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ABSTRACT

A genetic analysis of the prohibited species catch (PSC) of chum salmon (*Oncorhynchus keta*) collected during 2016 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. Samples were genotyped for 11 microsatellite markers from which stock contributions were estimated using the current chum salmon microsatellite baseline. In 2016, one genetic sample was collected for every 30.6 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 majority of the 114 chum salmon samples from the A-season were from Northeast Asia (37%) and Eastern GOA/Pacific Northwest (PNW) (37%) stocks. Based on the analysis of 2,701 chum salmon collected throughout the B-season, the largest stock groups in the catch were Eastern GOA/PNW (35%) and Northeast Asia (31%), followed by Western Alaska (19%), Southeast Asia (9%), Upper/Middle Yukon (5%), and Southwest Alaska (< 2%) stocks. The chum salmon caught in the Bering Sea in 2016 shared general patterns of stock distribution with those from past years, but differed by some finer-scale spatiotemporal strata. Of the 473 chum salmon samples from the GOA groundfish fisheries, the highest proportion was from Eastern GOA/PNW (93%) stocks, similar to previous years.

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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 2017a,b) 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 2016 from the U.S. Bering Sea walleye pollock (*Gadus chalcogrammus*) trawl fishery and the GOA groundfish fisheries. In the Bering Sea, the pollock fishery accounted for more than 98.8% of the total chum salmon taken in the groundfish fisheries (NMFS 2017). In the GOA, the majority (56%) of the chum salmon were caught in the pollock trawl fishery, with the remainder caught in other groundfish fisheries (NMFS 2016).

The National Marine Fisheries Service (NMFS) reporting areas associated with the groundfish fisheries are shown in Figure 1 and are presented later to describe the spatial distribution of the chum salmon catch and genetic samples. The data reporting tool, Alaska Fisheries Information Network (AKFIN[1]), developed by the Pacific States Marine Fisheries Commission (PSMFC) 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

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[1] AKFIN website

ADF&G groundfish statistical areas (Fig. 1). The AKFIN reports were used to construct spatial-temporal sets of genetic samples along the outer continental shelf from the 2016 chum salmon PSC.
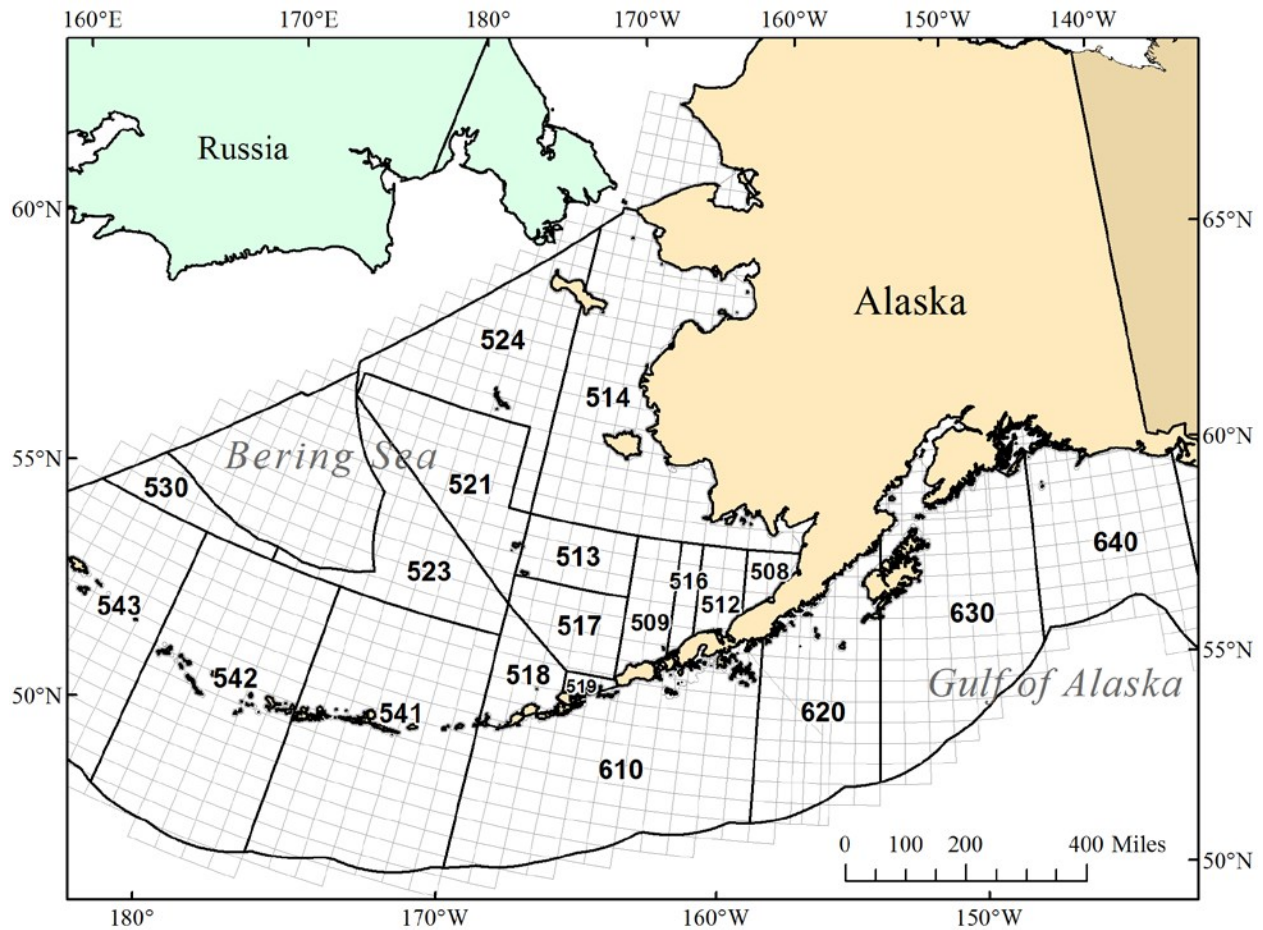
Figure 1. -- NMFS reporting areas associated with the Bering Sea-Aleutian Island and Gulf of Alaska groundfish fisheries are numbered and outlined in black. The ADF&G groundfish statistical areas are outlined in light gray.

For additional background and methods, this report is intended to be supplemented with the chum salmon reports prepared previously for the 2005-2015 Bering Sea trawl fisheries (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010, 2011a,b; Kondzela et al. 2012, 2013, 2016, 2017; 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 2016 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.

In 2016, an estimated 343,001 non-Chinook salmon (referred to hereafter as "chum salmon" because 99.9% of the non-Chinook salmon were chum salmon) were caught in the pollock-directed trawl fisheries and represent the third largest catch of chum salmon in the pollock fisheries since 1994 (NMFS 2017). This catch is substantially larger than the 1994-2015 average of 144,113 chum salmon and more than four times the median of 79,009 (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 3,726 chum salmon, 1% of the total Bering Sea chum salmon PSC, were caught. Of the chum salmon caught in the 2016 pollock trawl fishery, genetic samples were collected from 11,219 fish (NMFS 2016), which represents a sampling rate of 1 of every 30.6 chum salmon (or 3.3% of the chum salmon catch). This sampling rate is nearly identical to that in 2011-2015, the first 5 years of representative sampling.
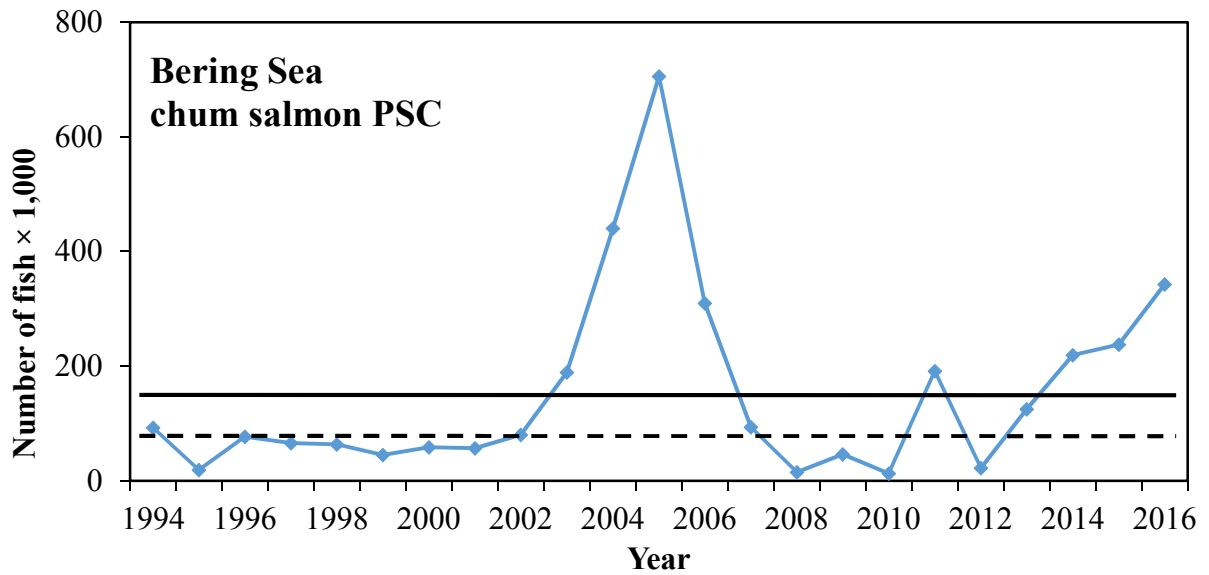
Figure 2. -- Yearly estimates for the non-Chinook salmon prohibited species catch (PSC) from the Bering Sea pollock-directed trawl fisheries (NMFS 2017). The solid horizontal line represents mean PSC and the dashed line represents median PSC, 1994-2015.

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 35-43) and two areas (NMFS reporting areas aggregated: 509, 513, and 516; 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 = 8.49, 24 d.f., P > 0.99). During the B-season, temporal biases were also minimal at finer spatial scales (Fig. 4; χ^2 = 7.86, 6 d.f., P = 0.25). The NMFS and ADF&G reporting area is known for samples collected at the haul-level from at-sea processors (hauls), but due to the uncertainty of catch location for samples collected at the trip-level from

shore-side processors (offloads) in which deliveries may contain mixed hauls from multiple

reporting areas, the reporting area of the chum salmon catch from offloads was identified as the

