Genetic Stock Composition Analysis of Chum Salmon from the Prohibited Species Catch of the 2015 Bering Sea Walleye Pollock Trawl Fishery and Gulf of Alaska Groundfish Fisheries

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ABSTRACT

A genetic analysis of the prohibited species catch (PSC) of chum salmon (*Oncorhynchus keta*) collected during 2015 from the federally managed walleye pollock (*Gadus chalcogrammus*) trawl fishery in the Bering Sea and from the federal groundfish fisheries in the Gulf of Alaska (GOA) was undertaken to determine the overall stock composition of the sample sets. Additionally, a genetic analysis was conducted of chum salmon collected in the southeastern Bering Sea during a test of a salmon excluder device. Samples were genotyped for 11 microsatellite markers from which stock contributions were estimated using the current chum salmon microsatellite baseline. In 2015, one genetic sample was collected for every 30.5 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. The small set of chum salmon samples (142) from the A-season were mostly from Northeast Asia (41%) and Eastern GOA/PNW (47%) stocks. Based on the analysis of 1,836 chum salmon collected throughout the B-season, the largest stock group in the catch was Eastern GOA/Pacific Northwest (PNW) (51%), followed by Northeast Asia (17%), Western Alaska (16%), Southeast Asia (10%), Upper/Middle Yukon (4%), and Southwest Alaska ($< 2\%$) stocks. The regional stock estimates for the 2015 chum salmon caught in the Bering Sea differed from most previous years, with contributions from Eastern GOA/PNW stocks surpassing those from Northeast Asia and Southeast Asia stocks. Of the 131 chum salmon samples from the GOA groundfish fisheries, the highest proportion was from Eastern GOA/PNW (88%) stocks. As with the Bering Sea fishery samples, the highest proportion of the 549 excluder device test samples were also from Eastern GOA/PNW (51%) stocks and included fish from multiple geographic regions despite being collected at small spatial and temporal scales.

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).

In this report, we present the genetic stock composition estimates for the samples of chum salmon PSC collected during 2015 from the U.S. Bering Sea walleye pollock (*Gadus chalcogrammus*) midwater trawl fishery and the GOA groundfish fisheries, as well as chum salmon collected in the Bering Sea during a test of a salmon excluder device. In the Bering Sea, the pollock fishery accounted for more than 97.7% of the total chum salmon taken in the groundfish fisheries (NMFS 2016a). In the GOA, the majority (42%) of the chum salmon were caught in the midwater trawl pollock fishery, with the remainder caught in other groundfish fisheries (NMFS 2016a).

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. A new data reporting tool was developed by the Pacific States Marine Fisheries Commission (PSMFC) that simplifies access to fishery information associated with the genetic samples of salmon PSC and is useful for organizing sample datasets at the finer resolution of ADF&G groundfish statistical areas (Fig. 1). The Alaska Fisheries

Information Network (AKFIN[1]) reports developed by the PSMFC were used to construct spatial-temporal clusters of genetic samples along the outer continental shelf from the 2015 chum salmon PSC.
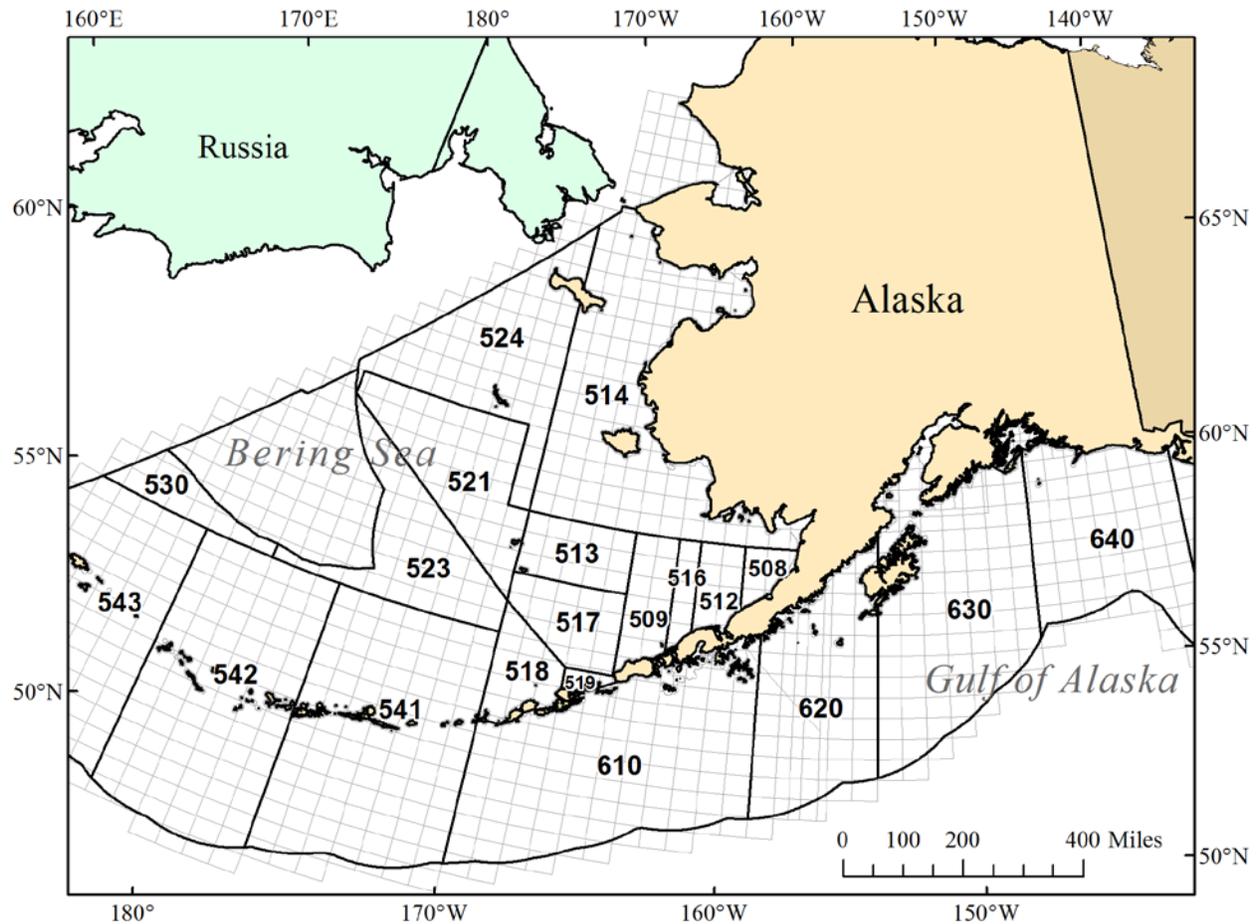
Figure 1. -- NMFS reporting areas associated with the Bering Sea-Aleutian Island and Gulf of Alaska groundfish fisheries are numbered and outlined in black. The ADF&G groundfish statistical areas are outlined in light gray.

For additional background and methods, this report is intended to be supplemented with the chum salmon reports prepared previously for the 2005-2014 Bering Sea trawl fisheries (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010, 2011a,b; Kondzela et al. 2012, 2013,

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2016; 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 2015 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 ABL.

In 2015, an estimated 237,796 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 (NMFS 2016a). This catch is substantially larger than the 1994-2014 average of 139,651 chum salmon and 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 November 1) (Fig. 3) in NMFS reporting areas 509-524 (Fig. 1). During the A-season, approximately 4,647 chum salmon, 2% of the total Bering Sea chum salmon PSC, were caught. Of the 236,686 chum salmon caught in the 2015 "midwater" pollock trawl fishery during the A- and B-seasons, genetic samples were collected from 7,762 fish, which represents a sampling rate of 1 of every 30.5 chum salmon (or 3.3% of the midwater trawl catch of chum salmon). This sampling rate is nearly identical to that in 2011-2014, the first 4 years of representative sampling.
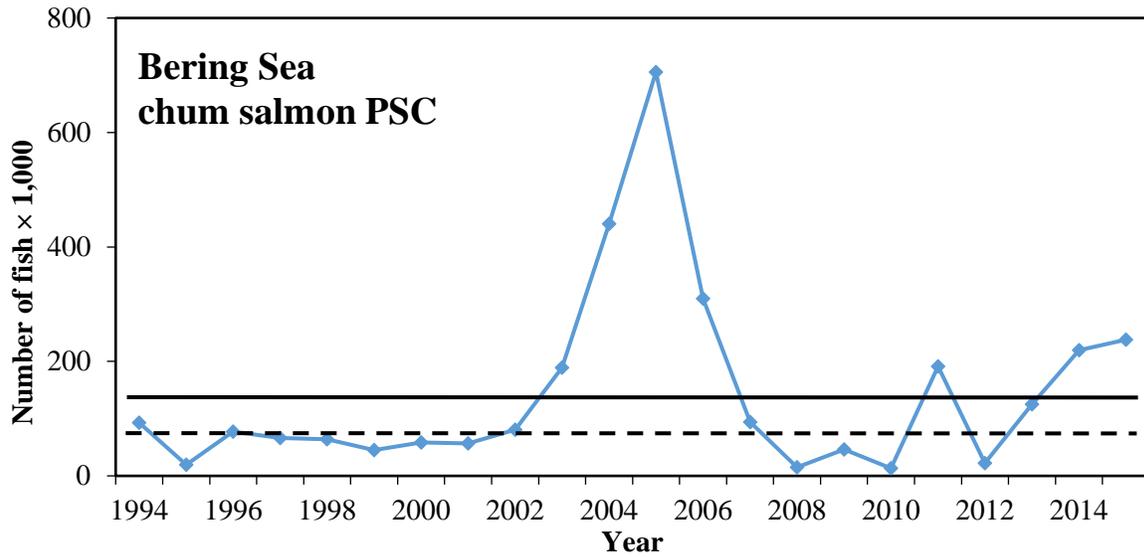
Figure 2. -- Yearly estimates for the non-Chinook salmon prohibited species catch (PSC) from the Bering Sea pollock-directed trawl fisheries (NMFS 2016a). The solid horizontal line represents mean PSC and the dashed line represents median PSC, 1994-2014.

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 35-42) and two areas (NMFS reporting areas aggregated: 509, 513, 517, 518 and 519; and 521, 523, and 524). Temporal bias by statistical week ending on Sunday was minimal (Fig. 3) when samples were pooled across management areas (χ^2 = 5.15, 17 d.f., P > 0.99). During the B-season, temporal biases were also minimal at finer spatial scales (Fig. 4; χ^2 = 3.06, 2 d.f., P = 0.22). Due to the uncertainty of catch location for samples collected from shore-side deliveries in which the hauls were mixed (74% of genetic samples were from catcher vessel offloads; 26% 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.
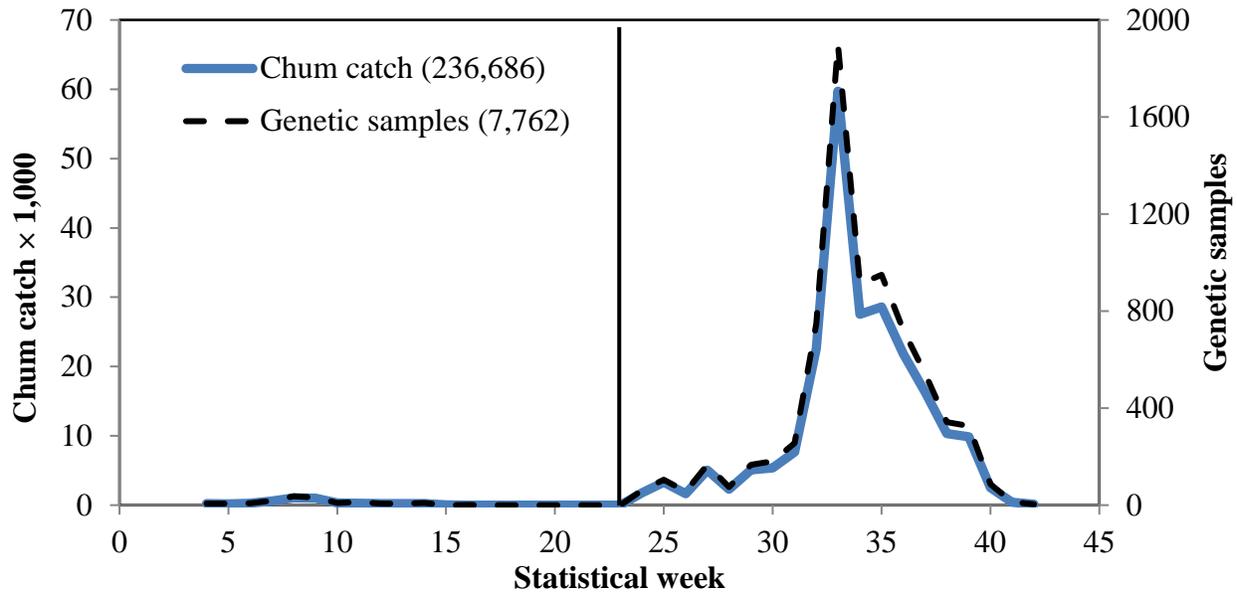
Figure 3. -- Number of Bering Sea chum salmon caught (solid line) and genetic samples collected (dashed line) from the 2015 Bering Sea pollock midwater trawl fishery by statistical week. Weeks 1-23 correspond to the A-season, whereas weeks 24-42 correspond to the B-season, the demarcation of which is a vertical line.
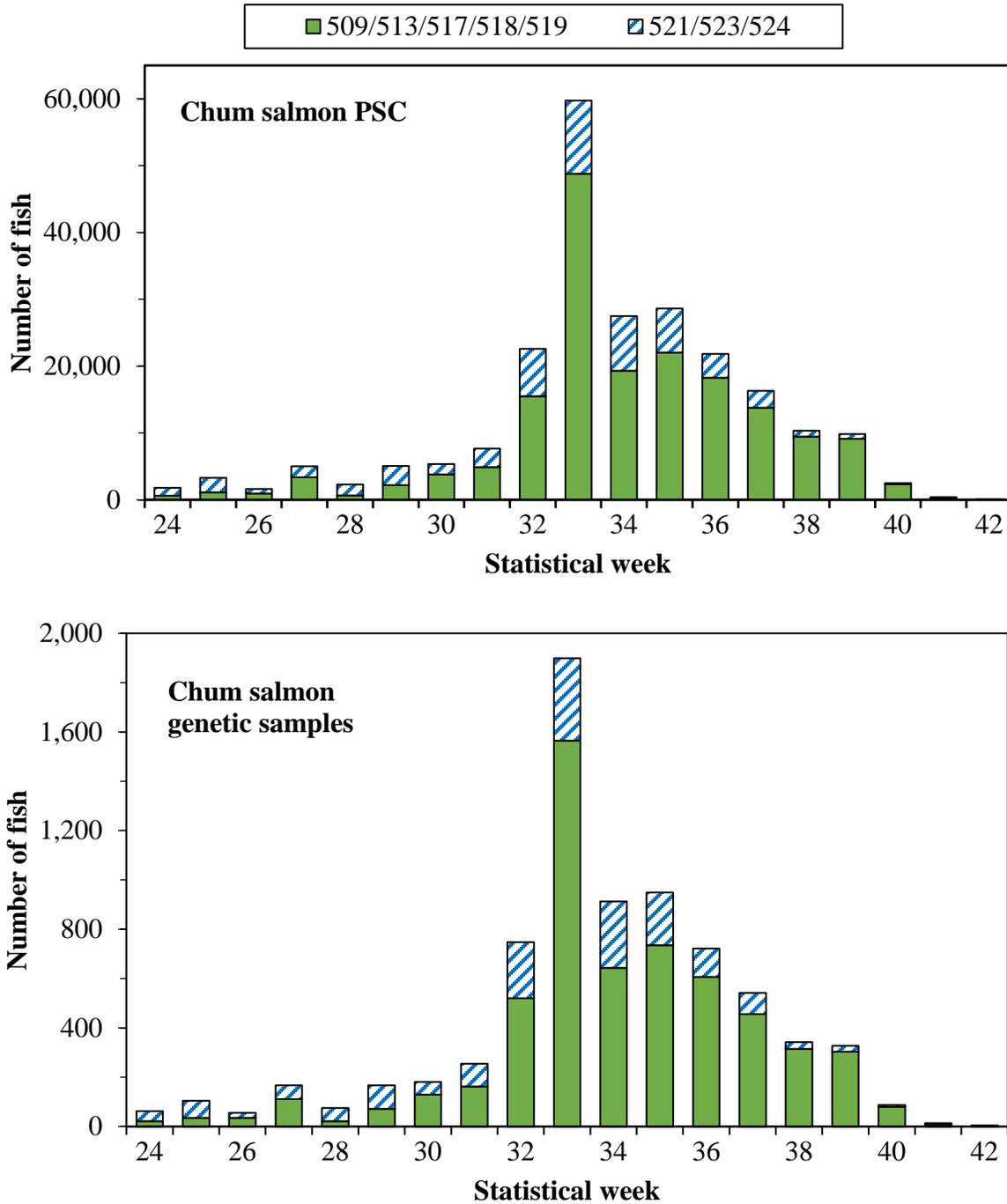
Figure 4. -- Number of Bering Sea chum salmon caught and genetic samples collected from the 2015 Bering Sea pollock B-season by statistical week and NMFS reporting area (designated in the legend).

