



NOAA Technical Memorandum NMFS-AFSC-292

doi:10.7289/V54J0C29

Genetic Stock Composition Analysis of Chum Salmon Bycatch from the 2013 Bering Sea Walleye Pollock Trawl Fishery

by

J. A. Whittle, S. C. Vulstek, C. M. Kondzela, and J. R. Guyon

U.S. DEPARTMENT OF COMMERCE
National Oceanic and Atmospheric Administration
National Marine Fisheries Service
Alaska Fisheries Science Center

February 2015

NOAA Technical Memorandum NMFS

The National Marine Fisheries Service's Alaska Fisheries Science Center uses the NOAA Technical Memorandum series to issue informal scientific and technical publications when complete formal review and editorial processing are not appropriate or feasible. Documents within this series reflect sound professional work and may be referenced in the formal scientific and technical literature.

The NMFS-AFSC Technical Memorandum series of the Alaska Fisheries Science Center continues the NMFS-F/NWC series established in 1970 by the Northwest Fisheries Center. The NMFS-NWFSC series is currently used by the Northwest Fisheries Science Center.

This document should be cited as follows:

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. doi:10.7289/V54J0C29.

Document available: <http://www.afsc.noaa.gov/Publications/AFSC-TM/NOAA-TM-AFSC-292.pdf>

Reference in this document to trade names does not imply endorsement by the National Marine Fisheries Service, NOAA.



NOAA Technical Memorandum NMFS-AFSC-292
doi:10.7289/V54J0C29

Genetic Stock Composition Analysis of Chum Salmon Bycatch from the 2013 Bering Sea Walleye Pollock Trawl Fishery

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

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

www.afsc.noaa.gov

U.S. DEPARTMENT OF COMMERCE

Penny S. Pritzker, Secretary

National Oceanic and Atmospheric Administration

Kathryn D. Sullivan, Under Secretary and Administrator

National Marine Fisheries Service

Eileen Sobeck, Assistant Administrator for Fisheries

February 2015

This document is available to the public through:

National Technical Information Service
U.S. Department of Commerce
5285 Port Royal Road
Springfield, VA 22161

www.ntis.gov

ABSTRACT

A genetic analysis of chum salmon (*Oncorhynchus keta*) bycatch from the 2013 Bering Sea walleye pollock (*Gadus chalcogrammus*) trawl fishery was undertaken to determine the overall stock composition of the sample set. Samples were genotyped for 11 microsatellite markers and results were estimated using the current chum salmon microsatellite baseline. Since 2011, genetic samples from the chum salmon bycatch were collected systematically to reduce sample biases that may exist in collections from previous years. In 2013, one genetic sample was collected for every 30.3 chum salmon caught in the 99.8% of the midwater trawl fishery that was sampled. Evaluation of sampling based on time, location, and vessel indicated that the genetic samples were representative of the total bycatch. Based on the analysis of 3,880 chum salmon bycatch samples collected throughout the 2013 Bering Sea trawl fishery, the Northeast Asia stocks dominated the sample set (45%); moderate contributions came from Southeast Asia (15%), Eastern Gulf of Alaska (GOA)/Pacific Northwest (PNW) (15%), and Western Alaska (18%) stocks, and smaller contributions came from Upper/Middle Yukon River (6%) and Southwest Alaska (1%) stocks. The regional stock estimates for the 2013 chum salmon bycatch were similar to those for the 2012 bycatch, but differed significantly from estimates for other years, especially for the Asian and the Eastern GOA/PNW regions. There were significant spatial differences in stock distribution with the Southeast Asia contribution higher in the northwestern U.S. waters of the Bering Sea than in the southeastern Bering Sea, and the Eastern GOA/PNW contribution highest in the easternmost area sampled in the southeastern Bering Sea. Analysis of temporal strata revealed changes in stock composition during the course of the fall “B” season with increasing contribution of Northeast Asia stocks, decreasing contribution of Eastern GOA/PNW stocks, and variable contribution from Southeast Asia and Western Alaska.

CONTENTS

ABSTRACT.....	iii
CONTENTS.....	v
INTRODUCTION	1
SAMPLE DISTRIBUTION.....	3
GENETIC STOCK COMPOSITION	9
Laboratory Analyses	9
Laboratory Quality Control.....	10
Data Analyses - Stock Composition	11
Data Analyses - Subsampling Effects.....	14
COMPARISON WITH PREVIOUS ESTIMATES	17
TEMPORAL STRATIFICATION	20
SPATIAL STRATIFICATION	22
SUMMARY	27
Sampling Issues	27
Stock Composition Estimates	27
Temporal and Spatial Effects.....	28
Application of Estimates.....	30
ACKNOWLEDGMENTS	30
CITATIONS	31
APPENDICES	35
Appendix I	35
Appendix II	41

INTRODUCTION

It is important to understand the stock composition of Pacific salmon (*Oncorhynchus* spp.) caught in Bering Sea groundfish fisheries because this area is a known feeding habitat for multiple brood years of chum salmon (*O. keta*) from many different localities in North America and Asia (Myers et al. 2007, Davis et al. 2009, Urawa et al. 2009). Determining the geographic origin of salmon caught in federally managed fisheries is essential to understanding the effects that fishing has on chum salmon stocks, especially those with conservation concerns (NPFMC 2012). This report includes genetic stock identification results for the chum salmon bycatch samples collected from the 2013 U.S. Bering Sea walleye pollock (*Gadus chalcogrammus*) midwater trawl fishery. National Marine Fisheries Service (NMFS) reporting areas associated with the groundfish fishery are shown in Figure 1 and are presented later to describe the spatial distribution of the chum salmon bycatch and genetic samples.

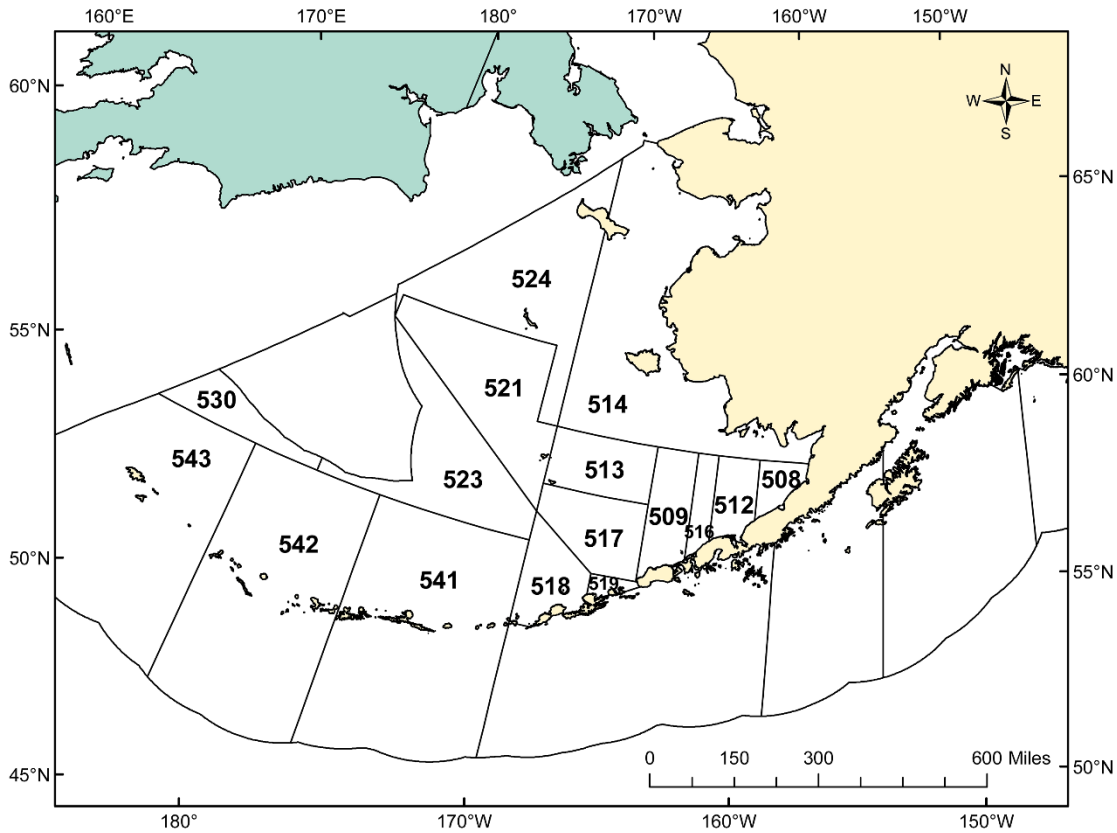


Figure 1. -- NMFS reporting areas associated with the Bering Sea-Aleutian Island groundfish fishery.

We present the stock composition estimates for the 2013 chum salmon bycatch samples collected from the Bering Sea. For additional background and methods, this report is intended to be supplemented with the chum salmon reports prepared previously for the 2005–2012 Bering Sea trawl fisheries (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2011a,b; Gray et al. 2010; Kondzela et al. 2012, 2013; Vulstek et al. 2014). The chum salmon bycatch is designated as non-Chinook in the NMFS database and comprises over 99% of the non-Chinook category (NPFMC 2005).

SAMPLE DISTRIBUTION

Genetic samples were collected from the chum salmon bycatch of the Bering Sea pollock fishery by the Alaska Fisheries Science Center's (AFSC) North Pacific Groundfish and Halibut Observer Program (Observer Program) in 2013 for analysis at the AFSC's Auke Bay Laboratories. Sampling was changed in 2011 from previous years to implement a systematic sampling protocol recommended by Pella and Geiger (2009). With a goal to sample every 30th chum salmon, axillary processes (for genetic analysis) and scales (for ageing) were collected throughout the season and stored together in coin envelopes that were labeled, frozen, and shipped to the Auke Bay Laboratories (ABL).

In 2013, an estimated 125,316 chum salmon were taken as bycatch in the pollock-directed trawl fisheries, accounting for more than 98% of the total chum salmon bycatch taken in the Bering Sea groundfish fisheries (NMFS 2014). The remaining 1.5% of the chum bycatch was taken in other groundfish fisheries. This was the sixth largest non-Chinook salmon bycatch in the pollock fisheries between 1994 and 2013, and nearly double the median of 71,612 (Fig. 2), but less than the average of 135,663. The 2013 genetic samples were collected from the midwater pollock trawl fishery during the B-season (June 10 to December 31) in North Pacific Fishery Management Council (NPFMC) reporting areas 509-524 (Fig. 1). Of the 124,986 chum salmon caught in this fishery and season, genetic samples were collected from 4,123 fish, which represents a sampling rate of 1 of every 30.3 chum salmon (or 3.3% of the midwater trawl chum salmon bycatch). This sampling rate is nearly identical to that in 2011–2012, the first two years of representative sampling.

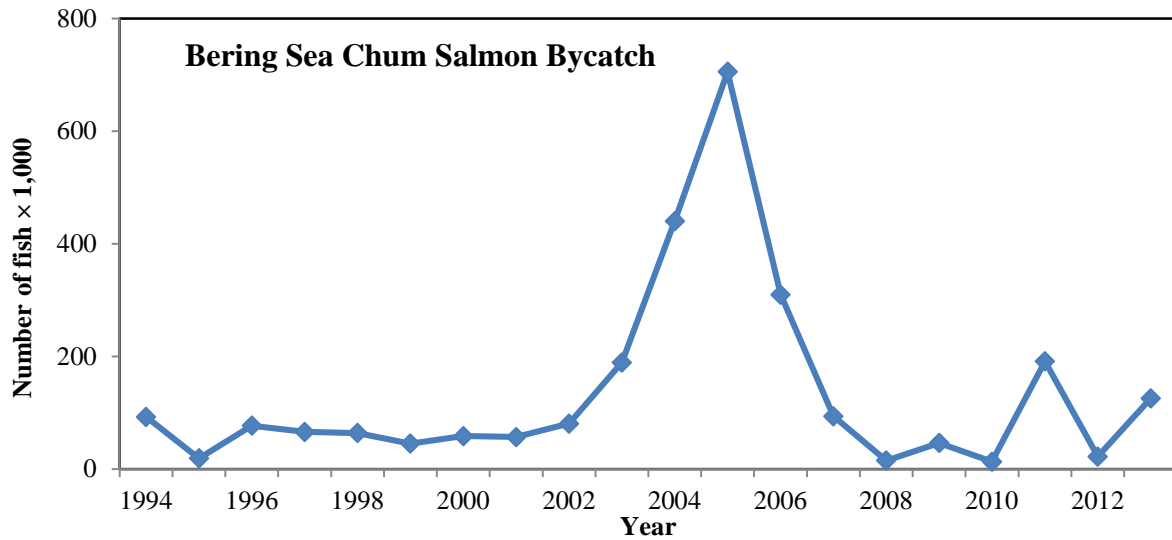


Figure 2. -- Yearly estimates for the non-Chinook salmon bycatch from the Bering Sea pollock directed trawl fisheries (NMFS 2014).

Biases and errors associated with past collections of genetic samples from the bycatch (NMFS 2009, Pella and Geiger 2009) have the potential to affect stock composition estimates. The systematic sampling protocols recommended by Pella and Geiger (2009) were implemented in 2011 to reduce sampling error and bias, the efficacy of which was evaluated by comparing the genetic sample distributions and the overall bycatch estimates with Chi-square tests. Temporal bias by statistical week ending on Sunday was minimal (Fig. 3) when samples were pooled across management areas ($\chi^2 = 1.44$, 17 *d.f.*, $P > 0.99$). Nearly all of the chum salmon bycatch occurred in the pollock B-season (99.8%), where temporal biases were also minimal at finer spatial scales (Fig. 4; $\chi^2 = 3.99$, 6 *d.f.*, $P = 0.68$). Low counts in some time/area combinations were pooled prior to testing and for subsequent stock composition analyses: Early, Middle, and Late time periods (weeks 24-29, 30-34, and 35-43) and NMFS reporting areas 517 and 519 together, and 521, 523, and 524 together. Due to the uncertainty of catch location for samples collected from shore-side deliveries in which the hauls were mixed (88% of genetic samples were from catcher vessel offloads; 12% from catcher processor and mothership hauls), the

NMFS reporting area of the entire catch of a fishing trip was identified as the area of the most abundant haul.

