Genetic Stock Composition Analysis of the Chinook Salmon Bycatch from the 2013 Bering Sea Walleye Pollock (*Gadus chalcogrammus*) Trawl Fishery

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

www.afsc.noaa.gov

ABSTRACT

A genetic analysis of samples from the Chinook salmon (*Oncorhynchus tshawytscha*) bycatch of the 2013 Bering Sea-Aleutian Island (BSAI) trawl fishery for walleye pollock (*Gadus chalcogrammus*) was undertaken to determine the overall stock composition of the bycatch. 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 2013, 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 1,246 Chinook salmon bycatch samples collected throughout the 2013 BSAI walleye pollock trawl fishery, Coastal Western Alaska stocks dominated the sample set (50%) with smaller contributions from British Columbia (16%), North Alaska Peninsula (14%), 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 Upper Yukon stocks and higher contributions of West Coast U.S. and NW Gulf of Alaska stocks during the "B" season.

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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 Pacific 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 the Chinook salmon bycatch samples collected from the U.S. Bering Sea-Aleutian Island (BSAI) pollock trawl fishery. National Marine Fisheries Service (NMFS) geographical statistical areas associated with the BSAI groundfish fishery (areas 509-524) are
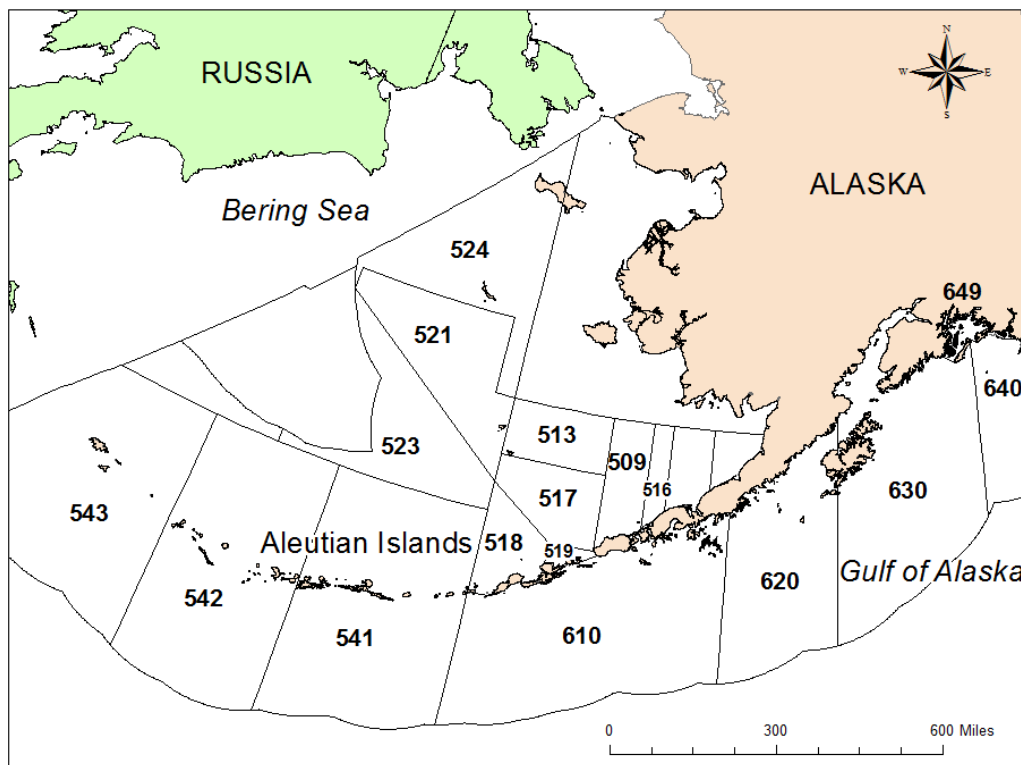

Figure 1. -- NMFS statistical areas associated with the Bering Sea-Aleutian Island (BSAI) and Gulf of Alaska (GOA) groundfish fisheries.

shown in Figure 1 and are used later in the report to describe the spatial distribution of the Chinook salmon bycatch and genetic samples.