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.

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 ± 5.3 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 100 vessels that participated in the midwater trawl fishery during the A and B-seasons caught chum salmon. On 43% of the vessels, the chum salmon catch was undersampled, but by only a small number – based on the systematic sampling protocol, only 128 fish (1.6% of expected) were not sampled. The ratio of genetic sampling did not differ between hauls and offloads (t-test; $P = 0.69$).
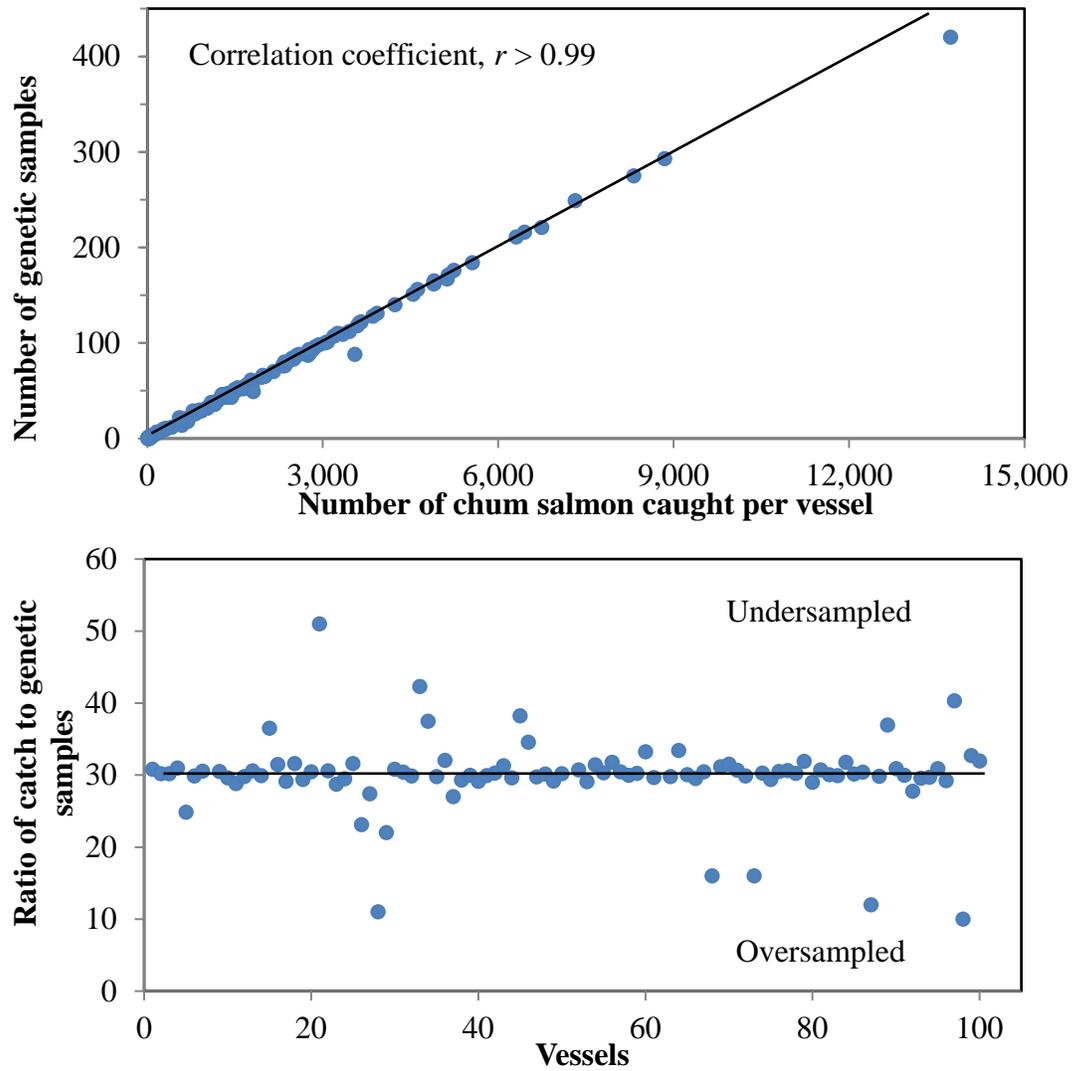
Figure 5. -- Bering Sea chum salmon catch and genetic samples from the 2015 Bering Sea pollock A and B-seasons. Number of genetic samples collected from the total number of chum salmon caught from each of 100 vessels; black diagonal line represents the expected sampling rate (top panel). The ratio of 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). Three vessels with 8, 23, and 30 chum salmon caught and zero fish sampled are not shown in bottom panel.

Gulf of Alaska

The estimated PSC of chum salmon in the GOA (NMFS 2016b) 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., Guthrie et al. 2016). However, in 2015, chum

salmon samples were collected in the GOA (AFSC 2014) primarily from the pollock trawl fishery, which caught about 45% of the chum salmon PSC in the GOA (Fig. 6). The chum salmon caught in the non-pollock fisheries between the B and C pollock seasons (weeks 23-34; Fig. 7), were spread nearly evenly across the halibut, rockfish, and sablefish fisheries, with a small remainder from the arrowtooth flounder fishery. This is the second year in a row that the number of chum salmon genetic samples collected from the GOA groundfish fisheries was large enough to run a mixed-stock analysis. Approximately 16% of the chum salmon caught in the pollock fisheries were collected for genetic samples, whereas less than 1% of chum salmon caught in other GOA groundfish fisheries were sampled. The available sample set included 145 samples from the pollock fishery from NMFS reporting areas 610, 620, and 630 during primarily the pollock C and D seasons[2], and 5 samples from other fisheries (Figs. 1, 7, 8).

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[2] 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.
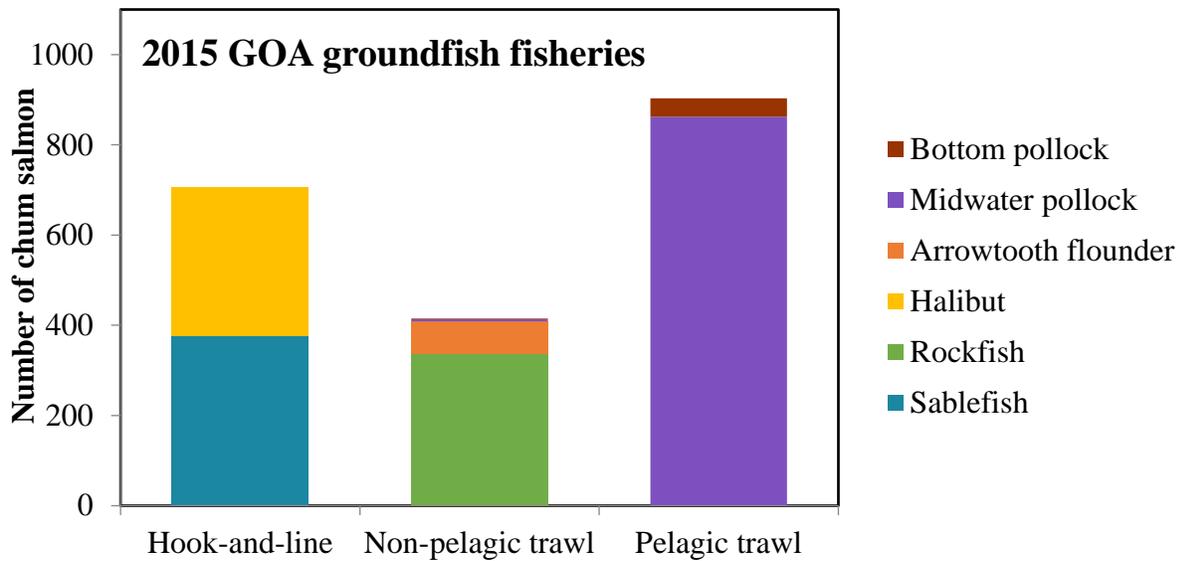
Figure 6. -- Estimated number of chum salmon caught (total of 2,032 fish) in the 2015 Gulf of Alaska groundfish fisheries by target species. The 7 chum salmon caught in the Pacific cod fishery are not shown.
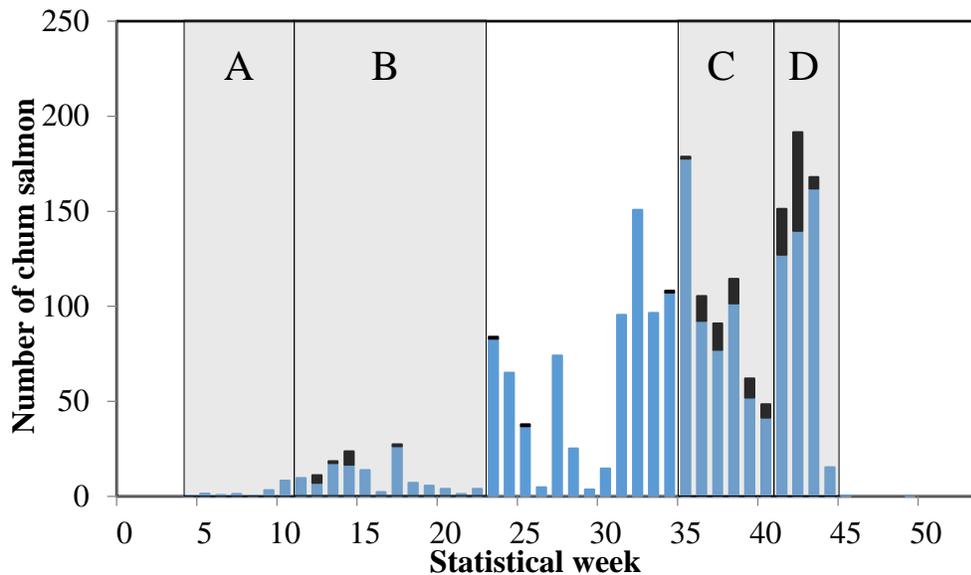
Figure 7. -- Number of chum salmon caught (blue plus black) and genetic samples collected (black) from the 2015 Gulf of Alaska groundfish fisheries by statistical week. Grayed areas with letter designations refer to NMFS management seasons for pollock in the Western and Central Regulatory Areas (NMFS reporting areas 610-630).
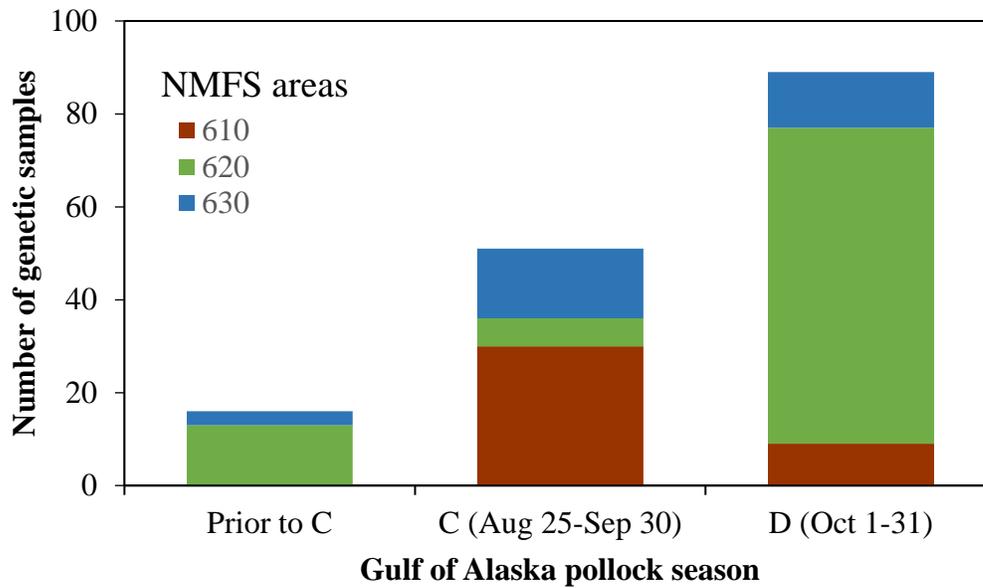
Figure 8. -- Number of chum salmon genetic samples collected from the 2015 Gulf of Alaska groundfish fisheries by pollock season and NMFS reporting areas.

