Extension of Genetic Stock Composition Analysis to the Chinook Salmon Bycatch in the Gulf of Alaska Walleye Pollock (*Gadus chalcogrammus*) Trawl Fisheries, 2012

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September 15, 2014

ABSTRACT

The genetic stock composition of the Chinook salmon (*Oncorhynchus tshawytscha*) samples from the 2012 federal Gulf of Alaska (GOA) trawl fishery for walleye pollock (*Gadus chalcogrammus*) was extended to provide an overall stock composition for the fishery bycatch and stock-specific harvests. Genetic samples were collected opportunistically in 2012 from Chinook salmon taken in the bycatch of this fishery. These samples had previously been genotyped for 43 single nucleotide polymorphism (SNP) DNA markers and results were estimated using the available coastwide baseline of SNP markers for Chinook salmon. However, the opportunistic nature of the samples raised concerns about applying the proportional composition of the samples to the entire bycatch because of unknown, but potentially significant, biases. Here we investigate the most appropriate means by which this extension can be made. While sample sizes varied widely and did not achieve the 10% target used to sample bycatch in the Bering Sea, using a stratified estimator weighted by stratum-specific bycatch, it was possible to estimate the stock composition of the total catch with acceptable accuracy and precision. Based on the reanalysis of 948 Chinook salmon bycatch samples, the proportions of reporting groups did not change significantly from previously published values: British Columbia (50%), West Coast U.S. (28%), and Coastal Southeast Alaska (19%) comprised the largest reporting groups.

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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. Genetic stock identification (GSI) results for the set of Chinook salmon bycatch samples collected in 2012 from the U.S. GOA pollock trawl fisheries were completed in 2013 by Auke Bay Laboratories and reported to the North Pacific Fishery Management Council (NPFMC) in April of 2014 (Guthrie et al. 2014). However, the opportunistic nature of sampling raised concerns about applying the proportional composition of the samples to the entire bycatch because of unknown but potentially significant biases. The NPFMC recommended in April of 2014 that methods be explored to produce a reliable stock composition estimate for the bycatch in the entire 2012 fishery. To achieve this goal the following objectives need to be accomplished:

1) Investigate the extent to which Chinook salmon bycatch samples taken during 2012 GOA pollock fishery can be used to estimate stock-specific bycatch for the fishery.

2) Provide stock-specific composition, bycatch estimates, and associated summary statistics.

For the purposes of this report, stocks will be defined as the genetically identifiable reporting groups reported in Templin et al. (2011) and used in Guthrie et al. (2013).

SAMPLE DISTRIBUTION

A complete description of sampling the Chinook salmon bycatch in the GOA pollock fishery is provided by Guthrie et al. (2014). For the purposes of this analysis we provide the

following overview. In the 2012 GOA pollock fishery, there was no initial requirement for full

retention of Chinook salmon caught in the prohibited species catch although there were efforts

from industry to facilitate the collection of samples in anticipation of Amendment 93 to the GOA

groundfish fishery management plan. This plan required retention of all salmon intercepted in

the pollock fisheries in the Western and Central GOA until an observer was able to count the

number of salmon and collect scientific data or biological samples from a proportion of those

salmon. The intention was to take genetic samples from the bycatch proportionately, one in
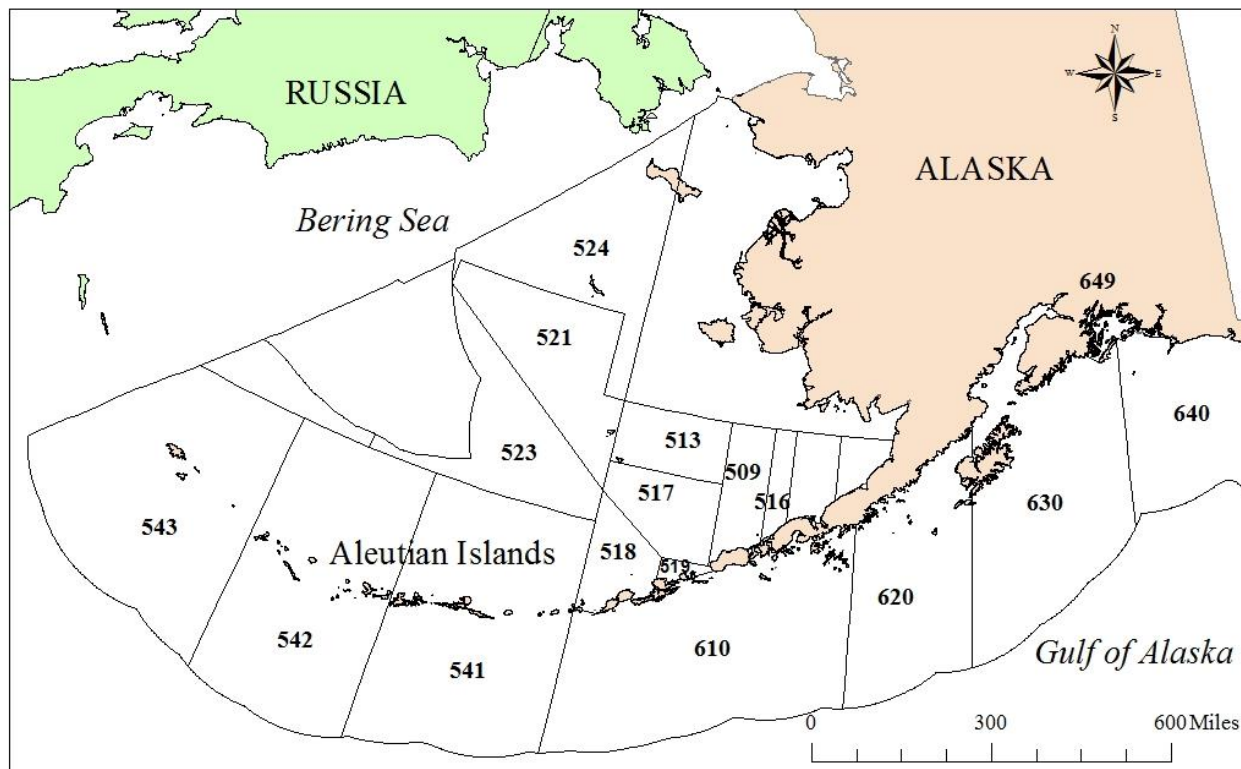
every 10 Chinook salmon encountered.

