



NOAA Technical Memorandum NMFS-AFSC-244

# **Genetic Stock Composition Analysis of Chinook Salmon Bycatch Samples from the 2011 Bering Sea and Gulf of Alaska Trawl Fisheries**

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

**U.S. DEPARTMENT OF COMMERCE**  
National Oceanic and Atmospheric Administration  
National Marine Fisheries Service  
Alaska Fisheries Science Center

March 2013

## NOAA Technical Memorandum NMFS

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This document should be cited as follows:

Guthrie, C. M. III, H. T. Nguyen, and J. R. Guyon. 2013. Genetic stock composition analysis of Chinook salmon bycatch samples from the 2011 Bering Sea and Gulf of Alaska trawl fisheries. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-244, 28 p.

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

Alaska Fisheries Science Center  
Auke Bay Laboratories  
17109 Pt. Lena Loop Road  
Juneau, AK 99801

*[www.afsc.noaa.gov](http://www.afsc.noaa.gov)*

## **U.S. DEPARTMENT OF COMMERCE**

Rebecca M. Blank, Acting Secretary

### **National Oceanic and Atmospheric Administration**

Kathryn D. Sullivan, Acting Under Secretary and Administrator

### **National Marine Fisheries Service**

Samuel D. Rauch III, Acting Assistant Administrator for Fisheries

March 2013

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## ABSTRACT

A genetic analysis of samples from the Chinook salmon (*Oncorhynchus tshawytscha*) bycatch of the 2011 Bering Sea-Aleutian Island (BSAI) and Gulf of Alaska (GOA) pollock trawl fisheries 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 2011, genetic samples from the Bering Sea were collected using a systematic random sampling protocol from one out of every 10 Chinook salmon encountered. Based on the analysis of 2,473 Chinook salmon bycatch samples collected throughout the 2011 BSAI walleye pollock (*Theragra chalcogramma*) trawl fishery, Coastal Western Alaska stocks dominated the sample set (68%) with smaller contributions from North Alaska Peninsula (9%), British Columbia (8%), and U.S. west coast (6%) 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 Yukon River stocks during the “B” season. Genetic samples were also collected from Chinook salmon taken in the bycatch of the 2011 Gulf of Alaska (GOA) pollock trawl fisheries. In contrast with the Bering Sea, genetic samples were collected opportunistically in the GOA during 2011; 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 240 Chinook salmon bycatch samples, British Columbia (40%) and U.S. west coast (26%) stocks comprised the largest stock groups with smaller contributions from Northwest GOA (15%) and Coastal Southeast Alaska (14%) stocks.



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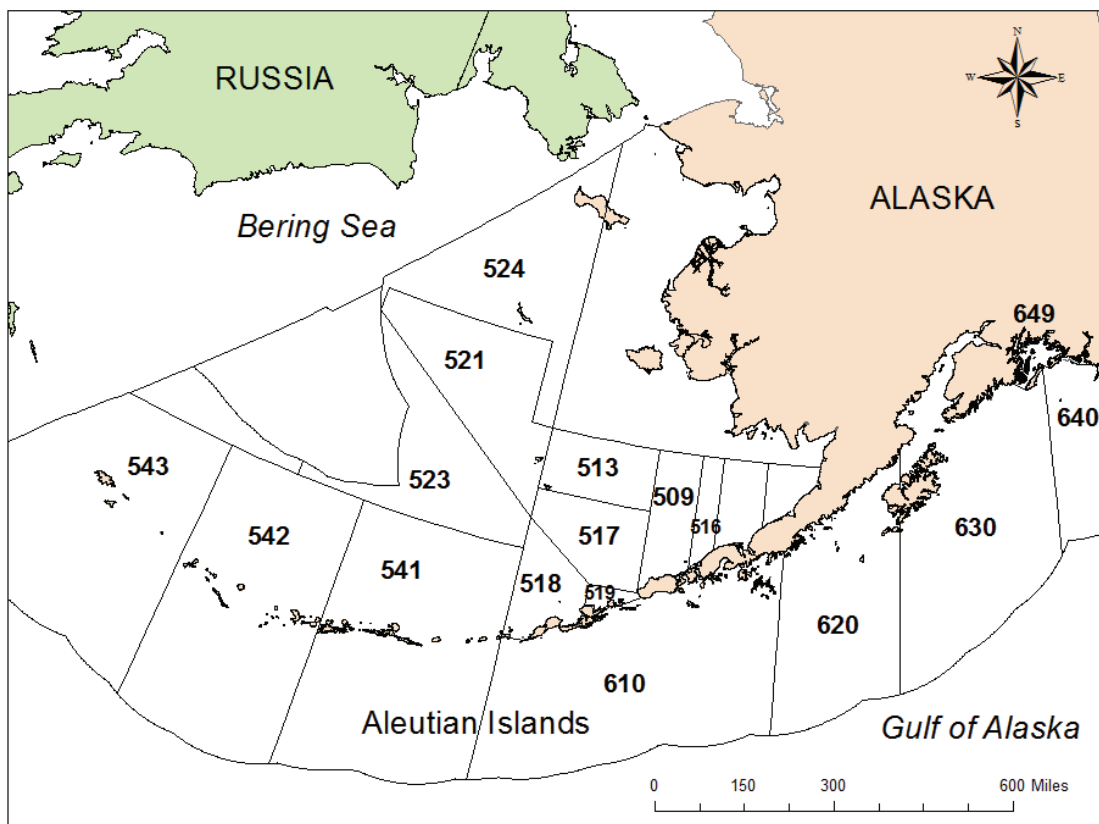
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## INTRODUCTION

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 2011. 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 2005-2010 Chinook salmon bycatch (NMFS 2009; Guyon et al. 2010a and b; Guthrie et al. 2012; Larson et al. 2013). For additional information regarding background and methodology, this report is intended to be supplemented with the Chinook salmon bycatch report prepared previously for the 2008 Bering Sea trawl fishery (Guyon et al. 2010a).

## SAMPLE DISTRIBUTION

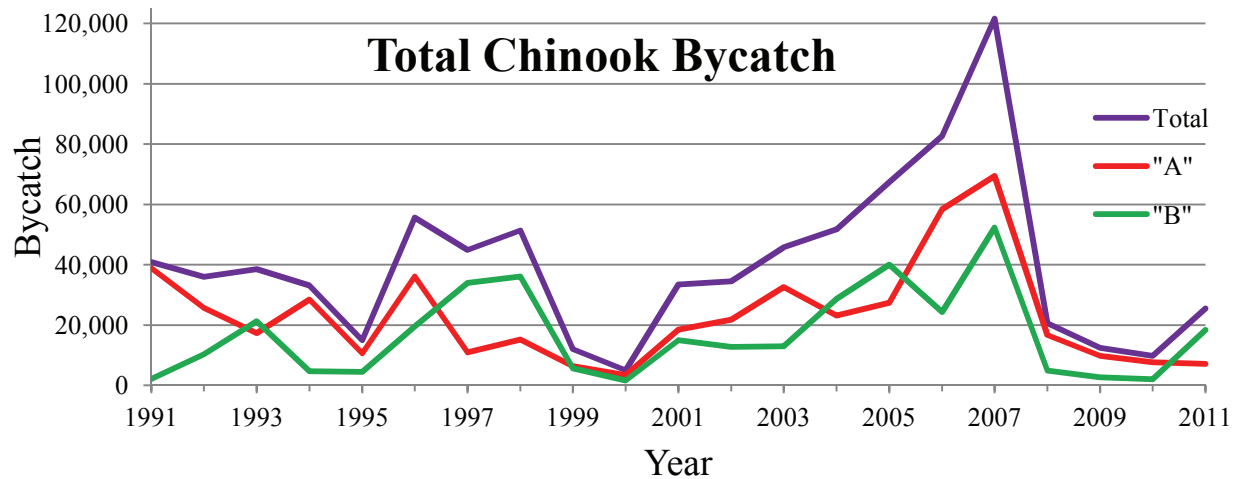
Samples were collected from the Chinook salmon bycatch by the Alaska Fisheries Science Center's (AFSC) Fisheries Monitoring and Analysis Division (FMA) for its Auke Bay Laboratories (ABL). Amendment 91 to the Fishery Management Plan for Groundfish of the BSAI Management Area was enacted in 2010 and included 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 the North Pacific Groundfish Observer program to

collect genetic samples from one out of every 10 Chinook salmon encountered as bycatch in the BSAI pollock fishery. In the 2011 GOA pollock fishery, there was no requirement for full retention of Chinook salmon caught in the prohibited species catch and genetic samples were collected opportunistically when encountered by observers.

