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Genetic Stock Composition Analysis of Chum Salmon from the Prohibited Species Catch of the 2014 Bering Sea Walleye Pollock Trawl Fishery and Gulf of Alaska Groundfish Fisheries

by
C. M. Kondzela, J. A. Whittle, D. Yates, S. C. Vulstek,
H. T. Nguyen, and J. R. Guyon

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H. T. Nguyen, and J. R. Guyon

Alaska Fisheries Science Center
Auke Bay Laboratories
17109 Pt. Lena Loop Road
Juneau, AK 99801

www.afsc.noaa.gov

U.S. DEPARTMENT OF COMMERCE
Penny. S. Pritzker, Secretary
National Oceanic and Atmospheric Administration
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ABSTRACT

A genetic analysis of the prohibited species catch (PSC) of chum salmon (*Oncorhynchus keta*) collected during 2014 from the federally managed walleye pollock (*Gadus chalcogrammus*) trawl fishery in the Bering Sea and the federal groundfish fisheries in the Gulf of Alaska (GOA) was undertaken to determine the overall stock composition of the sample sets. Samples were genotyped for 11 microsatellite markers from which stock contributions were estimated using the current chum salmon microsatellite baseline. In 2014, one genetic sample was collected for every 30.2 chum salmon caught in the Bering Sea midwater trawl fishery. The evaluation of sampling in the Bering Sea based on time, location, and vessel indicated that the genetic samples were representative of the total chum salmon PSC in the Bering Sea. Based on the analysis of 1,741 chum salmon collected throughout the 2014 Bering Sea trawl fishery, the largest stock group in the catch was Northeast Asia (37%), followed by Eastern GOA/Pacific Northwest (PNW) (24%), Southeast Asia (19%), Western Alaska (18%), Upper/Middle Yukon (2%), and Southwest Alaska (< 1%) stocks. The regional stock estimates for the 2014 chum salmon caught in the Bering Sea were similar to those in 2013, with the exception of a lower contribution from Upper/Middle Yukon stocks in 2014. As in previous years, there were some significant differences in stock proportions throughout the season and across areas. For the first time, a small set of chum salmon samples from the GOA groundfish fisheries were available for genetic analysis. The highest proportion of the 273 chum salmon sampled in the GOA groundfish fisheries were from Eastern GOA/PNW (92%) stocks.

CONTENTS

INTRODUCTION

Pacific salmon (*Oncorhynchus* spp.) are prohibited species in the federally managed Bering Sea and Gulf of Alaska (GOA) groundfish fisheries, which are subject to complex management rules (NPMFC 2013, 2014) that are in part designed to reduce prohibited species catch (PSC). It is important to understand the stock composition of Pacific salmon caught in these fisheries, which take place in areas that are 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 samples of chum salmon collected during 2014 from 1) the U.S. Bering Sea walleye pollock (*Gadus chalcogrammus*) midwater trawl fishery and 2) for the first time, the GOA groundfish fisheries. In the Bering Sea, the pollock fishery accounted for more than 97.9% of the total chum salmon taken in the groundfish fisheries (NMFS 2015); the remaining chum salmon were taken in other groundfish fisheries. In the GOA, about half of the chum salmon were caught in the midwater trawl pollock fishery, with the remainder caught in other groundfish fisheries (NMFS 2014). 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 catch and genetic samples.

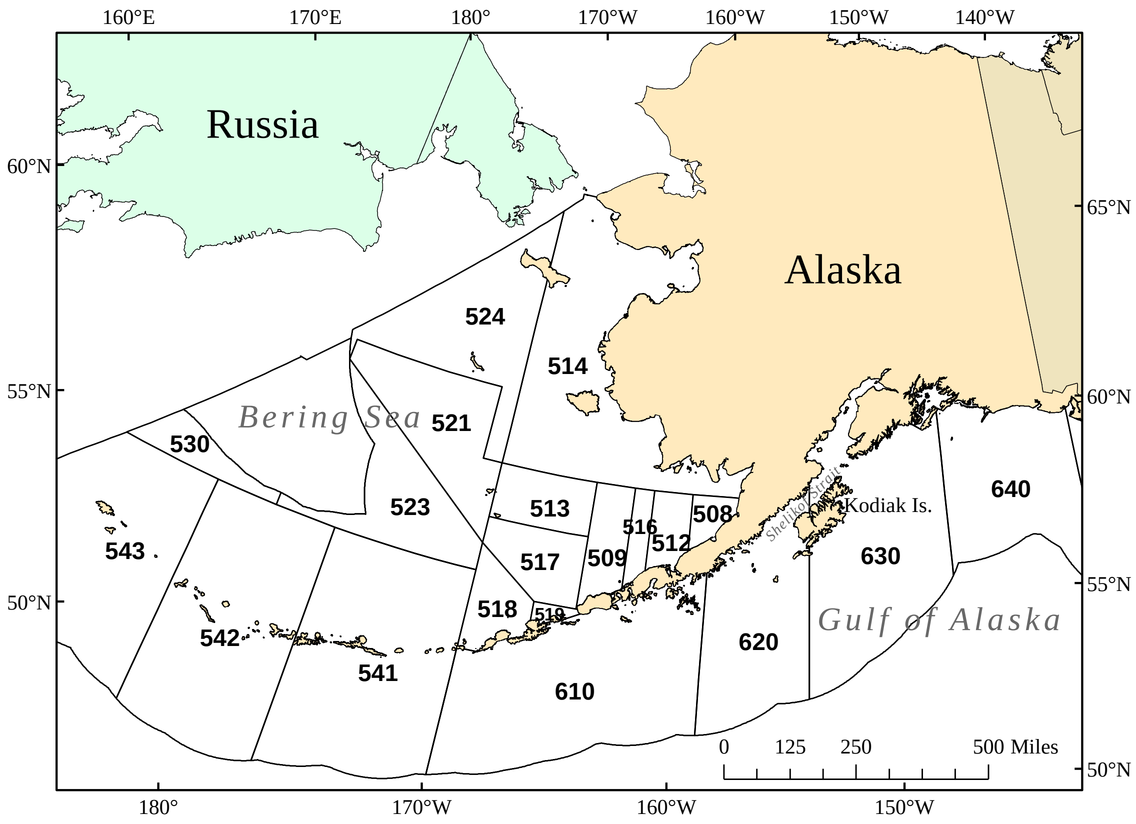

Figure 1. -- NMFS reporting areas associated with the Bering Sea-Aleutian Island and Gulf of Alaska groundfish fisheries.

In this report, we present the stock composition estimates for the samples of 2014 chum salmon PSC collected from the Bering Sea and GOA. For additional background and methods, this report is intended to be supplemented with the chum salmon reports prepared previously for the 2005-2013 Bering Sea trawl fisheries (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010, 2011a,b; Kondzela et al. 2012, 2013; Vulstek et al. 2014; Whittle et al. 2015). The chum salmon PSC is designated as non-Chinook (*O. tshawytscha*) in the NMFS database and comprises over 95% of the non-Chinook category in the Bering Sea (NPFMC 2007).

SAMPLE DISTRIBUTION

Bering Sea

Genetic samples were collected from the chum salmon caught in the Bering Sea pollock fishery by the Alaska Fisheries Science Center's (AFSC) North Pacific Groundfish and Halibut Observer Program (Observer Program) in 2014 for analysis at the AFSC's Auke Bay Laboratories (ABL). Sampling was changed in 2011 from previous years (Faunce 2015, Cahalan et al. 2014) to implement a systematic sampling protocol recommended by Pella and Geiger (2009). With a goal to sample every 30th chum salmon, axillary processes (for genetic analysis) and scales (for ageing) were collected throughout the season and stored together in coin envelopes that were labeled, frozen, and shipped to the ABL.

In 2014, an estimated 219,428 chum salmon were caught in the pollock-directed trawl fisheries and represent the fourth largest catch of non-Chinook salmon in the pollock fisheries since 1994. This catch is substantially larger than the average of 139,651 chum salmon and nearly three times the median of 77,236 (Fig. 2). As in previous years, nearly all of the chum salmon were caught during the pollock B-season (10 June to 31 December) (Fig. 3) in NMFS reporting areas 509-524 (Fig. 1). Of the 218,787 chum salmon caught in the 2014 midwater pollock trawl fishery during the B-season, genetic samples were collected from 7,237 fish, which represents a sampling rate of 1 of every 30.2 chum salmon (or 3.3% of the midwater trawl catch of chum salmon). This sampling rate is nearly identical to that in 2011-2013, the first 3 years of representative sampling.

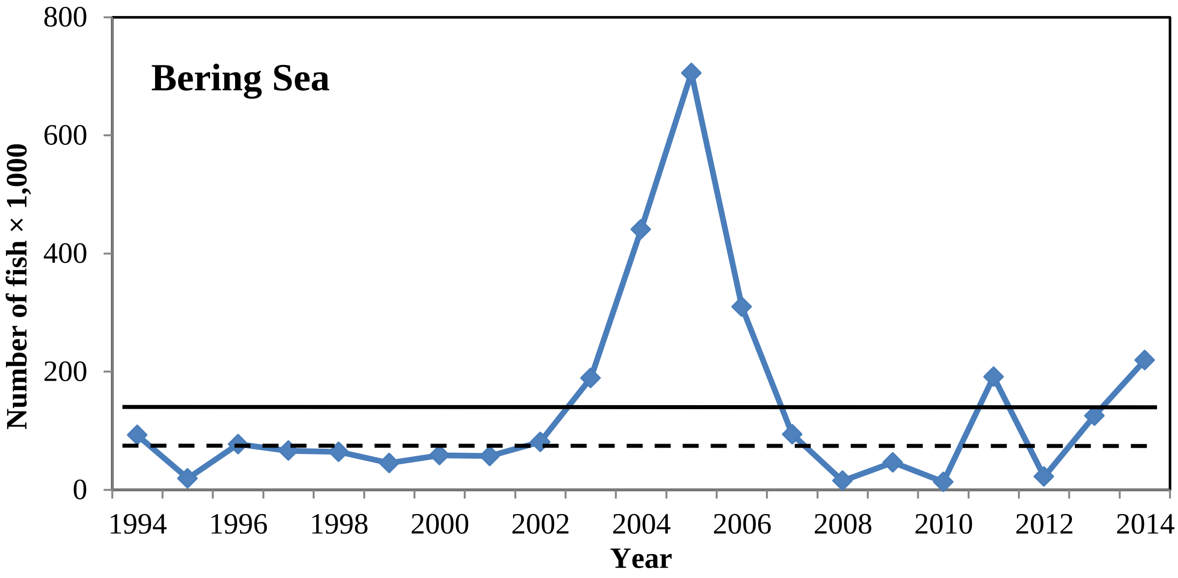

Figure 2. -- Yearly estimates for the non-Chinook salmon PSC from the Bering Sea pollock-directed trawl fisheries (NMFS 2015). The solid horizontal line represents mean PSC and the dashed line represents median PSC.