area where most of the pollock were caught during a fishing trip.
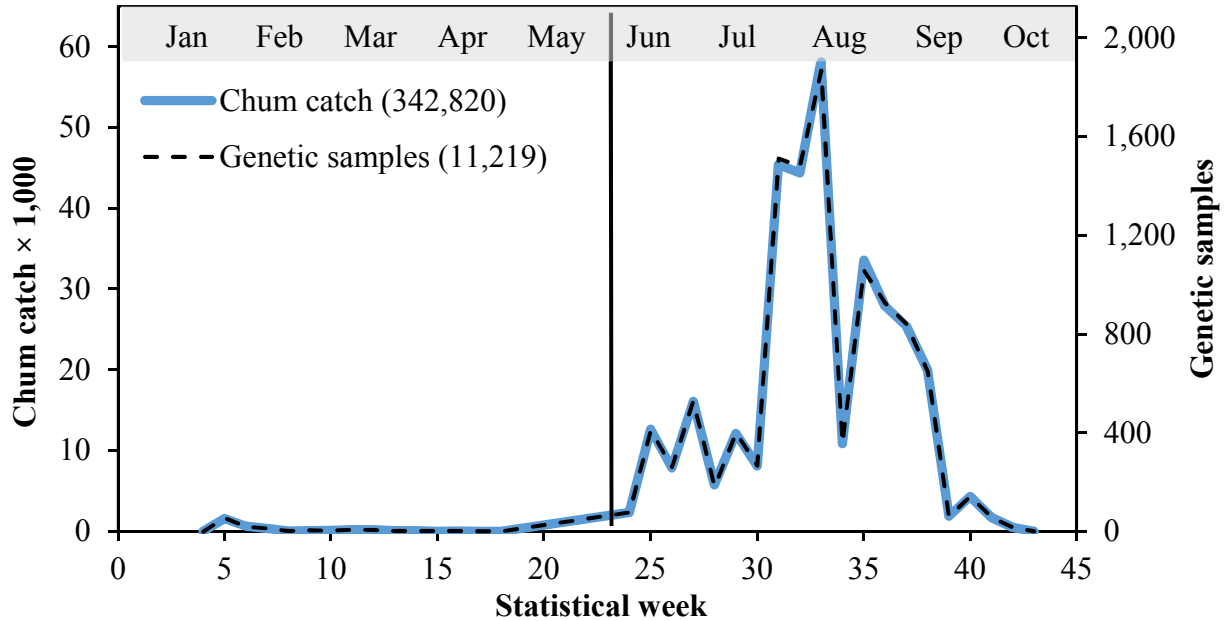
Figure 3. -- Number of Bering Sea chum salmon caught (solid line) and genetic samples collected (dashed line) from the 2016 Bering Sea pollock trawl fishery by statistical week. Weeks 1-23 correspond to the A-season, whereas weeks 24-43 correspond to the B-season, the demarcation of which is a vertical line.
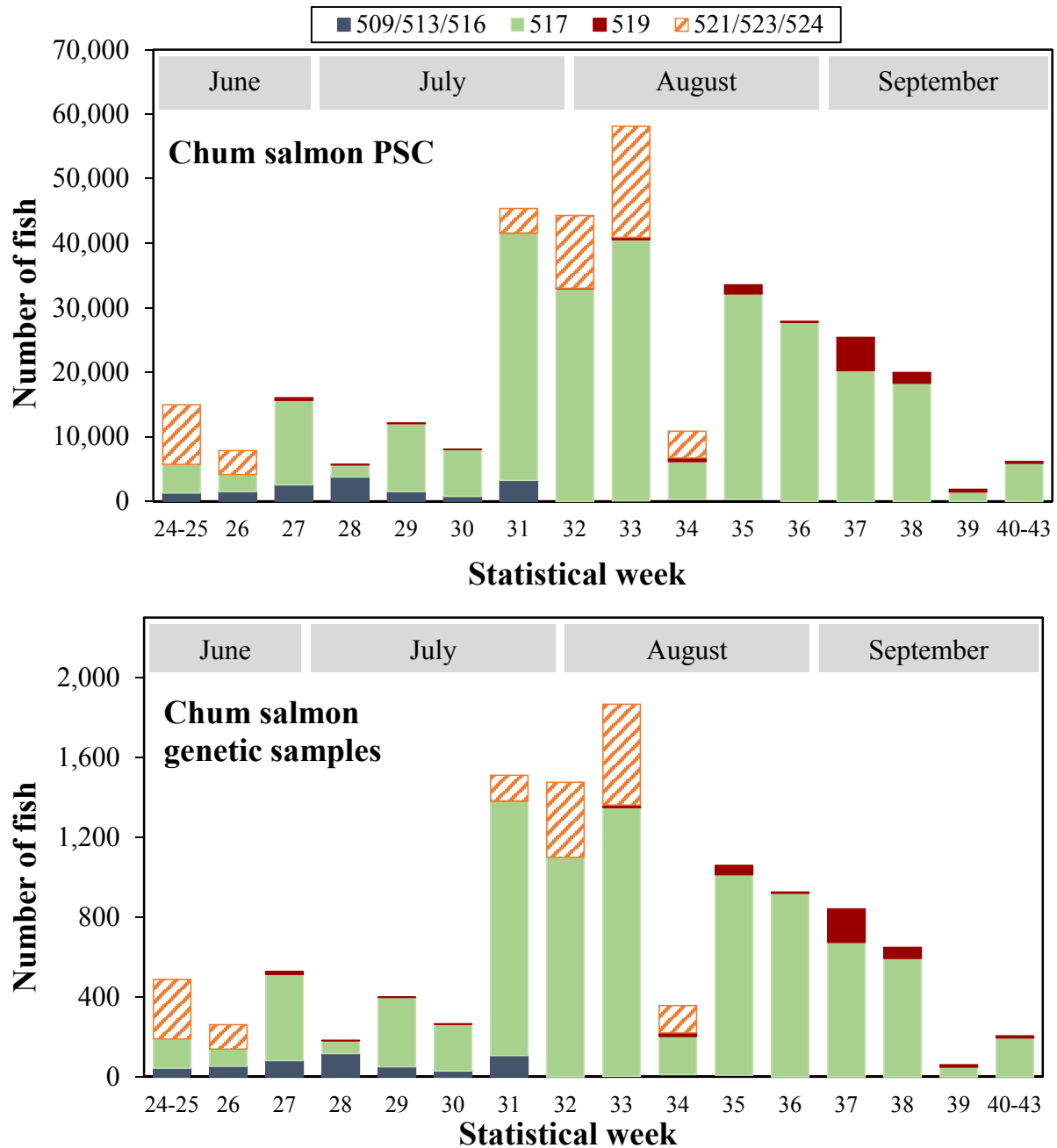
Figure 4. -- Number of Bering Sea chum salmon caught (top) and genetic samples collected (bottom) from the 2016 Bering Sea pollock B-season by statistical week and NMFS reporting area (designated in the legend).

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). The sampling ratio of numbers of chum salmon caught to numbers of genetic samples per vessel was 30.4 ± 2.6 fish (mean ± S.D.; unweighted by proportion of bycatch each vessel caught), which is close to the protocol sampling goal of one genetic sample collected from every 30th chum salmon caught. All 102 vessels that participated in the midwater trawl fishery during the A- and B-seasons caught chum salmon. In 2016, about 43% of the chum salmon PSC was counted from at-sea hauls and 57% from shoreside offloads. By vessel, the 1:30 ratio of genetic sampling did not differ between hauls and offloads (t-test; P = 0.33).
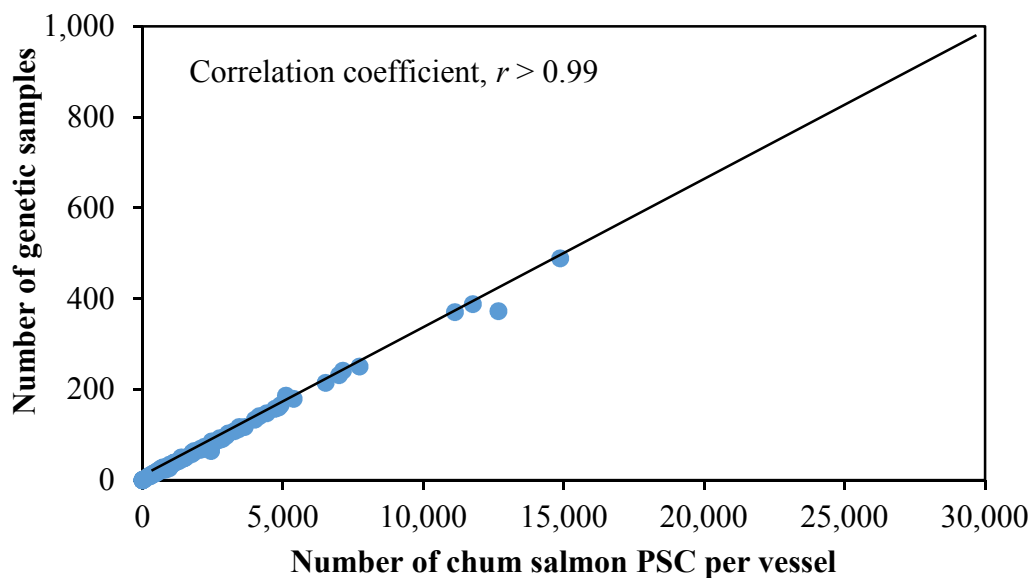
Figure 5. -- Bering Sea chum salmon catch and genetic samples from the 2016 Bering Sea pollock A- and B-seasons. Number of genetic samples collected from the total number of chum salmon caught from each of 102 vessels; black diagonal line represents the expected sampling rate.

Gulf of Alaska

The estimated PSC of chum salmon in the GOA (NMFS 2016) 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. 2017). In 2016, chum salmon samples were collected in the GOA (AFSC 2015) primarily from the pollock trawl fishery, which caught about 56% of the chum salmon PSC in the GOA (Fig. 6). The majority of chum salmon from the non-pollock fisheries were caught between the B and C pollock seasons (May 31-August 24; Fig. 7) in the arrowtooth flounder, sablefish, rockfish, and halibut fisheries. This is the third 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 26% 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 507 samples from the pollock fishery from NMFS reporting areas 610, 620, and 630 during primarily the pollock C- and D-seasons[2], and 2 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.
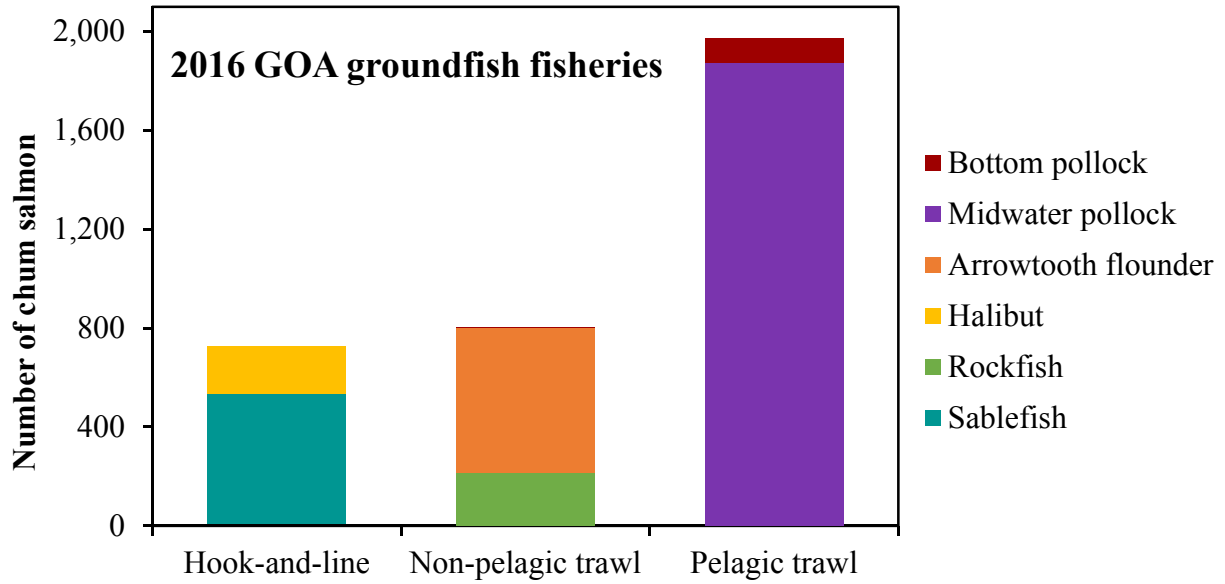
Figure 6. -- Estimated number of chum salmon caught (N = 3,518) in the 2016 Gulf of Alaska groundfish fisheries by target species. The 17 chum salmon caught in the Pacific cod, shallow-water flatfish, and flathead sole fisheries are not shown.
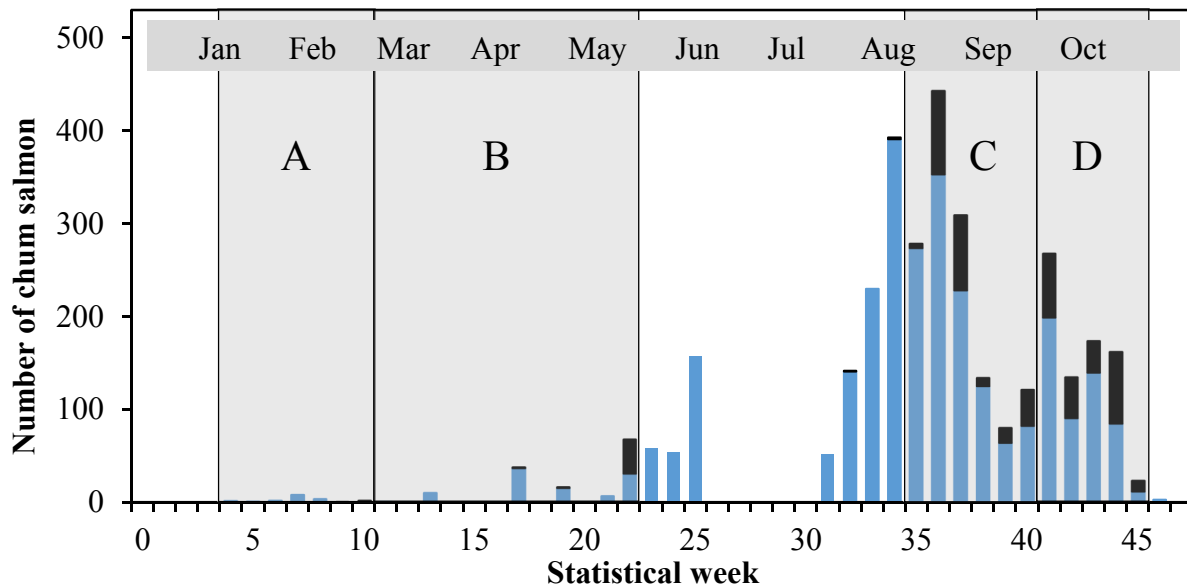
Figure 7. -- Number of chum salmon caught (blue plus black) and genetic samples collected (black) from the 2016 Gulf of Alaska groundfish fisheries by statistical week. Grayed areas with letter designations approximate the NMFS management seasons for pollock in the Western and Central Regulatory Areas (NMFS reporting areas 610-630).
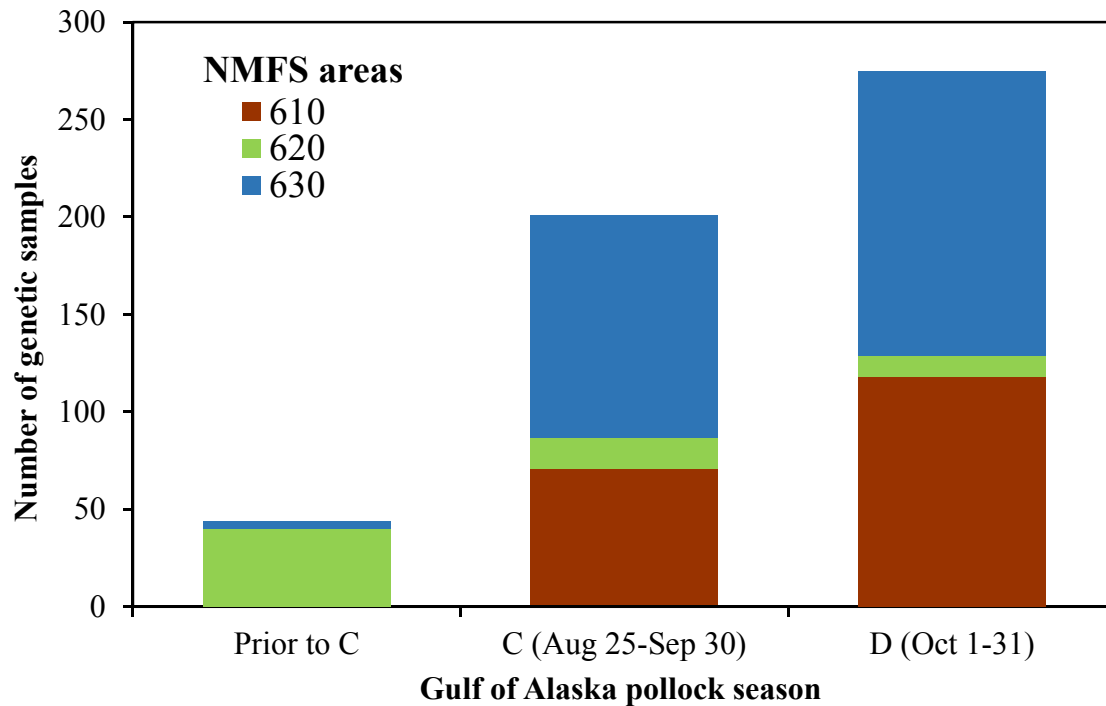
Figure 8. -- Number of chum salmon genetic samples collected from the 2016 Gulf of Alaska groundfish fisheries by pollock season and NMFS reporting areas.

