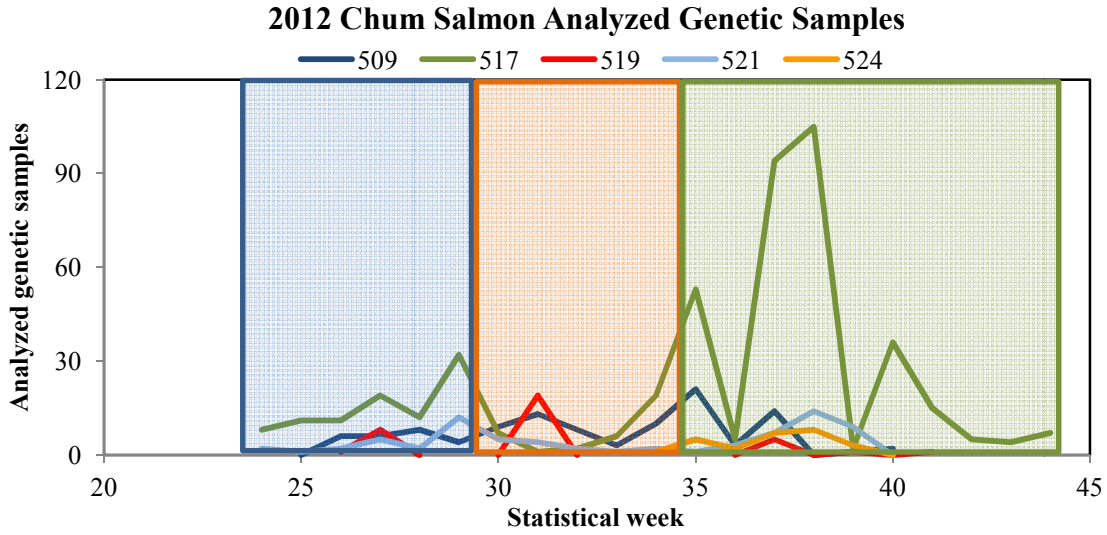


Figure 8. -- Analyzed genetic samples from the 2012 “B” season chum salmon bycatch identified by early (blue), middle (brown), and late (green) temporal groupings. NMFS reporting areas are designated in the legend.

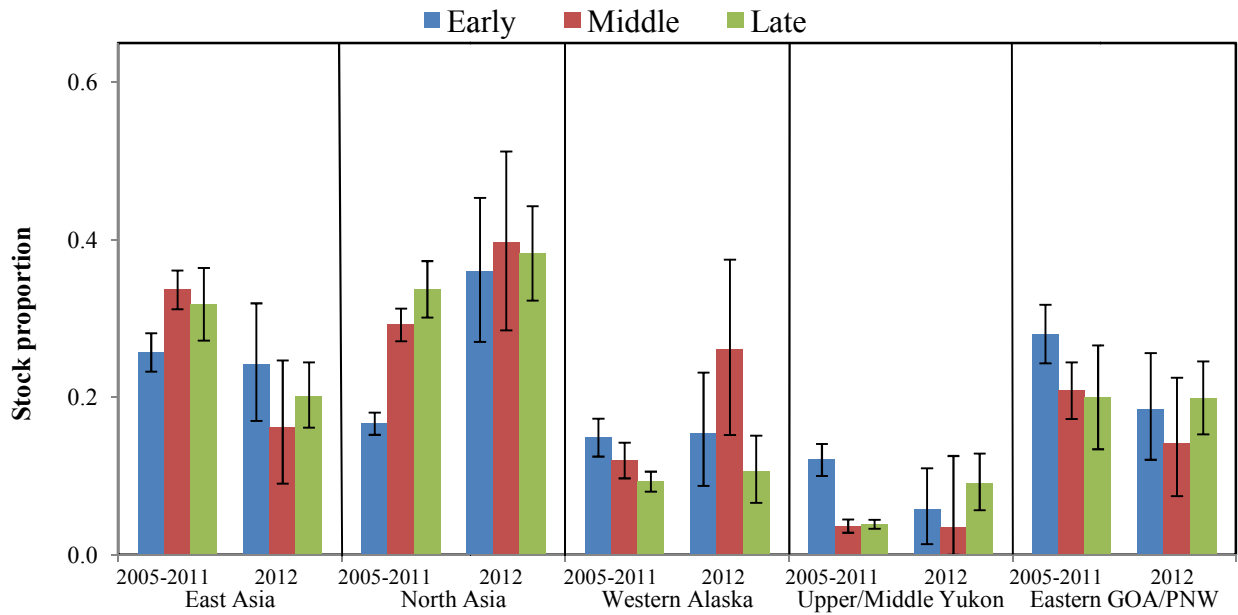


Figure 9. -- BAYES stock composition estimates for the early, middle, and late periods (defined in Table 5) from the 2005–2011 (mean) and 2012 chum salmon bycatch. Standard errors of the mean estimates are shown for the combined years; 95% BAYES credible intervals are shown for the 2012 analysis. Not 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. Gelman and Rubin shrink statistics were in all cases 1.02 or less and suggested strong convergence to a single posterior distribution. The stock composition estimates of the 2012 genetic samples differed only slightly across the three time periods within regions, except for the contribution from Western Alaska that increased during the middle time period (Weeks 30-34; Fig. 9).