Biases and errors associated with past collections of genetic samples from the salmon PSC have the potential to affect stock composition estimates (NMFS 2009, Pella and Geiger 2009). The systematic sampling protocols recommended by Pella and Geiger (2009) were implemented in the Bering Sea pollock fisheries in 2011 to reduce sampling error and bias, the efficacy of which was evaluated by comparing the genetic sample distributions and the overall PSC estimates with Chi-square tests. Low sample sizes in some time/area combinations were pooled prior to testing: Early, Middle, and Late time periods (weeks 24-29, 30-34, and 35-40) and three areas (NMFS reporting areas aggregated: 509, 517 and 519; 513 and 514; and 521, 523, and 524). During the B-season, temporal bias by statistical week ending on Sunday was minimal (Fig. 3) when samples were pooled across management areas ($\chi^2 = 1.12$, 15 d.f., $P > 0.99$). Temporal biases were also minimal at finer spatial scales (Fig. 4; $\chi^2 = 1.19$, 4 d.f., $P = 0.88$). Due to the uncertainty of catch location for samples collected from shore-side deliveries in which the hauls were mixed (67% of genetic samples were from catcher vessel offloads; 33% from catcher processor and mothership hauls), the NMFS reporting area of the chum salmon catch from offload deliveries was identified as the area where most of the pollock were caught during a fishing trip.

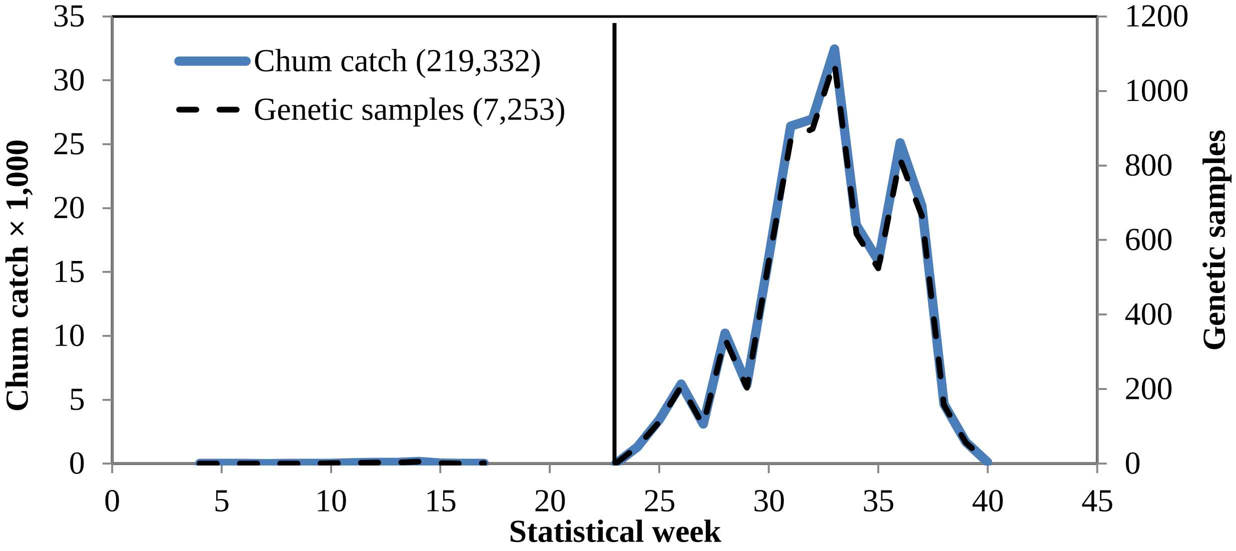

Figure 3. -- Number of Bering Sea chum salmon caught (solid line) and genetic samples collected (dashed line) from the 2014 Bering Sea pollock midwater trawl fishery by statistical week. Weeks 1-23 correspond to the A-season, whereas weeks 24-40 correspond to the B-season, the demarcation of which is a vertical line.

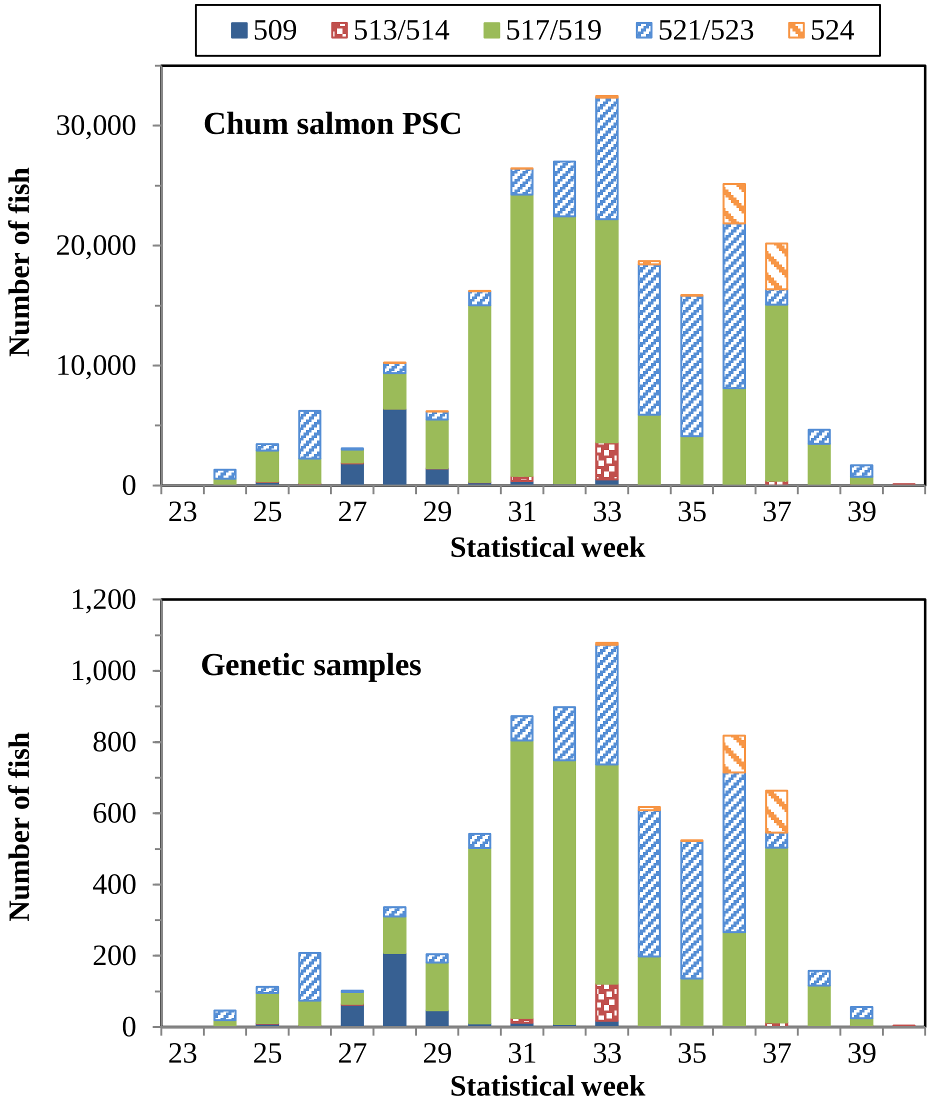

Figure 4. -- Number of Bering Sea chum salmon caught and genetic samples collected from the 2014 Bering Sea pollock B-season by statistical week and NMFS reporting area (designated in the legend).

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, the chum salmon catch was subsampled for genetic samples across a large range of chum salmon catch per vessel (Fig. 5, top panel). The sampling ratio of numbers of chum salmon caught to numbers of genetic samples per vessel was 29.9 ± 2.6 fish (mean ± S.D.; unweighted by proportion of bycatch each vessel caught), which is very close to the protocol sampling goal of one genetic sample collected from every 30th chum salmon caught (Fig. 5, bottom panel). All 88 vessels that participated in the midwater trawl fishery during the B-season caught chum salmon. By vessel, about 60% of the chum salmon catch was undersampled, but by only a small number – based on the systematic sampling protocol, only 56 fish (0.8% of expected) were not sampled. Excluding the two vessels with small chum salmon catches (two samples from each of 32 and 37 chum salmon, respectively), the variance of the ratio of number of chum caught to number of genetic samples collected from under- and oversampled vessels was about equal ($P < 0.317$; one-tail F-test).

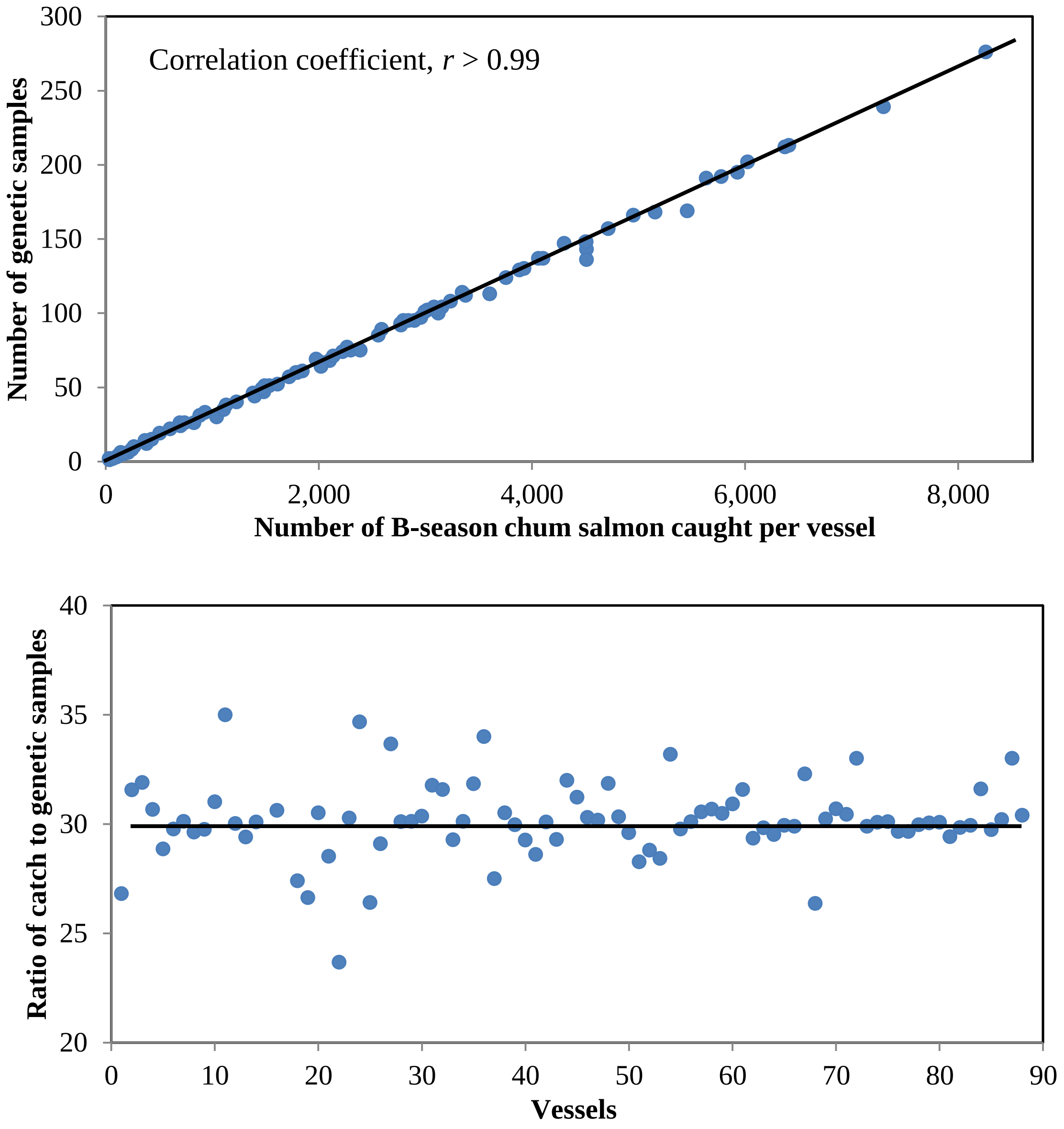

Figure 5. -- Bering Sea chum salmon catch and genetic samples from the 2014 Bering Sea pollock B-season. Number of genetic samples collected from the total number of chum salmon caught from each of 88 vessels; black diagonal line represents the expected sampling rate (top panel). The ratio of total number of chum salmon caught to number of genetic samples collected per sampled vessel; black horizontal line represents the expected sampling ratio (bottom panel). Two vessels with the ratios of 16.0 and 18.5 (two samples collected from 32 and 37 chum salmon caught, respectively) are not shown.

