NOAA Technical Memorandum NMFS-AFSC-XXX

Genetic Stock Composition Analysis of Chum Salmon from the Prohibited Species Catch of the 2018 Bering Sea Walleye Pollock Trawl Fishery and Gulf of Alaska Groundfish Fisheries

J. A. Whittle, C. M. Kondzela, J. T. Watson, P. D. Barry, Hv. T. Nguyen, E. M. Yasumiishi, D. Nicolls, and W. A. Larson

Auke Bay Laboratories
Alaska Fisheries Science Center
National Marine Fisheries Service
National Oceanic and Atmospheric Administration
17109 Lena Point Loop Road
Juneau, AK 99801

U.S. DEPARTMENT OF COMMERCE
xxxxx, Secretary
National Oceanic and Atmospheric Administration
xxxxxx, Under Secretary and Administrator
National Marine Fisheries Service
Xxxxxx, Assistant Administrator for Fisheries

February 2021

This document is available to the public through:

ABSTRACT

Chum salmon (*Oncorhynchus keta*) that are caught in Alaska's federally-managed groundfish trawl fisheries are designated as prohibited species catch (PSC). We analyzed genetic stock compositions of chum salmon PSC samples collected from the 2018 walleye pollock (*Gadus chalcogrammus*) fishery in the Bering Sea and from the federal groundfish fisheries in the Gulf of Alaska (GOA). Samples were genotyped for 11 microsatellite markers from which stock contributions were estimated using a range-wide chum salmon microsatellite baseline. In 2018, one genetic sample was collected from approximately every 32 chum salmon caught in the Bering Sea midwater pollock trawl fishery. The evaluation of sampling in the Bering Sea based on time, location, and vessel indicated that the number of genetic samples was representative of the total chum salmon PSC in the Bering Sea, with the exception that several high chum salmon catches were under-sampled due to lack of sampling materials. Based on the analysis of 2,193 chum salmon collected throughout the B-season, the largest stock group was Northeast Asia (49%), followed by Southeast Asia (18%), Western Alaska (15%), Eastern GOA/PNW (12%), Upper/Middle Yukon (3%), and Southwest Alaska (2%) stocks. The substantial increase in the proportion of Northeast Asia stocks and the decrease in Eastern GOA/PNW stocks in the past two years may be due to a temporal shift in bycatch occurrence. Most of the 2017-2018 Bering Sea chum salmon PSC was caught in a narrow window of time, several weeks earlier in the B-season than in past years. Similar to previous years, the majority of chum salmon caught in the Bering Sea B-season pollock fishery were age-4. The age-3 chum salmon were predominately from North American stocks, whereas most age-4 and age-5 chum salmon were from Asian stocks. The three fishing sectors -- catcher-processor, shoreside, and mothership -- had similar

stock proportions, although the total PSC numbers varied by sector. Of the 974 chum salmon samples from the GOA groundfish fisheries, the highest proportion was from Eastern GOA/PNW (87%) stocks, similar to previous years.

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 (NPFMC 2018, 2019) 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 for understanding the effects that fishing has on chum salmon stocks, especially those with conservation concerns (NPFMC 2012).

We present the genetic stock composition estimates for the samples of chum salmon PSC collected during 2018 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 95.7% of the total chum salmon taken in the groundfish fisheries (NMFS 2019a). In the GOA, the majority (88%) of the chum salmon were caught in the pollock trawl fishery, with the remainder caught in other groundfish fisheries (NMFS 2019b).

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 ADF&G groundfish statistical areas (Fig. 1). The AKFIN reports were used to construct spatial-

---

[1] AKFIN website

temporal sets of genetic samples from the 2018 chum salmon PSC caught along the outer
continental shelf.
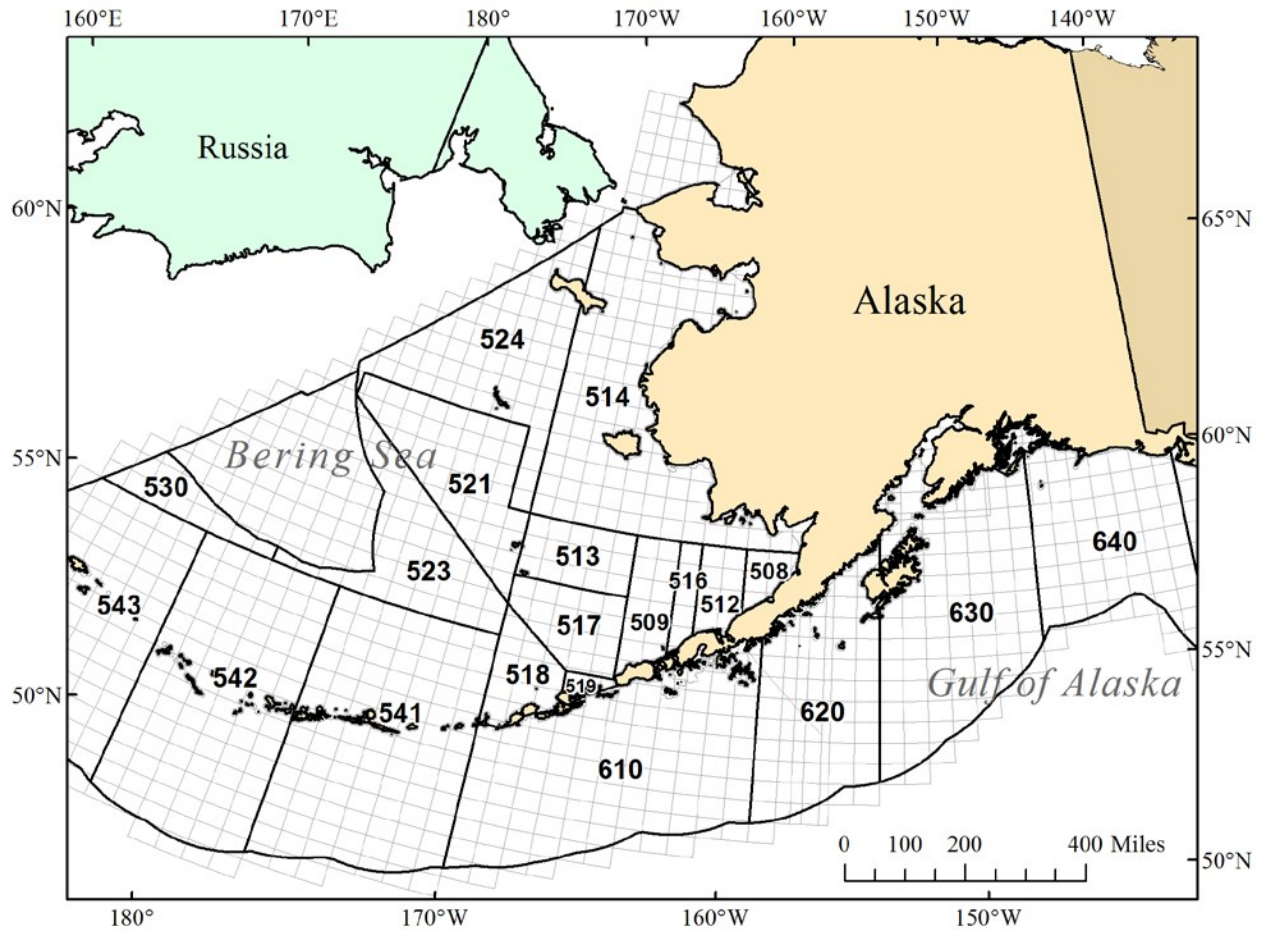
Figure 1. -- NMFS reporting areas associated with the Bering Sea-Aleutian Island and Gulf of
Alaska groundfish fisheries are numbered and outlined in black. The ADF&G
groundfish statistical areas are outlined in light gray.

For additional background and methods, this report is intended to be supplemented with
the chum salmon reports prepared previously for the 2005-2016 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, 2018). 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 2018 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 axillary processes (for genetic analysis) and scales (for ageing) from every 30th chum salmon throughout the season.

In 2018, an estimated 295,062 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 sixth largest catch of chum salmon in the pollock fisheries since 1994 (NMFS 2019a). This catch is nearly twice the 1994-2017 average of 166,396 chum salmon and more than three times the median of 86,662 (Fig. 2). As in previous years, nearly all (99.9%) of the chum salmon were caught during the pollock B-season (approximately 10 June to November 1) (Fig. 3) in NMFS reporting areas 509-524 (Fig. 1). The peak abundance of the chum salmon PSC in 2018 occurred very early in the B-season, 2-3 weeks earlier than in 2017, which also peaked several weeks earlier than previous years, and more than a month earlier than in 2011-2016 (Fig. 4). Genetic samples were collected from 9,188 fish (NMFS 2019b), which represents a sampling rate of 1 of every 32.1 chum salmon (or 3.12% of the chum salmon catch).
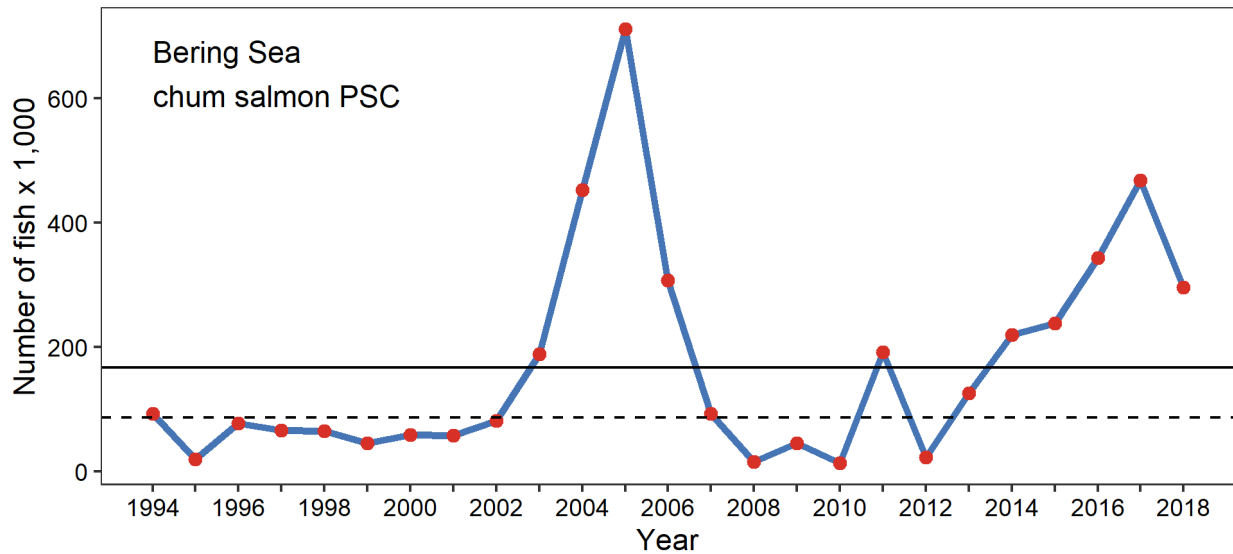
Figure 2. -- Yearly estimates for the non-Chinook salmon prohibited species catch (PSC) from the Bering Sea pollock-directed trawl fisheries (NMFS 2019a). The solid horizontal line represents mean PSC and the dashed line represents median PSC, 1994-2017.

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 strata were pooled prior to testing. For the entire year, weeks 3-16, 22-23, and 39-40 were pooled. For the B-season, weeks 23-24, 30-31, 32-34, and 36-40, and three areas of aggregated NMFS reporting areas (509, 513), (517, 519), and (521, 523, 524) were pooled. Temporal bias by statistical weeks (ending on Saturday) appears to be minimal (Fig. 3) when samples were pooled across management areas, although the Chi-square test was highly significant ($\chi^2 = 71.1$, 17 d.f., P << 0.001), due primarily to under-sampling during weeks 26-27. During the B-season, temporal biases also appear minimal at finer spatial scales (Fig. 5), but the Chi-square test was highly significant; ($\chi^2 = 101.7$, 18 d.f., P << 0.001) due primarily to under-sampling in aggregated NMFS reporting areas (517, 519) and