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

In 2012, an estimated 18,845 Chinook salmon were taken as bycatch in the GOA pollock

trawl fisheries in Districts 610, 620, 630, 640 and 649 (Fig. 1; NMFS 2012); this was less than

half the estimated 44,779 fish that were taken in the 2010 bycatch (Fig. 2). Tissues for genetic
analysis were sampled from 1,008 fish, corresponding to a sampling rate of 5% for the season.
This was fewer than the 10% sampling goal and these samples were not taken proportional to the
overall bycatch within each statistical week (Fig. 3) or area (District or grouping of Districts)
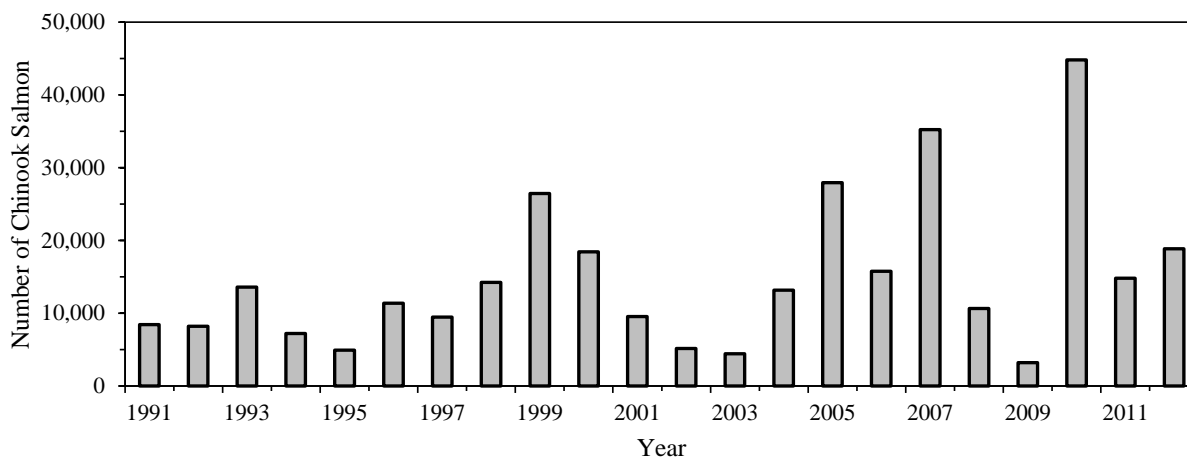(Fig. 4).

Figure 2.– Yearly estimates for the Chinook salmon bycatch from the Gulf of Alaska pollock trawl
fishery (NMFS 2012).

