

Genetic Stock Composition Analysis of Chinook Salmon Bycatch Samples from the 2015 Gulf of Alaska Trawl Fisheries

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Genetic Stock Composition Analysis of Chinook Salmon Bycatch Samples from the 2015 Gulf of Alaska Trawl Fisheries

C. M. Guthrie III, Hv. T. Nguyen, A. E. Thomson, and J. R. Guyon

Auke Bay Laboratories
Alaska Fisheries Science Center
National Marine Fisheries Service
National Oceanic and Atmospheric Administration
7600 Sand Point Way NE
Seattle, WA 98115-6349

U.S. DEPARTMENT OF COMMERCE

VACANT, Secretary

National Oceanic and Atmospheric Administration
Benjamin Friedman, Acting Under Secretary and Administrator
National Marine Fisheries Service
Samuel D. Rauch III, Acting Assistant Administrator for Fisheries

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ABSTRACT

A genetic analysis of samples from the Chinook salmon (Oncorhynchus tshawytscha) bycatch of the 2015 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 2015, 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 second year for this sampling protocol and resulted in the largest available genetic sample set to date with 17.8% of the salmon bycatch successfully genotyped. Based on the analysis of 2,414 Chinook salmon bycatch samples, British Columbia (51%), West Coast U.S. (32%), Coastal Southeast Alaska (14%), and Northwest Gulf of Alaska stocks (3%) comprised the largest stock groups. In 2015, genetic samples from the bycatch of the GOA rockfish catcher vessel (CV) fishery were collected by the fishing industry using a census sampling protocol where every Chinook salmon encountered was sampled. Based on the genotyping of 635 Chinook salmon bycatch samples collected from the 2015 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 (73%) with smaller contributions from British Columbia (19%), Coastal Southeast Alaska (5%), and Northwest GOA (3%) stocks. Based on the genotyping of 300 Chinook salmon bycatch samples collected throughout the 2015 GOA arrowtooth flounder trawl fishery from the catcherprocessors (CP), West Coast U.S. stocks (WA/OR/CA) represented the largest stock grouping

(47%) with smaller contributions from British Columbia (38%), Coastal Southeast Alaska (12%), and Northwest GOA (1%) stocks.

CONTENTS

ABSTRACT	iii
CONTENTS	
INTRODUCTION	
SAMPLE DISTRIBUTION	2
GENETIC STOCK COMPOSITION - PROCEDURE	
GENETIC STOCK COMPOSITION - RESULTS	10
SUMMARY	
Sampling Issues	
Stock Composition Estimates	
Application of These Estimates	
ACKNOWLEDGMENTS	
CITATIONS	29
APPENDIX	31

INTRODUCTION

The Gulf of Alaska (GOA) is known as a 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 Chinook salmon bycatch samples collected in the GOA from the (1) trawl fisheries for walleye pollock (*Gadus chalcogrammus*), (2) catcher vessel (CV) trawl fisheries for rockfish (*Sebastes* spp.), and (3) catcher-processor (CP) trawl fisheries for arrowtooth flounder (*Atheresthes* stomias). The National Marine Fisheries Service (NMFS) geographical statistical

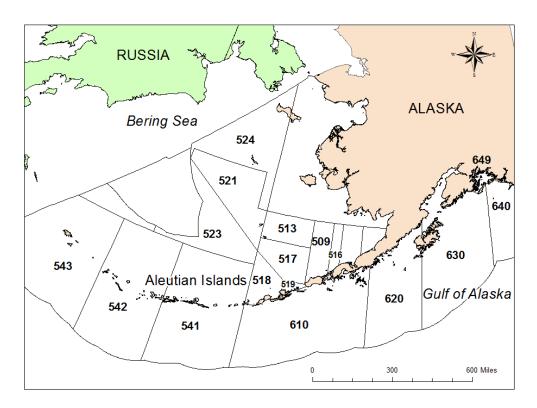


Figure 1. -- NMFS statistical areas associated with the Bering Sea-Aleutian Island (BSAI – Areas 509-543) and Gulf of Alaska (GOA – Areas 610-649) groundfish fisheries.

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 2015 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, 2016; 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

GOA 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 (NPGOP) 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 2015 from the GOA. Axillary process tissues were stored in coin envelopes which were labeled, frozen, and shipped to the AFSC's 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 (38) 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 2015, an estimated 13,612 Chinook salmon were taken as bycatch in the GOA pollock trawl fisheries (NMFS 2016). 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 2015 Chinook salmon bycatch was 2,414 fish, corresponding to a sampling rate of 17.7%. 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.

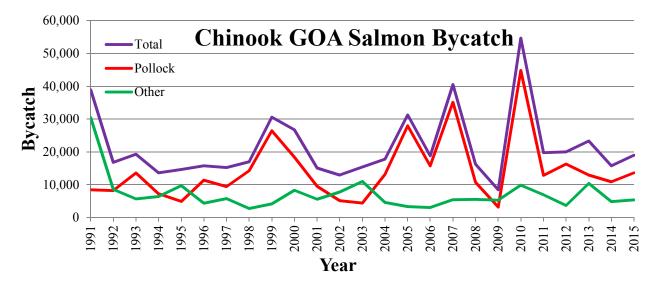


Figure 2. -- Yearly estimates for the Chinook salmon bycatch from the Gulf of Alaska (GOA) trawl fisheries (NMFS 2016).