In addition, some differences were observed in the pattern of 2012 within-season temporal stock contributions from the trends reported previously with the 2005–2011 chum salmon bycatch samples. The contribution from East Asia during the middle and late time periods in 2012 was significantly lower than in previous years, although during the late time period the contribution was more than double that observed in 2011 (Kondzela et al. 2013). The nearly uniform contribution from North Asia across the three time periods in 2012 differs from the pattern of this region in previous years, where the proportion contributed to the bycatch increased as the season progressed; during the first time period the contribution in 2012 was nearly two-fold higher than the previous 7-year average. The proportion of the bycatch contributed by Western Alaska chum salmon stocks increased in the middle of the season (Weeks 30-34), whereas on average in previous years, the proportion decreased over the course of the season. The contribution from the Upper/Middle Yukon did not decrease as the season progressed as has been observed in previous years. The unusually high contribution from the Eastern GOA/PNW in the latest period (Weeks 35-44) that was observed in 2011 did not recur in 2012. This analysis 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 2012, for the second year, 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 2012 genetic samples were spatially split into two broad areas (Fig. 1): the southeastern Bering Sea (NMFS reporting areas 509, 513, 517, 519; $n = 580$ samples) and the central Bering Sea (NMFS reporting areas 521, 524; $n = 93$ samples). BAYES stock composition estimates were made as described previously for each of the two spatial strata. Gelman and Rubin shrink statistics were 1.01 or less for both datasets and suggested strong convergence to a single posterior distribution. The stock composition estimates differed between the spatial strata (Fig. 10). About three-quarters of the contribution to the central Bering Sea and more than half of the contribution to the southeastern Bering Sea were from Asian stocks. Stocks from the Eastern GOA/PNW provided the highest contribution from North America in both Bering Sea areas. North Asia fish, the largest contributor to the bycatch in both Bering Sea areas, were caught in nearly equal proportions, but East Asia fish had a higher contribution in the central Bering Sea (34%) than in the southeastern Bering Sea (19%). Except for the Upper/Middle Yukon region, which had nearly equally low contribution in both broad areas, contributions from North American stocks appeared to be higher in the southeastern Bering Sea than in the central Bering

Sea, but the small sample size of the central Bering Sea dataset resulted in large, overlapping credible intervals.

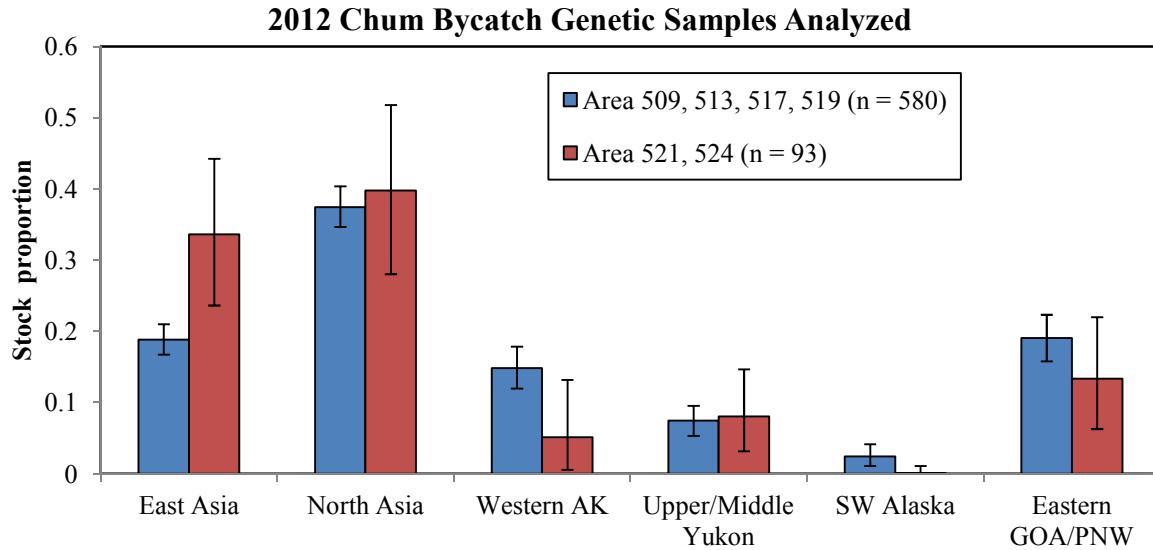


Figure 10. -- BAYES stock composition estimates and 95% credible intervals for the 2012 chum salmon bycatch genetic samples from the NMFS reporting areas of the central (521, 524) and southeastern (509, 513, 517, 519) Bering Sea.

To better understand the bycatch stock distribution across time and space, the 2012 sample set from Area 517 was large enough to split into two time periods (Table 6). Samples from all other areas were not included due to small sample sizes in those areas.

Table 6. -- Spatial and temporal groupings from the 2012 chum salmon bycatch genetic sample sets across two time periods (Table 5) for the reporting area with the most samples.

Reporting area	Time period	Number of samples
517	early-middle	124
517	late	310

BAYES stock composition estimates were made for the two time periods in NMFS reporting area 517 as described above. The Gelman and Rubin shrink statistics were below 1.02. The stock distribution did not change significantly across time, particularly for the Asian and

Eastern GOA/PNW regions (Fig. 11). The apparent change in contributions from the Western Alaska and the Upper/Middle Yukon regions during the two time periods was not significant due to overlapping 95% credible intervals. The contribution from Southwest Alaska was very low in both time periods.