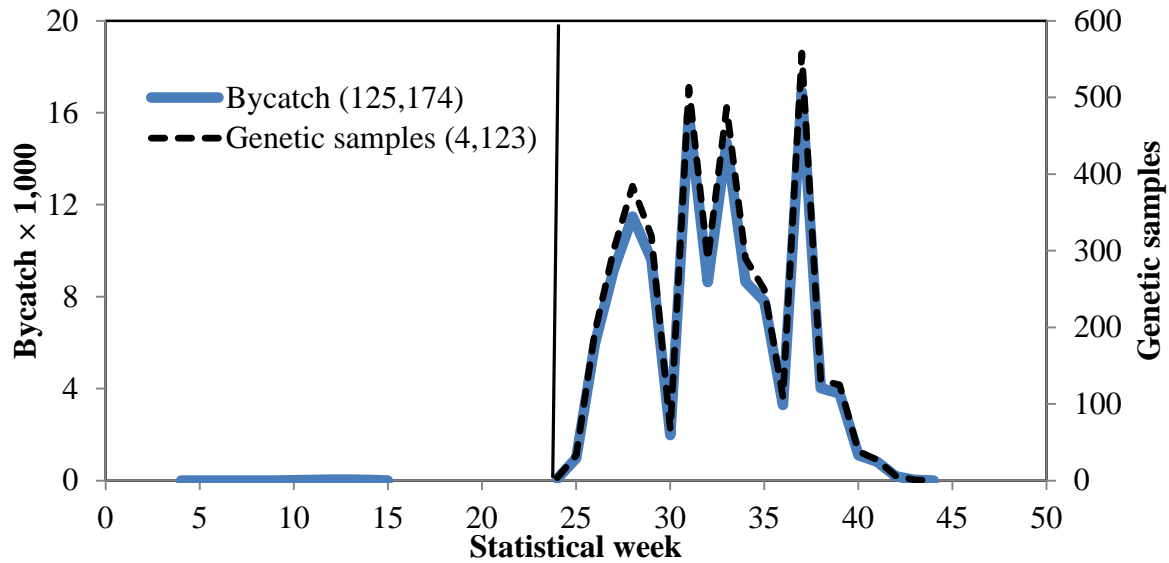


Figure 3. -- Number of Bering Sea chum salmon bycatch and genetic samples from 2013 by statistical week. Total numbers of chum salmon caught in the Bering Sea pollock midwater trawl fishery (solid line) compared with the 4,123 genetic samples collected in the B-season (dashed line). Weeks 1-23 correspond to the groundfish A-season, whereas weeks 24-50 correspond to the B-season, the demarcation of which is a vertical line.

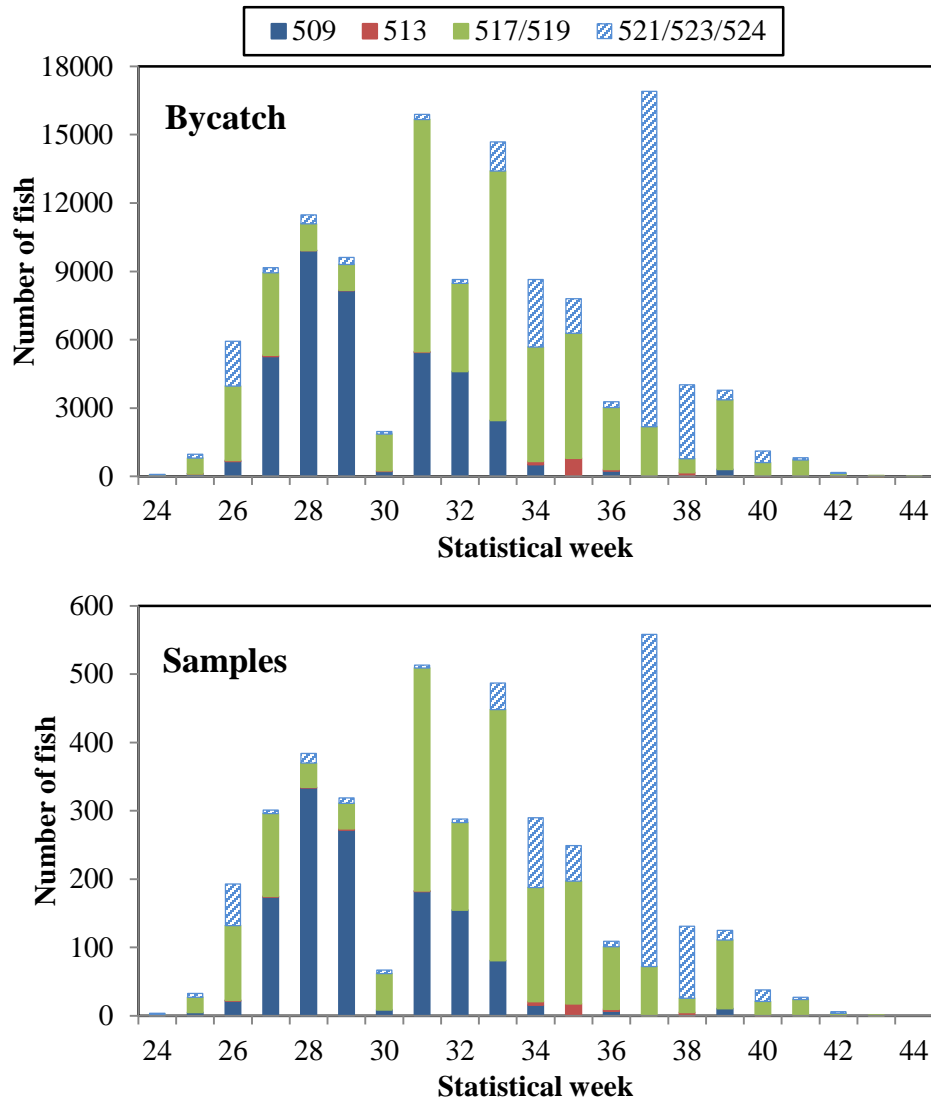


Figure 4. -- Number of Bering Sea chum salmon bycatch and genetic samples collected from the 2013 B-season by statistical week and NMFS reporting area (designated in the legend).

The systematic collecting protocol was also evaluated by comparing the total number of chum salmon caught on each vessel to the number of genetic samples collected from each vessel. During the B-season, > 99% of the chum salmon bycatch was subsampled for genetic samples across a large range of chum salmon bycatch per vessel (Fig. 5, top panel). Of the bycatch that was sampled, the mean sampling ratio of numbers of bycatch to numbers of genetic samples per vessel was 30.3 fish, which is very close to the protocol sampling goal of one genetic sample

collected from every 30th chum salmon caught (Fig. 5, bottom panel). All but 1 of the 86 vessels that participated in the midwater trawl fishery caught chum salmon. By vessel, slightly more than half the bycatch was undersampled, but based on the systematic sampling protocol, only 43 fish (1% of expected) were not sampled. The variance of the numbers of genetic samples from undersampled vessels was about two times higher than the variance from oversampled vessels ($P = 0.004$; one-tail F -test, excluding the vessel with 1 sample from 14 bycatch).

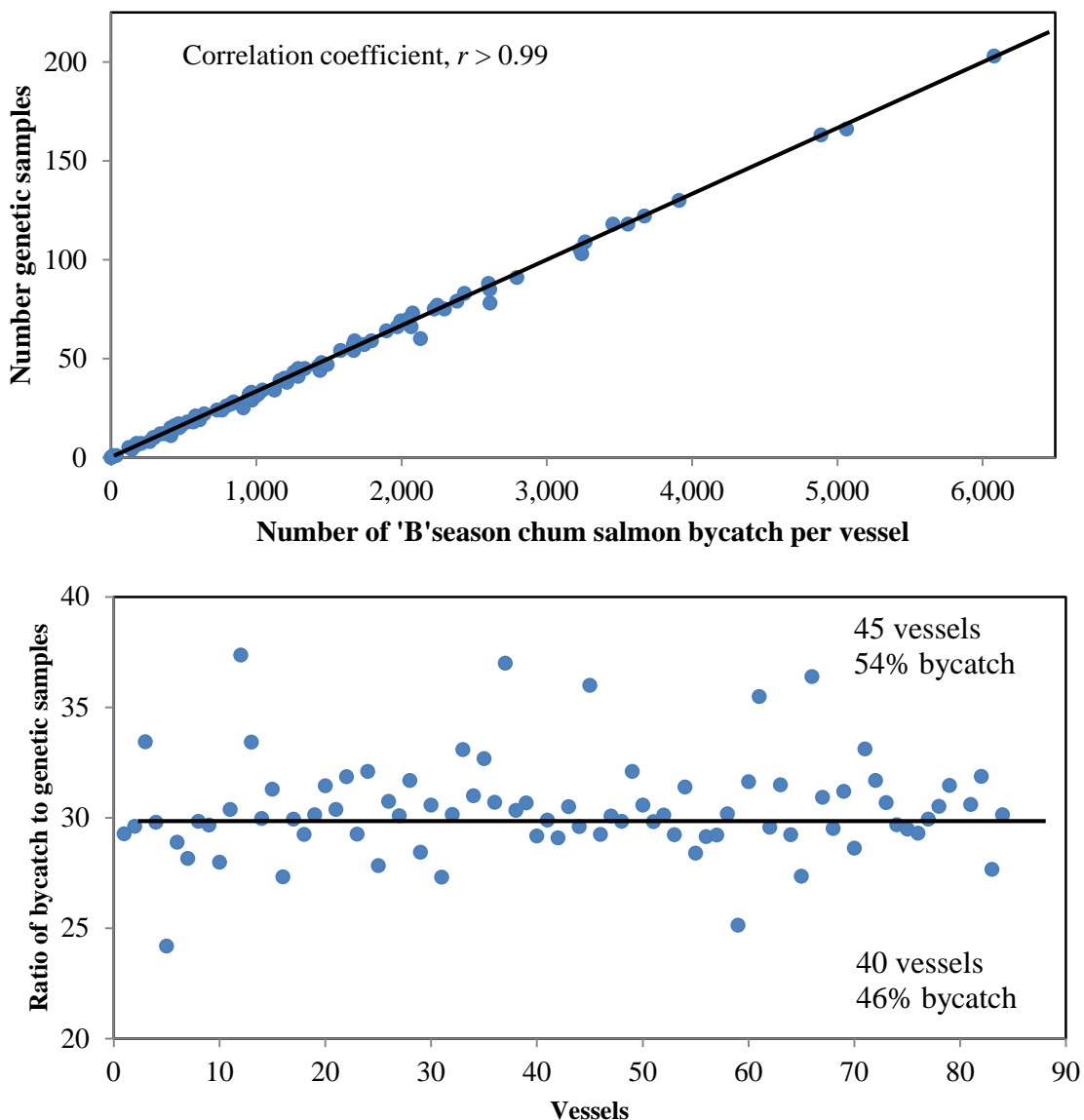


Figure 5. -- Bering Sea chum salmon bycatch and genetic samples from the 2013 pollock B-season. Number of genetic samples collected from the total number of chum salmon bycatch from each of 85 vessels; black diagonal line represents the expected sampling rate (top panel). The ratio of total number of bycatch sampled to number of genetic samples collected per sampled vessel; black horizontal line represents the expected sampling ratio (bottom panel). One vessel with the ratio of 14 (1 sample from 14 bycatch) is not shown.

GENETIC STOCK COMPOSITION

Laboratory Analyses

DNA was extracted from the axillary processes of all 4,094 chum salmon sampled from the bycatch during the B-season that were shipped to ABL. DNA extraction and microsatellite genotyping was performed as described previously (Guyon et al. 2010). Samples were genotyped for the following 11 microsatellite loci: *Oki100* (Beacham et al. 2009a), *Omm1070* (Rexroad et al. 2001), *Omy1011* (Spies et al. 2005), *One101*, *One102*, *One104*, *One114* (Olsen et al. 2000), *Ots103* (Nelson and Beacham 1999), *Ots3* (Greig and Banks 1999), *Ots68* (Williamson et al. 2002), and *Ssa419* (Cairney et al. 2000). Thermal cycling for the amplification of DNA fragments with polymerase chain reaction (PCR) was performed on a dual 384-well GeneAmp PCR System 9700 (Applied Biosystems, Inc.). Samples from the PCR reactions were diluted into 96-well plates for analysis by a 48-capillary, 36 cm array on the ABI 3730xl Genetic Analyzer (Applied Biosystems, Inc.). Genotypes were double-scored with GeneMapper 5.0 software (Applied Biosystems, Inc.) and exported to Excel (Microsoft, Inc.) spreadsheets.

Of the 4,094 bycatch samples analyzed, 3,889 bycatch samples were successfully genotyped for 8 or more of the 11 loci (Table 1). Nine pairs of duplicate genotypes were detected with GenAlEx 6.5 (Peakall and Smouse 2006, 2012); one sample from each pair was removed from further analysis. The remaining 3,880 bycatch samples had genetic information for an average of 10.9 loci. There were six alleles observed in six individuals that were not present in the chum salmon baseline; the single-locus genotypes for these individuals were removed from further analysis. The weekly distribution of genetic samples collected in the field (4,123), shipped to ABL and genotyped (4,094), and analyzed for stock estimation (3,880) did not differ from that expected from the total bycatch based on the sampling protocol (Table 2).

Table 1. -- Number of genetic samples successfully genotyped for chum salmon bycatch from the 2013 Bering Sea midwater pollock trawl fishery.

Number loci	Bycatch samples
11	3,612
10	193
9	47
8	28
< 8	214

Table 2. -- Chi-square tests for goodness of fit used to compare the weekly distribution of genetic samples collected, genotyped, and analyzed with the expected number of samples (total bycatch per week/30).

Sample set	X^2	<i>d.f.</i>	<i>P</i> -value
Collected	1.437	17	> 0.99
Genotyped	3.325	17	> 0.99
Analyzed	22.806	17	0.16

Laboratory Quality Control

Quality control of sample handling and genotyping was examined by plating DNA from the eight samples in the left-most column of each of 44 elution plates onto four 96-well plates for a total of 352 samples that were then processed for genotyping as described above. Genotypes from the quality control dataset were then compared to the genotypes of the original dataset (Table 3). Overall, the genotyping error was low; across 11 loci there were a total of 60 differences in 7,446 alleles in the original and quality control datasets, which represented an overall discrepancy rate of 0.81%.