The temporal distribution of genetic samples from the 2012 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 was
sampled in the earlier period (Fig. 3). We also compared the spatial distribution of genetic
samples with the Chinook salmon bycatch by NMFS statistical area over time, for early
(statistical weeks 3-14) and late (statistical weeks 34-44) seasons, which indicated that there was
less bycatch and fewer samples in the early season – dominated by Area 620 – and majority of
the bycatch and samples in the late season were from Area 610 (Fig. 4).
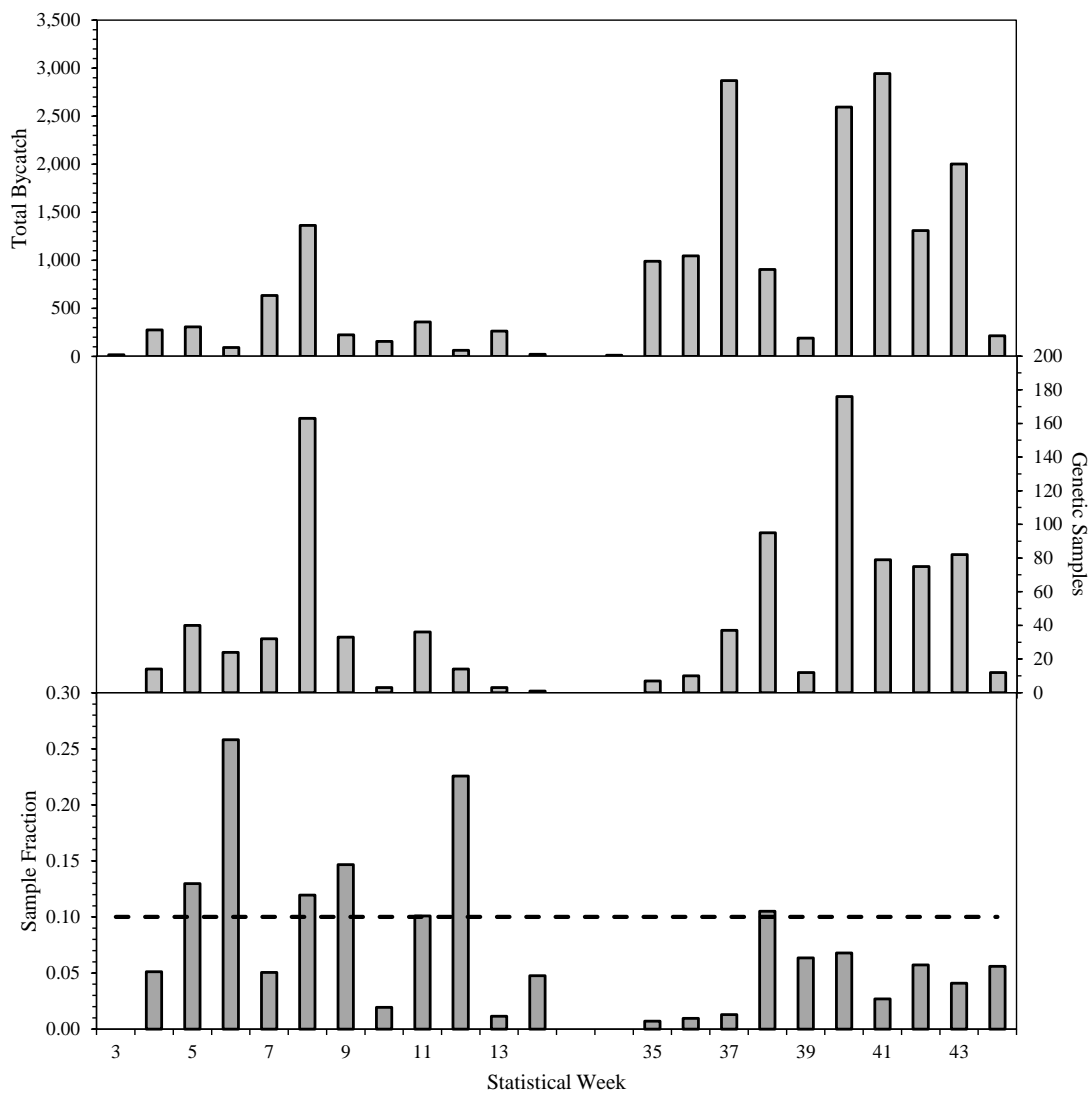
Figure 3.− Number of Chinook salmon bycatch reported (top), genetic samples used for genetic stock identification (middle) and proportion of fish sampled (bottom) by statistical week in 2012 Gulf of Alaska pollock trawl fishery. Dashed line in bottom graph indicates 10% sample fraction.
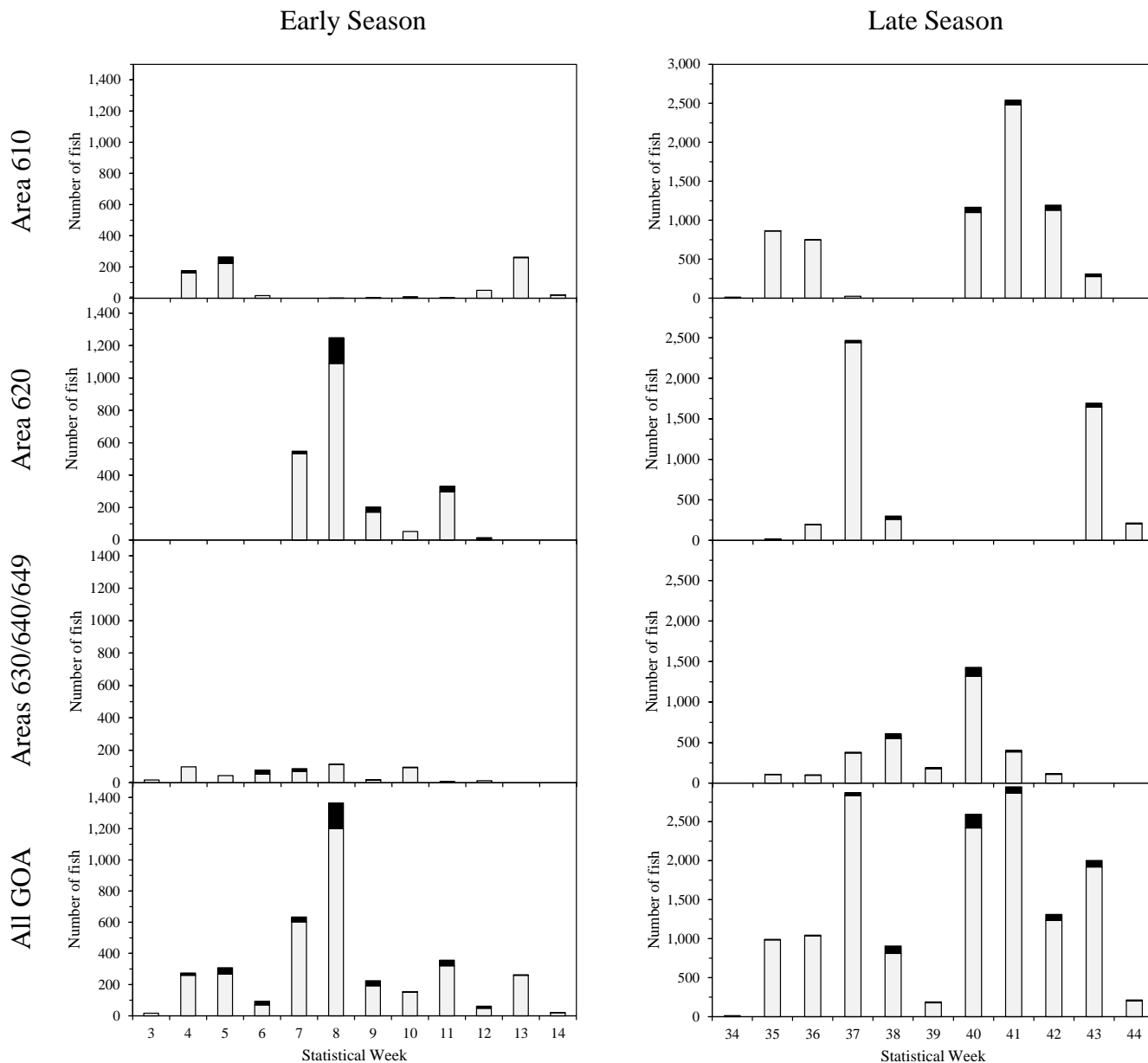
Figure 4.– 2012 Gulf of Alaska Chinook salmon bycatch and samples used for genetic stock identification (black section of bar), by time and area strata. Note the difference in y-axis scale between early and late season strata.