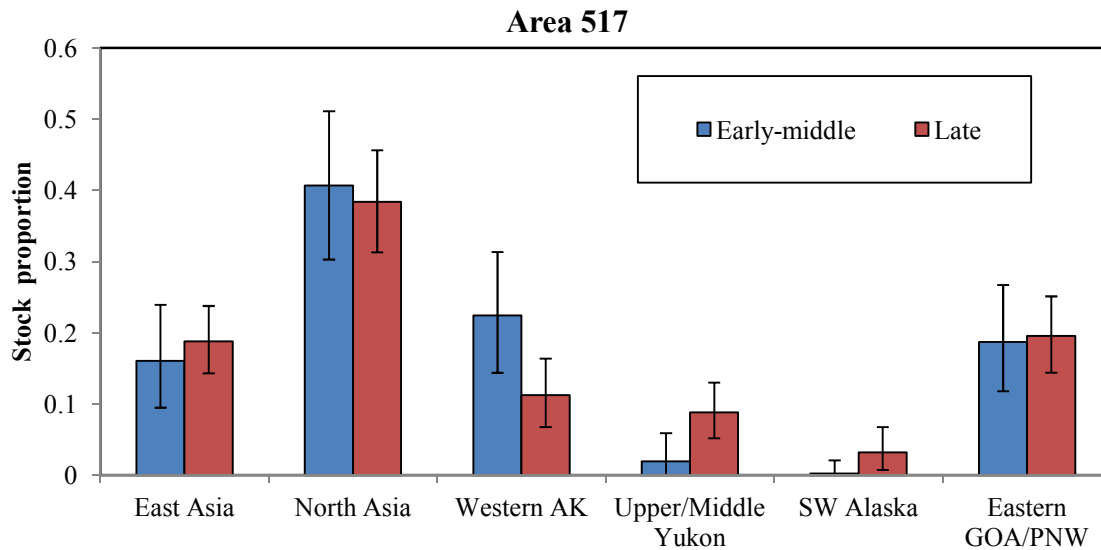


Figure 11. -- BAYES stock composition estimates and 95% credible intervals for the NMFS reporting area 517 for the early-middle and late time periods (Table 7) from the 2012 chum salmon bycatch genetic samples.

SALMON EXCLUDER DEVICE

Tests of salmon excluder devices were performed in 2012 (Gauvin et al. 2013) in the catcher vessel operational area (CVOA), north of Unimak Pass and off the northeastern coast of Unalaska Island (Fig. 12). The purpose of salmon excluder devices is to reduce the amount of salmon bycatch by allowing salmon to exit the trawl while simultaneously retaining groundfish. During the tests, a recapture net outside of the excluder device caught salmon that escaped the modified trawl. Three hauls in late-summer/fall 2012 contained a relatively large number of chum salmon from which genetic samples were taken (Table 7). A mixed stock analysis of these

samples provided an opportunity to determine the extent to which chum salmon stocks aggregate within a narrow geographic and temporal window.