Salmon Excluder Device Samples

Tests of salmon excluder devices were performed in 2015 northwest of Unimak Island in the catcher vessel operational area (CVOA) of the Bering Sea (Gauvin 2016; Fig. 9). The purpose of the 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. Five hauls in late August 2015 contained a relatively large number of chum salmon from which genetic samples were taken (Table 1). 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.

Table 1. -- Collection information for the five salmon excluder device collections of chum salmon caught in late summer 2015 and analyzed for genetic stock composition.

Vessel haul	N	Latitude (N)	Longitude (W)	Haul date
113	201	54.8917	165.3833	8/27/2015
115	74	54.8500	165.2767	8/30/2015
116	168	54.8850	165.2450	8/30/2015
117	56	54.8050	165.1283	8/30/2015
118	50	54.7300	165.1967	8/31/2015
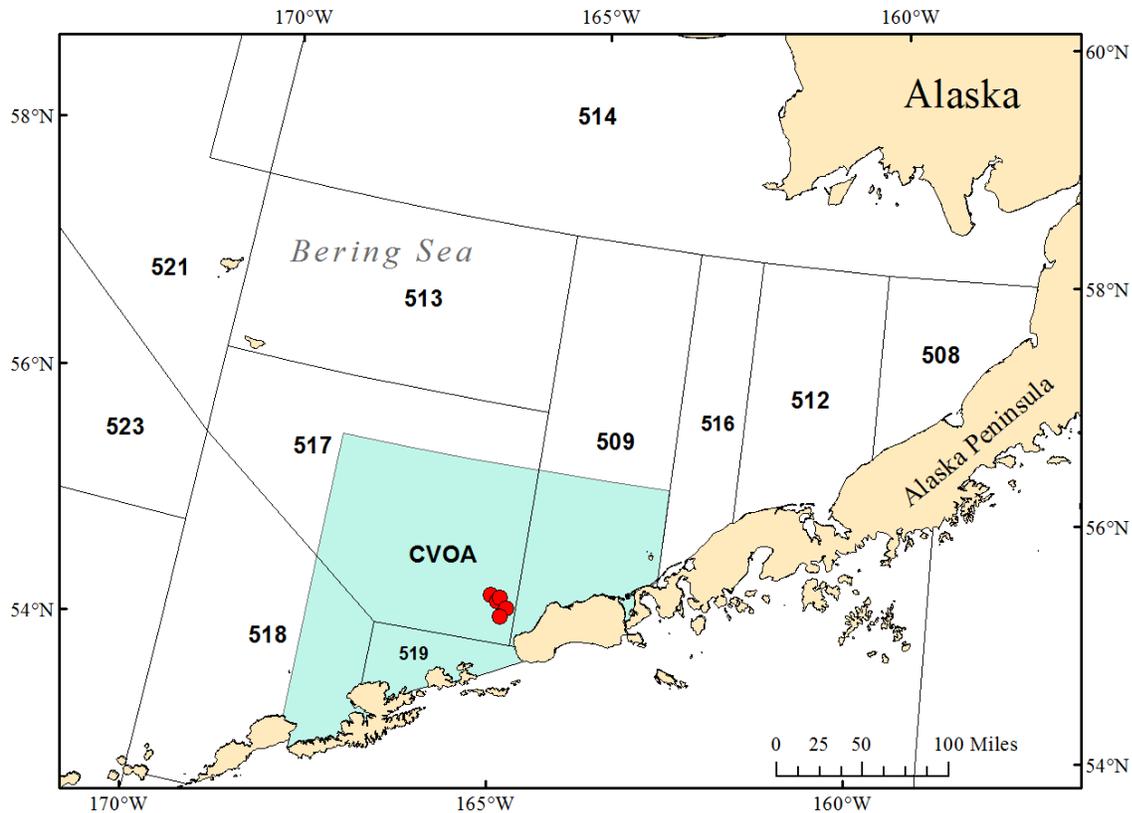
Figure 9. -- Locations of salmon excluder device test samples of chum salmon collected in late summer 2015 (red dots). Catcher vessel operation area (CVOA) is highlighted.

LABORATORY ANALYSES

Bering Sea: Fishery and Salmon Excluder Device Samples

Chum salmon samples from the B-season were subsampled in order to minimize laboratory costs while limiting potential bias of mixed-stock estimates. The total sample set of 7,612 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 1,892 chum salmon caught in the B-season and all of the 149 chum salmon sampled in the A-season. An additional 569 samples were selected for the 4-cluster analysis to increase the sample sizes in each time-area category to approximately 200 samples.

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 2,619 chum salmon bycatch samples and 559 excluder device samples analyzed from the Bering Sea, >97% were successfully genotyped for 8 or more of the 11 loci for an average of 10.9 loci (Table 2). With GenAlEx 6.5 (Peakall and Smouse 2006, 2012), no duplicate genotypes were detected in the Bering Sea bycatch samples and three were found in the excluder device samples from which one sample of each duplicate pair was 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 NMFS Observer sampling protocol (Table 3).

Table 2. -- Number of genetic samples genetically analyzed for chum salmon from the 2015
Bering Sea midwater pollock trawl fishery and salmon excluder test.

Number loci	Fishery	Excluder
11	2,436	534
10	79	14
9	16	3
8	18	1
< 8	70	7

Table 3. -- Observed number of samples (N) from the B-season and 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 40-42 were pooled to provide sample sizes > 4 in all time
categories.

Sample set	N	X^2	d.f.	P-value
Collected vs. expected	7,612	4.92	16	> 0.99
Genotyped vs. ¼ expected	1,892	3.95	16	> 0.99
Analyzed vs. ¼ expected	1,836	8.49	16	0.93

Quality control of sample handling and genotyping was examined by plating DNA from
the eight samples in the left-most column of each of 36 elution plates for a total of 288 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 4). Overall, the
genotyping error was low; across 11 loci there were a total of 23 differences in 5,750 alleles
between the original and quality control datasets, which represented an overall discrepancy rate
of 0.40%.

Table 4. -- Number of allele differences by locus between the original and quality control datasets for 2015 Bering Sea fishery and excluder samples with non-questionable genotypes.

Locus	Number alleles compared	Number allele differences	Percent difference
Oki100	524	3	0.57
Omm1070	528	2	0.38
Omy1011	532	2	0.38
One101	526	1	0.19
One102	532	2	0.38
One104	514	1	0.19
One114	512	1	0.20
Ots103	512	2	0.39
Ots3	534	6	1.12
OtsG68	512	2	0.39
Ssa419	524	1	0.19

Gulf of Alaska

DNA extraction and microsatellite genotyping was performed as described above. Of the 150 chum salmon samples analyzed, 10 samples amplified DNA from a species other than chum salmon and were excluded from further analysis. No duplicate genotypes were detected and 131 samples were successfully genotyped for 8 or more of the 11 loci, for an average of 10.9 loci (Table 5).

Table 5. -- Number of genetic samples genetically analyzed for chum salmon collected from the 2015 Gulf of Alaska groundfish fisheries.

Number loci	Number samples
11	121
10	6
9	1
8	3
< 8	9

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 two elution plates for a total of 16 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 there were a total of three differences in 306 alleles between the original and quality control datasets, which represented an overall discrepancy rate of 0.98%.

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. 10). 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.
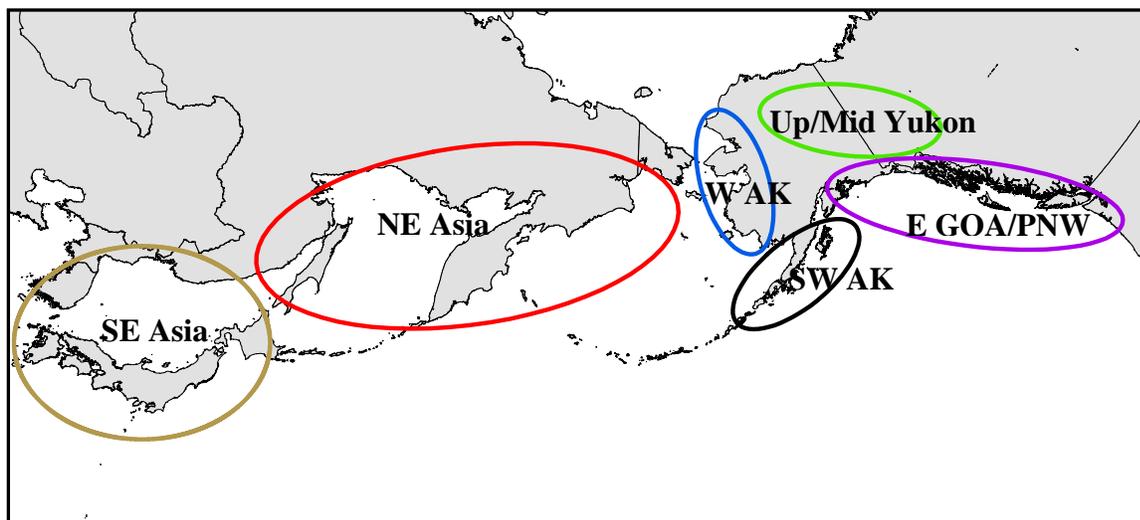
Figure 10. -- Six regional groups of baseline chum salmon populations used in this report were as follows: Southeast Asia, Northeast Asia, Western Alaska, Upper/Middle Yukon, Southwest Alaska, and the Eastern Gulf of Alaska/Pacific Northwest.

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, 2016; Vulstek et al. 2014; Whittle et al. 2015), the stock composition analysis for the 2015 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 (Table 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[3]. 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 1.00-1.01 (Table 6; Appendix II), 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 (2.5^{th} and 97.5^{th} 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 (Munro et al. 2012). The $P = 0$ statistic is the frequency of the 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. For example, the $P = 0$ value associated with the Southwest Alaska stock estimate from the A-season sample set (Table 6A) indicates that there is a 91% probability that essentially zero chum salmon from this stock were caught in this season.

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[3] 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.

Table 6. -- Regional stock composition estimates of chum salmon samples collected from 2015
trawl 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.

A. Bering Sea pollock trawl fishery, A-season, n = 142

Region	Mean	S.D.	2.5%	Median	97.5%	P = 0	Shrink
Southeast Asia	0.0318	0.0189	0.0051	0.0285	0.077	0.011	1.00
Northeast Asia	0.4096	0.0495	0.3138	0.4094	0.5062	0	1.00
Western Alaska	0.0633	0.0251	0.0213	0.0609	0.1186	0.001	1.00
Upper/Middle Yukon	0.0194	0.0149	0	0.0164	0.0557	0.174	1.00
Southwest Alaska	0.0056	0.0097	0	0.0009	0.0339	0.912	1.00
Eastern GOA/PNW	0.4703	0.0465	0.3802	0.4701	0.5618	0	1.00

B. Bering Sea pollock trawl fishery, B-season, n = 1,836

Region	Mean	S.D.	2.5%	Median	97.5%	P = 0	Shrink
Southeast Asia	0.0966	0.0075	0.0825	0.0964	0.1118	0	1.00
Northeast Asia	0.1746	0.0116	0.1522	0.1745	0.1978	0	1.00
Western Alaska	0.1596	0.0113	0.1380	0.1595	0.1824	0	1.00
Upper/Middle Yukon	0.0390	0.0071	0.0259	0.0387	0.0536	0	1.00
Southwest Alaska	0.0161	0.0051	0.0072	0.0158	0.0273	0	1.00
Eastern GOA/PNW	0.5141	0.0130	0.4888	0.5142	0.5395	0	1.00

C. Gulf of Alaska groundfish fisheries, n = 131

Region	Mean	S.D.	2.5%	Median	97.5%	P = 0	Shrink
Southeast Asia	0.0328	0.0168	0.0078	0.0303	0.072	0.030	1.00
Northeast Asia	0.0498	0.0289	0.0025	0.0465	0.1145	0.037	1.00
Western Alaska	0.0296	0.0197	0	0.0272	0.0745	0.149	1.00
Upper/Middle Yukon	0.0021	0.0050	0	0.0001	0.0168	1.000	1.00
Southwest Alaska	0.0040	0.0085	0	0.0003	0.0301	0.999	1.00
Eastern GOA/PNW	0.8818	0.0319	0.8139	0.8839	0.9372	0	1.00

D. Bering Sea salmon excluder device, n = 549

Region	Mean	S.D.	2.5%	Median	97.5%	P = 0	Shrink
Southeast Asia	0.0100	0.0052	0.0023	0.0092	0.0223	n/a	1.00
Northeast Asia	0.1358	0.0215	0.0954	0.1352	0.1797	n/a	1.00
Western Alaska	0.2356	0.0234	0.1910	0.2350	0.2831	n/a	1.00
Upper/Middle Yukon	0.0864	0.0161	0.0554	0.0861	0.1193	n/a	1.00
Southwest Alaska	0.0255	0.0146	0.0032	0.0236	0.0577	n/a	1.00
Eastern GOA/PNW	0.5066	0.0244	0.4583	0.5065	0.5547	n/a	1.00

COMPARISON WITH PREVIOUS ESTIMATES

Bering Sea

Stock compositions were estimated for the small sample set of chum salmon from the

A-season, but this was the first time since salmon PSC have been collected that the sample set

from the early season was large enough for genetic analysis; thus, there are no other years with

which to compare the 2015 stock compositions.