METHODS

DNA was extracted from axillary process tissue and genotyping was performed as described previously (Guyon et al. 2010a) using a Sequenom MassARRAY iPLEX platform[1] (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 A), 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 and b; Guthrie et al. 2012, 2013, and 2014; Larson et al. 2013). From the 2012 GOA Chinook salmon bycatch, a total of 1,008 samples were analyzed of which 948 were successfully genotyped for 35 or more of the 43 SNP loci (average of 41 markers/sample), a success rate of 94%. For further details see Guthrie et al. (2014).

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 3-14) and late season (statistical weeks 34-44). As described in Guthrie et al. (2014), the samples were separated into three spatial strata that corresponded to Areas 610, 620, and the aggregate 630/640/649. Thus there were six strata, each with a corresponding mixture sample and observed bycatch. Areas 630, 640 and 649 were combined because of the generally small bycatch compared to Areas 610 and 620.

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[1] Reference to trade names does not imply endorsement by the National Marine Fisheries Service, NOAA.

Table 1.– Chinook salmon bycatch harvest, number of genotyped samples and sample fraction of bycatch for 2012 Gulf of Alaska Pollock fishery stratified temporally and spatially into six strata. Early season includes statistical weeks 3 through 14 and late season includes statistical weeks 34 through 44.

Area	Early season			Late season		
	Bycatch	Sample size	Sample fraction	Bycatch	Sample size	Sample fraction
610	806	60	0.074	6,856	233	0.034
620	2,399	253	0.105	4,887	135	0.028
630/640/649	568	50	0.088	3,329	217	0.065

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 six 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 (Guthrie et al. 2014).

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

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

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 0 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: 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 six strata ranged from 568 in the combined Area 630/640/649 in the early season to 6,856 in Area 610 in the late season (Table 1). Sample sizes for GSI within these six strata ranged from 50 to 253. Generally strata with low sample sizes (Area 610 and combined areas 630/640/649 for the early season) also had low bycatch so that sample fractions, while not achieving the target 10%, were above the overall average sample fraction of 5% for the 2012 GOA season (> 7%). At the same time, while all other strata had lower sample fractions (2.8-6.5%), the sample sizes were of reasonable size (≥135 fish) given the relatively larger bycatches.

Stock composition estimates

The stock composition results indicate that 96.6% of the total bycatch in GOA comprised three reporting groups: British Columbia contributing the most (50%), followed by the West Coast U.S. (28%) and Coastal Southeast Alaska (19%) (Table 2). There were sufficient samples to allow further analysis of temporal and spatial differences in the bycatch.

When strata were combined across areas within season, estimates for the early season (statistical weeks 3-14) showed British Columbia contributed the most (41%), followed by Coastal Southeast Alaska (33%) and the West Coast U.S. (23%) (Table 3). For the late season

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(statistical weeks 34-44), British Columbia (52%) predominated, followed by the West Coast

U.S. (29%), and Coastal Southeast Alaska (15%) (Table 4).

