# Genetic Stock Composition Analysis of the Chinook Salmon Bycatch Samples from the 2014 Gulf of Alaska Trawl Fishery

by
C. M. Guthrie, III, Hv. T. Nguyen,  and  J. R. Guyon

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## ABSTRACT

A genetic analysis of samples from the Chinook salmon (*Oncorhynchus tshawytscha*) bycatch of the 2014 Gulf of Alaska (GOA) trawl fisheries for walleye pollock (*Gadus chalcogrammus*), rockfish (*Sebastes* spp.), and arrowtooth flounder (*Atheresthes stomias)* was undertaken to determine the stock composition of the sample sets. Samples were genotyped for 43 single nucleotide polymorphism (SNP) DNA markers and results were estimated using the Alaska Department of Fish and Game (ADF&G) SNP baseline. In 2014, genetic samples were collected from Chinook salmon taken in the bycatch of the Gulf of Alaska (GOA) pollock trawl fisheries using a simple random sample protocol with trip being the primary unit. This is the first year for this sampling protocol and resulted in the largest available genetic sample set to date with 10.7% of the salmon bycatch successfully genotyped.  Based on the analysis of 1,163 Chinook salmon bycatch samples, British Columbia (43%), West Coast U.S. (35%), Coastal Southeast Alaska (16%), and Northwest Gulf of Alaska stocks (5%) comprised the largest stock groups.  Weighting the available sample sets to the total bycatch by season and statistical area did not appreciably change the overall stock composition.  In 2014, genetic samples from the bycatch of the rockfish catcher vessel (CV) fishery in the central GOA were collected by the fishing industry using a census sampling protocol where every Chinook salmon encountered was sampled.  Based on the genotyping of 398 Chinook salmon bycatch samples collected from the 2014 GOA rockfish CV trawl fishery in NMFS Statistical Areas 620 and 630, West Coast U.S. stocks (WA/OR/CA) represented the largest stock grouping (72%) with smaller contributions from British Columbia (17%), Coastal Southeast Alaska (7%), and Northwest GOA (3%) stocks. Based on the genotyping of 404 Chinook salmon bycatch samples collected throughout the 2014 GOA arrowtooth flounder trawl fishery from the catcher-processors (CP) FV *Vaerdal* and FV *US*

*Intrepid*; West Coast U.S. stocks (WA/OR/CA) represented the largest stock grouping (51%) with smaller contributions from British Columbia (36%), Coastal Southeast Alaska (10%), Northeast GOA (2%) and Northwest GOA (2%) stocks.

# CONTENTS

# INTRODUCTION

The Bering Sea and the Gulf of Alaska (GOA) are known feeding habitats 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 Chinook salmon bycatch samples collected in the GOA from the (1) trawl fisheries for walleye pollock (*Gadus chalcogrammus*), (2) catcher vessel trawl fisheries for rockfish (*Sebastes* spp.) in the central GOA, and (3) catcher processor trawl fisheries for arrowtooth flounder (*Atheresthes stomias).* The National Marine Fisheries Service (NMFS)
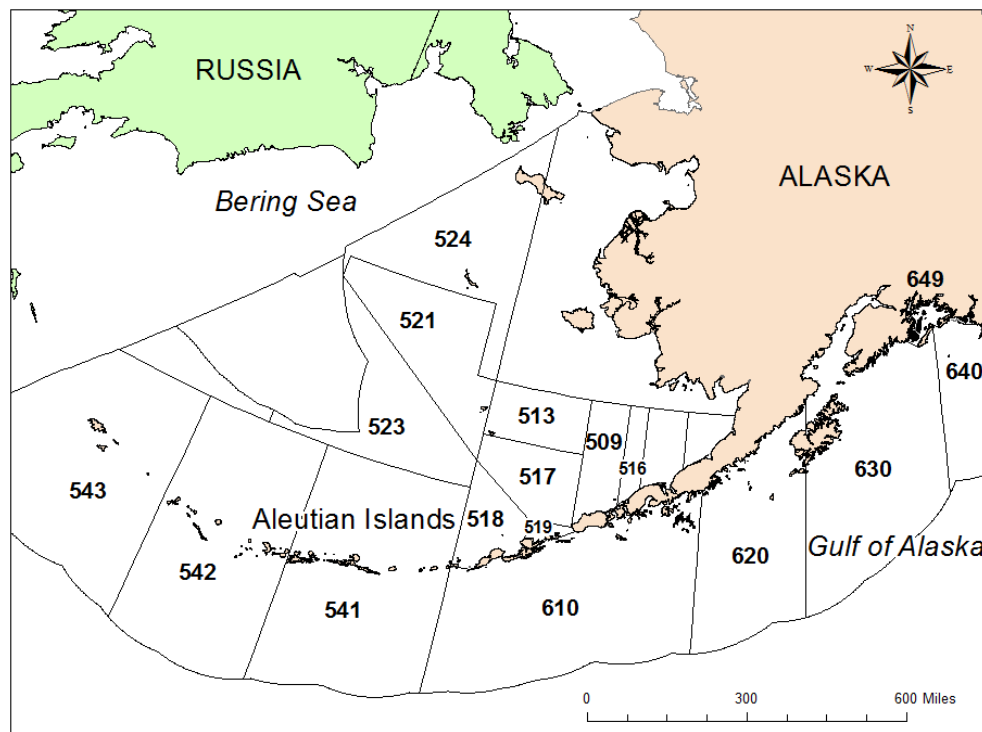


**Figure 1**. -- NMFS statistical areas associated with the Bering Sea-Aleutian Island (BSAI – Areas 509-543) and Gulf of Alaska (GOA – Areas 610-649) groundfish fisheries.

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.

The goal of this report is to present stock composition estimates for samples collected from the bycatch of the 2014 GOA federal trawl fisheries, but it is important to understand the limitations of each sample set for making accurate estimates of the entire bycatch or comparing estimates between samples or years. All analyses use a single nucleotide polymorphism (SNP) baseline provided by ADF&G (Templin et al. 2011) and this is the same baseline used to estimate previous stock compositions of samples from the Chinook salmon bycatch of the federally managed GOA trawl fisheries (Guthrie et al. 2013; Guyon et al. 2014, 2015a, 2015b; Larson et al. 2013). For additional information regarding background and methodology refer to the Chinook salmon bycatch report prepared previously for the 2008 Bering Sea trawl fishery (Guyon et al. 2010).

## SAMPLE DISTRIBUTION

### Gulf of Alaska Pollock Trawl Fishery

Amendment 93 to the GOA groundfish fishery management plan required industry retain all Chinook salmon caught as bycatch in the GOA pollock trawl fishery. This retention requirement was aimed at providing observers with complete access to the bycatch to support genetic stock composition analyses. However Amendment 93 did not mandate complete observer coverage, and not all GOA pollock trips were 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. Recognizing these limitations in the GOA, starting in 2014, the observer program implemented a simple random sampling (SRS) protocol with

respect to trip for the collection of genetic samples in the GOA (Faunce et al. 2014). This method randomly samples from trips and censuses the salmon bycatch encountered in each associated delivery to the processor (Faunce 2015). Samples of axillary process tissue for genetic analysis were collected throughout 2014 from the GOA. Axillary process tissues were stored in coin envelopes which were labeled, frozen, and shipped to Auke Bay Laboratories (ABL). The majority of the Chinook salmon bycatch genetic tissue samples were derived from the bottom and midwater pollock trawl fishery. Those samples (31) identified as originating from a non-pollock fishery (from trips in which the predominant target species by weight was not pollock) were removed from the analyses.

In 2014, an estimated 10,877 Chinook salmon were taken as bycatch in the GOA pollock trawl fisheries (NMFS 2015). The year with the highest overall Chinook bycatch in the GOA was 2010 (Fig. 2) when an estimated 44,819 fish were taken. The genotyped sample set for the 2014 Chinook salmon bycatch was 1,163 fish, corresponding to a sampling rate of 10.7%. This is the largest sample set by both number and proportion for the incidental catch of Chinook salmon captured in the GOA pollock trawl fishery.
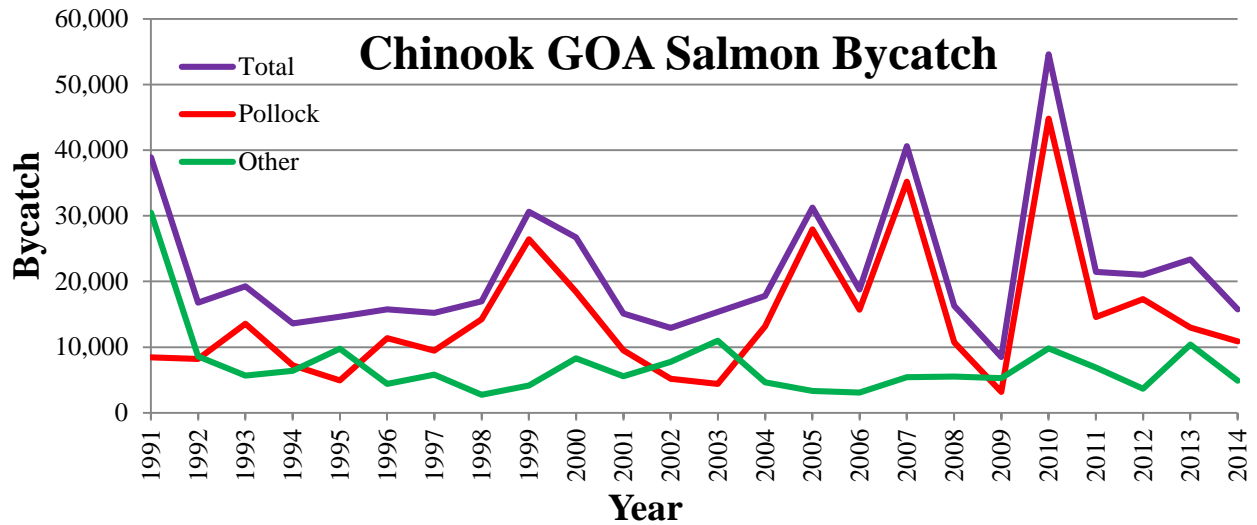
**Figure 2**. -- Yearly estimates for the Chinook salmon bycatch from the GOA trawl fisheries (NMFS 2015).