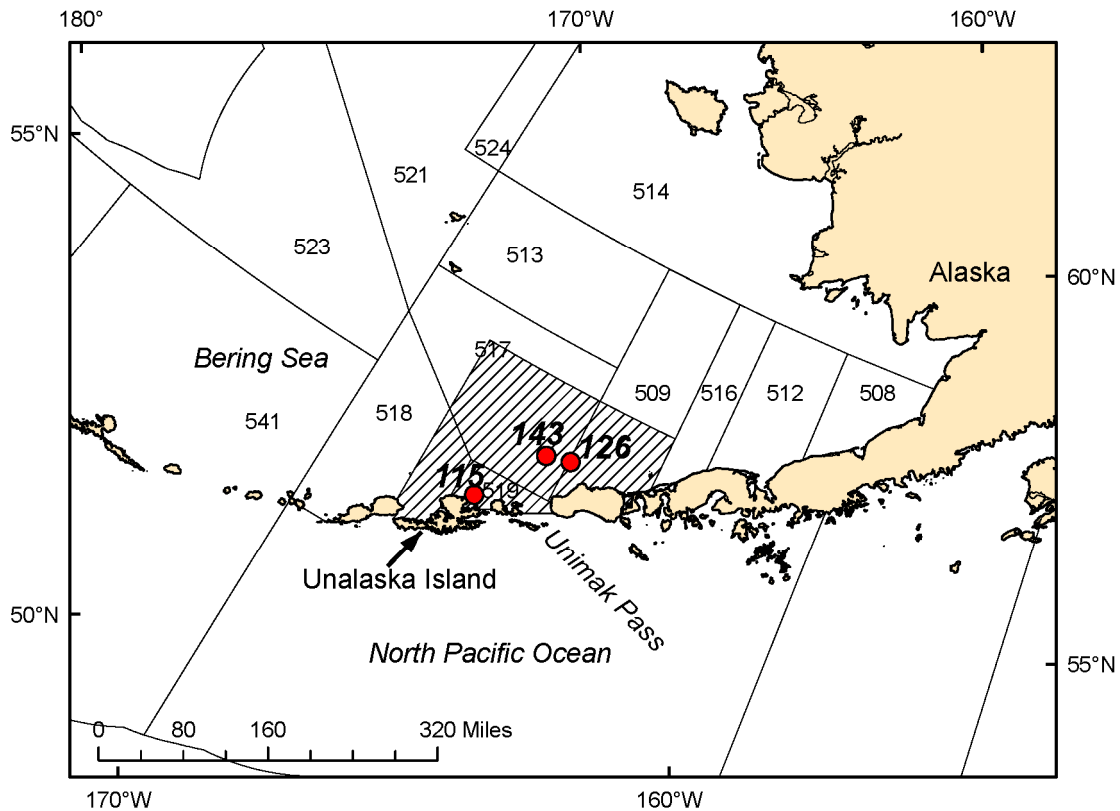


Figure 12. -- Locations and haul numbers of excluder device test samples of chum salmon collected in late-summer/fall 2012. Catcher vessel operational area is marked as the black dashed area.

Table 7. -- Collection information for the three salmon excluder device samples collected in late summer/fall 2012 and analyzed for genetic stock composition.

Haul	n	NMFS area	Latitude	Longitude	Haul date
115	115	519	54° 6' 36" N	166° 32' 24" W	8/25/2012
126	120	509	55° 6' 0" N	164° 57' 0" W	8/31/2012
143	72	517	55° 1' 12" N	165° 31' 12" W	9/19/2012

BAYES stock composition estimates were made as described previously for the total excluder device samples. Contribution proportions for the total excluder device samples were similar to those observed for the total bycatch, with a majority of fish originating from North Asia, lesser contributions from East Asia, Western Alaska, and Eastern GOA/PNW, and very low contributions from the Upper/Middle Yukon and Southwest Alaska (Table 8).

Table 8. --Regional BAYES stock composition estimates for 307 excluder-device chum salmon samples collected in 2012. 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
<i>East Asia</i>	0.105	0.020	0.069	0.104	0.145	1.00
<i>North Asia</i>	0.552	0.036	0.482	0.552	0.622	1.00
<i>Western Alaska</i>	0.156	0.027	0.105	0.155	0.211	1.00
<i>Upper/Middle Yukon</i>	0.053	0.017	0.022	0.052	0.088	1.00
<i>Southwest Alaska</i>	0.001	0.004	0.000	0.000	0.014	1.01
<i>Eastern GOA/PNW</i>	0.133	0.023	0.092	0.133	0.180	1.00

BAYES stock composition estimates were also made for the three individual trawl hauls (Table 7). Even at the smallest spatial and temporal scale of sampling, that is a single trawl haul, chum salmon from the entire geographic distribution of the species comingle during their summer-fall residence in the Bering Sea (Fig. 13). Stock composition estimates of samples from the three hauls were generally similar, with a few exceptions that may be due to differences in the sampling date, location, or both of individual hauls. The largest contribution in all three hauls was from North Asia, which appeared highest in the westernmost haul (Haul 115), but 95% credible intervals of this region overlap among the three hauls. The significantly lower contribution from Eastern GOA/PNW stocks in Haul 115 may be explained by the more western location and slightly earlier sampling date for that haul.

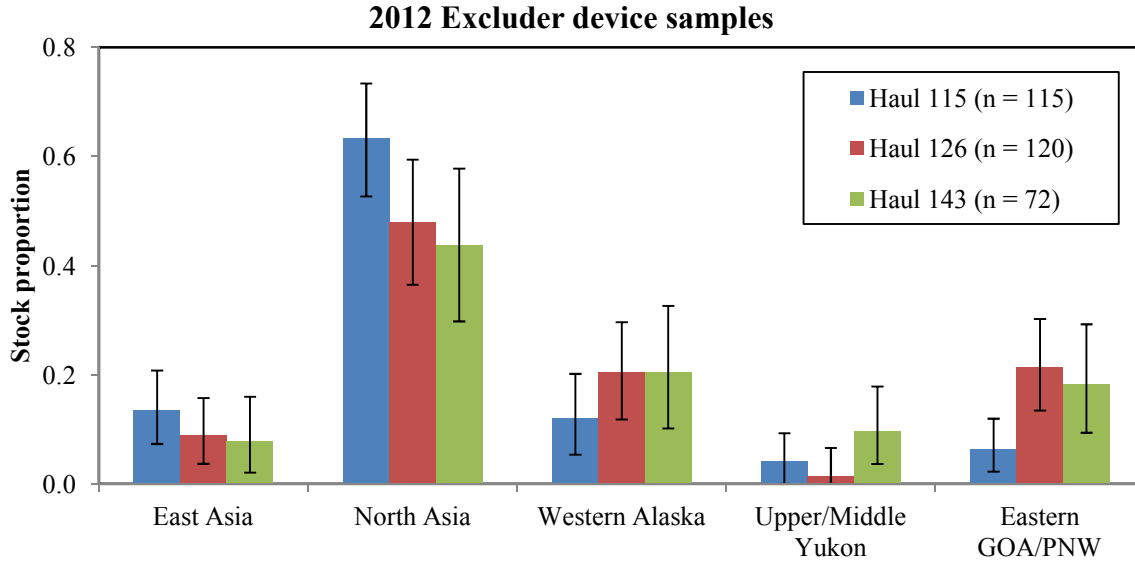


Figure 13. -- BAYES stock composition estimates and 95% credible intervals for the chum salmon collected in 2012 from three excluder-device test hauls (Table 7). Not shown is the Southwest Alaska region for which estimates never exceeded 0.7%.