Samples of axillary process tissue for genetic analysis were collected throughout 2011 from the BSAI and GOA. Axillary process tissue was stored in coin envelopes which were labeled, frozen, and shipped to ABL. The majority of the Chinook salmon bycatch genetic samples were derived from the bottom and midwater pollock trawl fishery, with the exception of 12 samples from BSAI where the target species was Pacific cod (*Gadus macrocephalus*).

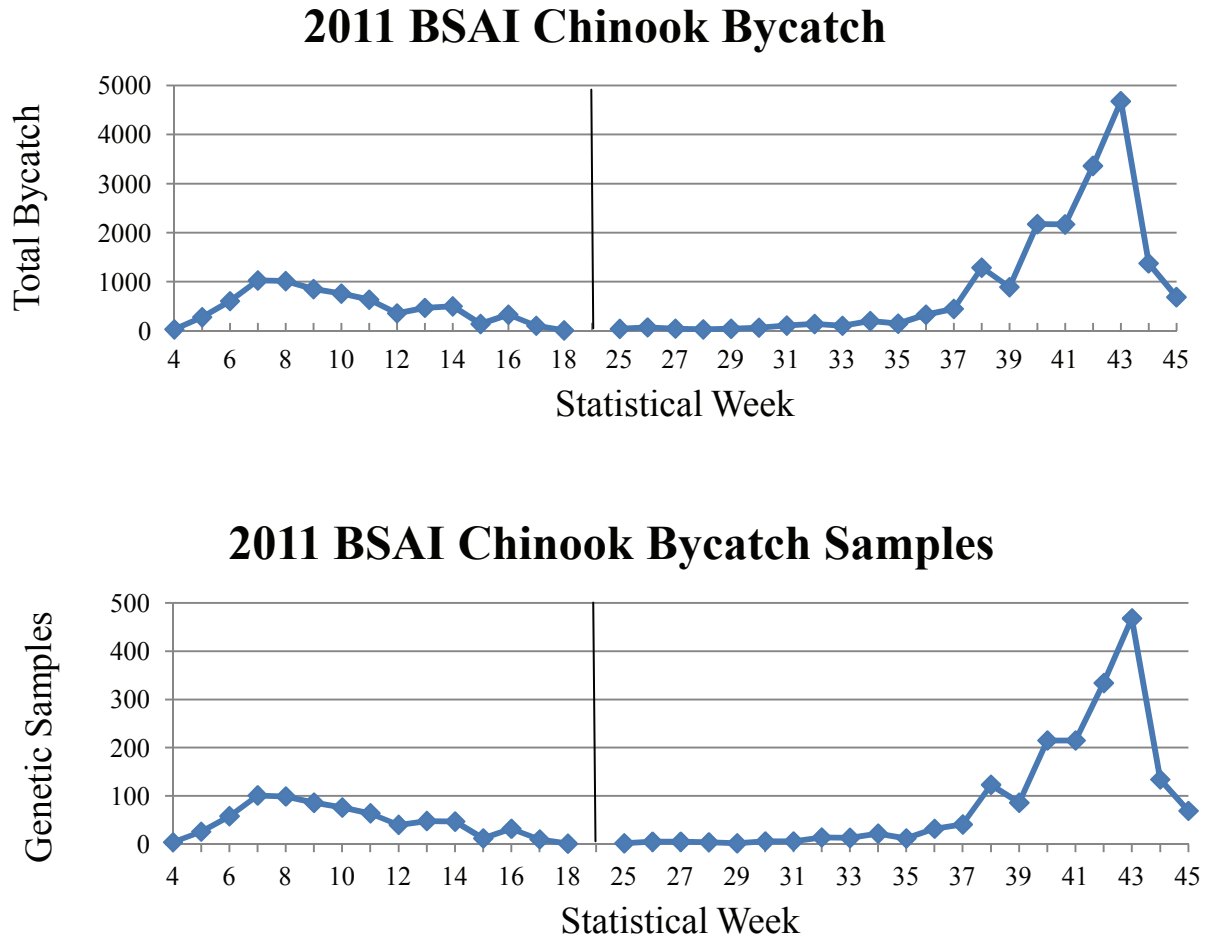
#### Bering Sea-Aleutian Islands

In 2011, an estimated 25,499 Chinook salmon were taken in the bycatch of BSAI pollock trawl fisheries (NMFS 2012), of which 7,136 were estimated from the trawl “A” season and 18,363 were estimated for the “B” season. Since 1991, the year with the highest overall Chinook bycatch in the BSAI was 2007 (Fig. 2) when an estimated 121,770 fish were taken. The genetic sample set for the 2011 “A” season Chinook salmon bycatch was 695 fish, corresponding to a sampling rate of 9.7%. The genetic sample set for the 2011 “B” season Chinook bycatch was 1,778 fish, corresponding to a sampling rate of 9.7%. The annual sampling rate for the entire year was 9.7%. There were more Chinook salmon taken in the “B” season than in the “A” season for the first time since 2005 (Fig. 2).