Potential spatial and temporal biases associated with the 2014 Chinook salmon GOA bycatch sample sets were visually evaluated by comparing the genetic sample distribution with the estimated overall distribution of bycatch showing similarities in their temporal distribution (Fig. 3). To evaluate the sample spatial distribution, the GOA Chinook salmon bycatch was compared with the bycatch samples by statistical area over time (Fig. 4) highlighting time/space sample distribution issues present in the sample set.

## 2014 GOA Pollock Trawl Chinook Bycatch
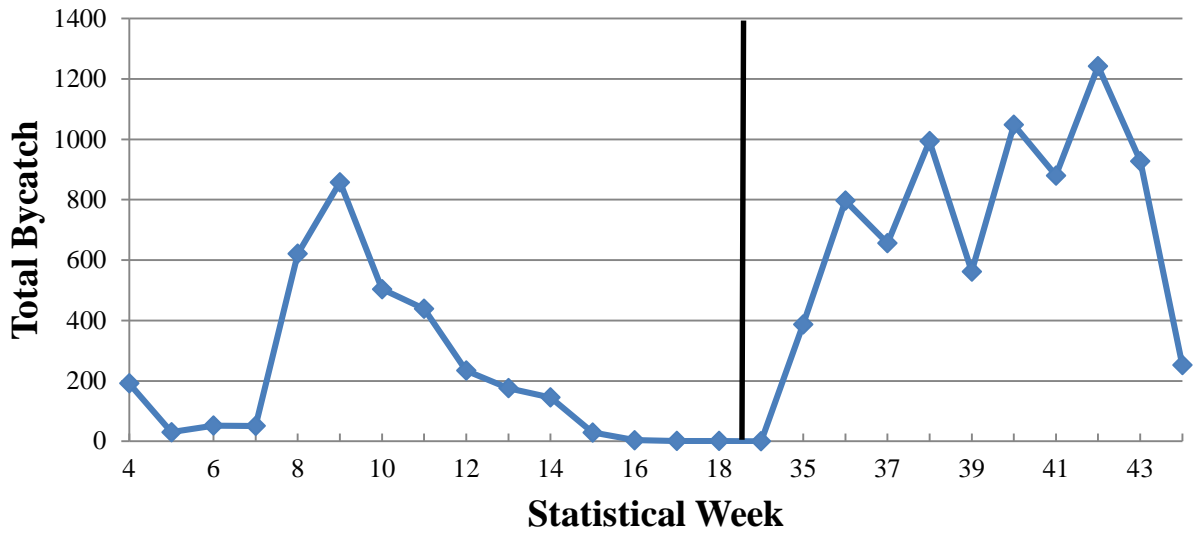


## 2014 GOA Pollock Trawl Chinook Bycatch Samples
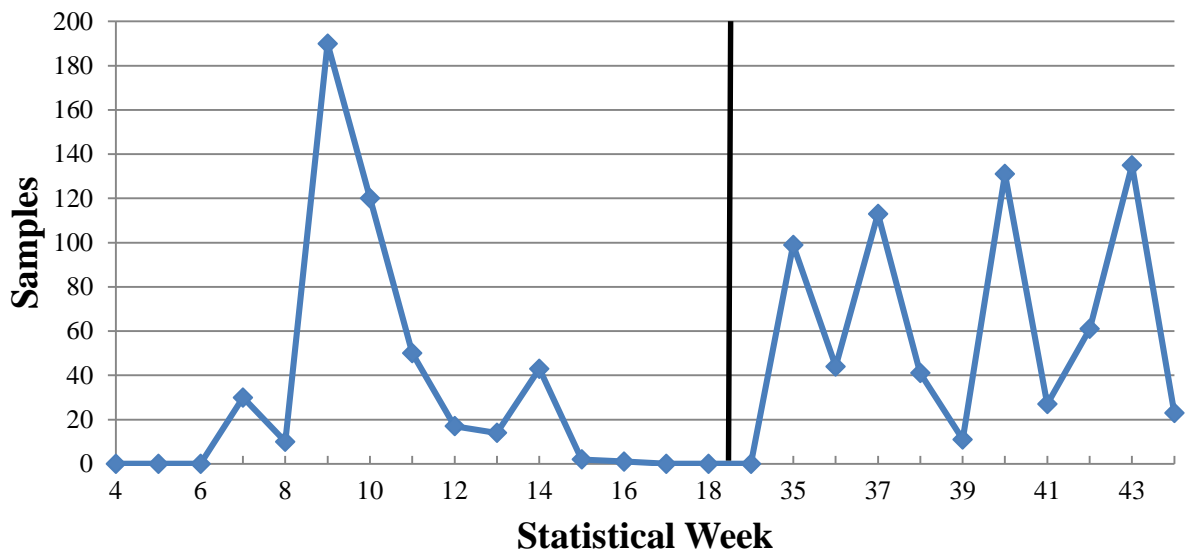


**Figure 3**. -- Number of Chinook salmon bycatch and genetic samples by statistical week. Top panel: Distribution of all Chinook salmon caught in the 2014 GOA pollock trawl fishery. Bottom panel: Distribution of the 1,163 genotyped samples from the 2014 bycatch. The vertical line separates weeks 18 and 35 when no fishing occurred.
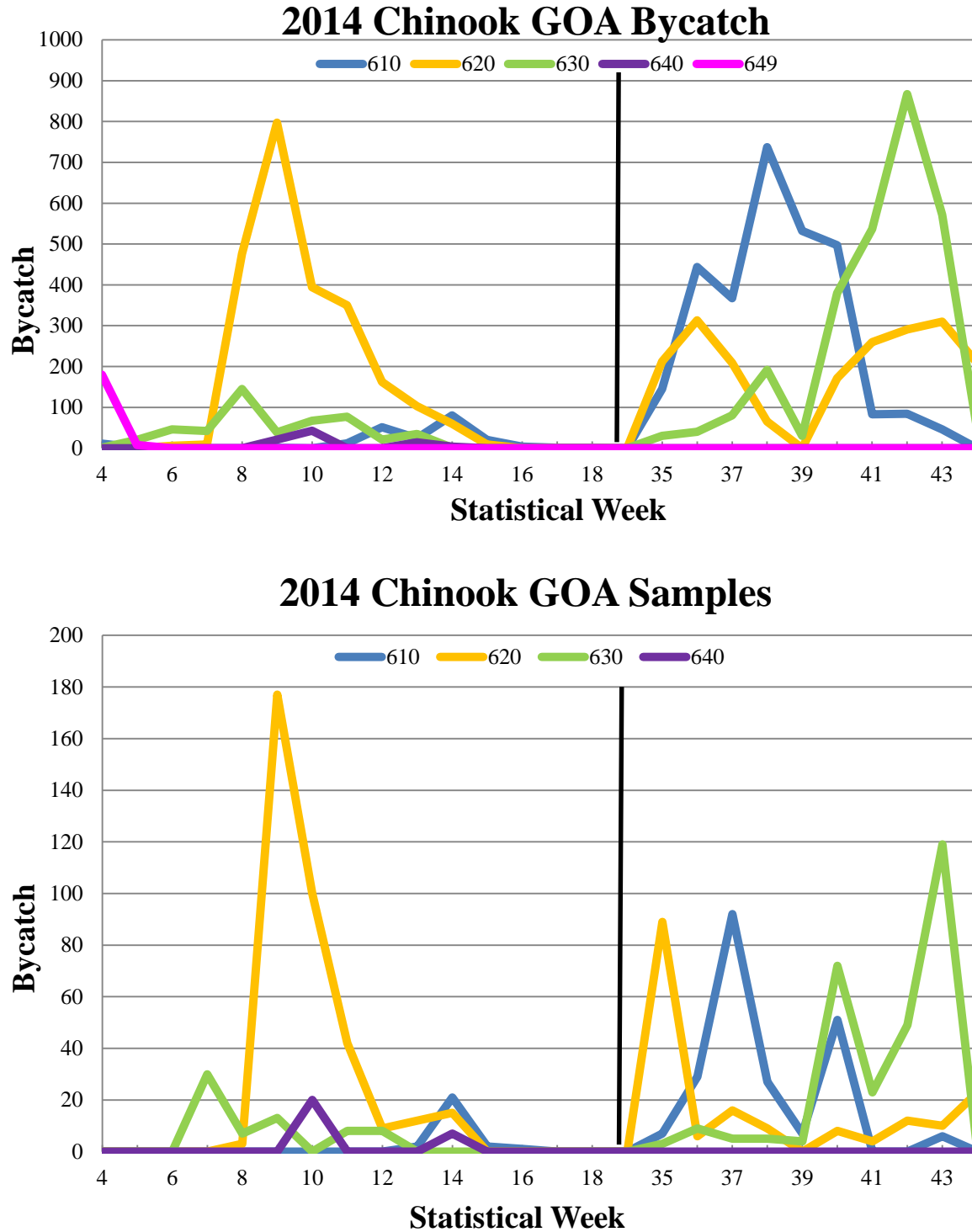
**Figure 4**.-- Comparison of the Chinook salmon bycatch by time and area with the distribution of available genetic samples. Top panel: Distribution of the estimated Chinook salmon caught in the 2014 GOA pollock trawl fishery. Bottom panel: Distribution of the 1,163 genotyped samples from the 2014 bycatch. The vertical line separates weeks 18 and 35 when no fishing occurred.