Potential spatial and temporal biases associated with the 2015 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).

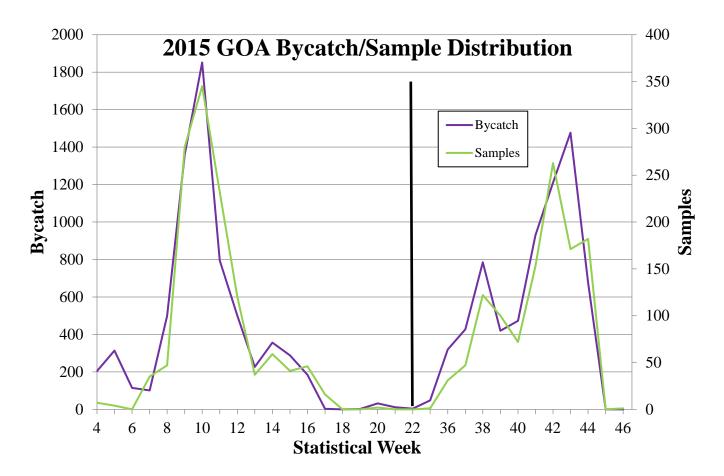
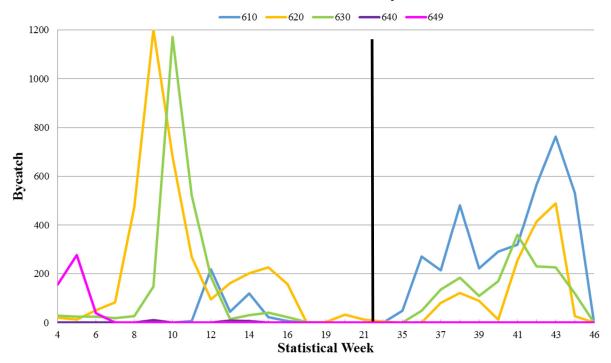


Figure 3.-- Number of Chinook salmon bycatch and genetic samples by statistical week. Distribution of all Chinook salmon caught in the 2015 Gulf of Alaska (GOA) pollock trawl fishery versus the distribution of the 2,414 genotyped samples from the 2015 bycatch. Bycatch from Areas 640 (n = 20) and 649 (n = 471) were omitted since they were not sampled. The line separates weeks 22 and 35 when no fishing occurred.

2015 Chinook GOA Bycatch



2015 Chinook GOA Samples

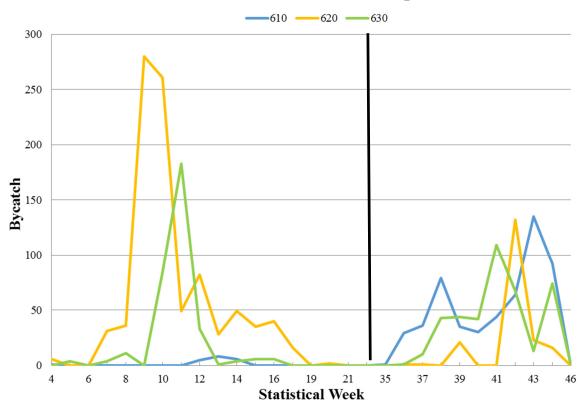


Figure 4. -- Comparison of the Chinook salmon bycatch by time and area with the distribution of available genetic samples. Top panel: Distribution of the estimated Chinook salmon caught in the 2015 Gulf of Alaska (GOA) pollock trawl fishery. Bottom panel: Distribution of the 2,414 genotyped samples from the 2015 bycatch. The line separates weeks 22 and 35 when no fishing occurred.

GOA Rockfish CV Trawl Fishery

Samples were collected from the Chinook salmon bycatch of the federally managed 2015 Alaska GOA CV rockfish trawl fishery 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), 2014 (Guthrie et al. 2016) and 2015 whereby genetic samples (axillary processes) and biological information were collected from every Chinook salmon encountered in the bycatch. Axillary process (AXP) tissues were stored in coin envelopes which were labeled, frozen, and shipped to the ABL. Between 4 May and 16 November 2015 (week numbers 19-47), genetic samples were collected from 638 Chinook salmon. Because samples were taken from the overall bycatch, the sample distribution is considered to be the bycatch distribution. The bycatch enumeration by statistical week is shown in Figure 5 and the sample collection area is approximated in Figure 6.

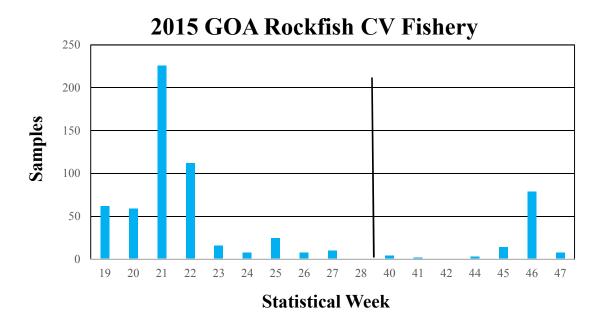


Figure 5. -- Genetic samples collected by Alaska Groundfish Data Bank from the census of the Chinook salmon bycatch in the 2015 Gulf of Alaska (GOA) rockfish catcher vessel (CV) trawl fishery plotted by statistical week. The line shows the demarcation between weeks 28 and 40 when there was no Chinook salmon bycatch.

