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U.S. DEPARTMENT OF COMMERCE
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National Marine Fisheries Service
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C. M. Guthrie III, H. T. Nguyen, and J. R. Guyon

Alaska Fisheries Science Center
Auke Bay Laboratories
17109 Lena Point Loop Road
Juneau AK 99801

www.afsc.noaa.gov

U.S. DEPARTMENT OF COMMERCE
Penny. S. Pritzker, Secretary
National Oceanic and Atmospheric Administration
Kathryn D. Sullivan, Under Secretary and Administrator
National Marine Fisheries Service
Eileen Sobeck, Assistant Administrator for Fisheries

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ABSTRACT

A genetic analysis of samples from the Chinook salmon (*Oncorhynchus tshawytscha*) bycatch of the 2012 Bering Sea-Aleutian Island (BSAI) and Gulf of Alaska (GOA) trawl fisheries for walleye pollock (*Gadus chalcogrammus*) was undertaken to determine the stock composition of the sample set. 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 2012, genetic samples from the Bering Sea were collected using a systematic random sampling protocol where one out of every 10 Chinook salmon encountered was sampled. Based on the analysis of 1,111 Chinook salmon bycatch samples collected throughout the 2012 BSAI walleye pollock trawl fishery, Coastal Western Alaska stocks dominated the sample set (63%) with smaller contributions from North Alaska Peninsula (11%), British Columbia (10%), and West Coast U.S. (OR/CA/WA) (7%) stocks. Analysis of temporal groupings within the pollock "A" and "B" seasons revealed changes in stock composition during the course of the year with lower contributions of North Alaska Peninsula and higher contributions of British Columbia and West Coast U.S. stocks during the "B" season. Genetic samples were also collected from Chinook salmon taken in the bycatch of the 2012 Gulf of Alaska (GOA) pollock trawl fisheries. In contrast with the Bering Sea, genetic samples were collected opportunistically in the GOA during 2012; consequently, the resulting stock composition estimates should be considered as stock compositions of the sample set rather than a representative composition of the entire GOA Chinook salmon bycatch. Based on the analysis of 948 Chinook salmon bycatch samples, British Columbia (49%), West Coast U.S. (28%), and Coastal Southeast Alaska (20%) stocks comprised the largest stock groups. We also produced stock composition estimates of Chinook salmon from tests of salmon excluder devices performed in February 2012 in an area north of Unimak Pass in the Bering Sea. Stock composition results showed that the majority of the 249 Chinook salmon collected in the 2012 excluder device test originated from Coastal Western Alaska (69%) and the North Alaska Peninsula (12.4%). These were very similar to the stock composition estimates from the 2012 BSAI “A” season.

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 a set of Chinook salmon bycatch samples collected from the U.S. Bering Sea-Aleutian Island (BSAI) and GOA pollock trawl fisheries. National Marine Fisheries Service

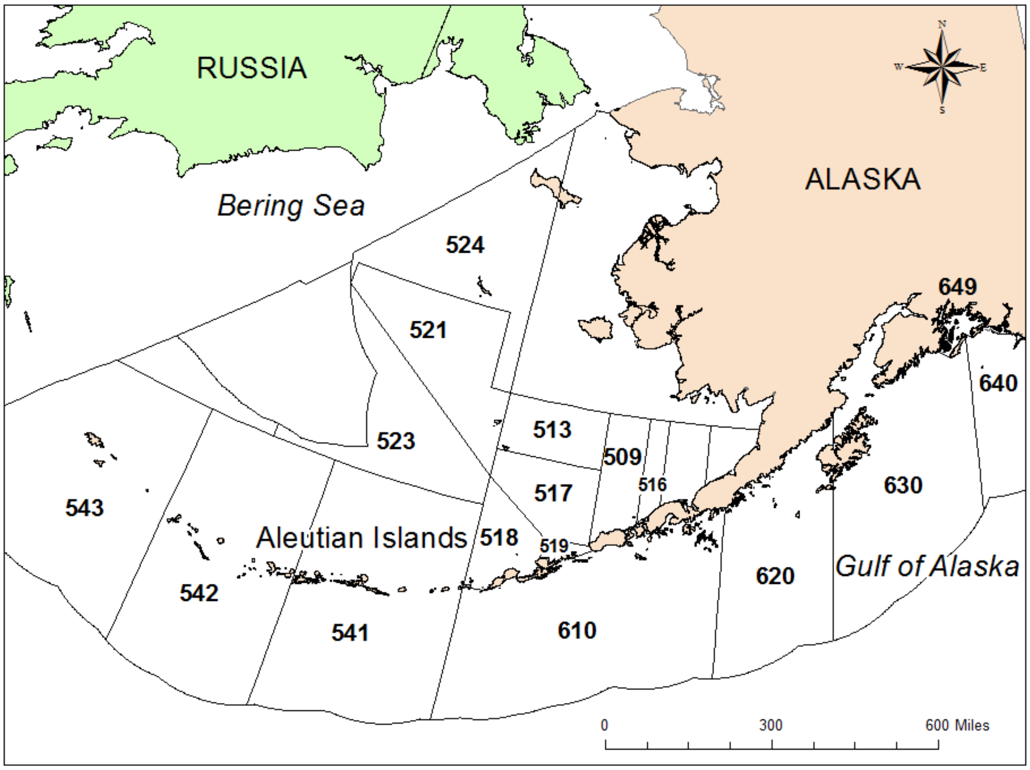

Figure 1. -- NMFS statistical areas associated with the Bering Sea-Aleutian Island (BSAI) and Gulf of Alaska (GOA) groundfish fisheries.

(NMFS) geographical statistical areas associated with the groundfish fishery are shown in Figure 1 and are used later in the report to describe the spatial distribution of the Chinook salmon bycatch and genetic samples.

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

Stock composition estimates of Chinook salmon obtained from 2012 tests of a salmon excluder device were also included in this report. Salmon excluder device tests were performed in February 2012 in an area north of Unimak Pass in the Bering Sea (Fig. 2). The aim of the salmon excluder device is to reduce salmon bycatch by allowing salmon to exit the trawl while simultaneously retaining groundfish. During the test, the recapture net was positioned outside the excluder allowing for the collection of all salmon that escaped the modified trawl.

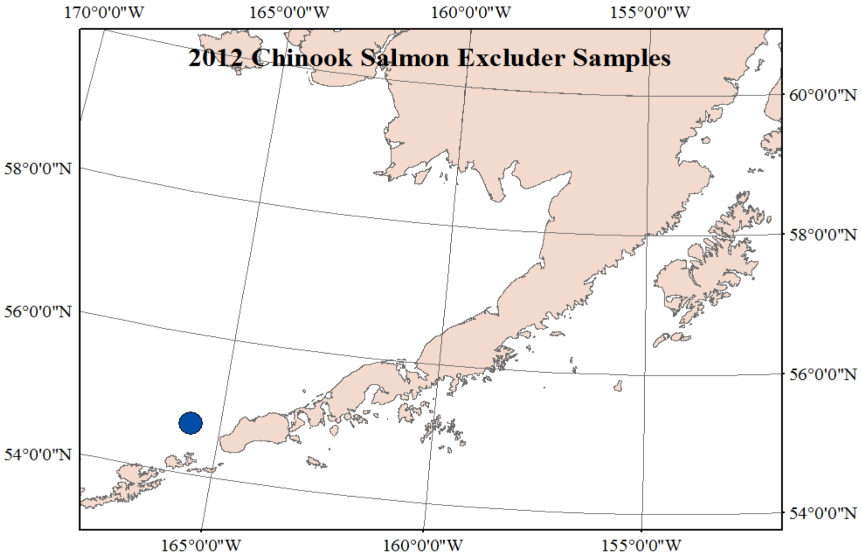

Figure 2. -- Position of samples collected in the 2012 salmon excluder device test. Plotted is the combined position of the 249 genotyped genetic samples as the hauls from the FV *Destination* and FV *Starbound* were so close together.