LABORATORY ANALYSES

Chum salmon samples from the Bering Sea pollock B-season were subsampled in order to minimize laboratory costs while limiting potential bias of mixed-stock estimates. The total sample set of 11,043 chum salmon was sorted by cruise, haul or offload, and specimen number, and every 4th sample was selected for analysis (see Whittle et al. 2015 for subsampling effects). DNA was extracted from the axillary processes of 2,762 chum salmon sampled in the B-season, all of the 121 chum salmon sampled in the A-season, and all of the 509 chum salmon sampled in the GOA groundfish fisheries. An additional 573 samples were selected for the 4-cluster spatial analysis to increase the sample sizes to approximately 200 samples in each time-area category.

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.).

Of the 3,947 chum salmon bycatch samples from the Bering Sea and GOA, 97% were

successfully genotyped for 8 or more of the 11 loci for an average of 10.9 loci (Table 1). Four

duplicate genotypes were detected in the Bering Sea bycatch samples with GenAlEx 6.5 (Peakall

and Smouse 2006, 2012); one sample of each duplicate pair was removed from further analysis.

Twenty-four GOA samples were determined to be non-chum and 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 NMFS observer sampling protocol (Table 2; AFSC 2015).

Table 1. -- Number of genetic samples analyzed for chum salmon from the 2016 Bering Sea
pollock trawl fishery and Gulf of Alaska groundfish fisheries.

Number loci	Genetic samples
11	3,619
10	136
9	31
8	31
<8	130

Table 2. -- 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 41-43 were pooled to provide sample sizes > 4 in all time categories.

Sample set	N	X^2	d.f.	P-value
Collected vs. expected	11,094	7.60	17	0.97
Genotyped vs. ¼ expected	2,762	3.05	17	> 0.99
Analyzed vs. ¼ expected	2,701	8.06	17	0.97

Quality control of sample handling and genotyping was examined by reanalyzing 8.4% of the samples: DNA was plated from the eight samples in the left-most column of each elution plate for a total of 344 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). The genotyping error was low; across 11 loci there were a total of 114 differences in 7,074 alleles between the original and quality control datasets, which represented an overall discrepancy rate of 1.61%.

Table 3. -- Number of allele differences by locus between the original and quality control datasets for 2016 Bering Sea midwater pollock trawl fishery and Gulf of Alaska groundfish fisheries samples with non-questionable genotypes.

Locus	Number alleles compared	Number allele differences	Percent difference
Oki100	622	18	2.89
Omm1070	640	24	3.75
Omy1011	644	9	1.40
One101	624	27	4.33
One102	624	12	1.92
One104	648	3	0.46
One114	652	3	0.46
Ots103	652	4	0.61
Ots3	676	7	1.04
OtsG68	642	4	0.62
Ssa419	650	3	0.46

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 saved 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 GOA/Pacific Northwest (PNW) (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.
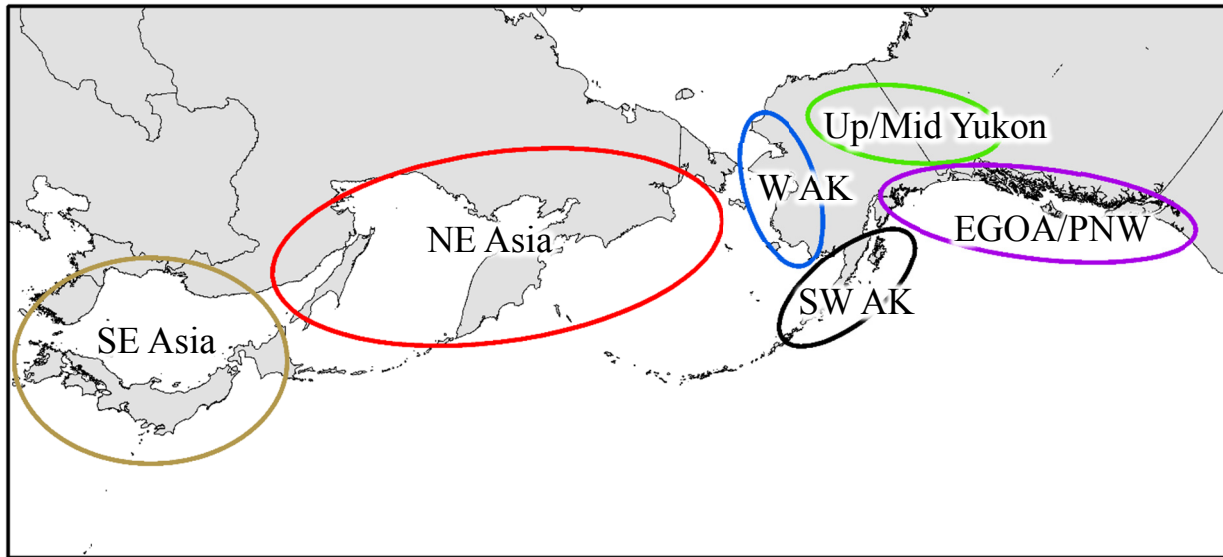
Figure 9. -- Six regional groups of baseline chum salmon populations used in this report.

As with previous analyses of chum salmon PSC (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010, 2011a,b; Kondzela et al. 2012, 2013, 2016, 2017; Vulstek et al. 2014; Whittle et al. 2015), the stock composition analysis for the 2016 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 4; 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 MCMC chains of 100,000 iterations (burn-in of 50,000) 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. Convergence was assessed with Gelman-Rubin shrink factors, which were all 1.00-1.05 (Table 4; 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 mean, standard deviation, median, 95% credible interval (2.5[th] and 97.5[th] percentile of the MCMC iterates in the posterior output), and $P = 0$, 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 Upper/Middle Yukon stock estimate from the A-season sample set (Table 4) indicates that there is a 98.6% 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 4. -- Regional stock composition estimates of chum salmon collected from 2016 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-Rubin shrink factor.

A. Bering Sea pollock trawl fishery, A-season, (PSC = 3,726, n = 114)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink
SE Asia	726	0.195	0.039	0.124	0.193	0.277	0	1.00
NE Asia	1,388	0.372	0.061	0.257	0.372	0.496	0	1.00
W Alaska	117	0.032	0.026	0	0.027	0.094	0.155	1.00
Up/Mid Yukon	15	0.004	0.008	0	0.001	0.027	0.986	1.00
SW Alaska	93	0.025	0.032	0	0.009	0.105	0.451	1.02
E GOA/PNW	1,387	0.372	0.057	0.261	0.372	0.485	0	1.01

B. Bering Sea pollock trawl fishery, B-season, (PSC = 339,094, n = 2,701)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink
SE Asia	29,908	0.088	0.006	0.077	0.088	0.100	0	1.00
NE Asia	103,254	0.305	0.011	0.282	0.304	0.327	0	1.00
W Alaska	65,411	0.193	0.011	0.172	0.193	0.214	0	1.00
Up/Mid Yukon	18,006	0.053	0.007	0.041	0.053	0.067	0	1.00
SW Alaska	4,374	0.013	0.004	0.006	0.012	0.022	0	1.00
E GOA/PNW	118,174	0.349	0.010	0.328	0.348	0.369	0	1.00

C. Gulf of Alaska groundfish fisheries, (PSC = 3,518, n = 473)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink
SE Asia	37	0.010	0.005	0.002	0.010	0.023	0.759	1.00
NE Asia	92	0.026	0.010	0.009	0.025	0.049	0.006	1.00
W Alaska	62	0.018	0.007	0.006	0.017	0.034	0.062	1.00
Up/Mid Yukon	4	0.001	0.003	0	0.000	0.009	1.000	1.00
SW Alaska	55	0.016	0.009	0.001	0.015	0.036	0.257	1.00
E GOA/PNW	3,268	0.929	0.015	0.898	0.930	0.955	0	1.00

COMPARISON WITH PREVIOUS ESTIMATES

Bering Sea

This was the second year in a row that the sample set from the A-season was large enough for genetic analysis. The stock composition results from 2016 were similar to 2015 for all regions, with the exception of Southeast Asia, which had a significantly larger stock contribution in 2016 than in 2015 (Fig. 10).
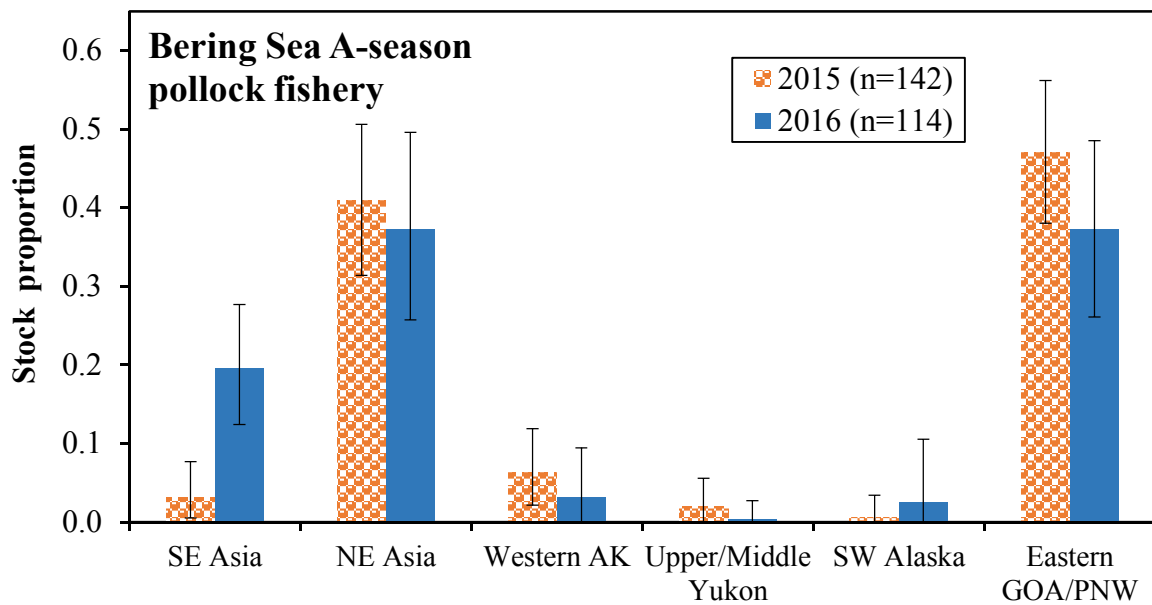
Figure 10. -- Stock composition estimates and 95% BAYES credible intervals for the 2015 and 2016 chum salmon genetic samples from the Bering Sea pollock A-season.

