



NOAA Technical Memorandum NMFS-AFSC-291

**Genetic Stock Composition
Analysis of the Chinook Salmon
Bycatch in the Gulf of Alaska Walleye
Pollock (*Gadus chalcogrammus*)
Trawl Fisheries, 2013**

by
J. R. Guyon, C. M. Guthrie III, A.R. Munro, J. Jasper, and
W.D. Templin

U.S. DEPARTMENT OF COMMERCE
National Oceanic and Atmospheric Administration
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Genetic Stock Composition Analysis of the Chinook Salmon Bycatch in the Gulf of Alaska Walleye Pollock (*Gadus chalcogrammus*) Trawl Fisheries, 2013

by
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ABSTRACT

The genetic stock composition of Chinook salmon (*Oncorhynchus tshawytscha*) samples from the 2013 U.S. Gulf of Alaska (GOA) trawl fishery for walleye pollock (*Gadus chalcogrammus*) was prepared to estimate stock-specific harvests. Genetic samples were collected in 2013 from Chinook salmon taken as bycatch in this fishery predominantly from NMFS statistical areas 620, 630, and 640. Samples were genotyped for 43 single nucleotide polymorphism (SNP) DNA markers and the results were estimated using the available coastwide baseline of SNP markers for Chinook salmon. While sample sizes varied widely and did not achieve the 10% target used to sample bycatch in the Bering Sea, by using a stratified estimator weighted by stratum-specific bycatch, it was possible to estimate the stock composition of the bycatch with acceptable accuracy and precision for NMFS statistical areas 620, 630, and 640, areas which comprised 84% of the bycatch in 2013. Based on the analysis of 693 Chinook salmon bycatch samples, the proportions of reporting groups were determined to be as follows: British Columbia (43%), U.S. West Coast (42%), coastal Southeast Alaska (11%), Northwest GOA (3%), and others (< 1%). No stock composition estimates are provided for statistical areas 610 or 649 due to the small size of the bycatch or the limited number of available genetic samples.

CONTENTS

ABSTRACT	iii
CONTENTS	v
INTRODUCTION	1
SAMPLE DISTRIBUTION	2
METHODS	6
RESULTS	9
SUMMARY	19
ACKNOWLEDGMENTS	21
CITATIONS	23
APPENDIX	25

INTRODUCTION

The Gulf of Alaska (GOA) provides feeding habitat for multiple brood years of Chinook salmon (*Oncorhynchus tshawytscha*) originating from many different localities in North America and Asia. Determining the geographic origin and stock composition of salmon caught in federally managed fisheries is essential to understanding whether fisheries management could address conservation concerns. This report provides genetic stock identification results for a set of Chinook salmon bycatch samples collected from the U.S. GOA pollock trawl fisheries. National Marine Fisheries Service (NMFS) geographical statistical areas associated with the groundfish fishery are shown in Figure 1 and are used later in the report to describe the spatial distribution of the Chinook salmon bycatch and genetic samples.

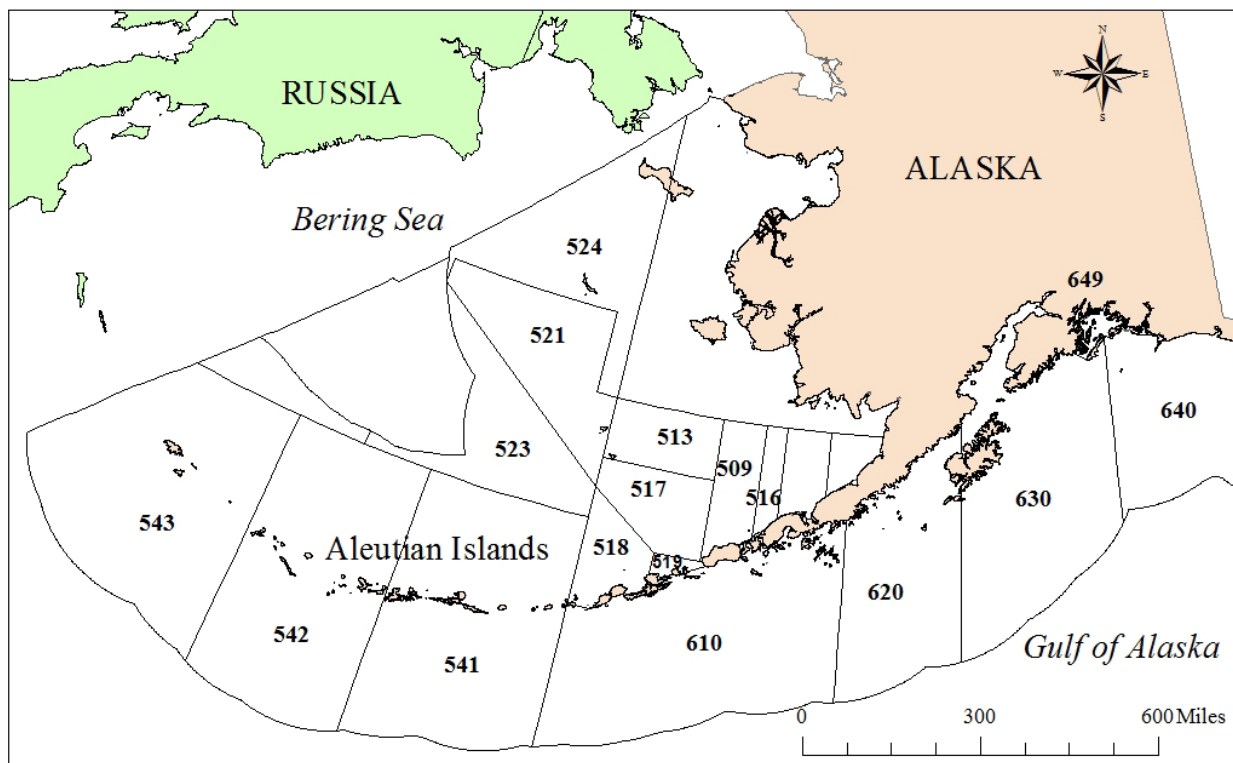


Figure 1. -- NMFS statistical areas associated with the Bering Sea-Aleutian Island (BSAI – areas 509-543) and Gulf of Alaska (GOA – areas 610-649) groundfish fisheries.

The goal of this report is to present stock composition estimates for samples collected from the bycatch of the 2013 federally managed pollock trawl fishery in the GOA, but it is important to understand the limitations for making accurate estimates of the entire bycatch imposed by the genetic baseline and the sampling distribution, both of which are addressed below. The analysis uses a single nucleotide polymorphism (SNP) baseline provided by the Alaska Department of Fish and Game (ADF&G) (Templin et al. 2011) and is the same baseline used previously to estimate the stock composition of samples from the 2005-2012 Chinook salmon bycatch (NMFS 2009; Guyon et al. 2010a, b, 2014; Guthrie et al. 2012, 2013, 2014; Larson et al. 2013).