(521, 523, 524) during weeks 26 and 27. 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.
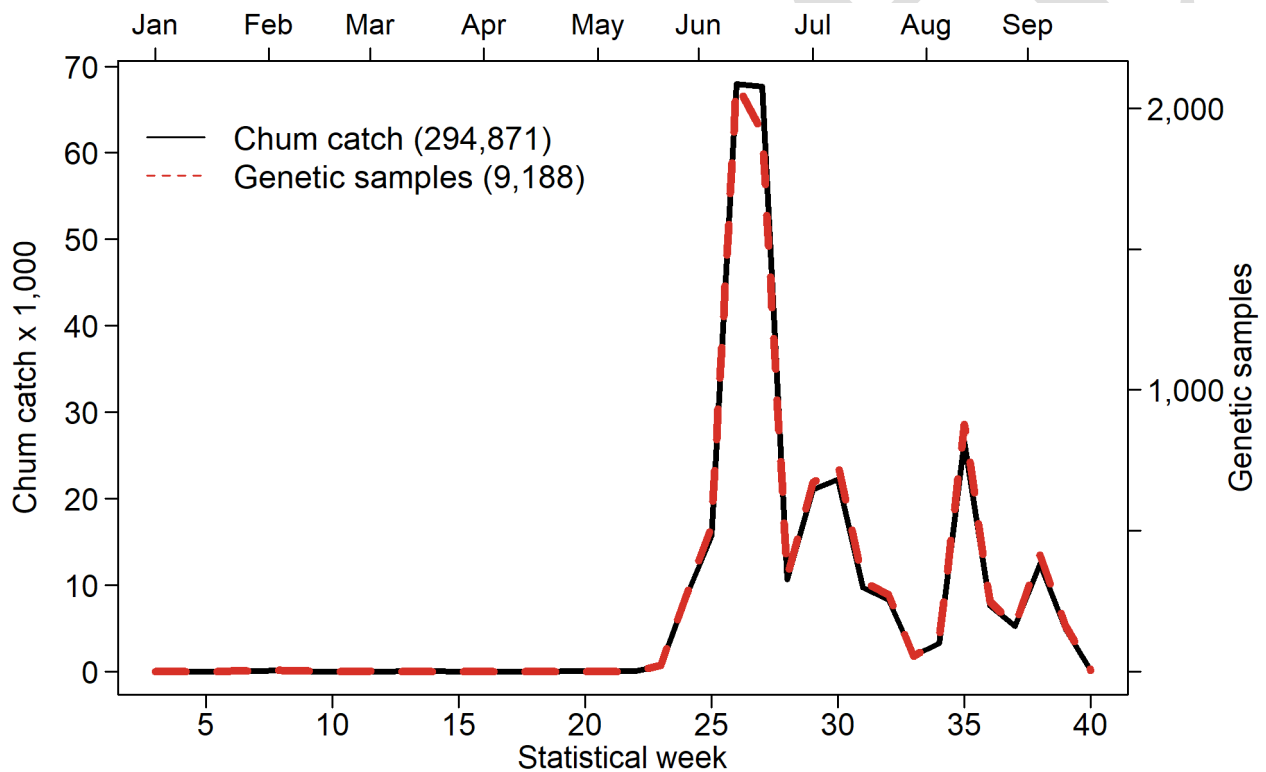
Figure 3. -- Number of Bering Sea chum salmon caught (black, solid line) and genetic samples collected (red, dashed line) from the 2018 Bering Sea pollock trawl fishery by statistical week. Weeks 1-22 correspond to the A-season, whereas weeks 23-40 correspond to the B-season.
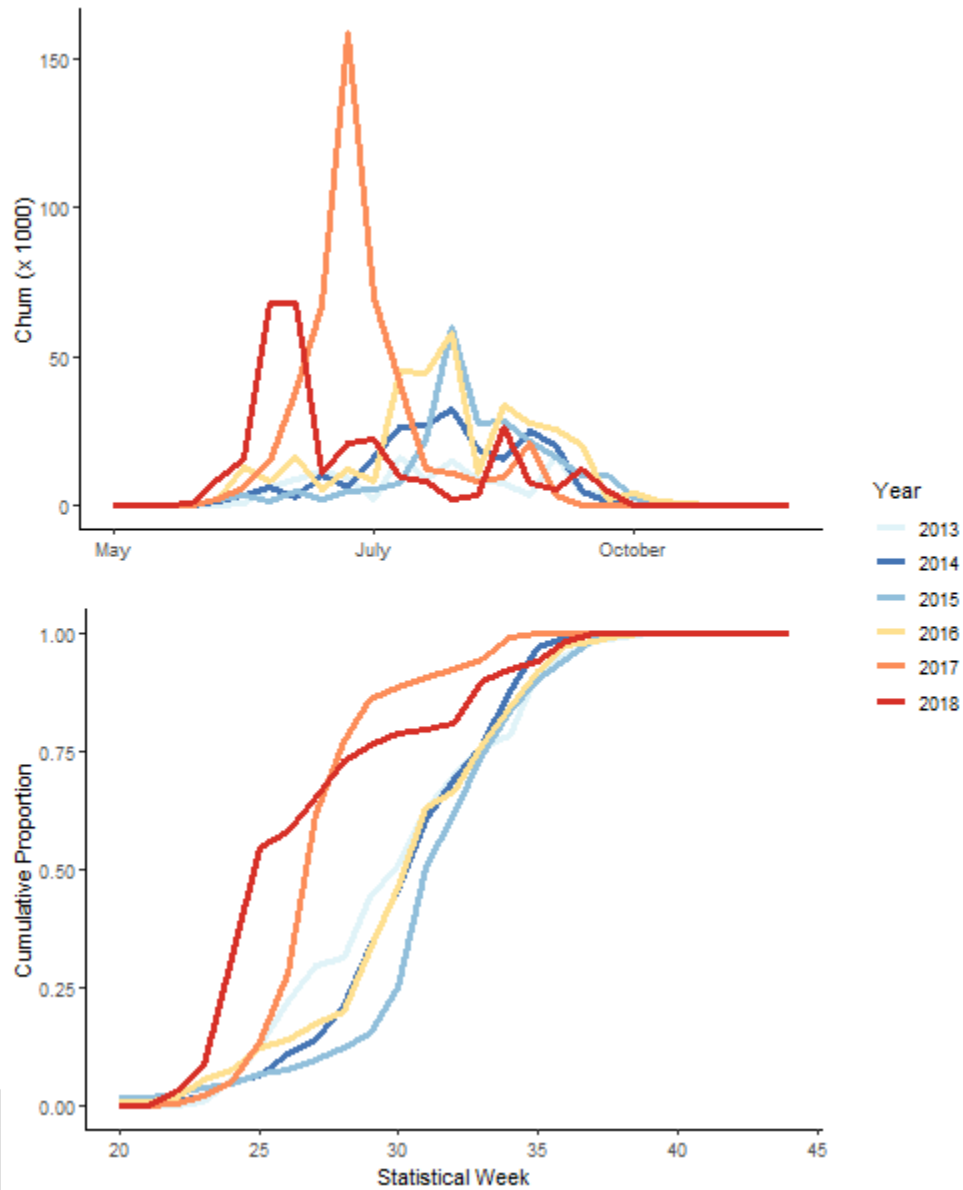
Figure 4. -- Number of chum salmon caught during the B-season (top) and cumulative proportion of bycatch (bottom) from the Bering Sea pollock trawl fishery by statistical week for years 2013 to 2018.
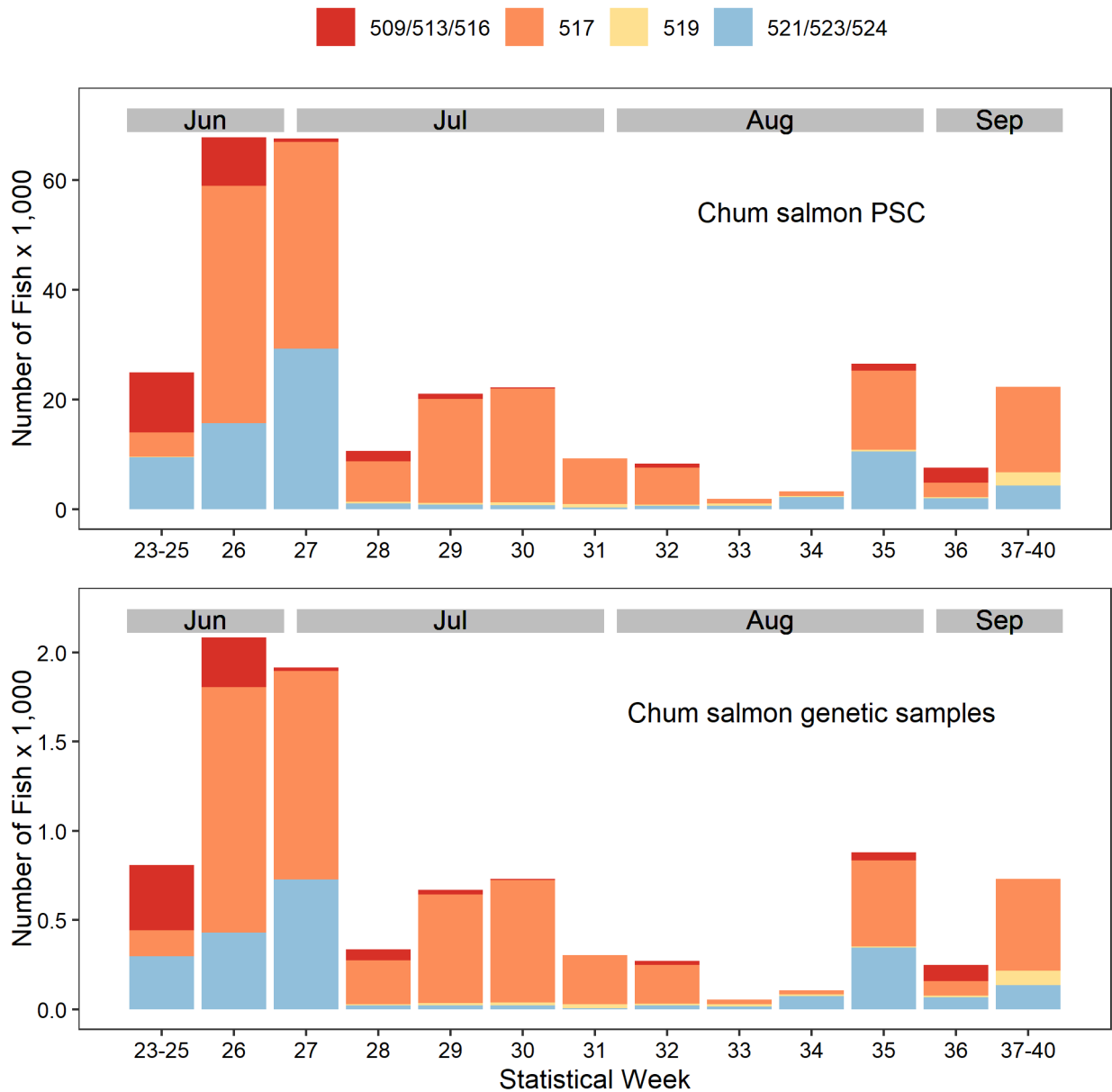
Figure 5. -- Number of Bering Sea chum salmon caught (top) and genetic samples collected (bottom) from the 2018 Bering Sea pollock B-season by statistical week and NMFS reporting area (designated in the legend).

The systematic collecting protocol was also evaluated by comparing the total number of chum salmon caught on each vessel to the number of genetic samples collected from each vessel during 2018. Of the 97 vessels that participated in the midwater trawl fishery during the A- and B-seasons, 90 vessels caught chum salmon. The chum salmon catch was subsampled by observers for genetic samples across a large range (0 – 20,000 fish) of chum salmon catch per vessel (Fig.

6). Per vessel, the ratio of numbers of genetic samples to numbers of chum salmon caught was 1 in 31.0 ± 3.7 fish (mean $\pm$ S.D.; unweighted by proportion of bycatch each vessel caught), which is close to the protocol sampling goal of one genetic sample from every 30th chum salmon caught. In 2018, 47% of the chum salmon PSC was counted from at-sea hauls and 53% from shoreside offloads. By vessel, the sampling ratio was 1 in 32.3 fish and 1 in 30.2 fish for at-sea and shoreside offloads respectively, a non-significant difference (t-test; $P = 0.12$). Several catcher-processor vessels had at-sea sampling rates lower than expected for some hauls (Fig. 6) due to large catches and insufficient sampling materials. The under-sampling of the catcher-processor vessel with the highest PSC explains most of the sampling bias observed across temporal and spatial strata described above (Figs. 3, 5).
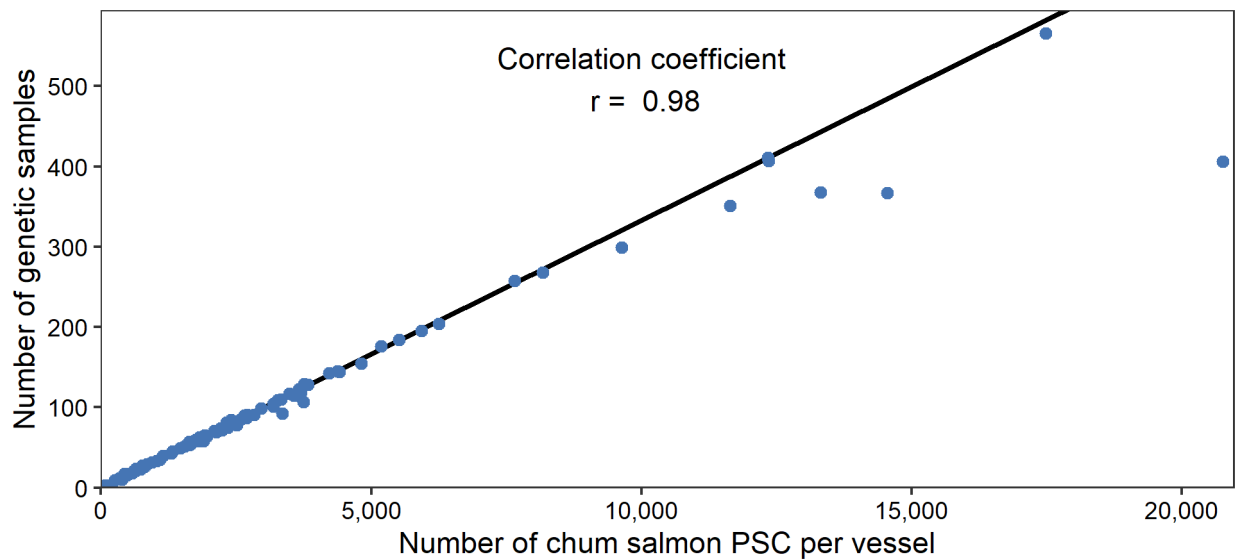
Figure 6. -- Bering Sea chum salmon catch and genetic samples from the 2018 Bering Sea pollock A- and B- seasons. Number of genetic samples collected from the total number of chum salmon caught from each of 90 vessels; black diagonal line represents the expected sampling rate.

Gulf of Alaska

The estimated PSC of chum salmon in the GOA (NMFS 2019b) 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. 2019). In 2018, chum salmon samples were collected in the GOA (AFSC 2017) primarily from the pollock trawl fishery, which caught about 88% of the chum salmon PSC in the GOA (Fig. 7). The majority of chum salmon from the non-pollock fisheries were caught in the shallow-water flatfish, rockfish, sablefish, and halibut fisheries between the pollock B- and C- seasons (May 31-August 24; Fig. 8). Approximately 14% 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 1,052 samples from the pollock fishery from NMFS reporting areas 610, 620, and 630 during primarily the pollock C- and D- seasons[2], and 3 samples from the rockfish fishery (Figs. 1, 8, 9).

---

[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 (Table 3).
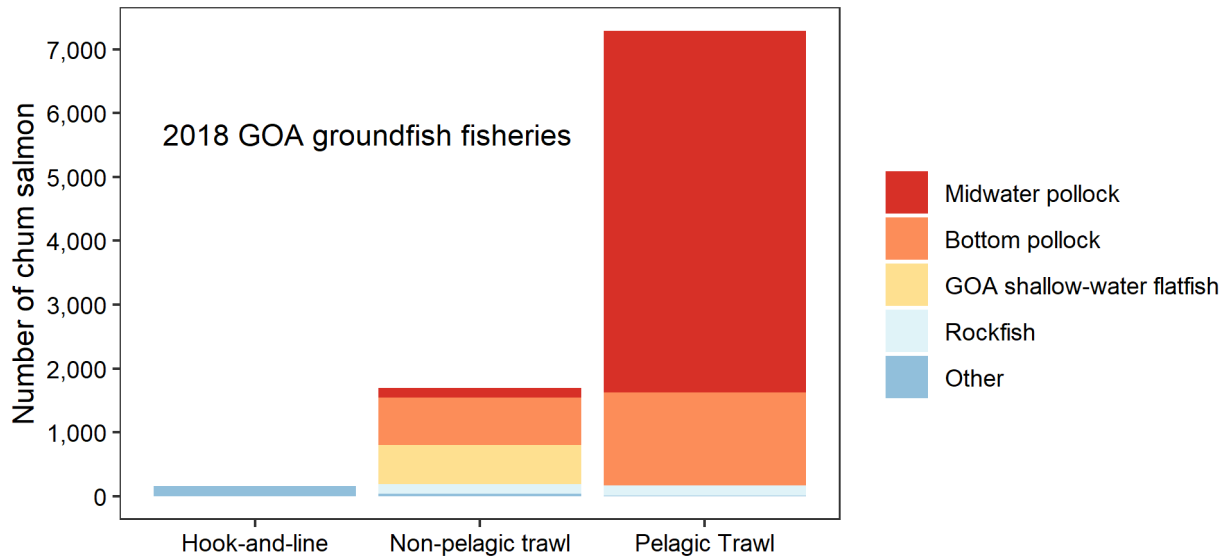
Figure 7. -- Estimated number of chum salmon caught (n = 9,149) in the 2018 Gulf of Alaska groundfish fisheries by target species. The 210 chum salmon caught in the Atka mackerel, arrowtooth flounder, halibut, Pacific cod, rex sole, and sablefish fisheries were combined as "Other".
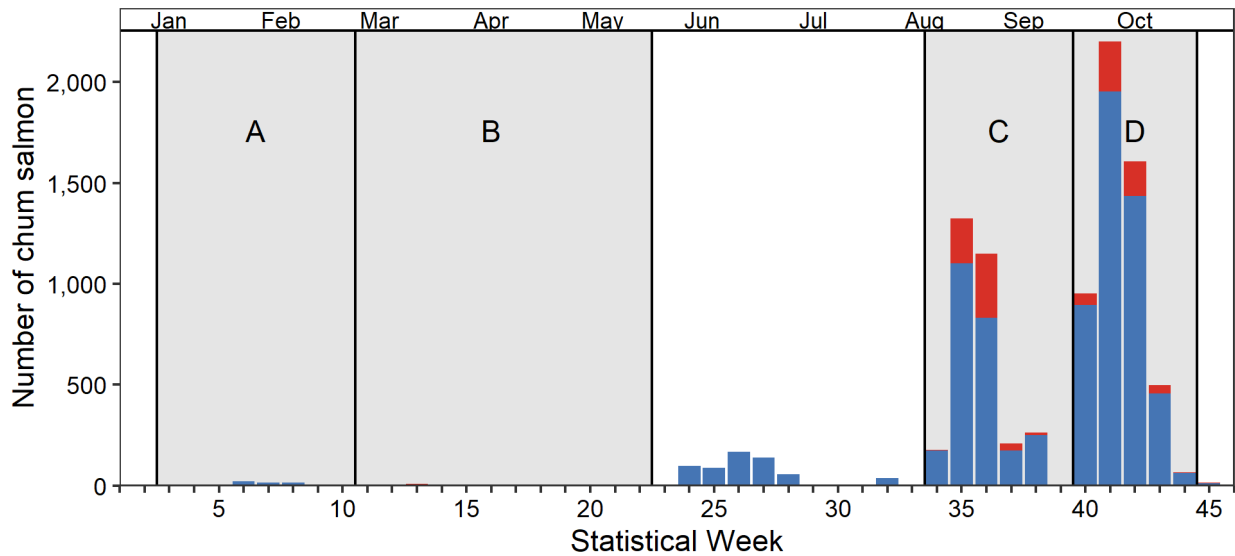
Figure 8. -- Number of chum salmon caught (blue plus red) and genetic samples collected (red) from the 2018 Gulf of Alaska groundfish fisheries by statistical week. Grayed areas with letter designations distinguish the NMFS management seasons for pollock in the Western and Central Regulatory Areas (NMFS reporting areas 610-630).
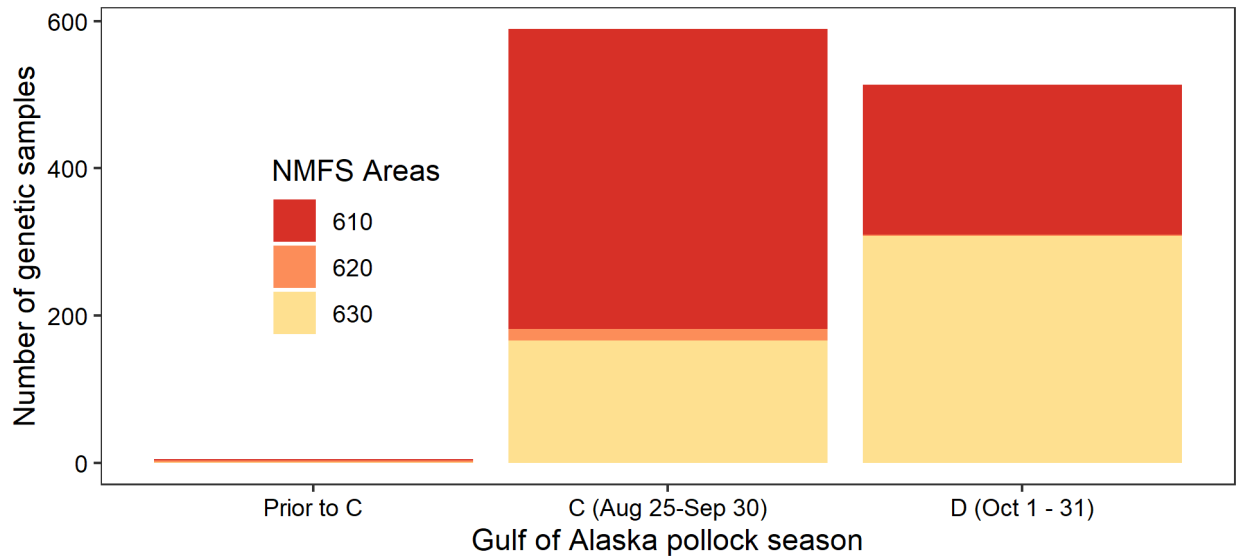
Figure 9. -- Number of chum salmon genetic samples collected from the 2018 Gulf of Alaska groundfish fisheries by pollock season and NMFS reporting areas.