In 2013, genetic samples were collected by the AFSC's North Pacific Groundfish Observer Program (NPGOP) from the Chinook salmon bycatch of the BSAI pollock fishery using the systematic sampling protocols recommended previously (Pella and Geiger 2009). The number of available samples and the unbiased methodology in which they were collected facilitated the extrapolation of the sample stock composition to the overall Chinook bycatch from the BSAI pollock trawl fishery in 2013. Stock composition analyses were performed using the single nucleotide polymorphism (SNP) baseline provided by the Alaska Department of Fish and Game (ADF&G) (Templin et al. 2011), the same baseline that was used previously to estimate stock composition of samples from the 2005-2012 Chinook salmon bycatch (NMFS 2009; Guyon et al. 2010a, b; Guthrie et al. 2012, 2013, and 2014; 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).

SAMPLE DISTRIBUTION

Samples were collected from the Chinook salmon bycatch by the NPGOP for analysis at AFSC's 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 NPGOP to collect genetic samples from one out of every 10 Chinook salmon encountered as bycatch in the BSAI pollock fishery. Samples of axillary

process tissue were collected from the Chinook salmon bycatch throughout 2013. Axillary process tissues were stored in coin envelopes which were labeled, frozen, and shipped to ABL for analysis.

In 2013, an estimated 13,033 Chinook salmon were taken in the bycatch of BSAI pollock trawl fisheries (NMFS 2014). Of the total bycatch, 8,236 were from the trawl "A" season and 4,797 were from the "B" season. These estimates are very similar to the Chinook salmon bycatch estimates from 2012, and represent a 49% reduction of the total Chinook salmon bycatch from 2011 levels (Fig. 2). 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. In 2013, there were 1,273 genetic samples from the BSAI Chinook salmon bycatch collected by the NPGOP; of those 1,246 were successfully genotyped for an overall sampling rate of 9.6% ("A" season -792 fish, 9.6% sampling rate; "B" season - 454 fish, 9.5% sampling rate).
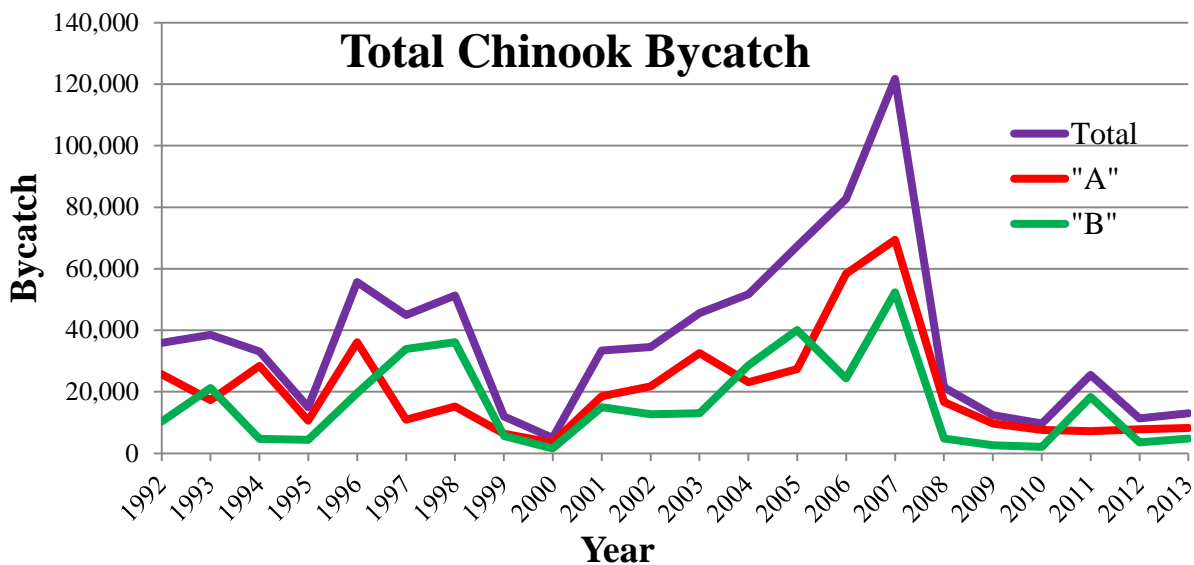
Figure 2. -- Yearly, "A" season, and "B" estimates for the Chinook salmon bycatch from the BSAI pollock trawl fishery (NMFS 2014).