SAMPLE DISTRIBUTION

Amendment 93 to the GOA groundfish fishery management plan requires industry retain all Chinook salmon caught as bycatch in the GOA pollock trawl fishery. This retention requirement is aimed at providing observers with complete access to this bycatch to support genetic stock composition analyses. However Amendment 93 does not mandate complete observer coverage, and not all GOA pollock trips are observed at-sea. Consequently, the North Pacific Groundfish Observer Program lacked the ability to know in advance the delivery times and locations of all GOA pollock deliveries. In 2013 the observer program monitored about 9 in 10 pollock deliveries in Kodiak -- where most GOA pollock deliveries take place -- and in Alaska as a whole (Faunce et al. 2014).

In 2013, an estimated 13,510 Chinook salmon were taken as bycatch in the GOA pollock trawl fisheries in National Marine Fisheries Service (NMFS) statistical areas 610, 620, 630, 640 and 649 (Fig. 1; NMFS 2014); this was less than a third of the estimated 44,862 Chinook salmon

that were taken as bycatch in the 2010 pollock fishery (Fig. 2). Tissues for genetic analysis were sampled from 737 fish, of which 693 were successfully genotyped from areas 620, 630, and 640 (see below) corresponding to a sampling rate of 5.1% for the season which is the highest rate yet attained in the GOA, but below the 10% sampling goal. When the number of samples was compared with the overall bycatch, potential temporal (Fig. 3) and spatial (Fig. 4) biases became apparent within the available sample set.

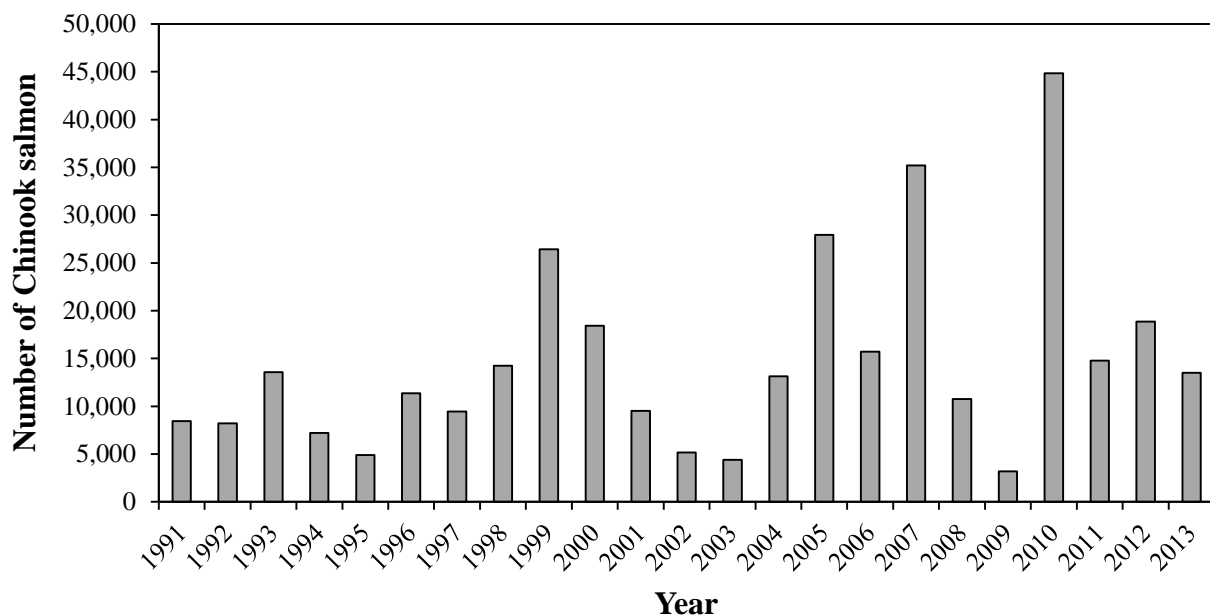


Figure 2. -- Yearly estimates for the Chinook salmon bycatch from the Gulf of Alaska pollock trawl fishery (NMFS 2014).

The temporal distribution of genetic samples (693) from the 2013 Chinook salmon GOA bycatch was compared to the overall distribution of bycatch by statistical week, which indicated that bycatch could be separated into two temporal periods and that a higher proportion of fish were sampled in the earlier period (statistical weeks 4-13, Fig. 3). We also compared the spatial distribution of genetic samples (693) with the Chinook salmon bycatch by NMFS statistical area over time, for early (statistical weeks 4-13) and late (statistical weeks 35-44) seasons, which

indicated that the bycatch was dominated by Area 620 (Fig. 4). Not shown in Figure 4, are areas 610 (2,161 bycatch estimate, 5 genetic samples), 640-late season (3 bycatch estimate, no genetic samples), and 649 (27 bycatch estimate, no genetic samples).