Gulf of Alaska

The estimated PSC of chum salmon in the GOA (NMFS 2015) is 1-2 orders of magnitude lower than in the Bering Sea and has been a lower management priority than the typically larger catches of Chinook salmon (e.g., Guyon et al. 2015). However, in 2014, chum salmon samples were collected in the GOA (AFSC 2013) primarily from the pollock trawl fishery, which catches about 50% of the chum salmon PSC in the GOA (Fig. 6). Of the chum salmon caught in the non-pollock fisheries between the B and C pollock seasons (weeks 23-34; Fig. 7), about half were from the rockfish fisheries and the remainder was split evenly between the sablefish and arrowtooth flounder fisheries. This is the first time that the number of chum salmon genetic samples collected from the GOA groundfish fisheries was large enough to run a mixed-stock analysis. The available sample set included 263 samples from the catcher vessel pollock fishery offloads, primarily from NMFS reporting area 620 during the pollock C season[1], and 10 samples from other fisheries (Figs. 1, 7, 8).

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[1] Pollock caught in Gulf of Alaska Western and Central Regulatory Areas (NMFS reporting areas 610-630): A season (Jan. 20 to Mar. 10), B season (Mar. 10 to May 31), C season (Aug. 25 to Oct. 1), D season (Oct 1. to Nov. 1), published in the Federal Register.

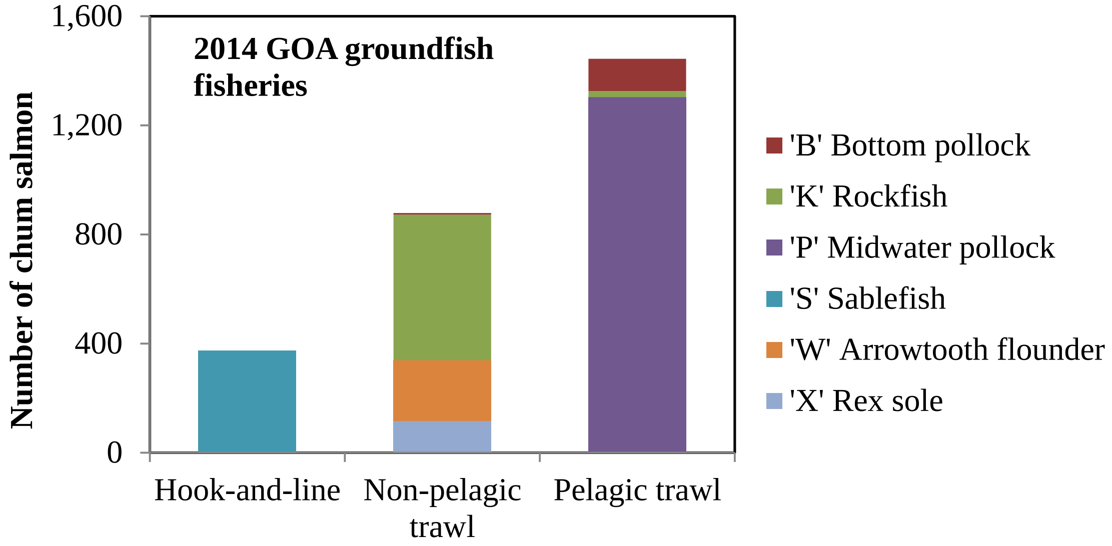

Figure 6. -- Estimated number of chum salmon caught in the 2014 GOA groundfish fisheries (total of 2,699 fish) by target species. Letter designations are those used in the NMFS Alaska Region catch reports (NMFS 2015).

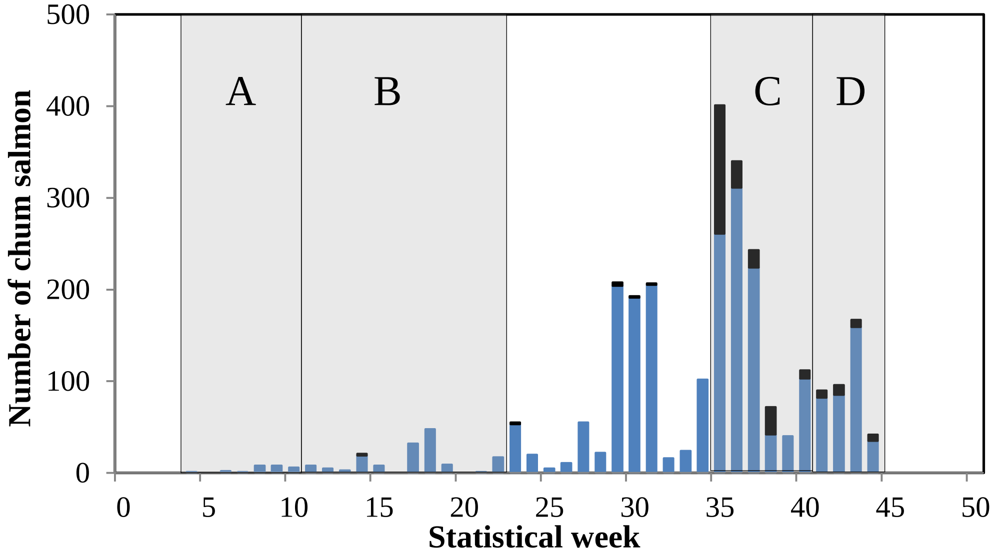

Figure 7. -- Number of chum salmon caught (blue plus black) and genetic samples collected (black) from the 2014 GOA groundfish fisheries by statistical week. Grayed areas with letter designations refer to NMFS management seasons for pollock in the Western and Central Regulatory Areas (NMFS reporting areas 610-630).

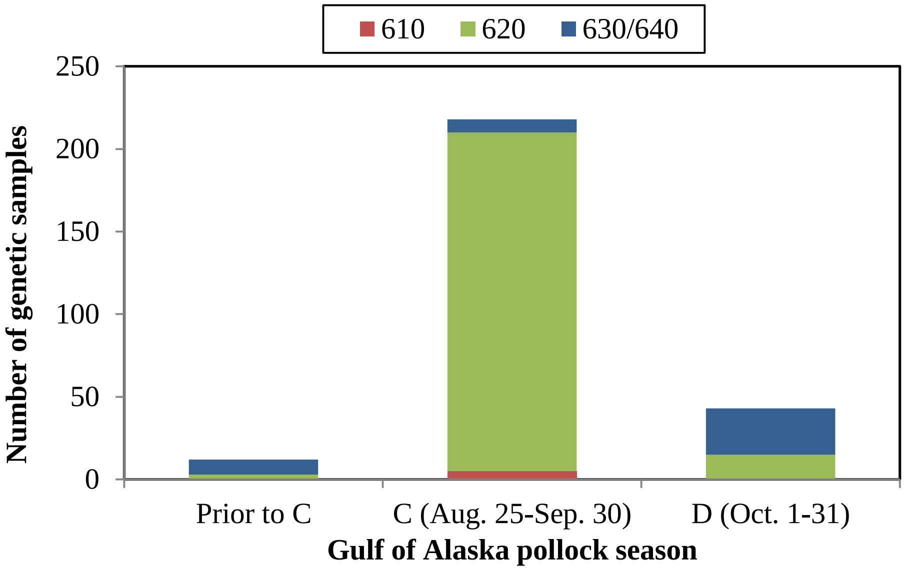

Figure 8. -- Number of chum salmon genetic samples collected from the 2014 GOA groundfish fisheries by pollock season and NMFS reporting areas (designated in the legend).

LABORATORY ANALYSES

Bering Sea

Chum salmon samples from the B-season were subsampled in order to minimize laboratory costs while limiting bias of mixed-stock estimates. The total sample set of 7,237 chum salmon was sorted by cruise, haul or offload, and specimen number and then every 4th sample was selected for analysis (see Whittle et al. 2015 for subsampling effects). DNA was extracted from the axillary processes of 1,826 chum salmon. DNA extraction and microsatellite genotyping was performed as described previously (Guyon et al. 2010). 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* (Beacham et al. 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 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 48-capillary, 36 cm array on the ABI 3730*xl* Genetic Analyzer (Applied Biosystems, Inc.). Genotypes were double-scored with GeneMapper 5.0 software (Applied Biosystems, Inc.) and exported to Excel (Microsoft, Inc.) spreadsheets.

Of the 1,826 chum salmon samples analyzed, three samples amplified DNA from a species other than chum salmon and were excluded. For 8 or more of the 11 loci, 1,744 samples were successfully genotyped. Three pairs of duplicate genotypes were detected with GenAlEx 6.5 (Peakall and Smouse 2006, 2012); one sample from each pair was removed from further analysis. The remaining 1,741 samples had genetic information for an average of 10.9 loci (Table 1). There were five alleles observed in seven individuals that were not present in the chum salmon baseline; the single-locus genotypes for these individuals were removed from further analysis. The weekly distribution of genetic samples collected in the field during the B-season and those further subsampled and analyzed did not differ from the total number of chum salmon caught based on the sampling protocol (Table 2).

Table 1. -- Number of genetic samples genetically analyzed for chum salmon from the 2014 Bering Sea midwater pollock trawl fishery.

Number loci	**Number samples**
11	1,639
10	55
9	38
8	12
< 8	79

Table 2. -- Chi-square tests for goodness of fit used to compare 1) the weekly distribution of genetic samples collected with the expected number of samples (total chum salmon caught per week/30), and 2) the samples genotyped and analyzed with ¼ of the samples expected. Weeks 39 and 40 were pooled to provide sample sizes > 4 in all time categories.

Sample set	**N**	X^2	**d.f.**	**P-value**
Collected vs. expected	7,237	1.12	15	> 0.99
Genotyped vs. ¼ expected	1,823	3.11	15	> 0.99
Analyzed vs. ¼ expected	1,741	6.81	15	0.96

Quality control of sample handling and genotyping was examined by plating DNA from the eight samples in the left-most column of each of 20 elution plates for a total of 160 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; across 11 loci there were a total of 34 differences in 3,240 alleles in the original and quality control datasets, which represented an overall discrepancy rate of 1.05%.

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**
Oki100	304	1	0.33
Omm1070	286	5	1.75
Omy1011	288	2	0.69
One101	296	6	2.03
One102	286	3	1.05
One104	298	0	0
One114	296	4	1.35
Ots103	296	7	2.36
Ots3	306	3	0.98
OtsG68	290	1	0.34
Ssa419	294	2	0.68

Gulf of Alaska

DNA extraction and microsatellite genotyping was performed as described above. Of the 278 chum salmon samples analyzed, 5 samples amplified DNA from a species other than chum salmon and were excluded. For 8 or more of the 11 loci, 253 samples were successfully genotyped. One sample of the one duplicate pair detected was removed from further analysis. The remaining 252 samples had genetic information for an average of 10.8 loci (Table 4).