SAMPLE DISTRIBUTION

Samples were collected from the Chinook salmon bycatch by the Alaska Fisheries Science Center's (AFSC) Fisheries Monitoring and Analysis Division (FMA) for analysis at Auke Bay Laboratories (ABL). Amendment 91 to the North Pacific Fishery Management Council (NPFMC) fishery management plan for groundfish of the BSAI Management Area was enacted in 2010 and included retention of the salmon caught in the prohibited species catch. In 2011, a systematic random sampling design recommended by Pella and Geiger (2009) was implemented by FMA to collect genetic samples from one out of every 10 Chinook salmon encountered as bycatch in the BSAI pollock fishery. In the 2012 GOA pollock fishery, there was no requirement for full retention of Chinook salmon caught in the prohibited species catch and genetic samples were collected proportionately only when encountered by observers.

Samples of axillary process tissue for genetic analysis were collected from Chinook salmon throughout 2012 from the BSAI and GOA. Axillary process tissues were stored in coin envelopes which were labeled, frozen, and shipped to ABL. The majority of the Chinook salmon bycatch genetic tissue samples were derived from the bottom and midwater pollock trawl fishery.

Bering Sea-Aleutian Islands

In 2012, an estimated 11,343 Chinook salmon were taken in the bycatch of BSAI pollock trawl fisheries (NMFS 2012). Of the total bycatch, 7,764 were from the trawl “A” season and 3,579 were from the “B” season. There was a 56% reduction of the total Chinook salmon bycatch between 2011 and 2012, the majority was from the 2011”B” season (81%) (Fig. 3). Since 1991, the year with the highest overall Chinook bycatch in the BSAI was 2007 (Fig. 3) when an estimated 121,770 fish were taken. In 2012, the Chinook salmon bycatch in both the “A” and “B” seasons were genotyped at a rate of 9.8% (“A” season -759 fish; “B” season - 352 fish).

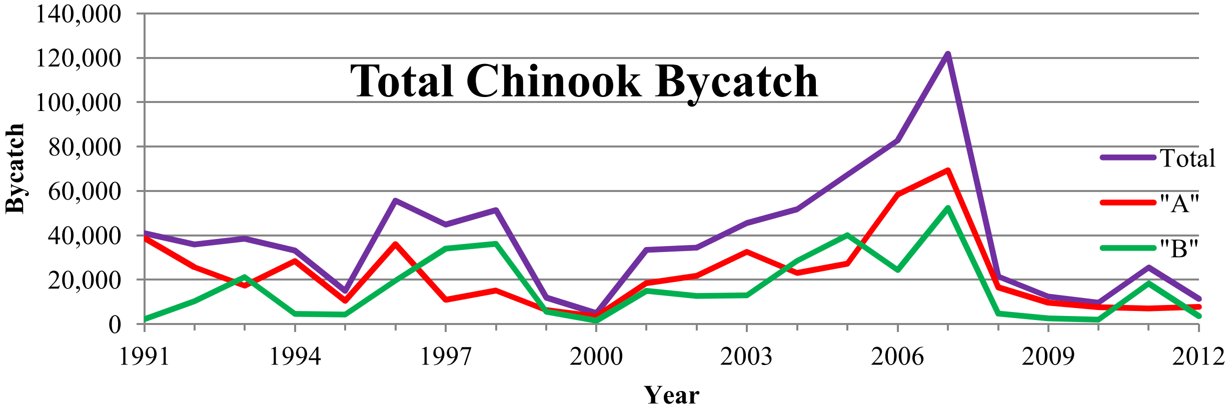

Figure 3. -- Yearly, “A” season, and “B” estimates for the Chinook salmon bycatch from the BSAI pollock trawl fishery (NMFS 2012).

Potential biases associated with the collection of genetic samples from the bycatch are well documented and have the potential to affect resulting stock composition estimates (Pella and Geiger 2009). Potential spatial and temporal biases associated with the 2012 Chinook salmon bycatch sample sets were evaluated by comparing the genetic sample distribution with the overall bycatch distribution (Fig. 4). During 2012, the overall bycatch and genetic samples were comparable in their temporal distribution. To evaluate the sample spatial distribution, the Chinook salmon bycatch was compared with the bycatch samples by statistical area over time (Fig. 5). Spatial and temporal sample biases can become more apparent at these higher resolution scales.

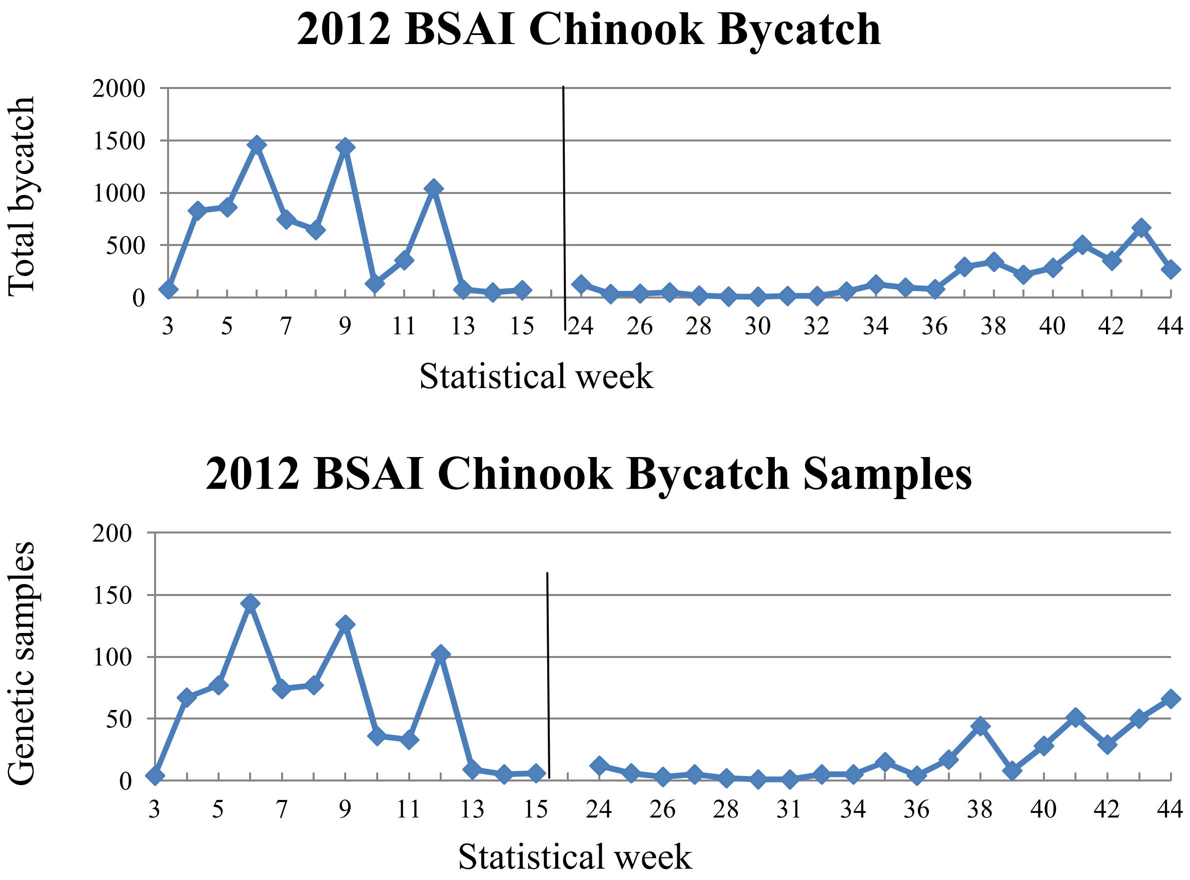

Figure 4. -- Number of Chinook salmon bycatch and genetic samples graphed by statistical week. Top panel: Distribution of all Chinook salmon caught in the 2012 Bering Sea pollock trawl fishery. Bottom panel: Distribution of the 1,111 genotyped samples from the 2012 bycatch. Weeks 3-15 correspond to the groundfish "A" season, whereas weeks 24-44 correspond to the "B" season, the demarcation of which is a vertical line.

2012 was the second year systematic random sampling was employed for collecting genetic tissue from the Bering Sea Chinook salmon bycatch and Figure 5 shows that the resulting samples were collected in proportion through time and space with the total catch. The sample spatial and temporal distribution was excellent in 2012 compared to previous years when samples were collected more opportunistically (Guyon et al. 2010a, 2010b; Guthrie et al. 2012).