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). Sample distributions for the 2013 Chinook salmon bycatch sample sets were evaluated by comparing the collection of genetic samples with the overall bycatch distribution which were comparable in their temporal distribution (Fig. 3). 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.
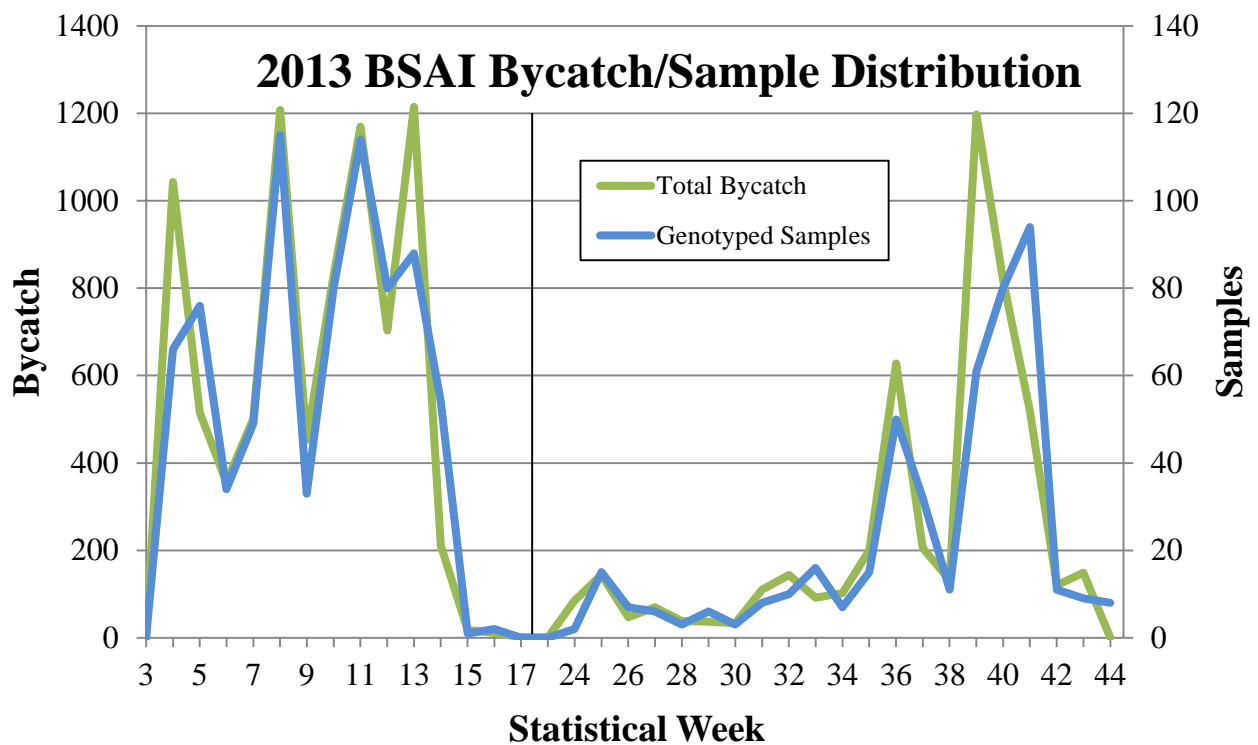
Figure 3. -- Number of Chinook salmon bycatch and genetic samples graphed by statistical week. Distribution of all Chinook salmon caught in the 2013 Bering Sea pollock trawl fishery (green line, left scale). Distribution of the 1,246 genotyped samples from the 2013 bycatch (blue line, right scale). Weeks 3-17 correspond to the groundfish "A" season, whereas weeks 23-44 correspond to the "B" season, the demarcation of which is a vertical line.