The stock composition results from the analysis of the 2016 chum salmon samples collected during the B-season were similar to the results from past years for four of the six regions, prior to and after systematic sampling was in effect (Fig. 11, upper panel). The two exceptions to this pattern were Southeast Asia stocks, which were lower than in previous years, and Eastern GOA/PNW stocks, which were higher than in years prior to systematic sampling. In 2016, Northeast Asia and Eastern GOA/PNW 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 2005-2016 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, 2017; 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 large variation in total chum salmon caught across the years (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.
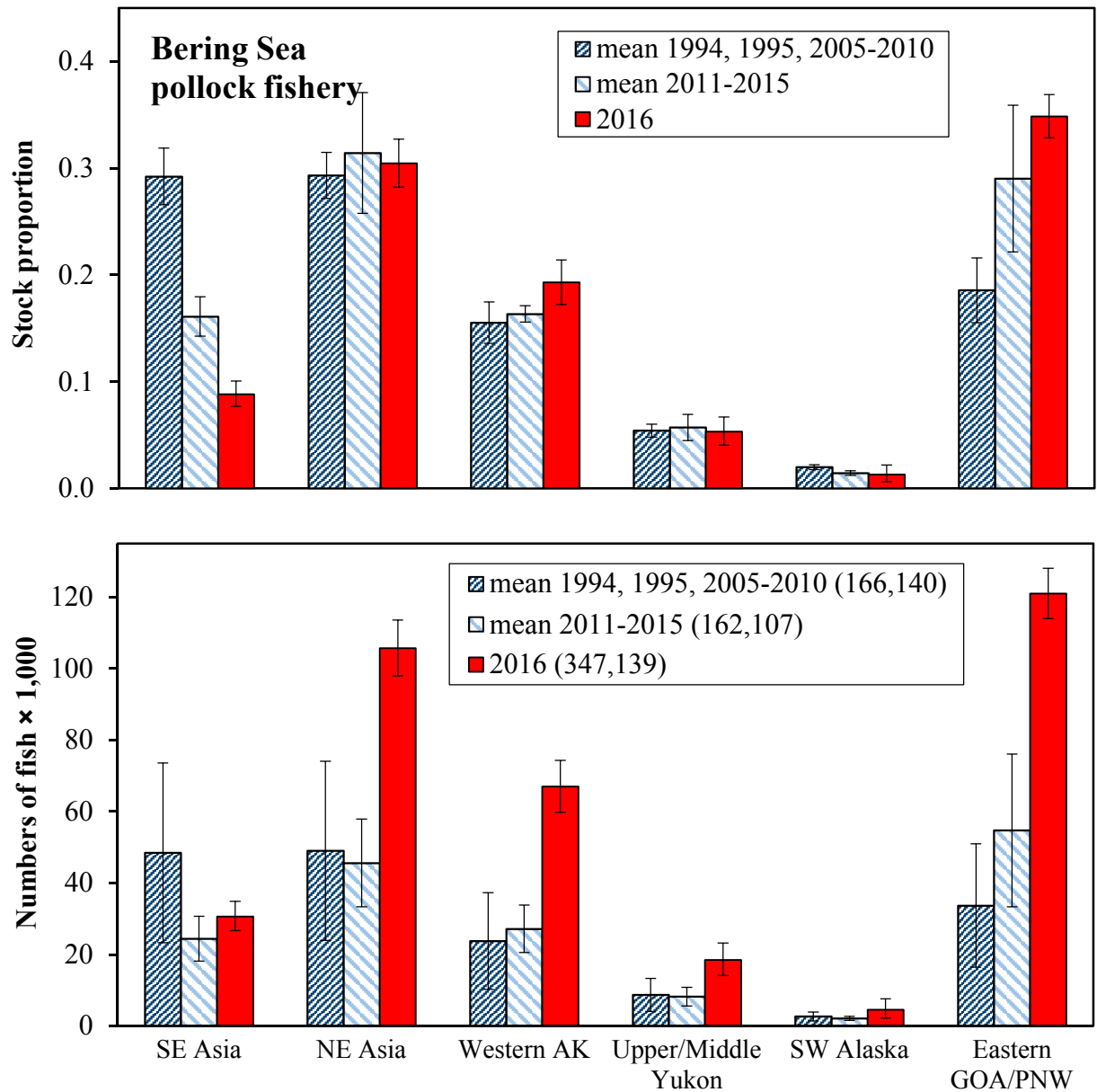
Figure 11. -- Comparison of the 2016 Bering Sea chum salmon stock composition estimates with the estimates from 2011 to 2015 (systematic sampling) and the unweighted mean estimates from 1994, 1995, and 2005-2010 (nonsystematic sampling). Proportions in top panel (B-season); numbers of fish (A+B seasons) in bottom panel, which for comparison purposes across years are based on the total chum salmon caught in all groundfish fisheries (NMFS 2017). Standard errors of the mean estimates are shown for the combined years; 95% BAYES credible intervals are shown for the 2016 analysis. Error bars are based on only the mixed-stock analyses and do not include errors associated with the overall annual PSC 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 2011-2016 are censuses.

Gulf of Alaska

In 2016, for the third 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 2016 GOA samples were nearly identical to the 2014-2015 estimates, with more than 90%

of the contribution from Eastern GOA/PNW stocks (Fig. 12). In all three 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 any of the three years (0.71-1.00 "P = 0"

values; Appendix II).
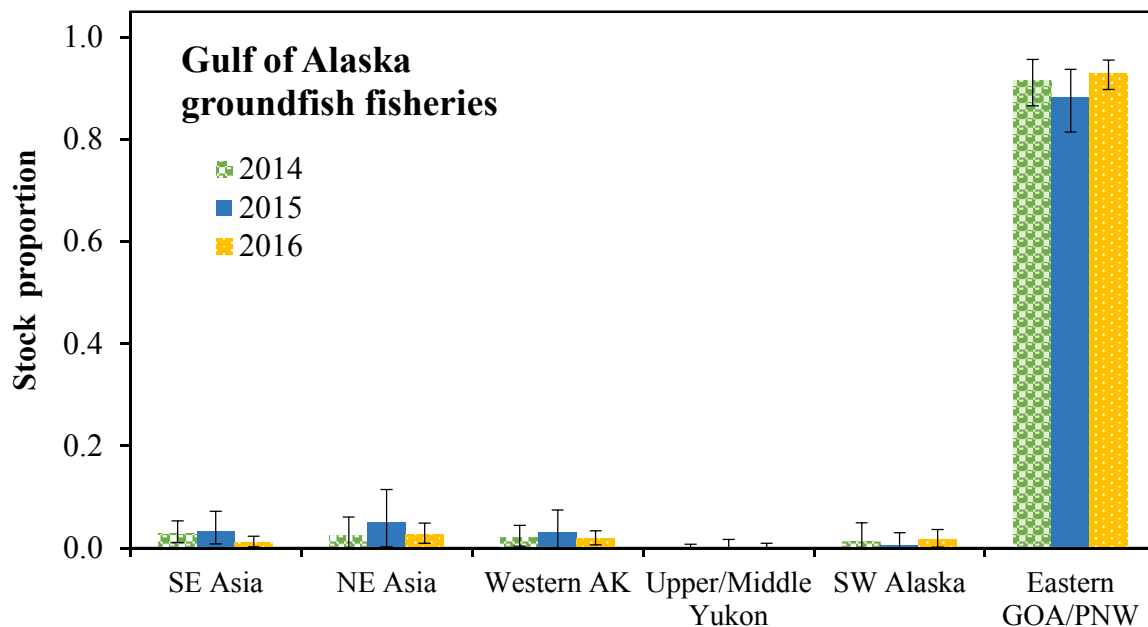
Figure 12. -- Stock composition estimates and 95% BAYES credible intervals for the 2014-2016
chum salmon genetic samples from the Gulf of Alaska groundfish fisheries.

TEMPORAL STRATIFICATION

Resolving 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 broader time scale of winter versus summer/fall. Although the dominant contribution from both seasons was from Eastern GOA/PNW and Northeast Asia stocks, there were significant differences in the stock contributions from other regions, particularly Southeast Asia, Western Alaska, and Upper/Middle Yukon (Tables 4A,B).

As with the 2005-2015 analyses, the 2016 Bering Sea sample set from the B-season was split into three time periods: Early, Middle, and Late (Table 5). Stock composition estimates were made as described previously for each of the three temporal strata (Appendix II).

Table 5. -- Temporal groups from the genetic sample sets of chum salmon caught in the 2016 Bering Sea, B-season pollock fishery.

Time period	Weeks	Dates	Number of samples
Early	24-29	June 10 – July 16	453
Middle	30-34	July 17 – August 20	1,333
Late	35-43	August 21 – October 22	915

The stock composition of chum salmon caught in the Bering Sea pollock fishery changed during the course of the season (Fig. 13). In 2016, genetic samples differed across the three time periods within three of the five regional groups. The contribution from Southeast Asia decreased significantly after the Early time period to a low level during the Middle and Late time periods, the Eastern GOA/PNW contribution increased across time, nearly doubling between the Early and Late time periods, and the Western Alaska contribution decreased slightly between the Middle and Late time periods. The slight increase in the Northeast Asia contribution after the Early time

period was not significant, and the Upper/Middle Yukon contribution was stable over the three time periods.