The stock composition results from the analysis of the 2015 chum salmon samples

collected during the B-season were notably different from past years, prior to and after

systematic sampling was in effect (Fig. 11, upper panel). For the first time since 2011, the

majority contribution came from Eastern GOA/PNW stocks, while in previous years Northeast

and Southeast Asia stocks generally dominated the regional contributions. 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 2005-2015 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, 2016; 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, 2005-2015

(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. 11, 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.
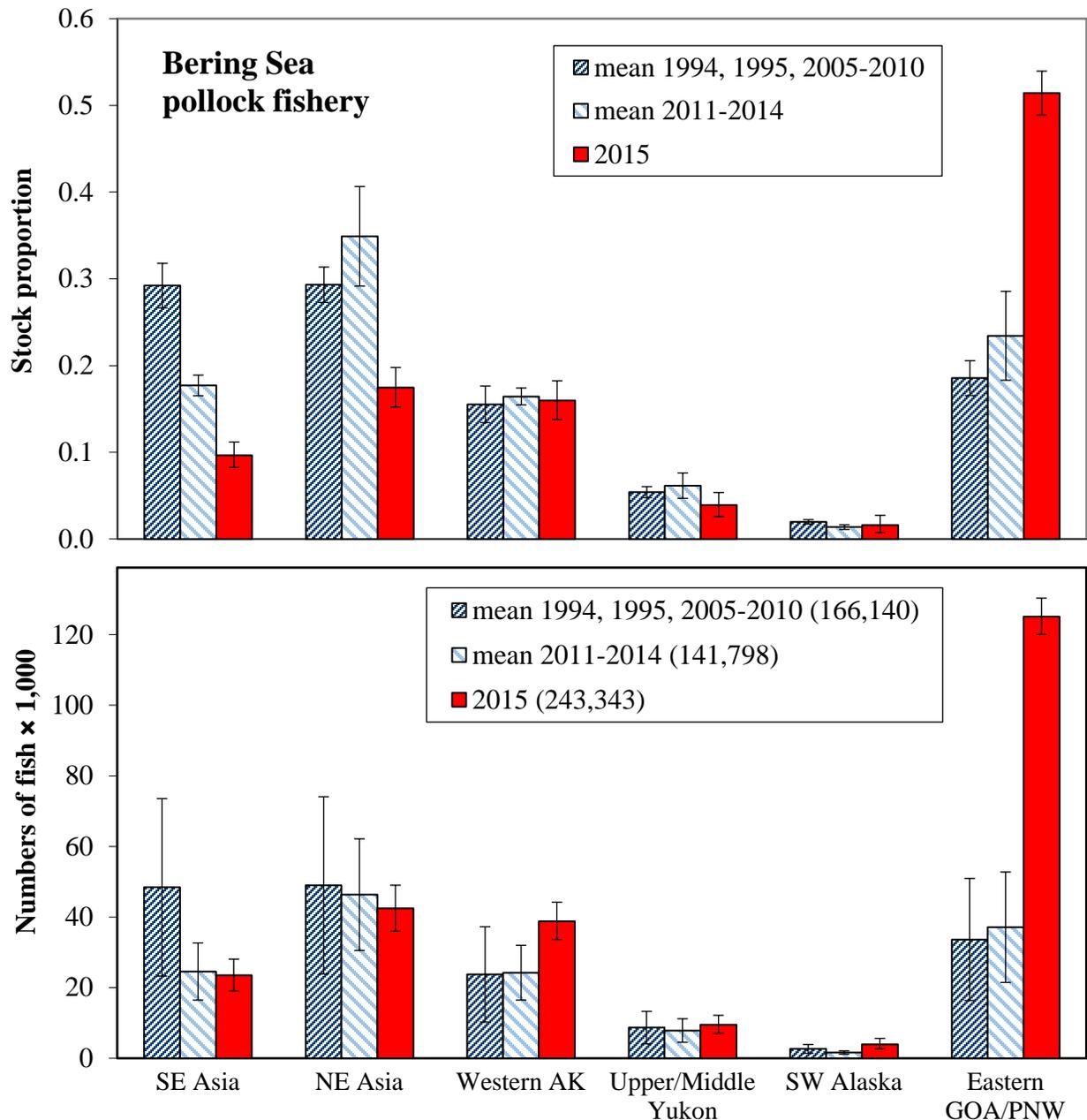
Figure 11. -- Comparison of the 2015 Bering Sea chum salmon stock composition estimates with the estimates from 2011 to 2014 (systematic sampling) and the unweighted mean estimates of available genetic samples from 1994, 1995, and 2005-2010 (non-systematic sampling). Proportions in top panel; numbers of fish in bottom panel, which for comparison purposes across years are based on the total chum salmon caught in all groundfish fisheries (NMFS 2016a). Standard errors of the mean estimates are shown for the combined years; 95% BAYES credible intervals are shown for the 2015 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 2011-2015 are censuses.

Gulf of Alaska

In 2015, for the second year in a row, samples from the PSC of chum salmon from the

GOA groundfish fisheries were available for genetic analysis. The stock composition estimates

of the 2015 GOA samples were nearly identical to the 2014 estimates, with nearly 90% of the

contribution from Eastern GOA/PNW stocks (Fig. 12). In both years, the contributions from all

other regions were 0-5%; chum salmon from the Upper/Middle Yukon and Southwest Alaska

regions were not present in the GOA samples in either year (0.71-1.00 "P = 0" values;

Appendix II).
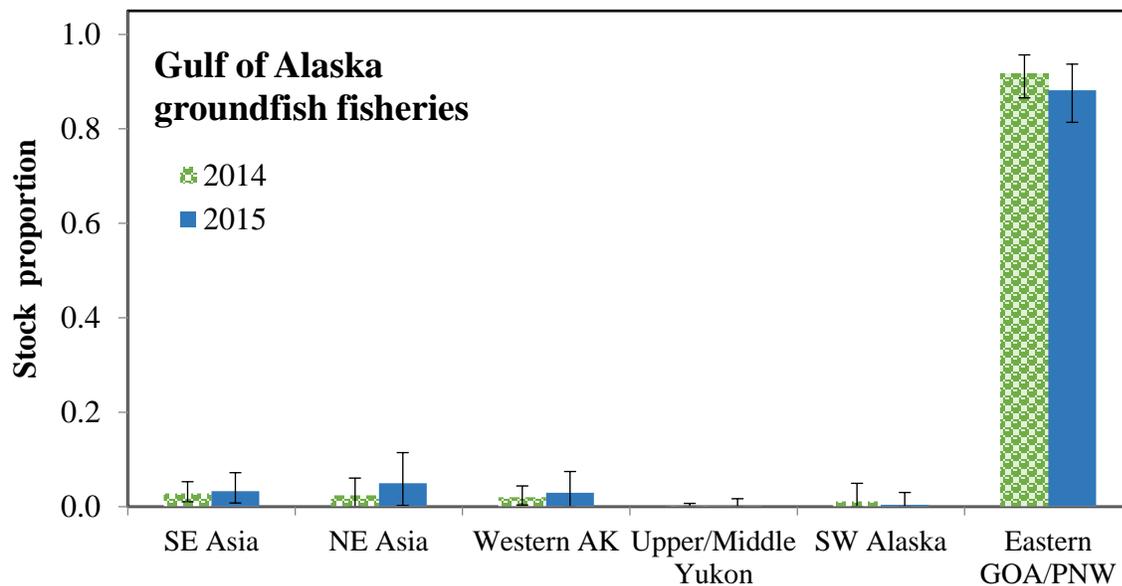
Figure 12. -- Stock composition estimates and 95% BAYES credible intervals for the 2014 and
2015 chum salmon genetic samples from the Gulf of Alaska groundfish fisheries.

Although comparisons of stock composition estimates of PSC with years prior to 2014

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 mid-August 2003 during an

extensive research survey that included the GOA (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, approximately 90% of the chum salmon caught in the 2014-2015 GOA groundfish fisheries were from Eastern GOA/PNW stocks and less than 5% 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, the Western Alaska Salmon Stock Identification Program (WASSIP)[4], focused in part on chum salmon caught in salmon fisheries south of the Alaska Peninsula (Munro et al. 2012; Templin et al. 2012). In the WASSIP, the salmon fishery[5] most proximate to the location of PSC chum salmon samples collected in the federal GOA groundfish fisheries was southwest of Kodiak Island. 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. Higher resolution of stock groupings of populations within the Eastern GOA/PNW region would be necessary to determine whether the high proportion of Eastern GOA/PNW stocks in the chum salmon PSC is a similar pattern to the interception of returning adults from local stocks in the July salmon fishery.

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[4] WASSIP is the largest salmon genetic stock identification study in history, analyzing stock composition of harvest in coastal Alaska fisheries from Kotzebue Sound to Chignik.
[5] Management of harvest of salmon caught in nearshore and offshore salmon fisheries is delegated to the state; Fishery Management Plan for the Salmon Fisheries in the EEZ off Alaska.

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.

Mixture analyses of samples from both the A and B-season provided an opportunity to compare stock contributions on the larger time scale of winter versus summer/fall. Although the dominant contribution from both seasons was from Eastern GOA/PNW stocks, there were significant differences in the stock contributions from other regions, particularly Northeast Asia and Western Alaska (Tables 6A,B).

As with the 2005-2014 analyses, the 2015 Bering Sea sample set from the B-season was temporally split into three 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).

Table 7. -- Temporal groups from the genetic sample sets of chum salmon caught in the 2015 Bering Sea, B-season pollock fishery.

Time period	Weeks	Dates	Number of samples
Early	24-29	10 June – 18 July	162
Middle	30-34	19 July – 22 August	959
Late	35-42	23 August – 17 October	715

The stock composition of chum salmon caught in the Bering Sea pollock fishery changed during the course of the season (Fig. 13). In 2015, genetic samples differed across the three time periods within three of the five regional groups. The contribution from Southeast Asia greatly decreased after the Early time period, and on the North American continent, the Western Alaska

contribution decreased across the B-season, whereas the Eastern GOA/PNW contribution in the Middle and Late time periods was more than four times higher than in the Early time period. The Northeast Asia and Upper/Middle Yukon contributions were each similar over the three time periods.

The averages of the 2005-2014 stock compositions for similar temporal strata are included for comparison purposes (Fig. 13). Some differences in the stock contributions by time period were observed between the 2015 and the 2005-2014 chum salmon samples. The contribution from Eastern GOA/PNW stocks during the Middle and Late time periods in 2015 was notably higher than in previous years. The contribution from Southeast Asia during the Early time period in 2015 was higher than the average of previous years. Both Asian regions had lower contributions in the Middle and Late periods than in previous years. The proportion of the chum salmon catch contributed by Western Alaska and Upper/Middle Yukon stocks was higher and lower, respectively, during the Early time period and similar to that observed in previous years during the Middle and Late time periods. 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.
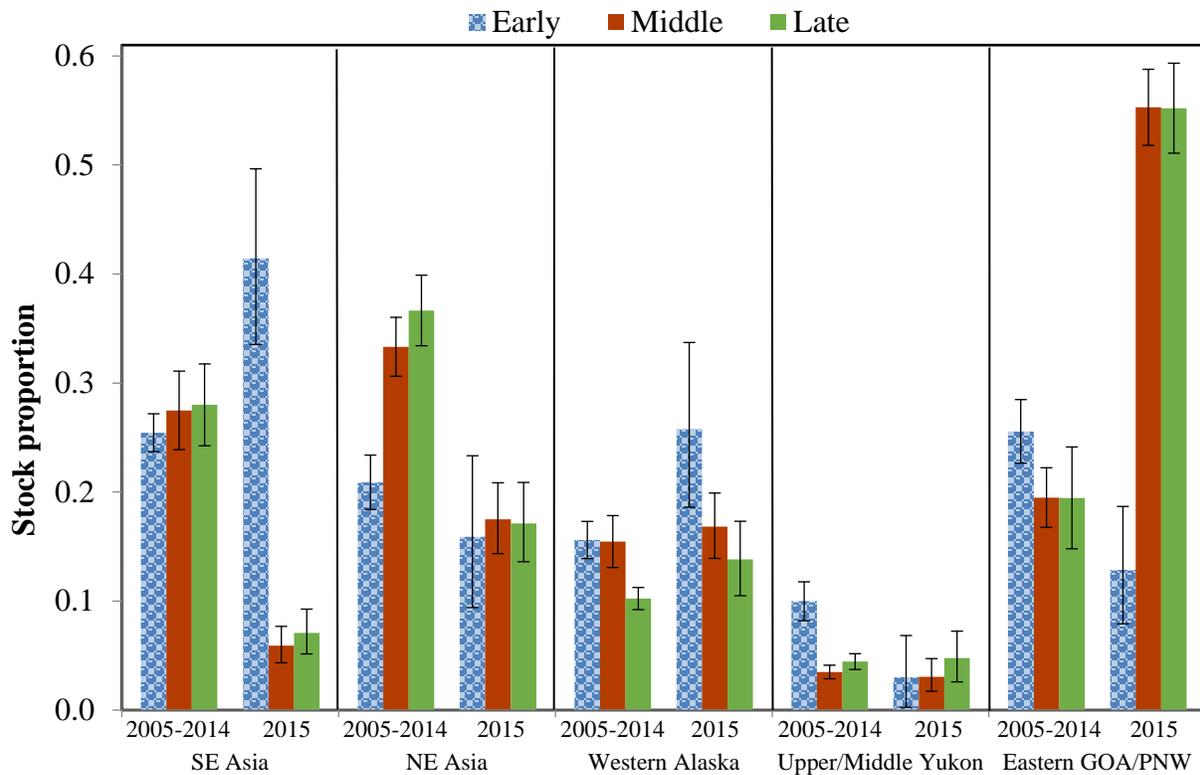
Figure 13. -- Stock composition estimates for the 2005-2014 (mean ± S.E.) and 2015 (± 95% BAYES credible intervals) chum salmon samples for the Early, Middle, and Late periods (defined in Table 7). Not shown is the Southwest Alaska region for which estimates never exceeded 5.6%.