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 full collection of 9,144 chum salmon received at ABL 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 2,287 chum salmon sampled in the Bering Sea B-season and all of the 1,055 chum salmon sampled in the GOA groundfish fisheries. An additional 313 samples were selected for the 4-cluster spatio-temporal analyses to increase the sample sizes to approximately 200 samples in each time-area stratum. Too few samples were collected from the Bering Sea A-season to analyze (PSC = 326; samples collected = 11).

DNA was extracted and microsatellite genotyping was performed (Guyon et al. 2010) for 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. 1998), *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 with the

GeneScan™ 600 LIZ™ Size Standard for analysis with 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 3,655 chum salmon bycatch samples from the Bering Sea and GOA, 95% were

successfully genotyped for 8 or more of the 11 loci for an average of 10.8 loci (Table 1). One

duplicate genotype was detected in the Bering Sea bycatch samples with GenAlEx 6.5 (Peakall

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

Table 1. -- Number of genetic samples analyzed for chum salmon from the 2018 Bering Sea
pollock trawl fishery and Gulf of Alaska groundfish fisheries.

Number loci	Genetic samples
11	3,065
10	290
9	61
8	59
<8	180

Quality control of sample handling and genotyping was examined by reanalyzing 8.8% of

the samples: DNA was plated from the eight samples in the left-most column of each elution plate

for a total of 320 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 2). Across 11 loci there were a total of 68 differences in 6,794 alleles between the original

and quality control datasets, which represented an overall discrepancy rate of 1.00%.

Table 2 -- Number of allele differences by locus between the original and quality control datasets for 2018 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	620	4	0.65
Omm1070	628	15	2.39
Omy1011	626	4	0.64
One101	594	14	2.36
One102	616	3	0.49
One104	624	1	0.16
One114	626	4	0.64
Ots103	622	5	0.80
Ots3	636	10	1.57
OtsG68	606	5	0.83
Ssa419	596	3	0.50

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 the data was formatted 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 (SE Asia), Northeast Asia (NE Asia), Western Alaska (WAK), Upper/Middle Yukon (Up/Mid Yukon), Southwest Alaska (SW AK), and the Eastern GOA/Pacific Northwest (EGOA/PNW) (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.
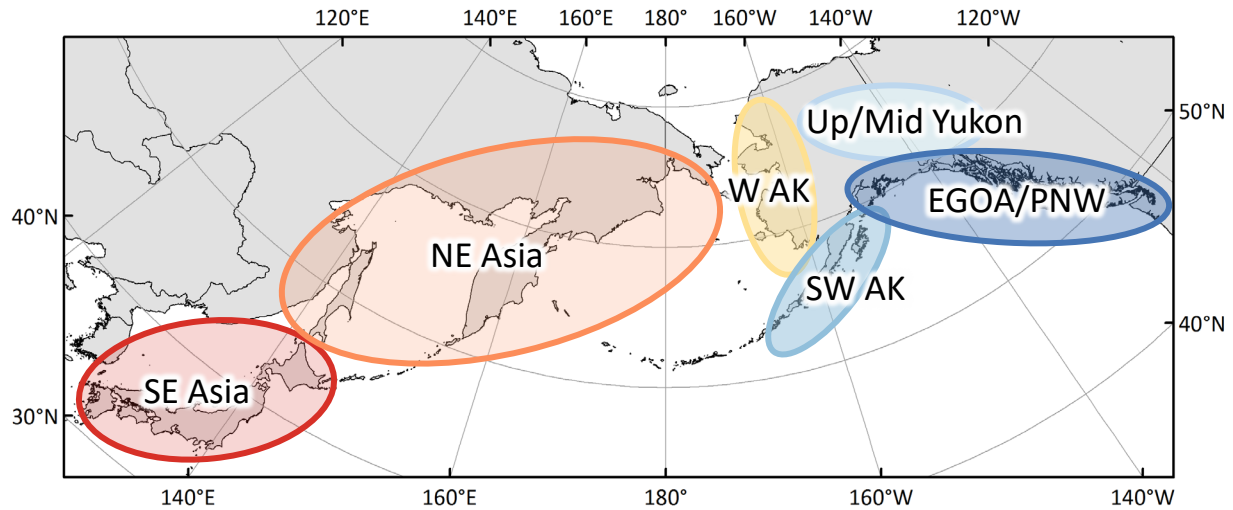
Figure 10. -- Six regional groups of baseline chum salmon populations used in this report.

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, 2018), the stock composition analysis for the 2018 chum salmon samples was performed with a Bayesian procedure (BAYES software; Pella and Masuda 2001). BAYES stock composition estimates based on data from all 11 loci were derived for the six regional groups (Table 3; 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

---

[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.

regions. Convergence was assessed with Gelman-Rubin shrink factors, which were 1.00-1.03 (Table 3; Appendix II) across all datasets, 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 Up/Mid Yukon stock estimate from the Gulf of Alaska sample set (Table 3B) indicates that there is a 67% probability that essentially zero chum salmon from this stock were caught in this season.

Recently a more computationally efficient mixed-stock analysis (MSA) program developed within the R statistical environment, *rubias* (Moran and Anderson 2019), was developed and adopted by the Alaska Department of Fish and Game for bycatch analyses in state managed salmon fisheries (Barclay 2020). We evaluated the effect of transitioning from BAYES to rubias by conducting MSA on 16 mixtures for the Bering Sea chum bycatch samples. The *rubias* package uses a Bayesian approach to the conditional MSA model that treats the relative frequencies of alleles in baseline stocks as if they were known without error. Additionally the package can correct for biases in reporting group estimates and provides the option to run the fully Bayesian model which treats the baseline allele frequencies as unknowns and estimates them from

the baseline and mixture samples. For all comparisons conducted in rubias, the MCMC sampling properties and prior distribution on stock proportions were identical to that of BAYES. The convergence of each chain was assessed with the Gelman-Rubin statistic (Gelman and Rubin 1992) estimated with the gelman.diag function in the coda library (Plummer et al. 2006) within R. No major differences were observed between inferences made with the two programs. All results presented below are from analyses with BAYES and comparisons between the two programs are reported in Appendix V.

Table 3. -- Regional stock composition estimates of chum salmon collected from 2018 Bering Sea and GOA trawl fisheries. BAYES mean proportion estimates are provided with standard deviations (SD), 95% credible intervals, median estimate, P = 0 statistic (values > 0.5 are shaded), and the Gelman-Rubin shrink factor. PSC is the number of chum salmon caught (census in Bering Sea and estimate in GOA) and n is the number of samples genetically analyzed.

A. Bering Sea pollock trawl fishery, B-season (PSC = 294,545; n = 2,193)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink
SE Asia	52,105	0.177	0.009	0.159	0.177	0.195	0	1.00
NE Asia	144,357	0.490	0.014	0.463	0.490	0.518	0	1.00
W Alaska	45,507	0.154	0.011	0.134	0.154	0.176	0	1.00
Up/Mid Yukon	10,044	0.034	0.005	0.024	0.034	0.045	0	1.00
SW Alaska	5,832	0.020	0.005	0.009	0.020	0.031	0	1.00
E GOA/PNW	36,671	0.124	0.009	0.108	0.124	0.142	0	1.00

B. Gulf of Alaska groundfish fisheries (PSC = 9,149; n = 974)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink
SE Asia	320	0.035	0.006	0.023	0.035	0.048	0	1.00
NE Asia	438	0.048	0.010	0.030	0.047	0.068	0	1.00
W Alaska	308	0.034	0.008	0.020	0.033	0.050	0	1.02
Up/Mid Yukon	61	0.007	0.004	0	0.006	0.015	0.673	1.03
SW Alaska	40	0.004	0.004	0	0.004	0.015	0.947	1.00
E GOA/PNW	7,981	0.872	0.012	0.847	0.873	0.896	0	1.00

COMPARISON WITH PREVIOUS ESTIMATES

Bering Sea

The stock composition results from the analysis of the 2018 chum salmon samples collected during the B-season were similar to the results from past years for three of the six regions (W Alaska, Up/Mid Yukon, and SW Alaska), prior to and after systematic sampling was in effect (Fig. 11, upper panel). Southeast Asia stock estimates were similar to those from previous years with systematic sampling. In 2018, NE Asia stocks dominated the regional contributions and the EGOA/PNW stocks were about half that of the average since systematic sampling went into effect. 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 2005-2018 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, 2018). 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 extrapolations being relatively free of sampling bias. The

location and timing of collections prior to 2011 was not always representative of the entire chum salmon PSC within a given year. In 2018, the numbers of chum salmon from SE Asia and EGOA/PNW stocks were higher and lower respectively, than in previous years (2011-2017) under systematic sampling. The above average bycatch in 2018 and the high proportion of NE Asia fish is reflected in high numbers of chum salmon intercepted from this region.
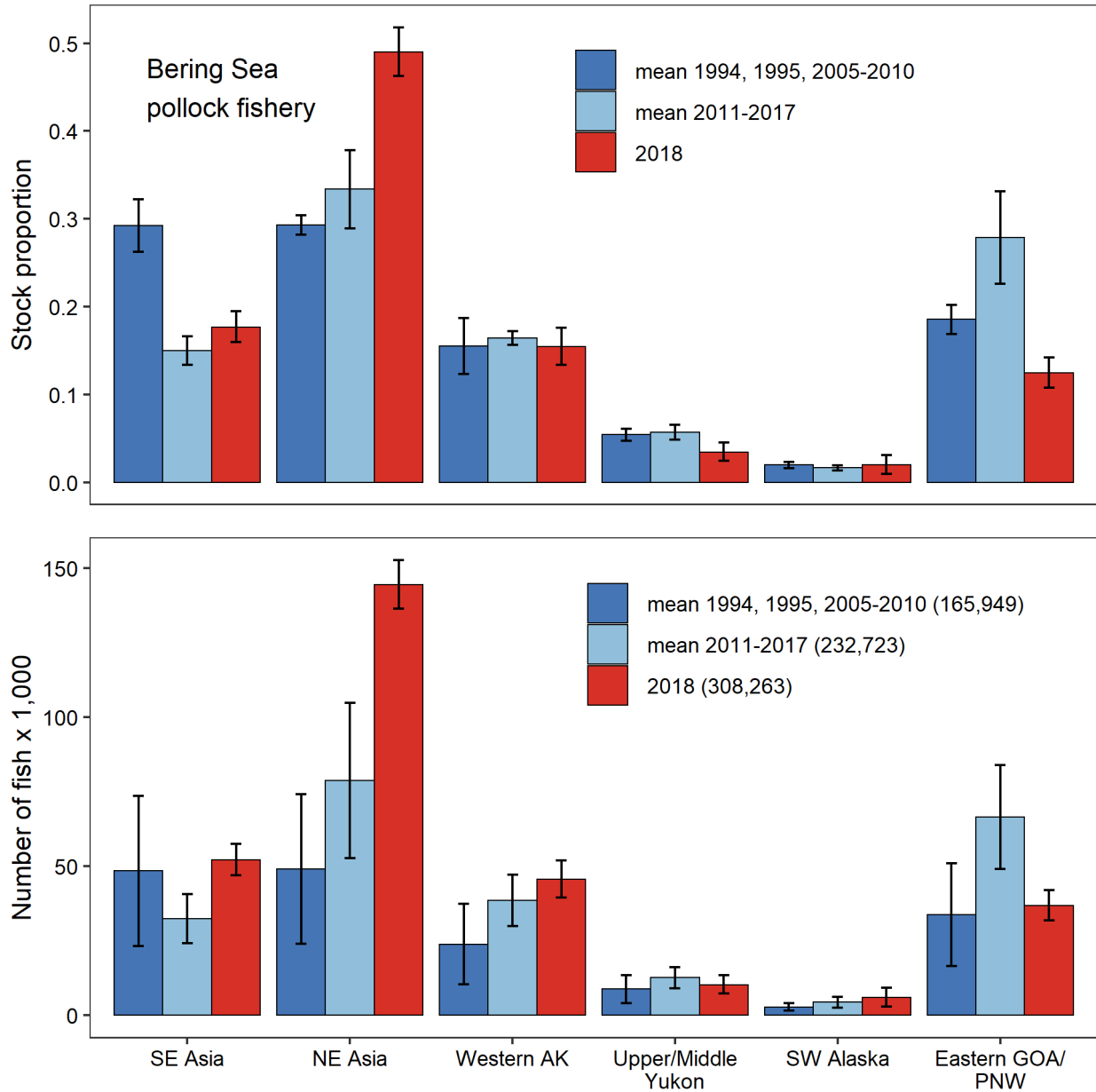
Figure 11. -- Comparison of the 2018 Bering Sea chum salmon stock composition estimates with the estimates from 2011 to 2017 (systematic sampling) and the unweighted mean estimates from 1994, 1995, and 2005-2010 (non-systematic sampling). Proportions in top panel (B-season); numbers of fish (A+B seasons) in bottom panel, which for comparison purposes across years are based on the total chum salmon caught in all groundfish fisheries (NMFS 2018). Standard errors of the mean estimates are shown for the combined years; 95% BAYES credible intervals are shown for the 2018 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 2011-2018 are censuses.

Gulf of Alaska

The stock composition estimates of the 2018 GOA chum salmon samples were nearly

identical to the 2014-2017 estimates, with 87% of the contribution from EGOA/PNW stocks (Fig.