The averages of the 2005-2015 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 2016 and the 2005-2015 chum salmon samples. The contribution from Eastern GOA/PNW stocks during the Middle and Late time periods in 2016 was notably higher than in previous years. The contribution from Southeast Asia during the Middle and Late time period in 2016 was lower than the average of previous years. The proportion of the chum salmon catch contributed by Western Alaska was higher during the Middle and Late time periods, and the Upper/Middle Yukon contribution was similar to that observed in previous years. 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.
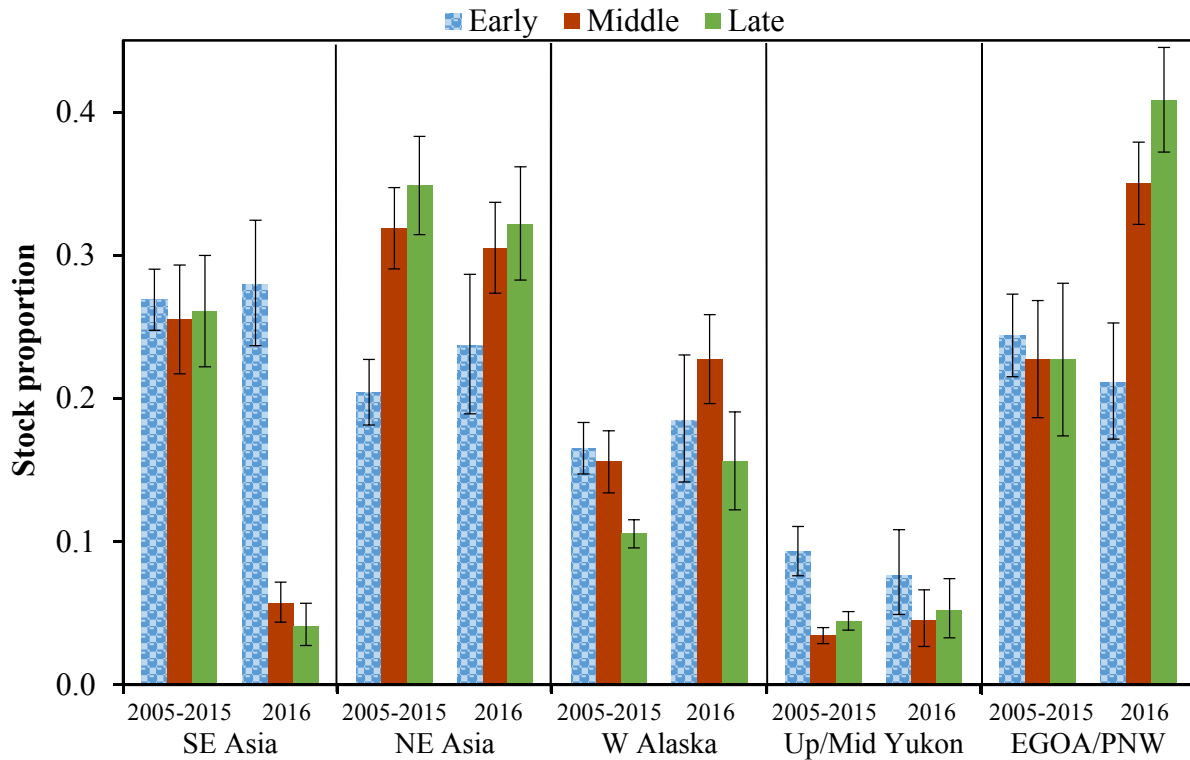
Figure 13. -- Stock composition estimates for the 2005-2015 (mean ± S.E.) and 2016 (± 95% BAYES credible intervals) chum salmon samples for the Early, Middle, and Late periods of the B-season (defined in Table 5). Not shown is the Southwest Alaska region for which estimates never exceeded 5.6%.

SPATIAL STRATIFICATION

Resolution 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 samples. In 2016, for the sixth year, the Observer Program undertook a complete census of chum salmon caught in the Bering Sea pollock trawl fisheries. About 43% of the chum salmon catch was counted and sampled at shoreside processing facilities. Of the shoreside offloads, about 60% of the chum salmon catch was from vessels that fished in one ADF&G statistical area during a trip. For the 40% of chum salmon catch offloaded from vessels that fished in multiple ADF&G statistical areas during a trip (17% of total chum salmon

catch), the area assigned to an offload was the area where the highest weight of pollock was caught.

The 2016 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, 516, 517, and 519). Stock compositions for the two spatial strata were estimated as described previously (Fig. 14; Appendix II). The contribution of stocks differed between the two spatial strata in a manner similar to that observed in 2015, with the exception of the Northeast Asia and Eastern GOA/PNW regions (Kondzela et al. 2017), which had nearly identical stock proportions between the two areas in 2016 but different proportions in 2015. Almost two-thirds of the contribution in the southeastern Bering Sea was from North American stocks, primarily from the Eastern GOA/PNW and Western Alaska regions. The contribution in the area west of 170°W was divided nearly evenly between North American and Asian stocks.
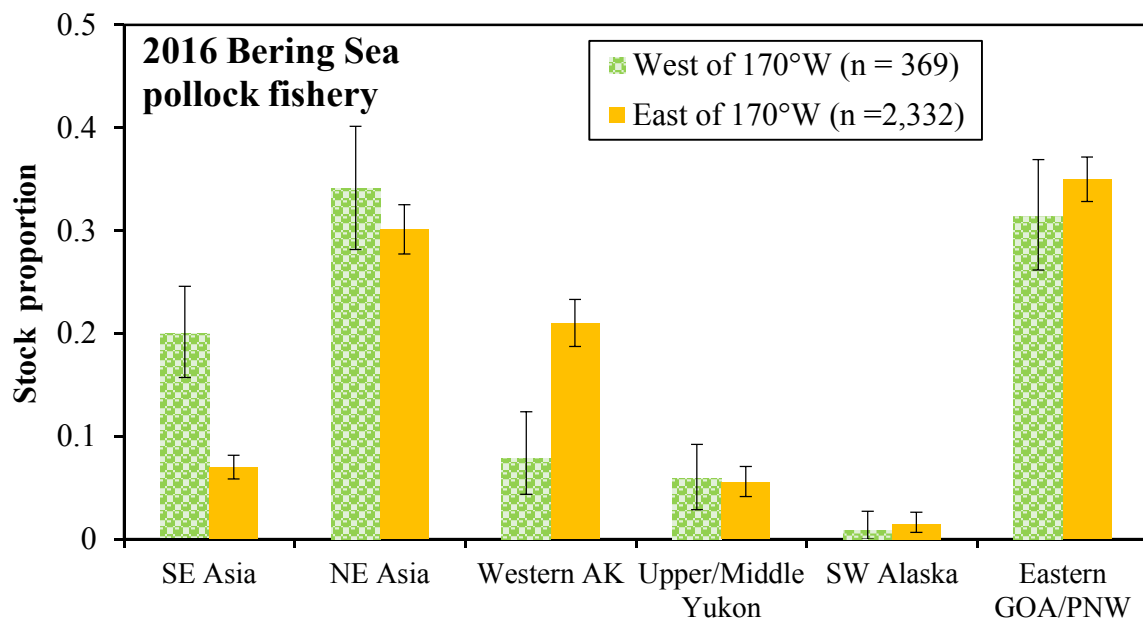
Figure 14. -- Stock composition estimates and 95% BAYES credible intervals for the 2016 chum salmon genetic samples collected during the B-season from the U.S. waters of the Bering Sea west of 170°W (aggregate area 521/523/524) and the southeastern Bering Sea east of 170°W (aggregate area 509/513/516/517/519).

To better understand the chum salmon stock distribution across both time and space, the 2016 samples from NMFS reporting area 517 were compared across Early, Middle, and Late time periods and samples from NMFS reporting area 521 were compared across Early and Middle time periods (Table 6). Samples from all other areas/time periods were not included due to small sample sizes.

Table 6. -- Spatial and temporal groups from the 2016 chum salmon genetic samples for the NMFS reporting areas and time periods (Table 5) with sufficient number of samples for analysis.

Reporting area	Time period	Number of samples
517	Early	262
	Middle	1,024
	Late	840
521	Early	102
	Middle	225

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, Southeast Asia stocks had the highest contribution during the Early time period, and decreased to a low level during the Middle and Late time periods. Northeast Asia stocks increased after the Early time period, although the 95% credible intervals overlap. Western Alaska stocks increased during the Middle time period, although the 95% credible intervals overlap, and then decreased during the Late time period. Eastern GOA/PNW stocks increased across all time periods. In area 521, the Southeast Asia stocks decreased five-fold and Eastern GOA/PNW stocks more than doubled after the Early time period. As in previous years, the contribution from Upper/Middle Yukon and Southwest

Alaska stocks was absent or 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.

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 locations of the chum salmon samples within each area are unknown. In addition, about 17% of the total chum salmon PSC was sampled from offload deliveries in which vessels fished in multiple areas. Thus, for an unknown proportion of the chum salmon samples, the area designation may not be correct.
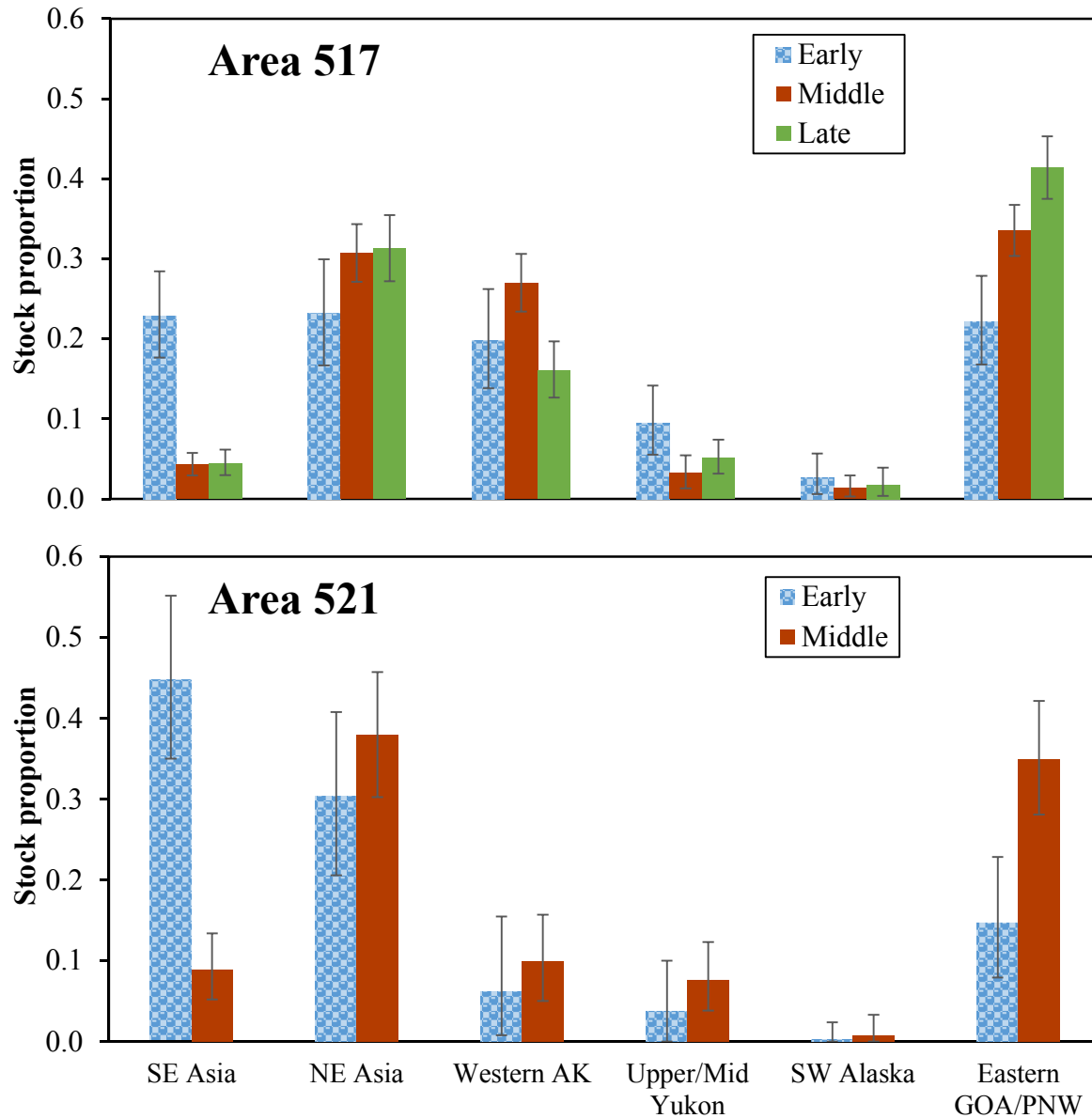
Figure 15. -- Stock composition estimates and 95% BAYES credible intervals for the 2016 chum
salmon genetic samples collected during the B-season from NMFS reporting area
517 for the Early, Middle, and Late time periods and from NMFS reporting area 521
for the Early and Middle time periods (Table 6).

In an effort to better understand the distribution of chum salmon stocks in the Bering Sea

PSC from the pollock fishery, stock composition estimates were obtained from four spatial

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 33-43)

time periods (Table 7; Appendix IV). There were fewer differences in stock estimates along the

continental shelf and across time periods in 2016 (Fig. 16; Appendix II) than in 2015. In the Early

time period, the pattern of stock proportions was similar between the two years. In 2016 there was

a gradient of stock proportions along the continental shelf with a higher proportion of chum

salmon from Asian stocks in the more northern portion of the fishery and a higher proportion of

chum salmon from North American stocks in the southeastern portion of the fishery, nearest to the

Alaska Peninsula. In the Late time period, the 2016 stock proportions for all six regions were

nearly constant across the continental shelf, unlike the pattern observed in 2015 in which the

Eastern GOA/PNW stock dominated Clusters 1-3 of the fishery. The two exceptions in 2016 were

the higher proportions of Western Alaska stocks in Cluster 1 and Southeast Asia stocks in

Cluster 4.