2013 was the third year systematic random sampling was employed for collecting genetic tissue from the Bering Sea Chinook salmon bycatch and Figure 4 shows that the resulting samples were collected in proportion through time and space with the total catch. As in 2011 and 2012, the sample spatial and temporal distribution was excellent in 2013 compared to previous years when samples were collected more opportunistically (Guyon et al. 2010a, 2010b; Guthrie et al. 2012, 2013, 2014).

2013 Chinook BSAI Bycatch

2013 Chinook BSAI Samples
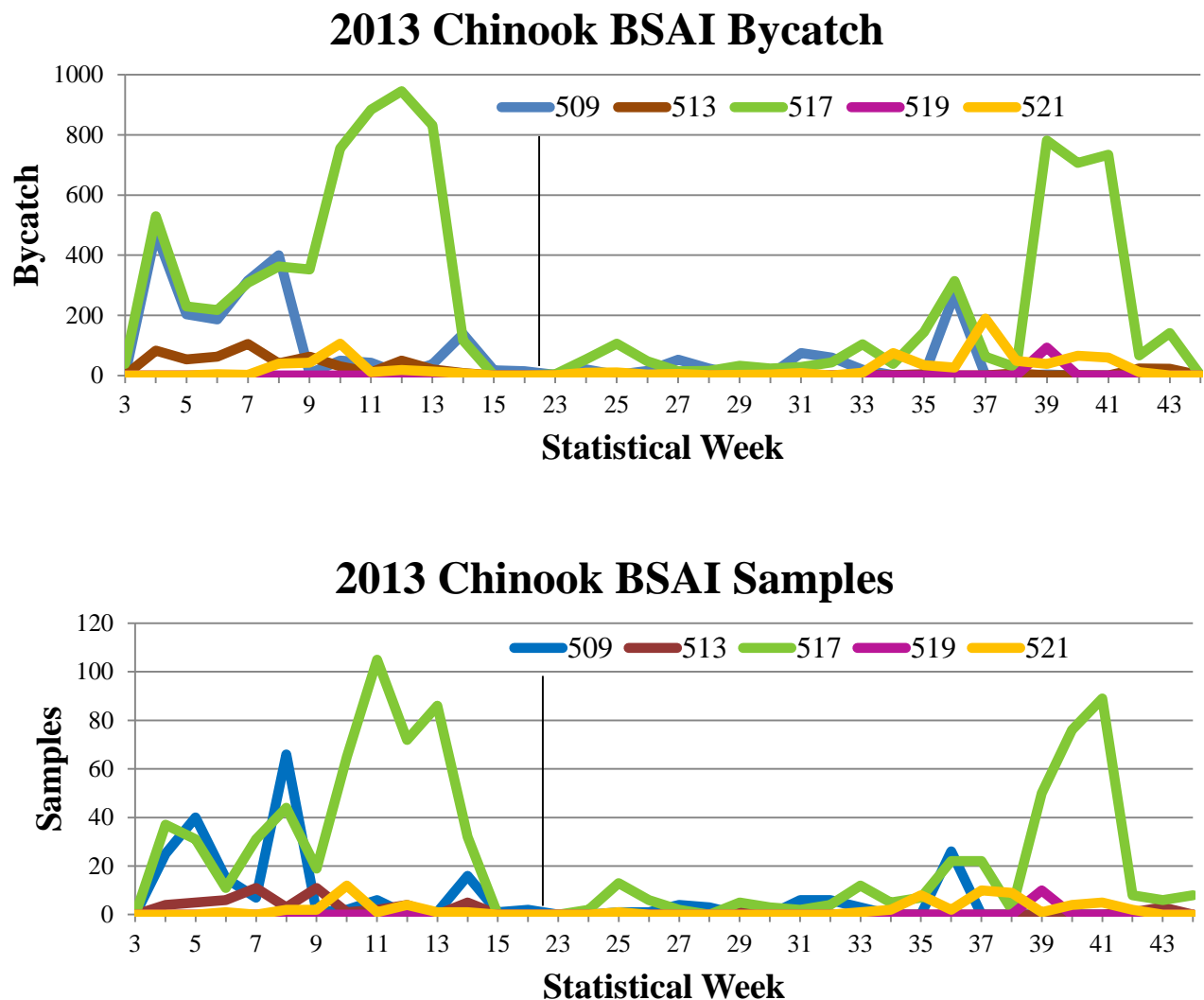
Figure 4. -- Comparison of the Chinook salmon bycatch by time and area with the distribution of available genetic samples. Top panel: Distribution of the Chinook salmon caught in the 2013 BSAI pollock trawl fishery. Not graphed were 2 fish from NMFS area 508 and 8 fish from NMFS area 524. Bottom panel: Distribution of the 1,246 genotyped samples from the 2013 bycatch. Not graphed was 1 fish from NMFS area 508. Weeks 3-16 correspond to the groundfish "A" season, whereas weeks 23-44 correspond to the "B" season, the demarcation of which is a vertical line.