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 673 individuals sampled from the 2012 chum salmon bycatch and 307 individuals from the late-summer/fall 2012 salmon excluder device tests. The limitations and results of this analysis are summarized below.

Sampling Issues

We highlight the reduced spatial and temporal biases in the 2012 sample set (Figs. 3 and 4) that were inherent in collections before 2011. Reduction of those biases improves the application of the 2012 genetic sample stock composition estimate to the entire chum salmon

bycatch. Implementation of Amendment 91 to the NPMFC 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 97.6% of the chum salmon bycatch from this fishery 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 2012 bycatch of Bering Sea chum salmon were predominantly from North Asia stocks (38.9%), although substantial contributions were also from East Asia (20.3%), Eastern GOA/PNW (17.6%), and Western Alaska (13.8%). The stock proportions from Asia in 2012 dominated the bycatch as in previous years; however, within this group, the 2012 estimates from North Asia and East Asia differed significantly from the 1994, 1995, 2005–2011 average contributions from these two regions. Although samples in 2012 were collected representatively from the pollock fishery 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

Our time-stratified analysis of the bycatch was limited to the pollock “B” season, when the majority of chum salmon are intercepted. For the most part, stock composition estimates changed little across the three sampling periods (Fig. 9). However, the relative stability of proportions in 2012 as compared to changes over the course of the season in previous years

suggest a shift in the temporal stratification of chum salmon stocks in the Bering Sea, changes in fishing or sampling locations, or both.

Spatial analysis comparing the central Bering Sea (NMFS reporting areas 524 and 521) and the southeastern Bering Sea (NMFS areas 509, 513, 517, and 519) suggested minor stock composition differences between the two areas. The majority of chum salmon bycatch in both broad areas originated from Asia, but there were differences in regional contributions between the two areas (Fig. 10). For example, the proportion of bycatch in the central Bering Sea from East Asia stocks was nearly twice that in the southeastern Bering Sea.

Limited sample size prevented examination of stock estimates on spatial and temporal strata except for an analysis of samples from NMFS reporting area 517 across two time periods. Stock composition proportions across time in this area were relatively stable (Fig. 11).

Salmon Excluder Device

Chum salmon from late-summer/fall 2012 excluder device samples provided an opportunity to examine the extent to which chum salmon stocks aggregate over the small spatial and temporal scales of a single trawl haul. Substantial mixing of stocks occurred among the total excluder samples (Table 8), as well as within each of three individual hauls (Fig. 13). Mixture proportions were similar to those of the overall 2012 bycatch samples, with most of the fish originating from North Asia and with substantial contributions from East Asia, Western Alaska, and the Eastern GOA/PNW.

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.

ACKNOWLEDGMENTS

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APPENDIX

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

DFO Num	Population name	Reg Num	Region	DFO Num	Population name	Reg Num	Region
41	Abashiri	1	East Asia	380	Dranka	2	North Asia
215	Avakumovka	1	East Asia	223	Hairusova	2	North Asia
40	Chitose	1	East Asia	378	Ivashka	2	North Asia
315	Gakko_River	1	East Asia	213	Kalininka	2	North Asia
292	Hayatsuki	1	East Asia	225	Kamchatka	2	North Asia
44	Horonai	1	East Asia	219	Kanchalan	2	North Asia
252	Kawabukuro	1	East Asia	379	Karaga	2	North Asia
313	Koizumi_River	1	East Asia	294	Kikchik	2	North Asia
300	Kushiro	1	East Asia	209	Kol	2	North Asia
37	Miomote	1	East Asia	233	Magadan	2	North Asia
391	Namdae_R	1	East Asia	211	Naiba	2	North Asia
231	Narva	1	East Asia	295	Nerpichi	2	North Asia
298	Nishibetsu	1	East Asia	381	Okhota	2	North Asia
293	Ohkawa	1	East Asia	212	Oklan	2	North Asia
297	Orikasa	1	East Asia	222	Ola	2	North Asia
214	Ryazanovka	1	East Asia	386	Olutorsky_Bay	2	North Asia
312	Sakari_River	1	East Asia	228	Ossora	2	North Asia
311	Shari_River	1	East Asia	224	Penzhina	2	North Asia
36	Shibetsu	1	East Asia	385	Plotnikova_R	2	North Asia
299	Shikiu	1	East Asia	221	Pymta	2	North Asia
253	Shiriuchi	1	East Asia	220	Tauy	2	North Asia
310	Shizunai	1	East Asia	383	Tugur_River	2	North Asia
217	Suifen	1	East Asia	226	Tym_	2	North Asia
35	Teshio	1	East Asia	230	Udarnitsa	2	North Asia
39	Tokachi	1	East Asia	290	Utka_River	2	North Asia
38	Tokoro	1	East Asia	208	Vorovskaya	2	North Asia
314	Tokushibetsu	1	East Asia	387	Zhypanova	2	North Asia
291	Toshibetsu	1	East Asia	348	Agiapuk	3	W Alaska
296	Tsugaruishi	1	East Asia	376	Alagnak	3	W Alaska
316	Uono_River	1	East Asia	3	Andreafsky	3	W Alaska
309	Yurappu	1	East Asia	357	Aniak	3	W Alaska
218	Amur	2	North Asia	301	Anvik	3	W Alaska
207	Anadyr	2	North Asia	80	Chulinak	3	W Alaska
384	Apuka_River	2	North Asia	347	Eldorado	3	W Alaska
382	Bolshaya	2	North Asia	358	George	3	W Alaska