Table 4. -- Number of genetic samples genetically analyzed for chum salmon collected from the 2014 Gulf of Alaska groundfish fisheries.

Number loci	Number samples
11	231
10	9
9	6
8	6
< 8	20

Quality control of sample handling and genotyping was examined by plating DNA from the 8 samples in the left-most column of each of the three elution plates for a total of 24 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; across 11 loci and 474 alleles, there were only two differences at locus *One102* in the original and quality control datasets, which represented an overall discrepancy rate of 0.42%.

GENETIC STOCK COMPOSITION

For the mixture genotypes, allele designations were standardized to match those in the Fisheries and Oceans Canada (DFO) chum salmon microsatellite baseline (Beacham et al. 2009b,c). Standardized genotypes were then exported from Excel as text files, and C++ or FORTRAN programs were used to format the data into mixture files compatible with software used for stock composition estimation. Stock compositions were determined by comparing mixture genotypes with allele frequencies from reference baseline populations. As described previously (Gray et al. 2010), with minor changes to regional group names, baseline populations were grouped into six regions: Southeast Asia, Northeast Asia, Western Alaska, Upper/Middle Yukon, Southwest Alaska, and the Eastern Gulf of Alaska/Pacific Northwest (Fig. 9). The regional groups 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 Appendix I.

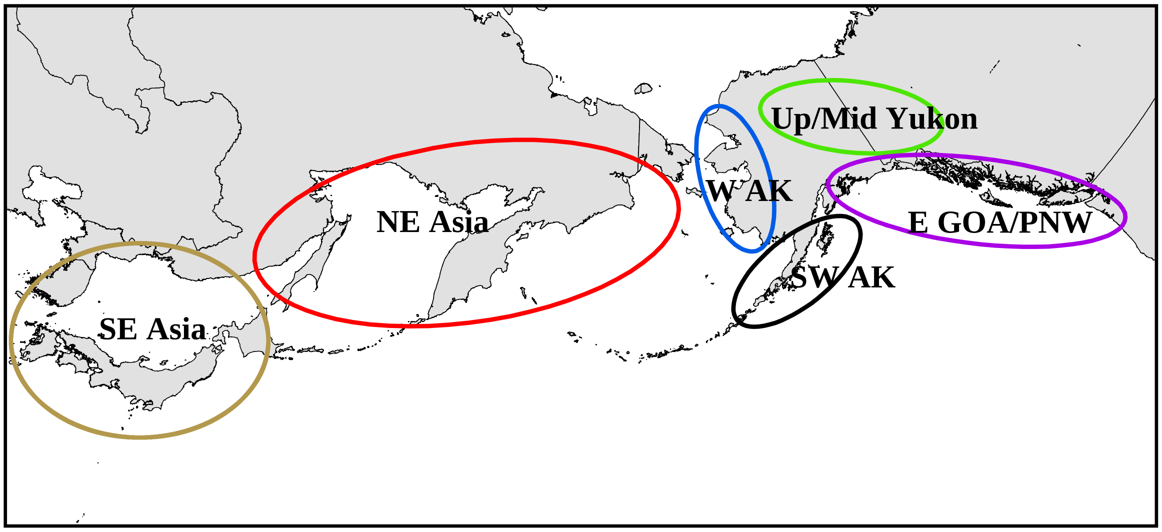

Figure 9. -- Six regional groups of baseline chum salmon populations used in this report were as follows: Southeast Asia (brown), Northeast Asia (red), Western Alaska (blue), Upper/Middle Yukon (green), Southwest Alaska (black), and the Eastern Gulf of Alaska/Pacific Northwest (purple).

As with previous analyses of chum salmon caught in the pollock trawl fishery (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010, 2011a,b; Kondzela et al. 2012, 2013; Vulstek et al. 2014; Whittle et al. 2015), the stock composition analysis for the 2014 chum salmon samples was performed with maximum-likelihood (SPAM 3.7 software; ADF&G 2003) and

Bayesian (BAYES software; Pella and Masuda 2001) procedures. The conditional maximum likelihood approach in SPAM compares the mixture genotypes directly with the baseline. In contrast, the Bayesian method uses an algorithm that can account for “missing” alleles in the baseline; that is, typically low frequency alleles present but not sampled in the baseline populations (Pella and Masuda 2001). Because the maximum-likelihood estimates were in close agreement with the Bayesian estimates, the maximum-likelihood estimates are not shown. BAYES stock composition estimates based on data from all 11 loci were derived for the six regional groups (Tables 5 and 6; Appendix II). For all estimates, the Dirichlet prior parameters for the stock proportions were defined by region to be $1/(GC_g)$, where C_g is the number of baseline populations in region g, and G is the number of regions[2]. For each analysis, six Monte Carlo chains of 100,000 iterations were run starting at disparate values of stock proportions 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. The first 50,000 iterations from each chain were discarded to remove the influence of the initial values. Convergence of the chains to posterior distributions of stock proportions was assessed with Gelman-Rubin shrink factors, which were all less than 1.04 (Tables 5 and 6), conveying strong convergence to a single posterior distribution (Gelman and Rubin 1992, Pella and Masuda 2001). A basic overview of the Bayesian method used for mixed-stock analysis in our report is presented in Appendix III.

The stock composition estimates were summarized by the following statistics: mean, standard deviation, median, 95% credible interval (2.5th and 97.5th percentile of the MCMC iterates in the posterior output), and a statistic called P = 0, which is the probability that a stock composition estimate is effectively zero (Habicht et al. 2012). The P = 0 statistic is the frequency

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[2] In analyses prior to the 2013 chum salmon PSC analysis, a flat prior (1/381) was assigned to each baseline population. Priors defined by region may reduce bias due to differences in how densely regions are represented by baseline populations.

of last half of the MCMC iterates of each chain combined that were less than a threshold that is calculated as 0.5 divided by the number of the chum salmon caught corresponding to the estimated proportion. This threshold is the value that would result in the estimated number of fish being rounded to zero fish when stock proportions are expanded to numbers of chum salmon caught. This statistic may be more useful than the credible interval for assessing the presence or absence of minor stocks.

Table 5. -- Regional stock composition estimates of 1,741 chum salmon samples from the 2014 **Bering Sea** pollock midwater trawl fishery. BAYES mean estimates are provided with standard deviations (S.D.), 95% credible intervals, median estimate, P = 0 statistic, and the Gelman and Rubin shrink factor.

Region	**Mean**	**S.D.**	**2.5%**	**Median**	**97.5%**	**P = 0**	**Shrink**
Southeast Asia	0.185	0.010	0.166	0.185	0.206	0	1.00
Northeast Asia	0.374	0.015	0.345	0.374	0.403	0	1.00
Western Alaska	0.177	0.012	0.154	0.177	0.201	0	1.00
Upper/Middle Yukon	0.021	0.006	0.010	0.021	0.033	0	1.00
Southwest Alaska	0.007	0.003	0.001	0.006	0.014	0.015	1.00
Eastern GOA/PNW	0.236	0.012	0.214	0.236	0.260	0	1.00

Table 6. -- Regional stock composition estimates of 252 chum salmon samples from the 2014 **Gulf of Alaska** groundfish fisheries. BAYES mean estimates are provided with standard deviations (S.D.), 95% credible intervals, median estimate, P = 0 statistic (values > 0.5 are shaded), and the Gelman and Rubin shrink factor.

Region	**Mean**	**S.D.**	**2.5%**	**Median**	**97.5%**	**P = 0**	**Shrink**
Southeast Asia	0.028	0.011	0.010	0.026	0.053	0.004	1.00
Northeast Asia	0.024	0.016	0.000	0.022	0.061	0.177	1.00
Western Alaska	0.020	0.011	0.004	0.019	0.044	0.150	1.00
Upper/Middle Yukon	0.001	0.002	0.000	0.000	0.007	1.000	1.00
Southwest Alaska	0.012	0.014	0.000	0.006	0.050	0.718	1.03
Eastern GOA/PNW	0.916	0.023	0.866	0.918	0.957	0	1.01

COMPARISON WITH PREVIOUS ESTIMATES

Bering Sea

The stock composition results from the analysis of the 2014 chum salmon samples were generally similar to the results from recent years when systematic sampling was in effect (Fig. 10, upper panel). One exception to this pattern was the significantly lower proportional contribution from the Upper/Middle Yukon in 2014 compared to all previous years. The extent to which year-to-year differences in regional stock contributions are attributable to differences in fishing locations and times or migration patterns of chum salmon is beyond the scope of this report. However, with systematic sampling of the Bering Sea chum salmon PSC in place, the role of these factors on the year-to-year variation of stock estimates will be easier to determine.

The 1994-1995 chum salmon stock composition estimates were produced with allozyme data (Wilmot et al. 1998), whereas the 2005-2014 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; Vulstek et al. 2014; Whittle et al. 2015). The allozyme (77 populations) and microsatellite DNA (381 populations) baselines have data from many of the same populations and have similar regional groups. The effect of the PSC on chum salmon populations is influenced by the overall size of the PSC relative to the number of adults that return to the rivers to spawn. The large variation in total chum salmon caught in 1994, 1995, 2005-2014 (Fig. 2) is reflected in the high standard errors of the mean number of chum salmon caught by region (unweighted by year) when stock composition estimates are extrapolated to the total chum salmon PSC from the Bering Sea groundfish fisheries (Fig. 10, lower panel). Since 2011, the genetic samples have been collected systematically, resulting in the numerical extrapolations being relatively free of sample bias. The location and timing of collections prior to 2011 was not always representative of the entire chum salmon PSC within a given year.