SPATIAL STRATIFICATION

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. This section is limited to analyses of the Bering Sea fishery and salmon excluder device samples.

Bering Sea Fishery

In 2015, for the fifth year, the Observer Program undertook a complete census of chum salmon caught in the Bering Sea pollock trawl fisheries. About 75% 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 2015 Bering Sea genetic samples from the B-season were split 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, 517, 518, 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. 14; Appendix II). The contribution of stocks differed between the spatial strata in a manner similar to that observed in 2014, with the exception of the Northeast Asia region (Kondzela et al. 2016). To a greater extent than in 2014, the preponderance of contribution in the southeastern Bering Sea was from North American stocks, primarily from the Eastern GOA/PNW region. Over half of the contribution to the area west of 170°W was from Asian stocks, although this component was lower than that observed in 2014 (70%).
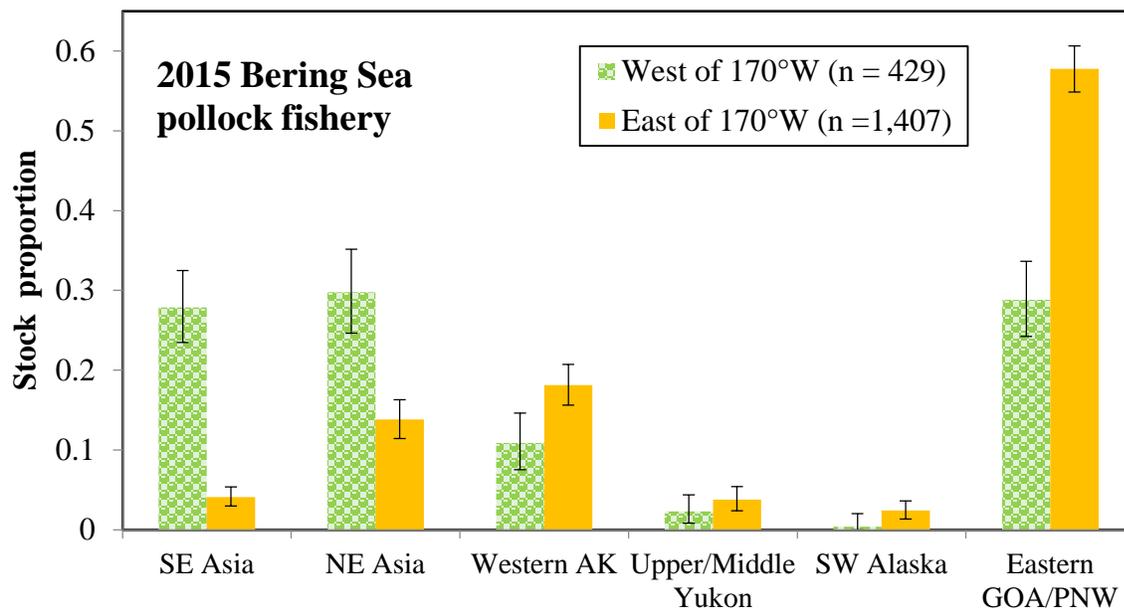
Figure 14. -- Stock composition estimates and 95% BAYES credible intervals for the 2015 chum salmon genetic samples from the U.S. waters of the Bering Sea west of 170°W (aggregate area 521/523/524) and the southeastern Bering Sea east of 170°W (aggregate area 509/513/517/518/519).

To better understand the chum salmon stock distribution across both time and space, the 2015 samples from areas 517 and 521 (Table 8) were compared across Early, Middle, and Late time periods. Samples from all other areas/time periods were not included due to small sample sizes.

Table 8. -- Spatial and temporal groups from the 2015 chum salmon genetic samples at three time periods (Table 7) for the reporting areas with the most samples.

Reporting area	Time period	Number of samples
517	Early	71
	Middle	698
	Late	593
521	Early	81
	Middle	235
	Late	107

Stock compositions were estimated for each spatial and temporal stratum as described above (Fig. 15; Appendix II). The major differences in regional stock contributions between area 517 and 521 mirror those observed in samples from east and west of 170°W (Fig. 14). Within each area some regional contributions varied across time. In area 517, Western Alaska stocks had the highest contribution during the Early time period, but decreased by more than half to a low level during the Middle and Late time periods. The reverse pattern was true for Eastern GOA/PNW stocks, which increased from a low contribution in the Early time period to more than triple the contribution of any other region in the Middle and Late time periods. In area 521, the Western Alaska stock contribution was very low after the Middle time period and the Eastern GOA/PNW stock contribution had a pattern similar, albeit less extreme, to that in area 517. The Southeast Asia stock contribution decreased after the Early time period in both areas. The Northeast Asia stock contribution was constant over time in area 517, but increased in area 521,

although the 95% credible intervals overlap. As in previous years, the contribution from

Upper/Middle Yukon and Southwest Alaska stocks was absent or very low in all time periods

and both areas. 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.
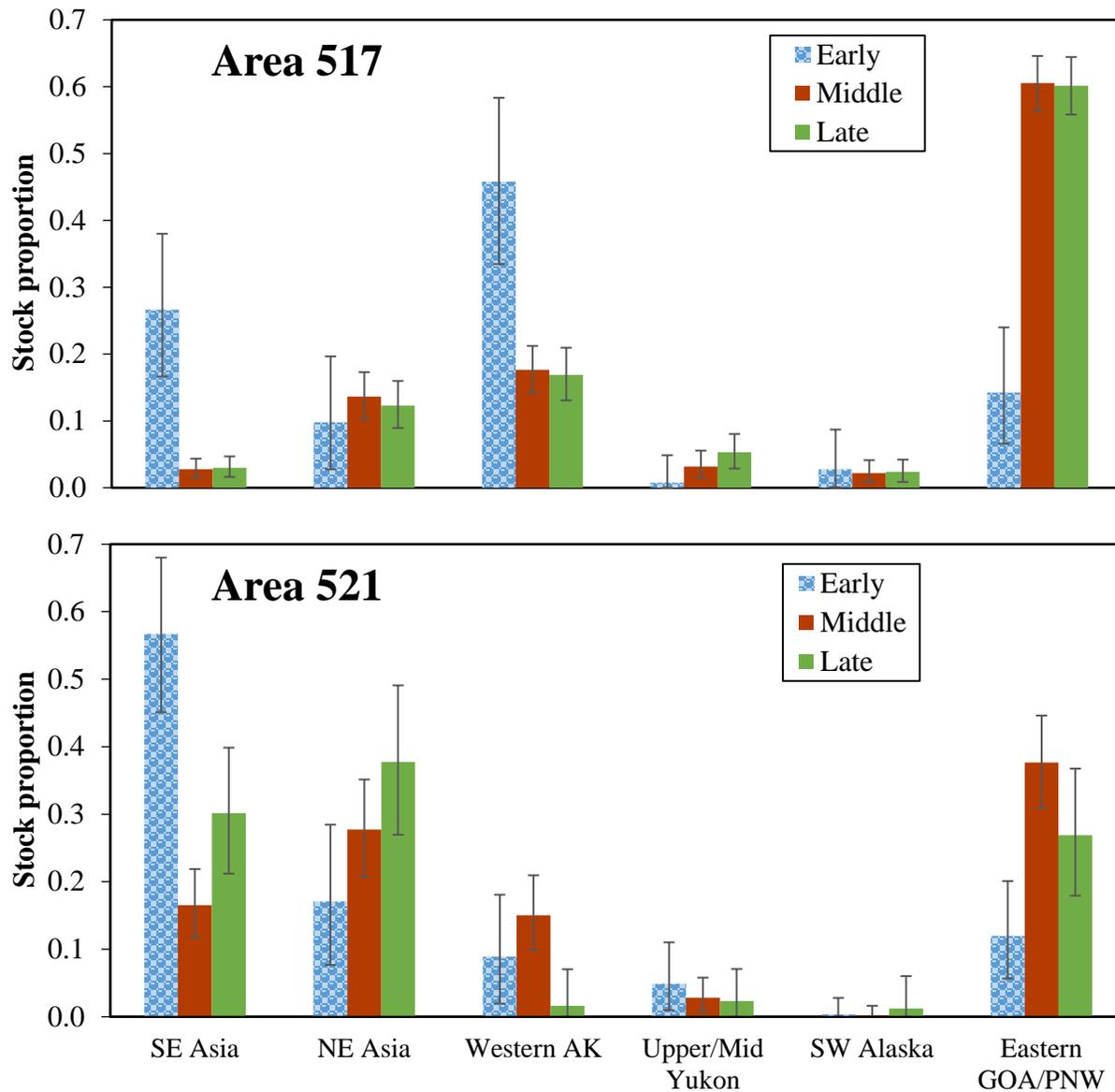
Figure 15. -- Stock composition estimates and 95% BAYES credible intervals for the 2015 chum salmon genetic samples from the NMFS reporting areas 517 and 521 for the Early, Middle, and Late time periods (Table 8).

In an effort to better understand the distribution of chum salmon stocks in the Bering Sea PSC from the pollock fishery at smaller spatial resolution than NMFS reporting areas, stock composition estimates were obtained from four clusters–based on ADF&G statistical areas–of chum salmon samples collected along the continental shelf edge during Early (statistical weeks 24-32) and Late (statistical weeks 33-42) time periods (Table 9; Appendix IV). There were some large differences in stock estimates along the continental shelf and over time (Fig. 16;

Appendix II). One of the most prominent differences was the higher proportion of Asian stocks

in the Early time period and the higher proportion of North American stocks in the Late time

period, especially from the Eastern GOA/PNW region. Another pattern of note was the higher

proportion of Asian stocks in the most northwestern samples (Cluster 4) in both time periods.

Table 9. -- Collection information for the four spatial clusters of chum salmon caught in two time periods, Early (weeks 24-32) and Late (weeks 33-42), during the 2015 B-season of the Bering Sea pollock fishery and analyzed for genetic stock composition.

Cluster	ADF&G areas	Time period	Samples received	Samples analyzed
1	635504-665530	Early	843	213
		Late	3,895	949
2	675500-685600	Early	190	186
		Late	286	195
3	695600-735630	Early	500	196
		Late	759	191
4	725730-785930	Early	245	197
		Late	461	190
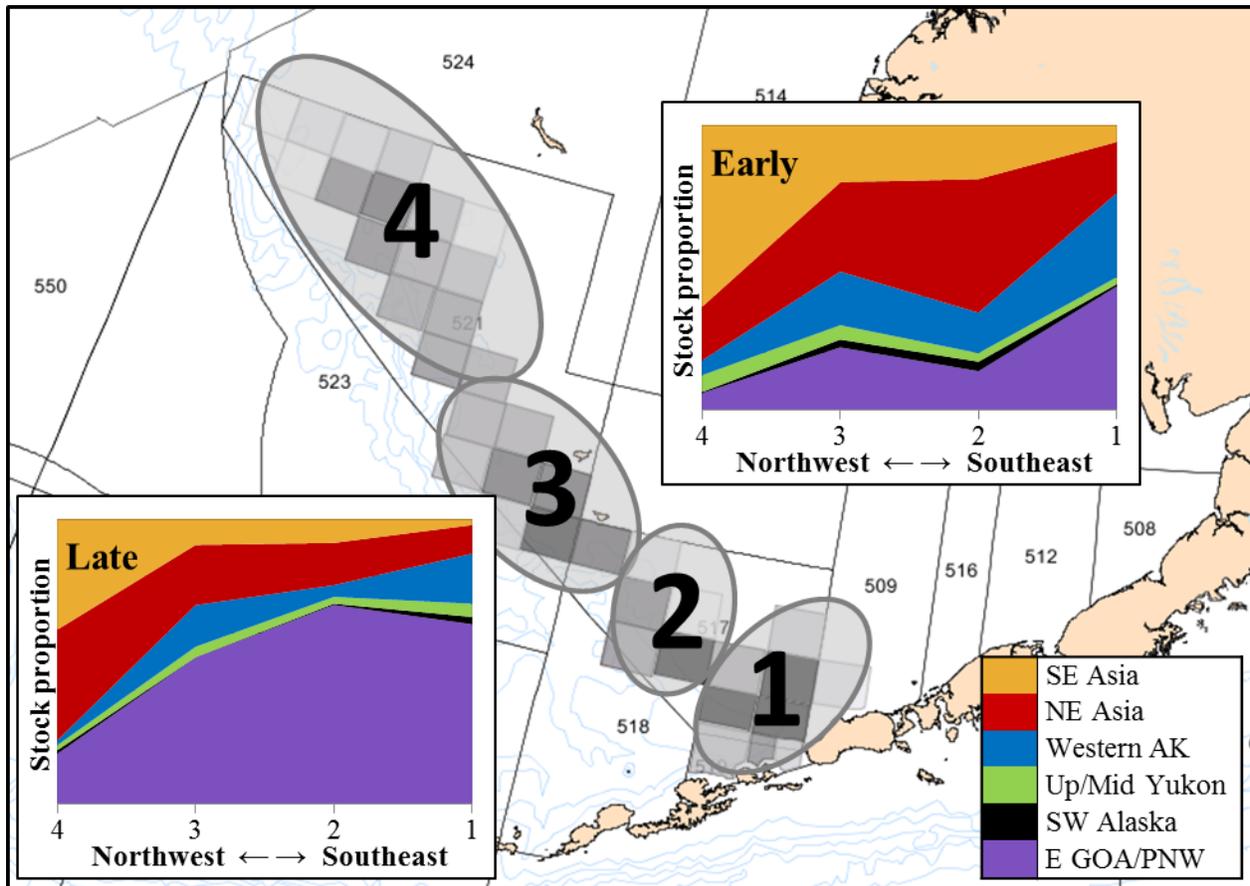
Figure 16. -- Stock composition estimates of chum salmon from four clusters of samples collected along the continental shelf edge during Early and Late time periods from the 2015 Bering Sea pollock fishery. ADF&G statistical areas are the gray squares within clusters. The Early time period is Weeks 24-32 and the Late time period is Weeks 33-42.

