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Genetic Stock Composition Analysis of the Chinook Salmon (*Oncorhynchus tshawytscha)* Bycatch from the 2016 Bering Sea Walleye Pollock (*Gadus chalcogrammus*) Trawl Fishery

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

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by

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

Auke Bay Laboratories
Alaska Fisheries Science Center
National Marine Fisheries Service
National Oceanic and Atmospheric Administration
17109 Pt. Lena Loop Road
Juneau, AK 99801

www.afsc.noaa.gov

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iii

ABSTRACT

A genetic analysis of samples from the Chinook salmon (*Oncorhynchus tshawytscha*) bycatch of the 2016 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 2016, 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 1,910 Chinook salmon bycatch samples collected throughout the 2016 BSAI walleye pollock trawl fishery, Coastal Western Alaska and British Columbia regions (34% and 29% respectively) dominated the sample set with smaller contributions from West Coast US (14%), and North Alaska Peninsula (13%) regions. 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 Coastal Western Alaska and North Alaska Peninsula regions and higher contributions of West Coast US, British Columbia, and NW Gulf of Alaska, regions during the "B" season when compared to the "A" season.

v

CONTENTS

INTRODUCTION

Pacific salmon (*Oncorhynchus* spp.) are prohibited species in the federally managed Bering Sea and Gulf of Alaska (GOA) groundfish fisheries, which are subject to complex management rules (NPMFC 2017a,b) that are in part designed to reduce prohibited species catch (PSC; hereafter referred to as "bycatch"). It is important to understand the stock composition of Pacific salmon caught in these fisheries, which take place in areas that are known feeding habitat for multiple brood years of Chinook salmon (*Oncorhynchus tshawytscha*) from many different localities in North America and Asia (Myers et al. 2007, Davis et al. 2009). Chinook salmon are economically valuable and highly prized in commercial, subsistence and sport fisheries. Determining the geographic origin of salmon caught in federally managed fisheries is essential to understanding the effects that fishing has on Chinook salmon stocks, especially those with conservation concerns (NPFMC 2012). This report provides genetic stock identification results for the Chinook salmon bycatch samples collected from the U.S. Bering Sea (BS) walleye pollock (*Gadus chalcogrammus*) trawl fishery. National Marine Fisheries Service (NMFS) geographical statistical areas (NMFS area) associated with the BS groundfish fishery (areas 509-524) and Alaska Department of Fish and Game (ADF&G) statistical areas (for details see http://www.adfg.alaska.gov/static/fishing/PDFs/commercial/chart03_bs.pdf) 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.

Amendment 91 to the North Pacific Fishery Management Council (NPFMC) Fishery Management Plan (FMP) for groundfish of the BSAI Management Area was enacted in 2010 and included retention of the all salmon caught in the pollock fishery. In 2011, a systematic random sampling design recommended by Pella and Geiger (2009) was implemented by the Alaska

2

Fisheries Science Center's (AFSC) Fisheries Management and Analysis (FMA) North Pacific Groundfish and Halibut Observer Program (Observer Program) to collect genetic samples from one out of every 10 Chinook salmon encountered as bycatch in the BS pollock fishery.

In 2016, genetic samples were collected by the Observer Program from the Chinook salmon bycatch of the BS pollock fishery by using the systematic sampling protocols recommended previously (Pella and Geiger 2009). The number of available samples and the unbiased sampling methodology facilitated the extrapolation of the sample stock composition to the overall Chinook bycatch from the BS pollock trawl fishery in 2016. Stock composition analyses were performed using the single nucleotide polymorphism (SNP) baseline provided by the ADF&G (Templin et al. 2011), the same baseline that was used previously to estimate stock composition of samples from the 2005-2015 Chinook salmon bycatch (NMFS 2009; Guyon et al. 2010a, b; Guthrie et al. 2012-2017; 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).
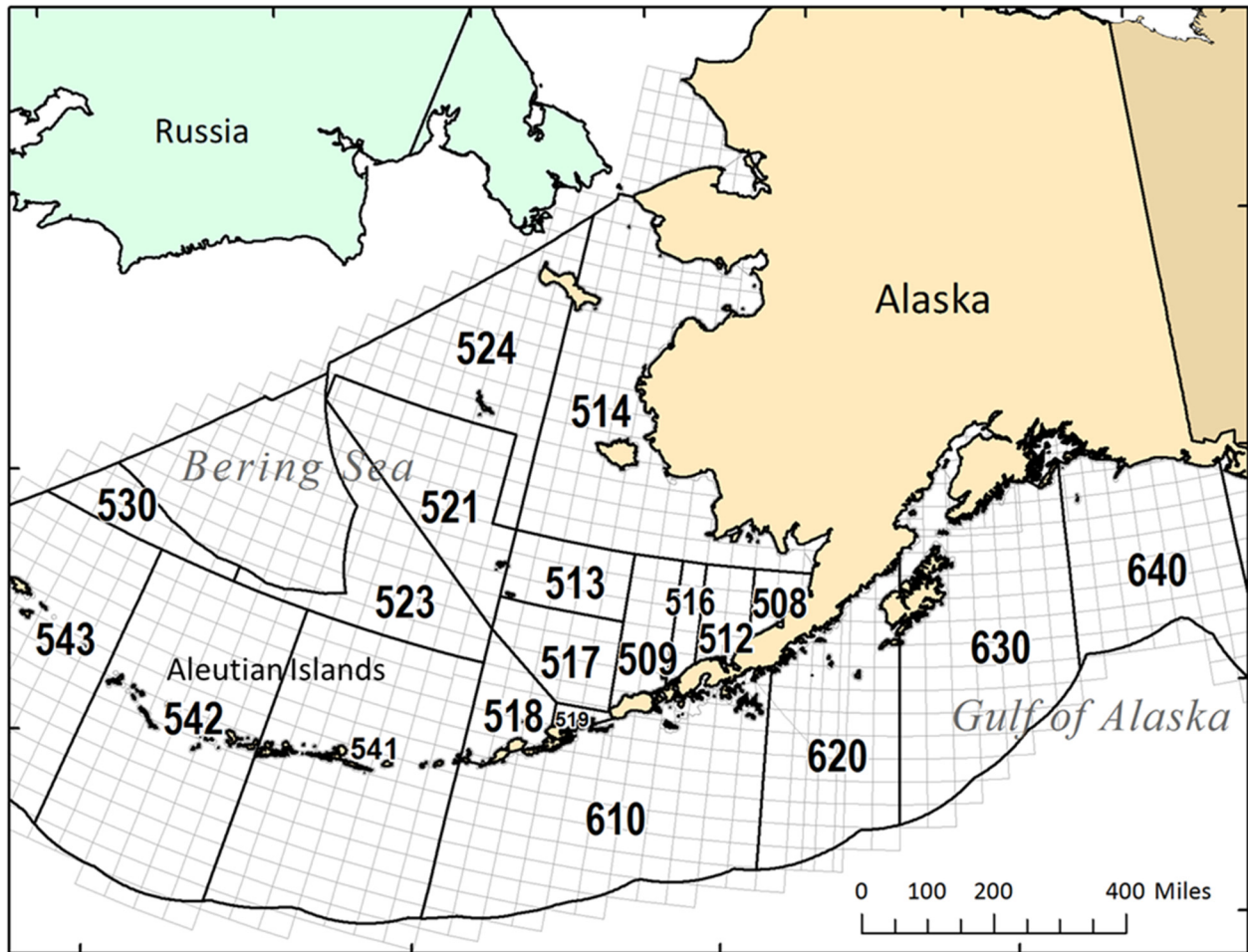
Figure 1. -- NMFS (outlined in black) and ADF&G (outlined in light gray) statistical areas associated with the Bering Sea and Gulf of Alaska groundfish fisheries.

SAMPLE DISTRIBUTION

Samples were collected from the Chinook salmon bycatch by the Observer Program for analysis at AFSC's Auke Bay Laboratories (ABL). Samples of axillary process tissue and scales were collected from the Chinook salmon bycatch throughout 2016. Axillary process tissues were stored in coin envelopes which were labeled, frozen, and shipped to ABL for analysis. Scales were collected as an additional source for genetic analysis, and for ageing if funding is available.