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 (see Appendix). This baseline was used previously for the genetic analysis of the 2005-2012 Chinook bycatch (NMFS 2009; Guyon et al. 2010a, b; Guthrie et al. 2012, 2013, 2014). 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 99.8% between the two chemistries for the 2013 controls confirmed the utility and compatibility of both genotyping methods.

From the 2013 Chinook salmon bycatch from the BSAI pollock trawl fishery, a total of 1,273 samples were analyzed of which 1,246 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 97.9%. These genotypes were analyzed using C++ programs written by the ABL's Genetics Program to check for duplicate samples and none were found. The remaining samples had genetic information for an average of 42.3 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).

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 1.03 or less for all the estimates, conveying strong convergence to a single posterior distribution (Pella and Masuda 2001).

Results (BAYES) suggest that 78% of the 792 samples from the "A" season originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska stock contributing the most (50%), followed by the North Alaska Peninsula (19%), and Upper Yukon (7%). The other major contributor was British Columbia (17%) (Table 1). For the "B" season, over 61% of the 454 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 (15%) and British Columbia (14%) (Table 2).

Table 1. -- Regional BAYES and SPAM stock composition estimates for the 792 Chinook salmon samples from the bycatch of the 2013 "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	**0.009**	0.004	0.004	0.009	0.017	**0.010**	0.004
Coast W AK	**0.502**	0.022	0.460	0.502	0.545	**0.497**	0.020
Mid-Yukon	**0.011**	0.006	0.000	0.010	0.026	**0.011**	0.005
Up Yukon	**0.072**	0.011	0.051	0.071	0.094	**0.069**	0.011
N AK Penn	**0.191**	0.018	0.157	0.191	0.228	**0.179**	0.016
NW GOA	**0.005**	0.007	0.000	0.002	0.024	**0.019**	0.008
Copper	**0.001**	0.001	0.000	0.000	0.005	**0.004**	0.003
NE GOA	**0.000**	0.001	0.000	0.000	0.004	**0.005**	0.003
Coast SE AK	**0.019**	0.007	0.008	0.019	0.034	**0.017**	0.006
BC	**0.170**	0.014	0.142	0.169	0.198	**0.167**	0.014
WA/OR/CA	**0.020**	0.006	0.010	0.019	0.033	**0.023**	0.006