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

Locus	Number alleles compared	Number allele differences	Percent difference
<i>Oki100</i>	682	4	0.59
<i>Omm1070</i>	664	12	1.81
<i>Omy1011</i>	680	7	1.03
<i>One101</i>	654	11	1.68
<i>One102</i>	678	7	1.03
<i>One104</i>	682	3	0.44
<i>One114</i>	688	2	0.29
<i>Ots103</i>	684	4	0.58
<i>Ots3</i>	680	2	0.29
<i>OtsG68</i>	680	3	0.44
<i>Ssa419</i>	674	5	0.74

Data Analyses – 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. 2008, Beacham et al. 2009b). Standardized genotypes were then exported from Excel as text files, and C++ or FORTRAN programs were used to format the data into mixture files compatible with software used for stock composition estimation. Stock compositions were determined by comparing mixture genotypes with allele frequencies from reference baseline populations. As described previously (Gray et al. 2010), with minor changes to regional group names, baseline populations were grouped into six regions: Southeast Asia, Northeast Asia, Western Alaska, Upper/Middle Yukon, Southwest Alaska, and the Eastern Gulf of Alaska/Pacific Northwest (Fig. 6). 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.

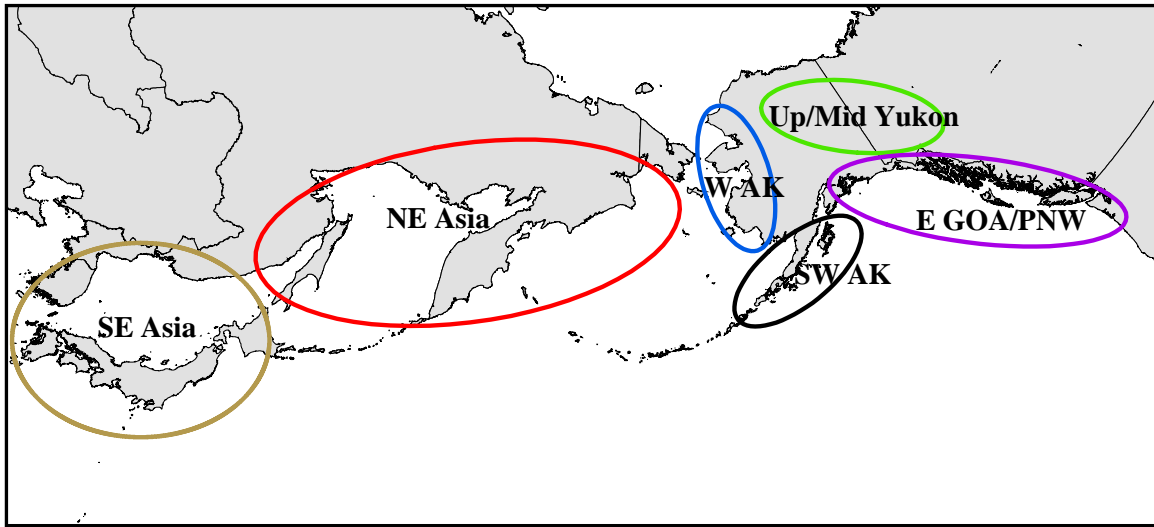


Figure 6. -- Six regional groups of baseline chum salmon populations used in this report were as follows: Southeast Asia (brown), Northeast Asia (red), Western Alaska (blue), Upper/Middle Yukon (green), Southwest Alaska (black), and the Eastern Gulf of Alaska/Pacific Northwest (purple).

As with previous chum salmon bycatch analyses (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010, 2011a,b; Kondzela et al. 2012, 2013; Vulstek et al. 2014), stock composition analysis for the 2013 chum salmon bycatch samples was performed with maximum-likelihood (SPAM 3.7 software; ADF&G 2003) and Bayesian (BAYES software; Pella and Masuda 2001) procedures. Because the maximum-likelihood estimates were in close agreement with the Bayesian estimates, the maximum-likelihood estimates are not shown. The Bayesian method uses an algorithm that can account for missing alleles in the baseline (Pella and Masuda 2001). BAYES stock composition estimates based on data from all 11 loci were derived for the six regional groups (Table 4; Appendix II). For all estimates, the Dirichlet prior parameters for the stock proportions were defined by region to be $1/(GC_g)$, where C_g is the number of baseline

populations in region g , and G is the number of regions¹. For each analysis, six Monte Carlo chains of 100,000 iterations were run starting at disparate values of stock proportions configured such that 95% of the stocks came from one designated region with weights equally distributed among the stocks of that region. The remaining 5% was equally distributed among remaining stocks from all other regions. The first 50,000 iterations from each chain were discarded to remove the influence of the initial values. Convergence of the chains to posterior distributions of stock proportions was assessed with Gelman-Rubin shrink factors, which were all 1.02 or less (Table 4), conveying strong convergence to a single posterior distribution (Gelman and Rubin 1992; Pella and Masuda 2001).

The stock composition estimates were summarized by the following statistics: mean, median, standard deviation, 95% credibility interval (2.5th and 97.5th percentile of the MCMC iterates in the posterior output), and a statistic called $P = 0$, which is the probability that a stock composition estimate is effectively zero (Habicht et al. 2012). The $P = 0$ statistic is the frequency of MCMC iterates that were less than a threshold that is calculated as 0.5 divided by the number of the reported bycatch 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 fish in the bycatch. This statistic may be more useful than the credibility interval for assessing the presence or absence of minor stocks.

¹ In bycatch analyses from previous years, a flat prior (1/381) was assigned to each baseline population. Priors defined by region may reduce bias due to differences in how densely regions are represented by baseline populations.

Table 4. -- Regional BAYES stock composition estimates for 3,880 chum salmon samples from the bycatch of the 2013 Bering Sea pollock midwater trawl fishery. BAYES mean estimates are provided with standard deviations (SD), 95% credible interval values, median estimate, $P = 0$ statistic, and the associated Gelman and Rubin shrink factor.

Region	Mean	SD	2.5%	Median	97.5%	$P = 0$	Shrink
Southeast Asia	0.1465	0.0063	0.1344	0.1464	0.1589	0	1.00
Northeast Asia	0.4489	0.0101	0.4292	0.4489	0.4686	0	1.00
Western Alaska	0.1809	0.0095	0.1626	0.1809	0.1996	0	1.01
Upper/Middle Yukon	0.0622	0.0066	0.0496	0.0621	0.0754	0	1.02
Southwest Alaska	0.0140	0.0029	0.0089	0.0138	0.0202	0	1.00
Eastern GOA/PNW	0.1475	0.0065	0.1351	0.1474	0.1604	0	1.00

Data Analyses – Subsampling Effects

The 2013 chum salmon bycatch from the Bering Sea was lower than during the peak years in the mid-2000s, but it was still one of the highest over the last two decades. The number of genetic samples analyzed in 2013 was more than double the number analyzed in previous years. This larger sample set provided an opportunity to examine the effects of subsampling the genetic samples on stock composition estimation, with the goal of reducing laboratory processing time and costs while maintaining stock composition estimate precision. The total sample set was first sorted by cruise, haul or offload, and specimen number and then split into subsets of samples that retained the systematic sampling in the field, albeit on a coarser scale: 1/2, 1/4, or 1/8 of the available genetic samples, which represents sampling every 60th, 120th, and 240th fish from the 2013 bycatch, respectively. The two subsets that contained half the samples were created by assigning every other sample to one of the two subsets. For the first of the smaller subsets, every 4th or 8th sample was chosen starting with the first sample in the total sample set. Remaining subsets were created by starting with the 2nd sample in the total sample set and then choosing every 4th or 8th sample, and so forth. Stock composition estimates for each sample subset were made as before, except that Monte Carlo chains of 50,000 iterations were run.

The stock composition estimates for the 1/2 sample sets were similar to each other and to the total sample set as determined by the overlap of 95% credible intervals for each regional group (Fig. 7; Appendix II). The mean difference of the six regional stock estimates of the 1/2 sample sets from the total sample set was less than 1% and the maximum difference was less than 2% of the overall stock proportions. As expected due to the larger sample size, the credible intervals were narrower for the total sample set than the 1/2 sample sets, but only by a margin of about 1% stock proportion. The highest variation in stock estimates occurred with the Upper/Middle Yukon region, although the maximum difference of stock estimates for this region was less than 3% between the 1/2 sample sets. As expected, the variation of the stock composition estimates increased with smaller sample sets. The 1/4 sample set estimates differed from the total sample set estimates by 0.05-4.06%; the range was about double that for the 1/8 sample sets (0.11-7.8%). In the smallest sample sets (1/8), the credible intervals of the lowest and highest estimates did not overlap for several regions (Northeast Asia, Western Alaska, Upper/Middle Yukon, and Southwest Alaska). The amount of variation in stock estimates also differed by stock region. For example, the Northeast Asia and Western Alaska regions had the most variation in stock estimates, whereas the Southwest Alaska and Southeast Asia regions had the least variation. Additionally, the probability that small estimates are effectively zero ($P = 0$); for example, Southwest Alaska, increased as sample size decreased.

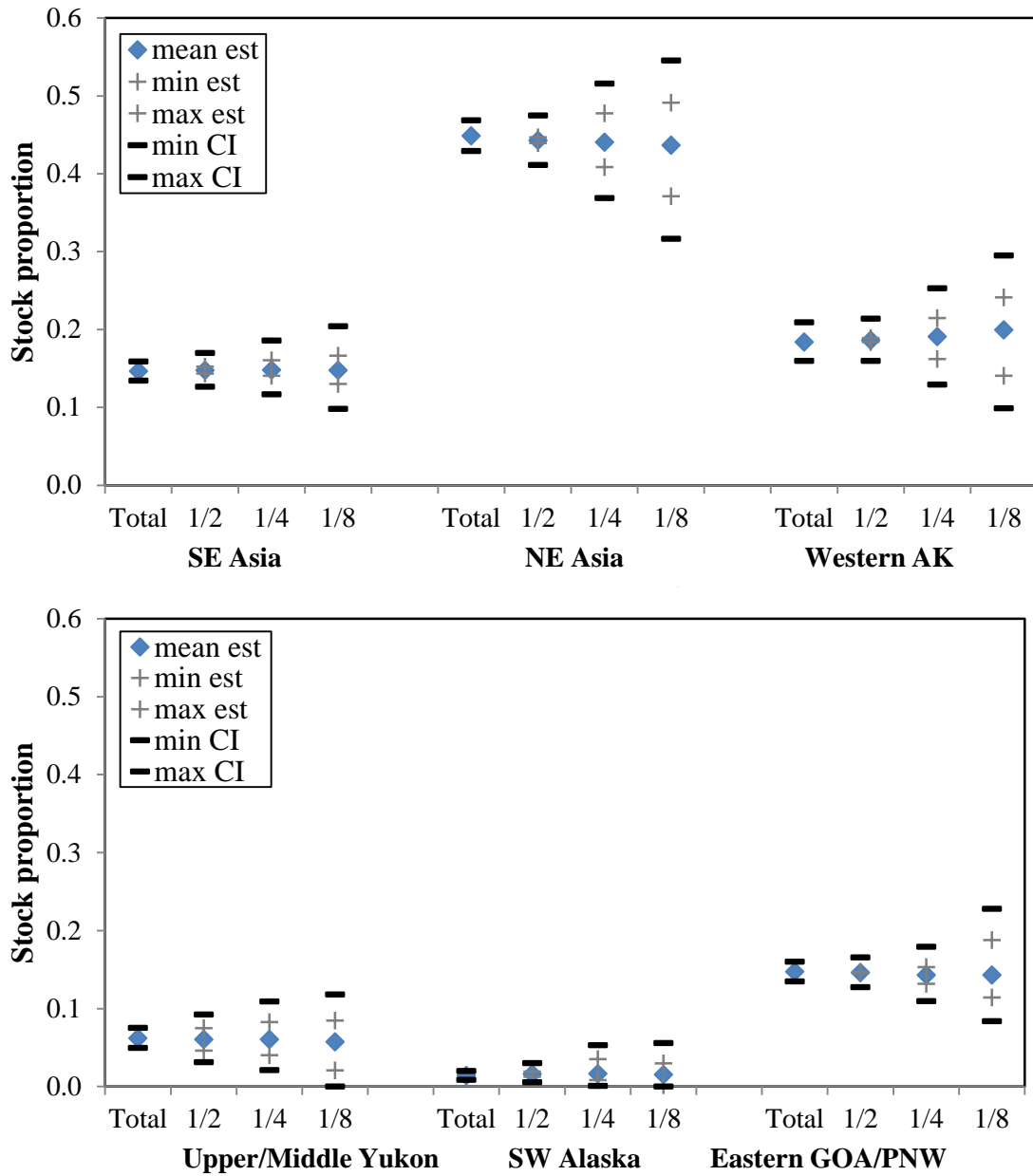


Figure 7. -- BAYES stock composition estimates (blue diamonds) and 95% credible intervals (black bars) for the 2013 chum salmon total bycatch sample set (3,880 samples) and for smaller sample sets created by splitting the total sample set into halves, quarters, and eighths. For the smaller sample sets (1/2, 1/4, and 1/8), the mean stock estimates, the lowest and highest stock estimates (grey crosses), and the 95% credible intervals of the lowest and highest stock estimates are shown.

COMPARISON WITH PREVIOUS ESTIMATES

The stock composition results from the analysis of the 2013 chum salmon bycatch samples were generally similar to the 2012 results, but differed somewhat from other previous estimates (Fig. 8, upper panel). The 2013 estimated contribution from Northeast Asia was higher than that of 2011 and the 1994, 1995, 2005–2010 average, whereas the contribution from Southeast Asia was slightly lower in comparisons across years. The 2013 Western Alaska, Upper/Middle Yukon, and Southwest Alaska contributions were similar to previous years. The 2013 contribution from the Eastern GOA/PNW was similar to all previous years, except 2011, which was a standout for this region. Contributions from the Upper/Middle Yukon and Southwest Alaska were below 10%, as in other years. The extent to which year-to-year differences in regional stock contributions are attributable to differences in fishing locations and times or migration patterns of chum salmon is beyond the scope of this report. However, with systematic sampling of the Bering Sea salmon bycatch in place, the role of these factors on the temporal variation of stock estimates will be easier to determine.