Salmon Excluder Device

Two of the five hauls from the salmon excluder device tests had large enough numbers of chum salmon (Table 1) to determine stock estimates for samples from each haul. Samples from proximate hauls provide a glimpse of the origin of chum salmon in the ocean on very fine spatial and temporal scales (3 days and < 9 km apart; Fig. 17; Appendix II). First, each haul contained a mix of fish from across the species geographic distribution, similar to the chum salmon PSC samples from the groundfish fisheries that are pooled across larger areas and time periods. For example, the stock compositions of the chum salmon from the excluder device hauls, which were collected in the

southeastern corner of area 517 during statistical weeks 35-36 (the Late time period), are similar to

those from the PSC collected at approximately the same time and location (green bars of Area 517 in

Fig. 15). Second, even at the small spatial and temporal scale of a single haul there were differences

in the stock contributions: the Upper/Middle Yukon contribution differed significantly between the

two hauls.
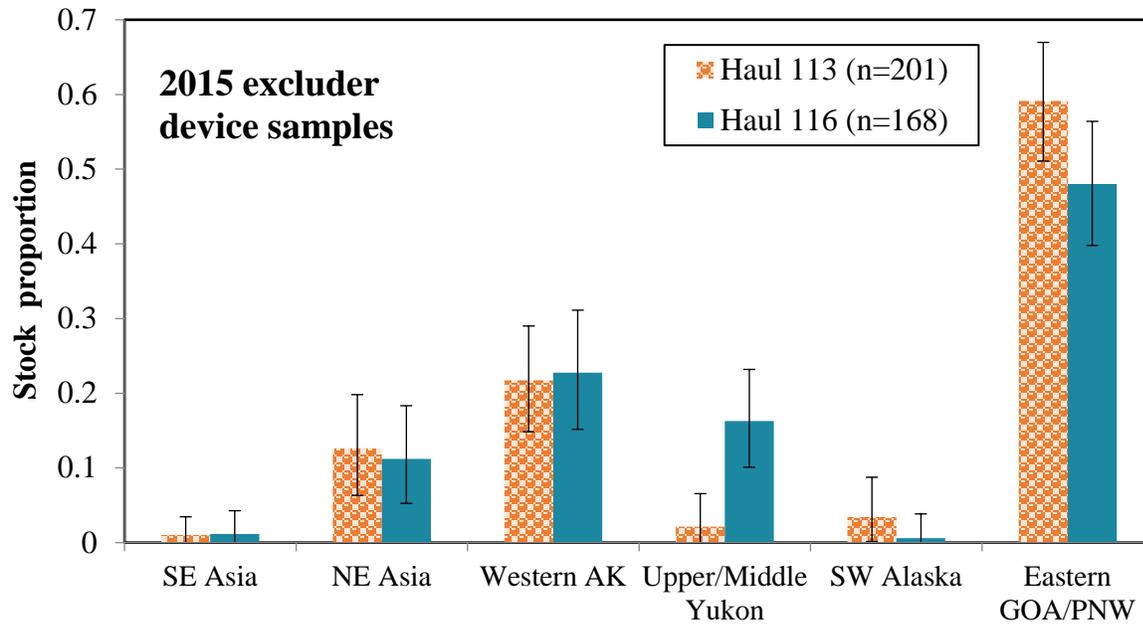
Figure 17. -- Stock composition estimates and 95% BAYES credible intervals for the 2015 chum
salmon genetic samples from Hauls 113 and 116 of the salmon excluder device tests
in the southeastern Bering Sea.

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 2015 chum salmon PSC based on 2,549 samples genotyped from the

Bering Sea, 131 samples genotyped from the GOA fisheries, and 549 samples genotyped from a

salmon excluder device test. The limitations and results of this analysis are summarized below and in Appendix II.

<div align="center">Sampling Issues</div>

Bering Sea

We highlight the reduced spatial and temporal biases in the Bering Sea 2015 sample set (Figs. 3 and 4) that were inherent in collections before 2011. Reduction of those biases improves the application of the 2015 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. This regulation led to the collection of representative samples from 98.4% of the chum salmon caught in this fishery for genetic analysis in 2015 (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 second year, a small sample set for genetic analysis. The distribution of chum salmon PSC samples collected is not representative of the

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[6] 75 FR 53026, August 30, 2010.
[7] Amendment 93 to the NPFMC fishery management plan for GOA groundfish (77 FR 42629, July 20, 2012).

groundfish fisheries as a whole. Most of the genetic samples (96%) were from the pollock trawl fishery, which in 2015 caught slightly less than half the chum salmon PSC in the GOA.

Stock Composition Estimates

Bering Sea

As in past years, only a very small portion of the total chum salmon PSC was caught during the A-season in 2015, but given the relatively high salmon bycatch in 2015, a small sample set was available for the first time for genetic analysis. Most of the samples (88%) were from Eastern GOA/PNW and Northeast Asia stocks (Table 6A).

About half of the genetic samples collected from chum salmon caught in the B-season 2015 Bering Sea pollock fishery were from Eastern GOA/PNW (51%) stocks and the other half of the samples were from approximately equal parts Asian and Alaska (western and southwest) stocks (Table 6B). This was the first year since 2011 that Eastern GOA/PNW stocks dominated the catch (see Fig. 8 in Whittle et al. 2015). Contribution from Upper/Middle Yukon stocks was similar to previous years, and the pattern of low contribution from Southwest Alaska continued in 2015 (Fig. 11). Although chum salmon samples in 2015 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.

Gulf of Alaska

As in 2014, a very different pattern of stock origin was observed in the 2015 GOA chum salmon PSC samples. Nearly 90% of the chum salmon sampled from the GOA groundfish fisheries were from Eastern GOA/PNW stocks (Table 6C). The remaining contributions from the other five regions were very low, 0-5%.

Salmon Excluder Device

Chum salmon samples collected in late-summer 2015 during tests of a salmon excluder device in the southeastern Bering Sea 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 6D), with stock composition similar to that of the overall 2015 Bering Sea chum salmon PSC samples–approximately half of the fish originated from Eastern GOA/PNW stocks (Appendix II). Chum salmon from individual hauls were a mix of stocks from Northeast Asia to the Eastern GOA/PNW and there were some differences in stock compositions between hauls (Fig. 17).

Temporal and Spatial Effects

The A-season stock compositions differed from those of the B-season primarily by a higher contribution from Northeast Asia stocks and lower contributions from Southeast Asia and Western Alaska stocks (Table 6A,B); differences in other regional estimates were minor. Whether the differences are due to the spatially contracted distribution of chum salmon PSC in the Bering Sea during the A-season or to seasonal differences is unknown.

The finer-scale 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 2015 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. 13). By time period, some differences were observed in the stock composition estimates of chum salmon PSC collected in 2015 and in previous years, notably for the Eastern GOA/PNW and Southeast Asia stocks. Other differences in stock composition estimates occurred during the Middle and Late time periods for Northeast

Asia stocks and during the Early time period for Western Alaska and Upper/Middle Yukon stocks.

Spatial analysis suggested that over half of the chum salmon from U.S. waters of the Bering Sea east of 170°W originated from Eastern GOA/PNW stocks. West of 170°W, the majority of chum salmon originated from nearly equal contributions of Southeast Asia, Northeast Asia, and Eastern GOA/PNW stocks (Fig. 14). The proportion of chum salmon from Asian stocks in the western area was higher than that in the southeastern Bering Sea, whereas the proportion of chum salmon from North America, particularly from Western Alaska and Eastern GOA/PNW stocks, were higher in the southeastern Bering Sea.

An examination of chum salmon stock estimates on both spatial and temporal strata of the Bering Sea pollock fishery during the B-season indicates that stocks are not randomly distributed (Figs. 13-16). Stocks from Asia dominate in the more northwestern areas of the fishery and stocks from North America, particularly from the Eastern GOA/PNW region, are more abundant later in 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.

ACKNOWLEDGMENTS

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APPENDICES

Appendix Table 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	DFO num.	Population name	Reg num.	Region
41	Abashiri	1	SE Asia	213	Kalininka	2	NE Asia
215	Avakumovka	1	SE Asia	225	Kamchatka	2	NE Asia
40	Chitose	1	SE Asia	219	Kanchalan	2	NE Asia
315	Gakko_River	1	SE Asia	379	Karaga	2	NE Asia
292	Hayatsuki	1	SE Asia	294	Kikchik	2	NE Asia
44	Horonai	1	SE Asia	209	Kol	2	NE Asia
252	Kawabukuro	1	SE Asia	233	Magadan	2	NE Asia
313	Koizumi_River	1	SE Asia	211	Naiba	2	NE Asia
300	Kushiro	1	SE Asia	295	Nerpichi	2	NE Asia
37	Miomote	1	SE Asia	381	Okhota	2	NE Asia
391	Namdae_R	1	SE Asia	212	Oklan	2	NE Asia
231	Narva	1	SE Asia	222	Ola	2	NE Asia
298	Nishibetsu	1	SE Asia	386	Olutorsky_Bay	2	NE Asia
293	Ohkawa	1	SE Asia	228	Ossora	2	NE Asia
297	Orikasa	1	SE Asia	224	Penzhina	2	NE Asia
214	Ryazanovka	1	SE Asia	385	Plotnikova_R	2	NE Asia
312	Sakari_River	1	SE Asia	221	Pymta	2	NE Asia
311	Shari_River	1	SE Asia	220	Tauy	2	NE Asia
36	Shibetsu	1	SE Asia	383	Tugur_River	2	NE Asia
299	Shikiu	1	SE Asia	226	Tym_	2	NE Asia
253	Shiriuchi	1	SE Asia	230	Udarnitsa	2	NE Asia
310	Shizunai	1	SE Asia	290	Utka_River	2	NE Asia
217	Suifen	1	SE Asia	208	Vorovskaya	2	NE Asia
35	Teshio	1	SE Asia	387	Zhypanova	2	NE Asia
39	Tokachi	1	SE Asia	348	Agiapuk	3	W Alaska
38	Tokoro	1	SE Asia	376	Alagnak	3	W Alaska
314	Tokushibetsu	1	SE Asia	3	Andreafsky	3	W Alaska
291	Toshibetsu	1	SE Asia	357	Aniak	3	W Alaska
296	Tsugaruishi	1	SE Asia	301	Anvik	3	W Alaska
316	Uono_River	1	SE Asia	80	Chulinak	3	W Alaska
309	Yurappu	1	SE Asia	347	Eldorado	3	W Alaska
218	Amur	2	NE Asia	358	George	3	W Alaska
207	Anadyr	2	NE Asia	307	Gisasa	3	W Alaska
384	Apuka_River	2	NE Asia	371	Goodnews	3	W Alaska
382	Bolshaya	2	NE Asia	288	Henshaw_Creek	3	W Alaska
380	Dranka	2	NE Asia	339	Imnachuk	3	W Alaska
223	Hairusova	2	NE Asia	361	Kanektok	3	W Alaska
378	Ivashka	2	NE Asia	362	Kasigluk	3	W Alaska