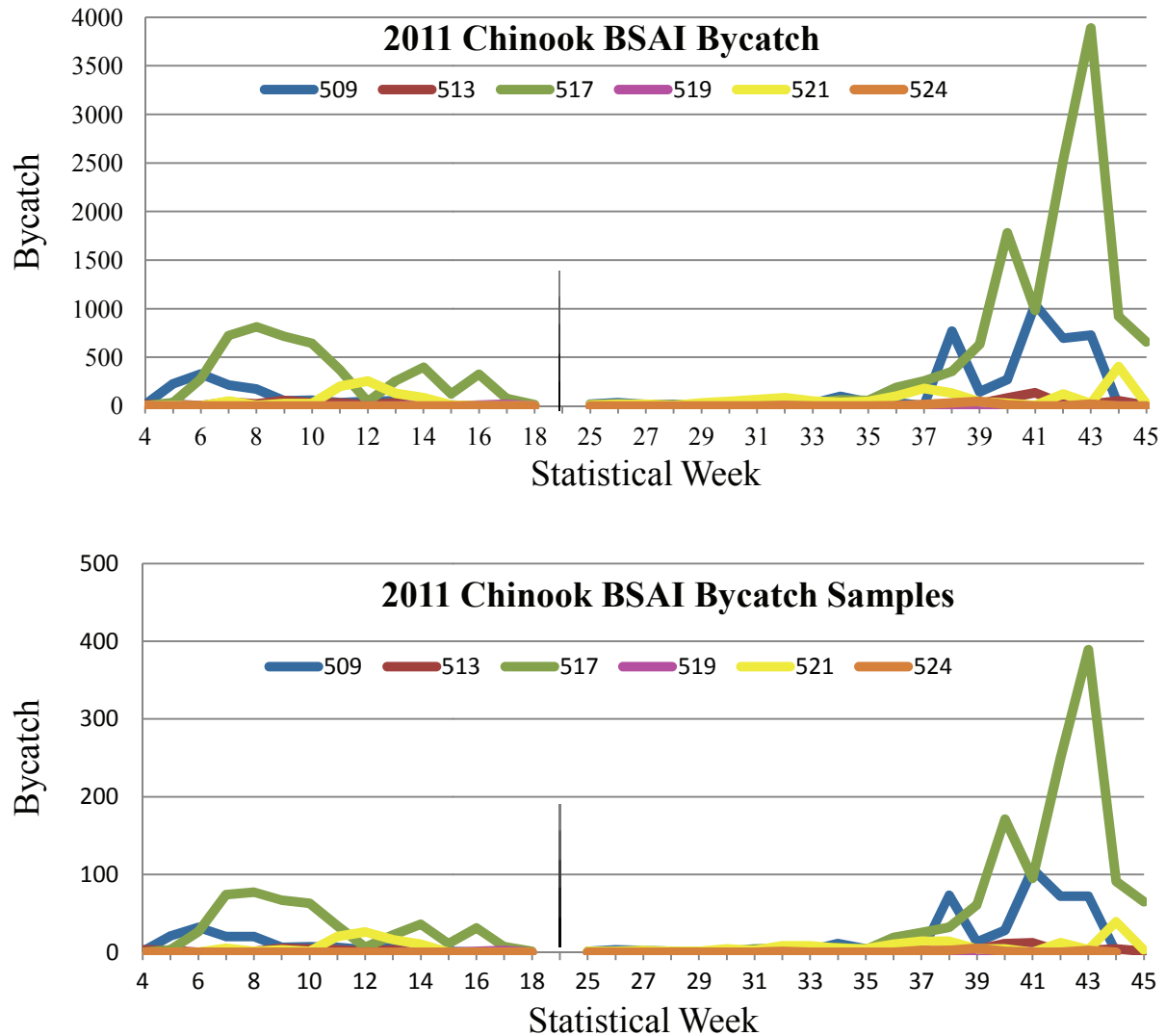
**Figure 2.** -- Yearly, “A” season, and “B” season estimates for the Chinook salmon bycatch from the BSAI pollock trawl fishery (NMFS 2012).

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 2011 Chinook salmon bycatch sample sets were evaluated by comparing the genetic sample distribution with the overall bycatch distribution (Fig. 3). During 2011, 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. 4). Spatial and temporal sample biases can become more apparent at these higher resolution scales. For samples collected from offloads in which the vessel fished in multiple areas, the sample location of the entire catch of a fishing trip was identified as the location of the most abundant haul, although generally those areas were in close proximity to each other.



**Figure 3.**-- Number of Chinook salmon bycatch and genetic samples graphed by statistical week. Top panel: Distribution of all Chinook salmon caught in the 2011 Bering Sea pollock trawl fishery. Bottom panel: Distribution of the available 2,473 genetic samples from the 2011 bycatch. Weeks 4-18 correspond to the groundfish “A” season, whereas weeks 25-45 correspond to the “B” season, the demarcation of which is a vertical line.

2011 was the first year systematic random sampling was employed for collecting genetic tissue from the Bering Sea Chinook salmon bycatch and Figure 4 shows that the resulting Chinook salmon bycatch samples were collected in proportion through time and space with the total catch. The sample spatial and temporal distribution was excellent in 2011 compared to previous years when samples were collected more opportunistically (Guyon et al. 2010a, 2010b; Guthrie et al. 2012).

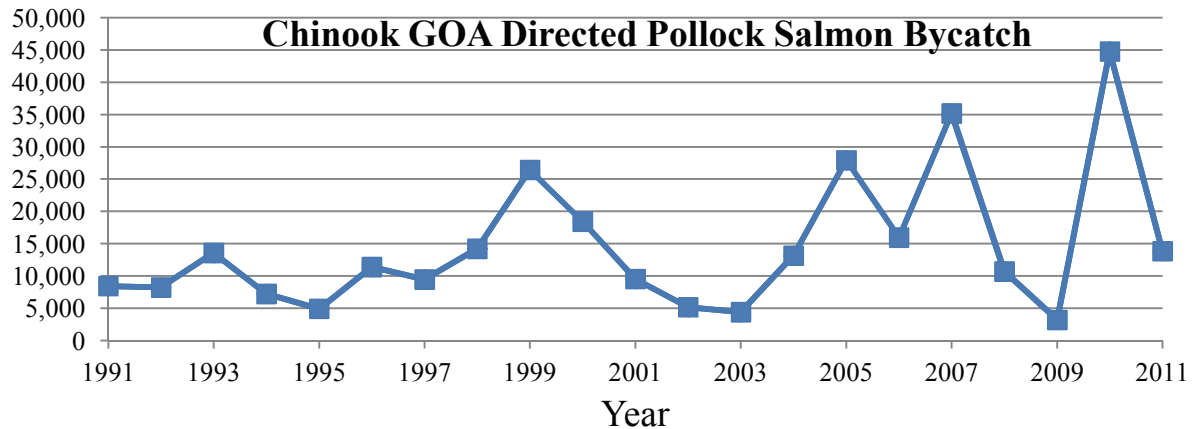


**Figure 4.--** Comparison of the Chinook salmon bycatch by time and area with the distribution of available genetic samples. Top panel: Distribution of the estimated Chinook salmon caught in the 2011 BSAI pollock trawl fishery. Bottom panel: Distribution of the available 2,473 genetic samples from the 2011 bycatch. Not graphed were 11 fish from area 541, and 1 from 542. Weeks 4-18 correspond to the groundfish “A” season, whereas weeks 25-45 correspond to the “B” season, the demarcation of which is a vertical line.