The 1994–1995 chum salmon bycatch stock composition estimates were produced with allozyme data (Wilmot et al. 1998), whereas the 2005–2013 estimates were derived from DNA-based microsatellite loci (Guyon et al. 2010; Marvin et al. 2011; Gray et al. 2010, 2011a,b; Kondzela et al. 2012, 2013; Vulstek et al. 2014). The allozyme (77 populations) and microsatellite DNA (381 populations) baselines have data from many of the same populations and have similar regional groups. The effect of the bycatch on chum salmon populations is influenced by the overall size of the bycatch relative to the returns. The large variation in total chum salmon bycatch in 1994, 1995, 2005–2013 (Fig. 2) is reflected in the high standard errors of the mean number of bycatch by region (unweighted by year) when stock composition estimates are extrapolated to the total bycatch from the Bering Sea groundfish fisheries (Fig. 8,

lower panel). Beginning in 2011, the genetic samples were collected systematically from the bycatch, resulting in the numerical extrapolations being relatively free of sample bias. The location and timing of collections from earlier years was not always representative of the entire bycatch within a given year.



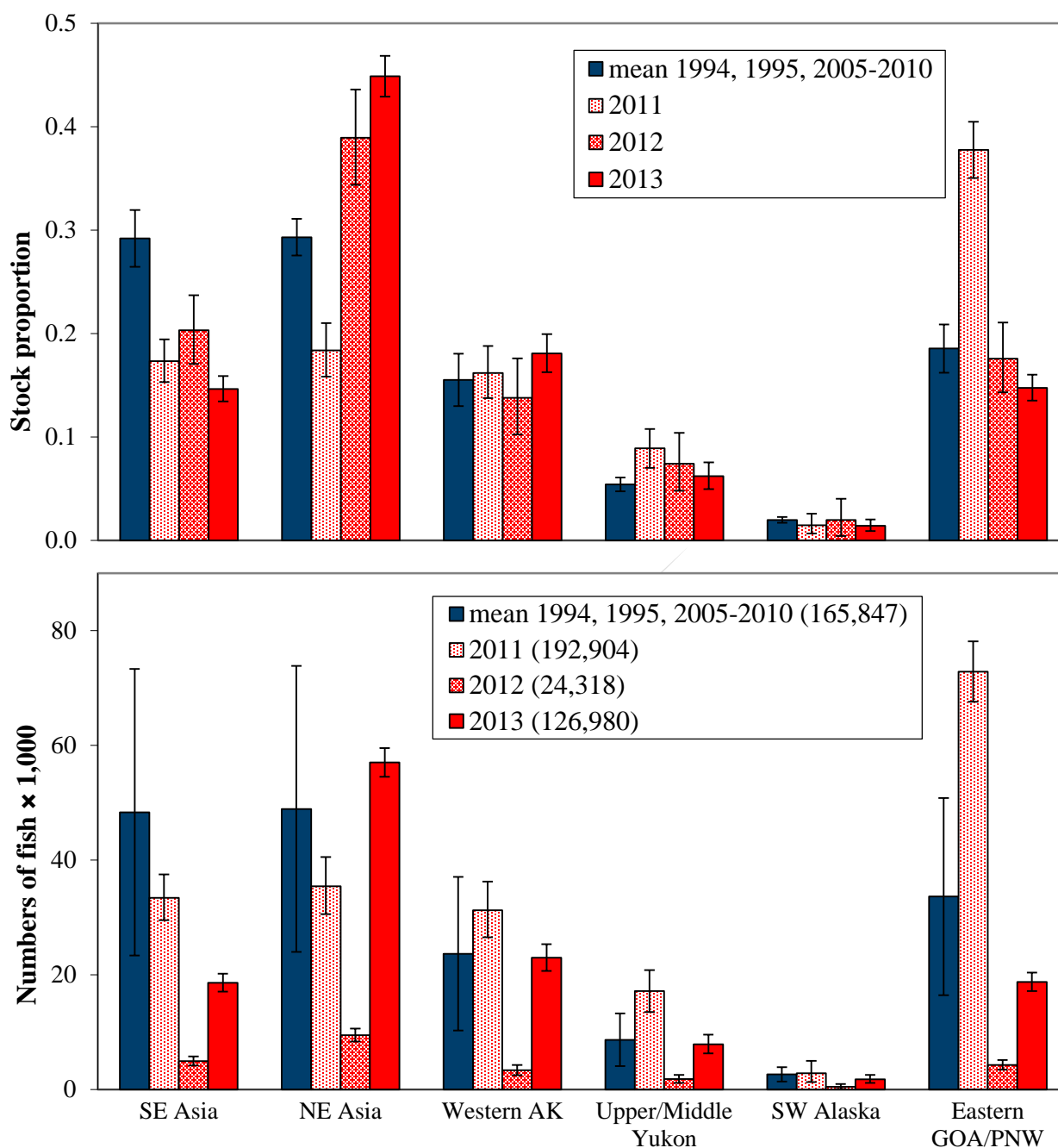


Figure 8. -- Comparison of the 2013 Bering Sea chum salmon bycatch stock composition estimates with the estimates from 2011 and 2012, and the unweighted mean estimates of available genetic samples from 1994, 1995, and 2005–2010. Proportions in top panel; numbers of fish in bottom panel, which for comparison purposes across years are based on the total chum salmon bycatch in all groundfish fisheries. Standard errors of the mean estimates are shown for the combined years; 95% BAYES credible intervals are shown for the 2011–2013 analyses. Error bars are based on only the mixed-stock analyses and do not include errors associated with the overall annual bycatch size estimation or potential biases in sample distribution. Total chum salmon bycatch from the Bering Sea groundfish fisheries is shown in parentheses in the bottom figure legend; 1994–2010 are estimates and 2011–2013 are censuses.

TEMPORAL STRATIFICATION

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

As with the 2005–2012 analyses, the 2013 sample set was temporally split into three B-season time periods: Early, Middle, and Late (Table 5). Stock composition analyses for 2013 and similar temporal strata of the average 2005–2012 chum salmon bycatch sample sets are included for comparison purposes (Fig. 9; Appendix II). Results from this analysis should be used cautiously because spatial differences exist in the time-stratified sample sets and these differences are known to affect the stock composition estimates.

Table 5. -- Temporal groups from the 2013 B-season chum salmon bycatch genetic sample sets.

Time period	Weeks	Dates	Number of samples
Early	24-29	June 10 – July 20	1,132
Middle	30-34	July 21 – August 24	1,582
Late	35-43	August 25 – October 24	1,166

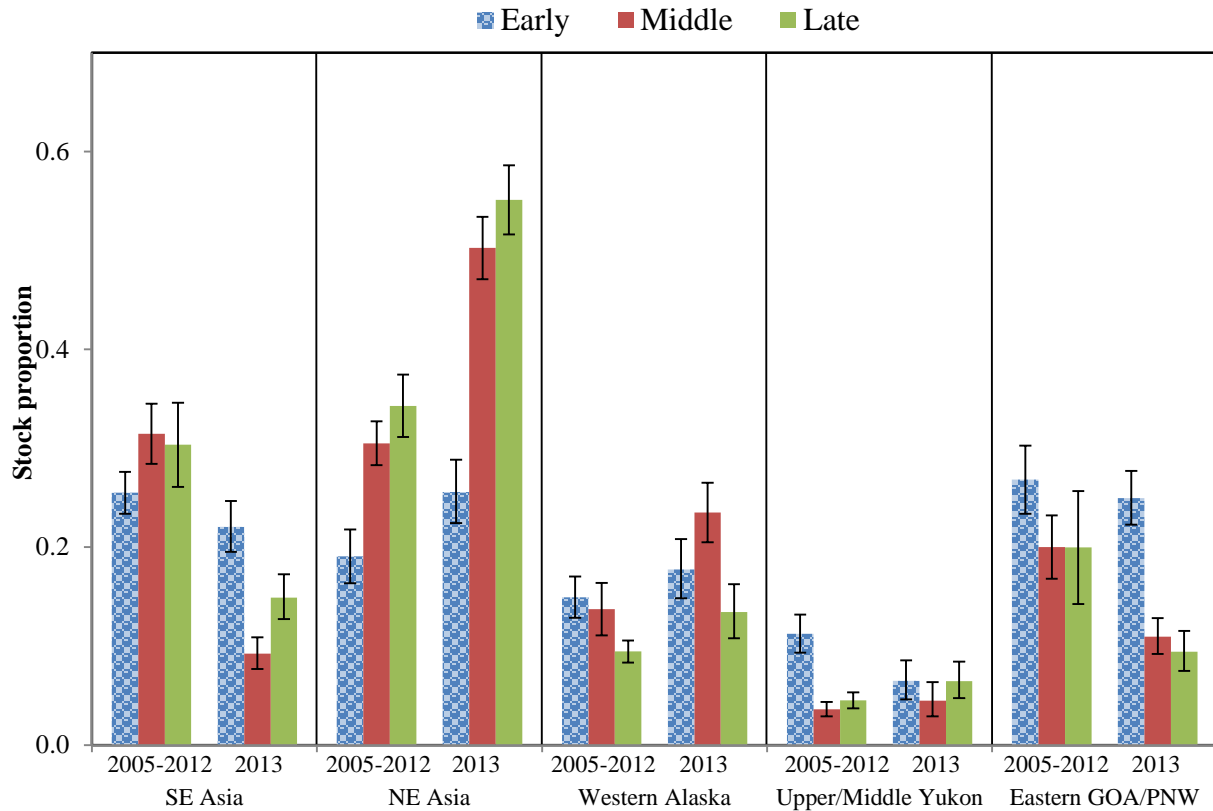


Figure 9. -- BAYES stock composition estimates for the 2005–2012 (mean) and 2013 chum salmon bycatch samples for the Early, Middle, and Late periods (defined in Table 5). Standard errors of the mean estimates are shown for the combined years; 95% BAYES credible intervals are shown for the 2013 analysis. Not shown is the Southwest Alaska region for which estimates never exceeded 5.6%.

BAYES stock composition estimates were made as described previously for each of the three temporal strata. Gelman and Rubin shrink factors were in all cases 1.00 and suggested strong convergence to a single posterior distribution. The stock composition estimates of the 2013 genetic samples differed across the three time periods within four of the five regional groups. The contribution from Southeast Asia decreased during the Middle time period and then increased in the Late time period, whereas the contribution from Northeast Asia doubled from the Early to Middle/Late time periods. On the North American continent, the Western Alaska contribution increased slightly in the Middle time period and then decreased in the Late time period, the Upper/Middle Yukon contribution remained stable over the three time periods, and

the Eastern GOA/PNW contribution decreased by about half after the Early time period (Fig. 9). In addition, some differences were observed between the pattern of 2013 temporal stock contributions and the trends reported previously with the 2005–2012 chum salmon bycatch samples. The contribution from Southeast Asia during the Middle and Late time periods in 2013 was lower than in previous years, although the 2013 distribution was similar to that observed in 2012 (Vulstek et al. 2014). The contribution from Northeast Asia across the three time periods in 2013 increased over the season to a greater extent than in previous years. The proportion of the bycatch contributed by Western Alaska chum salmon stocks increased in the middle of the season as observed in 2012, whereas on average in previous years, the proportions decreased over the course of the season. The contribution from the Upper/Middle Yukon remained relatively stable across time in 2013, unlike the decrease after the Early time period in previous years. The contribution from the Eastern GOA/PNW decreased to about half that observed in the first part of the season, a larger decrease than observed on average in previous years. This analysis demonstrates that stock composition of the chum salmon bycatch changes during the course of the season.

SPATIAL STRATIFICATION

Knowledge of the spatial distribution of the chum salmon bycatch is also important for better understanding the impacts of the pollock trawl fishery on salmon stocks. In 2013, for the third year, the Observer Program undertook a complete census of chum salmon bycatch from the Bering Sea trawl fisheries. Nearly 90% of the chum salmon bycatch was counted and sampled at shoreside facilities where catches were offloaded from vessels that theoretically can participate in multiple fishery management areas on a particular cruise before an offload. For vessels that

fished in multiple NMFS reporting areas during a trip, the area was identified as the area where most of the fishery target species were caught.

The 2013 genetic samples were spatially split into three areas (see Fig. 1): the U.S. waters of the Bering Sea west of longitude 170°W (areas 521, 523, and 524 aggregated due to small sample sizes in areas 523 and 524), and two areas in the southeastern Bering Sea east of longitude 170°W (area 509, and areas 513, 517, and 519 aggregated due to small sample sizes in areas 513 and 519). BAYES stock composition estimates were made as described previously for each of the three spatial strata. Gelman and Rubin shrink factors were 1.00 for all datasets and suggested strong convergence to a single posterior distribution. The stock composition estimates differed among the spatial strata (Fig. 10; Appendix II). About two-thirds of the contribution to the west of 170°W and about half of the contribution to the southeastern Bering Sea were from Asian stocks. Northeast Asia stocks, the largest contributor to the bycatch in all three Bering Sea areas, were highest in the aggregate area 513/517/519 of the southeastern Bering Sea. Southeast Asia stocks were about twice as frequent in waters west of 170°W as in the southeastern Bering Sea. Except for the Upper/Middle Yukon region, contributions from North American stocks were highest in the southeastern Bering Sea. The Eastern GOA/PNW stocks were more prevalent in area 509, the easternmost area fished, than in the other areas. Southwest Alaska had a nearly three-fold higher contribution to area 509 than to the other areas, but the contribution was low in all areas.