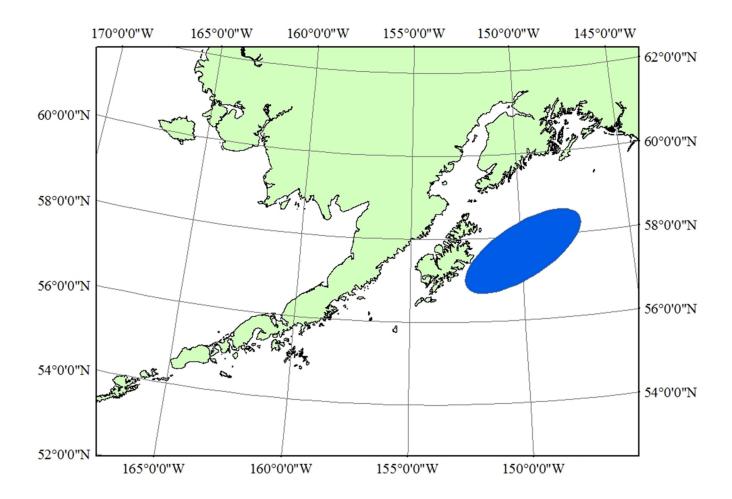


Figure 6. -- Relative location of the 638 Chinook salmon bycatch samples collected in NMFS Statistical Areas 620 and 630 by Alaska Groundfish Data Bank in the 2015 Gulf of Alaska rockfish trawl fishery.

GOA non-pollock CP Trawl Fishery

Samples were collected from the Chinook salmon bycatch of the federally managed 2015

Alaska GOA non-pollock catcher-processors (CP) trawl fisheries by the Alaska Seafood

Cooperative for analysis at ABL. Most of these samples were taken from the arrowtooth flounder fishery. Although there was no requirement for sample collection, the Alaska Seafood

Cooperative implemented an opportunistic sampling approach in 2015 to collect genetic samples (AXP) 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 17 November 2015 (NMFS Statistical Weeks 15 and 47), 365 Chinook salmon were sampled from catcher-processors in the arrowtooth flounder (323) and other non-pollock trawl (42) fisheries. Because samples were taken opportunistically from these vessels, the sample distribution is not considered representative of the entire bycatch but is used to indicate presence/absence of particular Chinook salmon stocks. The sample collection area for these fisheries is approximated in Figure 7.

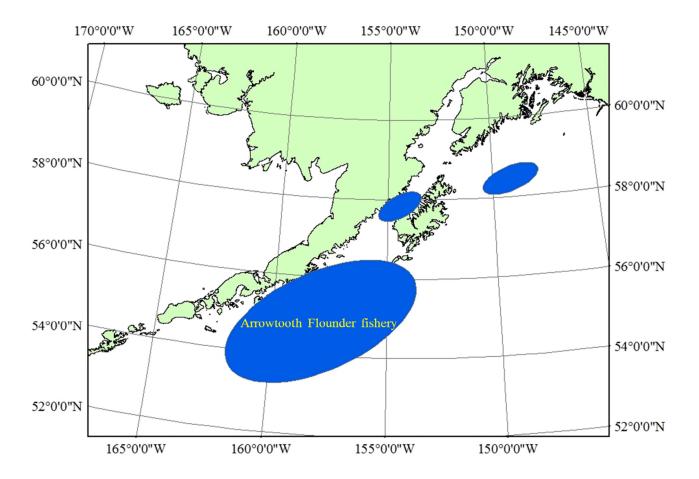


Figure 7. -- Approximate location 365 Chinook salmon bycatch samples collected by the catcher-processors of the Alaska Seafood Cooperative in the 2015 Gulf of Alaska non-pollock trawl fishery. The arrowtooth flounder trawl fishery (323 samples) is the western most group.

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, 2016; 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 2015 controls confirmed the utility and compatibility of both genotyping methods.

From the Chinook salmon bycatch from the 2015 GOA pollock trawl fishery, a total of 2,608 samples were analyzed of which 2,414 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 93%. The remaining samples had genetic information for an average of 41.6 of 43 markers.

From the Chinook salmon bycatch from the 2015 GOA rockfish CV trawl fishery, a total of 638 samples were analyzed of which 635 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 99.5%. The remaining samples had genetic information for an average of 42.3 of 43 markers.

From the Chinook salmon bycatch from the 2015 GOA CP trawl non-pollock trawl fishery, a total of 365 samples from the were analyzed of which 342 samples were successfully

genotyped for 35 or more of the 43 SNP loci, a success rate of 94%. The remaining samples had genetic information for an average of 41.9 of 43 markers.