DFO Num	Population name	Reg Num	Region	DFO Num	Population name	Reg Num	Region
307	Gisasa	3	W Alaska	2	Kluane	4	U/M Yukon
371	Goodnews	3	W Alaska	59	Kluane_Lake	4	U/M Yukon
288	Henshaw_Creek	3	W Alaska	181	Koyukuk_late	4	U/M Yukon
339	Imnachuk	3	W Alaska	90	Koyukuk_south	4	U/M Yukon
361	Kanektok	3	W Alaska	10	Minto	4	U/M Yukon
362	Kasigluk	3	W Alaska	6	Pelly	4	U/M Yukon
328	Kelly_Lake	3	W Alaska	439	Porcupine	4	U/M Yukon
340	Kobuk	3	W Alaska	83	Salcha	4	U/M Yukon
343	Koyuk	3	W Alaska	4	Sheenjek	4	U/M Yukon
363	Kwethluk	3	W Alaska	1	Tatchun	4	U/M Yukon
336	Kwiniuk_River	3	W Alaska	9	Teslin	4	U/M Yukon
303	Melozitna	3	W Alaska	84	Toklat	4	U/M Yukon
373	Mulchatna	3	W Alaska	360	Alagoshak	5	SW Alaska
372	Naknek	3	W Alaska	333	American_River	5	SW Alaska
330	Niukluk	3	W Alaska	366	Big_River	5	SW Alaska
329	Noatak	3	W Alaska	354	Coleman_Creek	5	SW Alaska
345	Nome	3	W Alaska	355	Delta_Creek	5	SW Alaska
302	Nulato	3	W Alaska	359	Egegik	5	SW Alaska
374	Nunsatuk	3	W Alaska	332	Frosty_Creek	5	SW Alaska
13	Peel_River	3	W Alaska	365	Gertrude_Creek	5	SW Alaska
322	Pikmiktalik	3	W Alaska	370	Joshua_Green	5	SW Alaska
331	Pilgrim_River	3	W Alaska	364	Meshik	5	SW Alaska
346	Shaktoolik	3	W Alaska	283	Moller_Bay	5	SW Alaska
341	Snake	3	W Alaska	369	Pumice_Creek	5	SW Alaska
368	Stuyahok_River	3	W Alaska	367	Stepovak_Bay	5	SW Alaska
375	Togiak	3	W Alaska	335	Sturgeon	5	SW Alaska
154	Tozitna	3	W Alaska	350	Uganik	5	SW Alaska
342	Unalakleet	3	W Alaska	334	Volcano_Bay	5	SW Alaska
344	Ungalik	3	W Alaska	356	Westward_Creek	5	SW Alaska
8	Big_Creek	4	U/M Yukon	239	Ahnuhati	6	E GOA/PNW
89	Big_Salt	4	U/M Yukon	69	Ahta	6	E GOA/PNW
86	Black_River	4	U/M Yukon	155	Ain	6	E GOA/PNW
87	Chandalar	4	U/M Yukon	183	Algard	6	E GOA/PNW
28	Chandindu	4	U/M Yukon	58	Alouette	6	E GOA/PNW
82	Cheena	4	U/M Yukon	325	Alouette_North	6	E GOA/PNW
81	Delta	4	U/M Yukon	270	Andesite_Cr	6	E GOA/PNW
7	Donjek	4	U/M Yukon	428	Arnoup_Cr	6	E GOA/PNW
5	Fishing_Br	4	U/M Yukon	153	Ashlulm	6	E GOA/PNW
88	Jim_River	4	U/M Yukon	156	Awun	6	E GOA/PNW
85	Kantishna	4	U/M Yukon	133	Bag_Harbour	6	E GOA/PNW