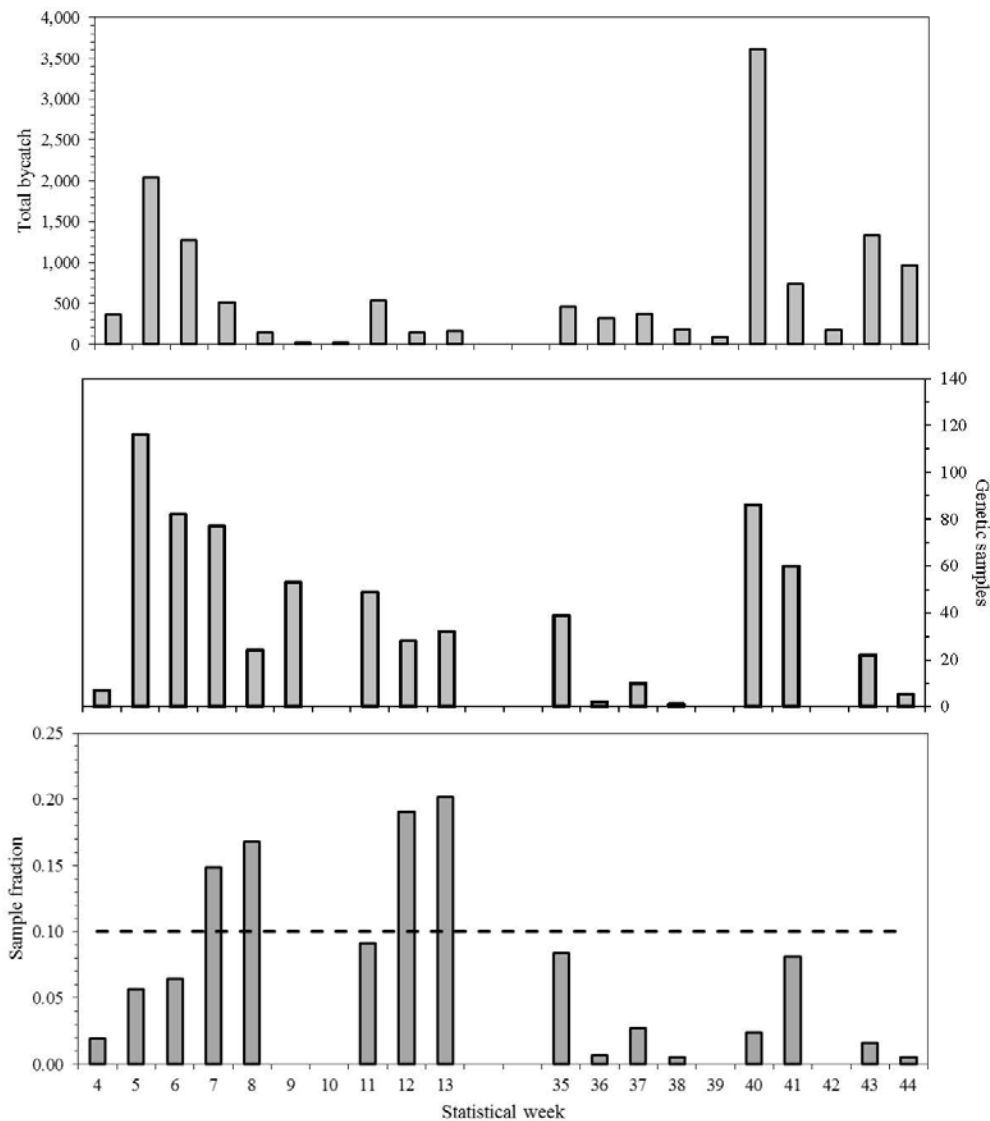


Figure 3. -- Number of Chinook salmon bycatch reported (top), genetic samples used for genetic stock identification (middle) and proportion of fish sampled (bottom) by statistical week in 2013 Gulf of Alaska pollock trawl fishery. Dashed line in bottom graph indicates 10% sample fraction. The week 9 sample fraction (bottom) is not shown since the number of samples (53) exceeded the total estimated bycatch (16), likely a result in how statistical weeks were calculated for this small sample set.

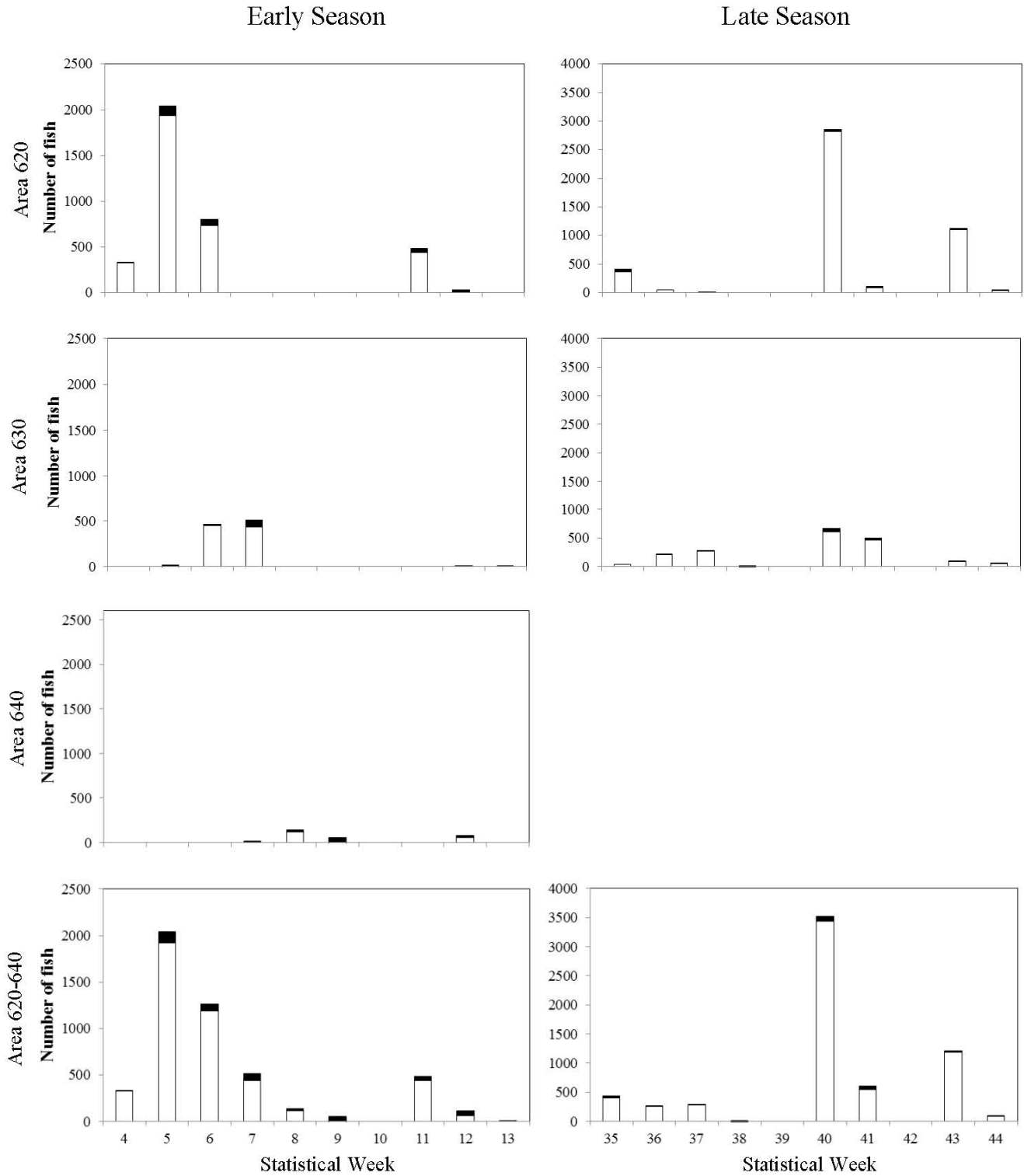


Figure 4. -- 2013 Gulf of Alaska Chinook salmon bycatch and samples used for genetic stock identification (black section of bar), by time and area strata. Note the difference in y-axis scale between early and late-season strata.

METHODS

Genotyping

DNA was extracted from collected axillary process tissue and genotyping was performed as described previously (Guyon et al. 2010a) using a Sequenom MassARRAY iPLEX platform (Gabriel et al. 2009) to genotype 43 SNP DNA markers represented in the Alaska Department of Fish and Game (ADF&G) Chinook salmon baseline (Templin et al. 2011). This baseline contains genetic information for 172 populations of Chinook salmon grouped into 11 broad-scale reporting groups (Appendix), which for this analysis will be considered stocks. This baseline was used previously to estimate stock composition of samples from the 2005-2012 Chinook salmon bycatch (NMFS 2009; Guyon et al. 2010a, b and 2014; Guthrie et al. 2012, 2013, and 2014; Larson et al. 2013). From the 2013 GOA Chinook salmon bycatch, a total of 737 samples were analyzed of which 698 were successfully genotyped for 35 or more of the 43 SNP loci (average of 41 markers/sample), a success rate of 95%. Five of the 698 samples were from area 610 (Table 1) and later excluded from the analysis (see below).