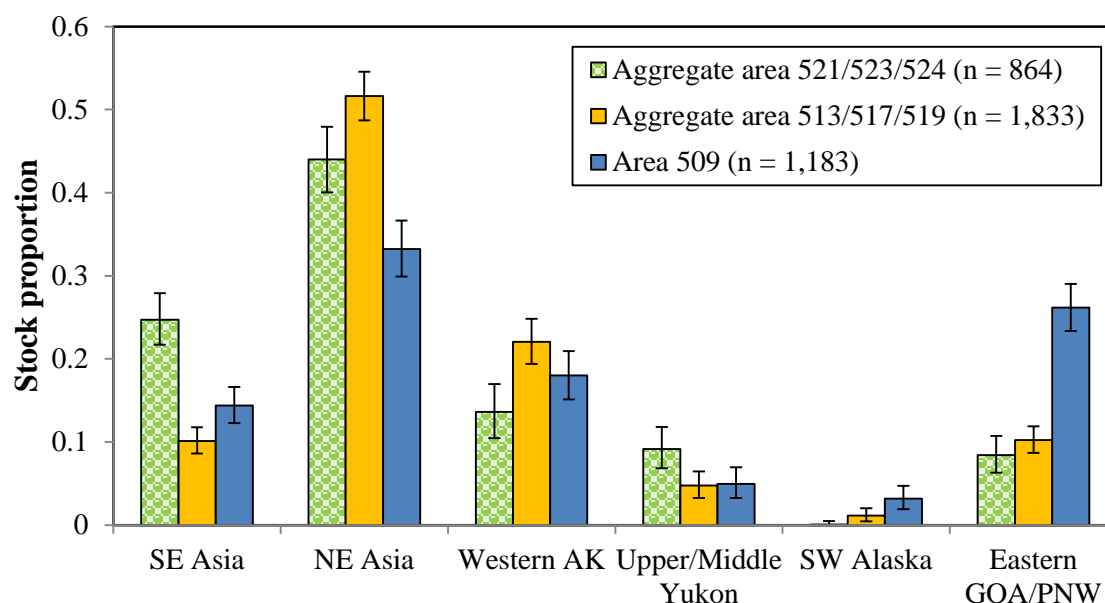


Figure 10. -- BAYES stock composition estimates and 95% credible intervals for the 2013 chum salmon bycatch genetic samples from the southeastern Bering Sea (area 509, and aggregate area 513/517/519) and U.S. waters west of long. 170° W (aggregate area 521/523/524).

To better understand the bycatch stock distribution across time and space, the 2013 sample set from area 509 was split into two time periods, and the sample sets from areas 517 and 521 were split into three time periods (Table 6). Samples from all other areas were not included due to small sample sizes in those areas.

Table 6. -- Spatial and temporal groups from the 2013 chum salmon bycatch genetic sample sets across three time periods (Table 5) for the reporting areas with the most samples.

Reporting area	Time period	Number of samples
509	Early	738
509	Middle	428
517	Early	304
517	Middle	1,004
517	Late	473
521	Early	85
521	Middle	144
521	Late	627

BAYES stock composition estimates were made for each of the spatial and temporal strata as described above (Fig. 11; Appendix II). The Gelman and Rubin shrink factors were 1.01 or less for all datasets. The Asian stock contribution changed significantly across time in a manner that was similar in the three reporting areas. Similar to results in 2011 (Kondzela et al. 2013), a recent year in which enough samples were available to stratify the data, the Northeast Asia contribution increased over time in all three areas, whereas the Southeast Asia contribution decreased over time for areas 517 and 521. The contribution from Western Alaska and the Upper/Middle Yukon remained relatively stable over time for all areas, whereas in 2011, the Upper/Middle Yukon stocks were infrequently encountered by the Late time period. The Eastern GOA/PNW contribution decreased over time for areas 509 and 517, unlike in 2011, and the increase in area 521 in the Late time period was far less than in 2011. As in previous years, the contribution from Southwest Alaska was very low in all time periods and areas. It should be noted that the numbers of fish from a region within a given area may not change over time, but the proportion will change if fish from other regions move into or out of the area.

Where it occurs, the similarity of stock distributions among the areas and time periods may be due at least in part to vessels fishing near area boundaries. For example, the southern corner of area 521 shares the northwestern edge of area 517. Latitude and longitude information was not available for many samples, so the location of the bycatch samples within each area is unknown. In addition, nearly 90% of the total bycatch was sampled from shoreside deliveries in which vessels may have fished in multiple areas. Thus, for an unknown proportion of the chum salmon bycatch samples, the area designation may not be correct.

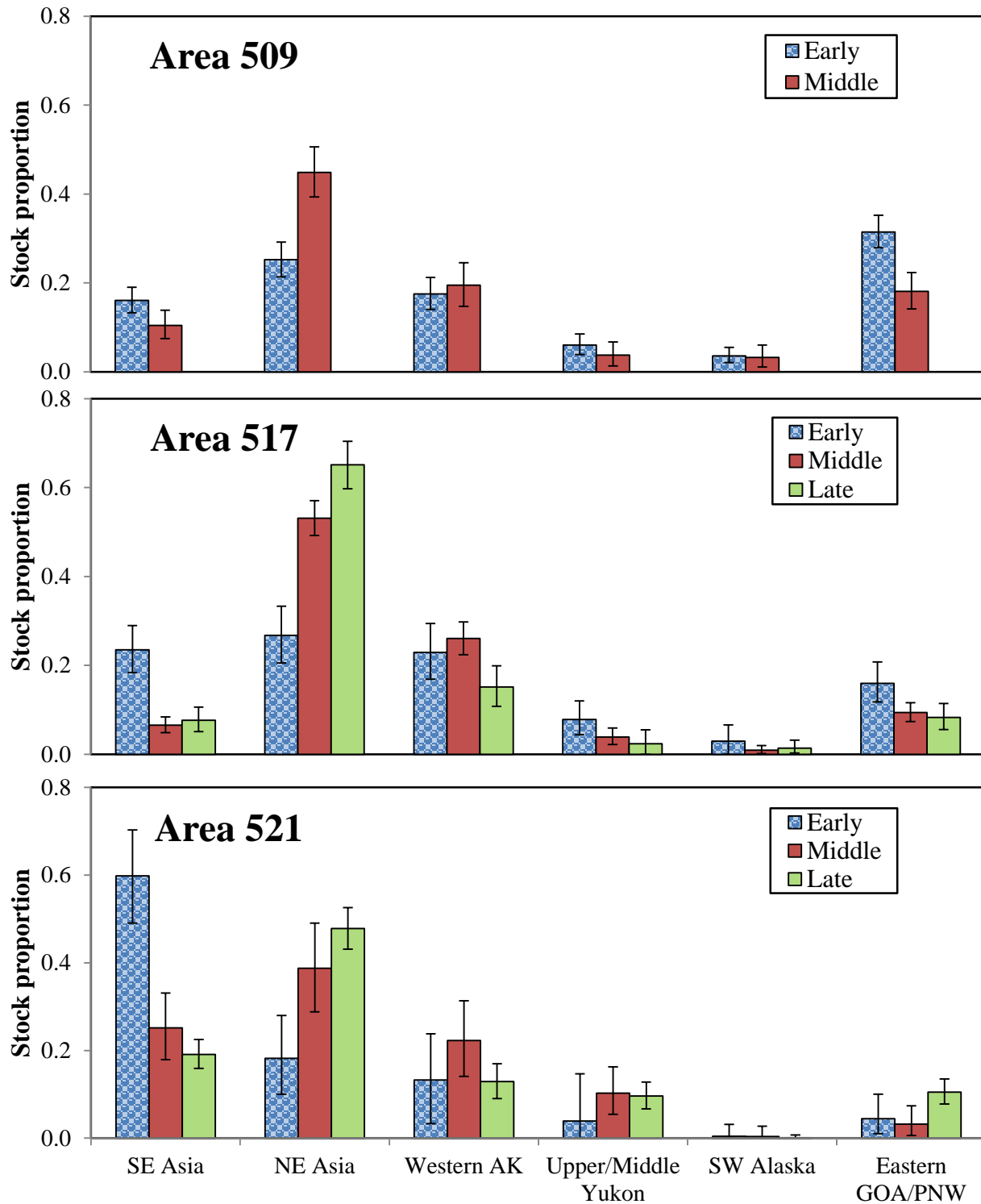


Figure 11. -- BAYES stock composition estimates and 95% credible intervals for the 2013 chum salmon bycatch genetic samples from the NMFS reporting area 509 for the Early and Middle time periods, and areas 517 and 521 for the Early, Middle, and Late time periods (Table 5).

SUMMARY

Stock composition estimates of the salmon bycatch in the Bering Sea groundfish fisheries are needed for fishery managers to understand the impact of these fisheries on salmon populations, particularly those in western Alaska. This report provides a stock composition analysis of 3,880 samples from the 2013 chum salmon bycatch. The limitations and results of this analysis are summarized below and in Appendix II.

Sampling Issues

We highlight the reduced spatial and temporal biases in the 2013 sample set (Figs. 3 and 4) that were inherent in collections before 2011. Reduction of those biases improves the application of the 2013 genetic sample stock composition estimates to the entire chum salmon bycatch. Implementation of Amendment 91 to the NPFMC fishery management plan for groundfish of the Bering Sea and Aleutian Islands Management Area (75 FR 53026, August 30, 2010; <https://www.federalregister.gov/articles/2010/08/30/2010-20618/fisheries-of-the-exclusive-economic-zone-off-alaska-chinook-salmon-bycatch-management-in-the-bering>) requires that all salmon taken as bycatch in the Bering Sea pollock fishery be sorted by species and counted to ensure compliance with the salmon bycatch caps for the pollock fishery. This new regulation led to the collection of representative samples from 99.8% of the chum salmon bycatch from this fishery for genetic analysis in 2013 (Fig. 5), and improved the capability to characterize the origin of salmon taken as bycatch in the Bering Sea pollock fishery.

Stock Composition Estimates

Overall, the genetic samples collected from the 2013 bycatch of Bering Sea chum salmon were predominantly from Northeast Asia stocks (44.9%), although moderate contributions were

also from Southeast Asia (14.7%), Eastern GOA/PNW (14.8%), and Western Alaska (18.1%) stocks. The stock proportions from Asia in 2013 dominated the bycatch as in previous years; however, within this group, the 2013 estimates from Northeast Asia and Southeast Asia differed significantly from some previous years (Fig. 8). Although samples in 2013 were collected representatively from the pollock fishery bycatch, there were differences in where and when genetic bycatch samples were collected from previous years, so that caution must be used in making year-to-year comparisons.

The 2013 chum salmon bycatch sample set was large enough to examine the effect of subsampling the total sample set on stock composition estimates. The stock composition estimates of the 1/2 sample sets were similar to each other and to the total sample set (Fig. 7), with most differences less than 1%. The differences increased when sample size was further decreased: 1/4 and 1/8 sample sets had maximum differences in stock estimates from the total sample set of 4% and 8%, respectively. Use of half the samples (about 2,000 samples) would reduce laboratory processing time and cost, as well as time required for data analyses, with negligible effect on stock composition estimates of the total bycatch. Even the use of 1/4 of the samples (about 1,000 samples) would provide stock estimates within 4% or less of the total sample set estimates. However, the use of fewer samples chosen from a systematic sampling protocol may preclude or limit more in-depth spatial, temporal, or potential age-specific analyses.

Temporal and Spatial Effects

The time-stratified analysis of the chum salmon bycatch was limited to the pollock B-season, when the majority of chum salmon are intercepted. Stock composition estimates of the 2013 bycatch changed across the three sampling periods, suggesting a shift in the temporal

stratification of chum salmon stocks in the Bering Sea, changes in fishing or sampling locations, or both (Fig. 9). The stock composition estimates of the 2013 bycatch shared a similar distribution to that observed across previous years for the Early time period, but not for the Middle time period, especially for the Southeast Asia and Western Alaska contributions, or the Late time period for the Southeast Asia contribution.

Spatial analysis that compared the samples from the U.S. waters of the Bering Sea west of long. 170°W (aggregate area 521/523/524) and from the southeastern Bering Sea (area 509; and aggregate area 513/517/519) suggested that the majority of chum salmon bycatch in all three areas originated from the Northeast Asia region (Fig. 10). However, there were some differences in regional contributions among the areas. The proportion of bycatch from Southeast Asia stocks in the U.S. waters of the Bering Sea west of long. 170°W was nearly twice that in the southeastern Bering Sea. The majority of chum salmon bycatch in all but the eastern most area fished (area 509) in the Bering Sea was from Asia, whereas more than half of the bycatch in area 509 was from North America, with the highest contribution from the Eastern GOA/PNW.

An examination of stock estimates on both spatial and temporal strata suggests that although there were some differences in stock distribution across areas or time periods, there were also consistent temporal changes in stock distribution within areas (Fig. 11). For example, the Southeast Asia contribution decreased, the Northeast Asia contribution increased, and the Western Alaska and Upper/Middle Yukon contributions changed little over time in the three areas where most of the chum salmon were caught. The contribution from the Eastern GOA/PNW decreased in areas 509 and 517, but increased in area 521 across the season.

Application of Estimates

The extent to which any salmon stock is impacted as the bycatch in the Bering Sea trawl fishery is dependent on many factors including 1) the overall size of the bycatch, 2) the age of the salmon caught in the bycatch, 3) the age 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

The baseline used for these analyses was obtained through a web portal sponsored by Fisheries and Oceans Canada and developed in their Molecular Genetics Laboratory with genetic loci identified in a number of laboratories. Fishery information was provided by the AFSC's Fisheries Monitoring and Analysis Division and NMFS Alaska Regional Office (AKR), with particular thanks to Martin Loefflad, Julie Blair, Ren Narita, and Glenn Campbell. This document was peer reviewed by the AFSC and external reviewers Brandee Gerke of the AKR and Bill Templin and Nick DeCovich of the Alaska Department of Fish and Game for which we are especially grateful.

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.
- 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. W. Wallace, S. Sato, S. Urawa, N. V. Varnavskaya, K. D. Le, and M. Wetklo. 2008. Microsatellite stock identification of chum salmon on a Pacific Rim basis and a comparison with single nucleotide polymorphisms (SNPs). N. Pac. Anadr. Fish Comm. Doc. 1105. 77 p. (Available at <http://www.npafc.org>).
- 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.
- 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.* 30:318-320.
- 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.
- Habicht, C., A. R. Munro, 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 sockeye salmon stocks in fisheries of the Western Alaska Salmon Stock Identification Program (WASSIP), 2006-2008. Alaska Department of Fish and Game, Special Publication No. 12-24, Anchorage.
- 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-AFSC-243, 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.
- 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.
- Nelson, R. J., and T. D. Beacham 1999. Isolation and cross species amplification of microsatellite loci useful for study of Pacific salmon. *Anim. Genet.* 30:228-229.
- NMFS (National Marine Fisheries Service). 2014. BSAI non-Chinook salmon mortality estimates, 1991-present, National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Alaska Regional Office, Juneau, Alaska.
- 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). 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, 99510.