In 2016, an estimated 21,926 Chinook salmon were taken in the bycatch of BSAI pollock trawl fisheries (NMFS 2017). The Chinook salmon bycatch estimate is 38% below the historical

average (35,309) for the Bering Sea between 1991 and 2015 (Fig. 2) (Table 1). Since 1991, and

far below the highest overall Chinook bycatch in 2007 (Fig. 2) when an estimated 121,770 fish

were taken. Of the total 2016 bycatch, 16,828 were from the trawl "A" season (01/01/16 to

6/10/16) and 5,098 were from the "B" season (6/11/16 to 12/31/16).
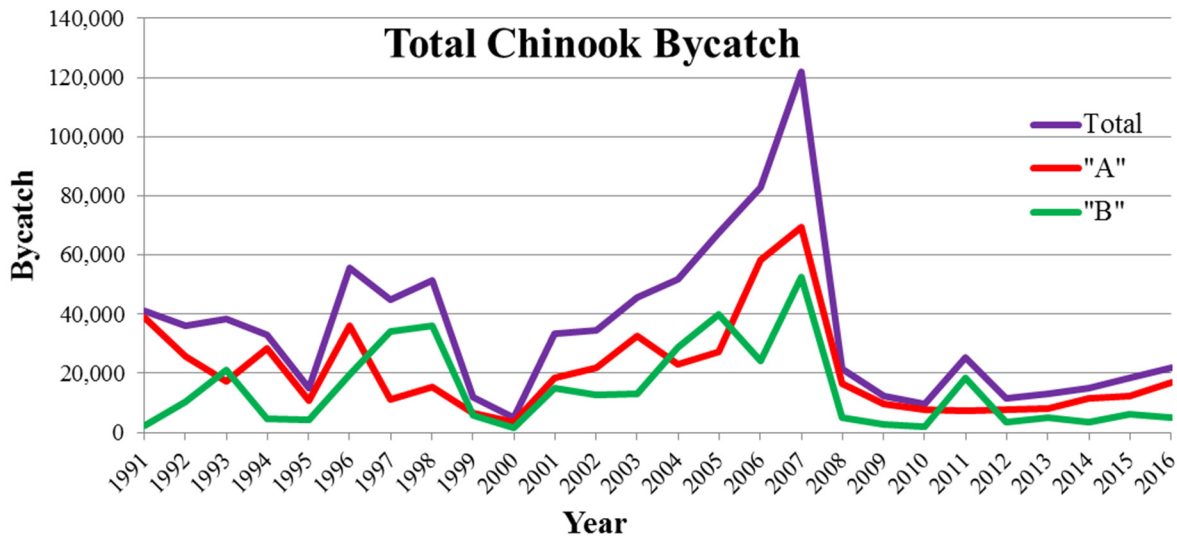
Figure 2. -- Yearly, "A" and "B" season estimates for the Chinook salmon bycatch from the Bering Sea
pollock trawl fishery (NMFS 2017).

In 2016, there were 2,148 genetic samples received from the BS Chinook salmon bycatch

collected by the observer program; of those 1,910 were successfully genotyped for an overall

genotyped sampling rate of 8.7% ("A" season had 1,488 fish, 8.8% sampling rate; "B" season

had 422 fish, 8.3% sampling rate).

Table 1. -- Annual, "A" and "B" season estimates for the Chinook salmon bycatch from the
Bering Sea-Aleutian Island pollock trawl fishery (NMFS 2017).

Year	Total	"A" Season	"B" Season
1991	40,906	38,791	2,114
1992	35,950	25,691	10,259
1993	38,516	17,264	21,252
1994	33,136	28,451	4,686
1995	14,984	10,579	4,405
1996	55,623	36,068	19,554
1997	44,909	10,935	33,973
1998	51,322	15,193	36,130
1999	11,978	6,352	5,627
2000	4,961	3,422	1,539
2001	33,444	18,484	14,961
2002	34,495	21,794	12,701
2003	45,586	32,609	12,977
2004	51,696	23,093	28,603
2005	67,362	27,331	40,030
2006	82,695	58,391	24,304
2007	121,770	69,420	52,350
2008	21,480	16,638	4,842
2009	12,369	9,711	2,658
2010	9,697	7,630	2,067
2011	25,499	7,137	18,362
2012	11,344	7,765	3,579
2013	13,034	8,237	4,797
2014	15,031	11,539	3,492
2015	18,329	12,304	6,025
2016	21,926	16,828	5,098

Potential biases primarily introduced through spatial and temporal aspects of genetic sample
collection from the bycatch are well documented and have the potential to affect resulting stock
composition estimates (Pella and Geiger 2009). The distributions of 2016 Chinook salmon
bycatch genetic samples were evaluated by comparing the collection of genetic samples with the
overall bycatch distribution (Figs. 3 and 4). The temporal distribution of samples collected and
successfully genotyped was evaluated across the two fishing seasons (Fig. 3). The sample spatial
distribution was compared with the total bycatch by NMFS statistical area (NMFS area) over

time (Fig. 4). 2016 was the sixth year that systematic random sampling was employed for

collecting genetic tissue from the Bering Sea Chinook salmon bycatch and Figure 4 shows the

resulting genetic samples were spatially and temporally representative of the total Chinook

bycatch (i.e., those fish not sampled for bycatch).. As in 2011-2015, the sample spatial and

temporal distribution were well aligned in 2016 compared to previous years when samples were