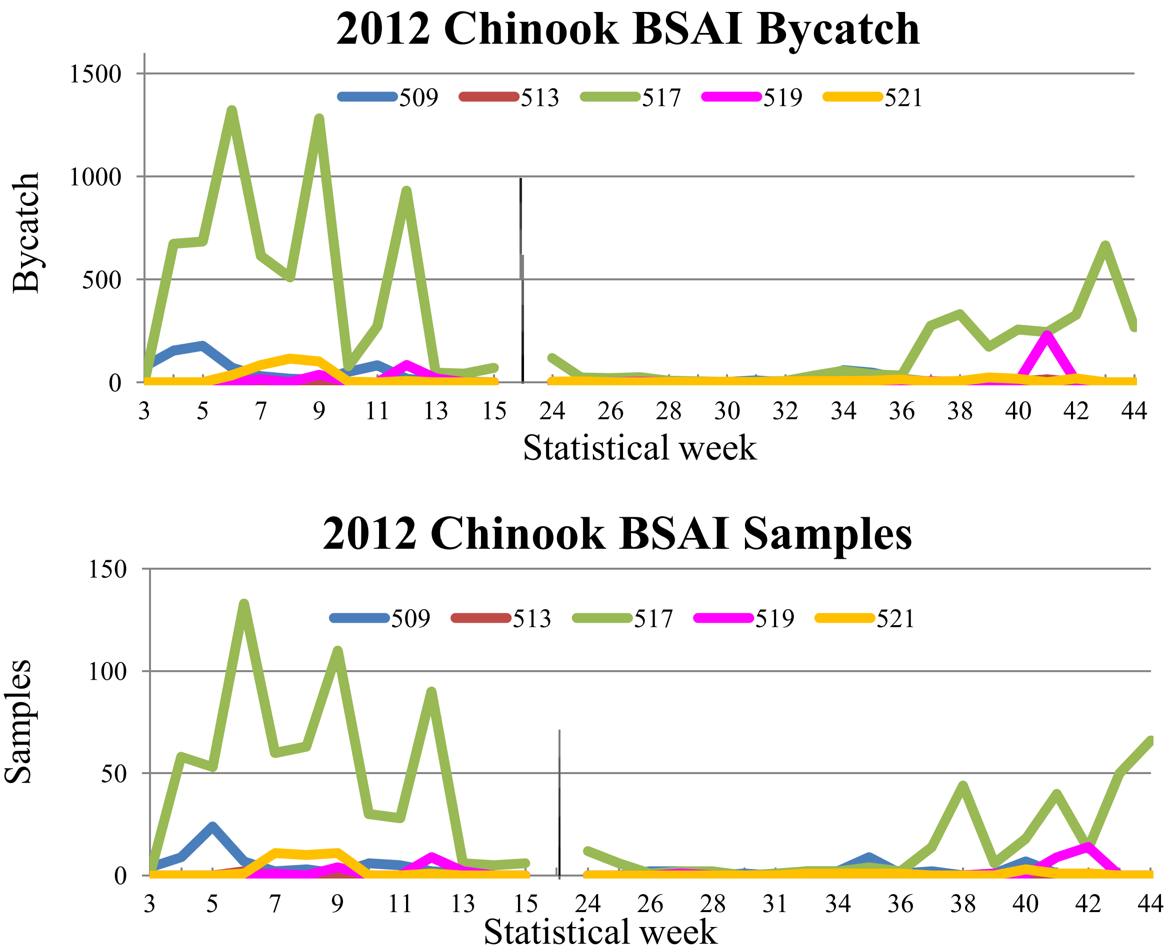

Figure 5. -- Comparison of the Chinook salmon bycatch by time and area with the distribution of available genetic samples. Top panel: Distribution of the estimated Chinook salmon caught in the 2012 BSAI pollock trawl fishery. Not graphed was 1 fish from NMFS area 523. Bottom panel: Distribution of the 1,111 genotyped samples from the 2012 bycatch. Weeks 3-15 correspond to the groundfish "A" season, whereas weeks 24-44 correspond to the "B" season, the demarcation of which is a vertical line.

Gulf of Alaska

In 2012, an estimated 18,845 Chinook salmon were taken as bycatch in the GOA pollock trawl fisheries (NMFS 2012). The year with the highest overall Chinook bycatch in the GOA was 2010 (Fig. 6) when an estimated 44,779 fish were taken. The genotyped sample set for the 2012 Chinook salmon bycatch was 948 fish, corresponding to a sampling rate of 5.0%. Unlike the BSAI samples, the sampling was not systematic with respect to the entire catch; consequently, the resulting stock composition estimates correspond to the sample set rather than the overall GOA Chinook salmon bycatch.

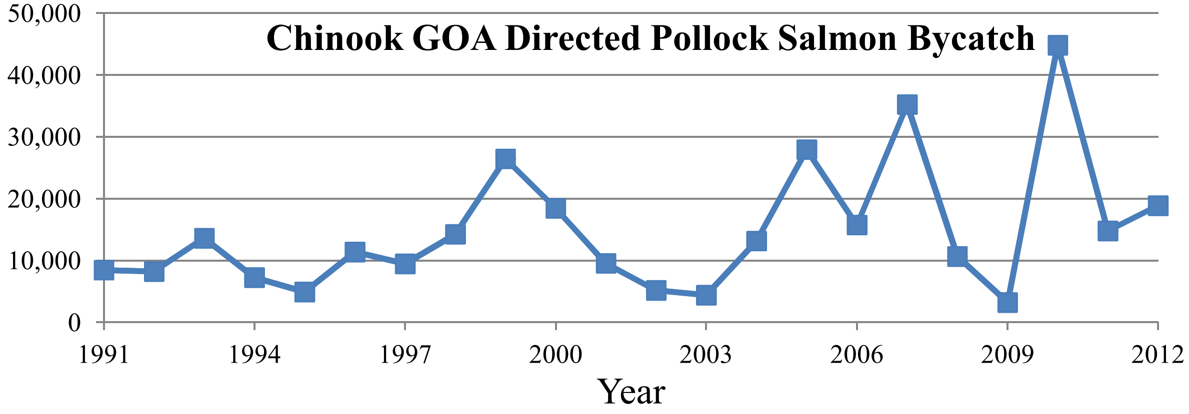

Figure 6. **--** Yearly estimates for the Chinook salmon bycatch from the GOA pollock trawl fishery (NMFS 2012).

Potential spatial and temporal biases associated with the 2012 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. 7). To evaluate the sample spatial distribution, the GOA Chinook salmon bycatch was compared with the bycatch samples by NMFS statistical area over time (Fig. 8) highlighting time/space sample distribution issues often associated with more opportunistic sampling. The samples were not representative of all areas; for example, NMFS areas 610 and 620 were underrepresented during the late season.