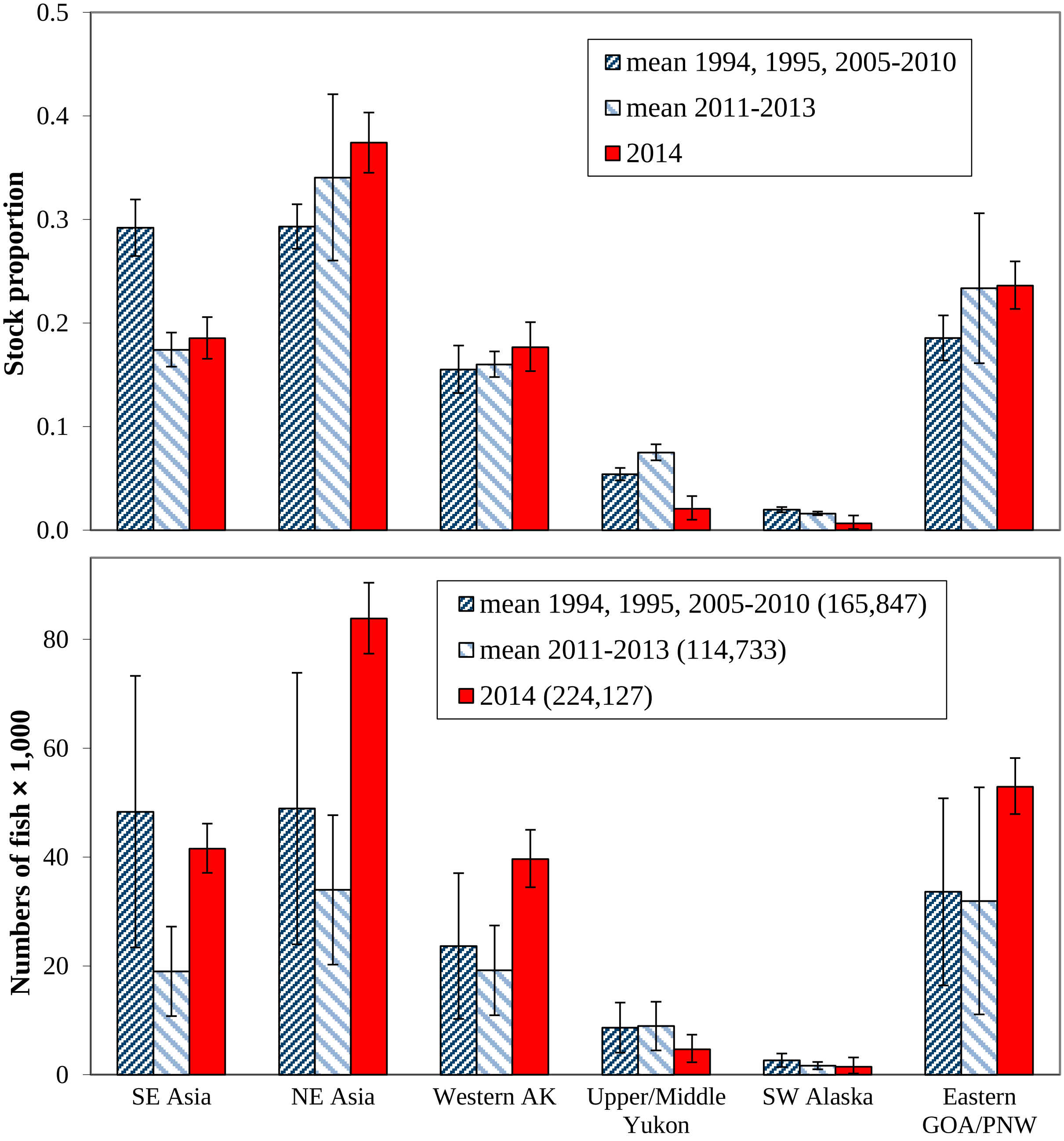

Figure 10. -- Comparison of the 2014 Bering Sea chum salmon stock composition estimates with the estimates from 2011-2013 (systematic sampling) and the unweighted mean estimates of available genetic samples from 1994, 1995, and 2005-2010 (non-systematic sampling). Proportions in top panel; numbers of fish in bottom panel, which for comparison purposes across years are based on the total chum salmon caught in all groundfish fisheries. Standard errors of the mean estimates are shown for the combined years; 95% BAYES credible intervals are shown for the 2014 analysis. Error bars are based on only the mixed-stock analyses and do not include errors associated with the overall annual prohibited species catch size estimation or potential biases in sample distribution. Total chum salmon caught in the Bering Sea groundfish fisheries is shown in parentheses in the bottom figure legend; 1994-2010 are estimates and 2011-2014 are censuses.

Gulf of Alaska

For the first time, in 2014, samples from the PSC of chum salmon from the GOA groundfish fisheries were available for genetic analysis. Although comparisons of stock composition estimates of PSC with prior years cannot be made, two previous studies provide some insight into the stock distribution of chum salmon that inhabit the GOA and the south side of the Alaska Peninsula during late summer/early fall. In the first study, chum salmon were collected between 5-17 August 2003 during an extensive research survey that included the GOA (Fig. 11; Urawa et al. 2009). The chum salmon samples from the GOA were predominately from Eastern GOA/PNW (40%) and Western Alaska (30%) stocks, with lower contributions from Southwest Alaska (13%), Southeast and Northeast Asia (< 10% each), and Upper/Middle Yukon (< 3%) stocks. In contrast, more than 90% of the chum salmon caught in the 2014 GOA groundfish fisheries were from Eastern GOA/PNW stocks and less than 3% from each of all other regional stocks. These stock distribution differences may be due to collection dates separated by a month or more, yearly variation, or location of collection sites. For example, the samples from the research survey were collected over a much broader area and farther offshore than the samples from the groundfish fisheries.

The second study focused in part on chum salmon caught in salmon fisheries south of the Alaska Peninsula (Fig. 11). Chum salmon of uncertain origin are caught in nearshore (within 3 nautical miles of shore) and offshore (in the EEZ, 3-200 nautical miles from shore) salmon fisheries east of Prince William Sound, Cook Inlet, and the south side of the Alaska Peninsula, where harvest management of offshore fisheries is delegated to the state[3]. Uncertainty about the origin of chum and sockeye (*O. nerka*) salmon harvested south of the Alaska Peninsula led to implementation of the Western Alaska Salmon Stock Identification Program (WASSIP)[4]. The

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[3] Fishery Management Plan for the Salmon Fisheries in the EEZ off Alaska.

[4] Western Alaska Salmon Stock Identification Program.

WASSIP produced the largest salmon genetic stock identification study in history (Habicht et al. 2012). From this large study, it was determined that some state managed nearshore and offshore salmon fisheries on the south side of the Alaska Peninsula in June and July harvest a mix of chum salmon that originate from populations throughout their geographic distribution, whereas other salmon fisheries harvest primarily local area stocks (Templin et al. 2012). Stock contributions in some fisheries also shift during the summer season. In the WASSIP, the fishery most proximate to the location of PSC chum salmon samples collected in the federal GOA groundfish fisheries was on the easternmost end of the WASSIP study area, southwest of Kodiak Island (Fig. 11). Mixed-stock analyses of chum salmon samples collected from this nearshore fishery (Eastern District, Chignik Management Area, Westward Region) during 2007 and 2009 indicated a mix of stocks from Asia (11%), coastal western Alaska (20%), Alaska Peninsula (11%), Chignik/Kodiak (14%), and east of Kodiak (44%) in June, and mostly local stocks (Chignik/Kodiak, 84%) in July.

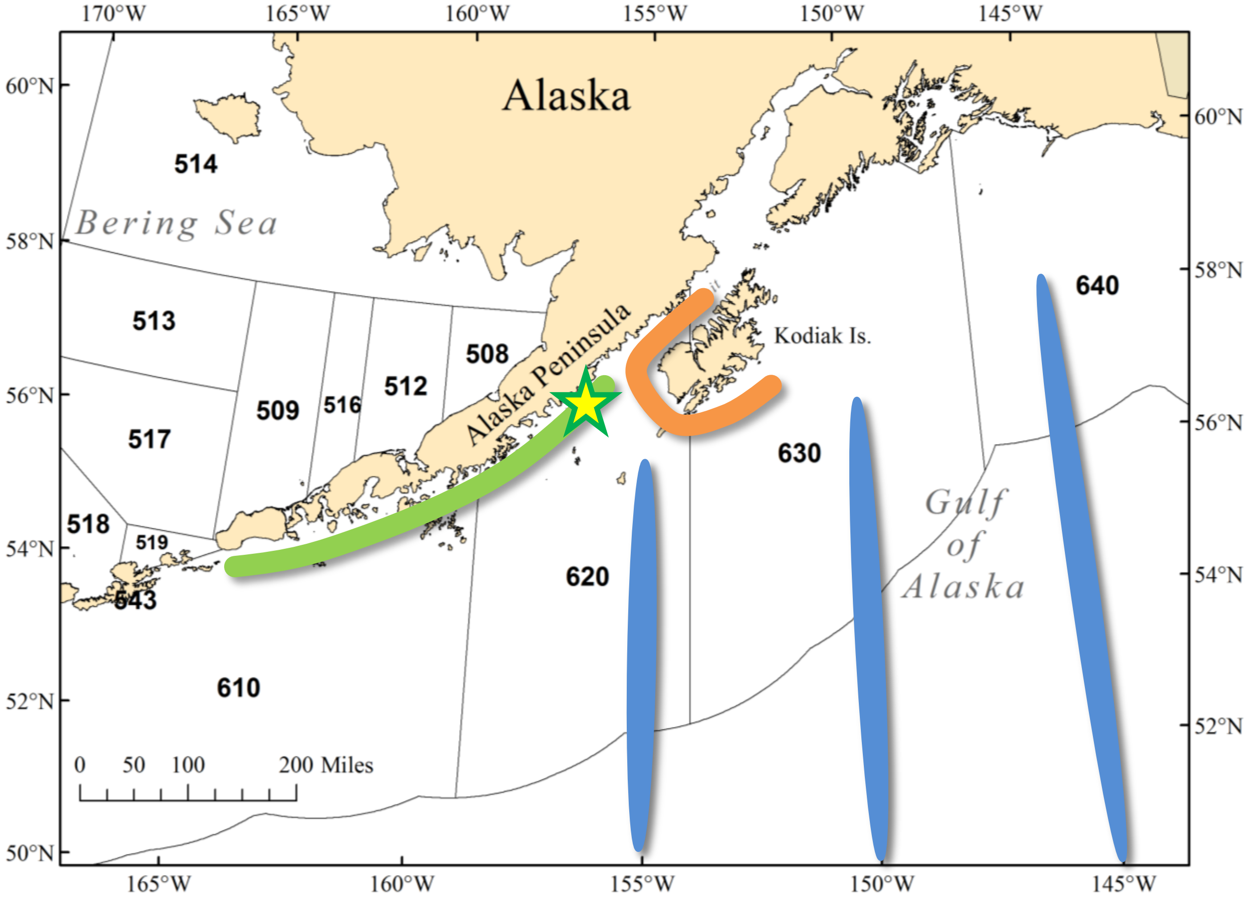

Figure 11. -- Location of chum salmon samples from 1) most of the prohibited species catch from the Gulf of Alaska groundfish fisheries during August-October in 2014 (orange line), 2) a Japanese research survey between 50-58°N and 145-155°W during August 2003 (blue areas), and 3) the portion of the WASSIP study south of the Alaska Peninsula during June and July in 2007-2009 (green line; star represents ADF&G's Eastern District, Chignik Management Area, Westward Region).

TEMPORAL STRATIFICATION

Knowledge of the temporal distribution of the chum salmon PSC is important for better understanding the seasonal impacts of the pollock trawl fishery on salmon stocks. If the chum salmon stock distribution changes consistently over time, it may be possible to manage the pollock fishery in a manner that minimizes effects on critical salmon stocks. This section is limited to analyses of the Bering Sea samples.

As with the 2005-2013 analyses, the 2014 Bering Sea sample set was temporally split into three B-season time periods: Early, Middle, and Late (Table 7). Stock composition estimates were made as described previously for each of the three temporal strata (Appendix II). Gelman and Rubin shrink factors were in all cases 1.00 and suggested strong convergence to a single posterior distribution (Appendix III).

Table 7. -- Temporal groups from the genetic sample sets of chum salmon caught in the 2014 Bering Sea, B-season pollock fishery.

Time period	**Weeks**	**Dates**	**Number of samples**
Early	24-29	10 June – 19 July	249
Middle	30-34	20 July – 23 August	957
Late	35-40	24 August – 4 October	535

The stock composition of chum salmon caught in the Bering Sea pollock fishery changed during the course of the season (Fig. 12). In 2014, genetic samples differed across the three time periods within two of the five regional groups. The contribution from Southeast Asia decreased during the Middle time period and then increased in the Late time period, and on the North American continent, the Western Alaska contribution decreased in the Late time period. The Northeast Asia and Upper/Middle Yukon contributions were similar over the three time periods, and although the Eastern GOA/PNW contribution increased after the Early time period, the 95% credible intervals overlap.