collected more opportunistically (Guyon et al. 2010a,b; Guthrie et al. 2012-2017).
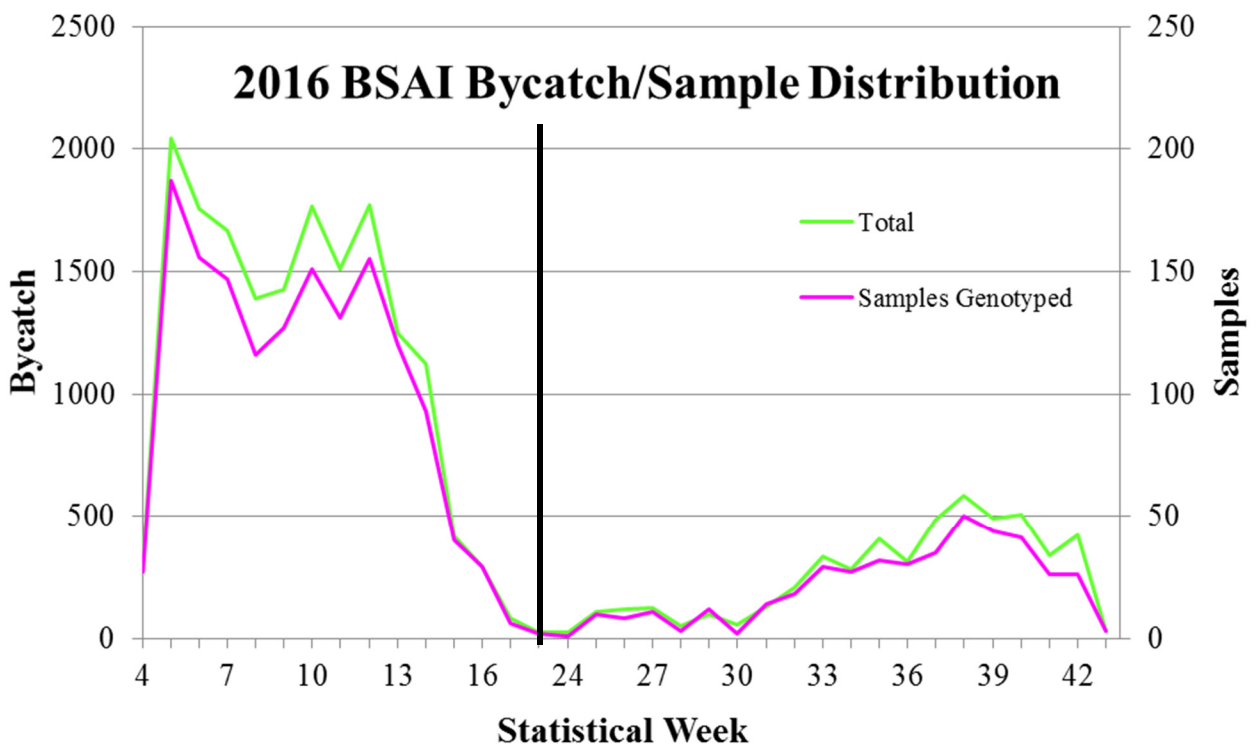
Figure 3. -- Number of Chinook salmon bycatch and genetic samples successfully genotyped graphed by statistical week. Weeks 4-18 correspond to the groundfish "A" season, whereas weeks 24-43 correspond to the "B" season, the demarcation of which is a vertical line.
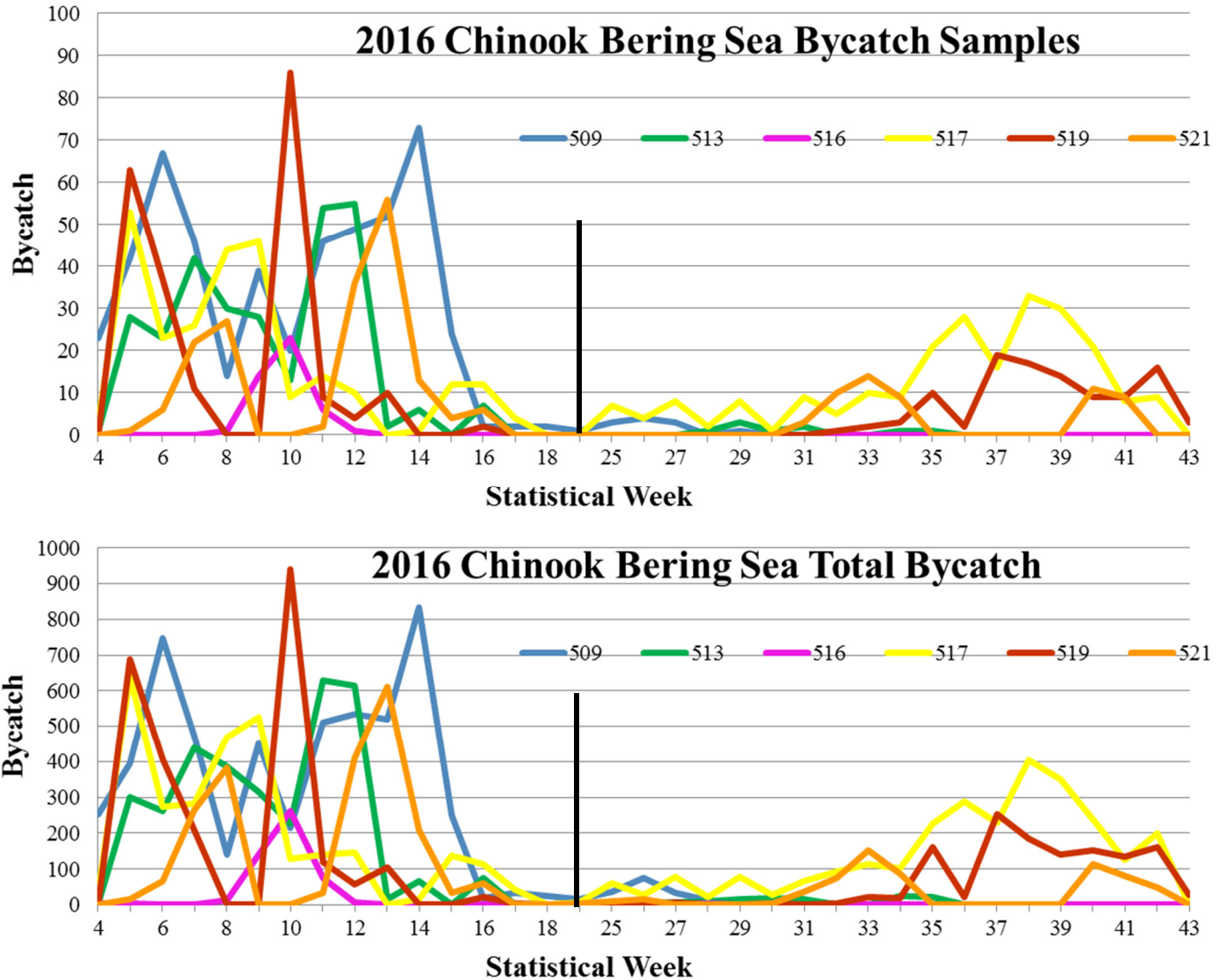
Figure 4. -- Comparison of the Chinook salmon bycatch by time and area with the distribution of available genetic samples. Top panel: Distribution of the 1,910 successfully genotyped samples from the 2016 bycatch. Not graphed were 11 fish from NMFS area 523. Bottom panel: Distribution of the Chinook salmon caught in the 2016 Bering Sea pollock trawl fishery. Not graphed were 136 fish each from NMFS area 523, and 5 fish from NMFS area 524. Weeks 4-18 correspond to the groundfish "A" season, whereas weeks 24-43 correspond to the "B" season, the demarcation of which is a vertical line.

LABORATORY ANALYSIS

DNA was extracted from axillary process tissue and genotyping was performed by using Taqman[TM] chemistries Applied Biosystems Inc. on a Life Technologies QuantStudio[TM] or by matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) (Guyon et al. 2010a) on a Sequenom MassARRAY iPLEX platform (Gabriel et al. 2009) for the 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 (also known as stock groups or reporting groups) (Appendix 1). Proof tests performed previously have shown the baseline to be suitable for stock composition analysis (Templin et al. 2011). Taqman[TM] assays were compared to internal controls for both open array (OA) and 384-well formats using the QuantStudio[TM]. The concordance rate between OA and 384 formats was 99.99%. In addition to internal MALDI-TOF chip controls, 10 (out of 384 on a chip) previously genotyped samples from ADF&G, which used TaqMan[TM] chemistries were included on each chip during the analyses and resulting genotypes were compared. Concordance rates of 99.9% between the two chemistries for the 2016 controls confirmed the utility and compatibility of both genotyping methods.

From the 2016 Chinook salmon bycatch from the Bering Sea pollock trawl fishery, a total of 2,148 samples were analyzed of which 1,910 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 88.9%. The remaining 1,910 successfully genotyped samples had genetic information for an average of 42 of 43 markers. Stock composition estimates were derived from BAYES software (Bayesian analysis; Pella and Masuda 2001; Appendix 2). The BAYES results were compared to SPAM software, (maximum likelihood analysis; ADF&G 2003) and both methods yielded almost identical stock composition estimates,

so only the BAYES results are reported here. BAYES software uses a Bayesian algorithm to produce stock composition estimates and can account for missing alleles in the baseline (Pella and Masuda 2001). 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% were 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 (Gelman and Rubin 1992), which were 1.02 or less for all the estimates, conveying strong convergence to a single posterior distribution (Pella and Masuda 2001).

STOCK COMPOSITION RESULTS

Results (BAYES) suggest that 60% of the 1,488 samples from the "A" season originated from Alaska river systems flowing into the Bering Sea (all regions north of the Aleutian Islands except for Russia) with the Coastal Western Alaska region contributing the most (39%), followed by the North Alaska Peninsula (17%), and Upper Yukon (2%). The other major contributors were British Columbia (26%), West Coast US (9%), and Coastal Southeast Alaska (4%) (Appendix 2). For the "B" season, over 81% of the 422 samples originated from regions south of the Aleutian chain with the British Columbia region contributing the most (37%), followed by the West Coast US (30%), Coastal Western Alaska 17%, Coastal Southeast Alaska (7%) and Northwest GOA (6%) regions, (Appendix 2).

For the entire year, 50% of the bycatch samples were estimated to be from Alaska river systems flowing into the Bering Sea with the Coastal Western Alaska region contributing the most (34%), trailed by the North Alaska Peninsula (13%), Upper Yukon (2%) and Middle Yukon (2%). Other contributors were British Columbia (29%), West Coast US (14%), Coastal Southeast Alaska (4%), and Northwest GOA (2%) (Appendix 2).