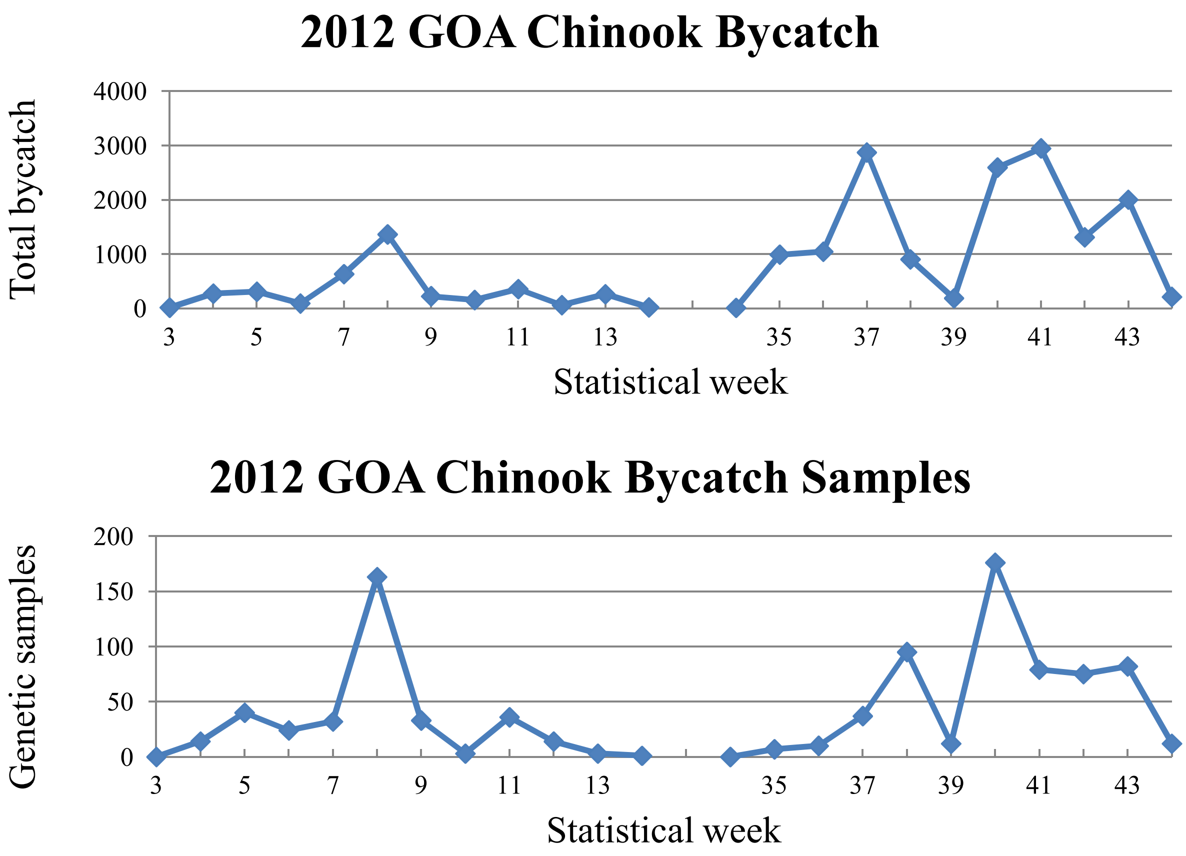

Figure 7. **--** Number of Chinook salmon bycatch and genetic samples by statistical week. Top panel: Distribution of all Chinook salmon caught in the 2012 GOA pollock trawl fishery. Bottom panel: Distribution of the 948 genotyped samples from the 2012 bycatch.

Excluder Samples

Chinook salmon from excluder tests were genetically sampled in test hauls that had greater than 50 samples, which in the spring of 2012, occurred in a single haul from each of two vessels (Table 1). Those hauls occurred within 2 days of each other in mid-February (Table 1). This provided for a unique sample set from which a large number of Chinook salmon genetic samples were collected at sea over a narrow geographic and temporal range; thus, providing an opportunity to determine the extent to which Chinook salmon stocks aggregated over this narrow window.

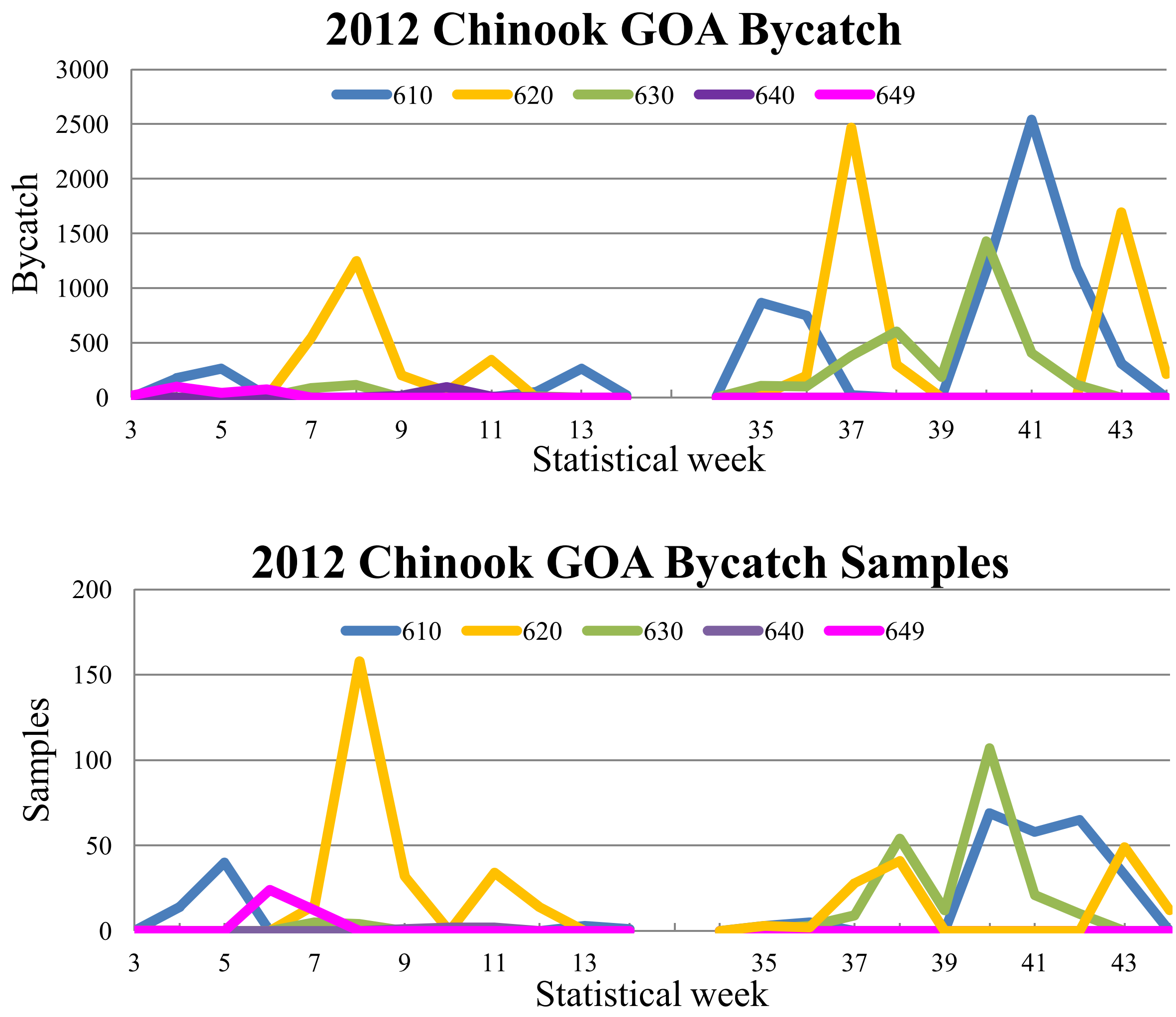

Figure 8. -- Comparison of the Chinook salmon bycatch by time and area with the distribution of available genetic samples. Top panel: Distribution of the estimated Chinook salmon caught in the 2012 GOA pollock trawl fishery. Bottom panel: Distribution of the 948 genotyped samples from the 2012 bycatch.

Table 1. -- Number of Chinook salmon samples collected from the 2012 salmon excluder device test. Genotyped refers to the number of samples successfully genotyped for greater than 80% of the SNP markers.

Vessel	**Location**	**Haul #**	**Date**	**Samples**	**Genotyped**
FV *Destination*	54 42 N, 165 30 W	28	2/16/2012	170	153
FV *Starbound*	54 44 N, 165 51W	65	2/14/2012	97	96

GENETIC STOCK COMPOSITION

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. 2010a) 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 2005-2011 Chinook bycatch (NMFS 2009; Guyon et al. 2010a, b,; Guthrie et al. 2012, 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 (Applied Biosystems Inc.). Concordance rates of 99.9% between the two chemistries for the 2012 controls confirmed the utility and compatibility of both genotyping methods.

From the 2012 Chinook salmon bycatch, a total of 2,126 samples were analyzed of which 2,059 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 96.8%. These genotypes were analyzed both in GenAlEx (Peakall and Smouse 2006) and using C++ programs written by the Auke Bay Laboratories Genetics Program to check for duplicate samples and none were found. Of the remaining samples, 1,111 originated from the BSAI and 948 from the GOA. The remaining samples had genetic information for an average of 41.1 of 43 markers. From a total of 267 excluder samples, 249 were successfully genotyped for an average of 40 of the 43 Chinook salmon SNP 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 2-11).

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 although an option was used within SPAM to allow Bayesian modeling of baseline allele frequencies (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 1.02 or less for all the estimates, conveying strong convergence to a single posterior distribution (Pella and Masuda 2001).