The averages of the 2005-2013 stock compositions for similar temporal strata are included for comparison purposes (Fig. 12). Some differences in the stock contributions by time period were observed between the 2014 and the 2005-2013 chum salmon samples. The contribution from Southeast Asia during the Middle period in 2014 was lower than the average of previous years, although the 2014 pattern of temporal stock contributions from Southeast Asia was similar to that observed in 2013 (Whittle et al. 2015). The contribution from Northeast Asia during the Early time period in 2014 was higher than in previous years. The proportion of the chum salmon catch contributed by Western Alaska stocks across time periods was more similar to that observed in 2013 than to the average in previous years. The distribution of contributions from the Upper/Middle Yukon across time was similar to that in previous years, although the estimates for all three time periods were about half that observed in previous years. Unlike previous years, including 2013, the contribution from the Eastern GOA/PNW increased as the season progressed. Results from the temporal 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.

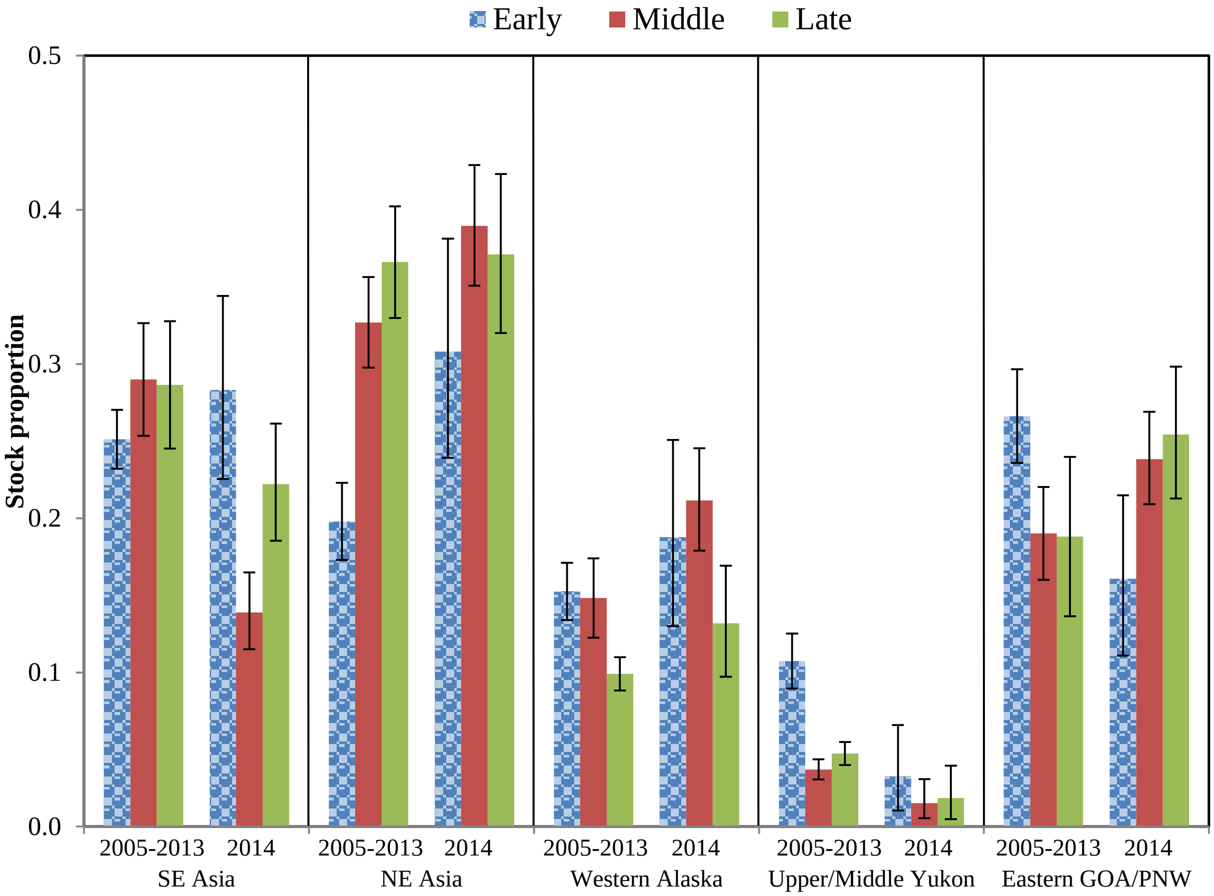

Figure 12. -- Stock composition estimates for the 2005-2013 (mean ± S.E.) and 2014 (± 95% BAYES credible intervals) chum salmon samples for the Early, Middle, and Late periods (defined in Table 7). Not shown is the Southwest Alaska region for which estimates never exceeded 5.6%.

SPATIAL STRATIFICATION

Bering Sea

Knowledge of the spatial distribution of the chum salmon PSC is also important for better understanding the impacts of the pollock trawl fishery on salmon stocks. In 2014, for the fourth year, the Observer Program undertook a complete census of chum salmon caught in the Bering Sea pollock trawl fisheries. About 66% of the chum salmon catch was counted and sampled at processing facilities where catches were offloaded from vessels that theoretically can fish in multiple fishery management areas before offloading the catch. For vessels that fished in multiple NMFS reporting areas during a trip, the area assigned to an offload was the area where the highest weight of pollock was caught.

The 2014 Bering Sea genetic samples were split spatially into two areas (see Fig. 1): the U.S. waters of the Bering Sea west of 170°W (areas 521, 523, and 524), and the southeastern Bering Sea, east of 170°W (areas 509, 513, 514, 517, and 519). NMFS reporting areas were aggregated to increase sample sizes for mixed-stock analyses. Stock compositions for the two spatial strata were estimated as described previously (Fig. 13; Appendix II). Gelman and Rubin shrink factors were 1.00 for all datasets and suggested strong convergence to a single posterior distribution (Appendix III). More than two-thirds of the contribution to the west of 170°W and about half of the contribution to the southeastern Bering Sea were from Asian stocks. Northeast Asia stocks were the largest contributor to the chum salmon catch in both Bering Sea areas, with nearly identical contributions in both areas. The contribution from other stocks differed between the spatial strata. Southeast Asia stocks were more than twice as frequent in waters west of 170°W as in the southeastern Bering Sea. Contributions from North American stocks were highest in the southeastern Bering Sea, particularly from the Western Alaska and Eastern GOA/PNW stocks.

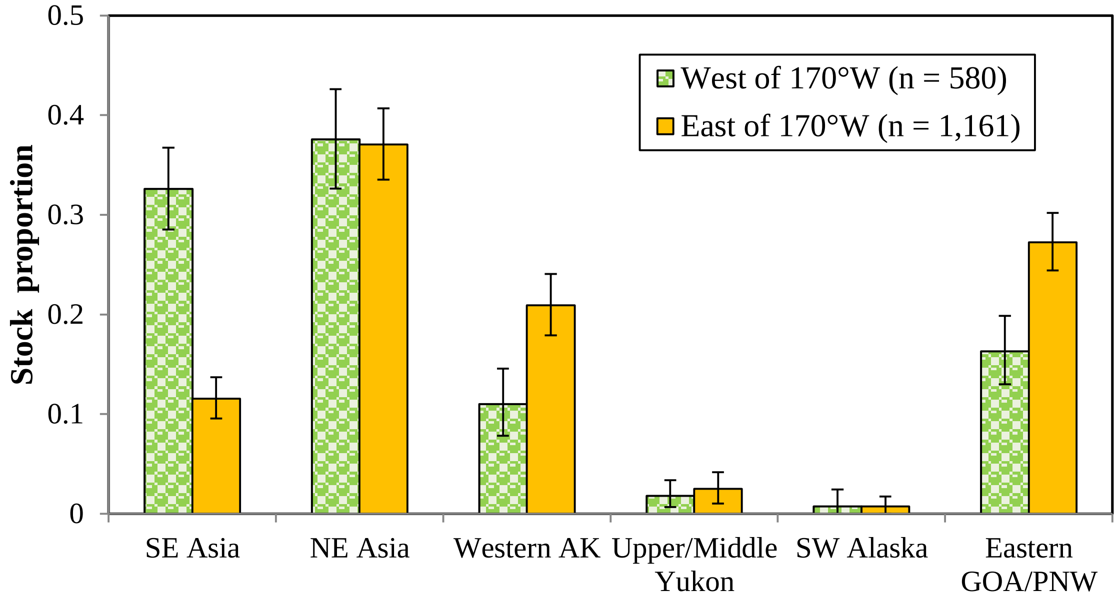

Figure 13. -- Stock composition estimates and 95% BAYES credible intervals for the 2014 chum salmon genetic samples from the U.S. waters of the Bering Sea west of 170°W (aggregate area 521/523/524) and the southeastern Bering Sea east of 170°W (aggregate area 509/513/514/517/519).

To better understand the chum salmon stock distribution across time and space, the 2014 samples from area 509 for the Early-Middle time periods and the samples from areas 517 and 521 for two time periods (Table 8) were compared. Samples from all other areas/time periods were not included due to small sample sizes.

Table 8. -- Spatial and temporal groups from the 2014 chum salmon genetic samples at two time periods (Table 7) for the reporting areas with the most samples.

Reporting area	**Time period**	**Number of samples**
509	Early-Middle	90
517	Early-Middle	784
517	Late	252
521	Early-Middle	295
521	Late	221

Stock compositions were estimated for each spatial and temporal stratum as described above (Fig. 14; Appendix II). The Gelman and Rubin shrink factors were 1.01 or less for all datasets, indicating that the stock composition estimates converged to a single posterior distribution (Appendix III). The Southeast Asia stock contribution for area 517 was the only Asian contribution that changed significantly (decreased) across time. The slight decrease in contribution across time from Western Alaska was not significant in area 517 or 521. The contribution from the Upper/Middle Yukon stocks was low in all three areas. The Eastern GOA/PNW contribution increased over time in area 517 and was similar during both time periods in area 521. As in previous years, the contribution from Southwest Alaska was absent or very low in all time periods and areas, with the exception of area 509 during the Early-Middle time period (Appendix II). 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.

Where it occurs, 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 chum salmon samples within each area is unknown. In addition, two-thirds of the total chum salmon PCS was sampled from offload deliveries in which vessels may have fished in multiple areas. Thus, for an unknown proportion of the chum salmon samples, the area designation may not be correct.