To investigate how stock compositions might vary among smaller areas, "A" season estimates were developed for five strata with sufficient numbers of samples as follows (Appendix 2, Figs. 1, 5-8): Saint George Island (335 samples, Fig. 6), Northwest Bering (554 samples, Fig. 7), Catcher Vessel Operation Area (CVOA) (715 samples, Fig. 8), Southeast Bering (934 samples, Fig. 7), and NMFS area 509 (501 samples, Fig. 1, 6) (NMFS 2017). It should be noted that some of these strata overlap. For the Saint George and Northwest Bering strata, the resulting stock compositions showed that 83% and 85% respectively were estimated to be from Alaska river systems flowing into the Bering Sea. The largest contributors were Coastal Western Alaska (51% for Saint George, 49% for Northwest Bering) and North Alaska Peninsula (23% for Saint George, 24% for Northwest Bering), followed by Upper Yukon (6% for Saint George and Northwest Bering). Fifteen percent of the samples from Saint George and 17% for Northwest Bering strata were from regions south of the Aleutians, where the largest contributors were British Columbia (8% for Saint George, 11% for Northwest Bering), and Coastal Southeast Alaska (4% for Saint George, 3% for Northwest Bering). For the Catcher Vessel Operational Area (CVOA), Southeast Bering, and NMFS area 509 strata, more than half of the resulting stock composition estimates were from regions south of the Aleutians. The largest contributors were British Columbia (36% for CVOA, 35% for Southeast Bering, 39% for NMFS area 509), West Coast US (14% for CVOA, 13% for Southeast Bering, 15% for NMFS area 509), and

Coastal Southeast Alaska (5% for CVOA, Southeast Bering and NMFS area 509). At least 40%
of CVOA (42%), Southeast Bering strata (46%), and NMFS area 509 (40%) were estimated to
be from Alaskan river systems flowing into the Bering Sea. The largest contributors were
Coastal Western Alaska (34% for CVOA, 34% for Southeast Bering, and 22% for NMFS area
509), and North Alaska Peninsula (8% for CVOA, 12% for Southeast Bering, 18% for NMFS
area 509).

Bering Sea "A" Season Area and Time Comparison

Figure 5. -- Comparison of area and time stock composition estimates from the 2016 Bering Sea Chinook salmon bycatch for "A" season: All (1,488 samples), Saint George Island (335 samples, Fig. 6), Northwest Bering (554 samples, Fig. 7), CVOA (715 samples, Fig. 8), Southeast Bering (934 samples, Fig. 7), and NMFS area 509 (501 samples, Fig. 6). Bering Sea "B" season (422 samples) and 2016 overall included for comparison. BAYES 95% credible intervals are plotted for estimates.

Figure 6. -- Location of Saint George Island (ADF&G Statistical Areas 705600, 695600, 685600, 705630, 695631, and 685630) and NMFS area 509 strata used in comparative stock composition estimates from the 2016 Bering Sea Chinook salmon bycatch for "A" season (NMFS 2016).
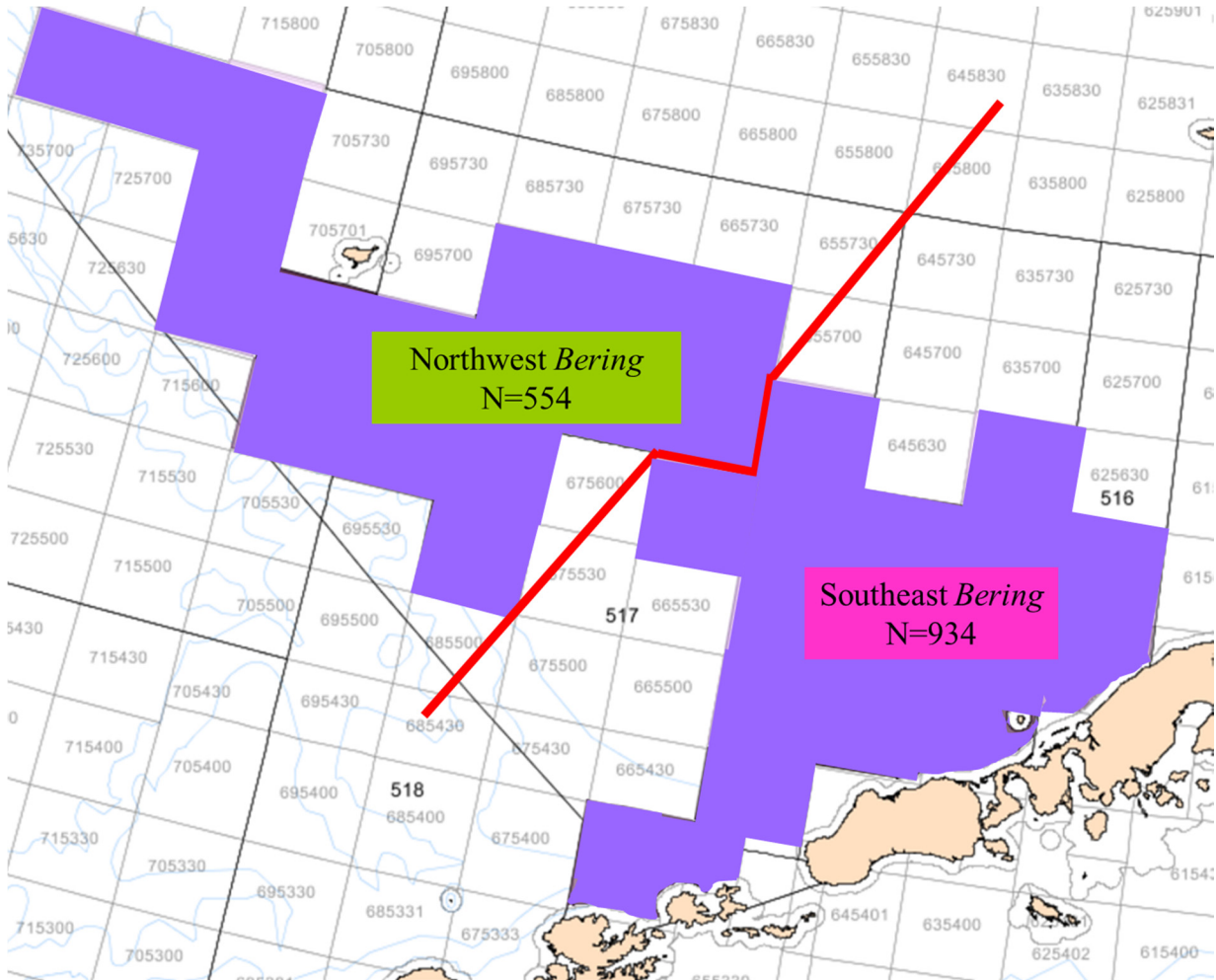
Figure 7. -- Location of Northwest Bering and Southeast Bering strata used in comparative stock composition estimates from the 2016 Bering Sea Chinook salmon bycatch for "A" season (NMFS 2016).
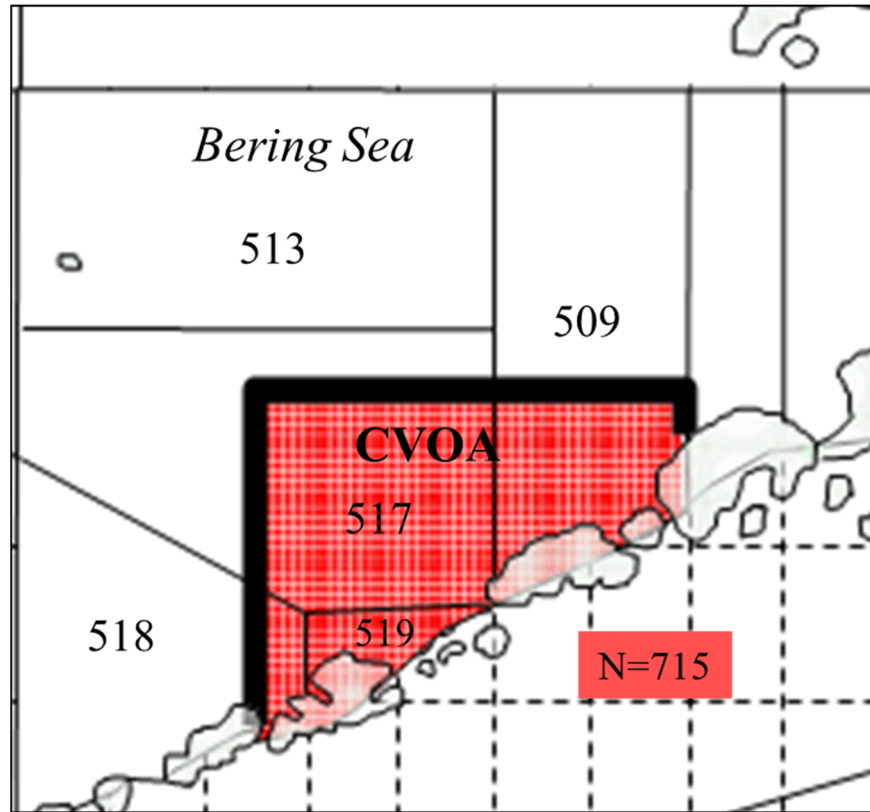
Figure 8. -- Location of Catcher Vessel Operational Area (CVOA) stratum used in comparative stock composition estimates from the 2016 Bering Sea Chinook salmon bycatch for "A" season (NMFS 2016).