GOA Rockfish CV Trawl Fishery

Samples were collected from the Chinook salmon bycatch of the federally managed 2014 Alaska CV rockfish trawl fishery in the central GOA by the Alaska Groundfish Data Bank (AGDB) for analysis at the ABL.  Although there was no requirement for sample collection, the AGDB implemented a census approach in 2013 (Guyon et al 2015b) and 2014 whereby genetic samples (axillary processes) and biological information were collected from every Chinook salmon encountered in the bycatch.  Axillary process tissues were stored in coin envelopes which were labeled, frozen, and shipped to the ABL.  Between 1 May and 15 November 2014 (week numbers 19-45), genetic samples were collected from 434 Chinook salmon from a census of 468. Because samples were taken from the overall bycatch, the sample distribution is considered to be the bycatch distribution.  The sample collection area is approximated in Figure 5 and the bycatch enumeration by statistical week is shown in Figure 6.
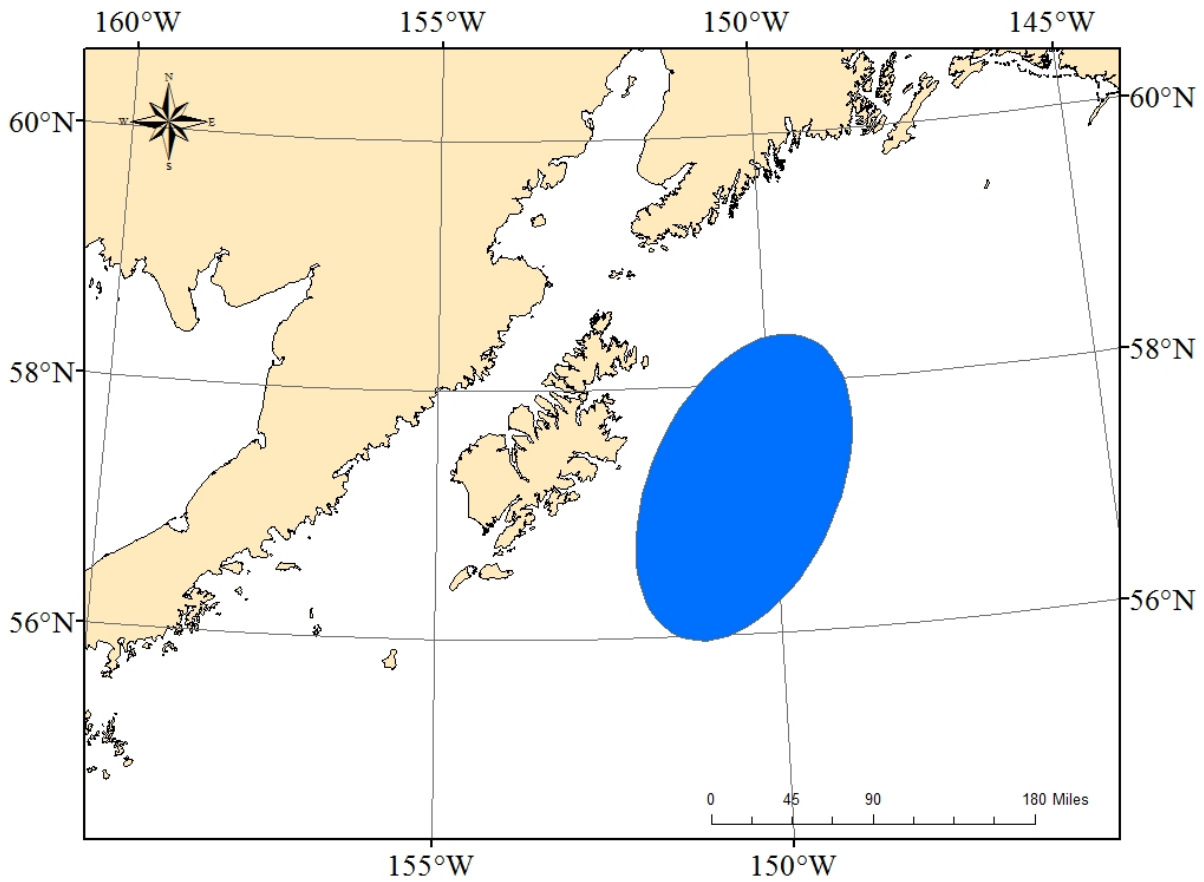
**Figure 5.** -- Relative location of Chinook salmon bycatch samples collected in NMFS Statistical Areas 620 and 630 by the Alaska Groundfish Data Bank in the 2014 GOA rockfish trawl fishery.

**2014 GOA Rockfish CV Fishery**
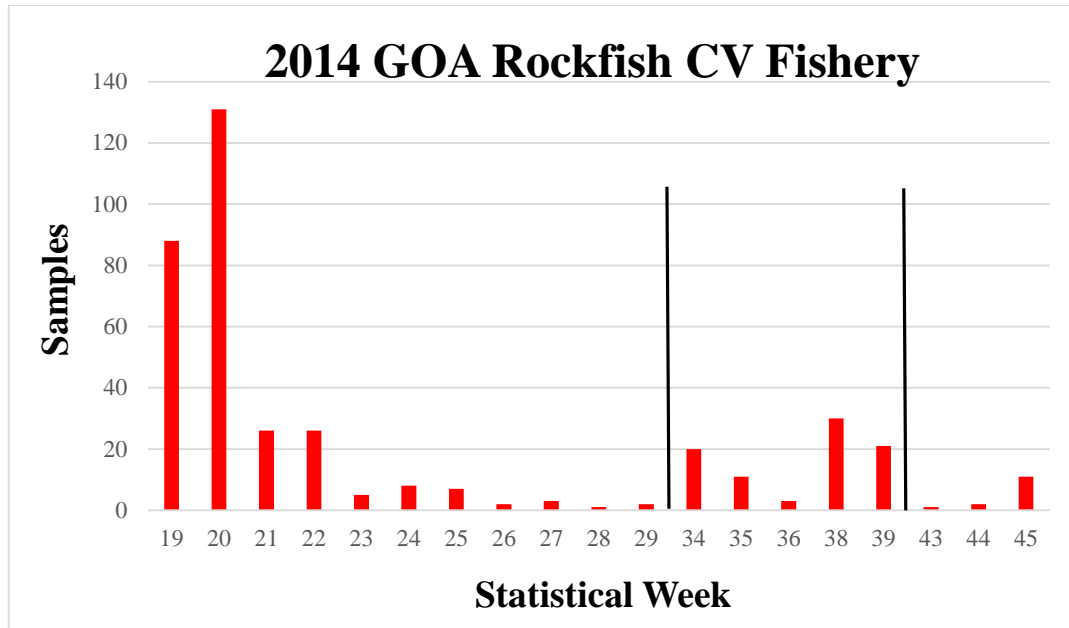
**Figure 6. --** Genetic samples collected by AGDB from the census of the Chinook salmon
bycatch in the 2014 GOA rockfish CV trawl fishery plotted by statistical week. The
lines show demarcations between weeks 29 and 34 and weeks 39 and 43 for which
no Chinook salmon bycatch was encountered.

GOA Arrowtooth Flounder Trawl Fishery

Samples were collected from the Chinook salmon bycatch of the federally managed

2014 Alaska GOA arrowtooth flounder trawl fishery by the Alaska Seafood Cooperative for

analysis at the AFSC's Auke Bay Laboratories. Although there was no requirement for sample

collection, the Alaska Seafood Cooperative implemented an opportunistic sampling approach in

2014 to collect genetic samples (axillary processes) and biological information from Chinook

salmon encountered in the bycatch. Axillary process tissues were stored in coin envelopes which

were labeled, frozen, and shipped to the ABL. Between 7 April and 22 May 2014 (NMFS