Bering Sea-Aleutian Islands

Results (BAYES) suggest that 88% of the 759 samples from the "A" season originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska stock contributing the most (68%), followed by the North Alaska Peninsula (16%), and Upper Yukon (3%). The other major contributor was British Columbia (7%) (Table 2). For the "B" season, over 53% of the 352 samples originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska region contributing the most (52%). This was followed by the West Coast U.S. stock (17%) and British Columbia (15%) (Table 3).

For the entire year, an estimated 77% of the bycatch samples were estimated to be from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska stock contributing the most (63%), trailed by the North Alaska Peninsula (11%). Other contributors were British Columbia (10%) and West Coast U.S. (7%) (Table 4). The “overall” and “A” season stock compositions were somewhat similar, which was anticipated given that 68% of the samples were from the “A” season.

Table 2. -- Regional BAYES and SPAM stock composition estimates for the 759 Chinook salmon samples from the bycatch of the 2012 “A” season BSAI 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	**0.005**	0.003	0.002	0.005	0.012	**0.005**	0.001
Coast W AK	**0.678**	0.022	0.634	0.679	0.721	**0.668**	0.020
Mid-Yukon	**0.012**	0.008	0.000	0.011	0.031	**0.021**	0.002
Up Yukon	**0.031**	0.008	0.016	0.031	0.048	**0.028**	0.003
N AK Penn	**0.162**	0.019	0.127	0.161	0.200	**0.150**	0.009
NW GOA	**0.002**	0.004	0.000	0.001	0.012	**0.009**	0.002
Copper	**0.000**	0.001	0.000	0.000	0.003	**0.004**	0.001
NE GOA	**0.001**	0.003	0.000	0.000	0.009	**0.004**	0.001
Coast SE AK	**0.017**	0.008	0.003	0.016	0.034	**0.023**	0.001
BC	**0.073**	0.011	0.052	0.073	0.096	**0.068**	0.003
WA/OR/CA	**0.019**	0.005	0.010	0.018	0.030	**0.019**	0.002

Table 3. -- Regional BAYES and SPAM stock composition estimates for the 352 Chinook salmon samples from the bycatch of the 2012 "B" season BSAI 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	**0.024**	0.008	0.011	0.023	0.043	**0.028**	0.008
Coast W AK	**0.521**	0.029	0.463	0.521	0.577	**0.501**	0.027
Mid-Yukon	**0.002**	0.003	0.000	0.000	0.011	**0.003**	0.003
Up Yukon	**0.010**	0.006	0.001	0.009	0.025	**0.010**	0.003
N AK Penn	**0.001**	0.003	0.000	0.000	0.008	**0.006**	0.002
NW GOA	**0.038**	0.014	0.013	0.036	0.069	**0.044**	0.010
Copper	**0.001**	0.002	0.000	0.000	0.005	**0.004**	0.000
NE GOA	**0.001**	0.002	0.000	0.000	0.006	**0.004**	0.000
Coast SE AK	**0.082**	0.018	0.045	0.081	0.119	**0.068**	0.005
BC	**0.153**	0.022	0.112	0.152	0.200	**0.166**	0.012
WA/OR/CA	**0.170**	0.021	0.131	0.170	0.213	**0.166**	0.015

Table 4. -- Regional BAYES and SPAM stock composition estimates for the 1,111 Chinook salmon samples from the bycatch of the 2012 BSAI 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	**0.011**	0.003	0.006	0.011	0.018	**0.011**	0.003
Coast W AK	**0.631**	0.018	0.594	0.631	0.666	**0.621**	0.016
Mid-Yukon	**0.010**	0.006	0.000	0.010	0.023	**0.013**	0.001
Up Yukon	**0.024**	0.006	0.013	0.024	0.037	**0.023**	0.002
N AK Penn	**0.108**	0.014	0.083	0.108	0.136	**0.102**	0.006
NW GOA	**0.014**	0.007	0.002	0.013	0.031	**0.022**	0.003
Copper	**0.000**	0.001	0.000	0.000	0.002	**0.001**	0.000
NE GOA	**0.001**	0.002	0.000	0.000	0.006	**0.004**	0.001
Coast SE AK	**0.034**	0.007	0.020	0.033	0.049	**0.038**	0.002
BC	**0.102**	0.010	0.083	0.102	0.123	**0.100**	0.004
WA/OR/CA	**0.066**	0.008	0.051	0.066	0.082	**0.065**	0.004

Gulf of Alaska

The BAYES results estimate that 99.6% of the 948 samples from the GOA originated from GOA/Pacific coastal regions, with the British Columbia contributing the most (49%), followed by the West Coast U.S. (28%) and Coastal Southeast Alaska (20%) (Table 5). Due to higher sample numbers, we were also able look at temporal and the geographical (NMFS statistical areas) differences. The BAYES estimates for the early season (statistical weeks 3-14) showed British Columbia contributed the most (42%), followed by Coastal Southeast Alaska (31%) and the West Coast U.S. (24%) (Table 6). For the late season (statistical weeks 34-44), British Columbia (52%) predominated, higher than the West Coast U.S. (30%), and Coastal Southeast Alaska (15%) (Table 7). The westernmost area, 610, had the largest BAYES estimates from British Columbia (69%) with smaller components from the West Coast U.S. (16%), and Coastal Southeast Alaska (12%) (Table 8). Moving east into NMFS area 620, the British Columbia composition dropped (39%) while those from the West Coast U.S. (31%), and Coastal Southeast Alaska (27%) increased almost two-fold (Table 9). The samples from the three easternmost areas (630, 640, and 649) were combined due to sample size, although most were from area 630 (226). British Columbia had the highest BAYES composition (38%), the West Coast U.S. increasing (36%), and Coastal Southeast Alaska (22%) dropping (Table 10).

Table 5. -- Regional BAYES and SPAM stock composition estimates for the 948 Chinook salmon samples from the bycatch of the 2012 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**	0.000	0.000	0.000	0.000	**0.000**	0.000
Coast W AK	**0.004**	0.004	0.000	0.003	0.013	**0.004**	0.002
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	0.003	**0.000**	0.000
NW GOA	**0.021**	0.005	0.012	0.020	0.032	**0.022**	0.003
Copper	**0.001**	0.001	0.000	0.000	0.005	**0.001**	0.000
NE GOA	**0.005**	0.003	0.001	0.005	0.012	**0.005**	0.000
Coast SE AK	**0.201**	0.018	0.167	0.200	0.238	**0.189**	0.007
BC	**0.492**	0.022	0.448	0.492	0.533	**0.506**	0.016
WA/OR/CA	**0.277**	0.016	0.246	0.276	0.308	**0.273**	0.012

Table 6. -- Regional BAYES and SPAM stock composition estimates for the 363 Chinook salmon samples from the bycatch of the 2012 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	**0.008**	0.008	0.000	0.007	0.028	**0.009**	0.005
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	0.002	**0.000**	0.000
N AK Penn	**0.000**	0.001	0.000	0.000	0.002	**0.000**	0.000
NW GOA	**0.008**	0.008	0.000	0.006	0.029	**0.012**	0.002
Copper	**0.000**	0.001	0.000	0.000	0.003	**0.000**	0.000
NE GOA	**0.005**	0.006	0.000	0.003	0.020	**0.007**	0.001
Coast SE AK	**0.312**	0.036	0.243	0.311	0.382	**0.269**	0.015
BC	**0.422**	0.037	0.350	0.422	0.496	**0.472**	0.025
WA/OR/CA	**0.244**	0.025	0.196	0.244	0.296	**0.231**	0.017

Table 7. -- Regional BAYES and SPAM stock composition estimates for the 585 Chinook salmon samples from the bycatch of the 2012 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**	0.000	0.000	0.000	0.001	**0.000**	0.000
Coast W AK	**0.001**	0.002	0.000	0.000	0.008	**0.002**	0.000
Mid-Yukon	**0.000**	0.000	0.000	0.000	0.001	**0.000**	0.000
Up Yukon	**0.000**	0.001	0.000	0.000	0.001	**0.000**	0.000
N AK Penn	**0.001**	0.002	0.000	0.000	0.006	**0.000**	0.000
NW GOA	**0.026**	0.007	0.014	0.026	0.041	**0.027**	0.005
Copper	**0.001**	0.002	0.000	0.001	0.006	**0.002**	0.000
NE GOA	**0.007**	0.004	0.001	0.006	0.017	**0.007**	0.000
Coast SE AK	**0.147**	0.019	0.111	0.146	0.186	**0.143**	0.006
BC	**0.520**	0.025	0.470	0.520	0.568	**0.522**	0.021
WA/OR/CA	**0.297**	0.020	0.259	0.297	0.338	**0.298**	0.017