When strata were combined across seasons within areas, the westernmost area, 610, had

the largest estimate from British Columbia (69%) with smaller components from the West Coast

U.S. (16%), and Coastal Southeast Alaska (12%) (Table 5). Moving east into NMFS area 620,

the estimated British Columbia contribution dropped (38%) while those from the West Coast

U.S. (36%) and Coastal Southeast Alaska (24%) increased at least two-fold (Table 6). For the

combined easternmost area (630, 640, and 649), estimates for British Columbia (37%), West

Coast U.S. (36%) and Coastal Southeast Alaska (24%) components were effectively the same as

those from area 620 (Table 7). For comparison purposes, the stock composition results were

plotted in Figure 5.

Table 2.– Stock composition estimates of the Chinook salmon bycatch of the 2012 Gulf of Alaska pollock trawl fishery using the stratified method (top table) compared with previously reported estimates (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 and n is the number of genetic samples used in the analysis.

| Reporting Group | Whole Season (H = 18,845; n = 948) | | | | | |
| | Proportion | 95% CI | | $P = 0$ | Median | SD |
		2.5%	97.5%			
Russia	0.000	0.000	0.002	0.63	0.000	0.001
Coastal Western AK	0.006	0.001	0.013	0.00	0.005	0.003
Middle Yukon R.	0.000	0.000	0.002	0.41	0.000	0.001
Upper Yukon R.	0.000	0.000	0.003	0.23	0.000	0.001
N AK Peninsula	0.001	0.000	0.004	0.41	0.000	0.001
NW Gulf of AK	0.020	0.011	0.033	0.00	0.020	0.006
Copper R.	0.001	0.000	0.004	0.11	0.001	0.001
NE Gulf of AK	0.005	0.001	0.012	0.00	0.004	0.003
Coastal SEAK	0.188	0.157	0.220	0.00	0.187	0.016
British Columbia	0.501	0.462	0.541	0.00	0.501	0.020
West Coast US	0.277	0.246	0.310	0.00	0.277	0.016

| Reporting Group | Guthrie et al. (2014) estimates | | | | | |
| | Proportion | 95% CI | | | Median | SD |
		2.5%	97.5%			
Russia	0.000	0.000	0.000		0.000	0.000
Coastal Western AK	0.004	0.000	0.013		0.003	0.004
Middle Yukon R.	0.000	0.000	0.001		0.000	0.000
Upper Yukon R.	0.000	0.000	0.001		0.000	0.000
N AK Peninsula	0.000	0.000	0.003		0.000	0.001
NW Gulf of AK	0.021	0.012	0.032		0.020	0.005
Copper R.	0.001	0.000	0.005		0.000	0.001
NE Gulf of AK	0.005	0.001	0.012		0.005	0.003
Coastal SEAK	0.201	0.167	0.238		0.200	0.018
British Columbia	0.492	0.448	0.533		0.492	0.022
West Coast US	0.277	0.246	0.308		0.276	0.016

Table 3.– Stock composition estimates for the Chinook salmon bycatch during the early season (weeks 3-14) of the 2012 Gulf of Alaska pollock trawl fishery – All areas. 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 | Early Season (All areas; H = 3,773; n = 363) | | | | | |
| | | 95% CI | | | | |
	Proportion	2.5%	97.5%	$P = 0$	Median	SD
Russia	0.000	0.000	0.002	0.83	0.000	0.001
Coastal Western AK	0.014	0.001	0.034	0.01	0.013	0.009
Middle Yukon R.	0.000	0.000	0.004	0.69	0.000	0.001
Upper Yukon R.	0.001	0.000	0.005	0.54	0.000	0.001
N AK Peninsula	0.000	0.000	0.004	0.73	0.000	0.001
NW Gulf of AK	0.007	0.000	0.024	0.09	0.005	0.007
Copper R.	0.001	0.000	0.006	0.56	0.000	0.002
NE Gulf of AK	0.004	0.000	0.016	0.05	0.003	0.004
Coastal SEAK	0.326	0.263	0.390	0.00	0.326	0.032
British Columbia	0.412	0.347	0.481	0.00	0.412	0.034
West Coast US	0.233	0.188	0.281	0.00	0.232	0.024

Table 4.– Stock composition estimates for the Chinook salmon bycatch during the late season (weeks 34-44) of the 2012 Gulf of Alaska pollock trawl fishery – All areas. 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 | Late Season (All areas; H = 15,072; n = 585) | | | | | |
| | | 95% CI | | | | |
	Proportion	2.5%	97.5%	$P = 0$	Median	SD
Russia	0.000	0.000	0.002	0.77	0.000	0.001
Coastal Western AK	0.003	0.000	0.011	0.03	0.003	0.003
Middle Yukon R.	0.000	0.000	0.002	0.61	0.000	0.001
Upper Yukon R.	0.000	0.000	0.003	0.45	0.000	0.001
N AK Peninsula	0.001	0.000	0.005	0.57	0.000	0.001
NW Gulf of AK	0.024	0.012	0.039	0.00	0.023	0.007
Copper R.	0.001	0.000	0.005	0.21	0.001	0.001
NE Gulf of AK	0.005	0.001	0.014	0.00	0.004	0.004
Coastal SEAK	0.153	0.118	0.191	0.00	0.152	0.019
British Columbia	0.524	0.477	0.571	0.00	0.524	0.024
West Coast US	0.289	0.251	0.328	0.00	0.288	0.020