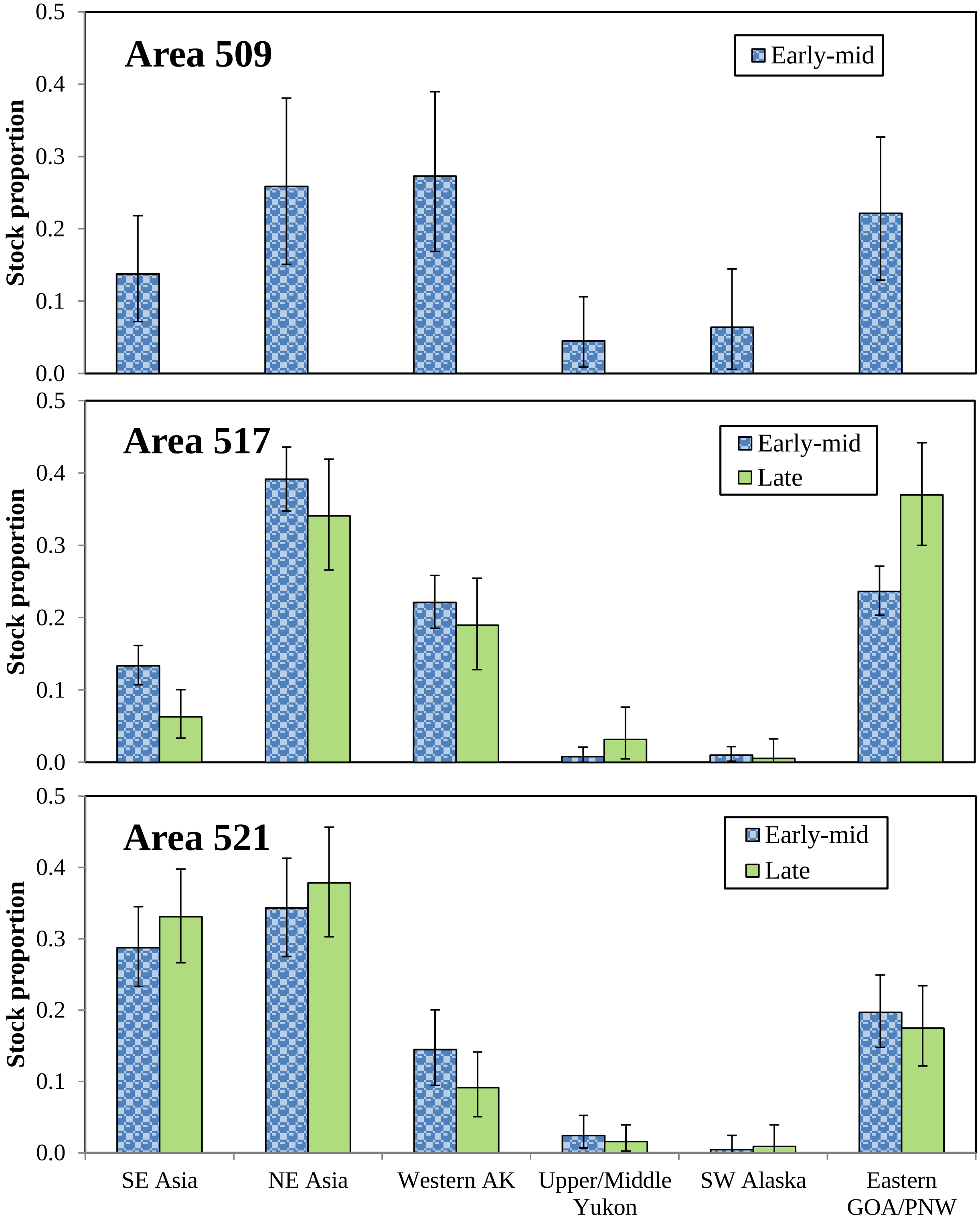

Figure 14. -- Stock composition estimates and 95% BAYES credible intervals for the 2014 chum salmon genetic samples from the NMFS reporting area 509 for the Early-Middle time period, and areas 517 and 521 for the Early-Middle and Late time periods (Table 8).

Gulf of Alaska

On a finer spatial scale, the stock composition estimates of two GOA subsets–154 samples collected from ADFG Statistical Area 555630[5], southwest of Kodiak Island, and 52 samples collected west of Kodiak Island in and near Shelikof Strait (Fig. 1)–were nearly identical to the estimates of the total dataset (not shown).

SUMMARY

Stock composition estimates of the salmon caught 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 the genetic stock composition analyses of the 2014 chum salmon PSC based on 1,741 and 252 samples genotyped from the Bering Sea and GOA fisheries, respectively. The limitations and results of this analysis are summarized below and in Appendix II.

Sampling Issues

Bering Sea

We highlight the reduced spatial and temporal biases in the Bering Sea 2014 sample set (Figs. 3 and 4) that were inherent in collections before 2011. Reduction of those biases improves the application of the 2014 genetic sample stock composition estimates to the entire chum salmon PSC. Implementation of Amendment 91 to the North Pacific Fishery Management Council fishery management plan for groundfish of the Bering Sea and Aleutian Islands Management Area[6] requires that all salmon caught in the Bering Sea pollock fishery be sorted by species and counted to ensure compliance with the salmon PSC limits for the pollock fishery.

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[5] ADFG statistical areas.

[6] 75 FR 53026, August 30, 2010.

This regulation led to the collection of representative samples from 99.2% of the chum salmon caught in this fishery for genetic analysis in 2014 (Fig. 5), and improved the capability to characterize the origin of salmon caught in the Bering Sea pollock fishery.

Gulf of Alaska

The GOA groundfish fisheries are complex and not all groundfish catches in the GOA are subject to observer coverage. The number of chum salmon caught in GOA federal fisheries is much lower than in the federal fisheries of the Bering Sea; however, recent expansion of sampling salmon PSC in the GOA[7] provided, for the first time, a small sample set for genetic analysis. Most of the samples (96%) were from the pollock trawl fishery, which in 2014 caught about half the chum salmon PSC in the GOA.

Stock Composition Estimates

Bering Sea

Overall, about half of the genetic samples collected from chum salmon caught in the 2014 Bering Sea pollock fishery were from Asia (37% Northeast Asia; 19% Southeast Asia), and the other half from North America, primarily from Eastern GOA/PNW (24%) and Western Alaska (18%) stocks (Table 5). The stock proportions from Asia in 2014 dominated the catch as in previous years (Fig. 10). Contribution from Upper/Middle Yukon (2%) stocks was significantly lower than in previous years and the pattern of low contribution from Southwest Alaska (< 1%) continued in 2014. Although chum salmon samples in 2014 were collected representatively from the pollock fishery, there were differences in where and when genetic samples were collected from previous years, so that caution must be used in making year-to-year comparisons.

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[7] Amendment 93 to the NPFMC fishery management plan for GOA groundfish (77 FR 42629, July 20, 2012).

Gulf of Alaska

A very different pattern of stock origin was observed in the GOA chum salmon samples. More than 90% of the chum salmon sampled from the GOA groundfish fisheries were from Eastern GOA/PNW stocks (Table 6). The remaining contributions from the other five regions were very low, 0-3%.

Temporal and Spatial Effects

The time-stratified analysis of the chum salmon samples was limited to the pollock B-season, when the majority of chum salmon are intercepted in the Bering Sea. Stock composition estimates of the 2014 chum salmon catch changed across the three sampling periods, suggesting a shift in the temporal stratification of chum salmon stocks in the Bering Sea, changes in fishing or sampling locations, or both (Fig. 12). The stock composition estimates of the 2014 chum salmon shared a similar distribution to that observed across previous years except for the Early time period for the Eastern GOA/PNW and for the Middle time period for the Southeast Asia and Western Alaska contributions.

Spatial analysis suggested that nearly half of the chum salmon from U.S. waters of the Bering Sea east of 170°W and over two-thirds of the chum salmon west of 170°W originated from Asian stocks (Fig. 13). The contribution from Northeast Asia was identical in both areas; however, there were some differences in contributions from other regions. The proportion of chum salmon from Southeast Asia stocks in the western area was much higher than that in the southeastern Bering Sea. Likewise, significantly higher proportions of chum salmon from Western Alaska and Eastern GOA/PNW stocks were found in the southeastern Bering Sea.

An examination of chum salmon stock estimates on both spatial and temporal strata of the Bering Sea pollock fishery suggests that overall the pattern of stock contributions was notably similar among the three reporting areas, although there were a few differences across areas or time periods (Fig. 14). For example, the Southeast Asia contribution was significantly higher in area 521 than in area 517. The stock contributions were stable across the two time periods in area 521, but in area 517, the contributions from Southeast Asia and Eastern GOA/PNW stocks changed across the season.

Application of Estimates

The extent to which any salmon stock is impacted by the Bering Sea and GOA trawl fisheries is dependent on many factors including 1) the overall size of the PSC, 2) the age of the salmon caught, 3) the age composition of the salmon stocks at return, 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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APPENDICES

Appendix I. -- Chum salmon populations in the Fisheries and Oceans Canada (DFO) microsatellite baseline with the regional designations used in the analyses of this report.

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

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

DFO Num	Population name	Reg Num	Region	DFO Num	Population name	Reg Num	Region
79	Bella_Coola	6	E GOA/PNW	269	Dog-tag	6	E GOA/PNW
49	Big_Qual	6	E GOA/PNW	177	Draney	6	E GOA/PNW
201	Big_Quilcene	6	E GOA/PNW	114	Duthie_Creek	6	E GOA/PNW
281	Bish_Cr	6	E GOA/PNW	427	East_Arm	6	E GOA/PNW
198	Bitter_Creek	6	E GOA/PNW	266	Ecstall_River	6	E GOA/PNW
103	Blackrock_Creek	6	E GOA/PNW	94	Elcho_Creek	6	E GOA/PNW
390	Blaney_Creek	6	E GOA/PNW	193	Ellsworth_Cr	6	E GOA/PNW
138	Botany_Creek	6	E GOA/PNW	203	Elwha	6	E GOA/PNW
264	Buck_Channel	6	E GOA/PNW	276	Ensheshese	6	E GOA/PNW
169	Bullock_Chann	6	E GOA/PNW	263	Fairfax_Inlet	6	E GOA/PNW
61	Campbell_River	6	E GOA/PNW	32	Fish_Creek	6	E GOA/PNW
323	Carroll	6	E GOA/PNW	429	Flux_Cr	6	E GOA/PNW
78	Cascade	6	E GOA/PNW	102	Foch_Creek	6	E GOA/PNW
76	Cayeghle	6	E GOA/PNW	179	Frenchman	6	E GOA/PNW
42	Cheakamus	6	E GOA/PNW	227	Gambier	6	E GOA/PNW
398	Cheenis_Lake	6	E GOA/PNW	96	Gill_Creek	6	E GOA/PNW
51	Chehalis	6	E GOA/PNW	166	Gilttoyee	6	E GOA/PNW
19	Chemainus	6	E GOA/PNW	145	Glendale	6	E GOA/PNW
47	Chilliwack	6	E GOA/PNW	135	Gold_Harbour	6	E GOA/PNW
392	Chilqua_Creek	6	E GOA/PNW	11	Goldstream	6	E GOA/PNW
117	Chuckwalla	6	E GOA/PNW	66	Goodspeed_River	6	E GOA/PNW
139	Clapp_Basin	6	E GOA/PNW	136	Government	6	E GOA/PNW
107	Clatse_Creek	6	E GOA/PNW	205	Grant_Creek	6	E GOA/PNW
118	Clyak	6	E GOA/PNW	100	Green_River	6	E GOA/PNW
62	Cold_Creek	6	E GOA/PNW	450	GreenRrHatchery	6	E GOA/PNW
77	Colonial	6	E GOA/PNW	237	Greens	6	E GOA/PNW
353	Constantine	6	E GOA/PNW	141	Harrison	6	E GOA/PNW
168	Cooper_Inlet	6	E GOA/PNW	438	Harrison_late	6	E GOA/PNW
197	County_Line	6	E GOA/PNW	64	Hathaway_Creek	6	E GOA/PNW
12	Cowichan	6	E GOA/PNW	234	Herman_Creek	6	E GOA/PNW
414	Crag_Cr	6	E GOA/PNW	17	Heydon_Cre	6	E GOA/PNW
161	Dak_	6	E GOA/PNW	407	Hicks_Cr	6	E GOA/PNW
259	Dana_Creek	6	E GOA/PNW	400	Homathko	6	E GOA/PNW
123	Date_Creek	6	E GOA/PNW	411	Honna	6	E GOA/PNW
250	Dawson_Inlet	6	E GOA/PNW	204	Hoodsport	6	E GOA/PNW
91	Dean_River	6	E GOA/PNW	185	Hooknose	6	E GOA/PNW
261	Deena	6	E GOA/PNW	406	Hopedale_Cr	6	E GOA/PNW
170	Deer_Pass	6	E GOA/PNW	412	Hutton_Head	6	E GOA/PNW
46	Demamiel	6	E GOA/PNW	278	Illiance	6	E GOA/PNW
210	Dipac_Hatchery	6	E GOA/PNW	152	Inch_Creek	6	E GOA/PNW
319	Disappearance	6	E GOA/PNW	146	Indian_River	6	E GOA/PNW

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

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

Appendix II. -- Regional stock composition estimates of chum salmon samples from the 2014 Bering Sea (BS) B-season, midwater pollock trawl fishery and the Gulf of Alaska (GOA) groundfish fisheries. BAYES mean estimates, standard deviations (SD), 95% credible intervals, median estimate, the probability that the stock estimate is equal to zero (P = 0; values > 0.5 are shaded; Habicht et al. 2012), and the Gelman-Rubin shrink factor are reported. For each stratum, prohibited species catch (PSC) is the number of chum salmon reported as caught and n is the number of genetic samples used in the analysis. Early season is Weeks 24-29, Middle season is Weeks 30-34, and Late season is Weeks 35-40.