#### Gulf of Alaska

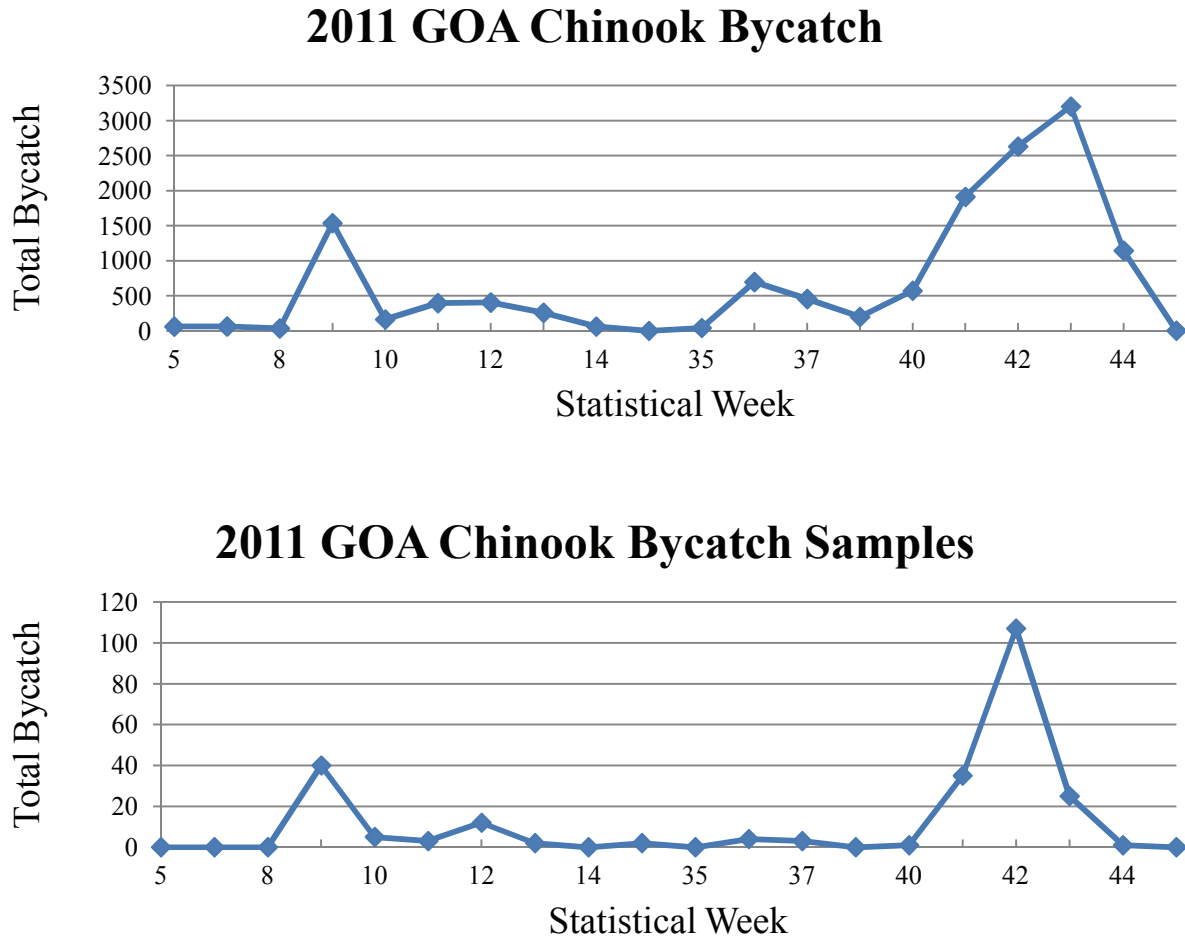
In 2011, an estimated 13,837 Chinook salmon were taken in the bycatch of GOA pollock trawl fisheries (NMFS 2012). The year with the highest overall Chinook bycatch in the GOA was 2010 (Fig. 5) when an estimated 44,779 fish were taken. The genetic sample set for the 2011

Chinook salmon bycatch was 240 fish, corresponding to a sampling rate of 1.7%. Unlike the BSAI samples, the sampling was not systematic; consequently, the resulting stock composition estimates correspond to the sample set rather than the overall GOA Chinook salmon bycatch.



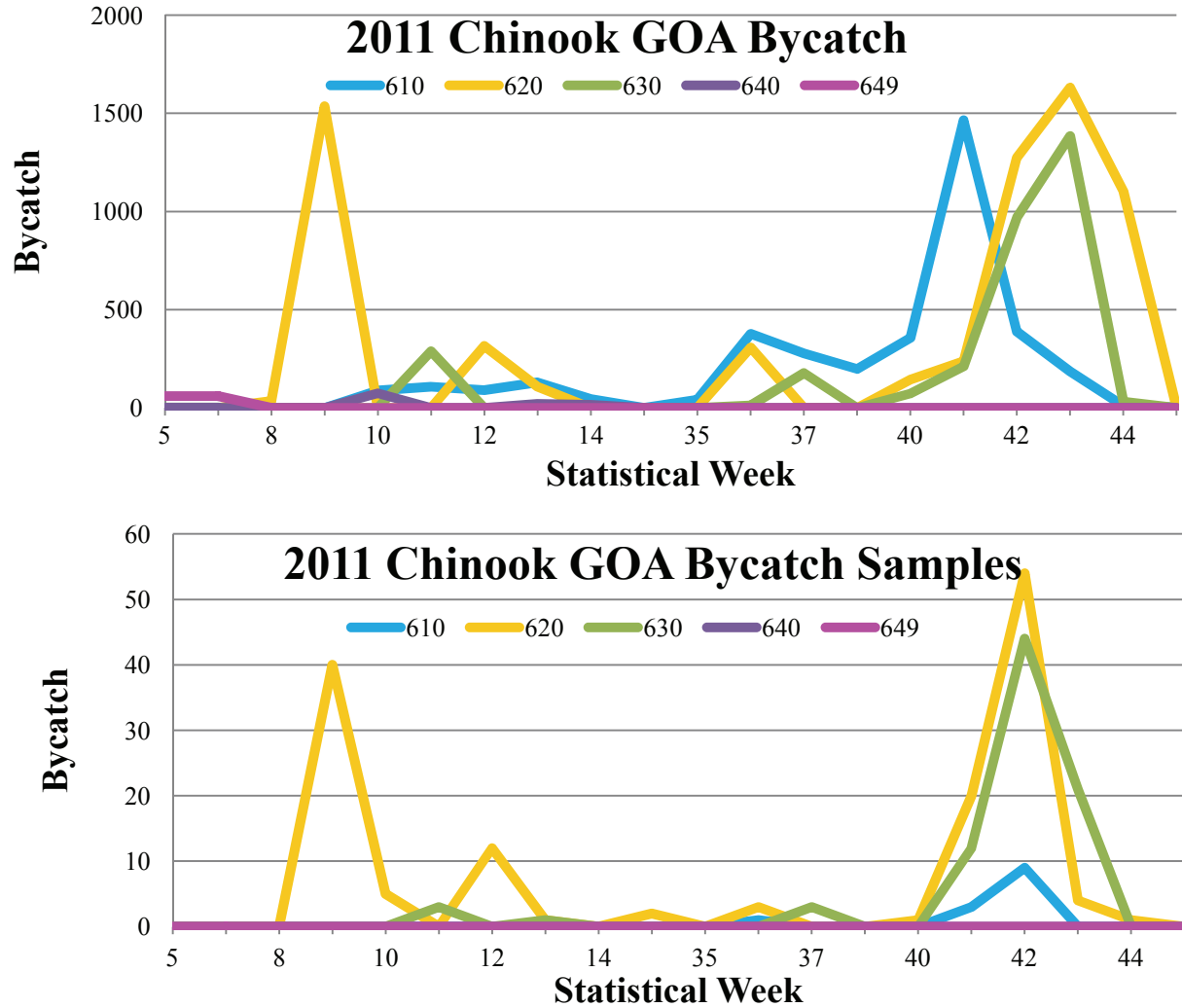
**Figure 5.** -- Yearly estimates for the Chinook salmon bycatch from the GOA pollock trawl fishery (NMFS 2012).

Potential spatial and temporal biases associated with the 2011 Chinook salmon GOA bycatch sample sets were evaluated by comparing the genetic sample distribution with the overall bycatch estimate distribution showing similarities in temporal distribution (Fig. 6). To evaluate the sample spatial distribution, the GOA Chinook salmon bycatch was compared with the bycatch samples by statistical area over time (Fig. 7) highlighting time/space sample distribution issues often associated with opportunistic sampling. The samples were not representative of all areas; for example, area 610 was underrepresented.



**Figure 6.--** Number of Chinook salmon bycatch and genetic samples by statistical week.  
 Top panel: Distribution of all Chinook salmon caught in the 2011 GOA pollock trawl fishery. Bottom panel: Distribution of the available 240 genetic samples from the 2011 bycatch.





**Figure 7.--** 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 2011 GOA pollock trawl fishery. Bottom panel: Distribution of the available 240 genetic samples from the 2011 bycatch.