Table 5.– Stock composition estimates for the Chinook salmon bycatch in Area 610 during the 2012 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.

| | | Area: 610 (All season; H = 7,662; n = 293) | | | | |
| | | 95% CI | | | | |
Reporting Group	Proportion	2.5%	97.5%	$P = 0$	Median	SD
Russia	0.000	0.000	0.002	0.86	0.000	0.001
Coastal Western AK	0.004	0.000	0.017	0.08	0.003	0.005
Middle Yukon R.	0.000	0.000	0.003	0.74	0.000	0.001
Upper Yukon R.	0.000	0.000	0.004	0.61	0.000	0.001
N AK Peninsula	0.000	0.000	0.003	0.78	0.000	0.001
NW Gulf of AK	0.025	0.009	0.048	0.00	0.024	0.010
Copper R.	0.000	0.000	0.004	0.65	0.000	0.001
NE Gulf of AK	0.009	0.001	0.026	0.00	0.008	0.007
Coastal SEAK	0.117	0.077	0.164	0.00	0.116	0.022
British Columbia	0.686	0.624	0.745	0.00	0.687	0.031
West Coast US	0.156	0.115	0.203	0.00	0.155	0.023

Table 6.– Stock composition estimates for the Chinook salmon bycatch in Area 620 during the 2012 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.

| | | Area: 620 (All season; H = 7,286; n = 388) | | | | |
| | | 95% CI | | | | |
Reporting Group	Proportion	2.5%	97.5%	$P = 0$	Median	SD
Russia	0.000	0.000	0.002	0.86	0.000	0.001
Coastal Western AK	0.008	0.000	0.020	0.02	0.007	0.005
Middle Yukon R.	0.000	0.000	0.003	0.75	0.000	0.001
Upper Yukon R.	0.000	0.000	0.004	0.62	0.000	0.001
N AK Peninsula	0.001	0.000	0.008	0.71	0.000	0.002
NW Gulf of AK	0.012	0.001	0.030	0.01	0.010	0.008
Copper R.	0.000	0.000	0.004	0.65	0.000	0.001
NE Gulf of AK	0.000	0.000	0.005	0.72	0.000	0.002
Coastal SEAK	0.236	0.180	0.296	0.00	0.235	0.030
British Columbia	0.380	0.314	0.449	0.00	0.380	0.034
West Coast US	0.362	0.302	0.423	0.00	0.362	0.031

Table 7.– Stock composition estimates for the Chinook salmon bycatch in Areas 630/640/649 of the 2012 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: 630/640/649 (All season; H = 3,897; n = 267) | | | | | |
| | Proportion | 95% CI | | $P = 0$ | Median | SD |
		2.5%	97.5%			
Russia	0.000	0.000	0.003	0.86	0.000	0.001
Coastal Western AK	0.004	0.000	0.021	0.22	0.002	0.006
Middle Yukon R.	0.000	0.000	0.003	0.77	0.000	0.001
Upper Yukon R.	0.001	0.000	0.004	0.65	0.000	0.001
N AK Peninsula	0.001	0.000	0.007	0.76	0.000	0.002
NW Gulf of AK	0.027	0.009	0.053	0.00	0.026	0.011
Copper R.	0.003	0.000	0.014	0.28	0.001	0.004
NE Gulf of AK	0.005	0.000	0.019	0.05	0.003	0.005
Coastal SEAK	0.236	0.166	0.303	0.00	0.237	0.035
British Columbia	0.365	0.294	0.450	0.00	0.363	0.040
West Coast US	0.358	0.297	0.420	0.00	0.358	0.031
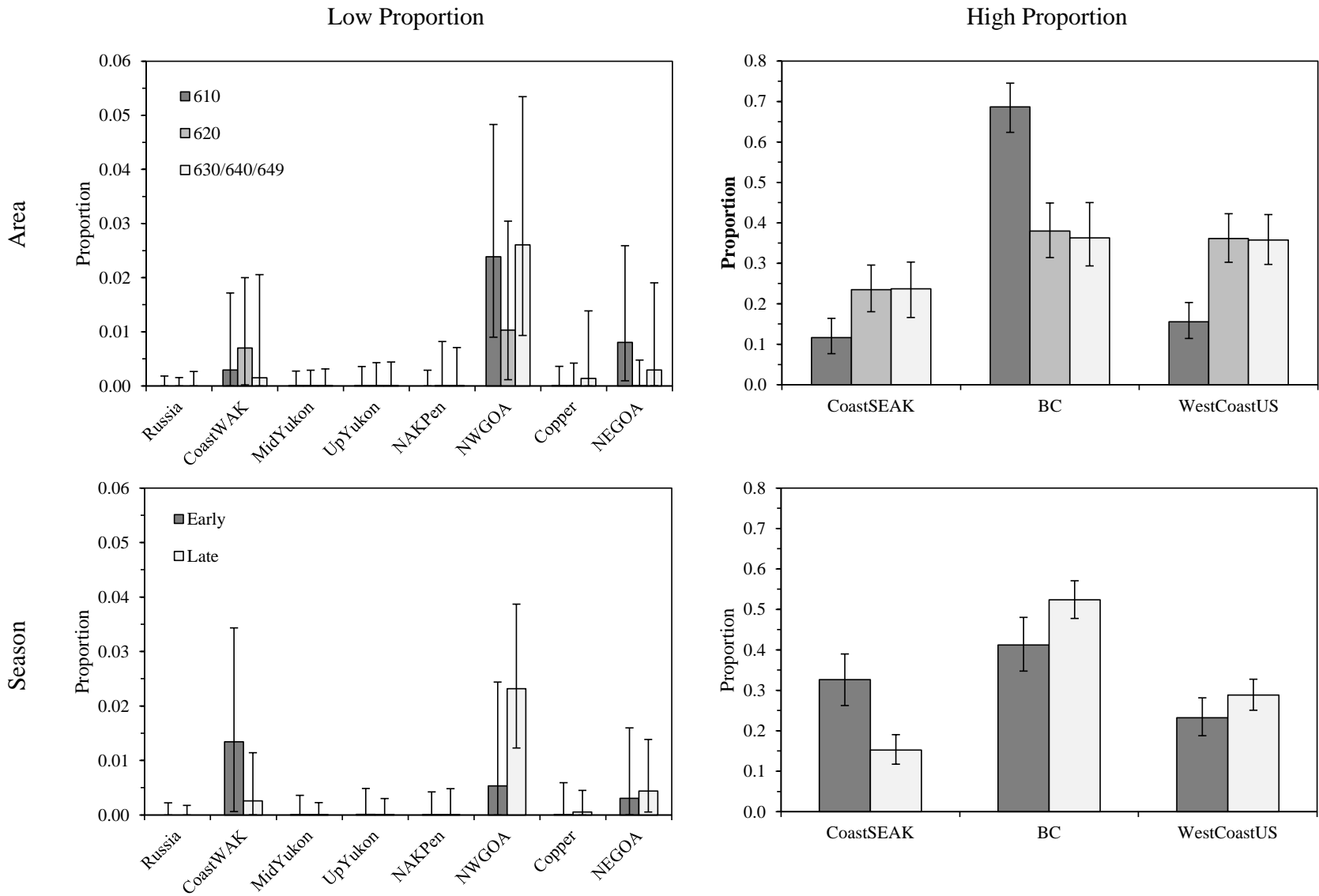
Figure 5.– 2012 Gulf of Alaska Chinook salmon stock composition estimates (median and 95% credibility intervals), by area (top) and temporal strata (bottom). Stocks estimated to be in low proportions (i.e. <10%) are plotted on the left while the more abundant stocks (>10%) the bycatch are plotted on the right.