BS Total sample set (PSC = 218,787, n = 1,741)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.185	0.010	0.166	0.185	0.206	0	1.00
NE Asia	0.374	0.015	0.345	0.374	0.403	0	1.00
Western Alaska	0.177	0.012	0.154	0.177	0.201	0	1.00
Upper/Middle Yukon	0.021	0.006	0.010	0.021	0.033	0	1.00
SW Alaska	0.007	0.003	0.001	0.006	0.014	0.015	1.00
Eastern GOA/PNW	0.236	0.012	0.214	0.236	0.260	0	1.00

BS Early season sample set (PSC = 30,460, n = 249)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.283	0.031	0.225	0.282	0.344	0	1.00
NE Asia	0.308	0.037	0.239	0.307	0.381	0	1.00
Western Alaska	0.188	0.031	0.130	0.187	0.251	0	1.00
Upper/Middle Yukon	0.033	0.014	0.011	0.031	0.066	0	1.00
SW Alaska	0.028	0.016	0.002	0.026	0.063	0.014	1.00
Eastern GOA/PNW	0.161	0.027	0.111	0.160	0.215	0	1.00

BS Middle season sample set (PSC = 120,717, n = 957)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.139	0.013	0.115	0.139	0.165	0	1.00
NE Asia	0.390	0.020	0.351	0.390	0.429	0	1.00
Western Alaska	0.212	0.017	0.179	0.212	0.245	0	1.00
Upper/Middle Yukon	0.015	0.007	0.005	0.014	0.031	0	1.00
SW Alaska	0.006	0.005	0.000	0.005	0.017	0.106	1.00
Eastern GOA/PNW	0.238	0.015	0.209	0.238	0.269	0	1.00

Appendix II. -- Continued.

BS Late season sample set (PSC = 67,610, n = 535)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.222	0.019	0.185	0.222	0.261	0	1.00
NE Asia	0.371	0.026	0.320	0.371	0.423	0	1.00
Western Alaska	0.132	0.018	0.097	0.131	0.169	0	1.00
Upper/Middle Yukon	0.019	0.009	0.005	0.017	0.040	0	1.00
SW Alaska	0.002	0.004	0.000	0.000	0.013	0.830	1.00
Eastern GOA/PNW	0.254	0.022	0.213	0.254	0.298	0	1.00

BS east of 170°W sample set, areas 509, 513, 514, 517, 519 (PSC = 144,869, n = 1,161)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.116	0.011	0.096	0.115	0.137	0	1.00
NE Asia	0.371	0.018	0.335	0.371	0.407	0	1.00
Western Alaska	0.209	0.016	0.179	0.209	0.241	0	1.00
Upper/Middle Yukon	0.025	0.008	0.010	0.025	0.042	0	1.00
SW Alaska	0.007	0.004	0.000	0.007	0.017	0.039	1.00
Eastern GOA/PNW	0.272	0.015	0.244	0.272	0.302	0	1.00

BS west of 170°W sample set, areas 521, 523, 524 (PSC = 73,918, n = 580)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.326	0.021	0.285	0.326	0.367	0	1.00
NE Asia	0.376	0.025	0.326	0.375	0.426	0	1.00
Western Alaska	0.110	0.017	0.078	0.110	0.146	0	1.00
Upper/Middle Yukon	0.018	0.007	0.007	0.017	0.034	0	1.00
SW Alaska	0.007	0.007	0.000	0.006	0.025	0.275	1.00
Eastern GOA/PNW	0.163	0.018	0.130	0.163	0.199	0	1.00

BS area 509 Early-Middle season sample set (PSC = 11,477, n = 90)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.138	0.038	0.072	0.135	0.218	0	1.00
NE Asia	0.259	0.059	0.151	0.256	0.381	0	1.00
Western Alaska	0.273	0.057	0.169	0.271	0.390	0	1.00
Upper/Middle Yukon	0.045	0.025	0.009	0.041	0.106	0.001	1.00
SW Alaska	0.064	0.036	0.006	0.060	0.144	0.010	1.00
Eastern GOA/PNW	0.222	0.051	0.129	0.219	0.327	0	1.00

Appendix II. -- Continued.

BS area 517 Early-Middle season sample set (PSC = 97,999, n = 784)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.133	0.014	0.107	0.133	0.162	0	1.00
NE Asia	0.391	0.023	0.348	0.391	0.436	0	1.00
Western Alaska	0.221	0.019	0.185	0.221	0.259	0	1.00
Upper/Middle Yukon	0.008	0.006	0.000	0.007	0.021	0.053	1.00
SW Alaska	0.010	0.005	0.001	0.010	0.022	0.016	1.00
Eastern GOA/PNW	0.236	0.017	0.203	0.236	0.271	0	1.00

BS area 517 Late season sample set (PSC = 30,857, n = 252)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.063	0.017	0.034	0.062	0.101	0	1.00
NE Asia	0.341	0.039	0.266	0.340	0.419	0	1.01
Western Alaska	0.189	0.032	0.128	0.189	0.255	0	1.00
Upper/Middle Yukon	0.032	0.019	0.005	0.029	0.076	0	1.01
SW Alaska	0.005	0.009	0.000	0.001	0.032	0.635	1.00
Eastern GOA/PNW	0.370	0.036	0.300	0.369	0.442	0	1.01

BS area 521 Early-Middle season sample set (PSC = 37,140, n = 295)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.288	0.029	0.234	0.287	0.345	0	1.00
NE Asia	0.343	0.035	0.275	0.343	0.413	0	1.00
Western Alaska	0.145	0.027	0.095	0.144	0.200	0	1.00
Upper/Middle Yukon	0.024	0.012	0.007	0.022	0.052	0	1.00
SW Alaska	0.004	0.007	0.000	0.001	0.024	0.671	1.00
Eastern GOA/PNW	0.197	0.026	0.148	0.196	0.249	0	1.00

BS area 521 Late season sample set (PSC = 28,919, n = 221)

Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.331	0.034	0.267	0.331	0.398	0	1.00
NE Asia	0.379	0.039	0.303	0.378	0.456	0	1.00
Western Alaska	0.091	0.023	0.051	0.090	0.141	0	1.00
Upper/Middle Yukon	0.016	0.010	0.003	0.014	0.039	0.005	1.00
SW Alaska	0.009	0.011	0.000	0.004	0.039	0.427	1.00
Eastern GOA/PNW	0.175	0.029	0.122	0.174	0.234	0	1.00

Appendix II. -- Continued.

GOA Total sample set (PSC = 2,699, n = 252)							
Region	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink Factor
SE Asia	0.028	0.011	0.010	0.026	0.053	0.004	1.00
NE Asia	0.024	0.016	0.000	0.022	0.061	0.177	1.00
Western Alaska	0.020	0.011	0.004	0.019	0.044	0.150	1.00
Upper/Middle Yukon	0.001	0.002	0.000	0.000	0.007	1.000	1.00
SW Alaska	0.012	0.014	0.000	0.006	0.050	0.718	1.03
Eastern GOA/PNW	0.916	0.023	0.866	0.918	0.957	0	1.01

Appendix III. -- Basic overview of Bayesian mixed-stock analysis (MSA) pertinent to the analysis of the chum salmon prohibited species catch (PSC).

MSA requires three components:

1. A mixture containing genotypes of samples of unknown origin (e.g., chum salmon PSC samples).

2. A baseline of allele frequencies of potentially contributing stocks in the mixture (same genetic markers as the mixture). The baseline is typically comprised of stock groups[8], populations that are grouped due to genetic similarity, geographic proximity, or political boundaries. For the chum salmon PSC we used the 381-population, 11-locus microsatellite baseline from Fisheries and Oceans Canada (DFO), with populations grouped into six regions.

3. A method to compare the mixture to the baseline to estimate the proportions of baseline populations, or more commonly stock groups, in the mixture. Two methods were used in our study:
    a. **Maximum-likelihood** method in program SPAM (Debevec et al. 2000; ADF&G 2003). For the chum salmon PSC samples, the likelihood method typically estimates stock proportions similar to those produced by the Bayesian method. A comparison of the stock proportions produced by the two methods provides a quality control check on the MSA.
    b. **Bayesian** method in program BAYES (Pella and Masuda 2001), described below.

MSA using the BAYES program requires several steps:

1. Assign parameters of the prior distribution for the unknown stock proportions. Typically an uninformative prior with parameters equal to 1/number of stocks is used unless independent information is available for setting an informative prior. If stock-group estimates are made, then an uninformative prior for the stock-group proportions is set (parameters equal to $1/GC_g$ where G is the number of groups and C_g is the number of baseline populations in group g).

2. Choose the number of Markov chain Monte Carlo (MCMC) samples to simulate from the posterior distribution of stock proportions (depends on the data, but 50,000 to 100,000 is commonly used in our salmon mixed-stock applications).

3. Run several sets of MCMC samples (at least 3 “chains”) with disparate values of initial mixture stock proportions such that most of the contribution comes from one stock or stock group. In the chum salmon PSC analyses, six chains were used, the first of which was started with 95% of the contribution coming from the first baseline region and 5% from all other regions. The other chains were similarly started.

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[8] Depending upon the context, stock groups are sometimes referred to as reporting groups or regional groups.

4. Evaluate convergence of stock proportion estimates to the posterior distribution. Two diagnostics implemented in the BAYES program help gauge convergence. Increase the number of MCMC samples until the stock estimates converge.
    a. **Within chains:** the Raftery and Lewis (1996) diagnostic is useful for determining the number of MCMC samples required to estimate quantiles of the posterior distribution with a specified accuracy and probability.
    b. **Across chains:** the Gelman and Rubin (1992) diagnostic compares the variation within a single chain for a given parameter (e.g., unknown stock proportion) to the total variation among chains and summarizes the two measures by a univariate statistic called the shrink factor. A shrink factor near 1 is consistent with convergence of the samples to the posterior distribution. A shrink factor >1.2 may indicate lack of convergence.

5. Once convergence is determined, the MCMC samples of stock composition estimates are combined from all chains and summarized (e.g., mean, median, standard deviation, 2.5% and 97.5% quantiles), typically from the last half of the chains to remove the influence of the initial values.

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