12). In all five years, the contributions from all other regions was very low; chum salmon from the

Up/Mid Yukon region were not present in the GOA samples in any of the five years ("P = 0"

value of 0.67-1.00; Appendix II).
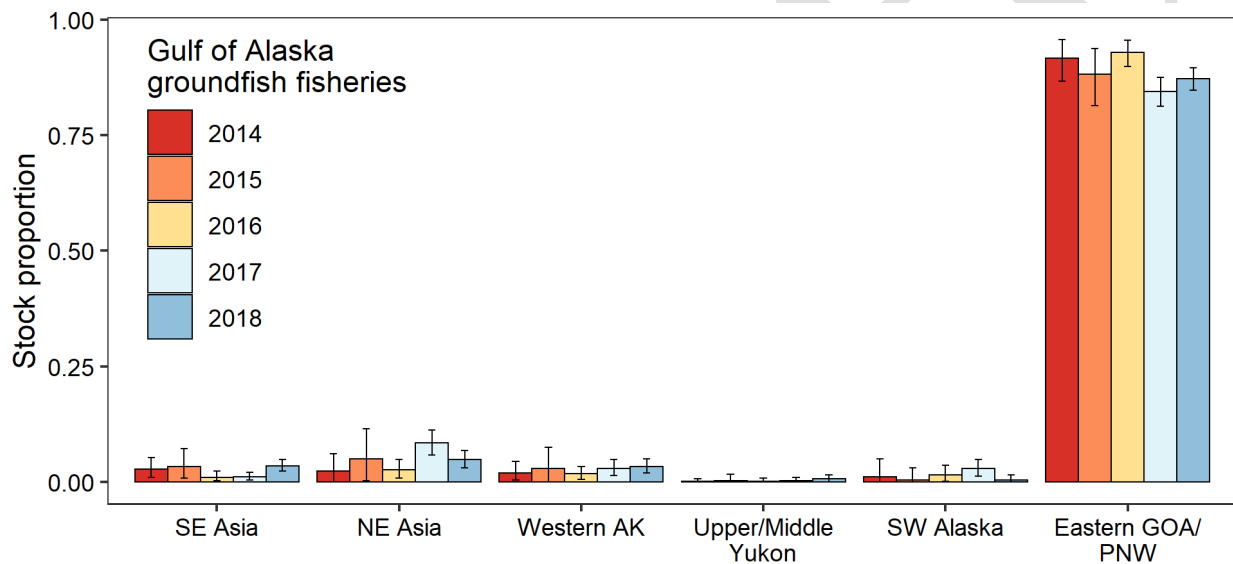
Figure 12. -- Stock composition estimates and 95% BAYES credible intervals for the 2014-2018
chum salmon collected from the Gulf of Alaska groundfish fisheries.

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.

As with the 2005-2017 analyses, the 2018 Bering Sea sample set from the B-season was split into three time periods: Early, Middle, and Late (Table 4). Stock composition estimates were made as described previously for each of the three temporal strata (Appendix II). Notably, more of the chum salmon PSC was caught earlier in the 2018 season than in previous years, a pattern also observed in 2017.

Table 4. -- Temporal groups from the genetic sample sets of chum salmon caught in the 2018 Bering Sea, B-season pollock fishery.

Time period	Weeks	Dates	Number of samples
Early	23-29	June 9 - July 21	1,384
Middle	30-34	July 22 - August 25	356
Late	35-40	August 26 - October 6	453

The stock composition of chum salmon caught in the 2018 Bering Sea pollock fishery changed during the course of the season (Fig. 13; Appendix II). The NE Asia contribution was the highest of all reporting groups in all three time periods. The NE Asia contributions were identical in the Early and Late time periods (46%) and higher during the Middle time period (66%). The contributions from SE Asia (22% to 10%) and Up/Mid Yukon (4% to 1%) decreased over the three time periods, while the EGOA/PNW contributions increased over three-fold (8% to 27%). The W Alaska contributions were similar in the Early and Late time periods, 18% and 14%, respectively, and lowest in the Middle time period (8%). The SW Alaska stock contributions have not exceeded 5.6% in any year and therefore data for this regional group is not included.

The 2011-2017 stock compositions for similar temporal strata are included for comparison purposes (Fig. 13). Across the years, the SE Asia contribution was higher in the Early time period than the Middle and Late time periods. The NE Asia contribution was higher in the 2018 Middle time period than in all other years or time periods. The NE Asia contributions varied across years

within each time period in a manner that was consistent across all three time periods, especially in the Middle and Late time periods. The W Alaska contributions were similar across years within each time period and slightly higher across years in the Early and Middle time periods than the Late time period. The Up/Mid Yukon contributions were consistently low across years at all three time periods. The EGOA/PNW contributions varied across years within each time period with nearly identical patterns of variation in the Middle and Late time periods; a decrease in contributions since 2015 continued in 2018. The inverse relationship of stock proportions across years between the NE Asia and E GOA/PNW regions during the Middle and Late time periods persisted in 2018. 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.
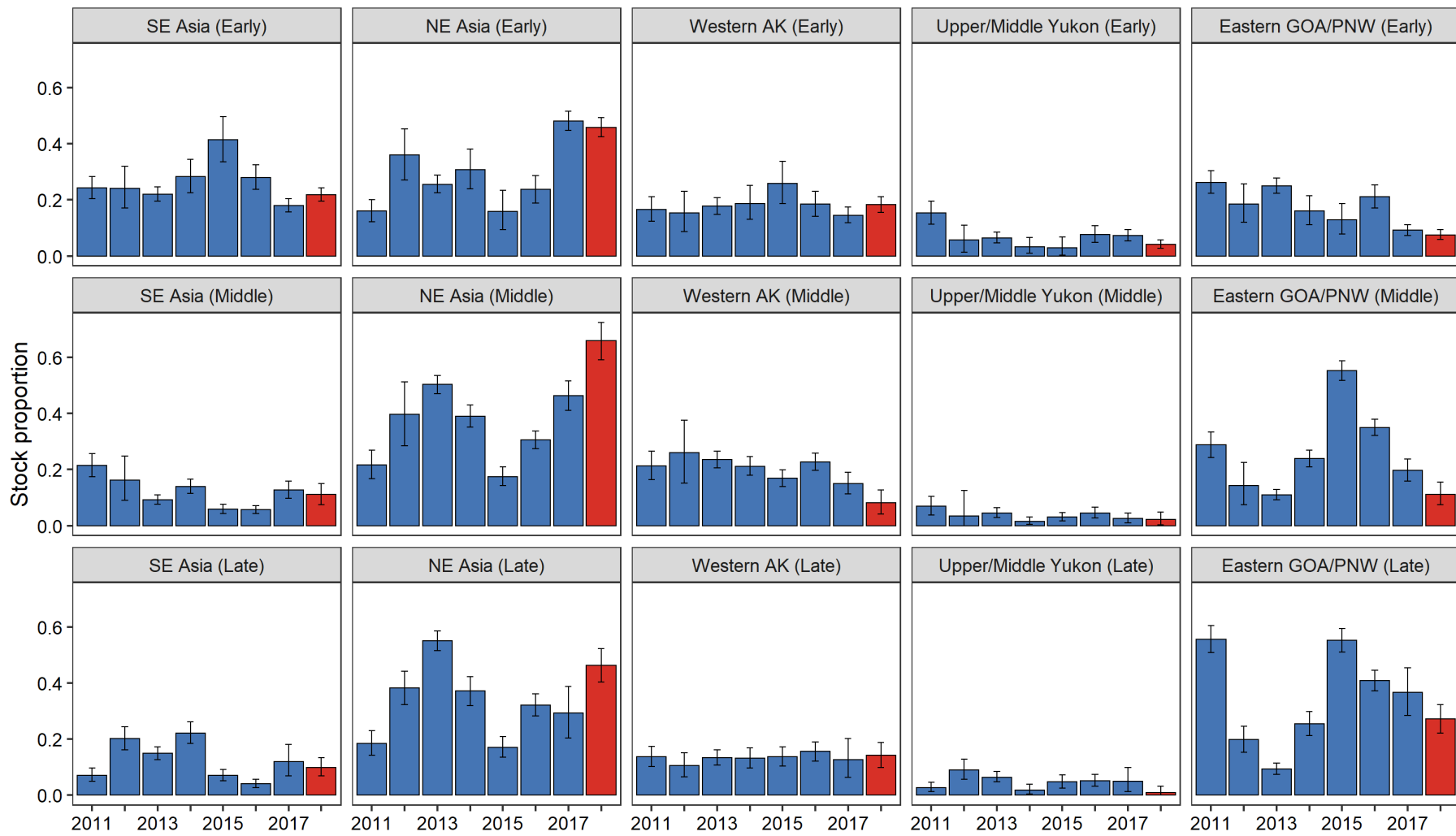
Figure 13 -- Stock composition estimates (mean ± 95% BAYES credible intervals) for the 2011-2018 chum salmon samples from the Early, Middle, and Late periods of the Bering Sea pollock B-season (defined in Table 4). Not shown is the SW Alaska region for which estimates never exceeded 5.6%. The current sampling year (2018) is denoted in red.

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 2018, for the eighth year, the Observer Program undertook a complete census of chum salmon caught in the Bering Sea pollock trawl fisheries. Approximately 50% of the chum salmon catch was counted and sampled at shoreside processing facilities; the remaining 50% was counted and sampled at sea. Of the shoreside offloads, 41% of the chum salmon catch was from vessels that fished in one ADF&G statistical area during a trip. For the 59% of chum salmon catch offloaded from vessels that fished in multiple ADF&G statistical areas during a trip (20% of total chum salmon catch), the area assigned to an offload was the area where the highest weight of pollock was caught.

The 2018 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, and 519). Stock compositions for the two spatial strata were estimated as described previously (Fig. 14; Appendix II). Approximately two-thirds of the contribution to the east and west of 170°W in the Bering Sea was from Asian stocks. NE Asia stocks were the largest contributor to the chum salmon catch with a slightly higher contribution (51%) in the area east of 170°W than in the west (42%). Southeast Asia stocks contributed more to waters west of 170°W than to the southeastern Bering Sea (26% vs. 15%), whereas the W Alaska stock contribution was higher in the east (17% vs. 11%). The contributions from other stocks were similar between the spatial strata.
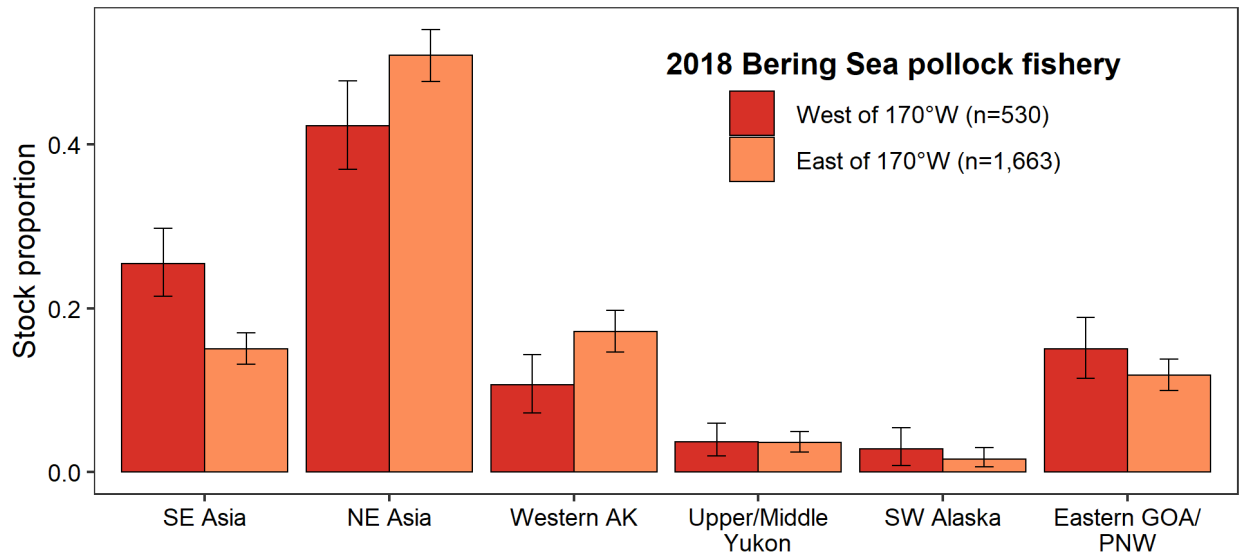
Figure 14. -- Stock composition estimates and 95% BAYES credible intervals for the 2018 chum salmon collected during the Bering Sea pollock B-season from the U.S. waters of the Bering Sea west of 170°W (aggregate area 521/523/524) and the southeastern Bering Sea east of 170°W (aggregate area 509/513/517/519).

To better understand the distribution of chum salmon stocks across time and space in the Bering Sea PSC from the pollock fishery, the 2018 stock composition estimates were compared from four spatial clusters and two time periods. Samples were aggregated into Early (statistical weeks 23-32) and Late (statistical weeks 33-40) time periods at four clusters that were based on ADF&G statistical areas along the continental shelf edge (Table 5; Fig. 15; Appendix IV). Excluded from this analysis are 205 samples (8%) from offloads of vessels that fished in more than one cluster. The NE Asia stocks dominated the chum salmon catch at all four clusters and both time periods, with the exception of the EGOA/PNW stock contribution in Cluster 3 during the Late time period (Fig. 16; Appendix II). Several stocks exhibited a gradient of contributions along the continental shelf. The SE Asia stocks were most prevalent in the northwest portion (Cluster 4) of the shelf in the Late time period, whereas the W Alaska stocks had higher contributions toward the southeastern Bering Sea (Cluster 1) in both time periods. The

EGOA/PNW stock contributions were highest in the Late time period in Clusters 1-3.

Contributions from the Up/Mid Yukon and SW Alaska stocks were low in all four clusters and

both time periods.

Table 5. -- Collection information for the four spatial clusters of chum salmon caught in two time periods, Early (weeks 23-32) and Late (weeks 33-40), during the 2018 Bering Sea pollock B-season and analyzed for genetic stock composition. The sample size (n = 57) of Cluster 4, Early time period, was too small for analysis.