Table 8. -- Regional BAYES and SPAM stock composition estimates for the 293 Chinook salmon samples from the bycatch of the 2012 GOA pollock trawl fishery from NMFS 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	**0.003**	0.004	0.000	0.001	0.013	**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	**0.000**	0.001	0.000	0.000	0.002	**0.000**	0.001
NW GOA	**0.025**	0.010	0.010	0.024	0.048	**0.025**	0.007
Copper	**0.000**	0.001	0.000	0.000	0.003	**0.000**	0.000
NE GOA	**0.008**	0.006	0.001	0.007	0.024	**0.012**	0.000
Coast SE AK	**0.117**	0.025	0.072	0.115	0.169	**0.099**	0.018
BC	**0.687**	0.032	0.620	0.688	0.748	**0.704**	0.035
WA/OR/CA	**0.160**	0.023	0.118	0.159	0.206	**0.157**	0.041

Table 9. -- Regional BAYES and SPAM stock composition estimates for the 388 Chinook salmon samples from the bycatch of the 2012 GOA pollock trawl fishery from NMFS 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	**0.009**	0.008	0.000	0.008	0.028	**0.010**	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	0.004	**0.000**	0.001
NW GOA	**0.013**	0.007	0.002	0.012	0.029	**0.012**	0.007
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	**0.000**	0.000
Coast SE AK	**0.272**	0.029	0.216	0.272	0.329	**0.247**	0.018
BC	**0.393**	0.032	0.332	0.392	0.458	**0.427**	0.035
WA/OR/CA	**0.313**	0.026	0.264	0.312	0.364	**0.305**	0.041

Table 10. **--** Regional BAYES and SPAM stock composition estimates for the 267 Chinook salmon samples from the bycatch of the 2012 GOA pollock trawl fishery from NMFS areas 630/640/649. 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**	0.006	0.000	0.000	0.020	**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**	0.002	0.000	0.000	0.005	**0.000**	0.000
NW GOA	**0.028**	0.011	0.009	0.026	0.053	**0.032**	0.008
Copper	**0.003**	0.004	0.000	0.001	0.015	**0.004**	0.000
NE GOA	**0.009**	0.008	0.000	0.008	0.028	**0.010**	0.001
Coast SE AK	**0.216**	0.033	0.154	0.215	0.283	**0.203**	0.013
BC	**0.384**	0.037	0.313	0.383	0.457	**0.397**	0.026
WA/OR/CA	**0.357**	0.031	0.298	0.356	0.418	**0.353**	0.026

Excluder Samples

Stock composition results showed that the majority of the 249 Chinook salmon samples collected in the 2012 Excluder device test originated from Coastal Western Alaska (69%) and the North Alaska Peninsula (12.4%) (Table 11), proportions that very closely represent the stock composition of the 2012 Chinook salmon bycatch from the BSAI “A” season. Since the sample numbers for each haul were relatively large, stock compositions were developed for each haul (Fig. 9). While the main contributing stocks were the same, there were differences in the relative proportions of fish originating from Coastal Western Alaska and the North Alaska Peninsula suggesting the potential for some stock aggregation effects (Fig. 9).

Table 11. **--** Regional BAYES and SPAM stock composition estimates for the 249 genotyped total excluder samples (153 from the FV *Destination* – Haul 28 and 96 from the FV *Starbound* – Haul 65). 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	**0.009**	0.007	0.001	0.008	0.026	**0.013**	0.008
Coast W AK	**0.690**	0.033	0.624	0.691	0.752	**0.654**	0.034
Mid-Yukon	**0.001**	0.003	0.000	0.000	0.011	**0.005**	0.005
Up Yukon	**0.000**	0.001	0.000	0.000	0.003	**0.000**	0.000
N AK Penn	**0.124**	0.024	0.080	0.122	0.175	**0.126**	0.025
NW GOA	**0.019**	0.015	0.000	0.017	0.054	**0.030**	0.014
Copper	**0.003**	0.005	0.000	0.000	0.017	**0.015**	0.009
NE GOA	**0.001**	0.003	0.000	0.000	0.009	**0.005**	0.005
Coast SE AK	**0.027**	0.015	0.000	0.026	0.058	**0.021**	0.011
BC	**0.069**	0.020	0.037	0.067	0.113	**0.071**	0.018
WA/OR/CA	**0.057**	0.015	0.031	0.056	0.090	**0.059**	0.015

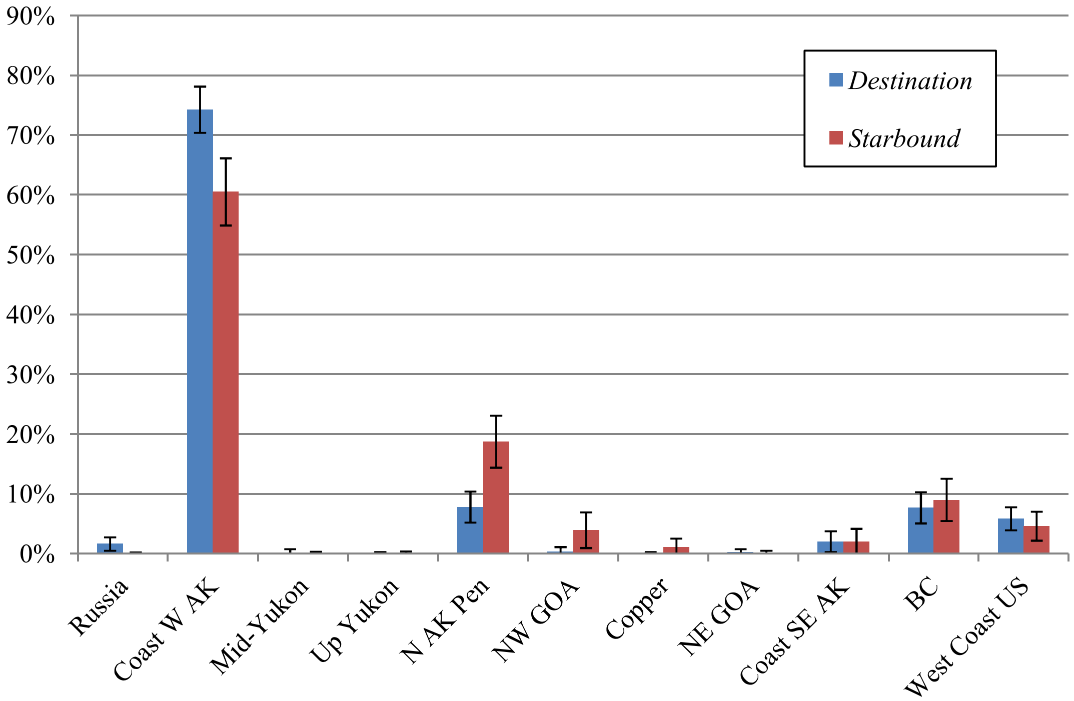

Figure 9. -- Comparison of stock proportions between 153 samples from the FV *Destination* (Haul 28) and 96 samples from the FV *Starbound* (Haul 65). The standard deviation of the estimate is plotted.

COMPARISON WITH PREVIOUS ESTIMATES

Although comparisons among years are complicated due to different sampling strategies employed in different years, stock compositions from the analysis of the 2012 "A" season Chinook salmon bycatch samples were in general agreement with the 2008, 2010, and 2011 "A" season estimates. For example, most samples continued to be from stocks originating from river systems directly flowing into the Bering Sea, although differences were apparent between the 2010 and the other 3 "A" season sample sets. The Upper and Middle Yukon estimated contribution continued to decrease in 2012 to levels similar to 2008 while the Coastal Western Alaska contributions increased (Fig. 10). Although the 2008, 2011, and 2012 "A" season contribution estimates were more similar, larger amounts of more southern stocks (Coastal Southeast Alaska, British Columbia, and West Coast U.S.) were estimated in both 2011 and 2012; than in 2008 (Fig. 10).