Table 7. -- Collection information for the four spatial clusters of chum salmon caught in two time periods, Early (weeks 24-32) and Late (weeks 33-43), during the 2016 B-season of the Bering Sea pollock fishery and analyzed for genetic stock composition.

Cluster	Time period	Samples received	Samples analyzed
1	Early	3,653	1,043
	Late	2,788	681
2	Early	440	185
	Late	2,167	535
3	Early	970	230
	Late	470	178
4	Late	187	184
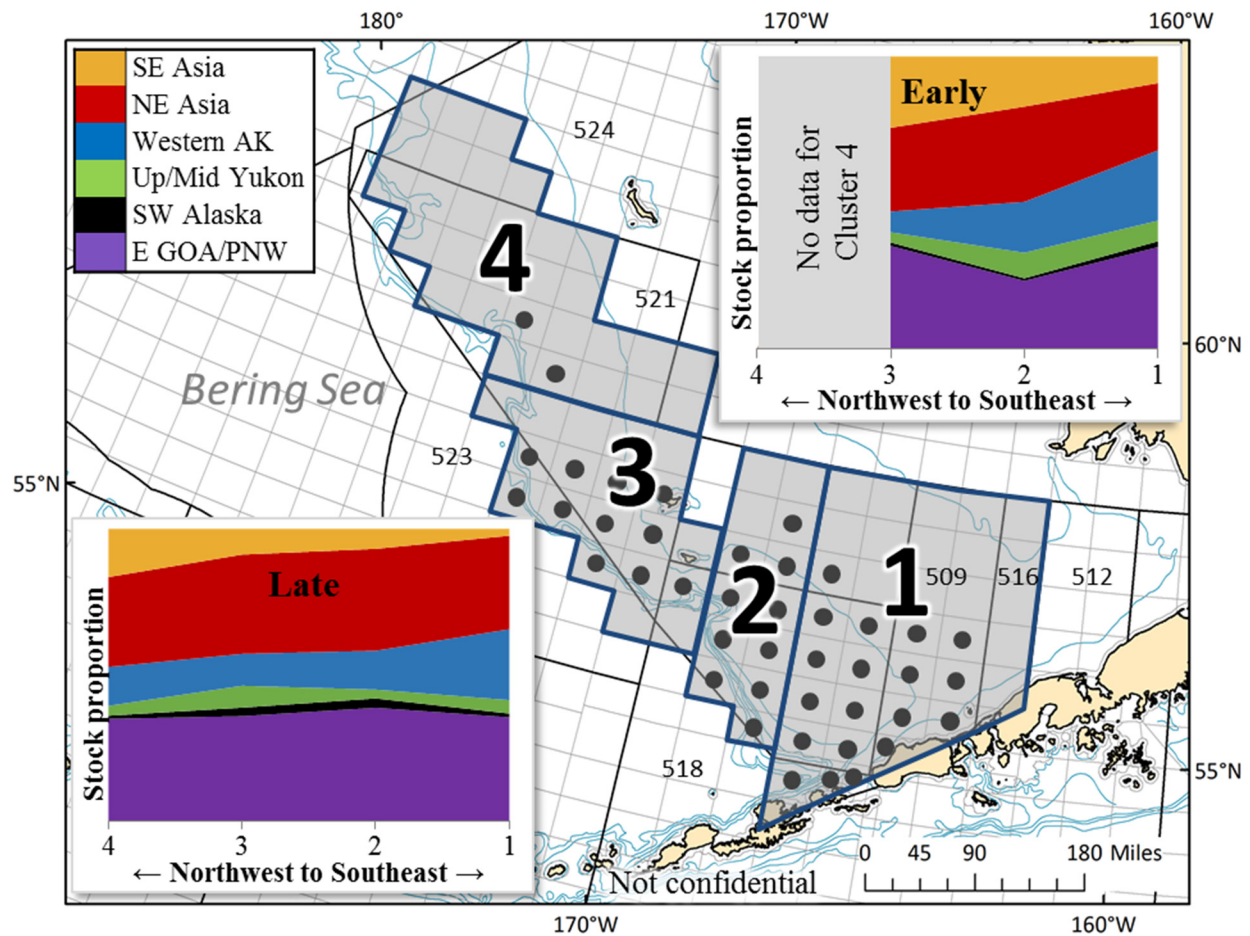
Figure 16. -- Stock composition estimates of chum salmon from four spatial clusters of samples collected along the continental shelf edge during Early (Weeks 24-32) and Late (Weeks 33-43) time periods from the 2016 Bering Sea pollock fishery. The four clusters of ADF&G statistical areas in which samples were collected in at least one year from 2013 to 2016 are highlighted in gray; ADF&G areas in which samples were collected in 2016 from at least 3 vessels are indicated with a dot. The sample size of the Early time period for the fourth cluster was too small for analysis.

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 2016 chum salmon PSC based on 3,344 samples genotyped from the

Bering Sea and 473 samples genotyped from the GOA fisheries. 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 2016 sample set (Figs. 3 and 4) that were inherent in collections before 2011. Reduction of those biases improves the application of the 2016 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[4] 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 98.2% of the chum salmon caught in this fishery for genetic analysis in 2016 (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[5] provided, for the third year, a small sample set for genetic analysis. The distribution of chum salmon PSC samples is not representative of the groundfish fisheries as a

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[4] 75 FR 53026, August 30, 2010.
[5] Amendment 93 to the NPFMC fishery management plan for GOA groundfish (77 FR 42629, July 20, 2012).

whole. Most of the genetic samples (98%) were from the pollock trawl fishery, which in 2016 caught just over 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 2016 A-season in, but given the relatively high salmon bycatch in 2016, a small sample set was available for the second year in a row for genetic analysis. Most of the samples (74%) were from Eastern GOA/PNW and Northeast Asia stocks (Table 4A). Except for an increase in the proportions from Southeast Asia stocks in 2016, the proportions from other regions were similar in 2015 and 2016 (Fig. 10).

Nearly two-thirds of the genetic samples collected from chum salmon caught in the B-season 2016 Bering Sea pollock fishery were from North America, with the majority from Eastern GOA/PNW (35%), followed by Western Alaska (19%), stocks. The contribution from Asian stocks was predominantly from Northeast Asia (31%) (Table 4B). The stock proportions from Southeast Asia were significantly lower than in previous years, while Eastern GOA/PNW proportions were higher than in years prior to systematic sampling (Fig. 11). Contributions from all other regions were similar to previous years, and the low contribution from Southwest Alaska continued in 2016. Although chum salmon samples in 2016 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 the previous two years, the stock proportions of the 2016 chum salmon PSC from the GOA had a very different pattern than that observed in the Bering Sea. In the GOA groundfish fisheries, 93% of the chum salmon sampled were from Eastern GOA/PNW stocks (Table 4C; Fig. 12). The remaining contributions from the other five regions were very low, 0-5%.

Temporal and Spatial Effects

The A-season stock compositions differed from those of the B-season primarily by a higher contribution from Southeast Asia stocks and lower contributions from Western Alaska and Upper/Middle Yukon stocks (Table 4A,B); differences were minor in other regional estimates. Whether the differences are due to the spatial contraction of the pollock fleet during the A-season or to seasonal differences in the oceanic distribution of chum salmon 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. As in previous years, stock composition estimates of the 2016 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 2016 and in previous years, notably for the Middle and Late time periods for Southeast Asia, Western Alaska, and Eastern GOA/PNW stocks.

Spatial analysis suggested that the majority of the chum salmon from U.S. waters of the Bering Sea east of 170°W originated from North American stocks, primarily from the Eastern GOA/PNW region. West of 170°W, the chum salmon originated from nearly equal contributions of Asian and North American stocks (Fig. 14). The proportion of chum salmon from Southeast

Asia 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 stocks, was 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 uniformly distributed (Figs. 15, 16). In general, the proportion of stocks from Asia are higher 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, although these patterns of stock distribution were more evident in the previous year.

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

CITATIONS

ADF&G (Alaska Department of Fish and Game). 2003. SPAM Version 3.7: Statistics program for analyzing mixtures. Alaska Dep. Fish Game, Comm. Fish. Division, Gene Conservation Laboratory, Anchorage, Alaska.

AFSC (Alaska Fisheries Science Center). 2015. 2016 Observer sampling manual. Fisheries Monitoring and Analysis Division, North Pacific Groundfish Observer Program. AFSC, 7600 Sand Point Way N.E., Seattle, Washington, 98115.

Beacham, T. D., K. D. Le, M. Wetklo, B. McIntosh, T. Ming, and K. M. Miller. 2009a. Population structure and stock identification of chum salmon from western Alaska determined with microsatellite and major histocompatibility complex variation, p. 141-160. *In* C. C. Krueger and C. E. Zimmerman (eds.), Pacific salmon: ecology and management in western Alaska's populations. Am. Fish. Soc., Symp. 70, Bethesda, Maryland.

Beacham, T. D., J. R. Candy, K. D. Le, and M. Wetklo. 2009b. Population structure of chum salmon (*Oncorhynchus keta*) across the Pacific Rim, determined from microsatellite analysis. Fish. Bull., U.S. 107:244-260.

Beacham, T. D., J. R. Candy, C. Wallace, S. Urawa, S. Sato, N. V. Varnavskaya, K. D. Le, and M. Wetklo. 2009c. Microsatellite stock identification of chum salmon on a Pacific Rim basis. N. Am. J. Fish. Manage. 29:1757-1776.

Beacham, T. D., L. Margolis, and R. J. Nelson. 1999. A comparison of methods of stock identification for sockeye salmon (*Oncorhynchus nerka*) in Barkley Sound, British Columbia. N. Pac. Anadr. Fish Comm. Bull. No. 1:227-239.

Cahalan, J., J. Gasper, and J. Mondragon. 2014. Catch sampling and estimation in the federal groundfish fisheries off Alaska, 2015 edition. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-286, 46 p.

Cairney, M., J. B. Taggart, and B. Hoyheim. 2000. Characterization of microsatellite and minisatellite loci in Atlantic salmon (*Salmo salar* L.) and cross-species amplification in other salmonids. Mol. Ecol. 9:2175-2178.

Davis, N. D., A. V. Volkov, A. Y. Efimkin, N. A. Kuznetsova, J. L. Armstrong, and O. Sakai. 2009. Review of BASIS salmon food habits studies. N. Pac. Anadr. Fish. Comm. Bull. 5:197-208.

Debevec, E. M., R. B. Gates, M. Masuda, J. Pella, J. Reynolds, and L. W. Seeb. 2000. SPAM (Version 3.2): statistics program for analyzing mixtures. J. Heredity 91:509-510.

Faunce, C. H. 2015. Evolution of observer methods to obtain genetic material from Chinook salmon bycatch in the Alaska pollock fishery. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-288, 28 p.

Gelman, A., and D. B. Rubin. 1992. Inference from iterative simulation using multiple sequences. Stat. Sci. 7:457-511.

Gray, A., T. McCraney, C. Kondzela, C. Marvin, and J. R. Guyon. 2011a. Genetic stock composition analysis of chum salmon bycatch samples from the 2007 Bering Sea trawl fisheries. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-220, 28 p.

Gray, A. K., W. T. McCraney, C. T. Marvin, C. M. Kondzela, H. T. Nguyen, and J. R. Guyon. 2011b. Genetic stock composition analysis of chum salmon bycatch samples from the 2008 Bering Sea groundfish fisheries. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-222, 29 p.

Gray, A., C. Marvin, C. Kondzela, T. McCraney, and J. R. Guyon. 2010. Genetic stock composition analysis of chum salmon bycatch samples from the 2009 Bering Sea trawl fisheries. Report to the North Pacific Fishery Management Council, 605 W. 4th Ave., Anchorage, Alaska, 99510, 23 p.

Greig, C., and M. A. Banks. 1999. Five multiplexed microsatellite loci for rapid response run identification of California's endangered winter Chinook salmon. Anim. Genet. 30:318320.

Guthrie, C. M. III, Hv. T. Nguyen, A. E. Thomson, and J. R. Guyon. 2017. Genetic stock composition analysis of Chinook salmon bycatch samples from the 2015 Gulf of Alaska trawl fisheries. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-343, 33 p. http://www.afsc.noaa.gov/Publications/AFSC-TM/NOAA-TM-AFSC-343.pdf

Guyon, J. R., C. Kondzela, T. McCraney, C. Marvin, and E. Martinson. 2010. Genetic stock composition analysis of chum salmon bycatch samples from the 2005 Bering Sea groundfish fishery. Report to the North Pacific Fishery Management Council, 605 W. 4th Ave., Anchorage, Alaska, 99510, 31 p.