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 1.05 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 99.94% of the 2,414 samples from the GOA originated from GOA/Pacific coastal regions, with the British Columbia grouping contributing

the most (51%), followed by the West Coast US (32%), Coastal Southeast Alaska (14%), and Northwest GOA (3%) (Table 1). The sample distribution was similar to the overall distribution (Figs. 3 and 4); except for the lack of samples from NMFS areas 640/649. Although care must be taken when comparing estimates across years due to the differences in sampling, the stock composition estimates in 2015 were very similar to that seen for previous years (Fig. 8).

Table 1. -- Regional BAYES and SPAM stock composition estimates for the 2,414 Chinook salmon samples from the bycatch of the 2015 Gulf of Alaska 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	<u>SD</u>	<u>2.5%</u>	Median	<u>97.5%</u>	SPAM	<u>SD</u>
Russia	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Coast W AK	0.000	0.001	0.000	0.000	0.003	0.001	0.000
Mid-Yukon	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Up Yukon	0.000	0.000	0.000	0.000	0.000	0.000	0.000
N AK Penn	0.000	0.001	0.000	0.000	0.002	0.001	0.000
NW GOA	0.026	0.004	0.019	0.026	0.033	0.025	0.001
Copper	0.001	0.001	0.000	0.001	0.004	0.002	0.000
NE GOA	0.002	0.001	0.000	0.001	0.005	0.003	0.000
Coast SE AK	0.136	0.009	0.119	0.136	0.154	0.134	0.003
BC	0.514	0.013	0.488	0.514	0.539	0.515	0.010
WA/OR/CA	0.321	0.011	0.300	0.321	0.343	0.320	0.008

Using information from a new tool provided by AKFIN (NMFS 2015), we were also able look at different temporal and the geographical (ADF&G statistical areas) differences which provided greater spatial precision than the NMFS statistical areas. We looked at seven different bycatch sample strata using this tool: Shumagin Islands (Fig. 9, Table 2); Shelikof Strait (SS) early, late, and overall (Fig. 10, Tables 3-5), and Southeast Kodiak Island (SKI) early, late, overall (Fig. 11, Tables 6-8). The western-most stratum, Shumagin Islands had the largest stock estimates from British Columbia (61%) with smaller components from the West Coast US

GOA Chinook Bycatch by Year

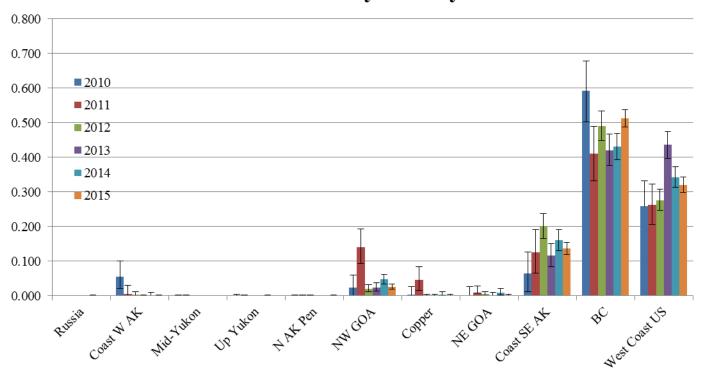


Figure 8. -- Comparison of yearly stock composition estimates (2010-2015) based on available genetic samples from the Gulf of Alaska (GOA) Chinook salmon bycatch. The same genetic baseline and general regional groupings were used in all analyses. BAYES 95% credible intervals are plotted for yearly estimates.

(21%), Coastal Southeast Alaska (14%) and Northwest GOA (3%) (Table 2) (Fig. 9). The BAYES estimates for the SS early (statistical weeks 7-17) showed British Columbia contributed the most (54%), followed by West Coast US (30%) and Coastal Southeast Alaska (14%) (Table 3). For the late season (statistical weeks 37-44), the West Coast US (54%) predominated, followed by British Columbia (24%), Coastal Southeast Alaska (16%), and Northwest GOA (5%) (Table 4). For overall SS British Columbia contributed the most (48%), followed by West Coast US (35%) and Coastal Southeast Alaska (14%) (Table 5). A comparison of SS early and SS late shows spatial stock differences between British Columbia (54% vs. 24%) and the West Coast US (30% vs. 54%) estimates (Fig. 12, Tables 3 and 4).

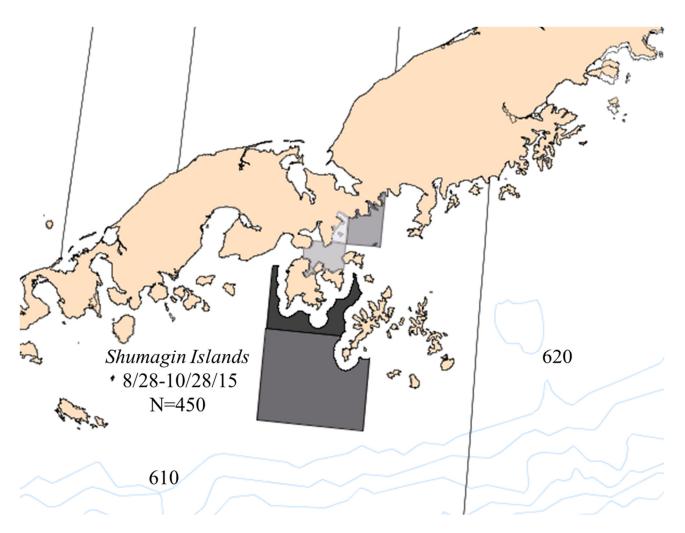


Figure 9. -- Location of the Shumagin Islands stratum used in comparative stock composition estimates from the 2015 Gulf of Alaska Chinook salmon bycatch (NMFS 2015).