Spatial cluster	Time period	Samples received	Samples analyzed
1	Early	2,236	524
1	Late	723	195
2	Early	2,533	615
2	Late	557	200
3	Early	1,545	367
3	Late	505	202
4	Late	142	135
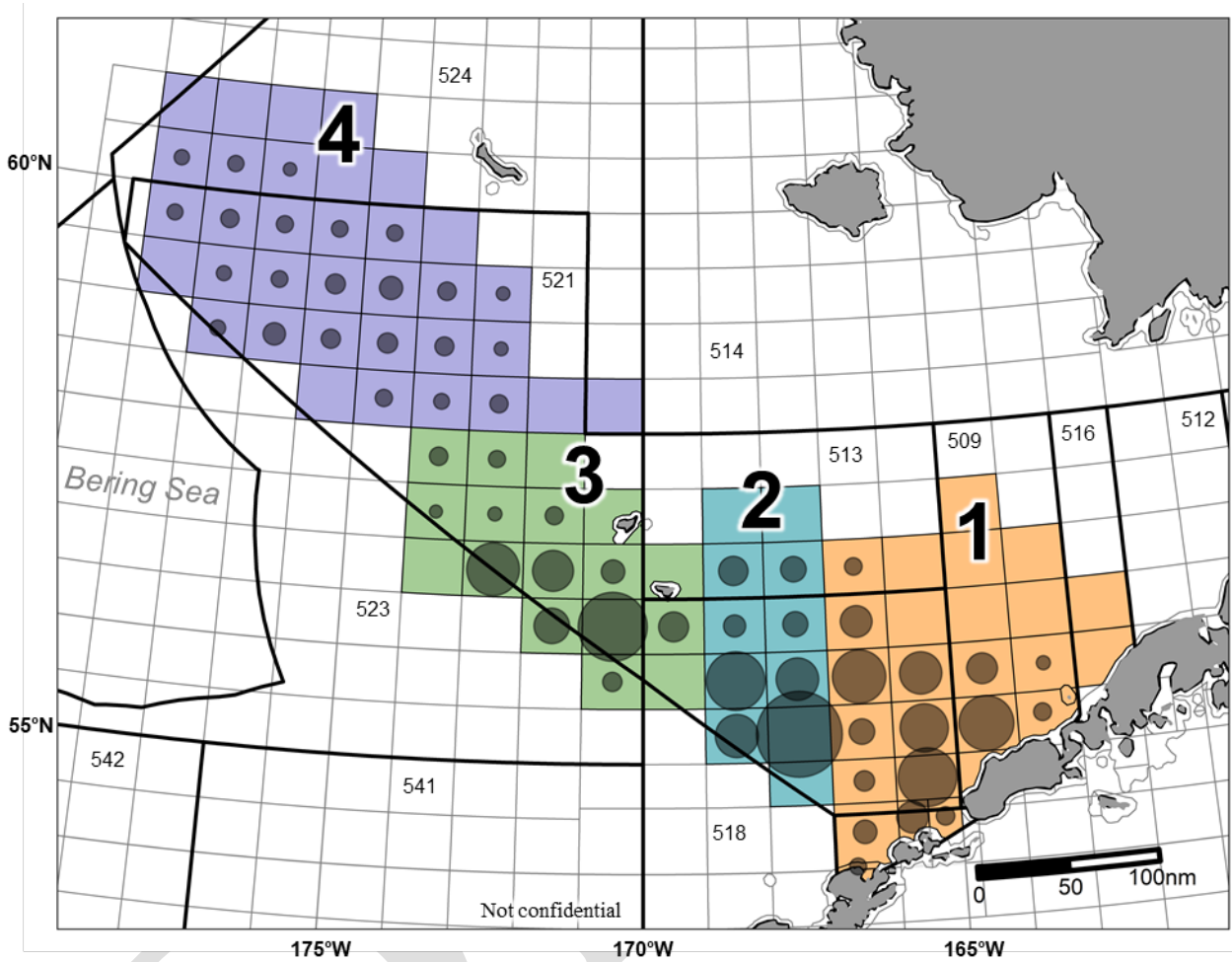
Figure 15. -- Four spatial clusters of ADF&G statistical areas in which chum salmon samples were collected in at least one year from 2013 to 2018 (highlighted); ADF&G areas in which samples were collected in 2018 from at least 3 vessels are indicated with circles sized relative to number of chum salmon bycatch. NMFS reporting areas associated with the Bering Sea-Aleutian Island groundfish fisheries are numbered and outlined in black.
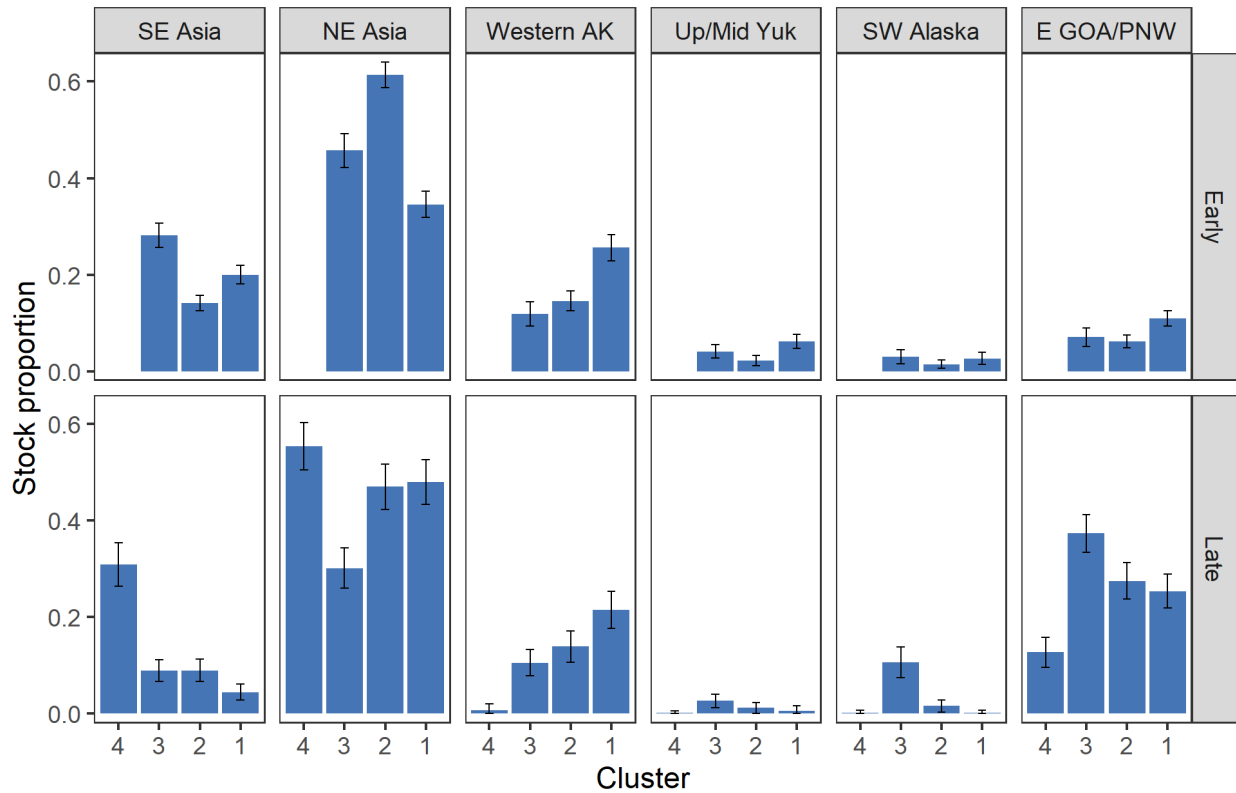
Figure 16. -- Stock composition estimates with 95% credible intervals from four spatial clusters of samples collected along the continental shelf edge (Fig. 15) during Early (Weeks 23-32) and Late (Weeks 33-40) time periods from the 2018 Bering Sea pollock fishery. The sample size of the 4th cluster, Early time period, was too small for analysis.

AGE STRATIFICATION

Stock estimates are provided by age strata of chum salmon. Scales collected from individual fish that were genotyped were read for age. Total age is the number of freshwater and saltwater annuli formed on the scales plus one to account for the winter spent rearing in freshwater. Approximately 80% of the successfully genotyped chum salmon caught in the 2018 Bering Sea pollock fishery B-season could be aged. The total age composition was 18% age-3, 68% age-4, 14% age-5, and <1% age-2 and age-6. These proportions were consistent with those observed in the 2016 and 2017 bycatch years. Stock composition was estimated for chum salmon, ages 3-5 (Fig. 17; Appendix II). Stock composition varied by age with a majority of age-3 fish from North

America, primarily from W Alaska and EGOA/PNW stocks, and a high proportion of the age-4 and age-5 fish from Asia, predominately from NE Asia stocks.
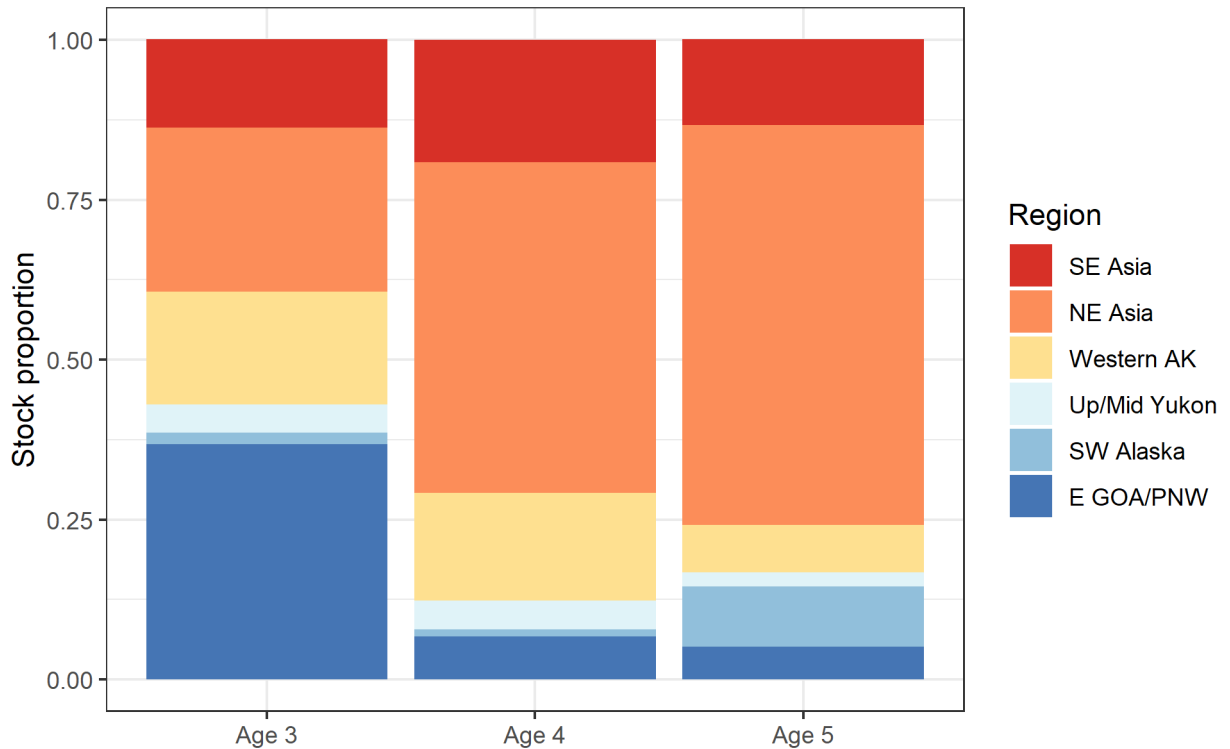
Figure 17. -- Stock composition estimates for the three predominate ages of chum salmon collected from the 2018 Bering Sea pollock B-season. Sample sizes were 303, 1,180, and 236 chum salmon for age-3, age-4, and age-5, respectively.

Stock estimates for many combinations of age, time, and spatial strata are available in Appendix II. The datasets with spatial strata (Clusters 1-4) include the extra samples added to increase the dataset sizes and are not necessarily representative of the entire bycatch. Full exploration of the stock estimates from the many multi-strata datasets are beyond the scope of this report, although several results are noted here (Fig. 18). The most striking difference in stock estimates are between age-3 and age-4 chum salmon regardless of time period or spatial strata; the EGOA/PNW and NE Asia stocks are more prevalent in age-3 and age-4 fish, respectively.
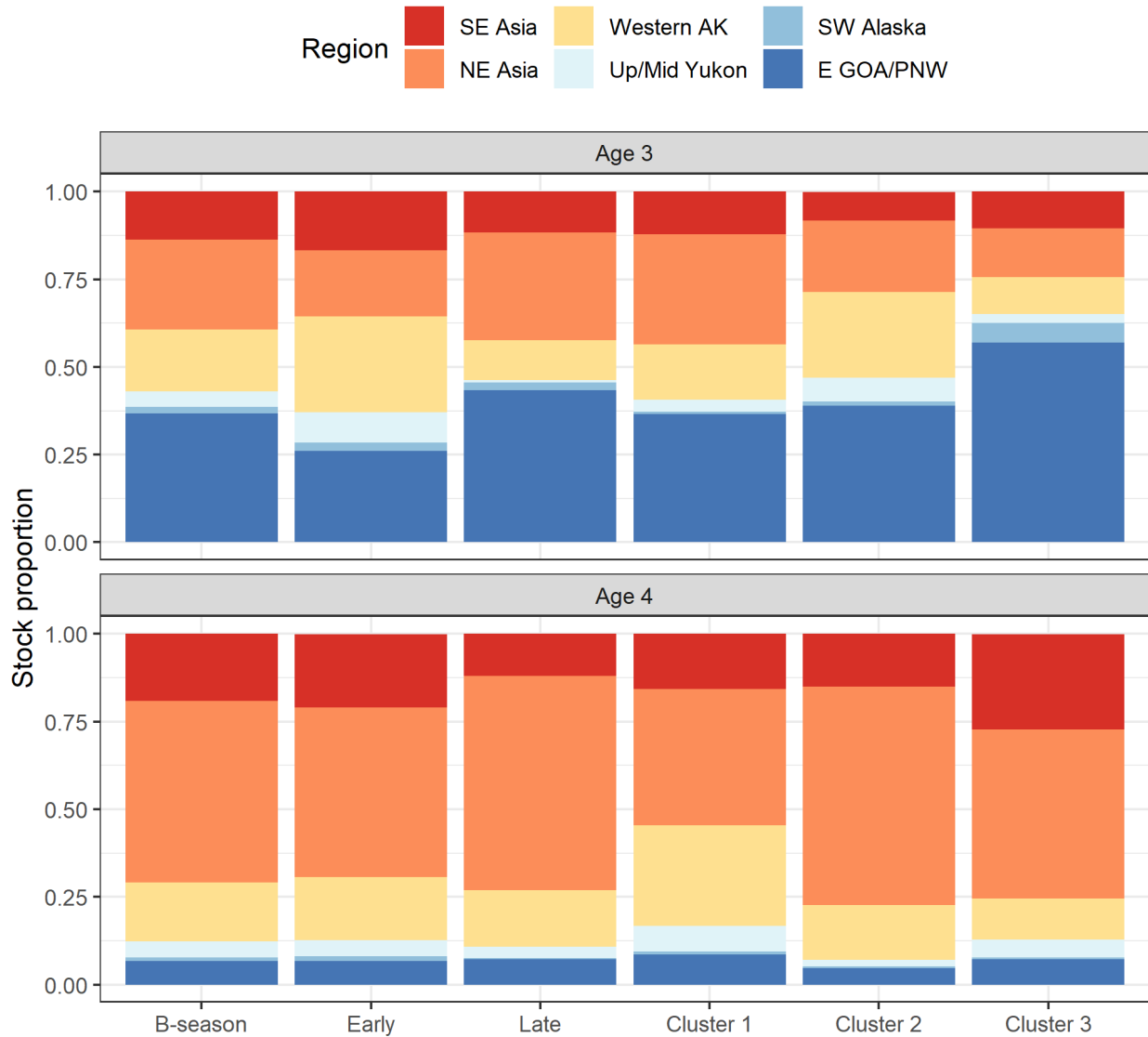
Figure 18. -- Stock composition estimates for the age-3 and age-4 chum salmon collected from the 2018 Bering Sea pollock B-season for the entire season, in two time periods, Early (weeks 23-32) and Late (weeks 33-40), and in three areas along the continental shelf (Clusters 1-3; Fig. 15). The sample sizes by age of the 4th cluster were too small for analysis.

FISHING SECTOR

In 2018, samples sizes were sufficient to analyze stock compositions for all three sectors:

catcher-processor, shoreside (catcher-vessel), and mothership (Fig. 19; Appendix II)[4]. The Bering

---

[4] The terms "shoreside" or "catcher-vessel" in this report are synonymous with the use of "inshore" in the Federal Register.

Sea pollock non-CDQ directed fishing allowances for these three sectors is split as 50%, 40%, and 10% allocations for the shoreside, catch-processors, and motherships, respectively[5]. Consistent with greater pollock quotas and fishing effort, More chum salmon were collected from each of the catcher-processor (126,248) and shoreside (147,417) sectors than the mothership sector (21,206). Most of the stock compositions were similar across fishing sectors (Fig. 19, upper panel). However, there were slight differences in contributions from SE Asia stocks in the shoreside and catcher-processor sectors, and a higher proportion of Up/Mid Yukon stocks in the mothership sector, although the numbers of fish from this region were similar in all three sectors (Fig. 19, lower panel).

---

[5] https://www.federalregister.gov/documents/2019/03/13/2019-04539/fisheries-of-the-exclusive-economic-zone-off-alaska-bering-sea-and-aleutian-islands-final-2019-and#p-32
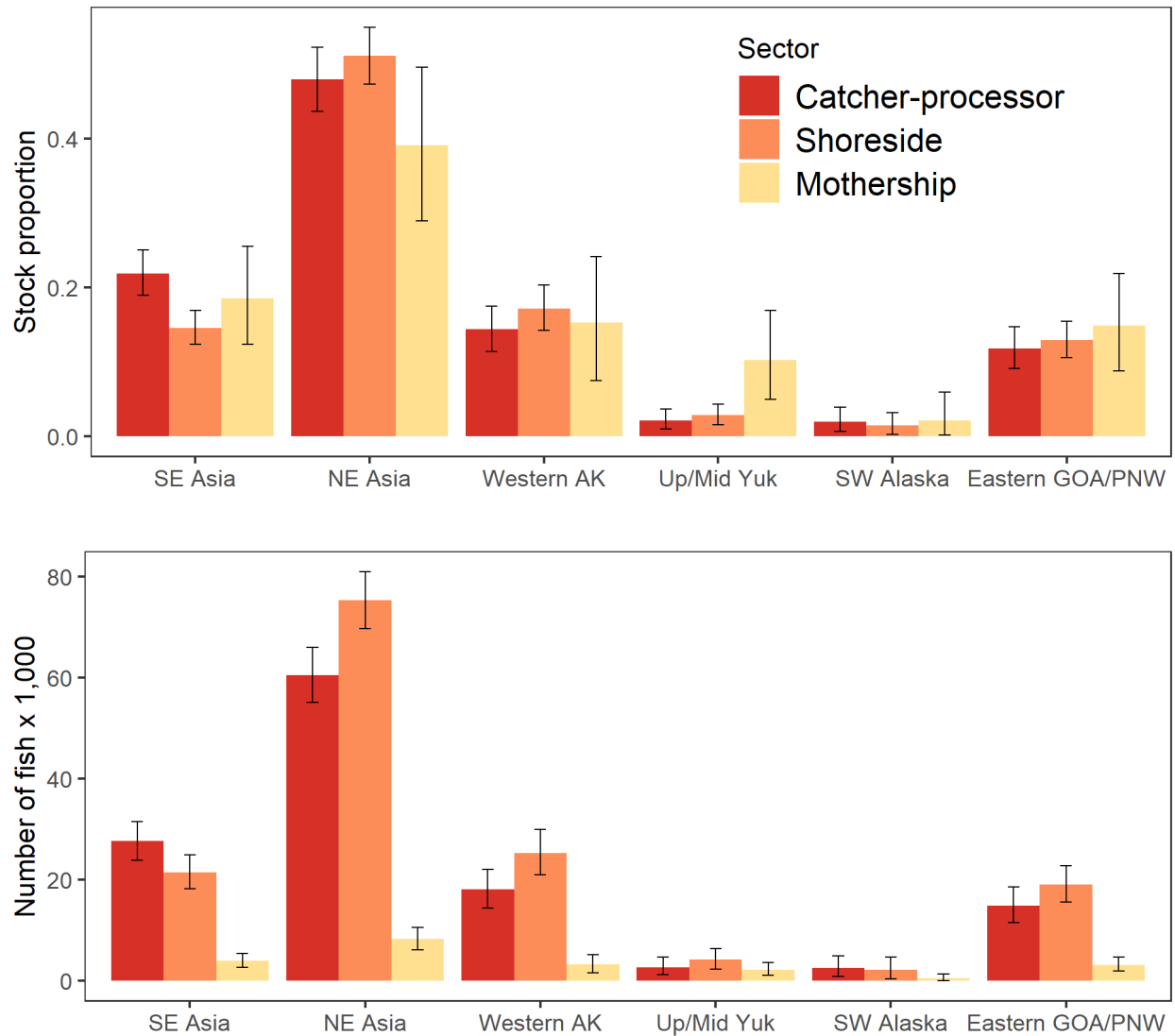
Figure 19. -- Stock composition estimates and 95% BAYES credible intervals for the 2018 chum salmon collected during the Bering Sea pollock B-season from the catcher-processor, shoreside, and mothership fishing sectors. Proportions in top panel; numbers of fish in bottom panel.