Kondzela, C. M., J. A. Whittle, S. C. Vulstek, Hv. T. Nguyen, and J. R. Guyon. 2017. 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. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-345, 64 p.

Kondzela, C. M., J. A. Whittle, D. Yates, S. C. Vulstek, H. T. Nguyen, and J. R. Guyon. 2016. 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. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-314, 49 p. http://dx.doi.org/10.7289/V5/TM-AFSC-314.

Kondzela, C. M., C. T. Marvin, S. C. Vulstek, H. T. Nguyen, and J. R. Guyon. 2013. Genetic stock composition analysis of chum salmon bycatch samples from the 2011 Bering Sea walleye pollock trawl fishery. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC243, 39 p.

Kondzela, C. M., W. T. McCraney, H. T. Nguyen, and J. R. Guyon. 2012. Genetic stock composition analysis of chum salmon bycatch samples from the 2010 Bering Sea groundfish fisheries. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-233, 29 p.

Marvin, C. T, S. L. Wildes, C. M. Kondzela, H. T. Nguyen, and J. R. Guyon. 2011. Genetic stock composition analysis of chum salmon bycatch samples from the 2006 Bering Sea groundfish fisheries. U. S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-220, 29 p.

Munro, A. R., C. Habicht, T. H. Dann, D. M. Eggers, W. D. Templin, M. J. Witteveen, T. T. Baker, K. G. Howard, J. R. Jasper, S. D. Rogers Olive, H. L. Liller, E. L. Chenoweth, and E. C. Volk. 2012. Harvest and harvest rates of chum salmon stocks in fisheries of the Western Alaska Salmon Stock Identification Program (WASSIP), 2007–2009. Alaska Department of Fish and Game, Special Publication No. 12-25, Anchorage.

Myers, K. W., N. V. Klovach, O. F. Gritsenko, S. Urawa, and T. C. Royer. 2007. Stock-specific distributions of Asian and North American salmon in the open ocean, interannual changes, and oceanographic conditions. N. Pac. Anadr. Fish. Comm. Bull. 4: 159-177.

NMFS (National Marine Fisheries Service). 2017. BSAI non-Chinook salmon mortality estimates, 1991-present, National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Alaska Regional Office, Juneau, Alaska. Retrieved on March 19, 2017 from https://alaskafisheries.noaa.gov/sites/default/files/reports/chum_salmon_mortality2017.pdf

NMFS (National Marine Fisheries Service). 2016. Catch Accounting System data. NMFS Alaska Regional Office. Data compiled by Alaska Fisheries Information Network for Alaska Fisheries Science Center, Juneau. [URL not publicly available as some information is confidential.]

NMFS (National Marine Fisheries Service). 2009. Bering Sea Chinook salmon bycatch management, Volume I. Final Environmental Impact Statement, National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Alaska Regional Office, Juneau, Alaska.

NPFMC (North Pacific Fishery Management Council). 2017a. Fishery management plan for groundfish of the Bering Sea and Aleutian Islands management area. North Pacific Fishery Management Council, 605 W. 4th Ave., Anchorage, Alaska, 99501. https://www.npfmc.org/wp-content/PDFdocuments/fmp/BSAI/BSAIfmp.pdf

NPFMC (North Pacific Fishery Management Council). 2017b. Fishery management plan for groundfish of the Gulf of Alaska. North Pacific Fishery Management Council, 605 W. 4th Ave., Anchorage, Alaska, 99501. https://www.npfmc.org/wp-content/PDFdocuments/fmp/GOA/GOAfmp.pdf

NPFMC (North Pacific Fishery Management Council). 2012. Bering Sea non-Chinook salmon PSC management measures, initial review draft environmental assessment. North Pacific Fishery Management Council, 605 W. 4th Ave., Anchorage, Alaska, 99501.

NPFMC (North Pacific Fishery Management Council). 2007. Environmental assessment/regulatory impact review/final regulatory flexibility analysis for modifying existing Chinook and chum salmon savings areas: Amendment 84 to the fishery management plan for groundfish of the Bering Sea and Aleutian Islands management area. North Pacific Fishery Management Council, 605 W. 4th Ave., Anchorage, Alaska, 99501.

Olsen, J. B., S. L. Wilson, E. J. Kretschmer, K. C. Jones, and J. E. Seeb. 2000. Characterization of 14 tetranucleotide microsatellite loci derived from sockeye salmon. Mol. Ecol. 9: 2185-2187.

Peakall, R., and P. E. Smouse. 2012. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research–an update. Bioinformatics 28:2537-2539.

Peakall, R., and P. E. Smouse. 2006. GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. Mol. Ecol. Notes 6:288-295.

Pella, J., and H. J. Geiger. 2009. Sampling considerations for estimating geographic origins of Chinook salmon bycatch in the Bering Sea pollock fishery. Alaska Dep. Fish Game Spec. Publ. No. SP 09-08.

Pella, J., and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. Fish. Bull., U.S. 99:151-167.

Raftery, A. E., and S. M. Lewis. 1996. Implementing MCMC, p. 115-130. *In* W. R. Gilks, S. Richardson, and D. J. Spiegelhalter (editors), Markov chain Monte Carlo in practice. Chapman & Hall, London.

Rexroad, C. E., R. L. Coleman, A. M. Martin, W. K. Hershberger, and J. Killefer. 2001. Thirty-five polymorphic microsatellite markers for rainbow trout (*Oncorhynchus mykiss*). Anim. Genet. 32:317-319.

Spies, I. B., D. J. Brasier, T. L. O'Reilly, T. R. Seamons, and P. Bentzen. 2005. Development and characterization of novel tetra-, tri-, and dinucleotide microsatellite markers in rainbow trout (*Oncorhynchus mykiss*). Mol. Ecol. Notes 5:278-281.

Urawa, S., S. Sato, P. A. Crane, B. Agler, R. Josephson, and T. Azumaya. 2009. Stock-specific ocean distribution and migration of chum salmon in the Bering Sea and North Pacific Ocean. N. Pac. Anadr. Fish Comm. Bull. 5:131-146.

Vulstek, S. C., C. M. Kondzela, C. T. Marvin, J. Whittle, and J. R. Guyon. 2014. Genetic stock composition analysis of chum salmon bycatch and excluder device samples from the 2012 Bering Sea walleye pollock trawl fishery. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-271, 35 p.

Whittle, J. A., S. C. Vulstek, C. M. Kondzela, and J. R. Guyon. 2015. Genetic stock composition analysis of chum salmon bycatch from the 2013 Bering Sea walleye pollock trawl fishery. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-292, 50 p.

Williamson, K. S., J. F. Cordes, and B. May. 2002. Characterization of microsatellite loci in Chinook salmon (*Oncorhynchus tshawytscha*) and cross-species amplification in other salmonids. Mol. Ecol. Notes 2:17-19.

Wilmot, R. L., C. M. Kondzela, C. M. Guthrie, and M. M. Masuda. 1998. Genetic stock identification of chum salmon harvested incidentally in the 1994 and 1995 Bering Sea trawl fishery. N. Pac. Anadr. Fish Comm. Bull. 1:285-299.

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 2016
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-
43. For the analyses of four spatial clusters, the Early time period is Weeks 24-
32 and the Late time period is Weeks 33-43.

GOA Total sample set (PSC = 3,518, n = 473)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	37	0.010	0.005	0.002	0.010	0.023	0.759	1.00
NE Asia	92	0.026	0.010	0.009	0.025	0.049	0.006	1.00
W Alaska	62	0.018	0.007	0.006	0.017	0.034	0.062	1.00
Up/Mid Yukon	4	0.001	0.003	0	0.000	0.009	1.000	1.00
SW Alaska	55	0.016	0.009	0.001	0.015	0.036	0.257	1.00
E GOA/PNW	3,268	0.929	0.015	0.898	0.930	0.955	0	1.00

BS A-season sample set (PSC = 3,726, n = 114)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	726	0.195	0.039	0.124	0.193	0.277	0	1.00
NE Asia	1,388	0.372	0.061	0.257	0.372	0.496	0	1.00
W Alaska	117	0.032	0.026	0	0.027	0.094	0.155	1.00
Up/Mid Yukon	15	0.004	0.008	0	0.001	0.027	0.986	1.00
SW Alaska	93	0.025	0.032	0	0.009	0.105	0.451	1.02
E GOA/PNW	1,387	0.372	0.057	0.261	0.372	0.485	0	1.01

BS B-season sample set (PSC = 339,094, n = 2,701)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	29,908	0.088	0.006	0.077	0.088	0.100	0	1.00
NE Asia	103,254	0.305	0.011	0.282	0.304	0.327	0	1.00
W Alaska	65,411	0.193	0.011	0.172	0.193	0.214	0	1.00
Up/Mid Yukon	18,006	0.053	0.007	0.041	0.053	0.067	0	1.00
SW Alaska	4,374	0.013	0.004	0.006	0.012	0.022	0	1.00
E GOA/PNW	118,174	0.349	0.010	0.328	0.348	0.369	0	1.00

Appendix II. -- Continued.

BS Early season sample set (PSC = 56,835, n = 453)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	15,885	0.280	0.022	0.237	0.279	0.325	0	1.00
NE Asia	13,453	0.237	0.025	0.189	0.236	0.287	0	1.00
W Alaska	10,497	0.185	0.023	0.142	0.184	0.230	0	1.00
Up/Mid Yukon	4,348	0.077	0.015	0.049	0.076	0.108	0	1.00
SW Alaska	659	0.012	0.007	0.002	0.011	0.027	0.006	1.00
E GOA/PNW	11,992	0.211	0.021	0.172	0.211	0.253	0	1.00

BS Middle season sample set (PSC = 166,973, n = 1,333)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	9,534	0.057	0.007	0.044	0.057	0.072	0	1.00
NE Asia	50,943	0.305	0.016	0.274	0.305	0.337	0	1.00
W Alaska	37,936	0.227	0.016	0.197	0.227	0.259	0	1.00
Up/Mid Yukon	7,597	0.046	0.010	0.027	0.045	0.067	0	1.00
SW Alaska	2,521	0.015	0.006	0.006	0.015	0.027	0	1.00
E GOA/PNW	58,457	0.350	0.015	0.322	0.350	0.379	0	1.00

BS Late season sample set (PSC = 115,286, n = 915)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	4,727	0.041	0.008	0.028	0.041	0.057	0	1.01
NE Asia	37,076	0.322	0.020	0.283	0.322	0.362	0	1.01
W Alaska	17,962	0.156	0.017	0.122	0.156	0.191	0	1.00
Up/Mid Yukon	6,018	0.052	0.011	0.033	0.052	0.074	0	1.01
SW Alaska	2,444	0.021	0.010	0.006	0.020	0.042	0	1.01
E GOA/PNW	47,060	0.408	0.019	0.372	0.408	0.445	0	1.01

BS area 517 sample set (PSC = 263,180, n = 2,126)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	17,001	0.065	0.006	0.053	0.065	0.077	0	1.00
NE Asia	80,586	0.306	0.013	0.281	0.306	0.332	0	1.00
W Alaska	55,478	0.211	0.012	0.188	0.211	0.235	0	1.00
Up/Mid Yukon	13,422	0.051	0.007	0.037	0.051	0.066	0	1.00
SW Alaska	3,948	0.015	0.005	0.006	0.014	0.027	0	1.00
E GOA/PNW	92,745	0.352	0.012	0.330	0.352	0.375	0	1.00

Appendix II. -- Continued.