For the "B" season, stock composition estimates were developed for NMFS areas 517 and 519 combined(334 samples, Figs. 1, 9, 10, Table 10) (NMFS 2016). Unlike for the 2015 samples, no estimates were developed for NMFS area 521 due to the small sample size and reduced fishing effort in this area. NMFS areas 517 and 519 had a slightly higher proportion of fish from regions southeast of the Aleutian Islands (84%), than the "B" season overall (81%).

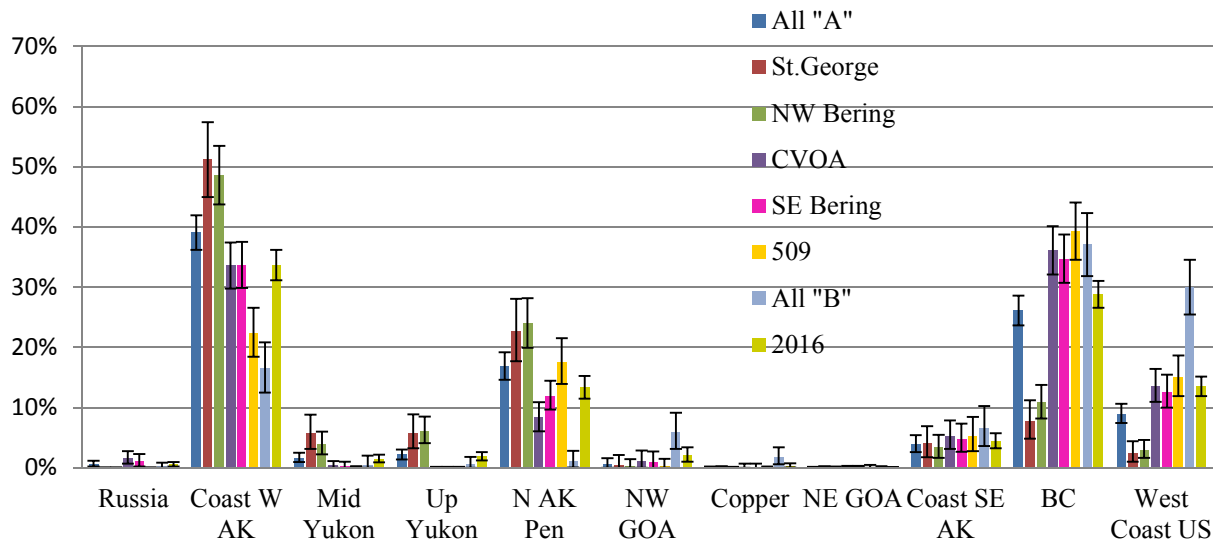# Bering Sea "B" Season Area and Time Comparison
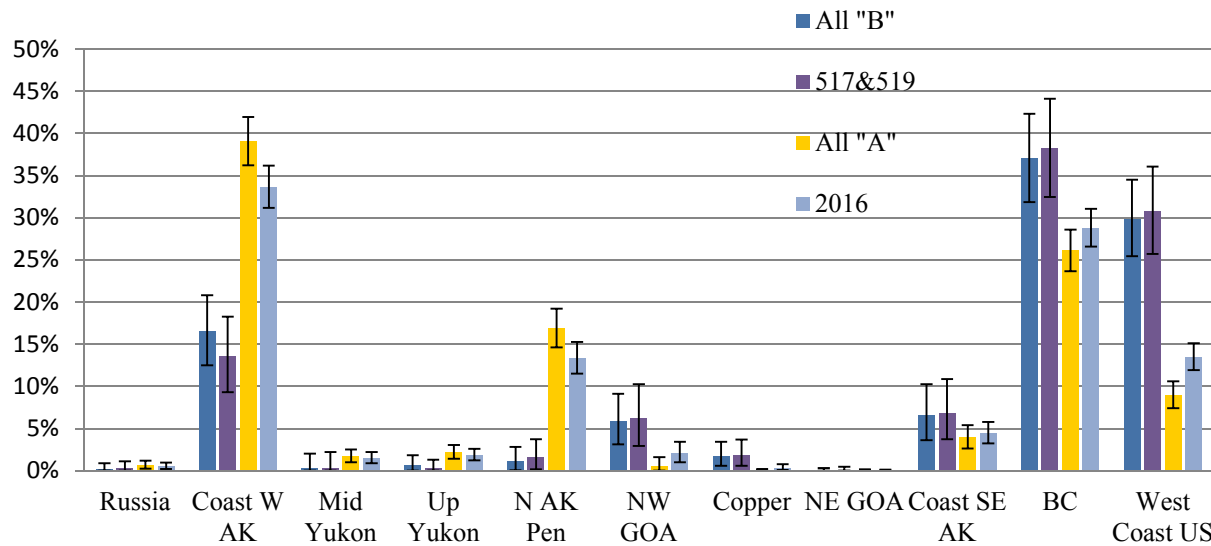
Figure 9. -- Comparison of area and time stock composition estimates from the 2016 Bering Sea Chinook salmon bycatch for "B" season: All (422 samples), and NMFS Areas 517/519 (334 samples). Bering Sea "A" season (1,488 samples) and 2016 overall included for comparison. BAYES 95% credible intervals are plotted for estimates.
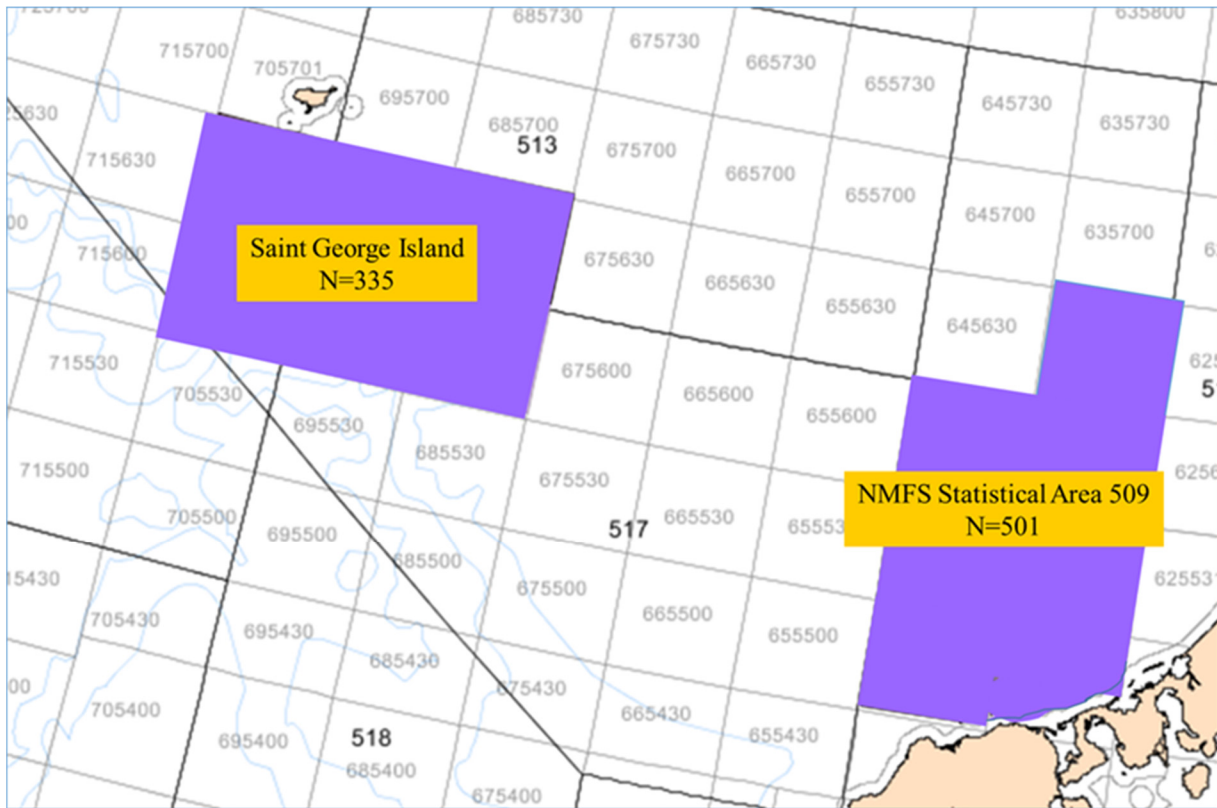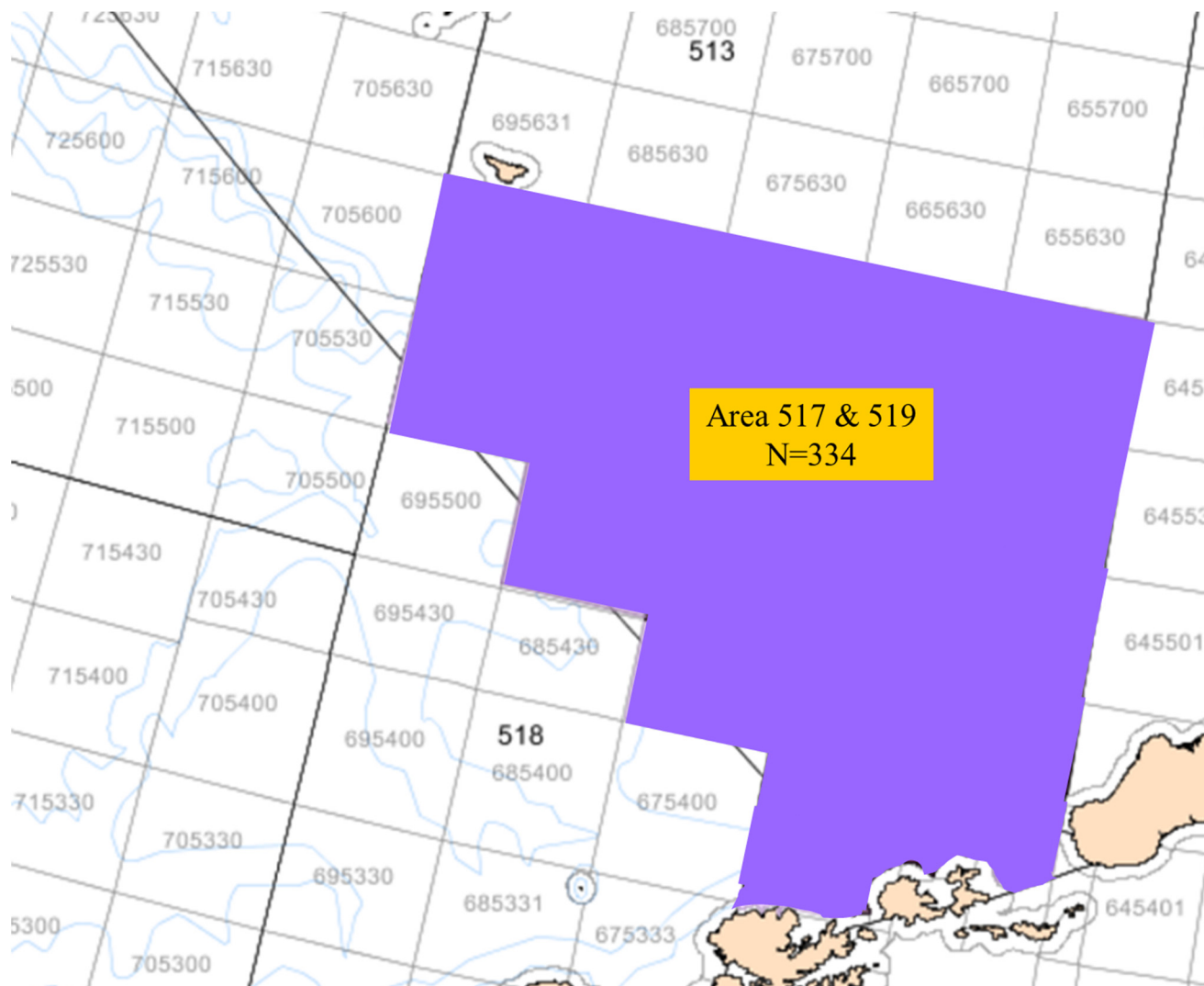
Figure 10. -- Location of samples from NMFS Statistical Areas 517 and 519 used in comparative stock composition estimates from the 2016 Bering Sea Chinook salmon bycatch for "B" season (NMFS 2016).