Table 1. -- Chinook salmon bycatch harvest, number of genotyped samples and sample fraction of bycatch for 2013 Gulf of Alaska pollock fishery stratified temporally and spatially. Early season includes statistical weeks 4 through 13 and late season includes statistical weeks 35 through 44.

Area	Early season			Late season		
	Bycatch	Sample size	Sample fraction	Bycatch	Sample size	Sample fraction
610	261	5	0.019	1,900	0	0.000
620	3,696	256	0.069	4,573	111	0.024
630	977	105	0.107	1,829	114	0.062
640	244	107	0.439	3	0	0.000
649	27	0	0.000	0	0	0.000

Stratification

The successfully genotyped samples were stratified both temporally and spatially (Table 1). Temporally, weekly samples were combined into two strata, which corresponded to early season (statistical weeks 4-13) and late season (statistical weeks 35-44). Spatially, the samples were separated into five strata that corresponded to NMFS statistical areas 610, 620, 630, 640, and 649. Due the limited number of samples or estimated bycatch, areas 610 (all year), 640 (late season), and 649 (all year) were excluded from further analysis. Thus five strata, each with a corresponding mixture sample and observed bycatch, were used to develop the composite stock composition estimate.

Stock composition estimates

The stock composition of the mixture representing each stratum was analyzed using the program BAYES (Pella and Masuda 2001) generally as described in Guthrie et al. (2014). The Dirichlet prior parameters for the stock proportions were defined to be one divided by the number of baseline populations. For each of the five strata, we ran 11 independent Markov Chain Monte Carlo (MCMC) chains of 20,000 iterations, initializing each chain by placing 90% of the allocation into one of each reporting group, and dividing the remaining 10% equally among the remaining groups, such that each group has one chain initialized at 90%. The first 10,000 iterations from each chain were discarded to remove the influence of the initial values.

To ensure that the BAYES output was an acceptable approximation of the stationary posterior distribution and that the stock composition estimates were valid, we assessed the 11 independent (MCMC) chains for convergence among chains using the Gelman-Rubin shrink factors that were computed for all stock groups.

For each reporting group, weighted average proportions were calculated from the following equation:

$$p_g = \frac{\sum_{t=1}^2 \sum_{s=1}^3 B_{t,s} p_{t,s,g}}{\sum_{t=1}^2 \sum_{s=1}^3 B_{t,s}}, \quad (\text{Eq. 1})$$

where $B_{t,s}$ was the bycatch occurring in season t of Area s ; $p_{t,s,g}$ was the proportion of reporting group g in this stratum; and p_g was the overall weighted average proportion of group g .

Applying Equation 1 across MCMC iterations contained within the BAYES posterior output files for all strata produced the posterior distribution of weighted averages from which summaries were derived.

Stock composition estimates were summarized from the posterior distributions of the MCMC iterates using the following statistics: mean and medians as measures of central tendency, the 95% credibility interval (i.e., the 2.5th and 97.5th percentiles), and standard deviation. We also report a statistic called $P = 0$, which is the probability that a stock composition estimate is effectively zero. This is the frequency of MCMC iterates in the posterior output that were less than a threshold that is calculated as 0.5 divided by the sum 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 is more useful for assessing support for the presence/absence of minor stocks than application of the credibility interval.

We report both the mean and median of the posterior distributions because at very small or very large stock compositions the posterior distributions may become skewed and the mean is more influenced by a few extreme iterates. Large differences between these statistics can be an

indication of skewness. Therefore, in these cases the median may be a preferred measure of central tendency of the posterior distribution. The drawbacks to the median, however, are as follows: 1) their summation across stocks does not equal 1; and 2) as a simple order statistic, they tend to ignore the evidence suggesting that the true value is not very small or large (as represented by the heavy tails).

Reporting group-specific bycatch estimates

Estimates of reporting group-specific bycatch were calculated by simply multiplying the stock composition point estimates by the sum of reported bycatch across strata. It should be noted that this assumes that the bycatch numbers are known with zero uncertainty.

RESULTS

Stratification

Bycatch in the five strata ranged from 244 in NMFS statistical area 640 in the early season to 4,573 in Area 620 in the late season (Table 1). Sample sizes for GSI within these five strata ranged from 105 to 256 with the sampling fraction ranging from 2.4% to 43.9%. Not included in the analysis are areas 610 (2,161 bycatch estimate, 5 genetic samples), 640-late season (3 bycatch estimate, no genetic samples), and 649 (27 bycatch estimate, no genetic samples).

Stock composition estimates

For the 2013 GOA Chinook salmon bycatch, our results showed that the genetic stock composition of the sample set was similar to the stratified estimate for areas 620, 630, and 640

(Fig. 5A), the location where 84% of the salmon bycatch was encountered. The stratified stock composition results indicate that 99% of the bycatch encountered in areas 620-640 was composed of four reporting groups: British Columbia (43%), U.S. West Coast (42%), coastal Southeast Alaska (11%), and NW GOA (3%) (Table 2, Fig. 5B). These results were similar to that seen previously for the 2012 GOA bycatch (Fig. 5B) (Guyon et al., 2014).

When strata were combined across areas 620-640 within season, stratified estimates for the early season (statistical weeks 4-13) showed British Columbia contributed the most (47%) followed by U.S. West Coast (40%) and coastal Southeast Alaska (12%) (Table 3, Fig. 5C). For the late season (statistical weeks 35-44), U.S. West Coast Chinook salmon were dominant (44%), followed by British Columbia (39%), coastal Southeast Alaska (11%), and NW GOA (6%) (Table 4, Fig. 5C).

When strata were combined across seasons within areas, Area 620 had a higher contribution from U.S. West Coast (46%) followed by British Columbia (41%), coastal Southeast Alaska (10%) and NW GOA (2%) (Table 5, Fig. 5D). Moving east into NMFS statistical area 630, the estimated British Columbia (48%), Coastal SEAK (16%), and NW GOA (8%) contributions increased while those from the U.S. West Coast (28%) decreased (Table 6, Fig. 5D). For the easternmost Area 640, estimates for the U.S. West Coast (67%) dominated, while British Columbia (27%), coastal Southeast Alaska (5%), and NW GOA (0%) components all decreased (Table 7, Fig. 5D).