BS area 517 Early season sample set (PSC = 32,564, n = 262)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	7,451	0.229	0.028	0.177	0.228	0.285	0	1.00
NE Asia	7,529	0.231	0.034	0.167	0.230	0.300	0	1.00
W Alaska	6,431	0.198	0.032	0.138	0.197	0.262	0	1.00
Up/Mid Yukon	3,094	0.095	0.022	0.055	0.094	0.141	0	1.00
SW Alaska	860	0.026	0.013	0.006	0.025	0.057	0.001	1.00
E GOA/PNW	7,203	0.221	0.028	0.168	0.220	0.279	0	1.00

BS area 517 Middle season sample set (PSC = 124,946, n = 1,024)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	5,298	0.042	0.007	0.029	0.042	0.058	0	1.00
NE Asia	38,358	0.307	0.018	0.271	0.307	0.344	0	1.00
W Alaska	33,660	0.269	0.018	0.234	0.269	0.306	0	1.00
Up/Mid Yukon	4,098	0.033	0.011	0.013	0.033	0.055	0	1.00
SW Alaska	1,674	0.013	0.007	0.003	0.012	0.029	0	1.00
E GOA/PNW	41,857	0.335	0.016	0.303	0.335	0.367	0	1.00

BS area 517 Late season sample set (PSC = 105,670, n = 840)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	4,692	0.044	0.008	0.030	0.044	0.061	0	1.01
NE Asia	33,032	0.313	0.021	0.272	0.313	0.355	0	1.01
W Alaska	16,971	0.161	0.018	0.127	0.160	0.197	0	1.00
Up/Mid Yukon	5,410	0.051	0.011	0.032	0.051	0.074	0	1.01
SW Alaska	1,849	0.018	0.009	0.004	0.016	0.039	0	1.01
E GOA/PNW	43,716	0.414	0.020	0.375	0.414	0.453	0	1.00

BS area 521 sample set (PSC = 44,785, n = 329)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	9,405	0.210	0.024	0.165	0.209	0.259	0	1.00
NE Asia	15,536	0.347	0.032	0.286	0.346	0.411	0	1.00
W Alaska	3,807	0.085	0.023	0.045	0.083	0.137	0	1.00
Up/Mid Yukon	2,656	0.059	0.019	0.023	0.059	0.097	0.001	1.00
SW Alaska	237	0.005	0.007	0	0.003	0.023	0.455	1.01
E GOA/PNW	13,149	0.294	0.028	0.241	0.293	0.349	0	1.00

Appendix II. -- Continued.

BS area 521 Early season sample set (PSC = 12,955, n = 102)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	5,809	0.448	0.052	0.350	0.448	0.552	0	1.00
NE Asia	3,927	0.303	0.052	0.206	0.302	0.408	0	1.00
W Alaska	803	0.062	0.040	0.008	0.054	0.155	0.000	1.00
Up/Mid Yukon	479	0.037	0.029	0	0.035	0.100	0.135	1.00
SW Alaska	40	0.003	0.007	0	0.000	0.024	0.927	1.00
E GOA/PNW	1,897	0.146	0.038	0.079	0.144	0.229	0	1.00

BS area 521 Middle season sample set (PSC = 31,449, n = 225)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	2,790	0.089	0.021	0.052	0.087	0.134	0	1.05
NE Asia	11,925	0.379	0.039	0.302	0.379	0.457	0	1.01
W Alaska	3,123	0.099	0.027	0.050	0.098	0.157	0	1.00
Up/Mid Yukon	2,393	0.076	0.022	0.038	0.075	0.123	0	1.00
SW Alaska	236	0.008	0.010	0.000	0.004	0.033	0.414	1.00
E GOA/PNW	10,985	0.349	0.036	0.281	0.349	0.421	0	1.00

BS east of 170°W sample set, areas 509, 513, 516, 517, 519 (PSC = 289,278, n = 2,332)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	20,192	0.070	0.006	0.059	0.070	0.082	0	1.00
NE Asia	86,986	0.301	0.012	0.277	0.301	0.325	0	1.00
W Alaska	60,719	0.210	0.012	0.187	0.210	0.233	0	1.00
Up/Mid Yukon	15,968	0.055	0.007	0.041	0.055	0.071	0	1.00
SW Alaska	4,252	0.015	0.005	0.006	0.014	0.026	0	1.01
E GOA/PNW	101,132	0.350	0.011	0.328	0.350	0.371	0	1.00

BS west of 170°W sample set, areas 521, 523, 524 (PSC = 49,816, n = 369)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	9,968	0.200	0.023	0.157	0.200	0.246	0	1.00
NE Asia	16,982	0.341	0.031	0.281	0.341	0.401	0	1.00
W Alaska	3,916	0.079	0.021	0.043	0.077	0.124	0	1.00
Up/Mid Yukon	2,934	0.059	0.016	0.029	0.058	0.092	0	1.00
SW Alaska	404	0.008	0.008	0	0.006	0.027	0.228	1.01
E GOA/PNW	15,617	0.314	0.027	0.262	0.313	0.369	0	1.00

Appendix II. -- Continued.

Cluster 1 Early sample set (PSC= 111,336, n=1,043)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	10,198	0.092	0.010	0.074	0.091	0.111	0	1.00
NE Asia	25,585	0.230	0.017	0.198	0.230	0.263	0	1.00
W Alaska	26,754	0.240	0.018	0.205	0.240	0.277	0	1.00
Up/Mid Yukon	7,883	0.071	0.013	0.047	0.070	0.097	0	1.00
SW Alaska	2,193	0.020	0.007	0.008	0.019	0.034	0	1.00
E GOA/PNW	38,734	0.348	0.016	0.316	0.348	0.380	0	1.00

Cluster 1 Late sample set (PSC= 88,941, n=681)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	2,055	0.023	0.007	0.012	0.023	0.038	0	1.00
NE Asia	28,479	0.320	0.023	0.275	0.320	0.367	0	1.00
W Alaska	21,622	0.243	0.023	0.199	0.243	0.288	0	1.00
Up/Mid Yukon	4,136	0.047	0.014	0.023	0.045	0.076	0	1.02
SW Alaska	1,103	0.012	0.008	0.002	0.011	0.031	0.001	1.00
E GOA/PNW	31,556	0.355	0.020	0.316	0.355	0.395	0	1.00

Cluster 2 Early sample set (PSC= 13,045, n=185)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	2,244	0.172	0.030	0.118	0.171	0.232	0	1.00
NE Asia	4,246	0.326	0.045	0.240	0.325	0.416	0	1.00
W Alaska	2,269	0.174	0.042	0.098	0.172	0.260	0	1.00
Up/Mid Yukon	1,144	0.088	0.029	0.036	0.087	0.147	0	1.00
SW Alaska	111	0.009	0.013	0	0.002	0.044	0.590	1.00
E GOA/PNW	3,032	0.232	0.034	0.169	0.231	0.302	0	1.00

Cluster 2 Late sample set (PSC= 73,346, n=535)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	4,980	0.068	0.012	0.046	0.067	0.093	0	1.00
NE Asia	25,612	0.349	0.026	0.298	0.349	0.402	0	1.01
W Alaska	9,784	0.133	0.020	0.096	0.133	0.174	0	1.00
Up/Mid Yukon	2,230	0.030	0.010	0.014	0.029	0.053	0	1.03
SW Alaska	2,340	0.032	0.012	0.012	0.031	0.059	0	1.01
E GOA/PNW	28,400	0.387	0.024	0.341	0.387	0.435	0	1.01

Appendix II. -- Continued.

Cluster 3 Early sample set (PSC= 29,591, n=320)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	7,229	0.244	0.026	0.195	0.244	0.297	0	1.00
NE Asia	8,463	0.286	0.031	0.227	0.286	0.348	0	1.00
W Alaska	2,110	0.071	0.022	0.033	0.070	0.118	0	1.00
Up/Mid Yukon	1,033	0.035	0.017	0.002	0.034	0.071	0.016	1.00
SW Alaska	346	0.012	0.008	0	0.010	0.030	0.048	1.01
E GOA/PNW	10,413	0.352	0.030	0.295	0.352	0.411	0	1.00

Cluster 3 Late sample set (PSC= 15,170, n=178)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	1,330	0.088	0.022	0.049	0.086	0.135	0	1.00
NE Asia	5,159	0.340	0.043	0.258	0.339	0.427	0	1.00
W Alaska	1,661	0.110	0.032	0.053	0.108	0.177	0	1.00
Up/Mid Yukon	1,141	0.075	0.025	0.032	0.073	0.129	0	1.00
SW Alaska	438	0.029	0.018	0.001	0.027	0.071	0.028	1.00
E GOA/PNW	5,440	0.359	0.040	0.284	0.358	0.438	0	1.00

Cluster 4 Late sample set (PSC= 6,931, n=184)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	1,143	0.165	0.030	0.109	0.164	0.228	0	1.00
NE Asia	2,134	0.308	0.045	0.223	0.307	0.399	0	1.00
W Alaska	925	0.133	0.033	0.073	0.132	0.203	0	1.00
Up/Mid Yukon	234	0.034	0.018	0.004	0.032	0.075	0.012	1.00
SW Alaska	73	0.011	0.015	0	0.004	0.053	0.588	1.00
E GOA/PNW	2,422	0.350	0.039	0.274	0.349	0.428	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[6], 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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[6] 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. -- Four spatial clusters of ADF&G groundfish statistical areas[7] of chum salmon PSC sampled from 2013 to 2016 during the B-season of the Bering Sea midwater pollock trawl fishery and analyzed for genetic stock composition. The areas sampled in 2016 in which at least three fishing vessels are represented are in bold (Fig. 16).

Cluster 1: 625504, 625531, 625600, 625630, 635501, **635504**, **635530**, **635600**, 635630, **645434**, **645501**, 645502, **645530**, **645600**, 645630, 645700, **655409**, **655410**, **655430**, **655500**, **655530**, **655600**, 655630, 655730, 665336, **665401**, 665403, 665404, **665430**, **665500**, **665530**, **665600**, **665630**, 665700

Cluster 2: **675430**, **675500**, **675530**, **675600**, **675630**, **675700**, 675730, **685500**, **685530**, **685600**, **685630**, 685700, 685730

Cluster 3: 695530, **695600**, 695631, 705530, **705600**, **705630**, **705701**, 705730, **715600**, **715630**, **715700**, 715730, **725630**, **725700**, 725730, **735630**, **735700**, 735730, 745730

Cluster 4: 705830, 715800, 725800, 725830, **735800**, 735830, 735900, 735930, 745800, **745830**, 745900, 745930, 755830, 755900, 755930, 756000, 765830, 765900, 765930, 766000, 766030, 775900, 775930, 776000, 776030, 785930, 786000, 786030

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[7] http://www.adfg.alaska.gov/index.cfm?adfg=fishingCommercialByFishery.statmaps

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AFSC-

365   GUTHRIE, C. M. III, HV. T. NGUYEN, A. E. THOMSON, K. HAUCH, and J. R. GUYON. 2018. Genetic stock composition analysis of the Chinook salmon (*Oncorhynchus tshawytscha*) bycatch from the 2016 Bering Sea walleye pollock (*Gadus chalcogrammus*) trawl fishery. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-365, 32 p.

364   SULLIVAN, J., and C. FAUNCE. 2018. Alternative sampling designs for the 2018 Annual Deployment Plan of the North Pacific Observer Program. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-364, 30 p. NTIS number pending.

363   STRASBURGER, W. W., J. H. MOSS, K. A. SIWICKE, and E. M. YASUMIISHI. 2018. Results from the eastern Gulf of Alaska ecosystem assessment, July through August 2016, 90 p. NTIS number pending.

362   ORR, A. J., J. D. HARRIS, K. A. HIRSCHBERGER, R. L. DELONG, G. S. SANDERS, and J. L. LAAKE 2017. Qualitative and quantitative assessment of use of offshore oil and gas platforms by the California sea lion (*Zalophus californianus*), 72 p. NTIS No.PB2018-100078.

361   MCCONNAUGHEY, R. A., K. E. BLACKHART , M. P. EAGELTON , and J. MARSH. 2017. Habitat assessment prioritization for Alaska stocks: Report of the Alaska Regional Habitat Assessment Prioritization Coordination Team, 102 p. NTIS No.PB2018-100160.

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358   FAUNCE, C., J. SULLIVAN, S. BARBEAUX, J. CAHALAN, J. GASPER, S. LOWE, and R. WEBSTER. 2017. Deployment performance review of the 2016 North Pacific Groundfish and Halibut Observer Program, 75 p. NTIS No. PB2017-102715.

357   LAMAN, E. A., C. N. ROOPER, S. C. ROONEY, K. A. TURNER, D. W. COOPER, and M. ZIMMERMANN. 2017. Model-based essential fish habitat definitions for Bering Sea groundfish species, 75 p. NTIS No. PB2017-102512.

356   CSEPP, D. J., D. C. HONEYFIELD, J. J. VOLLENWEIDER, and J. WOMBLE. 2017. Estuarine distribution, nutritional and thiaminase content of eulachon (*Thaleichthys pacificus*) in Southeast Alaska, with implications for Steller sea lions, 56 p. NTIS No. No. PB2017-102383.

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