Statistical Weeks 15 and 21), 560 Chinook salmon were sampled from two CP in the arrowtooth

flounder trawl fishery. This represents over 50% of the total Chinook salmon bycatch from that

fishery, but because samples were taken opportunistically, the sample distribution at this time is

not considered representative of the entire bycatch but is used to indicate presence/absence of

particular Chinook salmon stocks.  The sample collection area from the arrowtooth flounder

trawl fishery is approximated in Figure 7.
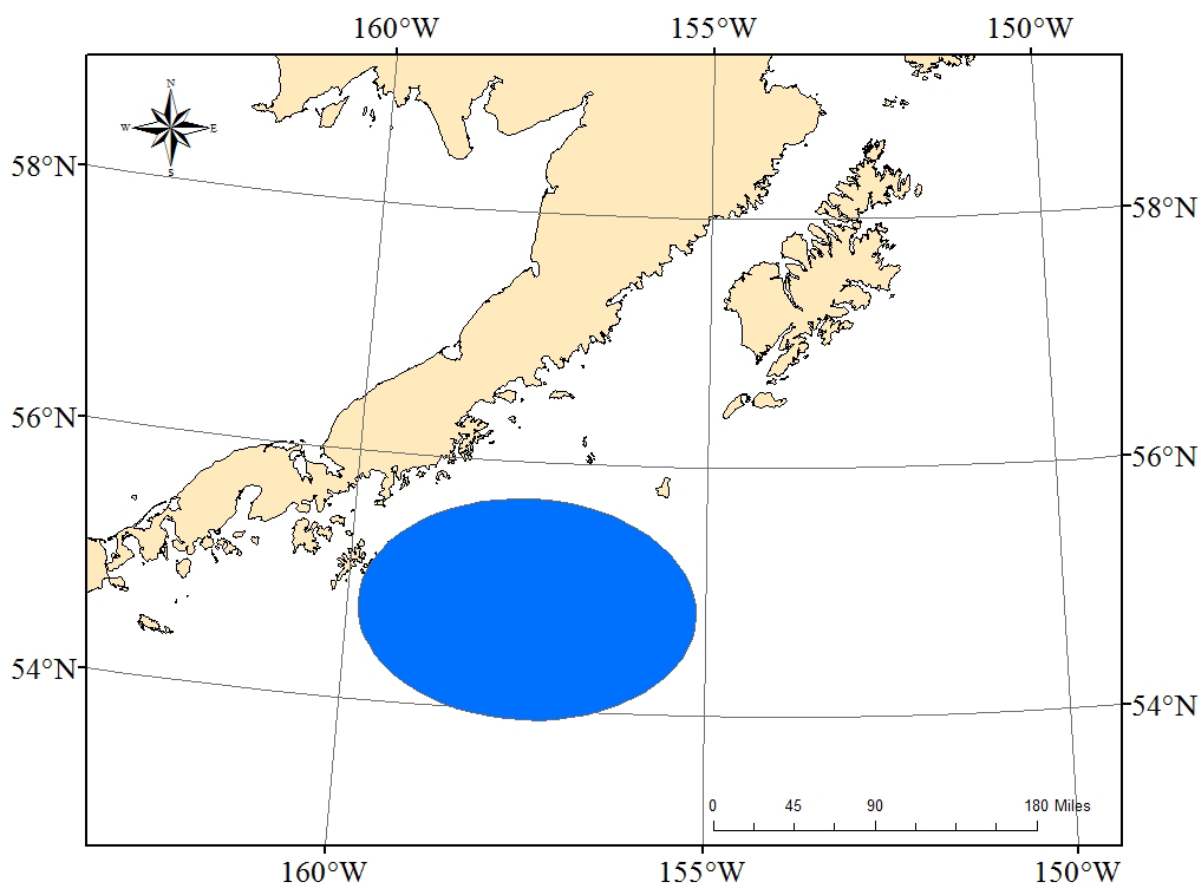


**Figure 7. --** Approximate location (NMFS Statistical Areas 610 and 620) of 560 Chinook
salmon bycatch samples collected by the Alaska Seafood Cooperative in the 2014
GOA arrowtooth flounder trawl fishery.

GENETIC STOCK COMPOSITION - PROCEDURE

DNA was extracted from axillary process tissue and matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) genotyping was performed as described previously (Guyon et al. 2010) using a Sequenom MassARRAY iPLEX platform (Gabriel et al. 2009) to genotype 43 SNP DNA markers represented in the Chinook salmon baseline (Templin et al. 2011). The SNP baseline contains genetic information for 172 populations of Chinook salmon grouped into 11 geographic regions. This baseline was used previously for the genetic analysis of the Chinook GOA bycatch (Guthrie et al. 2013; Guyon et al. 2014, 2015a, 2015b; Larson et al. 2013). In addition to internal MALDI-TOF chip controls, 10 previously genotyped samples were included on each chip during the analyses and resulting genotypes were compared to those from ADF&G, which used TaqMan chemistries (Thermo Fisher Scientific, Inc). Concordance rates of 99.8% between the two chemistries for the 2014 controls confirmed the utility and compatibility of both genotyping methods.

From the Chinook salmon bycatch from the 2014 GOA pollock trawl fishery, a total of 1,359 samples were analyzed of which 1,163 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 86%. These genotypes were analyzed using C++ programs written by the Auke Bay Laboratories' Genetics Program to check for duplicate samples and three were found which were previously removed from the analysis. The remaining samples had genetic information for an average of 40.3 of 43 markers.

From the Chinook salmon bycatch from the 2014 GOA rockfish CV trawl fishery, a total of 434 samples were analyzed of which 398 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 92%. These genotypes were analyzed using C++ programs

written by the Auke Bay Laboratories' Genetics Program to check for duplicate samples and 1 was found which was previously removed from the analysis. The remaining samples had genetic information for an average of 41.1 of 43 markers.

From the Chinook salmon bycatch from the 2014 GOA arrowtooth CP trawl fishery, a total of 445 samples from the *FV Værdal* were analyzed of which 301 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 68%. During processing, it was noted that these samples did not smell fresh indicating a potential sample quality issue. These genotypes were analyzed using C++ programs written by the Auke Bay Laboratories' Genetics Program to check for duplicate samples and none were found. The remaining samples had genetic information for an average of 40.2 of 43 markers. In the same fishery a total of 134 samples from the *FV US Intrepid* were analyzed of which 122 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 91%. Of the 122 samples successfully genotyped, 19 were not from the arrowtooth fishery and were not used in further analyses. These genotypes were analyzed using C++ programs written by the Auke Bay Laboratories' Genetics Program to check for duplicate samples and one was found which was previously removed from the analysis. The remaining samples had genetic information for an average of 41.8 of 43 markers. This resulted in a total of 404 samples from the 2014 GOA arrowtooth CP trawl fishery for use in stock composition analysis.

Stock composition estimates were derived using both BAYES (Bayesian analysis) and SPAM (maximum likelihood analysis) software and both methods yielded almost identical stock composition estimates (Tables 1, 3-12). BAYES software uses a Bayesian algorithm to produce stock composition estimates and can account for missing alleles in the baseline (Pella and Masuda 2001). In contrast, SPAM uses a conditional maximum likelihood approach in which the

mixture genotypes are compared directly with the baseline (ADF&G 2003). Convergence of the SPAM estimates was monitored with the "Percent of Maximum" value and all exceeded the 90% guaranteed percent achievement of the maximal likelihood. For each BAYES analysis, 11 Monte Carlo chains starting at disparate values of stock proportions were 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. For all estimates, a flat prior of 0.005814 (calculated as 1/172) was used for all 172 baseline populations. The analyses were completed for a chain length of 10,000 with the first 5,000 deleted during the burn-in phase when determining overall stock compositions. Convergence of the chains to posterior distributions of stock proportions was determined with Gelman and Rubin shrink statistics, which were 1.09 or less for all the estimates, conveying strong convergence to a single posterior distribution (Pella and Masuda 2001).

## GENETIC STOCK COMPOSITION - RESULTS

### GOA Pollock Trawl Fishery

The stock composition results estimate that 99.7% of the 1,163 samples from the GOA originated from GOA/Pacific coastal regions, with the British Columbia grouping contributing the most (43%), followed by the West Coast US (34%), Coastal Southeast Alaska (16%), and Northwest GOA (5%) (Table 1). Because the sample distribution did not match the overall distribution (Figs. 3 and 4, Table 2), efforts were made to develop a weighted stock composition to the overall catch using the protocols described previously in Guyon et al. 2014 and Guyon et al. 2015a. Briefly, the method involved developing stock compositions for each area and time strata identified in Table 2, and then weighting the overall estimate based on the relative size of the bycatch. All stock compositions for the weighted bycatch stock composition (Table 3) were

within the credible interval of the 2014 sample stock composition suggesting that both estimates were similar; consequently, all remaining estimates are unweighted. It was noted that the sample stock composition estimate for British Columbia was higher than the weighted estimate, a finding that can be attributed to a relatively higher percentage of samples from the early season (Table 2), a period which contained a higher proportion of fish from that area (Tables 4 and 5). Although care must be taken when comparing estimates across years due to the differences in sampling, the stock composition estimate and the weighted estimates in 2014 were very similar to that seen for previous years (Figure 8 and 9).

Due to higher sample numbers and sampling fractions available in 2014, we were also able look at temporal and the geographical (NMFS statistical areas) differences. The BAYES estimates for the early season (statistical weeks 4-16) showed British Columbia contributed the most (49%), followed by West Coast US (35%) and Coastal Southeast Alaska (14%) (Table 4). For the late season (statistical weeks 35-44), British Columbia (40%) predominated, followed by the West Coast US (33%), Coastal Southeast Alaska (18%), and Northwest GOA (7%) (Table 5). The western-most area, 610, had the largest stock estimates from British Columbia (52%) with smaller components from the West Coast US (28%), Coastal Southeast Alaska (12%) and Northwest GOA (7%) (Table 6) (Fig. 10). Moving east into area 620, the British Columbia composition dropped (38%) while those from the West Coast US (37%), and Coastal Southeast Alaska (20%) increased (Table 7) (Fig. 10). The samples from the two easternmost areas (630 and 640) were combined due to sample size, although most were from area 630 (354). British Columbia had the highest BAYES composition (42%), Northwest GOA steady (5%), West Coast US increasing (34%), and Coastal Southeast Alaska (17%) dropping (Table 8) (Fig. 10). The sample size within area 620 was large enough that temporal estimates could be derived for that

**Table 1**. – Regional BAYES and SPAM stock composition estimates for the 1,163 Chinook salmon samples from the bycatch of the 2014 GOA pollock trawl fishery. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

| Region | BAYES | SD | 2.5% | Median | 97.5% | SPAM | SD |
|---|---|---|---|---|---|---|---|
| Russia | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.002** | 0.000 |
| Coast W AK | **0.003** | 0.003 | 0.000 | 0.002 | 0.011 | **0.004** | 0.000 |
| Mid-Yukon | **0.000** | 0.000 | 0.000 | 0.000 | 0.001 | **0.002** | 0.000 |
| Up Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| N AK Penn | **0.000** | 0.000 | 0.000 | 0.000 | 0.001 | **0.000** | 0.000 |
| NW GOA | **0.048** | 0.007 | 0.035 | 0.048 | 0.063 | **0.045** | 0.003 |
| Copper | **0.003** | 0.003 | 0.000 | 0.002 | 0.012 | **0.005** | 0.001 |
| NE GOA | **0.010** | 0.005 | 0.002 | 0.009 | 0.021 | **0.015** | 0.001 |
| Coast SE AK | **0.161** | 0.015 | 0.131 | 0.161 | 0.192 | **0.151** | 0.005 |
| BC | **0.432** | 0.019 | 0.394 | 0.432 | 0.470 | **0.434** | 0.013 |
| WA/OR/CA | **0.343** | 0.015 | 0.314 | 0.343 | 0.373 | **0.341** | 0.012 |



**Figure 8.** -- Comparison of yearly stock composition estimates (2010-2014) based on available genetic samples from the GOA Chinook salmon bycatch. The same genetic baseline and general regional groupings were used in all analyses. BAYES 95% credible intervals are plotted for yearly estimates.