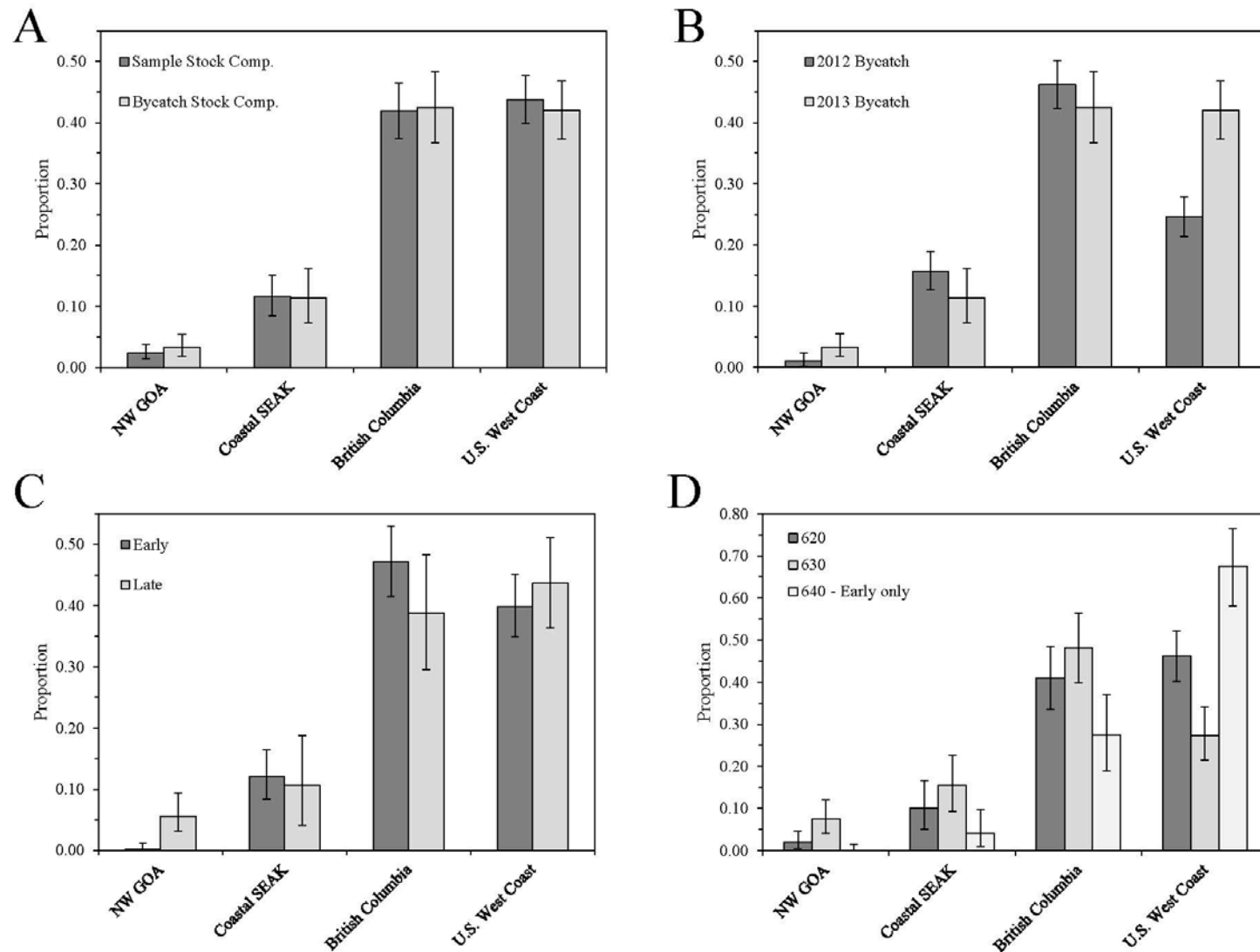


Figure 5. -- 2013 Gulf of Alaska Chinook salmon stock composition estimates (median and 95% credibility intervals) for the four most abundant stocks. Panel A – Genetic stock composition of the sample compared with the stratified estimate. Panel B – Comparison of the stratified stock composition estimate of the Chinook salmon bycatch from the 2012 GOA pollock trawl fishery (areas 610-649) with the 2013 estimate (areas 620-640). Panel C - Genetic stock composition of the early 2013 sample set with the late sample set. Panel D - Genetic stock composition of the spatial 2013 sample sets.

Table 2.-- Stock composition estimates of the Chinook salmon bycatch from areas 620-640 of the 2013 Gulf of Alaska (GOA) pollock trawl fishery using the stratified method where the stock composition estimate was weighted by the size of bycatch within each strata (top table) compared with unstratified stock composition estimate of the unweighted sample set (bottom table). Mean estimates are provided with the 95% credibility intervals (CI), probability that the stock contribution is 0 ($P = 0$), median value, and standard deviation (SD). H is the reported bycatch from areas 620-640 and n is the number of genetic samples used in the analysis.

2013 Stratified whole season (H = 11,319; n = 693)						
Reporting group	Proportion	95% CI		$P = 0$	Median	SD
		2.5%	97.5%			
Russia	0.000	0.000	0.002	0.709	0.000	0.001
Coastal W. AK	0.002	0.000	0.008	0.060	0.001	0.002
Middle Yukon R.	0.000	0.000	0.003	0.513	0.000	0.001
Upper Yukon R.	0.001	0.000	0.004	0.337	0.000	0.001
N AK Peninsula	0.000	0.000	0.004	0.554	0.000	0.001
NW GOA	0.034	0.019	0.055	0.000	0.033	0.009
Copper R.	0.002	0.000	0.009	0.166	0.001	0.003
NE GOA	0.001	0.000	0.007	0.389	0.000	0.002
Coastal SEAK	0.114	0.073	0.162	0.000	0.113	0.023
British Columbia	0.425	0.367	0.484	0.000	0.425	0.030
U.S. West Coast	0.420	0.373	0.468	0.000	0.420	0.024

2013 Unstratified sample estimate (n = 693)						
Reporting group	Proportion	95% CI		$P = 0$	Median	SD
		2.5%	97.5%			
Russia	0.000	0.000	0.001	0.830	0.000	0.014
Coastal W. AK	0.001	0.000	0.003	0.262	0.000	0.028
Middle Yukon R.	0.001	0.000	0.001	0.706	0.000	0.042
Upper Yukon R.	0.001	0.000	0.001	0.568	0.000	0.057
N AK Peninsula	0.001	0.000	0.001	0.752	0.000	0.071
NW GOA	0.025	0.014	0.038	0.000	0.024	0.085
Copper R.	0.002	0.000	0.005	0.533	0.000	0.099
NE GOA	0.003	0.000	0.011	0.540	0.000	0.113
Coastal SEAK	0.116	0.084	0.151	0.000	0.116	0.127
British Columbia	0.416	0.375	0.464	0.000	0.419	0.137
U.S. West Coast	0.434	0.399	0.477	0.000	0.438	0.151

Table 3. -- Stratified stock composition estimates for the Chinook salmon bycatch during the early season (weeks 4-13) of the 2013 Gulf of Alaska (GOA) pollock trawl fishery – areas 620-640. Mean estimates are provided with the 95% credibility intervals (CI), probability that the stock composition is 0 ($P = 0$), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis.