- NPFMC (North Pacific Fishery Management Council). 2005. Environmental assessment/regulatory impact review/initial regulatory flexibility assessment for modifying existing chum and Chinook salmon savings areas: amendment 84, secretariat review draft. North Pacific Fishery Management Council, 605 W. 4th Ave., Anchorage, Alaska, 99510.
- 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.
- 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.
- 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 I. -- Chum salmon populations in the DFO microsatellite baseline with the regional designations used in the analyses of this report.

DFO num.	Population name	Reg. num.	Region
41	Abashiri	1	SE Asia
215	Avakumovka	1	SE Asia
40	Chitose	1	SE Asia
315	Gakko_River	1	SE Asia
292	Hayatsuki	1	SE Asia
44	Horonai	1	SE Asia
252	Kawabukuro	1	SE Asia
313	Koizumi_River	1	SE Asia
300	Kushiro	1	SE Asia
37	Miomote	1	SE Asia
391	Namdae_R	1	SE Asia
231	Narva	1	SE Asia
298	Nishibetsu	1	SE Asia
293	Ohkawa	1	SE Asia
297	Orikasa	1	SE Asia
214	Ryazanovka	1	SE Asia
312	Sakari_River	1	SE Asia
311	Shari_River	1	SE Asia
36	Shibetsu	1	SE Asia
299	Shikiu	1	SE Asia
253	Shiriuchi	1	SE Asia
310	Shizunai	1	SE Asia
217	Suifen	1	SE Asia
35	Teshio	1	SE Asia
39	Tokachi	1	SE Asia
38	Tokoro	1	SE Asia
314	Tokushibetsu	1	SE Asia
291	Toshibetsu	1	SE Asia
296	Tsugaruishi	1	SE Asia
316	Uono_River	1	SE Asia
309	Yurappu	1	SE Asia
218	Amur	2	NE Asia
207	Anadyr	2	NE Asia
384	Apuka_River	2	NE Asia
382	Bolshaya	2	NE Asia

DFO num.	Population name	Reg. num.	Region
380	Dranka	2	NE Asia
223	Hairusova	2	NE Asia
378	Ivashka	2	NE Asia
213	Kalininka	2	NE Asia
225	Kamchatka	2	NE Asia
219	Kanchalan	2	NE Asia
379	Karaga	2	NE Asia
294	Kikchik	2	NE Asia
209	Kol	2	NE Asia
233	Magadan	2	NE Asia
211	Naiba	2	NE Asia
295	Nerpichi	2	NE Asia
381	Okhota	2	NE Asia
212	Oklan	2	NE Asia
222	Ola	2	NE Asia
386	Olutorsky_Bay	2	NE Asia
228	Ossora	2	NE Asia
224	Penzhina	2	NE Asia
385	Plotnikova_R	2	NE Asia
221	Pymta	2	NE Asia
220	Tauy	2	NE Asia
383	Tugur_River	2	NE Asia
226	Tym_	2	NE Asia
230	Udarnitsa	2	NE Asia
290	Utka_River	2	NE Asia
208	Vorovskaya	2	NE Asia
387	Zhypanova	2	NE Asia
348	Agiapuk	3	W Alaska
376	Alagnak	3	W Alaska
3	Andreafsky	3	W Alaska
357	Aniak	3	W Alaska
301	Anvik	3	W Alaska
80	Chulinak	3	W Alaska
347	Eldorado	3	W Alaska
358	George	3	W Alaska

DFO num.	Population name	Reg. num.	Region
307	Gisasa	3	W Alaska
371	Goodnews	3	W Alaska
288	Henshaw_Creek	3	W Alaska
339	Imnachuk	3	W Alaska
361	Kanektok	3	W Alaska
362	Kasigluk	3	W Alaska
328	Kelly_Lake	3	W Alaska
340	Kobuk	3	W Alaska
343	Koyuk	3	W Alaska
363	Kwethluk	3	W Alaska
336	Kwiniuk_River	3	W Alaska
303	Melozitna	3	W Alaska
373	Mulchatna	3	W Alaska
372	Naknek	3	W Alaska
330	Niukluk	3	W Alaska
329	Noatak	3	W Alaska
345	Nome	3	W Alaska
302	Nulato	3	W Alaska
374	Nunsatuk	3	W Alaska
13	Peel_River	3	W Alaska
322	Pikmiktalik	3	W Alaska
331	Pilgrim_River	3	W Alaska
346	Shaktoolik	3	W Alaska
341	Snake	3	W Alaska
368	Stuyahok_River	3	W Alaska
375	Togiak	3	W Alaska
154	Tozitna	3	W Alaska
342	Unalakleet	3	W Alaska
344	Ungalik	3	W Alaska
8	Big_Creek	4	U/M Yukon
89	Big_Salt	4	U/M Yukon
86	Black_River	4	U/M Yukon
87	Chandalar	4	U/M Yukon
28	Chandindu	4	U/M Yukon
82	Cheena	4	U/M Yukon
81	Delta	4	U/M Yukon
7	Donjek	4	U/M Yukon
5	Fishing_Br	4	U/M Yukon
88	Jim_River	4	U/M Yukon
85	Kantishna	4	U/M Yukon

DFO num.	Population name	Reg. num.	Region
2	Kluane	4	U/M Yukon
59	Kluane_Lake	4	U/M Yukon
181	Koyukuk_late	4	U/M Yukon
90	Koyukuk_south	4	U/M Yukon
10	Minto	4	U/M Yukon
6	Pelly	4	U/M Yukon
439	Porcupine	4	U/M Yukon
83	Salcha	4	U/M Yukon
4	Sheenjek	4	U/M Yukon
1	Tatchun	4	U/M Yukon
9	Teslin	4	U/M Yukon
84	Toklat	4	U/M Yukon
360	Alagoshak	5	SW Alaska
333	American_River	5	SW Alaska
366	Big_River	5	SW Alaska
354	Coleman_Creek	5	SW Alaska
355	Delta_Creek	5	SW Alaska
359	Egegik	5	SW Alaska
332	Frosty_Creek	5	SW Alaska
365	Gertrude_Creek	5	SW Alaska
370	Joshua_Green	5	SW Alaska
364	Meshik	5	SW Alaska
283	Moller_Bay	5	SW Alaska
369	Pumice_Creek	5	SW Alaska
367	Stepovak_Bay	5	SW Alaska
335	Sturgeon	5	SW Alaska
350	Uganik	5	SW Alaska
334	Volcano_Bay	5	SW Alaska
356	Westward_Creek	5	SW Alaska
239	Ahnuhati	6	E GOA/PNW
69	Ahta	6	E GOA/PNW
155	Ain	6	E GOA/PNW
183	Algard	6	E GOA/PNW
58	Alouette	6	E GOA/PNW
325	Alouette_North	6	E GOA/PNW
270	Andesite_Cr	6	E GOA/PNW
428	Arnoup_Cr	6	E GOA/PNW
153	Ashlulm	6	E GOA/PNW
156	Awun	6	E GOA/PNW
133	Bag_Harbour	6	E GOA/PNW

DFO num.	Population name	Reg. num.	Region
164	Barnard	6	E GOA/PNW
16	Bella_Bell	6	E GOA/PNW
79	Bella_Coola	6	E GOA/PNW
49	Big_Qual	6	E GOA/PNW
201	Big_Quilcene	6	E GOA/PNW
281	Bish_Cr	6	E GOA/PNW
198	Bitter_Creek	6	E GOA/PNW
103	Blackrock_Creek	6	E GOA/PNW
390	Blaney_Creek	6	E GOA/PNW
138	Botany_Creek	6	E GOA/PNW
264	Buck_Channel	6	E GOA/PNW
169	Bullock_Chann	6	E GOA/PNW
61	Campbell_River	6	E GOA/PNW
323	Carroll	6	E GOA/PNW
78	Cascade	6	E GOA/PNW
76	Cayeghle	6	E GOA/PNW
42	Cheakamus	6	E GOA/PNW
398	Cheenis_Lake	6	E GOA/PNW
51	Chehalis	6	E GOA/PNW
19	Chemainus	6	E GOA/PNW
47	Chilliwack	6	E GOA/PNW
392	Chilqua_Creek	6	E GOA/PNW
117	Chuckwalla	6	E GOA/PNW
139	Clapp_Basin	6	E GOA/PNW
107	Clatse_Creek	6	E GOA/PNW
118	Clyak	6	E GOA/PNW
62	Cold_Creek	6	E GOA/PNW
77	Colonial	6	E GOA/PNW
353	Constantine	6	E GOA/PNW
168	Cooper_Inlet	6	E GOA/PNW
197	County_Line	6	E GOA/PNW
12	Cowichan	6	E GOA/PNW
414	Crag_Cr	6	E GOA/PNW
161	Dak_	6	E GOA/PNW
259	Dana_Creek	6	E GOA/PNW
123	Date_Creek	6	E GOA/PNW
250	Dawson_Inlet	6	E GOA/PNW
91	Dean_River	6	E GOA/PNW
261	Deena	6	E GOA/PNW
170	Deer_Pass	6	E GOA/PNW

DFO num.	Population name	Reg. num.	Region
46	Demamiel	6	E GOA/PNW
210	Dipac_Hatchery	6	E GOA/PNW
319	Disappearance	6	E GOA/PNW
269	Dog-tag	6	E GOA/PNW
177	Draney	6	E GOA/PNW
114	Duthie_Creek	6	E GOA/PNW
427	East_Arm	6	E GOA/PNW
266	Ecstall_River	6	E GOA/PNW
94	Elcho_Creek	6	E GOA/PNW
193	Ellsworth_Cr	6	E GOA/PNW
203	Elwha	6	E GOA/PNW
276	Ensheshese	6	E GOA/PNW
263	Fairfax_Inlet	6	E GOA/PNW
32	Fish_Creek	6	E GOA/PNW
429	Flux_Cr	6	E GOA/PNW
102	Foch_Creek	6	E GOA/PNW
179	Frenchman	6	E GOA/PNW
227	Gambier	6	E GOA/PNW
96	Gill_Creek	6	E GOA/PNW
166	Gilttoyee	6	E GOA/PNW
145	Glendale	6	E GOA/PNW
135	Gold_Harbour	6	E GOA/PNW
11	Goldstream	6	E GOA/PNW
66	Goodspeed_River	6	E GOA/PNW
136	Government	6	E GOA/PNW
205	Grant_Creek	6	E GOA/PNW
100	Green_River	6	E GOA/PNW
450	GreenRrHatchery	6	E GOA/PNW
237	Greens	6	E GOA/PNW
141	Harrison	6	E GOA/PNW
438	Harrison_late	6	E GOA/PNW
64	Hathaway_Creek	6	E GOA/PNW
234	Herman_Creek	6	E GOA/PNW
17	Heydon_Cre	6	E GOA/PNW
407	Hicks_Cr	6	E GOA/PNW
400	Homathko	6	E GOA/PNW
411	Honna	6	E GOA/PNW
204	Hoodsport	6	E GOA/PNW
185	Hooknose	6	E GOA/PNW
406	Hopedale_Cr	6	E GOA/PNW

DFO num.	Population name	Reg. num.	Region
412	Hutton_Head	6	E GOA/PNW
278	Illiance	6	E GOA/PNW
152	Inch_Creek	6	E GOA/PNW
146	Indian_River	6	E GOA/PNW
92	Jenny_Bay	6	E GOA/PNW
115	Kainet_River	6	E GOA/PNW
144	Kakweiken	6	E GOA/PNW
268	Kalum	6	E GOA/PNW
395	Kanaka_Cr	6	E GOA/PNW
402	Kano_Inlet_Cr	6	E GOA/PNW
162	Kateen	6	E GOA/PNW
389	Kawkawa	6	E GOA/PNW
95	Kemano	6	E GOA/PNW
192	Kennedy_Creek	6	E GOA/PNW
238	Kennell	6	E GOA/PNW
351	Keta_Creek	6	E GOA/PNW
101	Khutze_River	6	E GOA/PNW
126	Khutzeymateen	6	E GOA/PNW
282	Kiltuish	6	E GOA/PNW
93	Kimsquit	6	E GOA/PNW
187	Kimsquit_Bay	6	E GOA/PNW
419	Kincolith	6	E GOA/PNW
273	Kispiox	6	E GOA/PNW
106	Kitasoo	6	E GOA/PNW
99	Kitimat_River	6	E GOA/PNW
275	Kitsault_Riv	6	E GOA/PNW
163	Kitwanga	6	E GOA/PNW
271	Kleanza_Cr	6	E GOA/PNW
437	Klewnuggit_Cr	6	E GOA/PNW
21	Klinaklini	6	E GOA/PNW
418	Ksedin	6	E GOA/PNW
125	Kshwan	6	E GOA/PNW
423	Kumealon	6	E GOA/PNW
112	Kwakusdis_River	6	E GOA/PNW
436	Kxngeal_Cr	6	E GOA/PNW
127	Lachmach	6	E GOA/PNW
262	Lagins	6	E GOA/PNW
131	Lagoon_Inlet	6	E GOA/PNW
448	LagoonCr	6	E GOA/PNW
167	Lard	6	E GOA/PNW