Looking at the SKI early, late, overall strata, the stock estimates were similar (Fig. 12, Tables 6-8) with British Columbia composition estimates the largest (48%, 43%, and 47%) followed by those from the West Coast US (38%, 36%, and 37%), and Coastal Southeast Alaska (14%, 16%, and 14%), respectively. Northwest GOA were absent from SKI early (Table 5, Fig. 12) but are present in late samples (4%) (Table 6, Fig. 12).

Table 2. -- Regional BAYES and SPAM stock composition estimates for the 450 Chinook salmon samples from the bycatch of the 2015 Gulf of Alaska pollock trawl fishery from around the Shumagin Islands. 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	<u>SD</u>	<u>2.5%</u>	Median	<u>97.5%</u>	SPAM	SD
Russia	0.000	0.001	0.000	0.000	0.002	0.001	0.000
Coast W AK	0.002	0.003	0.000	0.000	0.010	0.005	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	0.002	0.000
NW GOA	0.032	0.009	0.016	0.031	0.051	0.026	0.004
Copper	0.000	0.001	0.000	0.000	0.002	0.000	0.000
NE GOA	0.000	0.001	0.000	0.000	0.003	0.005	0.000
Coast SE AK	0.142	0.026	0.094	0.141	0.196	0.123	0.006
BC	0.612	0.033	0.547	0.613	0.675	0.631	0.028
WA/OR/CA	0.211	0.021	0.172	0.211	0.254	0.208	0.014

Table 3. -- Regional BAYES and SPAM stock composition estimates for the 918 Chinook salmon samples from the bycatch of the 2015 Gulf of Alaska pollock trawl fishery from early season (2/14-4/20/15) in Shelikof Strait. 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	<u>SD</u>	2.5%	Median	97.5%	SPAM	<u>SD</u>
Russia	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Coast W AK	0.002	0.002	0.000	0.000	0.008	0.002	0.001
Mid-Yukon	0.000	0.000	0.000	0.000	0.001	0.000	0.000
Up Yukon	0.000	0.000	0.000	0.000	0.001	0.000	0.000
N AK Penn	0.000	0.001	0.000	0.000	0.001	0.000	0.000
NW GOA	0.021	0.005	0.011	0.020	0.032	0.018	0.002
Copper	0.000	0.001	0.000	0.000	0.003	0.003	0.000
NE GOA	0.000	0.001	0.000	0.000	0.004	0.001	0.000
Coast SE AK	0.140	0.014	0.114	0.140	0.168	0.131	0.005
BC	0.535	0.020	0.497	0.535	0.574	0.550	0.018
WA/OR/CA	0.301	0.017	0.268	0.301	0.335	0.295	0.013

Table 4. -- Regional BAYES and SPAM stock composition estimates for the 225 Chinook salmon samples from the bycatch of the 2015 Gulf of Alaska pollock trawl fishery from late season in Shelikof Strait. 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	<u>SD</u>	<u>2.5%</u>	Median	<u>97.5%</u>	SPAM	<u>SD</u>
Russia	0.000	0.001	0.000	0.000	0.002	0.000	0.000
Coast W AK	0.003	0.004	0.000	0.001	0.015	0.004	0.001
Mid-Yukon	0.001	0.003	0.000	0.000	0.010	0.004	0.000
Up Yukon	0.000	0.001	0.000	0.000	0.004	0.000	0.000
N AK Penn	0.001	0.002	0.000	0.000	0.007	0.007	0.001
NW GOA	0.048	0.015	0.022	0.046	0.080	0.042	0.006
Copper	0.004	0.005	0.000	0.003	0.017	0.005	0.005
NE GOA	0.008	0.007	0.000	0.006	0.027	0.009	0.001
Coast SE AK	0.159	0.028	0.107	0.158	0.217	0.141	0.009
BC	0.237	0.033	0.175	0.236	0.305	0.249	0.020
WA/OR/CA	0.540	0.035	0.470	0.540	0.608	0.540	0.035

Table 5. -- Regional BAYES and SPAM stock composition estimates for the 1,179 Chinook salmon samples from the bycatch of the 2015 Gulf of Alaska pollock trawl fishery from Shelikof Strait. 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	<u>SD</u>	2.5%	Median	97.5%	SPAM	SD
Russia	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Coast W AK	0.002	0.002	0.000	0.001	0.007	0.002	0.000
Mid-Yukon	0.000	0.000	0.000	0.000	0.001	0.001	0.000
Up Yukon	0.000	0.000	0.000	0.000	0.001	0.000	0.000
N AK Penn	0.000	0.000	0.000	0.000	0.001	0.000	0.000
NW GOA	0.024	0.005	0.015	0.024	0.035	0.024	0.002
Copper	0.001	0.001	0.000	0.001	0.005	0.003	0.000
NE GOA	0.002	0.002	0.000	0.001	0.006	0.003	0.000
Coast SE AK	0.141	0.012	0.118	0.141	0.166	0.133	0.004
BC	0.484	0.018	0.450	0.484	0.519	0.493	0.014
WA/OR/CA	0.346	0.016	0.315	0.345	0.376	0.342	0.012