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 2018 chum salmon PSC based on 2,500 samples genotyped: 2,193

representative, plus 307 extra samples added to increase sample size for spatial-temporal datasets from the Bering Sea, and 974 samples 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 2018 sample set (Figs. 3 and 4) relative to sample biases that were inherent before 2011. 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 a more representative sampling protocol, which in 2018, was met for 93% of chum salmon PSC (Fig. 6). As in 2017, several catcher-processors with high chum salmon PSC early in the 2018 B-season under-sampled due to limited sampling materials. Nevertheless, most of the chum salmon PSC was representatively sampled in 2018 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 fifth year, a small sample set for genetic analysis. The distribution of chum salmon PSC samples is not representative of the groundfish fisheries as a

---

[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).

whole. Most of the genetic samples (99.4%) were from the pollock trawl fishery, which in 2018 caught 88% of the chum salmon PSC in the GOA.

Stock Composition Estimates

Bering Sea

Two-thirds of the genetic samples collected from chum salmon caught in the 2018 Bering Sea B-season pollock fishery were from Asia, with the majority from NE Asia (49%) stocks (Table 3A; Fig. 11). The contribution from North America was predominantly from W Alaska (15%) and EGOA/PNW (12%) stocks. The stock proportion from NE Asia significantly higher than in previous years. The SE Asia contribution was similar to years with systematic sampling and lower than years prior to systematic sampling. The EGOA/PNW contribution was significantly lower than in years prior to and after systematic sampling. The stock proportions from Alaska were similar to previous years. Although chum salmon sample collection in 2018 was largely representative for the pollock fishery, with the exception of lower than expected sample sizes from several under-sampled catcher-processor vessels early in the B-season, there were interannual differences in sampling (space and time) relative to previous years, so that caution must be used in making year-to-year comparisons.

Gulf of Alaska

As in the previous four years, the stock proportions of the 2018 chum salmon PSC from the GOA had a very different pattern than that observed in the Bering Sea. In the GOA groundfish fisheries, 87% of the chum salmon sampled were from EGOA/PNW stocks (Table 3B; Fig. 12). The remaining contributions from the other five regions were very low (0-5%).

Temporal and Spatial Effects

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 2018 chum salmon catch changed across the three sampling periods, suggesting a shift in the timing of chum salmon stocks in the Bering Sea, changes in fishing or sampling locations, or both (Fig. 13). We observed a higher contribution of SE Asia stocks during the Early time period, W Alaska stocks during the Early and Middle time periods, and EGOA/PNW stocks during the Middle and Late time periods. An inverse relationship of contribution across years between NE Asia and EGOA/PNW stocks was most evident during the Middle and Late time periods.

Spatial analysis indicated that the majority of the chum salmon from U.S. waters of the Bering Sea east and west of 170°W originated from Asian stocks, primarily from the NE Asia region (Fig. 14). The SE Asia stock contribution was higher west of 170°W, but the NE Asia stock contribution was higher east of 170°W, as was the W Alaska stock. The contributions of the other stocks were similar east and west of 170°W.

An examination of chum salmon stock estimates on both spatial and temporal strata of the 2018 Bering Sea pollock fishery during the B-season indicates that stocks are not uniformly distributed (Figs. 15 and 16). The proportion of stocks from SE Asia was higher in the most northwestern area of the fishery (e.g., Cluster 4) and earlier in the season. The NE Asia stocks dominated both time periods and all spatial strata. Of the North American stocks, the W Alaska stock contribution was higher toward the southeastern portion of the fishery (e.g., Cluster 1) in both time periods, the Up/Mid Yukon and SW Alaska contributions were low in both time periods and all spatial strata, and the EGOA/PNW contribution was higher in the Late time period, with no consistent pattern by spatial strata.

Age Stratification

About 80% of the genetic samples collected from chum salmon caught in the B-season Bering Sea pollock fishery could be aged, most of which were age-4 (68%). The majority of age-3 chum salmon were from North America (60.6%), primarily from W Alaska (17.6%) and EGOA/PNW (36.8%) stocks, and the majority of age-4 and age-5 chum salmon were from Asia (70.8% and 75.9% respectively), primarily from NE Asia stocks (Fig. 17). In general, this pattern was consistent at finer temporal and spatial scales (Fig. 18). Although a full exploration of the stock estimates from the many multi-strata datasets was not developed in this report, stock estimates for 2018 are available for many age-time-spatial strata in Appendix II.

Fishing Sector

Few differences were evident in the proportion of stocks from chum salmon collected in the three fishing sectors (Fig. 19, top panel). However, due to differences in total chum salmon PSC caught by each fishing sector, the number of chum salmon from Asian, W Alaska, and EGOA/PNW stocks in the catcher-processor and shoreside sectors was significantly higher than the mothership sector (Fig. 19, bottom panel).

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 abundance 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. 2017. 2018 Observer sampling manual. Fisheries Monitoring and Analysis Division, North Pacific Groundfish Observer Program. AFSC, 7600 Sand Point Way N.E., Seattle, Washington, 98115.

Barclay, A. W. 2020. Genetic stock identification of Upper Cook Inlet sockeye salmon harvest, 2019. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J20-01, Anchorage.

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. 1998. 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 III, C. M., Hv. T. Nguyen, M. Marsh, and J. R. Guyon. 2019. Genetic stock composition analysis of the Chinook salmon bycatch samples from the 2017 Gulf of Alaska trawl fisheries. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-390, 30 p. http://www.afsc.noaa.gov/Publications/AFSC-TM/NOAA-TM-AFSC-390.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.

Moran, B. M., and E. C. Anderson. 2019. Bayesian inference from the conditional genetic stock identification model. Canadian Journal of Fisheries and Aquatic Sciences 76:551–560.

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). 2019a. BSAI non-Chinook salmon mortality estimates, 1991-present, National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Alaska Regional Office, Juneau, Alaska. Retrieved on September 23, 2019 from https://www.fisheries.noaa.gov/sites/default/files/akro/chum_salmon_mortality2019.html

NMFS (National Marine Fisheries Service). 2019b. 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). 2018. Fishery management plan for groundfish of the Bering Sea and Aleutian Islands management area. North Pacific Fishery Management Council, 605 W. 4th Ave., Suite 306, Anchorage, Alaska, 99501. https://www.npfmc.org/wp-content/PDFdocuments/fmp/BSAI/BSAIfmp.pdf

NPFMC (North Pacific Fishery Management Council). 2019. Fishery management plan for groundfish of the Gulf of Alaska. North Pacific Fishery Management Council, 605 W. 4th Ave., Suite 306, 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.

Plummer M., N. Best, K. Cowles, and K. Vines. 2006. CODA: Convergence Diagnosis and Output Analysis for MCMC. *R News*, 6**:**7–11.

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.

Whittle, J. A., C. M. Kondzela, Hv. T. Nguyen, K. Hauch, D. Cuadra, and J. R. Guyon. 2018. Genetic stock composition analysis of chum salmon bycatch from the 2016 Bering Sea walleye pollock trawl fishery and Gulf of Alaska groundfish fisheries. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-366, 58 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 2018 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 23-29, Middle season is Weeks 30-34, and Late season is Weeks 35-40. For the analyses of four spatial clusters, the Early time period is Weeks 23-32 and the Late time period is Weeks 33-40. Sample sets with spatial strata by cluster have extra samples added to increase sample size, and may produce stock estimates that differ from sample sets that are representative of the bycatch.

GOA sample set (PSC = 9,149; n=974)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	320	0.035	0.006	0.023	0.035	0.048	0	1.00
NE Asia	438	0.048	0.010	0.030	0.047	0.068	0	1.00
W Alaska	308	0.034	0.008	0.020	0.033	0.05	0	1.02
Up/Mid Yukon	61	0.007	0.004	0	0.006	0.015	0.673	1.03
SW Alaska	40	0.004	0.004	0	0.004	0.015	0.947	1.00
E GOA/PNW	7,981	0.872	0.012	0.847	0.873	0.896	0	1.00

BS B-season sample set (PSC = 294,545; n=2,193)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	52,105	0.177	0.009	0.159	0.177	0.195	0	1.00
NE Asia	144,357	0.490	0.014	0.463	0.490	0.518	0	1.00
W Alaska	45,507	0.154	0.011	0.134	0.154	0.176	0	1.00
Up/Mid Yukon	10,044	0.034	0.005	0.024	0.034	0.045	0	1.00
SW Alaska	5,832	0.020	0.005	0.009	0.020	0.031	0	1.00
E GOA/PNW	36,671	0.124	0.009	0.108	0.124	0.142	0	1.00

BS Early sample set (PSC = 192,293; n=1,384)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	42,093	0.219	0.012	0.195	0.219	0.243	0	1.00
NE Asia	88,243	0.459	0.017	0.425	0.459	0.493	0	1.00
Western AK	35,132	0.183	0.014	0.156	0.183	0.211	0	1.00
Up/Mid Yukon	8,057	0.042	0.007	0.028	0.042	0.057	0	1.00
SW Alaska	4,365	0.023	0.006	0.012	0.022	0.036	0	1.00
E GOA/PNW	14,422	0.075	0.009	0.059	0.075	0.093	0	1.00

Appendix II. -- Continued.

BS Middle sample set (PSC = 45,316; n=356)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	5,007	0.110	0.019	0.075	0.110	0.151	0	1.00
NE Asia	29,845	0.659	0.034	0.591	0.659	0.723	0	1.00
Western AK	3,671	0.081	0.022	0.042	0.080	0.128	0	1.00
Up/Mid Yukon	1,006	0.022	0.012	0.002	0.021	0.048	0.013	1.01
SW Alaska	730	0.016	0.010	0	0.015	0.040	0.047	1.01
E GOA/PNW	5,062	0.112	0.021	0.074	0.111	0.155	0	1.01

BS Late sample set (PSC = 56,909; n=453)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	5,628	0.099	0.016	0.069	0.098	0.133	0	1.00
NE Asia	26,366	0.463	0.031	0.403	0.463	0.523	0	1.00
Western AK	8,075	0.142	0.022	0.100	0.141	0.188	0	1.00
Up/Mid Yukon	512	0.009	0.009	0	0.006	0.032	0.256	1.01
SW Alaska	871	0.015	0.014	0	0.013	0.046	0.165	1.01
E GOA/PNW	15,456	0.272	0.026	0.222	0.271	0.323	0	1.01

BS east of 170°W sample set (PSC = 216,960; n=1,663)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	32,566	0.150	0.010	0.132	0.150	0.170	0	1.00
NE Asia	110,368	0.509	0.016	0.477	0.509	0.540	0	1.00
Western AK	37,209	0.172	0.013	0.146	0.171	0.197	0	1.00
Up/Mid Yukon	7,789	0.036	0.006	0.024	0.036	0.050	0	1.00
SW Alaska	3,450	0.016	0.006	0.006	0.015	0.029	0	1.00
E GOA/PNW	25,580	0.118	0.010	0.099	0.118	0.138	0	1.00

BS west of 170°W sample set (PSC = 77,585; n=530)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	19,761	0.255	0.021	0.214	0.254	0.297	0	1.00
NE Asia	32,818	0.423	0.028	0.369	0.423	0.478	0	1.00
Western AK	8,263	0.106	0.018	0.072	0.106	0.143	0	1.00
Up/Mid Yukon	2,886	0.037	0.010	0.019	0.036	0.060	0	1.00
SW Alaska	2,203	0.028	0.012	0.008	0.028	0.054	0.001	1.00
E GOA/PNW	11,646	0.150	0.019	0.114	0.149	0.189	0	1.00

Appendix II. -- Continued.

Cluster 1 Early sample set (PSC = 69,371; n=524)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	13,867	0.200	0.019	0.164	0.200	0.238	0	1.00
NE Asia	23,988	0.346	0.028	0.293	0.345	0.401	0	1.00
Western AK	17,752	0.256	0.027	0.204	0.256	0.309	0	1.00
Up/Mid Yukon	4,301	0.062	0.015	0.036	0.061	0.093	0	1.00
SW Alaska	1,866	0.027	0.013	0.007	0.025	0.058	0.001	1.00
E GOA/PNW	7,596	0.110	0.016	0.081	0.109	0.142	0	1.00

Cluster 1 Late sample set (PSC = 21,907; n=195)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	968	0.044	0.017	0.017	0.042	0.081	0	1.00
NE Asia	10,509	0.480	0.046	0.389	0.480	0.571	0	1.00
Western AK	4,701	0.215	0.039	0.142	0.213	0.293	0	1.00
Up/Mid Yukon	127	0.006	0.010	0.000	0.001	0.037	0.676	1.00
SW Alaska	46	0.002	0.005	0.000	0.000	0.017	0.947	1.00
E GOA/PNW	5,556	0.254	0.035	0.188	0.253	0.325	0	1.00

Cluster 2 Early sample set (PSC = 80,742; n=615)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	11,401	0.141	0.016	0.112	0.141	0.173	0	1.00
NE Asia	49,568	0.614	0.026	0.563	0.614	0.664	0	1.00
Western AK	11,764	0.146	0.020	0.108	0.145	0.186	0	1.00
Up/Mid Yukon	1,801	0.022	0.010	0.005	0.021	0.046	0.006	1.00
SW Alaska	1,187	0.015	0.008	0.000	0.014	0.033	0.036	1.00
E GOA/PNW	5,014	0.062	0.013	0.038	0.061	0.090	0	1.01

Cluster 2 Late sample set (PSC = 16,688; n=200)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	1,490	0.089	0.023	0.050	0.087	0.140	0	1.00
NE Asia	7,838	0.470	0.047	0.379	0.469	0.563	0	1.00
Western AK	2,318	0.139	0.033	0.079	0.137	0.208	0	1.00
Up/Mid Yukon	202	0.012	0.011	0	0.009	0.040	0.214	1.00
SW Alaska	259	0.015	0.013	0	0.012	0.048	0.089	1.00
E GOA/PNW	4,583	0.275	0.038	0.202	0.274	0.351	0	1.00

Appendix II. -- Continued.