DFO num.	Population name	Reg. num.	Region
160	Little_Goose	6	E GOA/PNW
50	Little_Qua	6	E GOA/PNW
413	Lizard_Cr	6	E GOA/PNW
119	Lockhart-Gordon	6	E GOA/PNW
176	Lower_Lillooet	6	E GOA/PNW
137	Mace_Creek	6	E GOA/PNW
242	Mackenzie_Sound	6	E GOA/PNW
116	MacNair_Creek	6	E GOA/PNW
55	Mamquam	6	E GOA/PNW
121	Markle_Inlet_Cr	6	E GOA/PNW
27	Martin_Riv	6	E GOA/PNW
338	Mashiter_Creek	6	E GOA/PNW
	McLoughin_Cree		
109	k	6	E GOA/PNW
178	Milton	6	E GOA/PNW
194	Minter_Cr	6	E GOA/PNW
254	Mountain_Cr	6	E GOA/PNW
111	Mussel_River	6	E GOA/PNW
157	Naden	6	E GOA/PNW
337	Nahmint_River	6	E GOA/PNW
444	Nakut_Su	6	E GOA/PNW
14	Nanaimo	6	E GOA/PNW
122	Nangeese	6	E GOA/PNW
422	Nass_River	6	E GOA/PNW
399	Necleetsconnay	6	E GOA/PNW
113	Neekas_Creek	6	E GOA/PNW
321	Neets_Bay_early	6	E GOA/PNW
320	Neets_Bay_late	6	E GOA/PNW
173	Nekite	6	E GOA/PNW
104	Nias_Creek	6	E GOA/PNW
143	Nimpkish	6	E GOA/PNW
53	Nitinat	6	E GOA/PNW
191	Nooksack	6	E GOA/PNW
186	Nooseseck	6	E GOA/PNW
318	NorrishWorth	6	E GOA/PNW
159	North_Arm	6	E GOA/PNW
377	Olsen_Creek	6	E GOA/PNW
184	Orford	6	E GOA/PNW
287	Pa-aat_River	6	E GOA/PNW
260	Pacofi	6	E GOA/PNW
56	Pallant	6	E GOA/PNW

DFO num.	Population name	Reg. num.	Region
65	Pegattum_Creek	6	E GOA/PNW
48	Puntledge	6	E GOA/PNW
98	Quaal_River	6	E GOA/PNW
147	Quap	6	E GOA/PNW
108	Quartcha_Creek	6	E GOA/PNW
199	Quinault	6	E GOA/PNW
110	Roscoe_Creek	6	E GOA/PNW
397	Salmon_Bay	6	E GOA/PNW
195	Salmon_Cr	6	E GOA/PNW
134	Salmon_River	6	E GOA/PNW
200	Satsop	6	E GOA/PNW
236	Sawmill	6	E GOA/PNW
410	Seal_Inlet_Cr	6	E GOA/PNW
158	Security	6	E GOA/PNW
130	Sedgewick	6	E GOA/PNW
393	Serpentine_R	6	E GOA/PNW
317	Shovelnose_Cr	6	E GOA/PNW
249	Shustnini	6	E GOA/PNW
206	Siberia_Creek	6	E GOA/PNW
25	Silverdale	6	E GOA/PNW
196	Skagit	6	E GOA/PNW
274	Skeena	6	E GOA/PNW
171	Skowquiltz	6	E GOA/PNW
447	SkykomishRiv	6	E GOA/PNW
132	Slatechuck_Cre	6	E GOA/PNW
43	Sliammon	6	E GOA/PNW
15	Smith_Cree	6	E GOA/PNW
54	Snootli	6	E GOA/PNW
180	Southgate	6	E GOA/PNW
26	Squakum	6	E GOA/PNW
142	Squamish	6	E GOA/PNW
128	Stagoo	6	E GOA/PNW
265	Stanley	6	E GOA/PNW
52	Stave	6	E GOA/PNW
396	Stawamus	6	E GOA/PNW
409	Steel_Cr	6	E GOA/PNW
424	Stewart_Cr	6	E GOA/PNW
416	Stumaun_Cr	6	E GOA/PNW
327	Sugsaw	6	E GOA/PNW
324	Surprise	6	E GOA/PNW

DFO num.	Population name	Reg. num.	Region
75	Taaltz	6	E GOA/PNW
30	Taku	6	E GOA/PNW
18	Takwahoni	6	E GOA/PNW
251	Tarundl_Creek	6	E GOA/PNW
149	Theodosia	6	E GOA/PNW
22	Thorsen	6	E GOA/PNW
129	Toon	6	E GOA/PNW
279	Tseax	6	E GOA/PNW
202	Tulalip	6	E GOA/PNW
97	Turn_Creek	6	E GOA/PNW
430	Turtle_Cr	6	E GOA/PNW
247	Tuskwa	6	E GOA/PNW
165	Tyler	6	E GOA/PNW
33	Tzoonie	6	E GOA/PNW
124	Upper_Kitsumkal	6	E GOA/PNW
140	Vedder	6	E GOA/PNW
70	Viner_Sound	6	E GOA/PNW
45	Wahleach	6	E GOA/PNW
172	Walkum	6	E GOA/PNW
73	Waump	6	E GOA/PNW
232	Wells_Bridge	6	E GOA/PNW
352	Wells_River	6	E GOA/PNW
105	West_Arm_Creek	6	E GOA/PNW
267	Whitebottom_Cr	6	E GOA/PNW
326	Widgeon_Slough	6	E GOA/PNW
277	Wilauks_Cr	6	E GOA/PNW
120	Wilson_Creek	6	E GOA/PNW
401	Worth_Creek	6	E GOA/PNW
60	Wortley_Creek	6	E GOA/PNW
248	Yellow_Bluff	6	E GOA/PNW
434	Zymagotitz	6	E GOA/PNW

Appendix II. -- Stock composition estimates for the chum salmon bycatch samples from the 2013 Bering Sea midwater pollock trawl fishery. Mean and median estimates, standard deviations (SD), 95% credible intervals, the probability that the stock estimate is equal to zero ($P = 0$; values >0.5 are shaded; Habicht et al. 2012), and the Gelman-Rubin shrink factor are reported. Bycatch is the number of chum salmon reported for given strata and n is the number of genetic samples used in the analysis. Early season is Weeks 24-29, Middle season is Weeks 30-34, and Late season is Weeks 35-43.

Total sample set (Bycatch = 124,986; n = 3,880)							
Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1465	0.0063	0.1344	0.1464	0.1589	0	1.00
NE Asia	0.4489	0.0101	0.4292	0.4489	0.4686	0	1.00
Western Alaska	0.1809	0.0095	0.1626	0.1809	0.1996	0	1.01
Upper/Middle Yukon	0.0622	0.0066	0.0496	0.0621	0.0754	0	1.02
SW Alaska	0.0140	0.0029	0.0089	0.0138	0.0202	0	1.00
Eastern GOA/PNW	0.1475	0.0065	0.1351	0.1474	0.1604	0	1.00

First 1/2 subsample (Bycatch = 124,986, n = 1,940)							
Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1522	0.0089	0.1353	0.1521	0.1700	0	1.00
NE Asia	0.4466	0.0143	0.4184	0.4466	0.4747	0	1.00
Western Alaska	0.1888	0.0128	0.1640	0.1887	0.2141	0	1.00
Upper/Middle Yukon	0.0461	0.0080	0.0314	0.0458	0.0628	0	1.00
SW Alaska	0.0194	0.0050	0.0106	0.0190	0.0301	0	1.00
Eastern GOA/PNW	0.1470	0.0093	0.1291	0.1468	0.1655	0	1.00

Second 1/2 subsample (Bycatch = 124,986, n = 1,940)							
Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1434	0.0088	0.1265	0.1433	0.1609	0	1.00
NE Asia	0.4394	0.0143	0.4114	0.4394	0.4676	0	1.00
Western Alaska	0.1840	0.0127	0.1597	0.1839	0.2092	0	1.00
Upper/Middle Yukon	0.0751	0.0086	0.0584	0.0750	0.0923	0	1.00
SW Alaska	0.0127	0.0041	0.0055	0.0123	0.0216	0	1.00
Eastern GOA/PNW	0.1454	0.0092	0.1277	0.1453	0.1637	0	1.00

Appendix II. -- Continued.

First 1/4 subsample (Bycatch = 124,986, n = 970)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1605	0.0128	0.1360	0.1604	0.1860	0	1.00
NE Asia	0.4119	0.0200	0.3723	0.4120	0.4506	0	1.00
Western Alaska	0.2148	0.0192	0.1785	0.2146	0.2529	0	1.01
Upper/Middle Yukon	0.0425	0.0119	0.0213	0.0419	0.0675	0	1.00
SW Alaska	0.0354	0.0085	0.0202	0.0349	0.0532	0	1.00
Eastern GOA/PNW	0.1350	0.0129	0.1105	0.1346	0.1609	0	1.00

Second 1/4 subsample (Bycatch = 124,986, n = 970)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1494	0.0124	0.1261	0.1491	0.1746	0	1.00
NE Asia	0.4650	0.0194	0.4269	0.4651	0.5027	0	1.00
Western Alaska	0.1619	0.0171	0.1292	0.1618	0.1962	0	1.01
Upper/Middle Yukon	0.0829	0.0126	0.0598	0.0823	0.1091	0	1.02
SW Alaska	0.0089	0.0058	0.0011	0.0077	0.0231	0.0055	1.01
Eastern GOA/PNW	0.1319	0.0119	0.1096	0.1316	0.1561	0	1.00

Third 1/4 subsample (Bycatch = 124,986, n = 970)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1421	0.0123	0.1189	0.1418	0.1671	0	1.00
NE Asia	0.4774	0.0198	0.4386	0.4773	0.5158	0	1.00
Western Alaska	0.1800	0.0172	0.1475	0.1797	0.2145	0	1.00
Upper/Middle Yukon	0.0404	0.0104	0.0212	0.0400	0.0614	0	1.00
SW Alaska	0.0084	0.0043	0.0015	0.0078	0.0184	0.0107	1.00
Eastern GOA/PNW	0.1517	0.0130	0.1268	0.1515	0.1778	0	1.00

Appendix II. -- Continued.

Fourth 1/4 subsample (Bycatch = 124,986, n = 970)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1407	0.0124	0.1169	0.1404	0.1655	0	1.00
NE Asia	0.4084	0.0201	0.3689	0.4083	0.4480	0	1.00
Western Alaska	0.2073	0.0181	0.1721	0.2072	0.2432	0	1.01
Upper/Middle Yukon	0.0770	0.0122	0.0546	0.0764	0.1025	0	1.01
SW Alaska	0.0134	0.0060	0.0033	0.0128	0.0266	0.0019	1.00
Eastern GOA/PNW	0.1533	0.0132	0.1280	0.1531	0.1793	0	1.00

First 1/8 subsample (Bycatch = 124,986, n = 485)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1664	0.0183	0.1321	0.1659	0.2041	0	1.00
NE Asia	0.4266	0.0280	0.3719	0.4266	0.4816	0	1.00
Western Alaska	0.2079	0.0258	0.1592	0.2075	0.2600	0	1.00
Upper/Middle Yukon	0.0550	0.0166	0.0256	0.0540	0.0903	0	1.01
SW Alaska	0.0296	0.0118	0.0102	0.0284	0.0557	0	1.00
Eastern GOA/PNW	0.1144	0.0167	0.0839	0.1136	0.1487	0	1.00

Second 1/8 subsample (Bycatch = 124,986, n = 485)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1435	0.0176	0.1103	0.1431	0.1795	0	1.00
NE Asia	0.4376	0.0276	0.3836	0.4376	0.4923	0	1.00
Western Alaska	0.1991	0.0240	0.1529	0.1983	0.2478	0	1.00
Upper/Middle Yukon	0.0743	0.0146	0.0482	0.0736	0.1048	0	1.00
SW Alaska	0.0099	0.0081	0.0000	0.0082	0.0301	0.0741	1.00
Eastern GOA/PNW	0.1355	0.0173	0.1036	0.1349	0.1709	0	1.00

Appendix II. -- Continued.

Third 1/8 subsample (Bycatch = 124,986, n = 485)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1476	0.0176	0.1146	0.1472	0.1834	0	1.00
NE Asia	0.4747	0.0281	0.4198	0.4744	0.5306	0	1.00
Western Alaska	0.1675	0.0229	0.1243	0.1670	0.2144	0	1.00
Upper/Middle Yukon	0.0444	0.0141	0.0195	0.0436	0.0741	0	1.00
SW Alaska	0.0168	0.0083	0.0042	0.0155	0.0367	0.0005	1.00
Eastern GOA/PNW	0.1488	0.0185	0.1143	0.1482	0.1865	0	1.00

Fourth 1/8 subsample (Bycatch = 124,986, n = 485)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1517	0.0178	0.1183	0.1512	0.1882	0	1.00
NE Asia	0.3710	0.0279	0.3165	0.3708	0.4263	0	1.00
Western Alaska	0.2064	0.0273	0.1552	0.2057	0.2617	0	1.01
Upper/Middle Yukon	0.0740	0.0193	0.0385	0.0737	0.1130	0	1.01
SW Alaska	0.0091	0.0064	0.0003	0.0078	0.0249	0.0304	1.00
Eastern GOA/PNW	0.1879	0.0198	0.1501	0.1873	0.2279	0	1.00

Fifth 1/8 subsample (Bycatch = 124,986, n = 485)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1578	0.0178	0.1246	0.1574	0.1936	0	1.00
NE Asia	0.3840	0.0281	0.3291	0.3837	0.4403	0	1.00
Western Alaska	0.2411	0.0273	0.1883	0.2410	0.2952	0	1.00
Upper/Middle Yukon	0.0207	0.0143	0.0002	0.0180	0.0551	0.0248	1.00
SW Alaska	0.0278	0.0104	0.0114	0.0265	0.0520	0	1.00
Eastern GOA/PNW	0.1686	0.0197	0.1310	0.1681	0.2083	0	1.01

Appendix II. -- Continued.

Sixth 1/8 subsample (Bycatch = 124,986, n = 485)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1486	0.0175	0.1156	0.1481	0.1843	0	1.00
NE Asia	0.4913	0.0276	0.4380	0.4913	0.5456	0	1.00
Western Alaska	0.1406	0.0221	0.0989	0.1399	0.1857	0	1.00
Upper/Middle Yukon	0.0847	0.0159	0.0556	0.0839	0.1183	0	1.00
SW Alaska	0.0084	0.0059	0.0006	0.0072	0.0230	0.0165	1.00
Eastern GOA/PNW	0.1265	0.0172	0.0950	0.1258	0.1621	0	1.00

Seventh 1/8 subsample (Bycatch = 124,986, n = 485)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1365	0.0170	0.1044	0.1361	0.1712	0	1.00
NE Asia	0.4704	0.0273	0.4172	0.4707	0.5241	0	1.00
Western Alaska	0.2135	0.0245	0.1665	0.2131	0.2625	0	1.00
Upper/Middle Yukon	0.0313	0.0128	0.0108	0.0297	0.0610	0.0005	1.00
SW Alaska	0.0019	0.0035	0.0000	0.0002	0.0123	0.7387	1.00
Eastern GOA/PNW	0.1464	0.0176	0.1137	0.1458	0.1830	0	1.00

Eighth 1/8 subsample (Bycatch = 124,986, n = 485)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1300	0.0172	0.0981	0.1295	0.1652	0	1.00
NE Asia	0.4383	0.0294	0.3803	0.4380	0.4974	0	1.00
Western Alaska	0.2191	0.0255	0.1700	0.2188	0.2706	0	1.00
Upper/Middle Yukon	0.0743	0.0161	0.0451	0.0735	0.1084	0	1.00
SW Alaska	0.0205	0.0102	0.0050	0.0190	0.0442	0.0014	1.01
Eastern GOA/PNW	0.1178	0.0172	0.0855	0.1172	0.1526	0	1.00

Appendix II. -- Continued.