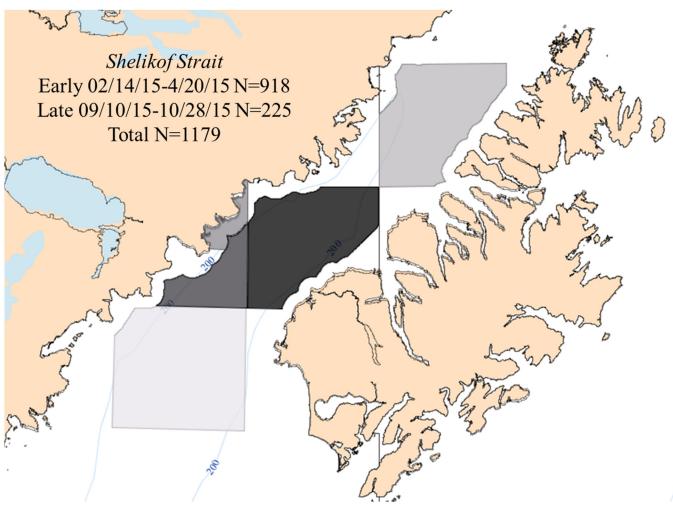


Figure 10. -- Location of the Shelikof Strait strata used in comparative stock composition estimates from the 2015 Gulf of Alaska Chinook salmon bycatch (NMFS 2015).

Table 6. -- Regional BAYES and SPAM stock composition estimates for the 262 Chinook salmon samples from the bycatch of the 2015 Gulf of Alaska pollock trawl fishery from early season offshore of Southeast Kodiak. 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	<u>SD</u>	<u>2.5%</u>	Median	<u>97.5%</u>	SPAM	<u>SD</u>
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	0.000	0.000
Up Yukon	0.000	0.001	0.000	0.000	0.003	0.000	0.000
N AK Penn	0.000	0.001	0.000	0.000	0.002	0.000	0.000
NW GOA	0.001	0.001	0.000	0.000	0.004	0.000	0.000
Copper	0.000	0.001	0.000	0.000	0.003	0.000	0.000
NE GOA	0.000	0.001	0.000	0.000	0.003	0.007	0.001
Coast SE AK	0.135	0.027	0.085	0.134	0.189	0.123	0.008
BC	0.483	0.036	0.412	0.483	0.554	0.493	0.031
WA/OR/CA	0.380	0.032	0.319	0.380	0.443	0.377	0.026

Table 7. -- Regional BAYES and SPAM stock composition estimates for the 304 Chinook salmon samples from the bycatch of the 2015 Gulf of Alaska pollock trawl fishery from late season offshore of Southeast Kodiak. 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	<u>SD</u>	2.5%	Median	<u>97.5%</u>	SPAM	<u>SD</u>
Russia	0.000	0.001	0.000	0.000	0.001	0.000	0.000
Coast W AK	0.006	0.006	0.000	0.004	0.023	0.003	0.001
Mid-Yukon	0.000	0.001	0.000	0.000	0.003	0.000	0.000
Up Yukon	0.000	0.001	0.000	0.000	0.003	0.000	0.000
N AK Penn	0.002	0.004	0.000	0.000	0.013	0.007	0.000
NW GOA	0.036	0.013	0.015	0.035	0.064	0.027	0.003
Copper	0.003	0.005	0.000	0.000	0.018	0.009	0.005
NE GOA	0.001	0.002	0.000	0.000	0.008	0.001	0.000
Coast SE AK	0.158	0.026	0.109	0.157	0.210	0.136	0.008
BC	0.434	0.034	0.368	0.434	0.503	0.457	0.027
WA/OR/CA	0.360	0.029	0.304	0.360	0.419	0.360	0.024

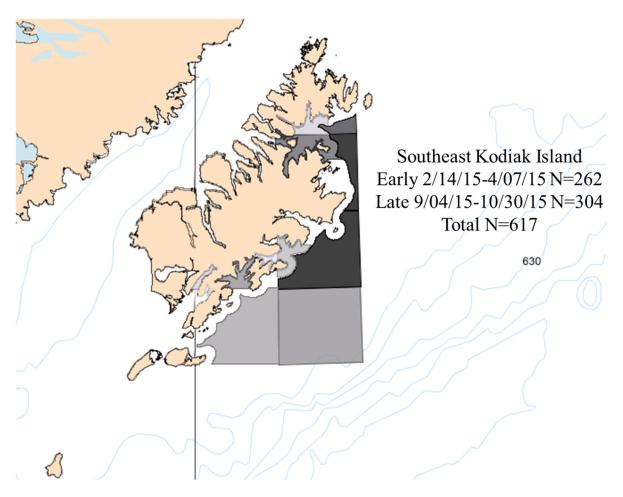


Figure 11. -- Location of the Kodiak Island strata used in comparative stock composition estimates from the 2015 Gulf of Alaska Chinook salmon bycatch (NMFS 2015).