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

From the 2011 Chinook salmon bycatch, a total of 2,756 samples were analyzed of which 2,720 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 98.7%. These genotypes were analyzed both in GenAlEx (Peakall and Smouse 2006) and using C++ programs written by the Auke Bay Laboratories Genetics Program to confirm data integrity which resulted in the removal of three fish with duplicate genotypes from adjacent wells. An additional four were removed for lack of area information. Of the remaining 2,713, there were 2,473 which from the BSAI and 240 were from the GOA. The remaining samples had genetic information for an average of 41.2 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 1-4).

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). Although Version 3.7b of the SPAM software allows Bayesian modeling of baseline allele frequencies, these options were not utilized for the stock composition analyses. Convergence of the SPAM estimates was monitored with the “Percent of

Maximum” value which was determined to be 90.7 (BSAI “A” estimate), 90.1 (BSAI “B” estimate), 90.3 (BSAI overall estimate) and 90.3 (GOA estimate), exceeding 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 all 1.05 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 85% of the 695 samples from the “A” season originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska stock contributing the most (54%), followed by the North Alaska Peninsula (22%), and Upper Yukon (7%). The other major contributor was British Columbia (7%) (Table 1). For the “B” season, over 79% of the 1,778 samples originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska region contributing the most (74%). This was followed by British Columbia (8%) and the U.S. west coast stock (6%) (Table 2).

**Table 1.** -- Regional BAYES and SPAM stock composition estimates for the 695 Chinook salmon samples from the bycatch of the 2011 “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.

<u>Region</u>	<u>BAYES</u>	<u>SD</u>	<u>2.5%</u>	<u>Median</u>	<u>97.5%</u>	<u>SPAM</u>	<u>SD</u>
Russia	<b>0.002</b>	0.002	0.000	0.001	0.006	<b>0.002</b>	0.002
Coast W AK	<b>0.540</b>	0.023	0.496	0.541	0.585	<b>0.536</b>	0.020
Mid-Yukon	<b>0.018</b>	0.008	0.006	0.017	0.036	<b>0.028</b>	0.004
Up Yukon	<b>0.074</b>	0.011	0.053	0.073	0.097	<b>0.071</b>	0.007
N AK Penn	<b>0.218</b>	0.019	0.181	0.218	0.257	<b>0.198</b>	0.012
NW GOA	<b>0.006</b>	0.006	0.000	0.004	0.022	<b>0.022</b>	0.003
Copper	<b>0.000</b>	0.001	0.000	0.000	0.002	<b>0.000</b>	0.000
NE GOA	<b>0.000</b>	0.001	0.000	0.000	0.002	<b>0.000</b>	0.000
Coast SE AK	<b>0.031</b>	0.009	0.016	0.030	0.049	<b>0.030</b>	0.002
BC	<b>0.072</b>	0.011	0.051	0.072	0.096	<b>0.075</b>	0.006
WA/OR/CA	<b>0.040</b>	0.008	0.026	0.039	0.056	<b>0.039</b>	0.004

**Table 2.** -- Regional BAYES and SPAM stock composition estimates for the 1,778 Chinook salmon samples from the bycatch of the 2011 “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.

<u>Region</u>	<u>BAYES</u>	<u>SD</u>	<u>2.5%</u>	<u>Median</u>	<u>97.5%</u>	<u>SPAM</u>	<u>SD</u>
Russia	<b>0.010</b>	0.003	0.006	0.010	0.016	<b>0.010</b>	0.002
Coast W AK	<b>0.738</b>	0.013	0.713	0.738	0.762	<b>0.733</b>	0.013
Mid-Yukon	<b>0.013</b>	0.005	0.005	0.013	0.022	<b>0.011</b>	0.001
Up Yukon	<b>0.007</b>	0.004	0.001	0.006	0.014	<b>0.008</b>	0.000
N AK Penn	<b>0.034</b>	0.007	0.022	0.034	0.048	<b>0.033</b>	0.003
NW GOA	<b>0.036</b>	0.009	0.020	0.035	0.055	<b>0.038</b>	0.003
Copper	<b>0.006</b>	0.003	0.000	0.006	0.012	<b>0.006</b>	0.001
NE GOA	<b>0.001</b>	0.002	0.000	0.000	0.008	<b>0.004</b>	0.000
Coast SE AK	<b>0.014</b>	0.005	0.006	0.014	0.024	<b>0.015</b>	0.001
BC	<b>0.078</b>	0.007	0.064	0.077	0.092	<b>0.078</b>	0.002
WA/OR/CA	<b>0.064</b>	0.006	0.053	0.064	0.077	<b>0.064</b>	0.003

**Table 3.** -- Regional BAYES and SPAM stock composition estimates for the 2,473 Chinook salmon samples from the bycatch of the 2011 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.

<u>Region</u>	<u>BAYES</u>	<u>SD</u>	<u>2.5%</u>	<u>Median</u>	<u>97.5%</u>	<u>SPAM</u>	<u>SD</u>
Russia	<b>0.008</b>	0.002	0.005	0.008	0.012	<b>0.008</b>	0.001
Coast W AK	<b>0.683</b>	0.012	0.660	0.683	0.706	<b>0.679</b>	0.011
Mid-Yukon	<b>0.016</b>	0.005	0.008	0.016	0.025	<b>0.017</b>	0.001
Up Yukon	<b>0.025</b>	0.005	0.016	0.024	0.034	<b>0.025</b>	0.002
N AK Penn	<b>0.086</b>	0.008	0.071	0.086	0.103	<b>0.079</b>	0.004
NW GOA	<b>0.026</b>	0.007	0.014	0.026	0.041	<b>0.033</b>	0.002
Copper	<b>0.003</b>	0.002	0.000	0.002	0.008	<b>0.004</b>	0.001
NE GOA	<b>0.001</b>	0.001	0.000	0.000	0.004	<b>0.002</b>	0.000
Coast SE AK	<b>0.018</b>	0.004	0.011	0.018	0.026	<b>0.019</b>	0.001
BC	<b>0.078</b>	0.006	0.066	0.078	0.090	<b>0.079</b>	0.002
WA/OR/CA	<b>0.057</b>	0.005	0.048	0.057	0.067	<b>0.056</b>	0.002

**Table 4.** -- Regional BAYES and SPAM stock composition estimates for the 240 Chinook salmon samples from the bycatch of the 2011 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.

<u>Region</u>	<u>BAYES</u>	<u>SD</u>	<u>2.5%</u>	<u>Median</u>	<u>97.5%</u>	<u>SPAM</u>	<u>SD</u>
Russia	<b>0.000</b>	0.001	0.000	0.000	0.001	<b>0.000</b>	0.000
Coast W AK	<b>0.006</b>	0.009	0.000	0.001	0.030	<b>0.006</b>	0.004
Mid-Yukon	<b>0.000</b>	0.001	0.000	0.000	0.002	<b>0.000</b>	0.000
Up Yukon	<b>0.000</b>	0.001	0.000	0.000	0.003	<b>0.000</b>	0.000
N AK Penn	<b>0.000</b>	0.001	0.000	0.000	0.002	<b>0.000</b>	0.000
NW GOA	<b>0.146</b>	0.025	0.100	0.145	0.198	<b>0.140</b>	0.018
Copper	<b>0.041</b>	0.017	0.011	0.040	0.078	<b>0.046</b>	0.010
NE GOA	<b>0.002</b>	0.006	0.000	0.000	0.021	<b>0.010</b>	0.001
Coast SE AK	<b>0.144</b>	0.032	0.085	0.142	0.211	<b>0.125</b>	0.009
BC	<b>0.402</b>	0.040	0.323	0.401	0.480	<b>0.410</b>	0.027
WA/OR/CA	<b>0.260</b>	0.030	0.205	0.260	0.320	<b>0.263</b>	0.022

For the entire year, an estimated 81% 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 (68%), trailed by the North Alaska Peninsula (9%). Other contributors were British Columbia (8%), and U.S. west coast (6%) (Table 3). The “overall” and “B” season stock compositions were similar, which was anticipated given that 72% of the samples were from the “B” season. In 2011, 72% of the Chinook salmon bycatch was from the “B” season of the Bering Sea pollock fishery.