## GOA Chinook Bycatch by Year



**Figure 9.** -- Comparison of yearly stock composition estimates (2010-2014) based on available genetic samples from the GOA Chinook salmon bycatch. The estimates were weighted for 2012-14. The same genetic baseline and general regional groupings were used in all analyses. BAYES 95% credible intervals are plotted for yearly estimates.



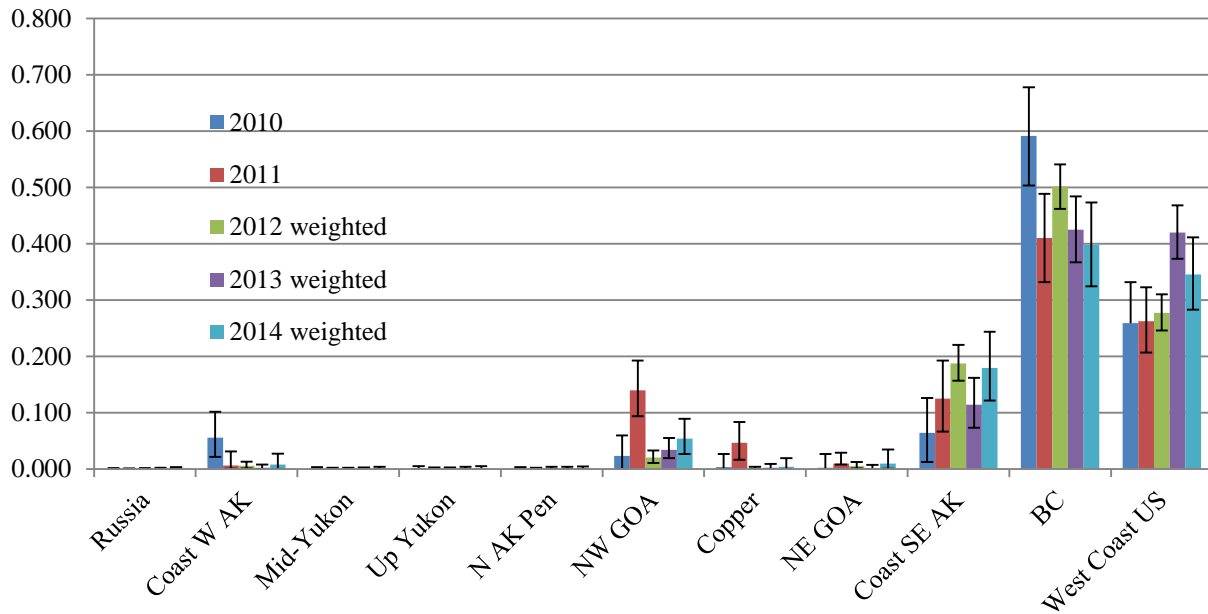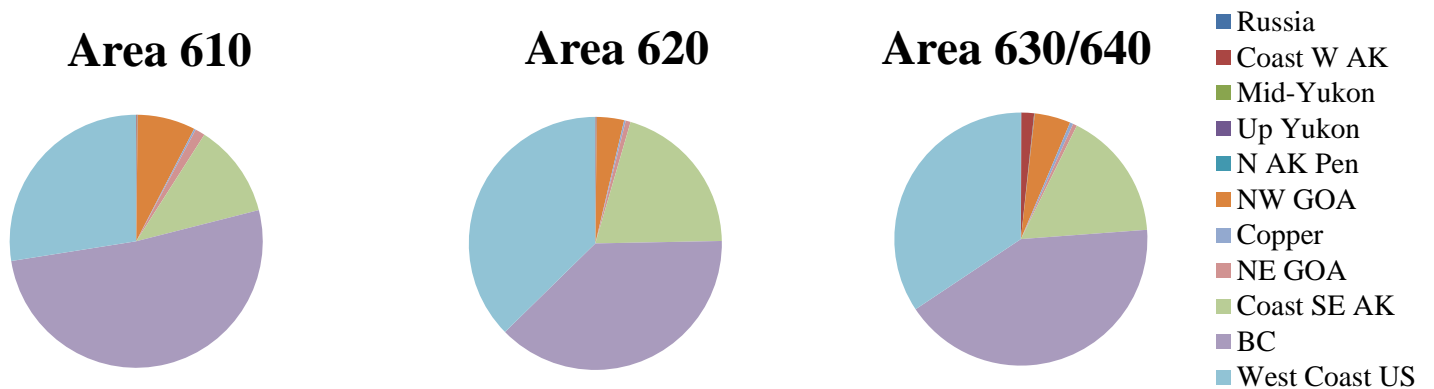**Figure 10.** -- Comparison of seasonal GOA NMFS Statistical Areas stock composition estimates based on available genetic samples from the Chinook salmon bycatch. The same regional groupings were used in all analyses.

**Table 2**.-- Chinook salmon bycatch harvest, number of genotyped samples and sample fraction of bycatch for 2014 Gulf of Alaska pollock fishery stratified temporally and spatially.  Early season includes statistical weeks 4 through 16 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  | 201     | 25          | 0.124           | 2935    | 219         | 0.075           |
| 620  | 2366    | 358         | 0.151           | 2039    | 178         | 0.087           |
| 630  | 494     | 66          | 0.134           | 2773    | 288         | 0.104           |
| 640  | 82      | 27          | 0.329           | 0       | 0           | 0.000           |
| 649  | 188     | 0           | 0.000           | 0       | 0           | 0.000           |

**Table 3**. – Weighted regional BAYES and SPAM stock composition estimates for the 1,163 Chinook salmon samples from the bycatch of the 2014 GOA pollock trawl fishery. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate.

| **Region** | **BAYES** | **SD** | **2.5%** | **Median** | **97.5%** |
|------------|-----------|--------|----------|------------|-----------|
| Russia     | 0.000     | 0.001  | 0.000    | 0.000      | 0.003     |
| Coast W AK | 0.008     | 0.008  | 0.000    | 0.006      | 0.027     |
| Mid-Yukon  | 0.000     | 0.001  | 0.000    | 0.000      | 0.004     |
| Up Yukon   | 0.000     | 0.002  | 0.000    | 0.000      | 0.005     |
| N AK Penn  | 0.000     | 0.002  | 0.000    | 0.000      | 0.004     |
| NW GOA     | 0.054     | 0.016  | 0.026    | 0.053      | 0.089     |
| Copper     | 0.004     | 0.006  | 0.000    | 0.002      | 0.019     |
| NE GOA     | 0.010     | 0.010  | 0.000    | 0.006      | 0.034     |
| Coast SE AK| 0.179     | 0.031  | 0.122    | 0.178      | 0.244     |
| BC         | 0.398     | 0.038  | 0.325    | 0.398      | 0.473     |
| WA/OR/CA   | 0.345     | 0.033  | 0.283    | 0.345      | 0.411     |

area (Tables 9 and 10), the results of which show a higher contribution from British Columbia

(47% vs. 16%) and lower contributions from Coastal Southeast Alaska (15% vs. 33%) and

Northwest GOA (1% vs. 6%) in the early season**.**

**Table 4**. -- Regional BAYES and SPAM stock composition estimates for the 478 Chinook salmon samples from the bycatch of the 2014 GOA pollock trawl fishery for the early season. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

| **Region** | **BAYES** | **SD** | **2.5%** | **Median** | **97.5%** | **SPAM** | **SD** |
|---|---|---|---|---|---|---|---|
| Russia | **0.000** | 0.000 | 0.000 | 0.000 | 0.001 | **0.000** | 0.000 |
| Coast W AK | **0.001** | 0.001 | 0.000 | 0.000 | 0.005 | **0.000** | 0.000 |
| Mid-Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.002** | 0.000 |
| Up Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| N AK Penn | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.001** | 0.002 |
| NW GOA | **0.017** | 0.007 | 0.007 | 0.017 | 0.032 | **0.017** | 0.001 |
| Copper | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| NE GOA | **0.007** | 0.005 | 0.000 | 0.007 | 0.019 | **0.006** | 0.000 |
| Coast SE AK | **0.138** | 0.022 | 0.097 | 0.137 | 0.182 | **0.128** | 0.006 |
| BC | **0.488** | 0.028 | 0.433 | 0.488 | 0.543 | **0.502** | 0.023 |
| WA/OR/CA | **0.349** | 0.023 | 0.304 | 0.349 | 0.395 | **0.344** | 0.019 |