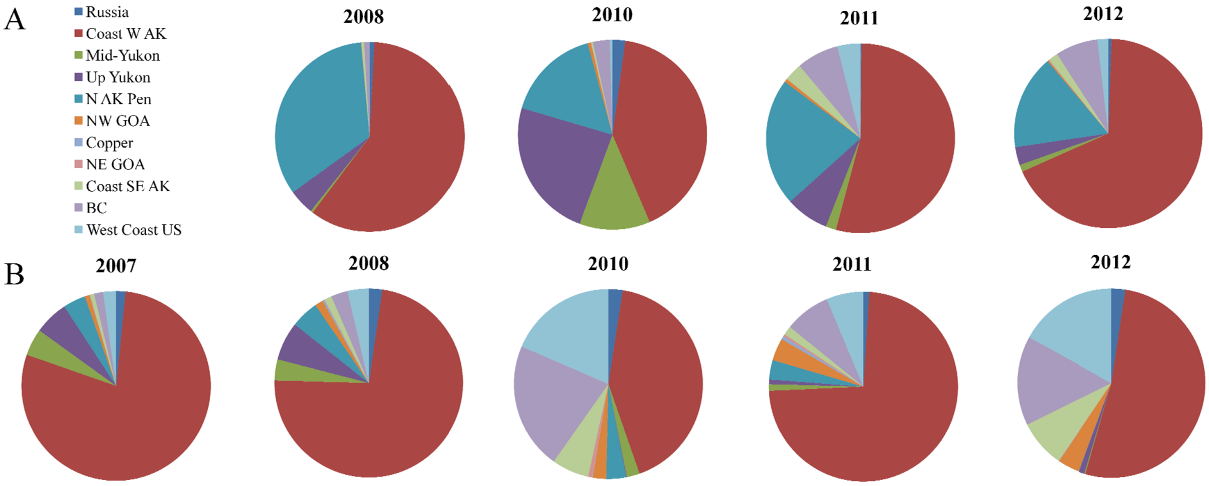

Figure 10. -- Comparison of "A" season genetic stock composition estimates for 2008, 2010-12 based on available genetic samples from the BSAI Chinook salmon bycatch. Comparison of "B" season genetic stock composition estimates for 2007, 2008, 2010-12 stock composition estimates based on available genetic samples from the BSAI "B" season Chinook salmon bycatch. The same genetic baseline and regional groupings were used in all analyses.

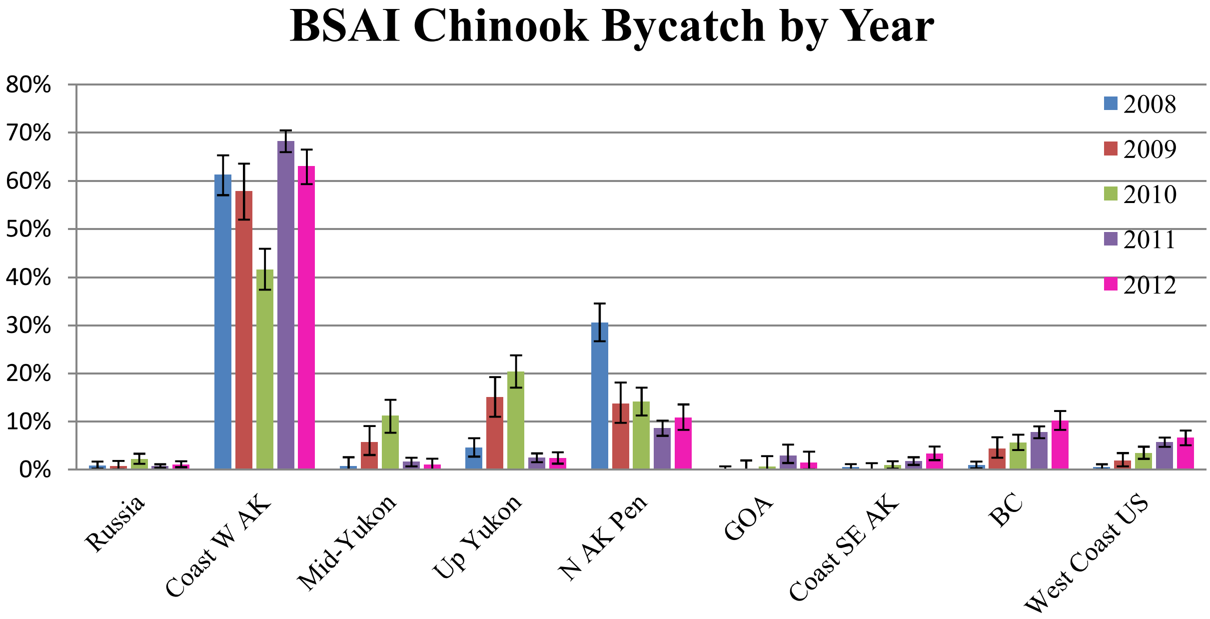

Figure 11. -- Comparison of yearly stock composition estimates (2008-2012) based on genetic samples from the BSAI Chinook salmon bycatch. The same genetic baseline and general regional groupings were used in all analyses. GOA group consists of combined values for NWGOA, Copper, and NE GOA. BAYES 95% credible intervals are plotted for yearly estimates.

The 2007, 2008, and 2011 “B” season stock composition estimates were similar with large amounts from Coastal Western Alaska (Fig. 10). In contrast with the other “B” season estimates, the 2010 and 2012 “B” season estimates identified larger contributions from British Columbia, West Coast U.S. and Coastal Southeast Alaska stocks. In contrast to 2011 and similar to most other previous years studied, most of the Chinook salmon bycatch occurred in 2012 during the “A” season. As in 2011, systematic random sampling was employed in 2012, where genetic samples were collected from one of every 10 Chinook salmon encountered.

While changes in sampling protocols between years necessitate caution in comparing analyses across years, when the stock compositions were analyzed for the entire year, Coastal Western Alaska stock compositions trended downward between 2008 and 2010 but increased in 2011, and remained at a similar level in 2012 (Fig. 11). North Alaska Peninsula stock compositions have remained consistent since 2009 reporting 11% of the bycatch in 2012 (Fig. 11). The upper and middle Yukon River contribution continued to be low in 2012, while Coastal Southeast Alaska, British Columbia and West Coast U.S. stock compositions continued their 5-year upward trend (Fig. 11).

For the GOA, the opportunistic sampling protocols employed between 2010 and 2012 limit the results to indentifying only presence of individual stocks; however, the greater number of available samples (948) allowed temporal and geographical analyses for the first time in 2012. Recognizing these limitations, Figure 12 shows the stock composition in the GOA of samples collected in 2010, 2011, and 2012. All years show an abundance of southern stock groups (British Columbia, West Coast U.S., and Coastal Southeast Alaska). The NW GOA dropped in abundance in 2012, similar to levels in 2010 and there was a corresponding increase in British Columbia and West Coast U.S. groups. There appear to be more Coastal Southeast Alaska fish

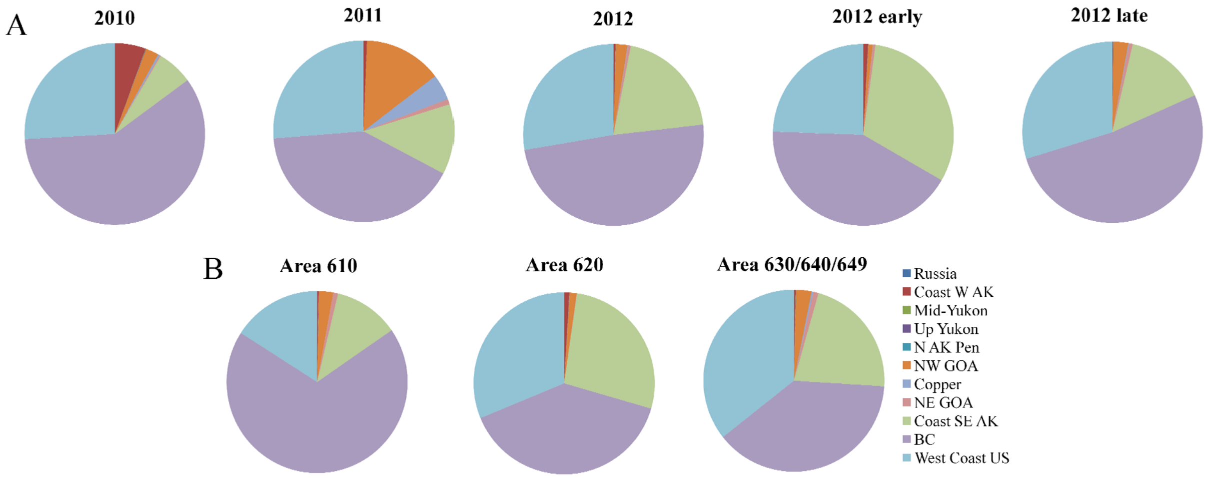

Figure 12. -- Comparison of genetic stock composition estimates for 2010-12 based on available genetic samples from the GOA Chinook salmon bycatch. Panel A shows comparisons across time. Panel B shows comparisons between NMFS Statistical Areas in 2012. The same genetic baseline and regional groupings were used in all analyses.