### Gulf of Alaska

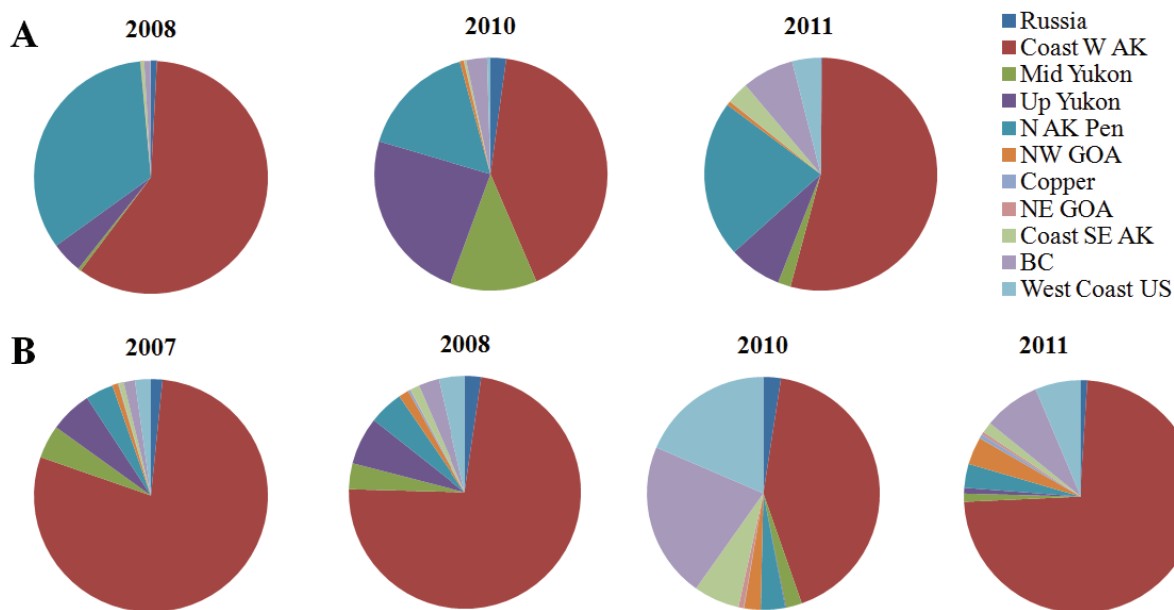
The BAYES results estimate that 99% of the 240 samples from the GOA originated from GOA/Pacific coastal regions, with the British Columbia contributing the most (40%), followed by the West Coast US (26%) and Coastal Southeast Alaska (14%; Table 4).

### 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 2011 “A” season Chinook salmon bycatch samples were in general agreement with the 2008 and 2010 “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 2011 “A” season sample sets including the Upper and Middle Yukon estimated contribution which decreased in 2011 while the Western Alaska and the North Alaska Peninsula estimated contributions increased (Fig. 8). Although the 2008 and 2011 “A” season contribution estimates

were more similar, larger amounts of more southern stocks (Coastal Southeast Alaska, British Columbia, and west coast US) were estimated in 2011 than 2008 and 2010.

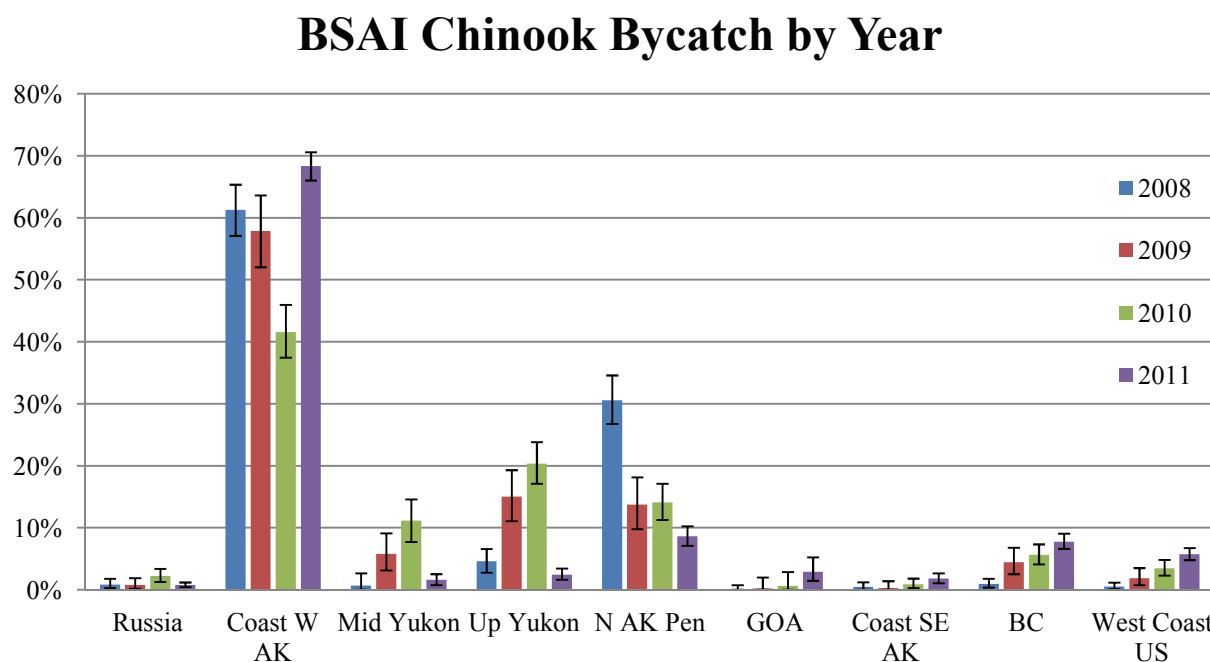
Likewise, the 2007, 2008, and 2011 “B” season stock composition estimates were similar with large amounts from Coastal Western Alaska (Fig 8.) In contrast with the 2010 “B” season estimate, the 2011 “B” season estimate identified smaller contributions from British Columbia, West Coast U.S. and Coastal Southeast Alaska stocks. Unlike previous years studied, most of the Chinook salmon bycatch occurred during the “B” season such that the sample set was relatively large this year. In addition, 2011 was the first year systematic random sampling was employed where genetic samples were collected from one of every 10 Chinook salmon encountered. The combined size of the sample set and the proportional sampling methods employed help make the 2011 “B” season estimates representative of the total catch.



**Figure 8.--** Comparison of “A” season genetic stock composition estimates for 2008,2010 and 2011 based on available genetic samples from the BSAI Chinook salmon bycatch. Comparison of “B” season genetic stock composition estimates for 2007, 2008, 2010, and 2011 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.

While changes in sampling protocols between years necessitate caution in comparing annual analyses across years, when the stock compositions were analyzed for the entire year, Coastal Western Alaska and North Alaska Peninsula stock compositions trended downward between 2008 and 2010 but increased in 2011 (Fig. 10). The Yukon River contribution dropped to its lowest levels in 2011, while British Columbia and West Coast U.S. stock compositions continued to trend upward (Fig. 9).