Cluster 3 Early sample set (PSC = 58,210; n=367)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	16,392	0.282	0.026	0.233	0.281	0.334	0	1.00
NE Asia	26,608	0.457	0.035	0.389	0.457	0.525	0	1.00
Western AK	6,939	0.119	0.025	0.074	0.118	0.173	0	1.00
Up/Mid Yukon	2,410	0.041	0.014	0.016	0.040	0.072	0	1.00
SW Alaska	1,746	0.030	0.014	0.007	0.028	0.063	0.001	1.00
E GOA/PNW	4,115	0.071	0.019	0.037	0.070	0.111	0	1.00

Cluster 3 Late sample set (PSC = 15,897; n=202)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	1,416	0.089	0.023	0.050	0.087	0.138	0	1.00
NE Asia	4,782	0.301	0.042	0.223	0.299	0.385	0	1.00
Western AK	1,669	0.105	0.027	0.057	0.103	0.164	0	1.00
Up/Mid Yukon	415	0.026	0.014	0.005	0.024	0.059	0.003	1.00
SW Alaska	1,682	0.106	0.032	0.047	0.104	0.172	0	1.00
E GOA/PNW	5,934	0.373	0.039	0.298	0.373	0.451	0	1.00

Cluster 4 Late sample set (PSC = 4,534; n=135)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	1,399	0.309	0.045	0.224	0.307	0.399	0	1.00
NE Asia	2,510	0.553	0.049	0.455	0.554	0.648	0	1.00
Western AK	34	0.007	0.013	0	0.001	0.044	0.814	1.00
Up/Mid Yukon	7	0.002	0.004	0	0	0.012	1.000	1.00
SW Alaska	9	0.002	0.005	0	0	0.016	1.000	1.00
E GOA/PNW	576	0.127	0.031	0.073	0.125	0.193	0	1.00

Catcher-processor sample set (PSC = 126,248; n=875)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	27,636	0.219	0.016	0.189	0.219	0.250	0	1.00
NE Asia	60,511	0.479	0.022	0.436	0.479	0.523	0	1.00
Western AK	18,129	0.144	0.015	0.114	0.143	0.174	0	1.00
Up/Mid Yukon	2,664	0.021	0.007	0.009	0.020	0.037	0	1.00
SW Alaska	2,487	0.020	0.008	0.006	0.019	0.039	0	1.00
E GOA/PNW	14,834	0.117	0.014	0.091	0.117	0.147	0	1.00

Appendix II. -- Continued.

Mothership sample set (PSC = 21,206; n=164)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	3,929	0.185	0.034	0.123	0.184	0.255	0	1.00
NE Asia	8,281	0.391	0.052	0.289	0.390	0.495	0	1.00
Western AK	3,238	0.153	0.042	0.075	0.151	0.242	0	1.00
Up/Mid Yukon	2,163	0.102	0.030	0.050	0.099	0.169	0	1.00
SW Alaska	447	0.021	0.015	0.001	0.018	0.059	0.021	1.00
E GOA/PNW	3,149	0.148	0.034	0.088	0.147	0.219	0	1.00

Shoreside sample set (PSC = 147,417; n=1,154)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	21,479	0.146	0.012	0.124	0.145	0.169	0	1.00
NE Asia	75,315	0.511	0.019	0.473	0.511	0.549	0	1.00
Western AK	25,238	0.171	0.015	0.142	0.171	0.203	0	1.00
Up/Mid Yukon	4,172	0.028	0.007	0.015	0.028	0.043	0	1.00
SW Alaska	2,182	0.015	0.008	0.002	0.014	0.031	0.002	1.00
E GOA/PNW	19,017	0.129	0.012	0.106	0.129	0.154	0	1.00

Age-3 Fish sample set (PSC = 50,656; n=303)

Region	Est. num.	Mean	SD	0.025	Median	0.975	P=0	Shrink Factor
SE Asia	6,965	0.138	0.021	0.098	0.137	0.182	0	1.00
NE Asia	13,008	0.257	0.034	0.192	0.256	0.326	0	1.00
Western AK	8,910	0.176	0.030	0.120	0.175	0.237	0	1.00
Up/Mid Yukon	2,224	0.044	0.016	0.016	0.043	0.080	0	1.00
SW Alaska	897	0.018	0.013	0.000	0.015	0.049	0.061	1.00
E GOA/PNW	18,652	0.368	0.032	0.307	0.368	0.432	0	1.01

Age-3 Cluster 1 sample set (PSC = 27,438; n=113)

Region	Est. num.	Mean	SD	0.025	Median	0.975	P=0	Shrink Factor
SE Asia	3,347	0.122	0.033	0.065	0.119	0.193	0	1.00
NE Asia	8,613	0.314	0.059	0.201	0.313	0.433	0	1.02
Western AK	4,338	0.158	0.046	0.078	0.155	0.257	0	1.02
Up/Mid Yukon	930	0.034	0.019	0.006	0.031	0.080	0	1.00
SW Alaska	156	0.006	0.011	0.000	0.001	0.040	0.669	1.00
E GOA/PNW	10,051	0.366	0.052	0.266	0.365	0.470	0	1.01

Appendix II. -- Continued.

Age-3 Cluster 2 sample set (PSC = 33,474; n=124)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	2,725	0.081	0.026	0.038	0.079	0.139	0	1.00
NE Asia	6,839	0.204	0.049	0.116	0.202	0.308	0	1.00
Western AK	8,191	0.245	0.050	0.151	0.243	0.347	0	1.00
Up/Mid Yukon	2,290	0.068	0.032	0.015	0.065	0.140	0	1.00
SW Alaska	415	0.012	0.016	0.000	0.006	0.055	0.303	1.00
E GOA/PNW	13,011	0.389	0.049	0.294	0.388	0.486	0	1.00

Age-3 Cluster 3 sample set (PSC = 32,686; n=115)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	3,403	0.104	0.029	0.053	0.102	0.168	0	1.00
NE Asia	4,560	0.140	0.044	0.063	0.136	0.233	0	1.00
Western AK	3,435	0.105	0.040	0.035	0.103	0.191	0	1.00
Up/Mid Yukon	860	0.026	0.016	0.004	0.023	0.066	0.001	1.00
SW Alaska	1,840	0.056	0.036	0.000	0.053	0.136	0.032	1.00
E GOA/PNW	18,589	0.569	0.055	0.458	0.569	0.675	0	1.00

Age-3 Early sample set (PSC = 19,754; n=114)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	3,331	0.169	0.036	0.105	0.167	0.244	0	1.00
NE Asia	3,718	0.188	0.050	0.098	0.185	0.294	0	1.00
Western AK	5,411	0.274	0.054	0.171	0.273	0.385	0	1.00
Up/Mid Yukon	1,693	0.086	0.034	0.030	0.082	0.162	0	1.00
SW Alaska	456	0.023	0.020	0.000	0.018	0.074	0.096	1.00
E GOA/PNW	5,146	0.261	0.046	0.175	0.259	0.354	0	1.00

Age-3 Late sample set (PSC = 27,803; n=189)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	3,211	0.116	0.026	0.070	0.114	0.171	0	1.00
NE Asia	8,538	0.307	0.043	0.225	0.306	0.394	0	1.00
Western AK	3,186	0.115	0.029	0.063	0.113	0.176	0	1.00
Up/Mid Yukon	178	0.006	0.008	0.000	0.003	0.030	0.471	1.00
SW Alaska	648	0.023	0.019	0.000	0.020	0.069	0.115	1.02
E GOA/PNW	12,041	0.433	0.041	0.353	0.433	0.515	0	1.01

Appendix II. -- Continued.

Age-4 Fish sample set (PSC = 197,275; n=1,180)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	37,739	0.191	0.013	0.166	0.191	0.217	0	1.00
NE Asia	101,932	0.517	0.019	0.479	0.517	0.553	0	1.00
Western AK	33,320	0.169	0.015	0.140	0.169	0.200	0	1.00
Up/Mid Yukon	8,956	0.045	0.008	0.031	0.045	0.062	0	1.00
SW Alaska	2,111	0.011	0.005	0.003	0.010	0.023	0	1.00
E GOA/PNW	13,237	0.067	0.009	0.050	0.067	0.086	0	1.00

Age-4 Cluster 1 sample set (PSC = 89,357; n=368)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	14,083	0.158	0.021	0.119	0.157	0.200	0	1.00
NE Asia	34,760	0.389	0.032	0.327	0.389	0.452	0	1.00
Western AK	25,538	0.286	0.034	0.219	0.286	0.350	0	1.00
Up/Mid Yukon	6,514	0.073	0.020	0.039	0.071	0.116	0	1.00
SW Alaska	768	0.009	0.011	0.000	0.004	0.036	0.334	1.00
E GOA/PNW	7,694	0.086	0.018	0.054	0.085	0.124	0	1.00

Age-4 Cluster 2 sample set (PSC = 119,047; n=441)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	17,881	0.150	0.019	0.114	0.149	0.190	0	1.00
NE Asia	74,226	0.624	0.029	0.565	0.624	0.680	0	1.00
Western AK	18,417	0.155	0.023	0.112	0.154	0.201	0	1.00
Up/Mid Yukon	2,274	0.019	0.010	0.000	0.018	0.041	0.037	1.00
SW Alaska	619	0.005	0.006	0.000	0.003	0.020	0.305	1.00
E GOA/PNW	5,643	0.047	0.014	0.024	0.046	0.077	0	1.00

Age-4 Cluster 3 sample set (PSC = 84,984; n=299)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	23,107	0.272	0.028	0.218	0.271	0.330	0	1.00
NE Asia	40,988	0.482	0.036	0.412	0.482	0.553	0	1.00
Western AK	9,977	0.117	0.025	0.072	0.116	0.170	0	1.00
Up/Mid Yukon	4,317	0.051	0.016	0.022	0.050	0.086	0	1.00
SW Alaska	442	0.005	0.007	0.000	0.002	0.024	0.408	1.00
E GOA/PNW	6,153	0.072	0.018	0.040	0.071	0.112	0	1.00

Appendix II. -- Continued.

Age-4 Early sample set (PSC = 168,598; n=973)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	35,068	0.208	0.015	0.180	0.208	0.237	0	1.00
NE Asia	81,804	0.485	0.021	0.445	0.485	0.526	0	1.00
Western AK	30,230	0.179	0.017	0.147	0.179	0.213	0	1.00
Up/Mid Yukon	7,806	0.046	0.009	0.030	0.046	0.065	0	1.00
SW Alaska	2,377	0.014	0.007	0.004	0.013	0.030	0	1.00
E GOA/PNW	11,313	0.067	0.010	0.049	0.067	0.087	0	1.00

Age-4 Late sample set (PSC = 30,451; n=207)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	3,645	0.120	0.027	0.072	0.118	0.176	0	1.00
NE Asia	18,624	0.612	0.046	0.520	0.612	0.701	0	1.00
Western AK	4,903	0.161	0.039	0.089	0.160	0.242	0	1.00
Up/Mid Yukon	1,017	0.033	0.023	0.000	0.033	0.082	0.105	1.00
SW Alaska	79	0.003	0.005	0.000	0.000	0.019	0.863	1.00
E GOA/PNW	2,180	0.072	0.023	0.032	0.070	0.120	0	1.00

Age-5 Fish sample set (PSC = 39,455; n=236)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	5,279	0.134	0.024	0.090	0.133	0.185	0	1.00
NE Asia	24,640	0.625	0.042	0.542	0.625	0.704	0	1.00
Western AK	2,908	0.074	0.029	0.023	0.072	0.135	0.001	1.00
Up/Mid Yukon	900	0.023	0.017	0.000	0.021	0.060	0.096	1.00
SW Alaska	3,701	0.094	0.032	0.037	0.093	0.159	0	1.00
E GOA/PNW	2,028	0.051	0.022	0.016	0.049	0.102	0	1.00

Age-5 Early sample set (PSC = 38,467; n=222)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	Shrink Factor
SE Asia	5,458	0.142	0.026	0.095	0.141	0.196	0	1.00
NE Asia	24,103	0.627	0.043	0.541	0.627	0.707	0	1.00
Western AK	3,297	0.086	0.031	0.031	0.084	0.150	0	1.00
Up/Mid Yukon	885	0.023	0.018	0.000	0.021	0.063	0.112	1.00
SW Alaska	3,404	0.088	0.033	0.037	0.084	0.161	0	1.01
E GOA/PNW	1,323	0.034	0.018	0.007	0.032	0.075	0.001	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) has been used in analyses in previous years. 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) and *rubias* (Moran and Anderson 2019), described below.

MSA using the BAYES and *rubias* programs 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.

---

[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. -- Four spatial clusters of ADF&G groundfish statistical areas[9] of chum salmon PSC sampled from 2013 to 2018 during the B-season of the Bering Sea midwater pollock trawl fishery and analyzed for genetic stock composition. The areas sampled in 2018 in which at least three fishing vessels are represented are in bold (Fig. 15).

Cluster 1: 625504, 625531, 625600, 625630, 625700, 625730, 635501, 635504, 635530, 635600, 635630, 635700, 635730, 645434, **645501**, 645502, **645530**, 645600, 645630, 645700, 645730, 655407, **655409**, 655410, **655430**, **655500**, **655530**, 655600, 655630, 655700, 655730, 665335, 665336, **665401**, 665403, 665404, **665430**, **665500**, **665530**, **665600**, 665630, 665700, 665730

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

Cluster 3: 695530, **695600**, 695631, 695632, **705530**, **705600**, **705630**, 705701, 705730, **715600**, **715630**, 715700, 715730, **725630**, 725700, **725730**, 735630, 735700, 735730, 745730

Cluster 4: 705800, 705830, 715800, 715830, 725800, 725830, 725900, **735800**, **735830**, **735900**, 735930, **745800**, **745830**, **745900**, **745930**, 746000, 755800, **755830**, **755900**, **755930**, 756000, 765830, **765900**, **765930**, 766000, 766030, 775830, 775900, **775930**, **776000**, 776030, 785900, 785930, 786000, 786030

---

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

Appendix V. – Comparison of rubias and BAYES genetic stock identification programs.

We evaluated the effect of transitioning from the software BAYES to rubias for MSA by conducting MSA on 19 mixtures for the Bering Sea chum bycatch samples. The *rubias* package uses a Bayesian approach to the conditional MSA model that treats the relative frequencies of alleles in baseline stocks as if they were known without error (conditional model). Additionally the package can correct for biases in reporting group estimates (bootstrap model) and provides the option to run the fully Bayesian model (full model) which treats the baseline allele frequencies as unknowns and estimates them from the baseline and mixture samples. For all comparisons, the MCMC sampling properties (Six chains initialized with 95% of the mixture originating from a single reporting group, 100000 MCMC samples with the first half discarded as burn-in) and prior distribution on stock proportions ($1/(GC_g)$) were similar to that of BAYES. Two subtle differences in sampling properties should be noted: 1) BAYES samples for the stock composition were thinned such that a single sample was retained for every 10 samples of the posterior distribution whereas no thinning occurred for rubias samples and 2) each of the chains for BAYES were combined after assessing convergence whereas a single sample of the posterior of rubias was used after assessing convergence. The convergence of each chain was assessed with the Gelman-Rubin statistic (Gelman and Rubin 1992) estimated with the gelman.diag function in the coda library (Plummer et al. 2006) within R.

For all 19 analyses comparing the conditional model of rubias with BAYES, we observed no convergence issues among the six MCMC chains. The point estimate of the Gelman-Rubin shrink factor ranged from 1.00 to 1.01 while the 95% C.I. ranged from 1.00 to 1.02. To retrieve bootstrap corrected samples from the posterior distribution, the difference between the bootstrapped mean reporting group proportion and conditional model estimates was added to each sample from the posterior distribution.

The mean difference between estimates made with the default conditional model of *rubias* and BAYES was 1.56% (± 1.48% SD) and 1.16 (± 137% SD) between the bootstrapped model and BAYES. Of the 114 estimates (19 analyses for 6 reporting groups), only two (1.8%) for the default model and three (2.6%) for the bootstrap model differed by more than 5% (Fig. V1). These three estimates were for the W AK, NE Asia, and SE Asia reporting groups in the East of 170 analysis. Compared with the default model of *rubias*, estimates of the contributions

of the NE and SE Asia reporting groups to mixtures was typically larger with BAYES, while estimates of the contribution of EGO/PNW and WAK were larger with *rubias*. (Fig. V1A, Table V1). Estimates of the contribution of W AK and NE Asia reporting groups have the largest mean bias correction (-2.6% and 1.5% respectively). This effectively shrinks the conditional model W AK reporting group estimates and inflates the NE Asia reporting estimates so that they more similarly match results from BAYES (Fig. V1).
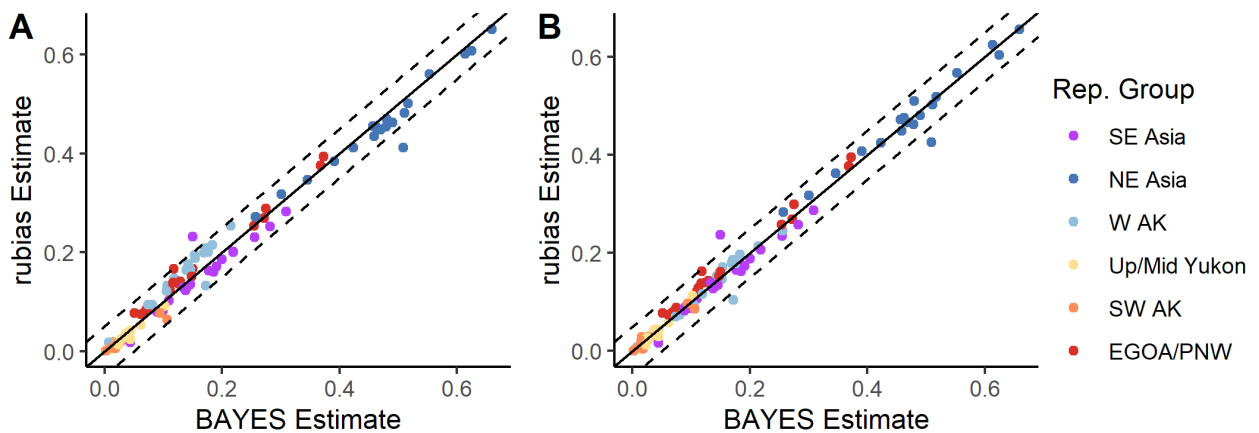
Figure V1. – Comparison of the stock composition estimates for each of the six reporting groups between MSA programs BAYES and the (A) default conditional MSA model in rubias and (B) the conditional model with bootstrapping over reporting groups. Twenty of the core analyses presented in this report were conducted in *rubias* with the conditional MSA model. Of the 114 estimates, only two (1.8%) differed by more than 5% (dotted lines) for the non-bootstrapped model while three differed by more than 5% for the bootstrapped model.