DFO num.	Population name	Reg num.	Region	DFO num.	Population name	Reg num.	Region
328	Kelly_Lake	3	W Alaska	6	Pelly	4	U/M Yukon
340	Kobuk	3	W Alaska	439	Porcupine	4	U/M Yukon
343	Koyuk	3	W Alaska	83	Salcha	4	U/M Yukon
363	Kwethluk	3	W Alaska	4	Sheenjek	4	U/M Yukon
336	Kwiniuk_River	3	W Alaska	1	Tatchun	4	U/M Yukon
303	Melozitna	3	W Alaska	9	Teslin	4	U/M Yukon
373	Mulchatna	3	W Alaska	84	Toklat	4	U/M Yukon
372	Naknek	3	W Alaska	360	Alagoshak	5	SW Alaska
330	Niukluk	3	W Alaska	333	American_River	5	SW Alaska
329	Noatak	3	W Alaska	366	Big_River	5	SW Alaska
345	Nome	3	W Alaska	354	Coleman_Creek	5	SW Alaska
302	Nulato	3	W Alaska	355	Delta_Creek	5	SW Alaska
374	Nunsatuk	3	W Alaska	359	Egegik	5	SW Alaska
13	Peel_River	3	W Alaska	332	Frosty_Creek	5	SW Alaska
322	Pikmiktalik	3	W Alaska	365	Gertrude_Creek	5	SW Alaska
331	Pilgrim_River	3	W Alaska	370	Joshua_Green	5	SW Alaska
346	Shaktoolik	3	W Alaska	364	Meshik	5	SW Alaska
341	Snake	3	W Alaska	283	Moller_Bay	5	SW Alaska
368	Stuyahok_River	3	W Alaska	369	Pumice_Creek	5	SW Alaska
375	Togiak	3	W Alaska	367	Stepovak_Bay	5	SW Alaska
154	Tozitna	3	W Alaska	335	Sturgeon	5	SW Alaska
342	Unalakleet	3	W Alaska	350	Uganik	5	SW Alaska
344	Ungalik	3	W Alaska	334	Volcano_Bay	5	SW Alaska
8	Big_Creek	4	U/M Yukon	356	Westward_Creek	5	SW Alaska
89	Big_Salt	4	U/M Yukon	239	Ahnuhati	6	E GOA/PNW
86	Black_River	4	U/M Yukon	69	Ahta	6	E GOA/PNW
87	Chandalar	4	U/M Yukon	155	Ain	6	E GOA/PNW
28	Chandindu	4	U/M Yukon	183	Algard	6	E GOA/PNW
82	Cheena	4	U/M Yukon	58	Alouette	6	E GOA/PNW
81	Delta	4	U/M Yukon	325	Alouette_North	6	E GOA/PNW
7	Donjek	4	U/M Yukon	270	Andesite_Cr	6	E GOA/PNW
5	Fishing_Br	4	U/M Yukon	428	Arnoup_Cr	6	E GOA/PNW
88	Jim_River	4	U/M Yukon	153	Ashlulm	6	E GOA/PNW
85	Kantishna	4	U/M Yukon	156	Awun	6	E GOA/PNW
2	Kluane	4	U/M Yukon	133	Bag_Harbour	6	E GOA/PNW
59	Kluane_Lake	4	U/M Yukon	164	Barnard	6	E GOA/PNW
181	Koyukuk_late	4	U/M Yukon	16	Bella_Bell	6	E GOA/PNW
90	Koyukuk_south	4	U/M Yukon	79	Bella_Coola	6	E GOA/PNW
10	Minto	4	U/M Yukon	49	Big_Qual	6	E GOA/PNW

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

DFO num.	Population name	Reg num.	Region	DFO num.	Population name	Reg num.	Region
152	Inch_Creek	6	E GOA/PNW	50	Little_Qua	6	E GOA/PNW
146	Indian_River	6	E GOA/PNW	413	Lizard_Cr	6	E GOA/PNW
92	Jenny_Bay	6	E GOA/PNW	119	Lockhart-Gordon	6	E GOA/PNW
115	Kainet_River	6	E GOA/PNW	176	Lower_Lillooet	6	E GOA/PNW
144	Kakweiken	6	E GOA/PNW	137	Mace_Creek	6	E GOA/PNW
268	Kalum	6	E GOA/PNW	242	Mackenzie_Sound	6	E GOA/PNW
395	Kanaka_Cr	6	E GOA/PNW	116	MacNair_Creek	6	E GOA/PNW
402	Kano_Inlet_Cr	6	E GOA/PNW	55	Mamquam	6	E GOA/PNW
162	Kateen	6	E GOA/PNW	121	Markle_Inlet_Cr	6	E GOA/PNW
389	Kawkawa	6	E GOA/PNW	27	Martin_Riv	6	E GOA/PNW
95	Kemano	6	E GOA/PNW	338	Mashiter_Creek	6	E GOA/PNW
192	Kennedy_Creek	6	E GOA/PNW	109	McLoughin_Cr	6	E GOA/PNW
238	Kennell	6	E GOA/PNW	178	Milton	6	E GOA/PNW
351	Keta_Creek	6	E GOA/PNW	194	Minter_Cr	6	E GOA/PNW
101	Khutze_River	6	E GOA/PNW	254	Mountain_Cr	6	E GOA/PNW
126	Khutzeymateen	6	E GOA/PNW	111	Mussel_River	6	E GOA/PNW
282	Kiltuish	6	E GOA/PNW	157	Naden	6	E GOA/PNW
93	Kimsquit	6	E GOA/PNW	337	Nahmint_River	6	E GOA/PNW
187	Kimsquit_Bay	6	E GOA/PNW	444	Nakut_Su	6	E GOA/PNW
419	Kincolith	6	E GOA/PNW	14	Nanaimo	6	E GOA/PNW
273	Kispiox	6	E GOA/PNW	122	Nangeese	6	E GOA/PNW
106	Kitasoo	6	E GOA/PNW	422	Nass_River	6	E GOA/PNW
99	Kitimat_River	6	E GOA/PNW	399	Necleetsconnay	6	E GOA/PNW
275	Kitsault_Riv	6	E GOA/PNW	113	Neekas_Creek	6	E GOA/PNW
163	Kitwanga	6	E GOA/PNW	321	Neets_Bay_early	6	E GOA/PNW
271	Kleanza_Cr	6	E GOA/PNW	320	Neets_Bay_late	6	E GOA/PNW
437	Klewnuggit_Cr	6	E GOA/PNW	173	Nekite	6	E GOA/PNW
21	Klinaklini	6	E GOA/PNW	104	Nias_Creek	6	E GOA/PNW
418	Ksedin	6	E GOA/PNW	143	Nimpkish	6	E GOA/PNW
125	Kshwan	6	E GOA/PNW	53	Nitinat	6	E GOA/PNW
423	Kumealon	6	E GOA/PNW	191	Nooksack	6	E GOA/PNW
112	Kwakusdis_River	6	E GOA/PNW	186	Nooseseck	6	E GOA/PNW
436	Kxngeal_Cr	6	E GOA/PNW	318	NorrishWorth	6	E GOA/PNW
127	Lachmach	6	E GOA/PNW	159	North_Arm	6	E GOA/PNW
262	Lagins	6	E GOA/PNW	377	Olsen_Creek	6	E GOA/PNW
131	Lagoon_Inlet	6	E GOA/PNW	184	Orford	6	E GOA/PNW
448	LagoonCr	6	E GOA/PNW	287	Pa-aat_River	6	E GOA/PNW
167	Lard	6	E GOA/PNW	260	Pacofi	6	E GOA/PNW
160	Little_Goose	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	324	Surprise	6	E GOA/PNW
48	Puntledge	6	E GOA/PNW	75	Taaltz	6	E GOA/PNW
98	Quaal_River	6	E GOA/PNW	30	Taku	6	E GOA/PNW
147	Quap	6	E GOA/PNW	18	Takwahoni	6	E GOA/PNW
108	Quartcha_Creek	6	E GOA/PNW	251	Tarundl_Creek	6	E GOA/PNW
199	Quinault	6	E GOA/PNW	149	Theodosia	6	E GOA/PNW
110	Roscoe_Creek	6	E GOA/PNW	22	Thorsen	6	E GOA/PNW
397	Salmon_Bay	6	E GOA/PNW	129	Toon	6	E GOA/PNW
195	Salmon_Cr	6	E GOA/PNW	279	Tseax	6	E GOA/PNW
134	Salmon_River	6	E GOA/PNW	202	Tulalip	6	E GOA/PNW
200	Satsop	6	E GOA/PNW	97	Turn_Creek	6	E GOA/PNW
236	Sawmill	6	E GOA/PNW	430	Turtle_Cr	6	E GOA/PNW
410	Seal_Inlet_Cr	6	E GOA/PNW	247	Tuskwa	6	E GOA/PNW
158	Security	6	E GOA/PNW	165	Tyler	6	E GOA/PNW
130	Sedgewick	6	E GOA/PNW	33	Tzoonie	6	E GOA/PNW
393	Serpentine_R	6	E GOA/PNW	124	Upper_Kitsumkal	6	E GOA/PNW
317	Shovelnose_Cr	6	E GOA/PNW	140	Vedder	6	E GOA/PNW
249	Shustnini	6	E GOA/PNW	70	Viner_Sound	6	E GOA/PNW
206	Siberia_Creek	6	E GOA/PNW	45	Wahleach	6	E GOA/PNW
25	Silverdale	6	E GOA/PNW	172	Walkum	6	E GOA/PNW
196	Skagit	6	E GOA/PNW	73	Waump	6	E GOA/PNW
274	Skeena	6	E GOA/PNW	232	Wells_Bridge	6	E GOA/PNW
171	Skowquiltz	6	E GOA/PNW	352	Wells_River	6	E GOA/PNW
447	SkykomishRiv	6	E GOA/PNW	105	West_Arm_Creek	6	E GOA/PNW
132	Slatechuck_Cre	6	E GOA/PNW	267	Whitebottom_Cr	6	E GOA/PNW
43	Sliammon	6	E GOA/PNW	326	Widgeon_Slough	6	E GOA/PNW
15	Smith_Cree	6	E GOA/PNW	277	Wilauks_Cr	6	E GOA/PNW
54	Snootli	6	E GOA/PNW	120	Wilson_Creek	6	E GOA/PNW
180	Southgate	6	E GOA/PNW	401	Worth_Creek	6	E GOA/PNW
26	Squakum	6	E GOA/PNW	60	Wortley_Creek	6	E GOA/PNW
142	Squamish	6	E GOA/PNW	248	Yellow_Bluff	6	E GOA/PNW
128	Stagoo	6	E GOA/PNW	434	Zymagotitz	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				

Appendix II. -- Regional stock composition estimates of chum salmon samples from the 2015
Bering Sea (BS) midwater pollock trawl fishery and the Gulf of Alaska (GOA)
groundfish fisheries. Estimated number of prohibited species catch (PSC),
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; Munro et al. 2012), and the Gelman-Rubin shrink factor
are reported. For each stratum, 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 35-42.
For the analyses of four clusters, the Early time period is Weeks 24-32 and the
Late time period is Weeks 33-42.

BS A-season sample set (PSC = 4,467, n = 142)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink factor
SE Asia	148	0.032	0.019	0.005	0.029	0.077	0.011	1.00
NE Asia	1,903	0.410	0.050	0.314	0.409	0.506	0	1.00
W Alaska	294	0.063	0.025	0.021	0.061	0.119	0.001	1.00
Up/Mid Yukon	90	0.019	0.015	0	0.016	0.056	0.174	1.00
SW Alaska	26	0.006	0.010	0	0.001	0.034	0.912	1.00
E GOA/PNW	2,185	0.470	0.047	0.380	0.470	0.562	0	1.00

BS B-season sample set (PSC = 232,039, n = 1,836)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink factor
SE Asia	22,415	0.097	0.008	0.083	0.096	0.112	0	1.00
NE Asia	40,514	0.175	0.012	0.152	0.175	0.198	0	1.00
W Alaska	37,033	0.160	0.011	0.138	0.160	0.182	0	1.00
Up/Mid Yukon	9,050	0.039	0.007	0	0.039	0.054	0	1.00
SW Alaska	3,736	0.016	0.005	0	0.016	0.027	0	1.00
E GOA/PNW	119,291	0.514	0.013	0.489	0.514	0.540	0	1.00

BS Early season sample set (PSC = 19,138, n = 162)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink factor
SE Asia	7,929	0.414	0.041	0.335	0.414	0.497	0	1.00
NE Asia	3,041	0.159	0.036	0.094	0.158	0.233	0	1.00
W Alaska	4,932	0.258	0.039	0.186	0.256	0.337	0	1.00
Up/Mid Yukon	576	0.030	0.017	0	0.028	0.068	0.017	1.00
SW Alaska	201	0.011	0.010	0	0.008	0.038	0.231	1.00
E GOA/PNW	2,459	0.129	0.028	0.079	0.127	0.187	0	1.00

Appendix II – Continued.

BS Middle season sample set (PSC = 122,880, n = 959)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	7,274	0.059	0.009	0.043	0.059	0.077	0	1.00
NE Asia	21,516	0.175	0.017	0.144	0.175	0.209	0	1.00
W Alaska	20,681	0.168	0.015	0.139	0.168	0.199	0	1.00
Up/Mid Yukon	3,760	0.031	0.008	0	0.030	0.047	0	1.00
SW Alaska	1,683	0.014	0.005	0	0.013	0.026	0	1.00
E GOA/PNW	67,953	0.553	0.018	0.518	0.553	0.588	0	1.00

BS Late season sample set (PSC = 90,021, n = 715)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	6,382	0.071	0.011	0.052	0.070	0.093	0	1.00
NE Asia	15,421	0.171	0.019	0.136	0.171	0.209	0	1.00
W Alaska	12,432	0.138	0.018	0.105	0.138	0.173	0	1.00
Up/Mid Yukon	4,303	0.048	0.012	0	0.047	0.072	0	1.00
SW Alaska	1,764	0.020	0.008	0	0.019	0.037	0.001	1.00
E GOA/PNW	49,710	0.552	0.021	0.511	0.552	0.593	0	1.00

BS east of 170°W sample set, areas 509, 513, 517, 518, 519 (PSC = 176.886, n = 1,407)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	7,235	0.041	0.006	0.030	0.041	0.054	0	1.00
NE Asia	24,428	0.138	0.012	0.115	0.138	0.163	0	1.00
W Alaska	32,069	0.181	0.013	0.156	0.181	0.207	0	1.00
Up/Mid Yukon	6,686	0.038	0.008	0	0.038	0.054	0	1.00
SW Alaska	4,281	0.024	0.006	0	0.024	0.036	0	1.00
E GOA/PNW	102,187	0.578	0.015	0.549	0.578	0.607	0	1.00

BS west of 170°W sample set, areas 521, 523, 524 (PSC = 55,153, n = 429)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	15,377	0.279	0.023	0.235	0.279	0.325	0	1.00
NE Asia	16,414	0.298	0.027	0.246	0.297	0.351	0	1.00
W Alaska	5,995	0.109	0.018	0.075	0.108	0.146	0	1.00
Up/Mid Yukon	1,263	0.023	0.009	0	0.022	0.044	0	1.00
SW Alaska	221	0.004	0.006	0	0.001	0.020	0.601	1.00
E GOA/PNW	15,884	0.288	0.024	0.242	0.288	0.337	0	1.00

Appendix II – Continued.