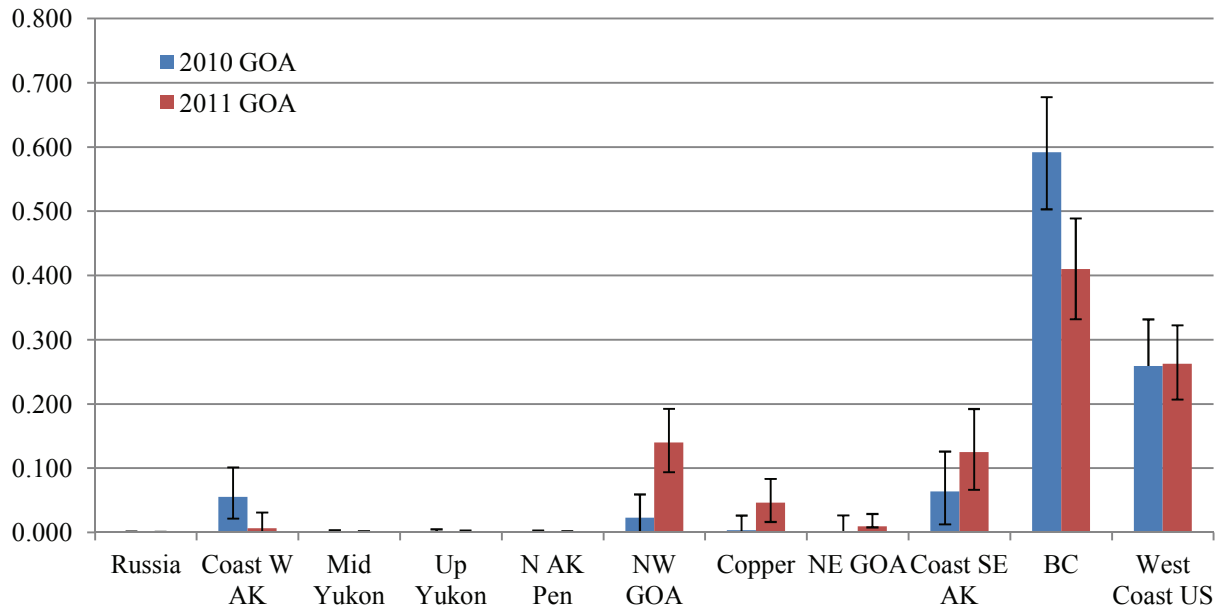
For the GOA, the opportunistic sampling protocols employed between 2010 and 2011 limit the results to indentifying only presence of individual stocks. In addition, available sample numbers were very low, with 161 samples from 2010 (0.4% sampling rate) and 240 samples in



**Figure 9.** -- Comparison of yearly stock composition estimates (2008-2011) based on genetic samples from the Bering Sea 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.



## 2010 and 2011 GOA Chinook Salmon Bycatch



**Figure 10.** -- Comparison of yearly stock composition estimates (2010-2011) 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.

2011 (1.7% sampling rate). Recognizing these limitations, Figure 10 shows the stock composition of the GOA collected in 2010 and 2011, and both years show an abundance of Southern stock groups; British Columbia, West Coast US, NW GOA, and Coastal Southeast Alaska.

### 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 the recent declaration of a fisheries disaster for Yukon River Chinook salmon in 2010 and 2012 by the U. S. Secretaries 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. The incidental harvest of Chinook salmon in the Bering Sea pollock fishery averaged 39,888 salmon per year during 1991-2011, but steadily 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 25,499 Chinook salmon in 2011, a number which is approximately 14,000 fish below the 20-year average, but the most since 2007.

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 14,574 salmon per year during 1991-2011, with a peak of 44,779 in 2010. The GOA Chinook salmon bycatch dropped to just below the 21-year average in 2011 to 13,837 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 a stock composition analysis of genetic sample sets from the 2011 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 Bering Sea Chinook salmon prohibited species catch, this is the first year from which representative samples have been collected. 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. 3 and 4). The observed genetic sampling rate in 2011 was 9.7%, the highest ever observed and in close agreement with the one in 10 sampling goal. The resulting Chinook salmon Bering Sea bycatch sample set was 2,473, about four times the size of the sample sets from previous Bering Sea analyses.

#### Gulf of Alaska

Although opportunistic sampling was employed in both 2010 and 2011 for the collection of the GOA Chinook salmon bycatch genetic samples, the sampling effort improved from a 0.4% sampling rate in 2010 to 1.7% in 2011 although the overall sample set remained quite small at 240 samples in 2011. The lack of representative samples and the small sample size preclude calculating statistically reliable stock composition estimates of the 2011 GOA Chinook salmon bycatch as a whole. Nonetheless the stock composition of the available samples provides at least an indication of stock presence.

### Stock Composition Estimates

#### Bering Sea-Aleutian Islands

Genetic stock composition analysis showed the majority of bycatch samples were from Alaskan stocks predominantly originating from river systems directly flowing into the Bering Sea. The Chinook salmon bycatch stock composition estimates for the 2011 “A” season differed from those of the 2011 “B” season, suggesting temporal differences in the available Chinook salmon stocks. This was especially apparent in the following stock groups: Coastal Western Alaska (54% vs. 74%), Middle/Upper Yukon (9% vs. 2%), and the North Alaska Peninsula (22% vs. 3%). For the first time since 2005, the size of the Bering Sea Chinook salmon bycatch was

higher in the “B” season than the “A” season. Approximately (72%) of the Chinook salmon genetic samples were collected from the 2011 “B” season, a result that might help explain differences in overall stock contribution between previous years (Fig. 9).

#### Gulf of Alaska

As in 2010, the opportunistic nature in which genetic samples were collected from the GOA Chinook salmon bycatch limits the 2011 stock composition results to presence indicators. As in 2010, the 2011 GOA Chinook salmon bycatch samples were predominantly from the west coast of the United States, British Columbia, and Coastal Southeast Alaska (Fig. 10).

#### 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 infer 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 and the small sample sets used for the GOA estimates limit the application of those estimates to presence of a stock group.

## ACKNOWLEDGMENTS

Genotyping for this analysis was funded by the Alaska Fisheries Science Center, National Marine Fisheries Service, the North Pacific Fisheries Research Foundation, and the Alaska Sustainable Salmon Fund. We are grateful to Chris Habicht and Bill Templin of the ADF&G Gene Conservation Laboratory for providing suggestions and advice regarding the analysis, and reviewing this report. We are also grateful for the help from the AFSC's FMA Program including Martin Loefflad, Liz Chilton, and the many participating observers who helped fulfill our request for genetic samples. MALDI-TOF genotyping and assay design performed in collaboration with Colleen Ramsower and Dr. Ryan Sprissler from the genotyping core facility at the University of Arizona. Phil Mundy and Adrian Celewycz helped review the report. Special thanks to AFSC editor James Lee for his fast and thorough editorial review of this document.



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## APPENDIX

Appendix 1.-- Chinook salmon populations in the ADF&G SNP baseline with the regional designations used in the analyses of this report.