Table 2. -- Regional BAYES and SPAM stock composition estimates for the 454 Chinook salmon samples from the bycatch of the 2013 "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	**0.009**	0.005	0.002	0.008	0.020	**0.008**	0.005
Coast W AK	**0.519**	0.028	0.464	0.519	0.573	**0.494**	0.027
Mid-Yukon	**0.019**	0.010	0.004	0.018	0.042	**0.018**	0.008
Up Yukon	**0.014**	0.009	0.000	0.013	0.034	**0.017**	0.008
N AK Penn	**0.059**	0.015	0.034	0.058	0.090	**0.065**	0.015
NW GOA	**0.069**	0.018	0.035	0.068	0.107	**0.085**	0.019
Copper	**0.001**	0.003	0.000	0.000	0.009	**0.005**	0.004
NE GOA	**0.000**	0.002	0.000	0.000	0.004	**0.002**	0.003
Coast SE AK	**0.019**	0.011	0.001	0.018	0.045	**0.017**	0.008
BC	**0.143**	0.019	0.108	0.143	0.182	**0.146**	0.018
WA/OR/CA	**0.148**	0.017	0.116	0.147	0.182	**0.145**	0.017

Table 3. -- Regional BAYES and SPAM stock composition estimates for the 1,246 Chinook salmon samples from the bycatch of the 2013 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	**0.009**	0.003	0.004	0.008	0.015	**0.009**	0.003
Coast W AK	**0.501**	0.018	0.467	0.501	0.535	**0.497**	0.018
Mid-Yukon	**0.018**	0.007	0.006	0.017	0.031	**0.014**	0.005
Up Yukon	**0.050**	0.008	0.035	0.050	0.067	**0.050**	0.008
N AK Penn	**0.142**	0.014	0.116	0.142	0.170	**0.136**	0.012
NW GOA	**0.034**	0.010	0.018	0.034	0.055	**0.043**	0.009
Copper	**0.001**	0.002	0.000	0.000	0.007	**0.004**	0.002
NE GOA	**0.000**	0.001	0.000	0.000	0.003	**0.003**	0.003
Coast SE AK	**0.024**	0.006	0.013	0.024	0.036	**0.018**	0.005
BC	**0.155**	0.011	0.134	0.155	0.178	**0.159**	0.011
WA/OR/CA	**0.067**	0.008	0.052	0.066	0.082	**0.067**	0.008

For the entire year, an estimated 71% 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 (50%), trailed by the North Alaska Peninsula (14%) and the Upper Yukon (5%). Other contributors were British Columbia (16%) and West Coast U.S. (7%) (Table 3).

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 2013 "A" season Chinook salmon bycatch samples were in general agreement with the 2008, and 2010-12 "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 4 "A" season sample sets. The Upper and Middle Yukon estimated

contribution in 2013 were at levels similar to 2011 and 2012, while the Coastal Western Alaska

contributions decreased slightly (Fig. 5). Although the 2008, 2011, 2012 and 2013 "A" season

contribution estimates were generally similar, 2013 continued the trend of increasing amounts of