**Table 5**. -- Regional BAYES and SPAM stock composition estimates for the 685 Chinook salmon samples from the bycatch of the 2014 GOA pollock trawl fishery for the late season. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

| **Region** | **BAYES** | **SD** | **2.5%** | **Median** | **97.5%** | **SPAM** | **SD** |
|---|---|---|---|---|---|---|---|
| Russia | **0.000** | 0.001 | 0.000 | 0.000 | 0.004 | **0.003** | 0.000 |
| Coast W AK | **0.006** | 0.006 | 0.000 | 0.005 | 0.020 | **0.008** | 0.001 |
| Mid-Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| Up Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.003 | **0.001** | 0.000 |
| N AK Penn | **0.000** | 0.001 | 0.000 | 0.000 | 0.001 | **0.000** | 0.000 |
| NW GOA | **0.068** | 0.011 | 0.047 | 0.067 | 0.091 | **0.064** | 0.005 |
| Copper | **0.007** | 0.007 | 0.000 | 0.005 | 0.023 | **0.010** | 0.002 |
| NE GOA | **0.013** | 0.008 | 0.001 | 0.012 | 0.030 | **0.020** | 0.002 |
| Coast SE AK | **0.183** | 0.020 | 0.145 | 0.182 | 0.222 | **0.174** | 0.007 |
| BC | **0.396** | 0.023 | 0.351 | 0.396 | 0.441 | **0.381** | 0.015 |
| WA/OR/CA | **0.327** | 0.019 | 0.292 | 0.327 | 0.365 | **0.338** | 0.015 |

**Table 6**. -- Regional BAYES and SPAM stock composition estimates for the 245 Chinook salmon samples from the bycatch of the 2014 GOA pollock trawl fishery from area 610. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

| Region | BAYES | SD | 2.5% | Median | 97.5% | SPAM | SD |
|---|---|---|---|---|---|---|---|
| Russia | **0.000** | 0.001 | 0.000 | 0.000 | 0.001 | **0.000** | 0.000 |
| Coast W AK | **0.001** | 0.002 | 0.000 | 0.000 | 0.008 | **0.000** | 0.000 |
| Mid-Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| Up Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.004 | **0.000** | 0.000 |
| N AK Penn | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| NW GOA | **0.074** | 0.018 | 0.042 | 0.073 | 0.112 | **0.068** | 0.010 |
| Copper | **0.002** | 0.004 | 0.000 | 0.000 | 0.014 | **0.004** | 0.004 |
| NE GOA | **0.013** | 0.010 | 0.000 | 0.011 | 0.036 | **0.026** | 0.002 |
| Coast SE AK | **0.120** | 0.025 | 0.074 | 0.119 | 0.172 | **0.120** | 0.008 |
| BC | **0.515** | 0.039 | 0.438 | 0.515 | 0.589 | **0.494** | 0.032 |
| WA/OR/CA | **0.275** | 0.034 | 0.213 | 0.274 | 0.344 | **0.288** | 0.022 |

**Table 7.** -- Regional BAYES and SPAM stock composition estimates for the 536 Chinook salmon samples from the bycatch of the 2014 GOA pollock trawl fishery from area 620. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

| Region | BAYES | SD | 2.5% | Median | 97.5% | SPAM | SD |
|---|---|---|---|---|---|---|---|
| Russia | **0.000** | 0.000 | 0.000 | 0.000 | 0.001 | **0.000** | 0.000 |
| Coast W AK | **0.001** | 0.003 | 0.000 | 0.000 | 0.009 | **0.004** | 0.000 |
| Mid-Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.001 | **0.002** | 0.000 |
| Up Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| N AK Penn | **0.000** | 0.001 | 0.000 | 0.000 | 0.003 | **0.000** | 0.001 |
| NW GOA | **0.035** | 0.009 | 0.019 | 0.034 | 0.054 | **0.032** | 0.004 |
| Copper | **0.002** | 0.003 | 0.000 | 0.000 | 0.012 | **0.005** | 0.002 |
| NE GOA | **0.006** | 0.006 | 0.000 | 0.005 | 0.021 | **0.017** | 0.001 |
| Coast SE AK | **0.202** | 0.025 | 0.155 | 0.201 | 0.252 | **0.175** | 0.008 |
| BC | **0.380** | 0.028 | 0.324 | 0.379 | 0.435 | **0.399** | 0.018 |
| WA/OR/CA | **0.373** | 0.022 | 0.330 | 0.373 | 0.417 | **0.364** | 0.018 |

**Table 8**. -- Regional BAYES and SPAM stock composition estimates for the 382 Chinook salmon samples from the bycatch of the 2014 GOA pollock trawl fishery from areas 630/640. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

| Region | BAYES | SD | 2.5% | Median | 97.5% | SPAM | SD |
|---|---|---|---|---|---|---|---|
| Russia | **0.001** | 0.002 | 0.000 | 0.000 | 0.007 | **0.005** | 0.000 |
| Coast W AK | **0.016** | 0.011 | 0.000 | 0.015 | 0.040 | **0.007** | 0.001 |
| Mid-Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.004 | **0.000** | 0.000 |
| Up Yukon | **0.001** | 0.001 | 0.000 | 0.000 | 0.005 | **0.003** | 0.000 |
| N AK Penn | **0.000** | 0.001 | 0.000 | 0.000 | 0.001 | **0.000** | 0.000 |
| NW GOA | **0.046** | 0.014 | 0.022 | 0.045 | 0.076 | **0.048** | 0.006 |
| Copper | **0.004** | 0.005 | 0.000 | 0.003 | 0.017 | **0.009** | 0.004 |
| NE GOA | **0.005** | 0.006 | 0.000 | 0.003 | 0.022 | **0.003** | 0.000 |
| Coast SE AK | **0.165** | 0.027 | 0.116 | 0.164 | 0.219 | **0.148** | 0.008 |
| BC | **0.418** | 0.032 | 0.356 | 0.418 | 0.481 | **0.439** | 0.023 |
| WA/OR/CA | **0.344** | 0.025 | 0.295 | 0.343 | 0.394 | **0.339** | 0.021 |

**Table 9**. -- Regional BAYES and SPAM stock composition estimates for the 358 Chinook salmon samples from the bycatch of the 2014 GOA pollock trawl fishery from early season in area 620. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

| Region | BAYES | SD | 2.5% | Median | 97.5% | SPAM | SD |
|---|---|---|---|---|---|---|---|
| Russia | **0.000** | 0.001 | 0.000 | 0.000 | 0.001 | **0.000** | 0.000 |
| Coast W AK | **0.001** | 0.002 | 0.000 | 0.000 | 0.006 | **0.000** | 0.000 |
| Mid-Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.003** | 0.000 |
| Up Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| N AK Penn | **0.000** | 0.001 | 0.000 | 0.000 | 0.004 | **0.002** | 0.003 |
| NW GOA | **0.020** | 0.008 | 0.007 | 0.019 | 0.039 | **0.021** | 0.002 |
| Copper | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| NE GOA | **0.008** | 0.006 | 0.000 | 0.007 | 0.022 | **0.007** | 0.001 |
| Coast SE AK | **0.145** | 0.023 | 0.103 | 0.145 | 0.192 | **0.132** | 0.007 |
| BC | **0.465** | 0.031 | 0.405 | 0.465 | 0.525 | **0.480** | 0.026 |
| WA/OR/CA | **0.360** | 0.027 | 0.308 | 0.359 | 0.413 | **0.356** | 0.022 |

**Table 10**. -- Regional BAYES and SPAM stock composition estimates for the 178 Chinook
salmon samples from the bycatch of the 2014 GOA pollock trawl fishery from late
season in area 620.  The BAYES mean estimates are also provided with standard
deviations (SD), 95% credible intervals, and the median estimate. Standard
deviations for the SPAM estimates were determined by the analysis of 1,000
bootstrap resamplings of the mixture.

| Region | BAYES | SD | 2.5% | Median | 97.5% | SPAM | SD |
|--------|-------|-----|------|--------|-------|------|-----|
| Russia | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| Coast W AK | **0.011** | 0.014 | 0.000 | 0.005 | 0.047 | **0.013** | 0.001 |
| Mid-Yukon | **0.000** | 0.002 | 0.000 | 0.000 | 0.005 | **0.000** | 0.000 |
| Up Yukon | **0.000** | 0.002 | 0.000 | 0.000 | 0.005 | **0.000** | 0.000 |
| N AK Penn | **0.001** | 0.004 | 0.000 | 0.000 | 0.011 | **0.000** | 0.000 |
| NW GOA | **0.058** | 0.021 | 0.022 | 0.056 | 0.104 | **0.052** | 0.009 |
| Copper | **0.009** | 0.012 | 0.000 | 0.005 | 0.040 | **0.018** | 0.005 |
| NE GOA | **0.012** | 0.016 | 0.000 | 0.003 | 0.054 | **0.036** | 0.005 |
| Coast SE AK | **0.335** | 0.045 | 0.248 | 0.335 | 0.425 | **0.275** | 0.021 |
| BC | **0.163** | 0.039 | 0.094 | 0.161 | 0.246 | **0.219** | 0.018 |
| WA/OR/CA | **0.410** | 0.038 | 0.338 | 0.410 | 0.485 | **0.383** | 0.032 |

Gulf of Alaska Rockfish CV Trawl Fishery

The stock composition results indicate that almost all of the 398 Chinook salmon samples

from the bycatch of the 2014 GOA rockfish CV trawl fishery originated from GOA/Pacific

coastal regions, with the West Coast U.S. (WA/OR/CA) contributing the most (72%) with

smaller contributions from British Columbia (17%), Coastal Southeast Alaska (7%), and

Northwest GOA (3%) stocks (Table 11). There were more West Coast U.S. (WA/OR/CA) (72%

vs. 60%) and less British Columbia (17% vs. 31%) present in 2014 (Fig. 11), but the majority

were still from southern regions (97% and 96%).