DFO Num	Population name	Reg Num	Region	DFO Num	Population name	Reg Num	Region
164	Barnard	6	E GOA/PNW	46	Demamiel	6	E GOA/PNW
16	Bella_Bell	6	E GOA/PNW	210	Dipac_Hatchery	6	E GOA/PNW
79	Bella_Coola	6	E GOA/PNW	319	Disappearance	6	E GOA/PNW
49	Big_Qual	6	E GOA/PNW	269	Dog-tag	6	E GOA/PNW
201	Big_Quilcene	6	E GOA/PNW	177	Draney	6	E GOA/PNW
281	Bish_Cr	6	E GOA/PNW	114	Duthie_Creek	6	E GOA/PNW
198	Bitter_Creek	6	E GOA/PNW	427	East_Arm	6	E GOA/PNW
103	Blackrock_Creek	6	E GOA/PNW	266	Ecstall_River	6	E GOA/PNW
390	Blaney_Creek	6	E GOA/PNW	94	Elcho_Creek	6	E GOA/PNW
138	Botany_Creek	6	E GOA/PNW	193	Ellsworth_Cr	6	E GOA/PNW
264	Buck_Channel	6	E GOA/PNW	203	Elwha	6	E GOA/PNW
169	Bullock_Chann	6	E GOA/PNW	276	Ensheshese	6	E GOA/PNW
61	Campbell_River	6	E GOA/PNW	263	Fairfax_Inlet	6	E GOA/PNW
323	Carroll	6	E GOA/PNW	32	Fish_Creek	6	E GOA/PNW
78	Cascade	6	E GOA/PNW	429	Flux_Cr	6	E GOA/PNW
76	Cayeghle	6	E GOA/PNW	102	Foch_Creek	6	E GOA/PNW
42	Cheakamus	6	E GOA/PNW	179	Frenchman	6	E GOA/PNW
398	Cheenis_Lake	6	E GOA/PNW	227	Gambier	6	E GOA/PNW
51	Chehalis	6	E GOA/PNW	96	Gill_Creek	6	E GOA/PNW
19	Chemainus	6	E GOA/PNW	166	Gilttoyee	6	E GOA/PNW
47	Chilliwack	6	E GOA/PNW	145	Glendale	6	E GOA/PNW
392	Chilqua_Creek	6	E GOA/PNW	135	Gold_Harbour	6	E GOA/PNW
117	Chuckwalla	6	E GOA/PNW	11	Goldstream	6	E GOA/PNW
139	Clapp_Basin	6	E GOA/PNW	66	Goodspeed_River	6	E GOA/PNW
107	Clatse_Creek	6	E GOA/PNW	136	Government	6	E GOA/PNW
118	Clyak	6	E GOA/PNW	205	Grant_Creek	6	E GOA/PNW
62	Cold_Creek	6	E GOA/PNW	100	Green_River	6	E GOA/PNW
77	Colonial	6	E GOA/PNW	450	GreenRrHatchery	6	E GOA/PNW
353	Constantine	6	E GOA/PNW	237	Greens	6	E GOA/PNW
168	Cooper_Inlet	6	E GOA/PNW	141	Harrison	6	E GOA/PNW
197	County_Line	6	E GOA/PNW	438	Harrison_late	6	E GOA/PNW
12	Cowichan	6	E GOA/PNW	64	Hathaway_Creek	6	E GOA/PNW
414	Crag_Cr	6	E GOA/PNW	234	Herman_Creek	6	E GOA/PNW
161	Dak_	6	E GOA/PNW	17	Heydon_Cre	6	E GOA/PNW
259	Dana_Creek	6	E GOA/PNW	407	Hicks_Cr	6	E GOA/PNW
123	Date_Creek	6	E GOA/PNW	400	Homathko	6	E GOA/PNW
250	Dawson_Inlet	6	E GOA/PNW	411	Honna	6	E GOA/PNW
91	Dean_River	6	E GOA/PNW	204	Hoodsport	6	E GOA/PNW
261	Deena	6	E GOA/PNW	185	Hooknose	6	E GOA/PNW
170	Deer_Pass	6	E GOA/PNW	406	Hopedale_Cr	6	E GOA/PNW

DFO Num	Population name	Reg Num	Region	DFO Num	Population name	Reg Num	Region
412	Hutton_Head	6	E GOA/PNW	160	Little_Goose	6	E GOA/PNW
278	Illiance	6	E GOA/PNW	50	Little_Qua	6	E GOA/PNW
152	Inch_Creek	6	E GOA/PNW	413	Lizard_Cr	6	E GOA/PNW
146	Indian_River	6	E GOA/PNW	119	Lockhart-Gordon	6	E GOA/PNW
92	Jenny_Bay	6	E GOA/PNW	176	Lower_Lillooet	6	E GOA/PNW
115	Kainet_River	6	E GOA/PNW	137	Mace_Creek	6	E GOA/PNW
144	Kakweiken	6	E GOA/PNW	242	Mackenzie_Sound	6	E GOA/PNW
268	Kalum	6	E GOA/PNW	116	MacNair_Creek	6	E GOA/PNW
395	Kanaka_Cr	6	E GOA/PNW	55	Mamquam	6	E GOA/PNW
402	Kano_Inlet_Cr	6	E GOA/PNW	121	Markle_Inlet_Cr	6	E GOA/PNW
162	Kateen	6	E GOA/PNW	27	Martin_Riv	6	E GOA/PNW
389	Kawkawa	6	E GOA/PNW	338	Mashiter_Creek	6	E GOA/PNW
95	Kemano	6	E GOA/PNW	109	McLoughin_Creek	6	E GOA/PNW
192	Kennedy_Creek	6	E GOA/PNW	178	Milton	6	E GOA/PNW
238	Kennell	6	E GOA/PNW	194	Minter_Cr	6	E GOA/PNW
351	Keta_Creek	6	E GOA/PNW	254	Mountain_Cr	6	E GOA/PNW
101	Khutze_River	6	E GOA/PNW	111	Mussel_River	6	E GOA/PNW
126	Khutzeymateen	6	E GOA/PNW	157	Naden	6	E GOA/PNW
282	Kiltuish	6	E GOA/PNW	337	Nahmint_River	6	E GOA/PNW
93	Kimsquit	6	E GOA/PNW	444	Nakut_Su	6	E GOA/PNW
187	Kimsquit_Bay	6	E GOA/PNW	14	Nanaimo	6	E GOA/PNW
419	Kincolith	6	E GOA/PNW	122	Nangeese	6	E GOA/PNW
273	Kispiox	6	E GOA/PNW	422	Nass_River	6	E GOA/PNW
106	Kitasoo	6	E GOA/PNW	399	Necleetsconnay	6	E GOA/PNW
99	Kitimat_River	6	E GOA/PNW	113	Neekas_Creek	6	E GOA/PNW
275	Kitsault_Riv	6	E GOA/PNW	321	Neets_Bay_early	6	E GOA/PNW
163	Kitwanga	6	E GOA/PNW	320	Neets_Bay_late	6	E GOA/PNW
271	Kleanza_Cr	6	E GOA/PNW	173	Nekite	6	E GOA/PNW
437	Klewnuggit_Cr	6	E GOA/PNW	104	Nias_Creek	6	E GOA/PNW
21	Klinaklini	6	E GOA/PNW	143	Nimpkish	6	E GOA/PNW
418	Ksedin	6	E GOA/PNW	53	Nitinat	6	E GOA/PNW
125	Kshwan	6	E GOA/PNW	191	Nooksack	6	E GOA/PNW
423	Kumealon	6	E GOA/PNW	186	Nooseseck	6	E GOA/PNW
112	Kwakusdis_River	6	E GOA/PNW	318	NorrishWorth	6	E GOA/PNW
436	Kxngeal_Cr	6	E GOA/PNW	159	North_Arm	6	E GOA/PNW
127	Lachmach	6	E GOA/PNW	377	Olsen_Creek	6	E GOA/PNW
262	Lagins	6	E GOA/PNW	184	Orford	6	E GOA/PNW
131	Lagoon_Inlet	6	E GOA/PNW	287	Pa-aat_River	6	E GOA/PNW
448	LagoonCr	6	E GOA/PNW	260	Pacofi	6	E GOA/PNW
167	Lard	6	E GOA/PNW	56	Pallant	6	E GOA/PNW