Table 8. -- Regional BAYES and SPAM stock composition estimates for the 566 Chinook salmon samples from the bycatch of the 2015 Gulf of Alaska pollock trawl fishery from offshore of Southeast Kodiak. 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	<u>SD</u>	<u>2.5%</u>	Median	<u>97.5%</u>	SPAM	SD
Russia	0.000	0.000	0.000	0.000	0.001	0.000	0.000
Coast W AK	0.003	0.004	0.000	0.002	0.012	0.002	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	0.001	0.002	0.000	0.000	0.007	0.004	0.000
NW GOA	0.019	0.007	0.008	0.019	0.035	0.014	0.001
Copper	0.001	0.002	0.000	0.000	0.009	0.005	0.002
NE GOA	0.000	0.002	0.000	0.000	0.005	0.004	0.000
Coast SE AK	0.138	0.019	0.103	0.137	0.176	0.132	0.006
BC	0.470	0.025	0.420	0.470	0.520	0.474	0.020
WA/OR/CA	0.367	0.022	0.325	0.367	0.411	0.367	0.017

GOA by Area and Time Comparison

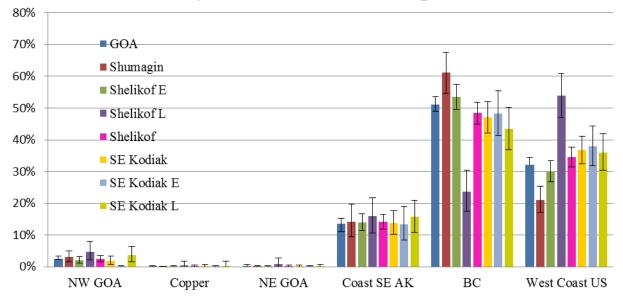


Figure 12. -- Comparison of area and time strata of stock composition estimates from the 2015 Gulf of Alaska (GOA) Chinook salmon bycatch: All (2414 samples), Shumagin Islands (450 samples, Fig. 9), Shelikof Strait (Fig. 10); Early (918), Late (225), and overall (1179), and Southeast Kodiak Island (Fig. 11); overall (566), Early (262), and Late (304). BAYES 95% credible intervals are plotted for yearly estimates.

Gulf of Alaska Rockfish CV Trawl Fishery

The stock composition results indicate that almost all of the 635 Chinook salmon samples from the bycatch of the 2015 GOA rockfish CV trawl fishery originated from GOA/Pacific coastal regions (99.9%), with the West Coast U.S. (WA/OR/CA) contributing the most (73%) with smaller contributions from British Columbia (19%), Coastal Southeast Alaska (5%), and Northwest GOA (3%) stocks (Table 9). The results were almost identical to 2014; West Coast U.S. (WA/OR/CA) (73% vs. 72%) and British Columbia (17%) (Fig. 11), the majority both years being from GOA/Pacific coastal regions (99.9% and 99.5%). The 2015 results differed in comparison to 2013 with more West Coast U.S. (WA/OR/CA) (73% vs. 60%) and less British Columbia (17% vs. 31%) present (Fig. 13).

Table 9. -- Regional BAYES and SPAM stock composition estimates for the 635 genotyped samples from the bycatch of the 2015 Gulf of Alaska rockfish catcher vessel 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	<u>SD</u>	<u>2.5%</u>	Median	<u>97.5%</u>	SPAM	<u>SD</u>
Russia	0.000	0.000	0.000	0.000	0.000	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	0.000	0.000	0.000	0.001	0.000	0.000
Up Yukon	0.000	0.000	0.000	0.000	0.001	0.000	0.000
N AK Penn	0.000	0.001	0.000	0.000	0.001	0.000	0.000
NW GOA	0.027	0.007	0.015	0.026	0.042	0.026	0.002
Copper	0.008	0.004	0.002	0.007	0.017	0.009	0.002
NE GOA	0.000	0.001	0.000	0.000	0.002	0.000	0.000
Coast SE AK	0.048	0.010	0.030	0.047	0.069	0.047	0.002
BC	0.189	0.018	0.155	0.189	0.225	0.182	0.009
WA/OR/CA	0.728	0.019	0.689	0.728	0.765	0.736	0.025

GOA Rockfish/Arrowtooth Chinook Bycatch by Year

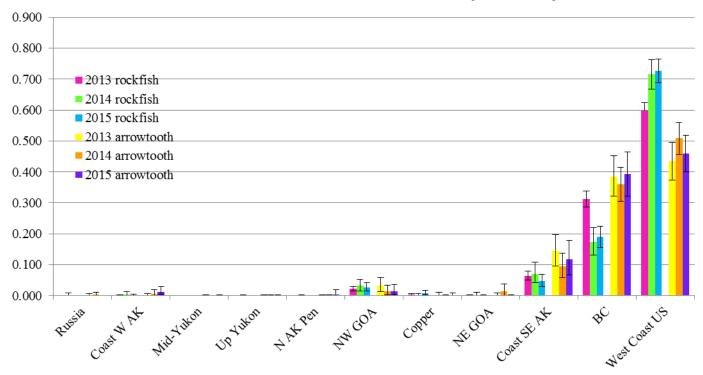


Figure 13. -- Comparison of stock composition estimates from Chinook salmon bycatch samples collected from the 2013, 2014 and 2015 Gulf of Alaska rockfish and arrowtooth trawl fishery.