**Table 11**. -- Regional BAYES and SPAM stock composition estimates for the 398 genotyped samples from the bycatch of the 2014 GOA rockfish CV trawl fishery. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

| Region | BAYES | SD | 2.5% | Median | 97.5% | SPAM | SD |
|---|---|---|---|---|---|---|---|
| Russia | **0.001** | 0.002 | 0.000 | 0.000 | 0.008 | **0.003** | 0.001 |
| Coast W AK | **0.003** | 0.004 | 0.000 | 0.002 | 0.013 | **0.003** | 0.000 |
| Mid-Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.001 | **0.000** | 0.000 |
| Up Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| N AK Penn | **0.000** | 0.001 | 0.000 | 0.000 | 0.003 | **0.000** | 0.000 |
| NW GOA | **0.032** | 0.010 | 0.015 | 0.031 | 0.053 | **0.027** | 0.006 |
| Copper | **0.001** | 0.002 | 0.000 | 0.000 | 0.006 | **0.003** | 0.001 |
| NE GOA | **0.001** | 0.003 | 0.000 | 0.000 | 0.010 | **0.002** | 0.001 |
| Coast SE AK | **0.071** | 0.017 | 0.041 | 0.070 | 0.108 | **0.074** | 0.004 |
| BC | **0.174** | 0.023 | 0.130 | 0.174 | 0.221 | **0.186** | 0.012 |
| WA/OR/CA | **0.717** | 0.024 | 0.669 | 0.717 | 0.763 | **0.703** | 0.032 |
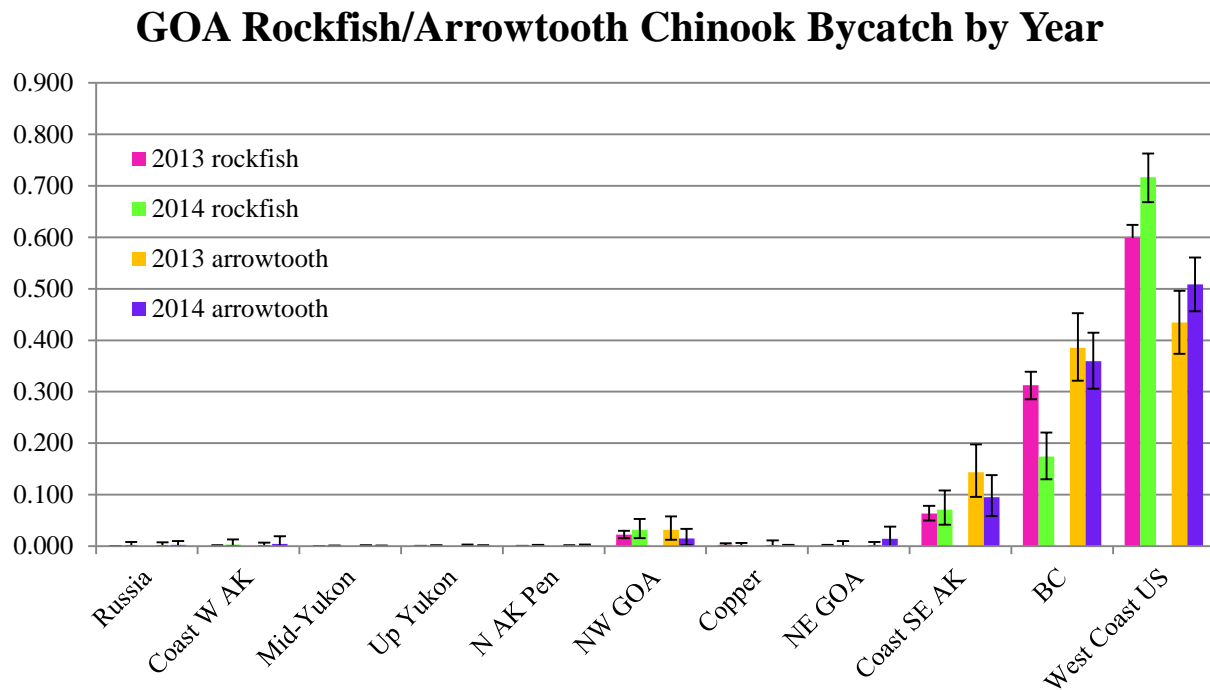


Figure 11. -- Comparison of stock composition estimates from Chinook salmon bycatch samples collected from the 2013 and 2014 GOA rockfish and arrowtooth trawl fishery.

Gulf of Alaska Arrowtooth Flounder Trawl Fishery

Stock composition estimates were made from the 404 Chinook salmon bycatch samples

collected throughout the 2014 GOA arrowtooth flounder trawl fishery from the catcher-

processors (CP) FV *Værdal* and FV *US Intrepid*. West Coast U.S. stocks (WA/OR/CA)

represented the largest stock grouping (51%) with smaller contributions from British Columbia

(36%), Coastal Southeast Alaska (10%), Northeast GOA (2%) and Northwest GOA (2%) stocks

(Table 12).  There were more West Coast U.S. (WA/OR/CA) (51% vs. 43%) and minutely less

British Columbia (36% vs. 38%) present in 2014 (Fig. 11), but the majority were from southern

regions (96%) in both years.

**Table 12**. -- Regional BAYES and SPAM stock composition estimates for the 404 genotyped
samples from the bycatch of the 2014 GOA arrowtooth trawl fishery. The BAYES
mean estimates are also provided with standard deviations (SD), 95% credible
intervals, and the median estimate. Standard deviations for the SPAM estimates were
determined by the analysis of 1,000 bootstrap resamplings of the mixture.

| Region | BAYES | SD | 2.5% | Median | 97.5% | SPAM | SD |
|---|---|---|---|---|---|---|---|
| Russia | **0.003** | 0.003 | 0.000 | 0.002 | 0.010 | **0.003** | 0.000 |
| Coast W AK | **0.005** | 0.006 | 0.000 | 0.003 | 0.019 | **0.006** | 0.003 |
| Mid-Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.001 | **0.002** | 0.000 |
| Up Yukon | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| N AK Penn | **0.000** | 0.001 | 0.000 | 0.000 | 0.003 | **0.000** | 0.000 |
| NW GOA | **0.015** | 0.008 | 0.002 | 0.014 | 0.034 | **0.017** | 0.003 |
| Copper | **0.000** | 0.001 | 0.000 | 0.000 | 0.002 | **0.000** | 0.000 |
| NE GOA | **0.015** | 0.010 | 0.000 | 0.014 | 0.038 | **0.017** | 0.001 |
| Coast SE AK | **0.095** | 0.020 | 0.058 | 0.094 | 0.138 | **0.067** | 0.004 |
| BC | **0.359** | 0.028 | 0.306 | 0.359 | 0.415 | **0.387** | 0.020 |
| WA/OR/CA | **0.509** | 0.027 | 0.456 | 0.509 | 0.561 | **0.500** | 0.025 |

SUMMARY

Communities in western Alaska and elsewhere are dependent on Chinook salmon for subsistence and commercial purposes. Decreasing Chinook salmon returns to western Alaska rivers have caused hardships in these communities and led to fisheries disaster declarations for Yukon River Chinook salmon in 2010 and 2012 by the U. S. Secretary of Commerce (Locke 2010, Blank 2012), and in the Kuskokwim Rivers, and Cook Inlet in 2012 (Blank 2012). Salmon-dependent communities have expressed concern regarding the numbers of salmon caught as bycatch in the Bering Sea trawl fishery (Gisclair 2009). The incidental harvest of Chinook salmon taken in the incidental catch from federally managed groundfish fisheries in the GOA averaged 21,718 salmon per year during 1991-2014, with an estimated peak of 54,607 in 2010. The bycatch from pollock trawl fishery is the largest component of the salmon bycatch in the GOA. In 2014, the GOA Chinook salmon bycatch was below the 24-year average in 2014 at 15,745 Chinook salmon of which 10,877 were estimated from the pollock trawl fishery and 4,868 from other fisheries including the rockfish and arrowtooth flounder trawl fisheries.

Stock composition estimates of the Chinook salmon bycatch are needed for pollock and salmon fishery managers to understand the biological effects of the incidental take of salmon in the trawl fishery. This report provides Chinook salmon bycatch stock composition analysis of genetic sample sets from the 2014 GOA federally managed trawl fisheries including the pollock, rockfish, and arrowtooth flounder fisheries. The results and limitations of these analyses are summarized below.

Sampling Issues

Due to efforts from the North Pacific Groundfish Observer Program and the many observers who collected samples, the number of available samples from the 2014 GOA pollock

trawl fishery was higher than in any previous year. As in analyses from 2012 and 2013 (Guyon et al. 2014, 2015a), efforts were made to normalize the available sample set to the size of the bycatch by area and season. The weighted stock composition was similar to the non-weighted stock composition and the resulting weighted estimate can be considered the current stock composition estimate for the bycatch from that fishery.