BS area 517 sample set (PSC = 172,641, n = 1,362)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	7,406	0.043	0.006	0.032	0.043	0.056	0	1.00
NE Asia	23,410	0.136	0.013	0.112	0.135	0.161	0	1.00
W Alaska	31,611	0.183	0.013	0.157	0.183	0.210	0	1.00
Up/Mid Yukon	6,474	0.038	0.008	0	0.037	0.054	0	1.00
SW Alaska	4,109	0.024	0.006	0	0.024	0.036	0	1.00
E GOA/PNW	99,631	0.577	0.015	0.548	0.577	0.607	0	1.00

BS area 517 Early season sample set (PSC = 8,388, n = 71)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	2,235	0.266	0.055	0.166	0.264	0.380	0	1.00
NE Asia	824	0.098	0.044	0.028	0.093	0.197	0	1.00
W Alaska	3,839	0.458	0.064	0.335	0.457	0.583	0	1.00
Up/Mid Yukon	63	0.008	0.014	0	0.001	0.049	0.732	1.00
SW Alaska	232	0.028	0.023	0	0.022	0.087	0.055	1.00
E GOA/PNW	1,196	0.143	0.045	0.066	0.139	0.240	0	1.00

BS area 517 Middle season sample set (PSC = 90,438, n = 698)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	2,505	0.028	0.007	0.015	0.027	0.044	0	1.00
NE Asia	12,345	0.137	0.018	0.103	0.136	0.173	0	1.00
W Alaska	15,962	0.177	0.018	0.142	0.176	0.212	0	1.00
Up/Mid Yukon	2,885	0.032	0.010	0	0.031	0.056	0	1.00
SW Alaska	1,999	0.022	0.009	0	0.021	0.041	0	1.00
E GOA/PNW	54,742	0.605	0.021	0.564	0.605	0.646	0	1.00

BS area 517 Late season sample set (PSC = 73,815, n = 593)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	2,207	0.030	0.008	0.016	0.029	0.047	0	1.00
NE Asia	9,094	0.123	0.018	0.089	0.123	0.160	0	1.00
W Alaska	12,467	0.169	0.020	0.131	0.169	0.210	0	1.00
Up/Mid Yukon	3,920	0.053	0.013	0	0.053	0.080	0	1.00
SW Alaska	1,735	0.024	0.009	0	0.023	0.042	0	1.00
E GOA/PNW	44,400	0.602	0.022	0.558	0.602	0.644	0	1.00

Appendix II – Continued.

BS area 521 sample set (PSC = 54,442 , n = 423)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	15,206	0.279	0.023	0.235	0.279	0.326	0	1.00
NE Asia	16,153	0.297	0.027	0.245	0.296	0.351	0	1.00
W Alaska	5,836	0.107	0.019	0.073	0.106	0.146	0	1.00
Up/Mid Yukon	1,100	0.020	0.009	0	0.019	0.041	0	1.00
SW Alaska	223	0.004	0.006	0	0.001	0.021	0.592	1.00
E GOA/PNW	15,924	0.293	0.024	0.246	0.292	0.341	0	1.00

BS area 521 Early season sample set (PSC = 9,619, n = 81)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	5,457	0.567	0.059	0.451	0.568	0.680	0	1.00
NE Asia	1,647	0.171	0.053	0.077	0.168	0.285	0	1.00
W Alaska	857	0.089	0.042	0.020	0.086	0.181	0.002	1.00
Up/Mid Yukon	471	0.049	0.026	0	0.045	0.110	0.001	1.00
SW Alaska	33	0.003	0.009	0	0.000	0.028	0.935	1.00
E GOA/PNW	1,154	0.120	0.037	0.057	0.117	0.201	0	1.00

BS area 521 Middle season sample set (PSC = 30,340, n = 235)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	5,015	0.165	0.026	0.118	0.165	0.219	0	1.00
NE Asia	8,419	0.278	0.037	0.208	0.277	0.352	0	1.00
W Alaska	4,563	0.150	0.028	0.099	0.149	0.210	0	1.00
Up/Mid Yukon	850	0.028	0.013	0	0.026	0.058	0	1.00
SW Alaska	67	0.002	0.005	0	0.000	0.016	0.905	1.00
E GOA/PNW	11,426	0.377	0.035	0.309	0.376	0.446	0	1.00

BS area 521 Late season sample set (PSC = 14,483, n = 107)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	4,370	0.302	0.047	0.212	0.301	0.399	0	1.00
NE Asia	5,467	0.378	0.057	0.270	0.377	0.491	0	1.00
W Alaska	235	0.016	0.020	0.000	0.009	0.070	0.321	1.00
Up/Mid Yukon	339	0.023	0.020	0	0.020	0.071	0.135	1.00
SW Alaska	180	0.012	0.018	0	0.004	0.060	0.469	1.00
E GOA/PNW	3,894	0.269	0.048	0.179	0.267	0.368	0	1.00

Appendix II – Continued.

Cluster 1 Early sample set (PSC = 25,417, n = 213)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	1,472	0.058	0.018	0.028	0.056	0.097	0	1.00
NE Asia	4,562	0.180	0.032	0.120	0.178	0.246	0	1.00
W Alaska	7,511	0.296	0.036	0.226	0.295	0.368	0	1.00
Up/Mid Yukon	613	0.024	0.016	0	0.021	0.064	0.028	1.00
SW Alaska	206	0.008	0.010	0	0.004	0.036	0.444	1.00
E GOA/PNW	11,054	0.435	0.037	0.363	0.435	0.508	0	1.00

Cluster 1 Late sample set (PSC = 118,231, n = 949)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	2,376	0.020	0.005	0.011	0.020	0.031	0	1.00
NE Asia	11,835	0.100	0.014	0.075	0.100	0.128	0	1.00
W Alaska	20,797	0.176	0.016	0.146	0.176	0.207	0	1.00
Up/Mid Yukon	5,533	0.047	0.010	0	0.046	0.068	0	1.00
SW Alaska	3,015	0.026	0.008	0	0.025	0.041	0	1.00
E GOA/PNW	74,675	0.632	0.018	0.597	0.632	0.666	0	1.00

Cluster 2 Early sample set (PSC = 5,712, n = 186)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	1,076	0.188	0.032	0.129	0.187	0.254	0	1.00
NE Asia	2,681	0.469	0.045	0.381	0.469	0.557	0	1.00
W Alaska	812	0.142	0.031	0.085	0.141	0.207	0	1.00
Up/Mid Yukon	170	0.030	0.015	0	0.028	0.065	0.003	1.00
SW Alaska	191	0.033	0.019	0	0.031	0.076	0.008	1.00
E GOA/PNW	783	0.137	0.030	0.083	0.135	0.200	0	1.00

Cluster 2 Late sample set (PSC = 8,701, n = 195)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	718	0.083	0.022	0.044	0.081	0.131	0	1.00
NE Asia	1,291	0.148	0.034	0.087	0.147	0.219	0	1.00
W Alaska	358	0.041	0.021	0.007	0.039	0.090	0.004	1.00
Up/Mid Yukon	210	0.024	0.013	0	0.023	0.053	0.024	1.00
SW Alaska	39	0.005	0.008	0	0.001	0.029	0.874	1.00
E GOA/PNW	6,085	0.699	0.036	0.627	0.700	0.768	0	1.00

Appendix II – Continued.

Cluster 3 Early sample set (PSC = 15,273, n = 196)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	3,056	0.200	0.030	0.144	0.199	0.263	0	1.00
NE Asia	4,780	0.313	0.043	0.231	0.312	0.400	0	1.00
W Alaska	2,877	0.188	0.039	0.116	0.187	0.269	0	1.00
Up/Mid Yukon	768	0.050	0.023	0	0.048	0.102	0	1.00
SW Alaska	418	0.027	0.017	0	0.025	0.067	0.020	1.00
E GOA/PNW	3,371	0.221	0.034	0.158	0.220	0.290	0	1.00

Cluster 3 Late sample set (PSC = 24,251, n = 191)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	2,178	0.090	0.023	0.050	0.088	0.139	0	1.00
NE Asia	5,124	0.211	0.039	0.140	0.210	0.292	0	1.01
W Alaska	3,548	0.146	0.032	0.088	0.145	0.212	0	1.00
Up/Mid Yukon	888	0.037	0.019	0	0.034	0.082	0.003	1.01
SW Alaska	36	0.002	0.004	0	0.000	0.012	0.980	1.00
E GOA/PNW	12,472	0.514	0.040	0.435	0.514	0.593	0	1.01

Cluster 4 Early sample set (PSC = 7,374, n = 197)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	4,700	0.637	0.037	0.564	0.638	0.709	0	1.00
NE Asia	1,386	0.188	0.035	0.124	0.187	0.259	0	1.00
W Alaska	383	0.052	0.023	0.012	0.050	0.102	0.001	1.00
Up/Mid Yukon	434	0.059	0.021	0	0.057	0.106	0	1.00
SW Alaska	32	0.004	0.008	0	0.001	0.027	0.913	1.00
E GOA/PNW	439	0.060	0.019	0.028	0.058	0.102	0	1.00

Cluster 4 Late sample set (PSC = 14,343, n = 190)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	5,556	0.387	0.039	0.313	0.387	0.464	0	1.00
NE Asia	5,581	0.389	0.045	0.304	0.388	0.479	0	1.00
W Alaska	235	0.016	0.015	0.000	0.013	0.053	0.166	1.00
Up/Mid Yukon	257	0.018	0.012	0	0.016	0.047	0.027	1.00
SW Alaska	178	0.012	0.012	0	0.009	0.044	0.255	1.00
E GOA/PNW	2,536	0.177	0.032	0.117	0.176	0.243	0	1.00

Appendix II – Continued.

BS salmon excluder test device, total sample set (n = 549)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	5	0.010	0.005	0.002	0.009	0.022	n/a	1.00
NE Asia	75	0.136	0.022	0.095	0.135	0.180	n/a	1.00
W Alaska	129	0.236	0.023	0.191	0.235	0.283	n/a	1.00
Up/Mid Yukon	47	0.086	0.016	0.055	0.086	0.119	n/a	1.00
SW Alaska	14	0.026	0.015	0.003	0.024	0.058	n/a	1.00
E GOA/PNW	278	0.507	0.024	0.458	0.507	0.555	n/a	1.00

BS salmon excluder test device, Haul 113 (n = 201)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	2	0.010	0.010	0	0.008	0.035	n/a	1.00
NE Asia	25	0.126	0.035	0.063	0.124	0.198	n/a	1.01
W Alaska	44	0.217	0.036	0.149	0.217	0.290	n/a	1.00
Up/Mid Yukon	4	0.021	0.019	0	0.018	0.066	n/a	1.00
SW Alaska	7	0.034	0.023	0.002	0.030	0.088	n/a	1.00
E GOA/PNW	119	0.591	0.041	0.511	0.592	0.670	n/a	1.00

BS salmon excluder test device, Haul 116 (n = 168)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	2	0.012	0.012	0	0.008	0.043	n/a	1.00
NE Asia	19	0.112	0.034	0.053	0.110	0.183	n/a	1.00
W Alaska	38	0.228	0.041	0.152	0.226	0.311	n/a	1.00
Up/Mid Yukon	27	0.163	0.034	0.101	0.161	0.232	n/a	1.00
SW Alaska	1	0.006	0.011	0	0.001	0.038	n/a	1.01
E GOA/PNW	81	0.480	0.043	0.398	0.480	0.564	n/a	1.00

GOA Total sample set (PSC = 1,823 , n = 131)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P = 0	Shrink factor
SE Asia	60	0.033	0.017	0.008	0.030	0.072	0.030	1.00
NE Asia	91	0.050	0.029	0.003	0.047	0.115	0	1.00
W Alaska	54	0.030	0.020	0.000	0.027	0.075	0.149	1.00
Up/Mid Yukon	4	0.002	0.005	0	0.000	0.017	1.000	1.00
SW Alaska	7	0.004	0.009	0	0.000	0.030	0.999	1.00
E GOA/PNW	1,608	0.882	0.032	0.814	0.884	0.937	0	1.00

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.

Appendix IV. -- [ADF&G groundfish statistical areas](http://www.adfg.alaska.gov/index.cfm?adfg=fishingCommercialByFishery.statmaps)
(http://www.adfg.alaska.gov/index.cfm?adfg=fishingCommercialByFishery.statmaps) of chum salmon PSC collected from the 2015 Bering Sea midwater pollock trawl fishery and analyzed for genetic stock composition by four spatial clusters.

Cluster 1: 625531, 635504, 635530, 645501, 645530, 655409, 655410, 655430, 655500, 655530, 665335, 665401, 665403, 665430, 665500, 665530

Cluster 2: 675500, 675530, 685500, 685530, 685600, 695530

Cluster 3: 695600, 695631, 705600, 705630, 715600, 715630, 715700, 715730, 725630, 725700, 735630

Cluster 4: 725730, 725800, 735700, 735730, 735800, 735830, 735900, 745800, 745830, 745900, 745930, 755830, 755900, 755930, 765830, 765900, 765930, 766000, 775900, 775930, 776000, 785930

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