COMPARISON WITH PREVIOUS ESTIMATES

In contrast to 2011 and similar to most other previous years studied, most of the Chinook salmon bycatch occurred in 2016 during the "A" season. Stock compositions from the analysis of the 2016 "A" season Chinook salmon bycatch showed that most samples continued to originate from river systems directly flowing into the Bering Sea but were lower than in previous years,

with an increase from GOA, BC, and West Coast US (Fig. 11). The Coastal Western Alaska
region continued to be the largest contributor in the 2016 "A" season, but was lower than in all
previous years.
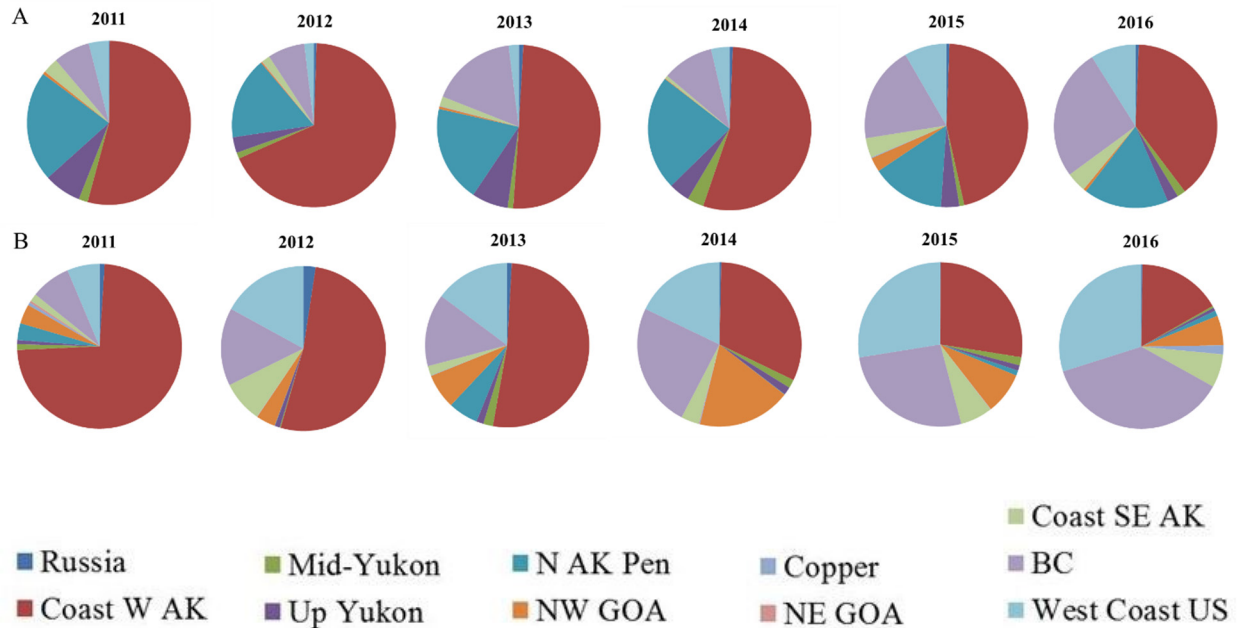
Figure 11. -- Comparison of "A" season (top) and "B" season (bottom) genetic stock composition
estimates for 2011-2016 from the Bering Sea Chinook salmon bycatch. The same genetic
baseline and regional groupings were used in all analyses.

The 2016 "B" season stock composition estimates from Coastal Western Alaska
continued to drop as observed across 2011-2015, a 57% decline since 2011 (Fig. 11). The 2016
"B" season estimates continued the trend of increased contributions from British Columbia, West
Coast US, and Coastal Southeast Alaska regions. The estimated relative contributions from these
more southern regions have increased 61% since 2011 (Fig. 11).