Similar to the 2013 rockfish CV trawl fishery in the central GOA, the fishing industry conducted a census approach in 2014 regarding the collection of genetic samples from every Chinook salmon encountered; consequently, the reported stock composition can be considered the overall stock composition for that fishery with the stipulation that samples were provided outside of the NMFS Observer System. While the sampling fraction was high, at this time stock composition estimates for the 2014 GOA CP arrowtooth flounder trawl fisheries should be considered point estimates since samples were collected opportunistically from two vessels participating in the fishery.

## Stock Composition Estimates

The derived stock composition estimates for Chinook salmon bycatch samples collected from federally managed trawl fisheries in the GOA continue to show that the vast majority of fish that are encountered derived from river systems that flow into the Gulf of Alaska and the Pacific Ocean.

## Application of These Estimates

The extent to which any salmon stock is impacted by the bycatch of the GOA 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 of the returning salmon, 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 contribution of a particular stock one year does not necessarily imply greater impact than a smaller contribution the next year.

## ACKNOWLEDGMENTS

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APPENDIX

Appendix. -- Chinook salmon populations in the ADF&G SNP baseline with the regional designations used in the analyses of this report. S.=South, R.=River, H.=Hatchery, and L.=Lake.

| Population name | Reg Num | Region Name | Population name | Reg Num | Region Name |
|---|---|---|---|---|---|
| Bistraya River | 1 | Russia | Henshaw Creek | 3 | Mid Yukon |
| Bolshaya River | 1 | Russia | Kantishna River | 3 | Mid Yukon |
| Kamchatka River late | 1 | Russia | Salcha River | 3 | Mid Yukon |
| Pakhatcha River | 1 | Russia | Sheenjek River | 3 | Mid Yukon |
| Andreafsky River | 2 | Coast W AK | S. Fork Koyukuk River | 3 | Mid Yukon |
| Aniak River | 2 | Coast W AK | Big Salmon River | 4 | Up Yukon |
| Anvik River | 2 | Coast W AK | Blind River | 4 | Up Yukon |
| Arolik River | 2 | Coast W AK | Chandindu River | 4 | Up Yukon |
| Big Creek | 2 | Coast W AK | Klondike River | 4 | Up Yukon |
| Cheeneetnuk River | 2 | Coast W AK | Little Salmon River | 4 | Up Yukon |
| Eek River | 2 | Coast W AK | Mayo River | 4 | Up Yukon |
| Gagaryah River | 2 | Coast W AK | Nisutlin River | 4 | Up Yukon |
| George River | 2 | Coast W AK | Nordenskiold River | 4 | Up Yukon |
| Gisasa River | 2 | Coast W AK | Pelly River | 4 | Up Yukon |
| Golsovia River | 2 | Coast W AK | Stewart River | 4 | Up Yukon |
| Goodnews River | 2 | Coast W AK | Takhini River | 4 | Up Yukon |
| Kanektok River | 2 | Coast W AK | Tatchun Creek | 4 | Up Yukon |
| Kisaralik River | 2 | Coast W AK | Whitehorse Hatchery | 4 | Up Yukon |
| Kogrukluk River | 2 | Coast W AK | Black Hills Creek | 5 | N AK Pen |
| Kwethluk River | 2 | Coast W AK | King Salmon River | 5 | N AK Pen |
| Mulchatna River | 2 | Coast W AK | Meshik River | 5 | N AK Pen |
| Naknek River | 2 | Coast W AK | Milky River | 5 | N AK Pen |
| Nushagak River | 2 | Coast W AK | Nelson River | 5 | N AK Pen |
| Pilgrim River | 2 | Coast W AK | Steelhead Creek | 5 | N AK Pen |
| Salmon R. -Pitka Fork | 2 | Coast W AK | Anchor River | 6 | NW GOA |
| Stony River | 2 | Coast W AK | Ayakulik River | 6 | NW GOA |
| Stuyahok River | 2 | Coast W AK | Benjamin Creek | 6 | NW GOA |
| Takotna River | 2 | Coast W AK | Chignik River | 6 | NW GOA |
| Tatlawiksuk River | 2 | Coast W AK | Crescent Creek | 6 | NW GOA |
| Togiak River | 2 | Coast W AK | Crooked Creek | 6 | NW GOA |
| Tozitna River | 2 | Coast W AK | Deception Creek | 6 | NW GOA |
| Tuluksak River | 2 | Coast W AK | Deshka River | 6 | NW GOA |
| Unalakleet River | 2 | Coast W AK | Funny River | 6 | NW GOA |
| Beaver Creek | 3 | Mid Yukon | Juneau Creek | 6 | NW GOA |
| Chandalar River | 3 | Mid Yukon | Karluk River | 6 | NW GOA |
| Chena River | 3 | Mid Yukon | Kasilof River mainstem | 6 | NW GOA |

| Population name | Reg Num | Region Name | Population name | Reg Num | Region Name |
|---|---|---|---|---|---|
| Kenai River mainstem | 6 | NW GOA | Kowatua River | 9 | Coast SE AK |
| Killey Creek | 6 | NW GOA | Little Tatsemenie River | 9 | Coast SE AK |
| Ninilchik River | 6 | NW GOA | Macaulay Hatchery | 9 | Coast SE AK |
| Prairie Creek | 6 | NW GOA | Medvejie Hatchery | 9 | Coast SE AK |
| Slikok Creek | 6 | NW GOA | Nakina River | 9 | Coast SE AK |
| Talachulitna River | 6 | NW GOA | Tahltan River | 9 | Coast SE AK |
| Willow Creek | 6 | NW GOA | Unuk R.-Deer Mountain H. | 9 | Coast SE AK |
| Bone Creek | 7 | Copper | Unuk River - LPW | 9 | Coast SE AK |
| E. Fork Chistochina River | 7 | Copper | Upper Nahlin River | 9 | Coast SE AK |
| Gulkana River | 7 | Copper | Big Qualicum River | 10 | BC |
| Indian River | 7 | Copper | Birkenhead River spring | 10 | BC |
| Kiana Creek | 7 | Copper | Bulkley River | 10 | BC |
| Manker Creek | 7 | Copper | Chilko River summer | 10 | BC |
| Mendeltna Creek | 7 | Copper | Clearwater River summer | 10 | BC |
| Otter Creek | 7 | Copper | Conuma River | 10 | BC |
| Sinona Creek | 7 | Copper | Damdochax Creek | 10 | BC |
| Tebay River | 7 | Copper | Ecstall River | 10 | BC |
| Tonsina River | 7 | Copper | Harrison River | 10 | BC |
| Big Boulder Creek | 8 | NE GOA | Kateen River | 10 | BC |
| Kelsall River | 8 | NE GOA | Kincolith Creek | 10 | BC |
| King Salmon River | 8 | NE GOA | Kitimat River | 10 | BC |
| Klukshu River | 8 | NE GOA | Klinaklini River | 10 | BC |
| Situk River | 8 | NE GOA | Kwinageese Creek | 10 | BC |
| Tahini River | 8 | NE GOA | Louis River spring | 10 | BC |
| Tahini River - Pullen Creek H. | 8 | NE GOA | Lower Adams River fall | 10 | BC |
| Andrews Creek | 9 | Coast SE AK | Lower Atnarko River | 10 | BC |
| Blossom River | 9 | Coast SE AK | Lower Kalum River | 10 | BC |
| Butler Creek | 9 | Coast SE AK | Lower Thompson River fall | 10 | BC |
| Chickamin River | 9 | Coast SE AK | Marble Creek | 10 | BC |
| Chickamin River-LPW | 9 | Coast SE AK | Middle Shuswap R. summer | 10 | BC |
| Chickamin R.Whitman L. H. | 9 | Coast SE AK | Morkill River summer | 10 | BC |
| Clear Creek | 9 | Coast SE AK | Nanaimo River | 10 | BC |
| Cripple Creek | 9 | Coast SE AK | Nechako River summer | 10 | BC |
| Crystal Lake Hatchery | 9 | Coast SE AK | Nitinat River | 10 | BC |
| Dudidontu River | 9 | Coast SE AK | Oweegee Creek | 10 | BC |
| Genes Creek | 9 | Coast SE AK | Porteau Cove | 10 | BC |
| Hidden Falls Hatchery | 9 | Coast SE AK | Quesnel River summer | 10 | BC |
| Humpy Creek | 9 | Coast SE AK | Quinsam River | 10 | BC |
| Kerr Creek | 9 | Coast SE AK | Robertson Creek | 10 | BC |
| Keta River | 9 | Coast SE AK | Salmon River summer | 10 | BC |
| King Creek | 9 | Coast SE AK | Sarita River | 10 | BC |

| Population name | Reg Num | Region Name | Population name | Reg Num | Region Name |
|---|---|---|---|---|---|
| Stuart River summer | 10 | BC | Lower Deschutes R. fall | 11 | West Coast US |
| Sustut River | 10 | BC | Lyons Ferry H. summer/fall | 11 | West Coast US |
| Torpy River summer | 10 | BC | Makah National Fish H. fall | 11 | West Coast US |
| Wannock River | 10 | BC | McKenzie River spring | 11 | West Coast US |
| Alsea River fall | 11 | West Coast US | Sacramento River winter | 11 | West Coast US |
| Carson Hatchery spring | 11 | West Coast US | Siuslaw River fall | 11 | West Coast US |
| Eel River fall | 11 | West Coast US | Soos Creek Hatchery fall | 11 | West Coast US |
| Forks Creek fall | 11 | West Coast US | Upper Skagit River summer | 11 | West Coast US |
| Hanford Reach | 11 | West Coast US | | | |
| Klamath River | 11 | West Coast US | | | |

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