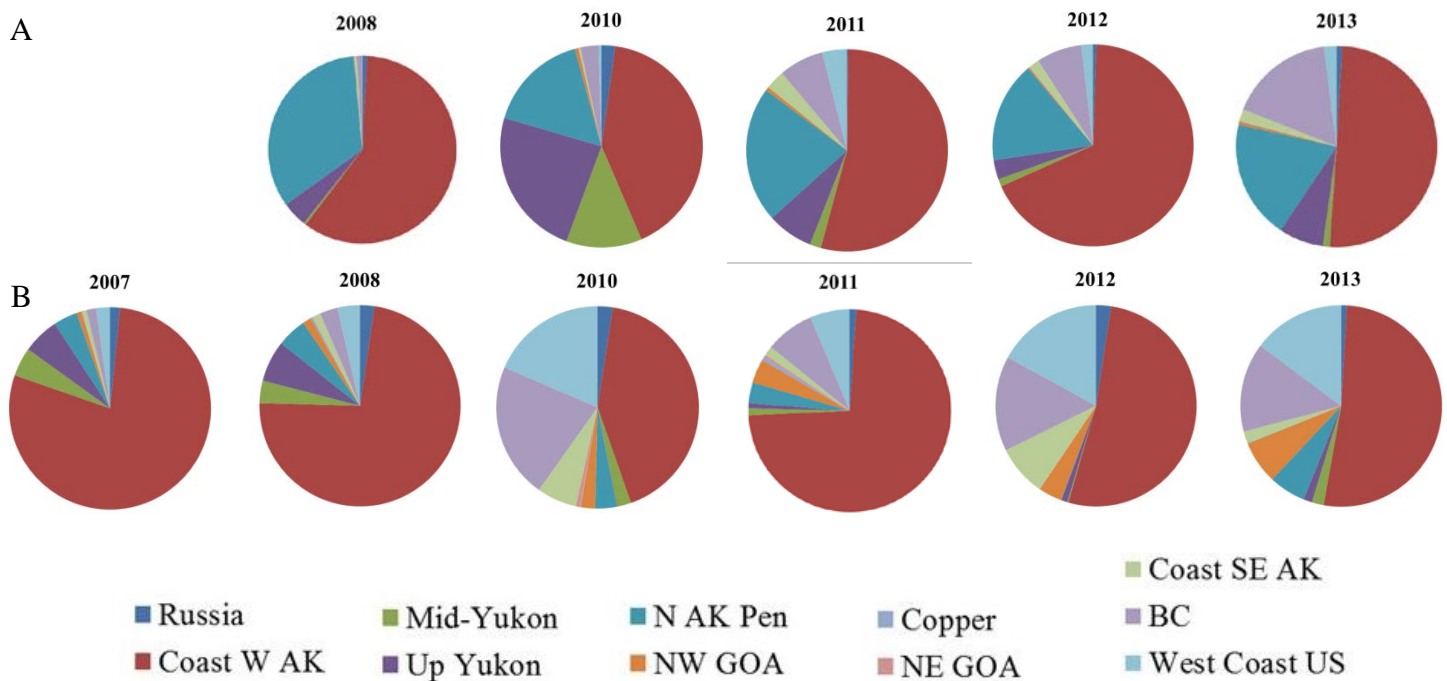southern stocks (Coastal Southeast Alaska, British Columbia, and West Coast U.S.) (Fig. 5).

Figure 5. -- Comparison of "A" season genetic stock composition estimates for 2008 and 2010-13 from the BSAI Chinook salmon bycatch. Comparison of "B" season genetic stock composition estimates for 2007, 2008, and 2010-13 stock composition estimates from the BSAI "B" season Chinook salmon bycatch. Estimates from 2011-13 are overall bycatch estimates whereas earlier compositions are of available sample sets. The same genetic baseline and regional groupings were used in all analyses.

The 2007, 2008, and 2011 "B" season stock composition estimates were similar with

large amounts from Coastal Western Alaska (Fig. 5). In contrast with the other "B" season

estimates, the 2010, 2012 and 2013 "B" season estimates identified larger contributions of the

sample set 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 2013 during the "A" season. As in 2011 and 2012, systematic random

sampling was employed in 2013, 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 are trending downward again in 2013 (Fig. 6). North Alaska

Peninsula stock compositions have remained consistent since 2009 composing 14% of the

bycatch in 2013 (Fig. 6). The upper and middle Yukon River contribution continued to be low

in 2013, while Coastal Southeast Alaska, British Columbia and West Coast U.S. stock