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 2012 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 whole fishery (Table 8), by season (Tables 9 and 10), and by statistical area (Tables 11-13).

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 R, Upper Yukon R, N AK Peninsula, and Copper R; 1-3 fish; Table 9), but the support for their absence from the bycatch during the early season ranged widely ($P = 0$ ranged from 0.54 for Upper Yukon R to 0.83 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 Scientific and Statistical Committee and the end users.

Table 8.– Reporting group-specific estimates of number of Chinook salmon taken as bycatch in the 2012 Gulf of Alaska pollock trawl fishery. Estimates are provided 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.

| Reporting Group | Whole Season (H = 18,845; n = 948) | | | | |
| | Mean | 95% CI | | Median | SD |
		2.5%	97.5%		
Russia	3	0	29	0	9
Coastal Western AK	106	20	242	97	57
Middle Yukon R.	5	0	37	1	12
Upper Yukon R.	9	0	50	3	15
N AK Peninsula	10	0	75	1	22
NW Gulf of AK	385	205	616	376	105
Copper R.	18	0	73	11	21
NE Gulf of AK	94	17	230	83	56
Coastal SEAK	3,536	2,955	4,149	3,528	305
British Columbia	9,450	8,710	10,194	9,450	378
West Coast US	5,229	4,632	5,846	5,225	309
Total	18,845				

Table 9.– Reporting group-specific estimates of number of Chinook salmon harvested in the bycatch during the early season (weeks 3-14) of the 2012 Gulf of Alaska pollock trawl fishery – all areas. Estimates are provided 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.

| Reporting Group | Early Season (All areas; H = 3,773; n = 363) | | | | |
| | Mean | 95% CI | | Median | SD |
		2.5%	97.5%		
Russia	1	0	8	0	3
Coastal Western AK	55	2	130	51	33
Middle Yukon R.	2	0	14	0	4
Upper Yukon R.	3	0	18	0	5
N AK Peninsula	2	0	16	0	5
NW Gulf of AK	27	0	92	20	26
Copper R.	3	0	22	0	7
NE Gulf of AK	16	0	60	11	16
Coastal SEAK	1,231	991	1,471	1,232	123
British Columbia	1,556	1,311	1,813	1,554	128
West Coast US	878	708	1,061	876	90
Total	3,774				

Table 10.– Reporting group-specific estimates of number of Chinook salmon harvested in the bycatch during the late season (weeks 34-44) of the 2012 Gulf of Alaska pollock trawl fishery – all areas. Estimates are provided 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.