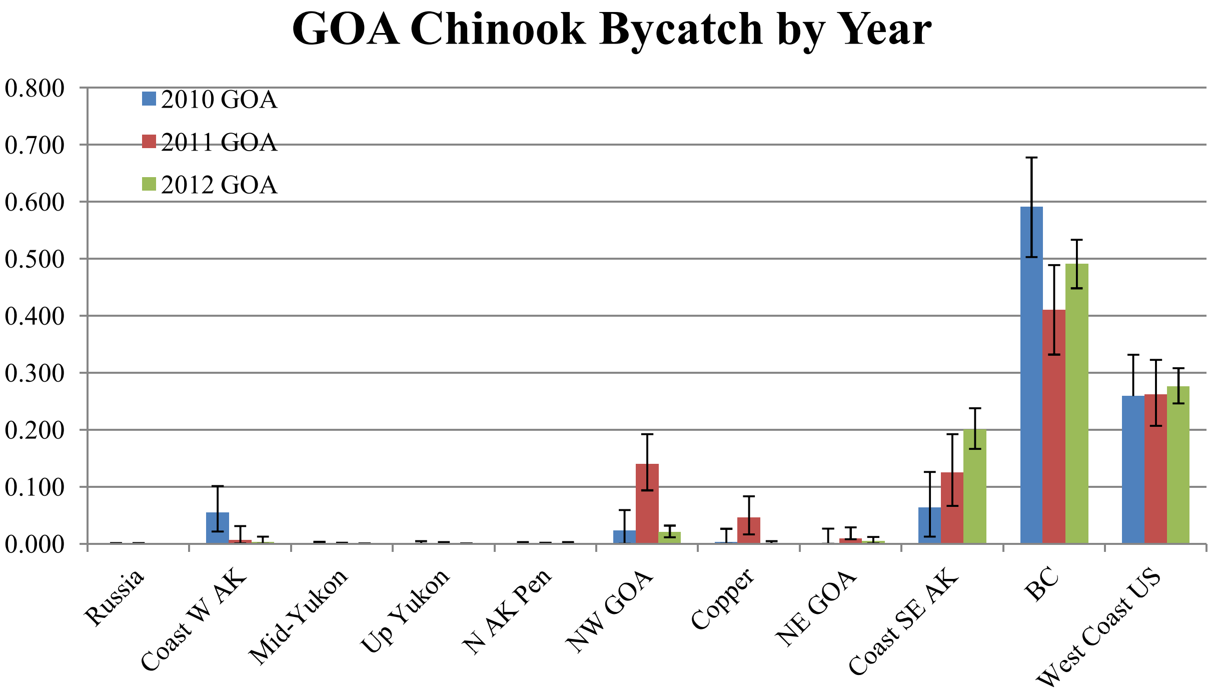

Figure 13. -- Comparison of yearly stock composition estimates (2010-2012) based on available genetic samples from the GOA Chinook salmon bycatch. The same genetic baseline and general regional groupings were used in all analyses. BAYES 95% credible intervals are plotted for yearly estimates.

early in 2012, than in late 2012 (Fig. 12A). There also appears to be more British Columbia fish in the west, in area 610, while the composition of West Coast U.S., and Coastal Southeast Alaska fish increased in the more eastern areas (620/630/640/649) (Fig.12B). Throughout all years, British Columbia remained the most abundant group, followed by the West Coast U.S., and the upward trending Coastal Southeast Alaska (Fig. 13)

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 in the Bering Sea pollock fishery averaged 38,624 salmon per year during 1991-2012, but increased to a peak of 121,638 in 2007. The Bering Sea Chinook salmon bycatch has abated in more recent years dropping to a total of 11,343 Chinook salmon in 2012, a number which is 27,281 fish below the 22-year average.

In addition to the Bering Sea, there is also a federally managed pollock trawl fishery in the Gulf of Alaska. The incidental harvest of Chinook salmon in the GOA averaged 14,647 salmon per year during 1991-2012, with a peak of 44,779 in 2010. The GOA Chinook salmon bycatch was above the 22-year average in 2012 at 18,850 Chinook salmon.

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 stock composition analysis of genetic sample sets from the 2012 Bering Sea and GOA Chinook salmon bycatch. The results and limitations of this analysis are summarized below.

Sampling Issues

Bering Sea-Aleutian Islands

With the implementation of systematic random sampling in the 2011 prohibited species catch, 2012 is the second year from which representative samples have been collected from the Chinook salmon bycatch. This represents a lot of effort over many years to develop standardized protocols for collecting sets of samples from numerous observers both at sea and in shore-based processing plants, the efforts of which are clearly apparent in the representative nature of the sample sets (Figs. 4 and 5). The observed genetic sampling rate in 2012 was 9.8%, the highest ever observed and in close agreement with the goal. The resulting Chinook salmon Bering Sea bycatch sample set was 1,111.

Gulf of Alaska

Although opportunistic sampling was employed for the collection of the GOA Chinook salmon bycatch genetic samples between 2010 and 2012, the sampling effort improved from a 0.4% sampling rate in 2010 to 1.7% in 2011 to 5.0% in the 2012. The overall sample set was larger than the two previous years combined at 948, although the lack of representative samples hinders calculating statistically reliable stock composition estimates of the 2012 GOA Chinook salmon bycatch as a whole. Nonetheless the stock composition of the available samples provides at least an indication of stock presence, although repeated estimates across years will eventually provide generalized composition estimates.

Stock Composition Estimates

Bering Sea-Aleutian Islands

Genetic stock composition analysis showed the majority of bycatch samples collected in the Bering Sea were from Alaskan stocks predominantly originating from river systems directly flowing into the Bering Sea. The stock composition of the Chinook salmon bycatch during the 2012 “A” season differed from the 2012 “B” season, demonstrating temporal differences in the stocks intercepted. This was especially apparent in the Coastal Western Alaska (68% vs. 52%) and the North Alaska Peninsula (16% vs. 0.1%) stock groups.

Salmon Excluder Test Samples

Genetic analysis showed that the samples collected from the spring 2012 salmon excluder device test were predominantly from Coastal Western Alaska with an overall stock composition very similar to the 2012 Bering Sea “A” season estimate. In addition, the sample set provided a unique opportunity to compare the stock composition of Chinook salmon taken at sea in two different hauls. Although the variance will increase with smaller sample sets, stock compositions for the Coastal Western Alaska and the North Alaska Peninsula stock groupings between hauls were outside the standard deviation intervals suggesting the potential for some degree of stock aggregation even over small spatial and temporal groupings.

Gulf of Alaska

As in previous years, the opportunistic nature in which genetic samples were collected from the GOA Chinook salmon bycatch limited the 2012 stock composition results to indicators of presence/absence, although the sample sizes were much improved allowing for temporal and geographic analyses. As in 2010 and 2011, the 2012 GOA Chinook salmon bycatch samples were predominantly from the west coast of the United States, British Columbia, and Coastal Southeast Alaska (Fig. 12).

Application of These Estimates

The extent to which any salmon stock is impacted by the bycatch of the Bering Sea trawl fishery is dependent on many factors including 1) the overall size of the bycatch, 2) the age of the salmon caught in the bycatch, 3) the age 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. Stock composition estimates for the Bering Sea Chinook salmon bycatch were performed using representative samples and the estimates are considered to be representative of the overall bycatch. Opportunistic sampling used for the GOA estimates limit the application of those estimates to presence of a stock group.

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APPENDIX

Chinook salmon populations in the ADF&G's single nucleotide polymorphisms (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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