DFO Num	Population name	Reg Num	Region	DFO Num	Population name	Reg Num	Region
65	Pegattum_Creek	6	E GOA/PNW	75	Taaltz	6	E GOA/PNW
48	Puntledge	6	E GOA/PNW	30	Taku	6	E GOA/PNW
98	Quaal_River	6	E GOA/PNW	18	Takwahoni	6	E GOA/PNW
147	Quap	6	E GOA/PNW	251	Tarundl_Creek	6	E GOA/PNW
108	Quartcha_Creek	6	E GOA/PNW	149	Theodosia	6	E GOA/PNW
199	Quinault	6	E GOA/PNW	22	Thorsen	6	E GOA/PNW
110	Roscoe_Creek	6	E GOA/PNW	129	Toon	6	E GOA/PNW
397	Salmon_Bay	6	E GOA/PNW	279	Tseax	6	E GOA/PNW
195	Salmon_Cr	6	E GOA/PNW	202	Tulalip	6	E GOA/PNW
134	Salmon_River	6	E GOA/PNW	97	Turn_Creek	6	E GOA/PNW
200	Satsop	6	E GOA/PNW	430	Turtle_Cr	6	E GOA/PNW
236	Sawmill	6	E GOA/PNW	247	Tuskwa	6	E GOA/PNW
410	Seal_Inlet_Cr	6	E GOA/PNW	165	Tyler	6	E GOA/PNW
158	Security	6	E GOA/PNW	33	Tzoonie	6	E GOA/PNW
130	Sedgewick	6	E GOA/PNW	124	Upper_Kitsumkal	6	E GOA/PNW
393	Serpentine_R	6	E GOA/PNW	140	Vedder	6	E GOA/PNW
317	Shovelnose_Cr	6	E GOA/PNW	70	Viner_Sound	6	E GOA/PNW
249	Shustnini	6	E GOA/PNW	45	Wahleach	6	E GOA/PNW
206	Siberia_Creek	6	E GOA/PNW	172	Walkum	6	E GOA/PNW
25	Silverdale	6	E GOA/PNW	73	Waump	6	E GOA/PNW
196	Skagit	6	E GOA/PNW	232	Wells_Bridge	6	E GOA/PNW
274	Skeena	6	E GOA/PNW	352	Wells_River	6	E GOA/PNW
171	Skowquiltz	6	E GOA/PNW	105	West_Arm_Creek	6	E GOA/PNW
447	SkykomishRiv	6	E GOA/PNW	267	Whitebottom_Cr	6	E GOA/PNW
132	Slatechuck_Cre	6	E GOA/PNW	326	Widgeon_Slough	6	E GOA/PNW
43	Sliammon	6	E GOA/PNW	277	Wilauks_Cr	6	E GOA/PNW
15	Smith_Cree	6	E GOA/PNW	120	Wilson_Creek	6	E GOA/PNW
54	Snootli	6	E GOA/PNW	401	Worth_Creek	6	E GOA/PNW
180	Southgate	6	E GOA/PNW	60	Wortley_Creek	6	E GOA/PNW
26	Squakum	6	E GOA/PNW	248	Yellow_Bluff	6	E GOA/PNW
142	Squamish	6	E GOA/PNW	434	Zymagotitz	6	E GOA/PNW
128	Stagoo	6	E GOA/PNW				
265	Stanley	6	E GOA/PNW				
52	Stave	6	E GOA/PNW				
396	Stawamus	6	E GOA/PNW				
409	Steel_Cr	6	E GOA/PNW				
424	Stewart_Cr	6	E GOA/PNW				
416	Stumaun_Cr	6	E GOA/PNW				
327	Sugsaw	6	E GOA/PNW				
324	Surprise	6	E GOA/PNW				

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