Reporting group	2013 Early season (areas 620, 630, 640; H = 4,917; n = 468)					
	Proportion	95% CI		$P = 0$	Median	SD
		2.5%	97.5%			
Russia	0.000	0.000	0.001	0.858	0.000	0.001
Coastal W. AK	0.001	0.000	0.006	0.276	0.000	0.002
Middle Yukon R.	0.000	0.000	0.002	0.731	0.000	0.001
Upper Yukon R.	0.000	0.000	0.003	0.598	0.000	0.001
N AK Peninsula	0.000	0.000	0.003	0.754	0.000	0.001
NW GOA	0.003	0.000	0.013	0.119	0.002	0.003
Copper R.	0.001	0.000	0.006	0.546	0.000	0.002
NE GOA	0.001	0.000	0.010	0.579	0.000	0.003
Coastal SEAK	0.122	0.084	0.164	0.000	0.121	0.020
British Columbia	0.472	0.414	0.530	0.000	0.472	0.029
U.S. West Coast	0.399	0.349	0.450	0.000	0.398	0.026

Table 4. -- Stratified stock composition estimates for the Chinook salmon bycatch during the late season (weeks 35-44) of the 2013 Gulf of Alaska (GOA) pollock trawl fishery – areas 620-630. Mean estimates are provided with the 95% credibility intervals (CI), probability that the stock composition is 0 ($P = 0$), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis.

Reporting group	2013 Late season (areas 620, 630; H = 6,402; n = 225)					
	Proportion	95% CI		$P = 0$	Median	SD
		2.5%	97.5%			
Russia	0.000	0.000	0.003	0.831	0.000	0.001
Coastal W. AK	0.002	0.000	0.014	0.253	0.001	0.004
Middle Yukon R.	0.000	0.000	0.005	0.714	0.000	0.002
Upper Yukon R.	0.001	0.000	0.006	0.587	0.000	0.002
N AK Peninsula	0.001	0.000	0.006	0.744	0.000	0.002
NW GOA	0.058	0.031	0.094	0.000	0.056	0.016
Copper R.	0.003	0.000	0.015	0.314	0.001	0.004
NE GOA	0.001	0.000	0.008	0.683	0.000	0.003
Coastal SEAK	0.109	0.042	0.188	0.000	0.107	0.037
British Columbia	0.388	0.296	0.483	0.000	0.388	0.048
U.S. West Coast	0.437	0.363	0.511	0.000	0.437	0.038

Table 5. -- Stratified stock composition estimates for the Chinook salmon bycatch in NMFS statistical area 620 during the 2013 Gulf of Alaska pollock trawl fishery – all season. Mean estimates are provided with the 95% credibility intervals (CI), probability that the stock composition is 0 ($P = 0$), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis.

Reporting group	Area 620 (All season; H = 8,269; n = 367)					
	Proportion	95% CI		$P = 0$	Median	SD
		2.5%	97.5%			
Russia	0.000	0.000	0.002	0.857	0.000	0.001
Coastal W. AK	0.002	0.000	0.010	0.277	0.000	0.003
Middle Yukon R.	0.000	0.000	0.004	0.725	0.000	0.001
Upper Yukon R.	0.001	0.000	0.004	0.595	0.000	0.001
N AK Peninsula	0.000	0.000	0.004	0.735	0.000	0.002
NW GOA	0.021	0.005	0.046	0.000	0.019	0.011
Copper R.	0.001	0.000	0.005	0.591	0.000	0.002
NE GOA	0.001	0.000	0.007	0.660	0.000	0.002
Coastal SEAK	0.103	0.050	0.165	0.000	0.101	0.029
British Columbia	0.410	0.335	0.485	0.000	0.410	0.038
U.S. West Coast	0.462	0.401	0.523	0.000	0.462	0.031

Table 6. -- Stratified stock composition estimates for the Chinook salmon bycatch in NMFS statistical area 630 of the 2013 Gulf of Alaska (GOA) pollock trawl fishery – all season. Mean estimates are provided with the 95% credibility intervals (CI), probability that the stock composition is 0 ($P = 0$), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis.

Reporting group	Area 630 (All season; H = 2,806; n = 219)					
	Proportion	95% CI		$P = 0$	Median	SD
		2.5%	97.5%			
Russia	0.000	0.000	0.004	0.857	0.000	0.002
Coastal W. AK	0.002	0.000	0.014	0.332	0.001	0.004
Middle Yukon R.	0.000	0.000	0.005	0.765	0.000	0.002
Upper Yukon R.	0.001	0.000	0.006	0.656	0.000	0.002
N AK Peninsula	0.001	0.000	0.006	0.797	0.000	0.002
NW GOA	0.075	0.040	0.120	0.000	0.074	0.021
Copper R.	0.007	0.000	0.032	0.318	0.003	0.009
NE GOA	0.002	0.000	0.015	0.635	0.000	0.005
Coastal SEAK	0.155	0.092	0.226	0.000	0.154	0.034
British Columbia	0.482	0.399	0.565	0.000	0.481	0.042
U.S. West Coast	0.275	0.214	0.341	0.000	0.274	0.032

Table 7. -- Stratified stock composition estimates for the Chinook salmon bycatch in NMFS statistical area 640 of the 2013 Gulf of Alaska (GOA) pollock trawl fishery – early season. Mean estimates are provided with the 95% credibility intervals (CI), probability that the stock composition is 0 ($P = 0$), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis.

Reporting group	Area 640 (Early season; H = 244; n = 107)					
	Proportion	95% CI		$P = 0$	Median	SD
		2.5%	97.5%			
Russia	0.000	0.000	0.002	0.971	0.000	0.014
Coastal W. AK	0.002	0.000	0.013	0.813	0.000	0.029
Middle Yukon R.	0.001	0.000	0.005	0.947	0.000	0.042
Upper Yukon R.	0.001	0.000	0.007	0.914	0.000	0.057
N AK Peninsula	0.001	0.000	0.004	0.961	0.000	0.071
NW GOA	0.003	0.000	0.014	0.835	0.000	0.085
Copper R.	0.002	0.000	0.007	0.924	0.000	0.099
NE GOA	0.002	0.000	0.005	0.950	0.000	0.113
Coastal SEAK	0.045	0.010	0.097	0.001	0.041	0.129
British Columbia	0.274	0.188	0.371	0.000	0.274	0.145
U.S. West Coast	0.668	0.581	0.764	0.000	0.676	0.153

Reporting group-specific bycatch estimates

The number of salmon taken from any single reporting group is dependent on both the relative stock proportion and total size of the bycatch. Using the reported number of Chinook salmon taken as bycatch in the 2013 GOA pollock trawl fishery and the estimated stock contributions, reporting group-specific harvest in the bycatch was calculated by multiplying the stock proportions by the total estimated bycatch. The resulting estimated take as bycatch for each reporting group was determined for the fishery in areas 620-640 (Table 8), by season (Tables 9 and 10), and by statistical area (Tables 11-13). Because of the lack of samples, Area 610 is not included in the 2013 GOA stock composition estimate although an estimated 2,161 Chinook salmon were taken in the pollock bycatch for that area.