To further access differences among each of the models available in *rubias* we analyzed the full B season mixture (n = 2193) with the full model. Results from all four models were concordant; however slight differences were apparent. Despite BAYES and the full model implementing a fully Bayesian approach, these two models produced the most discordant estimates. Further simulations are being undertaken to understand these discrepancies. The largest difference was for the EGO/PNW reporting group (9%); however on average the differences among the contributions of each reporting group were less than 3%. As noted

above, there were relatively minor differences observed between the conditional and bootstrap models of *rubias*. On average the estimates differed by 0.7% with a maximum difference of 2.07% for the W AK reporting group. With a total PSC for the B season of 294,545 chum salmon, which would translate to a difference of 6,087 fish.
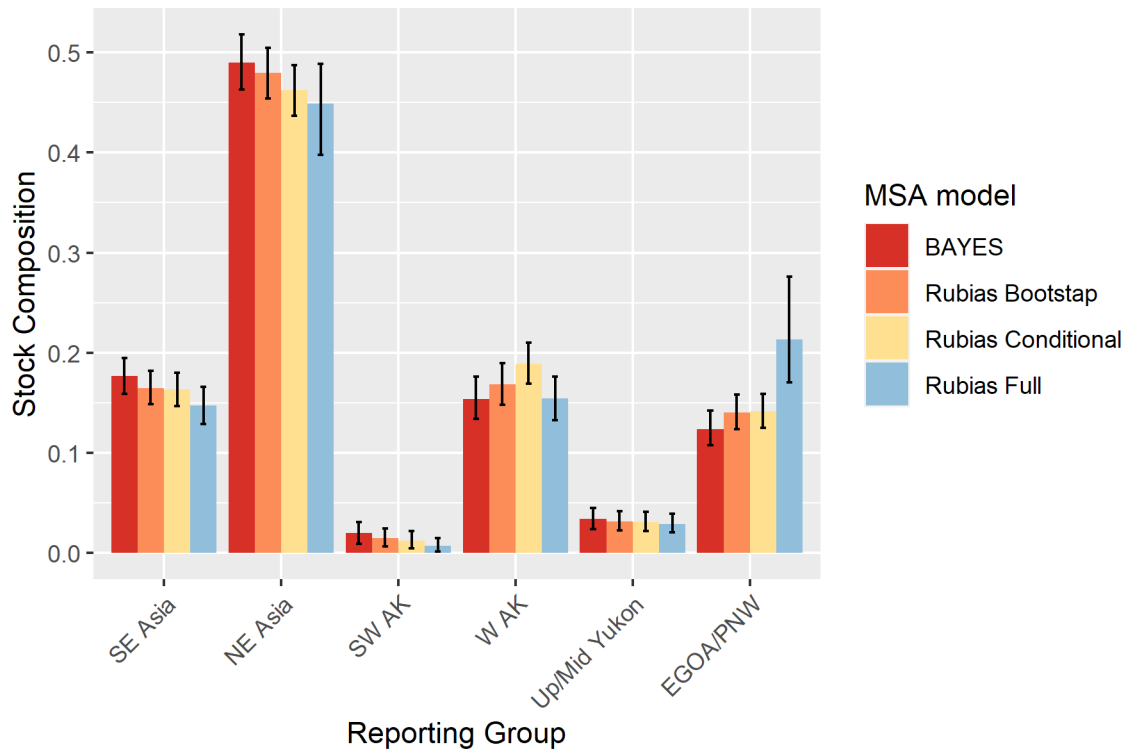
Figure V2. – Comparison of the stock composition estimates for the entire B season (n = 2193) for four MSA models: BAYES and three models implemented in *rubias*.

Overall, results from the conditional MSA model of rubias were concordant with results from BAYES and were produced substantially faster. Combined with the lack of reliance on a graphical user interface estimates can be produced in a more streamlined process. Results from the bootstrap model of *rubias* appeared to more closely match the results of BAYES suggesting that the model that accounts for biases in reporting group estimates may yield more accurate results than the default conditional model. While we compared the results of *rubias* to those of BAYES for these analyses, it should be apparent that BAYES results do not constitute

the true mixture compositions and only simulations of known proportions will demonstrate the accuracy of each model.

Table V1: Comparison of the stock composition estimates for each of the six reporting groups between MSA programs *rubias* (default conditional model) and BAYES for twenty core analyses.

Analysis	Region	BAYES Mean	2.5% CI	97.5% CI	rubias Mean	2.5% CI	97.5% CI	Difference
B season	SE Asia	0.177	0.159	0.195	0.163	0.147	0.180	0.014
	NE Asia	0.490	0.463	0.518	0.462	0.437	0.487	0.028
	W AK	0.154	0.134	0.176	0.189	0.169	0.210	0.035
	Up/Mid Yukon	0.034	0.024	0.045	0.031	0.022	0.041	0.003
	SW AK	0.020	0.009	0.031	0.013	0.005	0.022	0.007
	EGOA/PNW	0.124	0.108	0.142	0.142	0.125	0.159	0.018
WestOf170	SE Asia	0.255	0.214	0.297	0.231	0.194	0.271	0.024
	NE Asia	0.423	0.369	0.478	0.412	0.362	0.464	0.011
	W AK	0.106	0.072	0.143	0.133	0.099	0.171	0.027
	Up/Mid Yukon	0.037	0.019	0.060	0.035	0.018	0.056	0.002
	SW AK	0.028	0.008	0.054	0.020	0.005	0.039	0.008
	EGOA/PNW	0.150	0.114	0.189	0.167	0.132	0.205	0.017
EastOf170	SE Asia	0.150	0.132	0.170	0.232	0.194	0.271	0.082
	NE Asia	0.509	0.477	0.540	0.412	0.362	0.464	0.097
	W AK	0.172	0.146	0.197	0.133	0.099	0.171	0.039
	Up/Mid Yukon	0.036	0.024	0.050	0.035	0.018	0.056	0.001
	SW AK	0.016	0.006	0.029	0.020	0.005	0.039	0.004
	EGOA/PNW	0.118	0.099	0.138	0.167	0.132	0.205	0.049
Early	SE Asia	0.219	0.195	0.243	0.202	0.180	0.226	0.017
	NE Asia	0.459	0.425	0.493	0.435	0.404	0.467	0.024
	W AK	0.183	0.156	0.211	0.215	0.188	0.242	0.032
	Up/Mid Yukon	0.042	0.028	0.057	0.040	0.027	0.054	0.002
	SW AK	0.023	0.012	0.036	0.015	0.007	0.026	0.008
	EGOA/PNW	0.075	0.059	0.093	0.092	0.075	0.111	0.017

Table V1 continued

| Analysis | Region | BAYES | | | rubias | | | |
		Mean	2.5% CI	97.5% CI	Mean	2.5% CI	97.5% CI	Difference
Middle	SE Asia	0.110	0.075	0.151	0.103	0.071	0.141	0.007
	NE Asia	0.659	0.591	0.723	0.650	0.588	0.710	0.009
	W AK	0.081	0.042	0.128	0.095	0.056	0.140	0.014
	Up/Mid Yukon	0.022	0.002	0.048	0.019	0.002	0.041	0.003
	SW AK	0.016	0.000	0.040	0.010	0.000	0.029	0.006
	EGOA/PNW	0.112	0.074	0.155	0.123	0.086	0.165	0.011
Late	SE Asia	0.099	0.069	0.133	0.082	0.056	0.112	0.017
	NE Asia	0.463	0.403	0.523	0.452	0.397	0.508	0.011
	W AK	0.142	0.100	0.188	0.176	0.134	0.221	0.034
	Up/Mid Yukon	0.009	0.000	0.032	0.004	0.000	0.021	0.005
	SW AK	0.015	0.000	0.046	0.017	0.000	0.038	0.002
	EGOA/PNW	0.272	0.222	0.323	0.269	0.225	0.316	0.003
C1_Early	SE Asia	0.200	0.164	0.238	0.186	0.151	0.223	0.014
	NE Asia	0.346	0.293	0.401	0.347	0.299	0.396	0.001
	W AK	0.256	0.204	0.309	0.272	0.225	0.321	0.016
	Up/Mid Yukon	0.062	0.036	0.093	0.054	0.031	0.082	0.008
	SW AK	0.027	0.007	0.058	0.020	0.004	0.044	0.007
	EGOA/PNW	0.110	0.081	0.142	0.121	0.092	0.155	0.011
C1_Late	SE Asia	0.044	0.017	0.081	0.019	0.002	0.051	0.025
	NE Asia	0.480	0.389	0.571	0.470	0.384	0.557	0.010
	W AK	0.215	0.142	0.293	0.253	0.184	0.328	0.038
	Up/Mid Yukon	0.006	0.000	0.037	0.003	0.000	0.023	0.003
	SW AK	0.002	0.000	0.017	0.002	0.000	0.013	0.000
	EGOA/PNW	0.254	0.188	0.325	0.253	0.189	0.322	0.001
C2_Early	SE Asia	0.141	0.112	0.173	0.131	0.104	0.162	0.010
	NE Asia	0.614	0.563	0.664	0.601	0.553	0.647	0.013
	W AK	0.146	0.108	0.186	0.165	0.130	0.204	0.019
	Up/Mid Yukon	0.022	0.005	0.046	0.017	0.003	0.034	0.005
	SW AK	0.015	0.000	0.033	0.011	0.001	0.027	0.004
	EGOA/PNW	0.062	0.038	0.090	0.075	0.052	0.101	0.013
C2_Late	SE Asia	0.089	0.050	0.140	0.080	0.045	0.125	0.009
	NE Asia	0.470	0.379	0.563	0.448	0.365	0.533	0.022
	W AK	0.139	0.079	0.208	0.164	0.104	0.232	0.025
	Up/Mid Yukon	0.012	0.000	0.040	0.008	0.000	0.031	0.004
	SW AK	0.015	0.000	0.048	0.011	0.000	0.038	0.004
	EGOA/PNW	0.275	0.202	0.351	0.288	0.220	0.359	0.013

Table V1 continued

Analysis	Region	BAYES			rubias			
		Mean	2.5% CI	97.5% CI	Mean	2.5% CI	97.5% CI	Difference
C3_Early	SE Asia	0.282	0.233	0.334	0.252	0.206	0.301	0.030
	NE Asia	0.457	0.389	0.525	0.455	0.394	0.518	0.002
	W AK	0.119	0.074	0.173	0.147	0.102	0.196	0.028
	Up/Mid Yukon	0.041	0.016	0.072	0.038	0.015	0.066	0.003
	SW AK	0.030	0.007	0.063	0.023	0.004	0.049	0.007
	EGOA/PNW	0.071	0.037	0.111	0.085	0.052	0.124	0.014
C3_Late	SE Asia	0.089	0.050	0.138	0.080	0.045	0.125	0.009
	NE Asia	0.301	0.223	0.385	0.318	0.241	0.400	0.017
	W AK	0.105	0.057	0.164	0.122	0.071	0.182	0.017
	Up/Mid Yukon	0.026	0.005	0.059	0.022	0.004	0.050	0.004
	SW AK	0.106	0.047	0.172	0.064	0.023	0.115	0.042
	EGOA/PNW	0.373	0.298	0.451	0.394	0.320	0.469	0.021
C4_Late	SE Asia	0.309	0.224	0.399	0.282	0.205	0.365	0.027
	NE Asia	0.553	0.455	0.648	0.560	0.465	0.653	0.007
	W AK	0.007	0.000	0.044	0.018	0.000	0.060	0.011
	Up/Mid Yukon	0.002	0.000	0.012	0.001	0.000	0.011	0.001
	SW AK	0.002	0.000	0.016	0.002	0.000	0.013	0.000
	EGOA/PNW	0.127	0.073	0.193	0.137	0.081	0.204	0.010
Catcher Processor	SE Asia	0.219	0.189	0.250	0.200	0.172	0.228	0.019
	NE Asia	0.479	0.436	0.523	0.454	0.413	0.494	0.025
	W AK	0.144	0.114	0.174	0.172	0.142	0.204	0.028
	Up/Mid Yukon	0.021	0.009	0.037	0.020	0.009	0.034	0.001
	SW AK	0.020	0.006	0.039	0.015	0.003	0.030	0.005
	EGOA/PNW	0.117	0.091	0.147	0.139	0.113	0.167	0.022
Mothership	SE Asia	0.185	0.123	0.255	0.161	0.105	0.225	0.024
	NE Asia	0.391	0.289	0.495	0.384	0.295	0.475	0.007
	W AK	0.153	0.075	0.242	0.195	0.118	0.278	0.042
	Up/Mid Yukon	0.102	0.050	0.169	0.092	0.045	0.151	0.010
	SW AK	0.021	0.001	0.059	0.017	0.001	0.048	0.004
	EGOA/PNW	0.148	0.088	0.219	0.151	0.095	0.217	0.003
Shoreside	SE Asia	0.146	0.124	0.169	0.135	0.114	0.157	0.011
	NE Asia	0.511	0.473	0.549	0.481	0.446	0.516	0.030
	W AK	0.171	0.142	0.203	0.209	0.180	0.239	0.038
	Up/Mid Yukon	0.028	0.015	0.043	0.024	0.014	0.037	0.004
	SW AK	0.015	0.002	0.031	0.008	0.001	0.018	0.007
	EGOA/PNW	0.129	0.106	0.154	0.142	0.120	0.166	0.013

Table V1 continued

Analysis	Region	BAYES			rubias			
		Mean	2.5% CI	97.5% CI	Mean	2.5% CI	97.5% CI	Difference
Age3	SE Asia	0.138	0.098	0.182	0.123	0.087	0.164	0.015
	NE Asia	0.257	0.192	0.326	0.272	0.211	0.336	0.015
	W AK	0.176	0.120	0.237	0.200	0.148	0.256	0.024
	Up/Mid Yukon	0.044	0.016	0.080	0.024	0.007	0.049	0.020
	SW AK	0.018	0.000	0.049	0.006	0.000	0.025	0.012
	EGOA/PNW	0.368	0.307	0.432	0.375	0.316	0.436	0.007
Age4	SE Asia	0.191	0.166	0.217	0.171	0.148	0.195	0.020
	NE Asia	0.517	0.479	0.553	0.501	0.467	0.536	0.016
	W AK	0.169	0.140	0.200	0.199	0.171	0.228	0.030
	Up/Mid Yukon	0.045	0.031	0.062	0.043	0.029	0.059	0.002
	SW AK	0.011	0.003	0.023	0.008	0.001	0.020	0.003
	EGOA/PNW	0.067	0.050	0.086	0.078	0.060	0.098	0.011
Age5	SE Asia	0.134	0.090	0.185	0.129	0.087	0.178	0.005
	NE Asia	0.625	0.542	0.704	0.607	0.529	0.683	0.018
	W AK	0.074	0.023	0.135	0.095	0.046	0.155	0.021
	Up/Mid Yukon	0.023	0.000	0.060	0.014	0.000	0.046	0.009
	SW AK	0.094	0.037	0.159	0.077	0.030	0.129	0.017
	EGOA/PNW	0.051	0.016	0.102	0.078	0.039	0.123	0.027
							Mean	0.016
							SD	0.015