ADF&G number	Population name	Region number	Region
1	Bistraya River	1	Russia
2	Bolshaya River	1	Russia
3	Kamchatka River late	1	Russia
4	Pakhatcha River	1	Russia
8	Andreafsky River	2	Coast W AK
40	Aniak River	2	Coast W AK
9	Anvik River	2	Coast W AK
34	Arolik River	2	Coast W AK
54	Big Creek	2	Coast W AK
44	Cheeneetnuk River	2	Coast W AK
36	Eek River	2	Coast W AK
45	Gagaryah River	2	Coast W AK
41	George River	2	Coast W AK
10	Gisasa River	2	Coast W AK
7	Golsovia River	2	Coast W AK
33	Goodnews River	2	Coast W AK
35	Kanektok River	2	Coast W AK
38	Kisaralik River	2	Coast W AK
42	Kogruluk River	2	Coast W AK
37	Kwethluk River	2	Coast W AK
51	Mulchatna River	2	Coast W AK
53	Naknek River	2	Coast W AK
50	Nushagak River	2	Coast W AK
5	Pilgrim River	2	Coast W AK
48	Salmon River - Pitka Fork	2	Coast W AK
43	Stony River	2	Coast W AK
52	Stuyahok River	2	Coast W AK
46	Takotna River	2	Coast W AK
47	Tatlawiksuk River	2	Coast W AK
49	Togiak River	2	Coast W AK
11	Tozitna River	2	Coast W AK
39	Tuluksak River	2	Coast W AK
6	Unalakleet River	2	Coast W AK
17	Beaver Creek	3	Mid Yukon
18	Chandalar River	3	Mid Yukon
15	Chena River	3	Mid Yukon
12	Henshaw Creek	3	Mid Yukon
14	Kantishna River	3	Mid Yukon
16	Salcha River	3	Mid Yukon
19	Sheenjek River	3	Mid Yukon
13	South Fork Koyukuk River	3	Mid Yukon
27	Big Salmon River	4	Up Yukon

ADF&G number	Population name	Region number	Region
24	Blind River	4	Up Yukon
20	Chandindu River	4	Up Yukon
21	Klondike River	4	Up Yukon
26	Little Salmon River	4	Up Yukon
23	Mayo River	4	Up Yukon
30	Nisutlin River	4	Up Yukon
29	Nordenskiold River	4	Up Yukon
25	Pelly River	4	Up Yukon
22	Stewart River	4	Up Yukon
31	Takhini River	4	Up Yukon
28	Tatchun Creek	4	Up Yukon
32	Whitehorse Hatchery	4	Up Yukon
59	Black Hills Creek	5	N AK Pen
55	King Salmon River	5	N AK Pen
56	Meshik River	5	N AK Pen
57	Milky River	5	N AK Pen
58	Nelson River	5	N AK Pen
60	Steelhead Creek	5	N AK Pen
78	Anchor River	6	NW GOA
62	Ayakulik River	6	NW GOA
72	Benjamin Creek	6	NW GOA
61	Chignik River	6	NW GOA
69	Crescent Creek	6	NW GOA
76	Crooked Creek	6	NW GOA
65	Deception Creek	6	NW GOA
64	Deshka River	6	NW GOA
73	Funny River	6	NW GOA
70	Juneau Creek	6	NW GOA
63	Karluk River	6	NW GOA
77	Kasilof River mainstem	6	NW GOA
75	Kenai River mainstem	6	NW GOA
71	Killey Creek	6	NW GOA
79	Ninilchik River	6	NW GOA
67	Prairie Creek	6	NW GOA
74	Slikok Creek	6	NW GOA
68	Talachulitna River	6	NW GOA
66	Willow Creek	6	NW GOA
81	Bone Creek	7	Copper
82	E. Fork Chistochina River	7	Copper
85	Gulkana River	7	Copper
80	Indian River	7	Copper
87	Kiana Creek	7	Copper
88	Manker Creek	7	Copper
86	Mendeltna Creek	7	Copper
83	Otter Creek	7	Copper
84	Sinona Creek	7	Copper
90	Tebay River	7	Copper
89	Tonsina River	7	Copper
92	Big Boulder Creek	8	NE GOA

ADF&G number	Population name	Region number	Region
95	Kelsall River	8	NE GOA
96	King Salmon River	8	NE GOA
116	Klukshu River	8	NE GOA
91	Situk River	8	NE GOA
93	Tahini River	8	NE GOA
94	Tahini River - Pullen Creek Hatchery	8	NE GOA
111	Andrews Creek	9	Coast SE AK
110	Blossom River	9	Coast SE AK
102	Butler Creek	9	Coast SE AK
98	Chickamin River	9	Coast SE AK
99	Chickamin River - Little Port Walter	9	Coast SE AK
100	Chickamin River - Whitman Lake Hatchery	9	Coast SE AK
103	Clear Creek	9	Coast SE AK
104	Cripple Creek	9	Coast SE AK
112	Crystal Lake Hatchery	9	Coast SE AK
121	Dudidontu River	9	Coast SE AK
105	Genes Creek	9	Coast SE AK
114	Hidden Falls Hatchery	9	Coast SE AK
101	Humpy Creek	9	Coast SE AK
106	Kerr Creek	9	Coast SE AK
109	Keta River	9	Coast SE AK
97	King Creek	9	Coast SE AK
117	Kowatua River	9	Coast SE AK
118	Little Tatsemenie River	9	Coast SE AK
115	Macaulay Hatchery	9	Coast SE AK
113	Medvejie Hatchery	9	Coast SE AK
120	Nakina River	9	Coast SE AK
122	Tahltn River	9	Coast SE AK
108	Unuk River - Deer Mountain Hatchery	9	Coast SE AK
107	Unuk River - Little Port Walter	9	Coast SE AK
119	Upper Nahlin River	9	Coast SE AK
143	Big Qualicum River	10	BC
157	Birkenhead River spring	10	BC
128	Bulkley River	10	BC
148	Chilko River summer	10	BC
152	Clearwater River summer	10	BC
138	Conuma River	10	BC
124	Damdochax Creek	10	BC
130	Ecstall River	10	BC
158	Harrison River	10	BC
123	Kateen River	10	BC
125	Kincolith Creek	10	BC
133	Kitimat River	10	BC
135	Klinaklini River	10	BC
126	Kwinageese Creek	10	BC
153	Louis River spring	10	BC
154	Lower Adams River fall	10	BC
132	Lower Atnarko River	10	BC
131	Lower Kalum River	10	BC

ADF&G number	Population name	Region number	Region
155	Lower Thompson River fall	10	BC
139	Marble Creek	10	BC
156	Middle Shuswap River summer	10	BC
145	Morkill River summer	10	BC
136	Nanaimo River	10	BC
149	Nechako River summer	10	BC
140	Nitinat River	10	BC
127	Oweegee Creek	10	BC
137	Porteau Cove	10	BC
150	Quesnel River summer	10	BC
144	Quinsam River	10	BC
141	Robertson Creek	10	BC
146	Salmon River summer	10	BC
142	Sarita River	10	BC
151	Stuart River summer	10	BC
129	Sustut River	10	BC
147	Torpy River summer	10	BC
134	Wannock River	10	BC
168	Alsea River fall	11	West Coast US
166	Carson Hatchery spring	11	West Coast US
171	Eel River fall	11	West Coast US
160	Forks Creek fall	11	West Coast US
164	Hanford Reach	11	West Coast US
170	Klamath River	11	West Coast US
165	Lower Deschutes River fall	11	West Coast US
163	Lyons Ferry Hatchery summer/fall	11	West Coast US
159	Makah National Fish Hatchery fall	11	West Coast US
167	McKenzie River spring	11	West Coast US
172	Sacramento River winter	11	West Coast US
169	Siuslaw River fall	11	West Coast US
162	Soos Creek Hatchery fall	11	West Coast US
161	Upper Skagit River summer	11	West Coast US



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