Early season sample set (All areas; Bycatch = 37,239, n = 1,132)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.2205	0.0132	0.1954	0.2204	0.2466	0	1.00
NE Asia	0.2558	0.0163	0.2245	0.2556	0.2885	0	1.00
Western Alaska	0.1775	0.0153	0.1484	0.1772	0.2083	0	1.00
Upper/Middle Yukon	0.0648	0.0100	0.0462	0.0644	0.0856	0	1.00
SW Alaska	0.0319	0.0076	0.0181	0.0315	0.0478	0	1.00
Eastern GOA/PNW	0.2495	0.0139	0.2228	0.2494	0.2772	0	1.00

Middle season sample set (All areas; Bycatch = 49,826, n = 1,582)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.0924	0.0082	0.0770	0.0922	0.1090	0	1.00
NE Asia	0.5026	0.0161	0.4710	0.5026	0.5341	0	1.00
Western Alaska	0.2350	0.0152	0.2051	0.2349	0.2651	0	1.00
Upper/Middle Yukon	0.0448	0.0089	0.0290	0.0442	0.0637	0	1.00
SW Alaska	0.0154	0.0047	0.0073	0.0151	0.0255	0	1.00
Eastern GOA/PNW	0.1097	0.0093	0.0921	0.1095	0.1284	0	1.00

Late season sample set (All areas; Bycatch = 37,921, n = 1,166)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1490	0.0116	0.1273	0.1488	0.1725	0	1.00
NE Asia	0.5513	0.0180	0.5161	0.5513	0.5862	0	1.00
Western Alaska	0.1345	0.0139	0.1079	0.1343	0.1625	0	1.00
Upper/Middle Yukon	0.0646	0.0095	0.0473	0.0642	0.0844	0	1.00
SW Alaska	0.0062	0.0036	0.0009	0.0057	0.0147	0.1038	1.00
Eastern GOA/PNW	0.0943	0.0103	0.0750	0.0939	0.1154	0	1.00

Appendix II. -- Continued.

Area 509 sample set (All season; Bycatch = 38,005, n = 1,183)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1439	0.0111	0.1226	0.1437	0.1664	0	1.00
NE Asia	0.3324	0.0172	0.2990	0.3324	0.3665	0	1.00
Western Alaska	0.1801	0.0149	0.1513	0.1800	0.2095	0	1.00
Upper/Middle Yukon	0.0498	0.0094	0.0328	0.0493	0.0697	0	1.00
SW Alaska	0.0320	0.0072	0.0193	0.0315	0.0472	0	1.00
Eastern GOA/PNW	0.2618	0.0144	0.2336	0.2618	0.2901	0	1.00

Area 509 sample set (Early season; Bycatch = 27,177, n = 738)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1609	0.0146	0.1332	0.1606	0.1904	0	1.00
NE Asia	0.2523	0.0199	0.2136	0.2521	0.2919	0	1.00
Western Alaska	0.1751	0.0181	0.1406	0.1748	0.2123	0	1.00
Upper/Middle Yukon	0.0606	0.0118	0.039	0.0601	0.0853	0	1.00
SW Alaska	0.0363	0.0087	0.021	0.0356	0.0551	0	1.00
Eastern GOA/PNW	0.3148	0.0188	0.279	0.3146	0.3522	0	1.00

Area 509 sample set (Middle season; Bycatch = 13,272, n = 428)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1047	0.0161	0.0752	0.1040	0.1385	0	1.00
NE Asia	0.4486	0.0288	0.3933	0.4486	0.5059	0	1.00
Western Alaska	0.1950	0.0250	0.1475	0.1945	0.2458	0	1.00
Upper/Middle Yukon	0.0380	0.0138	0.0136	0.0371	0.0675	0.0012	1.00
SW Alaska	0.0323	0.0126	0.0113	0.0311	0.0602	0.0001	1.00
Eastern GOA/PNW	0.1813	0.0210	0.1414	0.1808	0.2232	0	1.00

Appendix II. -- Continued.

Area 517 sample set (Early season; Bycatch = 9,877, n = 304)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.2350	0.0269	0.1838	0.2341	0.2898	0	1.00
NE Asia	0.2675	0.0325	0.2057	0.2668	0.3332	0	1.00
Western Alaska	0.2294	0.0321	0.1688	0.2286	0.2943	0	1.00
Upper/Middle Yukon	0.0787	0.0195	0.0440	0.0774	0.1202	0	1.00
SW Alaska	0.0297	0.0171	0.0000	0.0288	0.0662	0.0509	1.00
Eastern GOA/PNW	0.1597	0.0230	0.1176	0.1590	0.2077	0	1.00

Area 517 sample set (Middle season; Bycatch = 31,602, n = 1,004)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.0656	0.0090	0.0491	0.0653	0.0842	0	1.00
NE Asia	0.5313	0.0202	0.4919	0.5312	0.5706	0	1.00
Western Alaska	0.2606	0.0188	0.2239	0.2605	0.2979	0	1.00
Upper/Middle Yukon	0.0390	0.0096	0.0219	0.0384	0.0594	0	1.00
SW Alaska	0.0093	0.0046	0.0019	0.0087	0.0198	0.0211	1.00
Eastern GOA/PNW	0.0943	0.0107	0.0740	0.0939	0.1159	0	1.00

Area 517 sample set (Late season; Bycatch = 14,994, n = 473)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.0764	0.0140	0.0510	0.0757	0.1061	0	1.00
NE Asia	0.6512	0.0270	0.5973	0.6513	0.7039	0	1.00
Western Alaska	0.1517	0.0232	0.1081	0.1510	0.1992	0	1.00
Upper/Middle Yukon	0.0239	0.0145	0.0002	0.0229	0.0550	0.0356	1.00
SW Alaska	0.0140	0.0076	0.0028	0.0127	0.0321	0.0039	1.00
Eastern GOA/PNW	0.0828	0.0150	0.0556	0.0822	0.1146	0	1.00

Appendix II. -- Continued.

Area 521 sample set (Early season; Bycatch = 3,072, n = 85)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.5980	0.0541	0.4906	0.5984	0.7029	0	1.00
NE Asia	0.1819	0.0458	0.1001	0.1794	0.2797	0	1.00
Western Alaska	0.1327	0.0537	0.0330	0.1333	0.2383	0.0006	1.00
Upper/Middle Yukon	0.0390	0.0430	0.0000	0.0233	0.1468	0.2761	1.01
SW Alaska	0.0041	0.0090	0.0000	0.0003	0.0314	0.9857	1.00
Eastern GOA/PNW	0.0444	0.0235	0.0101	0.0407	0.1001	0.0018	1.00

Area 521 sample set (Middle season; Bycatch = 4,756, n = 144)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.2515	0.0390	0.1789	0.2502	0.3310	0	1.00
NE Asia	0.3878	0.0516	0.2882	0.3873	0.4904	0	1.00
Western Alaska	0.2227	0.0437	0.1408	0.2209	0.3136	0	1.00
Upper/Middle Yukon	0.1024	0.0276	0.0543	0.1004	0.1627	0	1.00
SW Alaska	0.0036	0.0078	0.0000	0.0003	0.0273	0.9793	1.00
Eastern GOA/PNW	0.0320	0.0178	0.0060	0.0291	0.0740	0.0075	1.00

Area 521 sample set (Late season; Bycatch = 20,563, n = 627)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1909	0.0168	0.1590	0.1905	0.2250	0	1.00
NE Asia	0.4781	0.0239	0.4310	0.4780	0.5256	0	1.00
Western Alaska	0.1290	0.0202	0.0904	0.1285	0.1700	0	1.00
Upper/Middle Yukon	0.0960	0.0157	0.0667	0.0954	0.1281	0	1.00
SW Alaska	0.0009	0.0021	0.0000	0.0001	0.0072	1.0000	1.00
Eastern GOA/PNW	0.1050	0.0145	0.0780	0.1045	0.1348	0	1.00

Appendix II. -- Continued.

Area 513/517/519 sample set (All season; Bycatch = 58,311, n = 1,833)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.1013	0.0081	0.0861	0.1011	0.1177	0	1.00
NE Asia	0.5163	0.015	0.4869	0.5163	0.5454	0	1.00
Western Alaska	0.2206	0.0137	0.1942	0.2205	0.2482	0	1.00
Upper/Middle Yukon	0.0478	0.0082	0.0326	0.0475	0.0645	0	1.00
SW Alaska	0.0114	0.004	0.0046	0.0111	0.0203	0	1.00
Eastern GOA/PNW	0.1025	0.0082	0.0869	0.1023	0.1191	0	1.00

Area 521/523/524 sample set (All season; Bycatch = 28,670, n = 864)

Region	Proportion	SD	2.5%	Median	97.5%	$P = 0$	Shrink Factor
SE Asia	0.2472	0.0158	0.2171	0.2470	0.2790	0	1.00
NE Asia	0.4399	0.0203	0.4002	0.4398	0.4794	0	1.00
Western Alaska	0.1364	0.0165	0.1048	0.1362	0.1697	0	1.00
Upper/Middle Yukon	0.0916	0.0126	0.0686	0.0910	0.1183	0	1.00
SW Alaska	0.0007	0.0014	0.0000	0.0000	0.0050	1.0000	1.00
Eastern GOA/PNW	0.0842	0.0114	0.0631	0.0838	0.1075	0	1.00

RECENT TECHNICAL MEMORANDUMS

Copies of this and other NOAA Technical Memorandums are available from the National Technical Information Service, 5285 Port Royal Road, Springfield, VA 22167 (web site: www.ntis.gov). Paper and electronic (.pdf) copies vary in price.

AFSC-

- 291 GUYON, J. R., C. M. GUTHRIE III, A. R. MUNRO, J. JASPER, and W. D. TEMPLIN. 2015. Genetic stock composition analysis of the Chinook salmon bycatch in the Gulf of Alaska walleye pollock (*Gadus chalcogrammus*) trawl fisheries, 26 p. NTIS number pending.
- 290 GUTHRIE, C. M. III, HV. T. NGUYEN, and J. R. GUYON. 2015. Genetic stock composition analysis of the Chinook salmon bycatch from the 2013 Bering Sea walleye pollock (*Gadus chalcogrammus*) trawl fishery, 21 p. NTIS number pending.
- 289 GUYON, J. R., HV. T. NGUYEN, C. M. GUTHRIE III, J. BONNEY, K. MCGAULEY, K. HANSEN, and J. GAUVIN. 2015. Genetic stock composition analysis of Chinook salmon bycatch samples from the rockfish and arrowtooth flounder 2013 Gulf of Alaska trawl fisheries and the Gulf of Alaska salmon excluder device test, 19 p. NTIS number pending.
- 288 FAUNCE, C. H. 2015. Evolution of observer methods to obtain genetic material from Chinook salmon bycatch in the Alaska pollock fishery, 28 p. NTIS number pending.
- 287 ZIMMERMANN, M., and M. M. PRESCOTT. 2015. Smooth sheet bathymetry of the central Gulf of Alaska, 54p. NTIS number pending.
- 286 CAHALAN, J., J. GASPER, and J. MONDRAGON. 2014. Catch sampling and estimation in the federal groundfish fisheries off Alaska, 2005 edition, 46 p. NTIS number pending.
- 285 GUYON, J. R., C.M. GUTHRIE III, A. R. MUNRO, J. JASPER, and W. D. TEMPLIN. 2014. Extension of genetic stock composition analysis to the Chinook salmon bycatch in the Gulf of Alaska walleye pollock (*Gadus chalcogrammus*) trawl fisheries, 2012, 26 p. NTIS number pending.
- 284 HIMES-CORNELL, A., and K. KENT. 2014. Involving fishing communities in data collection: a summary and description of the Alaska Community Survey 2011, 171 p. NTIS number pending.
- 283 GARVIN, M. R., M. M. MASUDA, J. J. PELLA, P. D. BARRY, S. A. FULLER, R. J. RILEY, R. L. WILMOT, V. BRYKOV, and A. J. GHARRETT. 2014. A Bayesian cross-validation approach to evaluate genetic baselines and forecast the necessary number of informative single nucleotide polymorphisms, 59 p. NTIS number pending.
- 282 DALY, B. J., C. E. ARMISTEAD, and R. J. FOY. 2014. The 2014 eastern Bering Sea continental shelf bottom trawl survey: Results for commercial crab species, 167 p. NTIS No. PB2015-101255.
- 281 FAUNCE, C., J. CAHALAN, J. GASPER, T. A'MAR, S. LOWE, F. WALLACE, and R. WEBSTER. 2014. Deployment performance review of the 2013 North Pacific Groundfish and Halibut Observer Program, 74 p. NTIS No .PB2015-100579.
- 280 HIMES-CORNELL, A., and K. KENT. 2014. Involving fishing communities in data collection: a summary and description of the Alaska Community survey, 2010, 170 p. NTIS No PB2015-100578.
- 279 FISSEL, B. E. 2014. Economic indices for the North Pacific groundfish fisheries: Calculation and visualization, 47 p. NTIS No. PB2015-100577.
- 278 GODDARD, P., R. LAUTH, and C. ARMISTEAD. 2014. Results of the 2012 Chukchi Sea bottom trawl survey of bottomfishes, crabs, and other demersal macrofauna, 110 p. NTIS No.PB2015-100576.
- 277 ALLEN, B. M., and R. P. ANGLISS. Alaska marine mammal stock assessments, 2013, 294 p. NTIS No. PB2015-100575.