Reporting Group	Late Season (All areas; H = 15,072; n = 585)				
	Mean	95% CI 2.5%	97.5%	Median	SD
Russia	2	0	27	0	9
Coastal Western AK	51	0	172	39	46
Middle Yukon R.	4	0	34	0	11
Upper Yukon R.	6	0	45	1	14
N AK Peninsula	9	0	73	0	21
NW Gulf of AK	358	185	583	349	102
Copper R.	15	0	68	8	20
NE Gulf of AK	77	8	209	66	53
Coastal SEAK	2,304	1,772	2,873	2,297	281
British Columbia	7,894	7,196	8,601	7,894	358
West Coast US	4,351	3,782	4,937	4,347	295
Total	15,071				

Table 11.– Reporting group-specific estimates of number of Chinook salmon taken as bycatch in Area 610 during the 2012 Gulf of Alaska pollock trawl fishery – all season. Estimates are provided 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.

Reporting Group	Area: 610 (All season; H = 7,662; n = 293)				
	Mean	95% CI 2.5%	97.5%	Median	SD
Russia	1	0	14	0	6
Coastal Western AK	34	0	132	22	36
Middle Yukon R.	2	0	21	0	7
Upper Yukon R.	3	0	27	0	9
N AK Peninsula	2	0	22	0	9
NW Gulf of AK	192	69	370	183	78
Copper R.	3	0	28	0	9
NE Gulf of AK	72	7	199	62	51
Coastal SEAK	898	586	1,258	890	171
British Columbia	5,257	4,779	5,711	5,262	238
West Coast US	1,197	877	1,557	1,190	174
Total	7,661				

Table 12.– Reporting group-specific estimates of number of Chinook salmon taken as bycatch in Area 620 during the 2012 Gulf of Alaska pollock trawl fishery – all season. Estimates are provided 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.

| | Area: 620 (All season; H = 7,286; n = 388) | | | | |
| | | 95% CI | | | |
Reporting Group	Mean	2.5%	97.5%	Median	SD
Russia	1	0	11	0	5
Coastal Western AK	57	1	146	51	38
Middle Yukon R.	2	0	21	0	8
Upper Yukon R.	4	0	31	0	11
N AK Peninsula	6	0	60	0	18
NW Gulf of AK	86	8	222	75	56
Copper R.	3	0	31	0	10
NE Gulf of AK	3	0	35	0	12
Coastal SEAK	1,718	1,314	2,156	1,711	215
British Columbia	2,769	2,291	3,271	2,766	250
West Coast US	2,637	2,203	3,081	2,634	225
Total	7,286				

Table 13.– Reporting group-specific estimates of number of Chinook salmon taken as bycatch in Areas 630/640/649 during the 2012 Gulf of Alaska pollock trawl fishery – all season. Estimates are provided 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.

| | Area: 630/640/649 (All season; H = 3,897; n = 267) | | | | |
| | | 95% CI | | | |
Reporting Group	Mean	2.5%	97.5%	Median	SD
Russia	1	0	10	0	4
Coastal Western AK	15	0	80	6	22
Middle Yukon R.	1	0	12	0	4
Upper Yukon R.	2	0	17	0	5
N AK Peninsula	3	0	28	0	9
NW Gulf of AK	107	36	208	102	44
Copper R.	11	0	54	5	15
NE Gulf of AK	18	0	74	11	20
Coastal SEAK	920	648	1,181	923	136
British Columbia	1,424	1,145	1,755	1,414	156
West Coast US	1,395	1,159	1,638	1,393	122
Total	3,897				

SUMMARY

Using the stratified analysis described in this report we were able to extend the stock

composition estimates of the 2012 Chinook salmon GOA bycatch beyond the original GSI of

available samples to describe the entire bycatch. When the results of this stock composition

were compared with the results reported previously by Guthrie et al. (2014), the comparison

showed little change in the stock compositions from using the stratification process (Table 2).

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. In addition, the strata with small sample sizes had sample fractions

>7% and those strata with small sample fractions had reasonable sample sizes (smallest was 135

fish). Intentional stratification and subsequent weighting of stock composition estimates with

bycatch helped to further minimize potential bias.

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 the 2012 stock

compositions in the GOA were fairly consistent both spatially and temporally.

Third, bycatch in the GOA pollock fishery in 2012 was dominated by three reporting

groups (Coastal SEAK, British Columbia, and West Coast USA), making up about 97% of

bycatch. The other eight reporting groups were present in low abundance (<0.1 to 2%).

However, there was good evidence that some of these reporting groups were regularly

detectable, with probability of not being present ($P = 0$) low for most stocks. North Alaska

Peninsula and Middle Yukon River (41% each) and Russia (63%) 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, and these fish would have been in the western GOA during 2012. It would be reasonable to assume that stock compositions in the GOA bycatch change with fluctuations in production from rivers in SE 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.

ACKNOWLEDGMENTS

Monitoring and Analysis Division including Martin Loefflad, Liz Chilton, and the many

participating observers who provided genetic samples. Dr. Ellen Yasumiishi (NOAA), Eric Volk

(ADF&G), and others helped with the editorial review. MALDI-TOF genotyping and assay

design performed in collaboration with Colleen Ramsower and Dr. Ryan Sprissler from the

genotyping core facility at the University of Arizona.

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APPENDIX A

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)
West Coast U.S.		**14**	**111 (52-191)**