As in previous years since 2011, systematic random sampling was employed in 2016,
where genetic samples were collected from one of every 10 Chinook salmon encountered. While
changes in sampling protocols prior to 2011 necessitate caution in comparing analyses across
longer time periods, when the stock compositions were analyzed for the entire year, the Coastal

Western Alaska region contribution trended downward between 2008 and 2010 but increased in

2011, and then trended downward again through 2016 (Fig. 12). The North Alaska Peninsula

regional contribution composed 13% of the bycatch in 2016, a slight increase from 2015 (Fig.

12). The upper and middle Yukon River, GOA, and Coastal Southeast Alaska contributions

continued to be low in 2016, while contributions from the British Columbia, and West Coast US

regions have trended upward (Fig. 12).
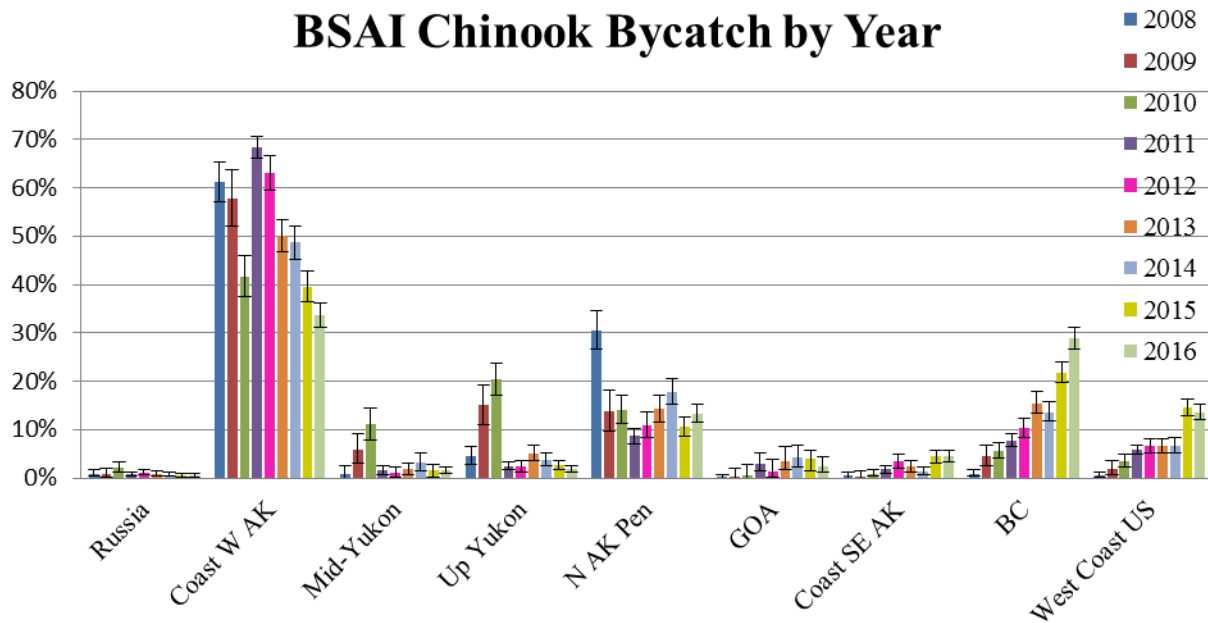
Figure 12. -- Comparison of yearly stock composition estimates (2008-2016) from the Bering Sea Chinook
salmon bycatch. Estimates from 2011-2016 are overall bycatch estimates, whereas earlier
estimates are of available sample sets. The same genetic baseline and general regional
groupings were used in all analyses. Gulf of Alaska (GOA) group consists of combined values
for Northwest GOA, Copper, and Northeast GOA. BAYES 95% credible intervals are plotted
for yearly estimates.

There was interest from the NPFMC Science and Statistical Committee (SSC) April 2017

meeting on how smaller strata stock compositions might change between years so "A" season

estimates were developed for the Northwest and Southeast Bering strata (Fig. 7) for which we

had an adequate number of samples (Fig. 13) for analyses (NPFMC 2017c). In the Northwest

Bering stratum there is a downward trend in the Coastal Western Alaska region contribution and an upward trend in the British Columbia and North Alaska Peninsula region contributions, especially between 2015 and 2016. The trend in the Southeast Bering stratum is similar except for 2014, when the Coastal Western Alaska and North Alaska Peninsula contribution increased, with a reciprocal decline in British Columbia and West Coast US regions.
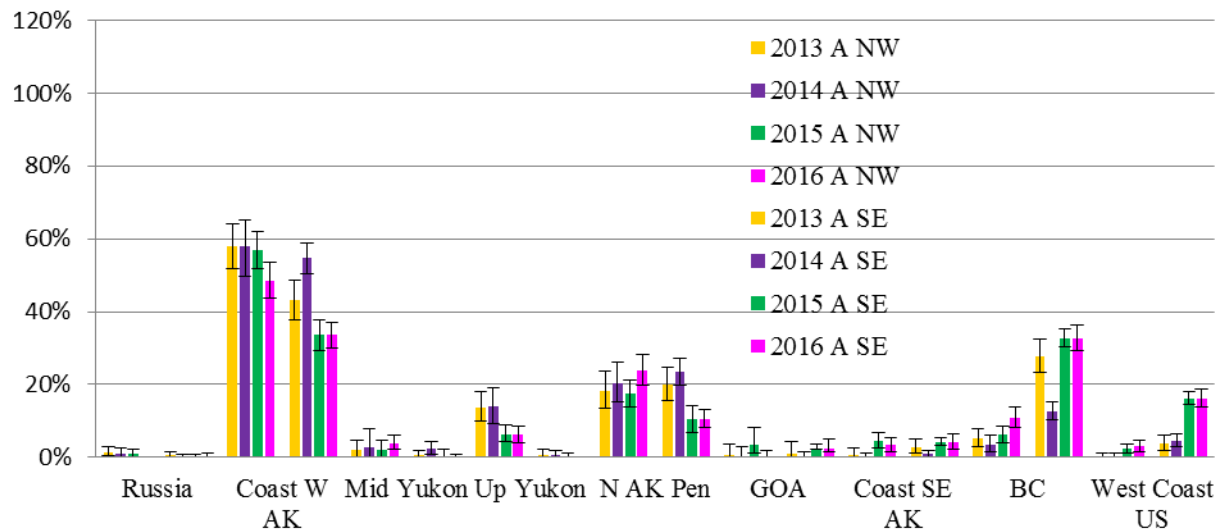
Figure 13. -- Comparison of yearly stock composition estimates (2013-2016) from the Bering Sea Chinook "A" season Northwest Bering and Southeast Bering strata. Gulf of Alaska (GOA) group consists of combined values for Northwest GOA, Copper, and Northeast GOA. BAYES 95% credible intervals are plotted for yearly estimates.

SUMMARY

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 35,309 salmon per year between 1991 and 2016, with a peak of 121,770 in 2007 (NMFS 2017). The Bering Sea Chinook salmon bycatch has abated in more recent years dropping to a total of 21,926 Chinook salmon in 2016,

well below the 26-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 (Ianelli and Stram 2015). This report provides stock

composition estimates of the Chinook salmon bycatch from the 2016 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 2011, 2016 is the sixth

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 number of successfully genotyped Chinook salmon from the Bering Sea bycatch samples

was 1,910, corresponding to an overall sampling rate in 2016 of 8.7%.

Stock Composition Estimates

Genetic stock composition analysis showed the majority of bycatch samples collected in

the Bering Sea were from Alaska originating from river systems directly flowing into the Bering

Sea. The stock composition of the Chinook salmon bycatch during the 2016 "A" season differed

from the 2016 "B" season, demonstrating temporal differences (Appendix 2; Fig.11). This was

especially apparent in the Coastal Western Alaska (39% vs. 17%), North Alaska Peninsula (17%

vs. 1%), NW GOA (1% vs. 6%), British Columbia (26% vs. 37%), and West Coast US (9% vs.

30%) stock groups. Spatial analysis showed that the stock compositions varied within season

depending upon where the salmon in the bycatch were caught. For example, during the "A"

season there was a higher concentration of Western Alaska origin Chinook intercepted in the northern areas of the Bering Sea, and southern (south of the Aleutians) origin Chinook intercepted in the southern areas of the Bering Sea (Fig. 5). One must also consider that the bycatch in the "A" season is over three times greater than the "B" season, and that the stock composition differences may be due to seasonal migration of stocks. For example, the estimated number of West Coast US fish only slightly increases from 1,506 in the "A" season to 1,524 in the "B" season (Appendix 2), while its proportion increases from 9% to 30%, likely due to the absence or lower proportion of other stock groups.