As an example of assessing the support for the presence/absence of reporting groups in the bycatch, in Tables 8-13 we highlighted reporting groups that had a 50% or greater probability

of being absent from the bycatch based on the $P = 0$ statistics reported in Tables 3-7. Reporting groups can have similar small estimates of the mean number of Chinook salmon in the bycatch (e.g., Russia, middle Yukon, upper Yukon, N Alaska Peninsula, Copper River, and NE GOA; 2-6 fish; Table 9), but the support for their absence from the bycatch during the early season ranged more widely ($P = 0$ ranged from 0.55 for Copper River to 0.86 for Russia; Table 3). The value of the $P = 0$ statistic is that, in conjunction with the other information presented, one can apply an appropriate critical value that helps them make their own interpretation of the level of support for the presence or absence of a given reporting group in the bycatch. Such a critical value should be made in consultation with the NPFMC Scientific and Statistical Committee and the end users.

Table 8. -- Reporting group-specific estimates of number of Chinook salmon taken as bycatch in the 2013 Gulf of Alaska (GOA) pollock trawl fishery – areas 620-640. Estimates are provided to the nearest fish with the mean, 95% credibility intervals (CI), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis. Shaded rows indicate stocks that have a >50% chance of not truly being present based on $P = 0$ in Table 2. A total of 13,510 Chinook salmon were reported as bycatch in the 2013 Gulf of Alaska pollock trawl fishery. The 2,191 fish not accounted for in these estimates include areas 610 (2,161 bycatch estimate, 5 genetic samples), 640-late season (3 bycatch estimate, no genetic samples), and 649 (27 bycatch estimate, no genetic samples). Total summed stock-specific harvest estimates might not equal reported harvest in table header because of rounding.

Reporting group	2013 bycatch whole season – areas 620-640 (H = 11,319; n = 693)				
	Mean	95% CI		Median	SD
		2.5%	97.5%		
Russia	2	0	23	0	8
Coastal W. AK	19	0	95	10	27
Middle Yukon R.	4	0	35	0	12
Upper Yukon R.	6	0	41	2	13
N AK Peninsula	5	0	45	0	15
NW GOA	385	209	618	375	105
Copper R.	25	0	103	14	30
NE GOA	11	0	74	2	22
Coastal SEAK	1,295	822	1,832	1,283	260
British Columbia	4,808	4,159	5,477	4,805	337
U.S. West Coast	4,757	4,224	5,293	4,757	273
Total	11,317				

Table 9. -- Reporting group-specific estimates of number of Chinook salmon harvested in the bycatch during the early season (weeks 4-13) of the 2013 Gulf of Alaska (GOA) pollock trawl fishery – areas 620-640. Estimates are provided to the nearest fish with the mean, 95% credibility intervals (CI), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis. Shaded rows indicate stocks that have a >50% chance of not truly being present based on $P = 0$ in Table 3. Total summed stock-specific harvest estimates might not equal reported harvest in table header because of rounding.

Early season (areas 620, 630, 640; H = 4,917; n = 468)					
Reporting group	Mean	95% CI		Median	SD
		2.5%	97.5%		
Russia	1	0	6	0	3
Coastal W. AK	5	0	28	2	8
Middle Yukon R.	1	0	12	0	4
Upper Yukon R.	2	0	15	0	5
N AK Peninsula	2	0	17	0	6
NW GOA	16	0	62	10	17
Copper R.	4	0	29	0	9
NE GOA	6	0	50	0	14
Coastal SEAK	599	414	808	595	101
British Columbia	2,323	2,038	2,605	2,322	144
U.S. West Coast	1,960	1,714	2,214	1,959	127
Total	4,919				

Table 10. -- Reporting group-specific estimates of number of Chinook salmon harvested in the bycatch during the late season (weeks 35-44) of the 2013 Gulf of Alaska (GOA) pollock trawl fishery – areas 620 and 630. Estimates are provided to the nearest fish with the mean, 95% credibility intervals (CI), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis. Shaded rows indicate stocks that have a >50% chance of not truly being present based on $P = 0$ in Table 4. Total summed stock-specific harvest estimates might not equal reported harvest in table header because of rounding.

Late season (areas 620, 630; H = 6,402; n = 225)					
Reporting group	Mean	95% CI		Median	SD
		2.5%	97.5%		
Russia	2	0	20	0	8
Coastal W. AK	14	0	88	4	25
Middle Yukon R.	3	0	31	0	11
Upper Yukon R.	4	0	37	0	12
N AK Peninsula	4	0	39	0	13
NW GOA	370	196	599	359	103
Copper R.	21	0	97	9	28
NE GOA	5	0	53	0	17
Coastal SEAK	696	267	1,201	684	240
British Columbia	2,485	1,893	3,095	2,485	306
U.S. West Coast	2,797	2,326	3,269	2,797	242
Total	6,401				

Table 11. -- Reporting group-specific estimates of number of Chinook salmon taken as bycatch in Area 620 during the 2013 Gulf of Alaska (GOA) pollock trawl fishery – all season. Estimates are provided to the nearest fish with the mean, 95% credibility intervals (CI), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis. Shaded rows indicate stocks that have a >50% chance of not truly being present based on $P = 0$ in Table 5. Total summed stock-specific harvest estimates might not equal reported harvest in table header because of rounding.

Reporting group	Area 620 (All season; H = 8,269; n = 367)				
	Mean	95% CI		Median	SD
		2.5%	97.5%		
Russia	1	0	14	0	7
Coastal W. AK	12	0	82	3	24
Middle Yukon R.	3	0	29	0	11
Upper Yukon R.	4	0	36	0	12
N AK Peninsula	4	0	37	0	13
NW GOA	173	43	379	160	88
Copper R.	5	0	43	0	13
NE GOA	6	0	59	0	18
Coastal SEAK	849	414	1,364	835	244
British Columbia	3,389	2,771	4,014	3,387	316
U.S. West Coast	3,821	3,317	4,322	3,822	257
Total	8,267				

Table 12. -- Reporting group-specific estimates of number of Chinook salmon taken as bycatch in Area 630 during the 2013 Gulf of Alaska (GOA) pollock trawl fishery – all season. Estimates are provided to the nearest fish with the mean, 95% credibility intervals (CI), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis. Shaded rows indicate stocks that have a >50% chance of not truly being present based on $P = 0$ in Table 6. Total summed stock-specific harvest estimates might not equal reported harvest in table header because of rounding.