Gulf of Alaska non-pollock CP Trawl Fishery

Stock composition estimates were made from the 342 Chinook salmon bycatch samples collected throughout the 2015 GOA non-pollock trawl fishery from the catcher-processors (CP). West Coast U.S. stocks (WA/OR/CA) represented the largest stock grouping (46%) with smaller contributions from British Columbia (39%), Coastal Southeast Alaska (12%), and Northwest GOA (2%) stocks (Table 10). Arrowtooth flounder was the target species for 300 of these samples, for which stock composition estimates were made. For arrowtooth only, West Coast U.S. stocks (WA/OR/CA) represented the largest stock grouping (47%) with smaller contributions from British Columbia (38%), Coastal Southeast Alaska (12%), and Northwest GOA (1%) stocks (Table 11). There were less West Coast U.S. (WA/OR/CA) (47% vs. 51%)

and the same amount British Columbia (38%) present in 2015 when compared to 2014 (Fig. 13), but the majority were from GOA/Pacific coastal regions (98.8% to (99.9%) in all years.

Table 10. -- Regional BAYES and SPAM stock composition estimates for the 342 genotyped samples from the bycatch of the 2015 Gulf of Alaska catcher-processor non-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	<u>2.5%</u>	Median	<u>97.5%</u>	SPAM	<u>SD</u>
Russia	0.000	0.000	0.000	0.000	0.001	0.000	0.000
Coast W AK	0.011	0.010	0.000	0.009	0.033	0.003	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	0.003	0.000	0.000
N AK Penn	0.003	0.005	0.000	0.001	0.016	0.003	0.000
NW GOA	0.015	0.010	0.000	0.013	0.038	0.020	0.001
Copper	0.001	0.002	0.000	0.000	0.006	0.005	0.000
NE GOA	0.001	0.002	0.000	0.000	0.007	0.003	0.000
Coast SE AK	0.117	0.028	0.068	0.116	0.175	0.105	0.006
BC	0.393	0.035	0.326	0.393	0.461	0.394	0.022
WA/OR/CA	0.459	0.028	0.405	0.459	0.514	0.467	0.026

Table 11. -- Regional BAYES and SPAM stock composition estimates for the 300 genotyped samples from the bycatch of the 2015 Gulf of Alaska catcher-processor arrowtooth flounder 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	<u>SD</u>	<u>2.5%</u>	Median	<u>97.5%</u>	SPAM	<u>SD</u>
Russia	0.000	0.001	0.000	0.000	0.001	0.000	0.000
Coast W AK	0.007	0.008	0.000	0.005	0.026	0.003	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	0.003	0.000	0.000
N AK Penn	0.005	0.006	0.000	0.002	0.020	0.004	0.000
NW GOA	0.013	0.009	0.000	0.012	0.035	0.013	0.001
Copper	0.001	0.002	0.000	0.000	0.008	0.007	0.000
NE GOA	0.000	0.001	0.000	0.000	0.003	0.000	0.000
Coast SE AK	0.124	0.029	0.073	0.122	0.187	0.109	0.007
BC	0.378	0.036	0.306	0.378	0.448	0.392	0.024
WA/OR/CA	0.472	0.030	0.413	0.472	0.530	0.473	0.028

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 1991-2015, 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 2015, the GOA Chinook salmon bycatch was below the 25-year average of 21,499 in 2015 at 18,973 Chinook salmon of which 13,612 were estimated from the pollock trawl fishery and 5,361 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 2015 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 2015 GOA pollock trawl fishery was higher than in any previous year, representing almost 18% of the total bycatch. The samples in 2015 were collected in similar proportions to the overall bycatch (Fig. 3), although small differences in spatial and temporal distributions remain (Fig. 4). Because the sample set represents such a large proportion of the total bycatch, and stock compositions separated spatially within seasons were very similar (Fig. 12), the overall estimate can be considered the bycatch stock composition from the 2015 GOA pollock trawl fishery.

Similar to the 2013 and 2014 GOA rockfish CV trawl fisheries, the fishing industry conducted a census approach in 2015 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. Stock composition estimates for the 2015 GOA CP arrowtooth flounder trawl fisheries should be considered point estimates as samples were collected by industry from 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 estimate the next.

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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.

	Reg			Reg	
Population name	num.	Region	Population name	num.	Region
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 RPitka 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

Reg Reg Population name num. Region Population name num. Region	
Population name num. Region Population name num. Region	
·	A TZ
Prairie Creek 6 NW GOA Medvejie Hatchery 9 Coast SE	
Slikok Creek 6 NW GOA Nakina River 9 Coast SE	
Talachulitna River 6 NW GOA Tahltan River 9 Coast SE	
Willow Creek 6 NW GOA Unuk RDeer Mountain H. 9 Coast SE	
Bone Creek 7 Copper Unuk River - LPW 9 Coast SE	
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	

	Reg			Reg	
Population name	num.	Region	Population name	num.	Region
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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