compositions continued their 6-year upward trend (Fig. 6).
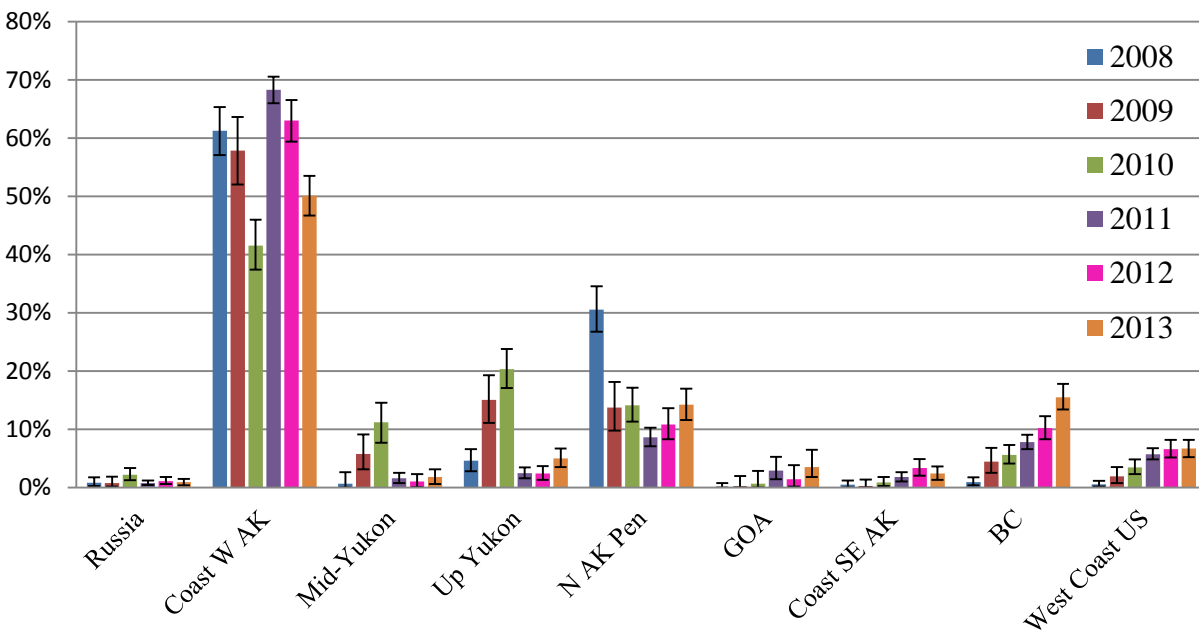
Figure 6. -- Comparison of yearly stock composition estimates (2008-2013) from the BSAI Chinook salmon bycatch. Estimates from 2011-13 are overall bycatch estimates whereas earlier compositions are of available sample sets. The same genetic baseline and general regional groupings were used in all analyses. GOA group consists of combined values for NWGOA, Copper, and NE GOA. BAYES 95% credible intervals are plotted for yearly estimates.

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 37,357 salmon per year during 1992-2013, but increased to a peak of 121,770 in 2007 (NMFS 2014). The Bering Sea Chinook salmon bycatch has abated in more recent years dropping to a total of 13,033 Chinook salmon in 2013, a number which is 24,324 fish below the 22-year average. 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 the Chinook salmon bycatch from the 2013 Bering Sea pollock trawl fishery. The results and limitations of this analysis are summarized below.

Sampling Issues

With the implementation of systematic random sampling in the 2011 prohibited species catch, 2013 is the third 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. 3 and 4). The observed genetic sampling rate in 2013 was 9.6%, not including the 27 samples that did not successfully genotype. The resulting final Chinook salmon Bering Sea bycatch sample set was 1,246.

Stock Composition Estimates

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 2013 "A" season differed from the 2013 "B" season, demonstrating temporal differences in the stocks intercepted. This was especially apparent in the North Alaska Peninsula (19% vs. 6%), Upper Yukon (7% vs. 1.4%), West Coast U.S. (2% vs. 15%), and NW GOA (1% vs. 7%) stock groups.

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 2013 Bering Sea Chinook salmon bycatch were performed using representative samples and the estimates are considered to be representative of the overall bycatch for this year.

ACKNOWLEDGMENTS

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APPENDIX

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

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

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

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

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