Reporting group	Area 630 (All season; H = 2,806; n = 219)				
	Mean	95% CI		Median	SD
		2.5%	97.5%		
Russia	1	0	12	0	5
Coastal W. AK	6	0	40	2	12
Middle Yukon R.	1	0	14	0	5
Upper Yukon R.	2	0	16	0	5
N AK Peninsula	2	0	18	0	6
NW GOA	211	111	335	207	58
Copper R.	20	0	91	8	26
NE GOA	5	0	43	0	13
Coastal SEAK	435	258	634	432	96
British Columbia	1,351	1,120	1,585	1,351	119
U.S. West Coast	771	600	956	768	91
Total	2,805				

Table 13. -- Reporting group-specific estimates of number of Chinook salmon taken as bycatch in areas 640 during the 2013 Gulf of Alaska (GOA) pollock trawl fishery – early season. Estimates are provided to the nearest fish with the mean, 95% credible intervals (CI), median value, and standard deviation (SD). H is the reported bycatch and n is the number of genetic samples used in the analysis. Shaded rows indicate stocks that have a >50% chance of not truly being present based on $P = 0$ in Table 7. Total summed stock-specific harvest estimates might not equal reported harvest in table header because of rounding.

Reporting group	Area 640 (Early season; H = 244; n = 107)				
	Mean	95% CI		Median	SD
		2.5%	97.5%		
Russia	0	0	1	0	3
Coastal W. AK	0	0	3	0	7
Middle Yukon R.	0	0	1	0	10
Upper Yukon R.	0	0	2	0	14
N AK Peninsula	0	0	1	0	17
NW GOA	1	0	3	0	21
Copper R.	0	0	2	0	24
NE GOA	0	0	1	0	28
Coastal SEAK	11	2	24	10	31
British Columbia	67	46	90	67	35
U.S. West Coast	163	142	186	165	37
Total	242				

SUMMARY

Using the stratified analysis described in this report, we report the stock composition estimates of the 2013 Chinook salmon bycatch from the federally managed GOA pollock trawl fishery in NMFS statistical areas 620, 630, and 640, the location where 84% of the bycatch occurred that year. We were not able to report stock composition estimates for the 2,161 Chinook salmon taken as bycatch in NMFS statistical area 610 because of the limited number of genetic samples (5). When the results of the bycatch stock composition were compared with the sample stock composition estimates, the comparison showed little change in the stock compositions using the stratification process (Fig. 5A). This probably results from a combination of three factors.

First, while sampling was opportunistic and did not achieve the targeted 10% sample fraction for the season or within each statistical week, the samples were distributed across time and area strata in an opportune way that provided adequate representation in this particular data set for an initial estimate. Second, stock compositions between early and late seasons (across all areas) and among areas (across seasons) were relatively similar (Tables 3-7; Fig. 5) suggesting that, like 2012, the 2013 stock compositions in the GOA were fairly consistent both spatially and temporally. Third, bycatch in the GOA pollock fishery in 2013 was dominated by four reporting groups (U.S. West Coast, British Columbia, coastal SEAK, and NW GOA) making up 99% of bycatch. The other seven reporting groups were present in low abundance (<1%). However, there was evidence that some of these reporting groups were regularly detectable, with probability of not being present ($P = 0$) averaging 0.39 for the low abundance stocks. Chinook salmon from Russia (71%), north Alaska Peninsula (55%), and middle Yukon River (51%) had the highest probability of truly being absent in the bycatch.

The convergence of these three factors mitigated the potential problems associated with using opportunistic samples, but this may not be the case in the future. Progress is being made to increase sampling of the bycatch, but until a stratified method of sampling (e.g., 1 in every 10 fish) is implemented, a post-analysis stratified weighted estimate method will be necessary. In addition, the consistent domination of stock composition by a small number of reporting groups may not continue in the future. Chinook salmon runs to the Pacific Northwest in 2013 and 2014 were large (WDFW 2014), and these fish would have been in the western GOA during 2013. It would be reasonable to assume that stock compositions in the GOA bycatch change with fluctuations in production from rivers in southeast Alaska, British Columbia, and the Pacific Northwest.

It should be noted that in this analysis we assume that there is no uncertainty in the reported bycatch numbers; therefore, the uncertainties presented in stock composition estimates and reporting group-specific bycatch numbers include only uncertainty associated with sampling and GSI analysis. In the future, incorporation of uncertainty in harvest numbers should be incorporated into the analysis to provide a more realistic assessment of the uncertainty in the bycatch stock composition estimates and probability of low abundance reporting groups being truly present in the bycatch.

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APPENDIX

Chinook salmon reporting groups for genetic stock identification using the ADF&G SNP baseline (from Templin et al. 2011). Too few samples were available to allow fine-scale resolution of the West Coast U.S. reporting group.

Reporting group		Number of populations	Mean sample size (range)
Broad	Fine		
Russia		4	
	Okhotsk Sea Coast	2	86 (77-94)
	Bering Sea Coast	2	85 (50-119)
Coastal West Alaska		27	
	Norton Sound	3	89 (72-112)
	Lower Yukon	4	202 (95-290)
	Kuskokwim Bay	3	253 (147-368)
	Lower Kuskokwim	11	166 (93-252)
	Upper Kuskokwim	2	143 (96-191)
	West Bristol Bay	4	100 (57-159)
	East Bristol Bay	2	88 (66-110)
Middle Yukon		8	
	Upper U.S. Yukon	5	106 (51-175)
	Tanana	3	189 (187-193)
Upper Yukon		13	
	Canada Border	2	164 (79-249)
	Pelly River	4	142 (99-197)
	Carmacks	5	99 (55-169)
	Takhini	2	202 (161-242)
North Alaska Peninsula		6	
	Port Heiden	2	87 (42-131)
	Port Moller	4	77 (51-95)
Northwest Gulf of Alaska		19	
	Chignik/Kodiak	3	117 (75-140)
	Susitna River	5	100 (52-251)
	Kenai Early	5	190 (95-266)
	Kenai Late	2	211 (119-302)
	Kasilof River	2	314 (306-321)
	Lower Kenai Peninsula	2	181 (162-200)
Copper		11	
	Upper Copper River	5	109 (50-157)
	Middle Copper	2	178 (144-211)

Reporting group		Number of populations	Mean sample size (range)
Broad	Fine		
	Lower Copper	4	70 (62-75)
Northeast Gulf of Alaska		7	
	Cape Fairweather	2	159 (143-174)
	Northern Southeast Alaska	5	134 (83-178)
Coastal Southeast Alaska		25	
	Chickamin River	6	141 (56-331)
	Unuk River	6	142 (94-397)
	Behm Canal	2	120 (95-144)
	Andrew Creek	5	214 (94-397)
	Transboundary Rivers	6	122 (86-143)
British Columbia		36	
	North Coast BC	5	86 (65-115)
	Skeena	4	112 (86-142)
	Central BC Coast	3	143 (141-144)
	South BC Mainland	2	119 (83-154)
	West Vancouver Island	5	125 (104-160)
	East Vancouver Island	3	121 (93-144)
	Upper Fraser	3	118 (94-154)
	Middle Fraser	4	168 (120-246)
	North Thompson	2	166 (153-179)
	South Thompson	3	97 (46-144)
	Lower Fraser	2	95 (93-96)
U.S. West Coast		14	111 (52-191)

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