Application of 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 annual escapement of the affected stocks. 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 2016 Bering Sea Chinook salmon bycatch were considered to be representative of the overall bycatch for this year.

23

ACKNOWLEDGMENTS

25

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APPENDICES

Appendix 1. -- 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	Population name	Reg num.	Region
Bistraya River	1	Russia	Henshaw Creek	3	Mid Yukon
Bolshaya River	1	Russia	Kantishna River	3	Mid Yukon
Kamchatka River late	1	Russia	Salcha River	3	Mid Yukon
Pakhatcha River	1	Russia	Sheenjek River	3	Mid Yukon
Andreafsky River	2	Coast W AK	S. Fork Koyukuk River	3	Mid Yukon
Aniak River	2	Coast W AK	Big Salmon River	4	Up Yukon
Anvik River	2	Coast W AK	Blind River	4	Up Yukon
Arolik River	2	Coast W AK	Chandindu River	4	Up Yukon
Big Creek	2	Coast W AK	Klondike River	4	Up Yukon
Cheeneetnuk River	2	Coast W AK	Little Salmon River	4	Up Yukon
Eek River	2	Coast W AK	Mayo River	4	Up Yukon
Gagaryah River	2	Coast W AK	Nisutlin River	4	Up Yukon
George River	2	Coast W AK	Nordenskiold River	4	Up Yukon
Gisasa River	2	Coast W AK	Pelly River	4	Up Yukon
Golsovia River	2	Coast W AK	Stewart River	4	Up Yukon
Goodnews River	2	Coast W AK	Takhini River	4	Up Yukon
Kanektok River	2	Coast W AK	Tatchun Creek	4	Up Yukon
Kisaralik River	2	Coast W AK	Whitehorse Hatchery	4	Up Yukon
Kogrukluk River	2	Coast W AK	Black Hills Creek	5	N AK Pen
Kwethluk River	2	Coast W AK	King Salmon River	5	N AK Pen
Mulchatna River	2	Coast W AK	Meshik River	5	N AK Pen
Naknek River	2	Coast W AK	Milky River	5	N AK Pen
Nushagak River	2	Coast W AK	Nelson River	5	N AK Pen
Pilgrim River	2	Coast W AK	Steelhead Creek	5	N AK Pen
Salmon 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	Population name	Reg num.	Region
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	Population name	Reg num.	Region
Stuart River summer	10	BC	Lower Deschutes R. fall	11	West Coast US
Sustut River	10	BC	Lyons Ferry H. summer/fall	11	West Coast US
Torpy River summer	10	BC	Makah National Fish H. fall	11	West Coast US
Wannock River	10	BC	McKenzie River spring	11	West Coast US
Alsea River fall	11	West Coast US	Sacramento River winter	11	West Coast US
Carson Hatchery spring	11	West Coast US	Siuslaw River fall	11	West Coast US
Eel River fall	11	West Coast US	Soos Creek Hatchery fall	11	West Coast US
Forks Creek fall	11	West Coast US	Upper Skagit River summer	11	West Coast US
Hanford Reach	11	West Coast US			
Klamath River	11	West Coast US			

Appendix 2. -- Regional BAYES stock composition percentage estimates and estimated numbers of different strata of Chinook salmon from the 2016 Bering Sea pollock trawl fisheries. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Sample sizes are adjacent to stratum designation. Total catch is the actual catch for each stratum from AKFIN reports (NMFS 2017). Figures 1, 3, 6, 7, 8 and 10 show strata locations and timing.

	"A" Season (N=1,488)				"B" Season (N=422)				*Bering Sea* all (N=1.910)			
	Est. #	Mean	SD	95% PI	Est. #	Mean	SD	95% PI	Est. #	Mean	SD	95% PI
Russia	108	0.6	0.25	(0.2,1.2)	12	0.2	0.24	(0.0,0.9)	114	0.5	0.19	(0.2,1.0)
Coast W AK	6,570	39.0	1.46	(36.2,41.9)	843	16.5	2.14	(12.5,20.8)	7,372	33.6	1.28	(31.2,36.2)
Mid Yukon	283	1.7	0.40	(1.0,2.5)	18	0.4	0.60	(0.0,2.0)	327	1.5	0.34	(0.9,2.2)
Up Yukon	365	2.2	0.43	(1.4,3.1)	34	0.7	0.48	(0.0,1.8)	406	1.9	0.35	(1.2,2.6)
N AK Pen	2,839	16.9	1.17	(14.6,19.2)	56	1.1	0.72	(0.0,2.8)	2,927	13.4	0.96	(11.5,15.3)
NW GOA	94	0.6	0.46	(0.0,1.6)	298	5.9	1.54	(3.1,9.1)	458	2.1	0.62	(1.0,3.4)
Copper	3	0.0	0.06	(0.0,0.2)	90	1.8	0.73	(0.6,3.4)	75	0.3	0.18	(0.1,0.8)
NE GOA	2	0.0	0.07	(0.0,0.2)	2	0.0	0.13	(0.0,0.3)	2	0.0	0.07	(0.0,0.1)
Coast SE AK	663	3.9	0.72	(2.6,5.4)	333	6.5	1.70	(3.6,10.2)	971	4.4	0.64	(3.3,5.8)
BC	4,394	26.1	1.26	(23.7,28.6)	1,888	37.0	2.68	(31.8,42.3)	6,312	28.8	1.14	(26.6,31.0)
West Coast US	1,506	9.0	0.81	(7.4,10.6)	1,524	29.9	2.33	(25.4,34.5)	2,960	13.5	0.82	(11.9,15.1)
Total Catch	16,828				5,098				21,926			

	Saint George I. "A" (N=335)				Area 509 "A" (N=501)				CVOA "A" (N=715)			
	Est. #	Mean	SD	95% PI	Est. #	Mean	SD	95% PI	Est. #	Mean	SD	95% PI
Russia	0	0.0	0.05	(0.0,0.1)	1	0.0	0.03	(0.0,0.1)	126	1.6	0.54	(0.7,2.8)
Coast W AK	1,969	51.2	3.15	(44.9,57.4)	1,208	22.4	2.07	(18.5,26.6)	2,684	33.6	1.96	(29.8,37.4)
Mid Yukon	219	5.7	1.45	(3.2,8.8)	1	0.0	0.09	(0.0,0.3)	30	0.4	0.30	(0.0,1.1)
Up Yukon	222	5.8	1.44	(3.3,8.9)	1	0.0	0.06	(0.0,0.2)	1	0.0	0.05	(0.0,0.2)
N AK Pen	873	22.7	2.64	(17.7,28.0)	949	17.6	1.94	(13.9,21.5)	668	8.4	1.22	(6.1,10.9)
NW GOA	14	0.4	0.61	(0.0,2.2)	13	0.2	0.43	(0.0,1.5)	84	1.1	0.81	(0.0,2.9)
Copper	1	0.0	0.10	(0.0,0.3)	1	0.0	0.08	(0.0,0.2)	7	0.1	0.20	(0.0,0.7)
NE GOA	1	0.0	0.11	(0.0,0.3)	2	0.0	0.15	(0.0,0.5)	2	0.0	0.13	(0.0,0.3)
Coast SE AK	156	4.1	1.32	(1.8,6.9)	287	5.3	1.45	(2.8,8.5)	424	5.3	1.20	(3.2,7.9)
BC	298	7.8	1.62	(4.9,11.2)	2,117	39.2	2.44	(34.5,44.0)	2,885	36.1	2.05	(32.1,40.1)
West Coast US	94	2.4	0.87	(1.0,4.4)	816	15.1	1.72	(11.9,18.6)	1,083	13.6	1.40	(10.9,16.4)
Total Catch	3,847				5,395				7,996			

	SE *Bering S.* "A" (N=934)				NW *Bering S.* "A" (N=554)				Areas 517/519 "B" (N=334)			
	Est. #	Mean	SD	95% PI	Est. #	Mean	SD	95% PI	Est. #	Mean	SD	95% PI
Russia	112	1.1	0.40	(0.5,2.0)	1	0.0	0.03	(0.0,0.1)	13	0.3	0.30	(0.0,1.1)
Coast W AK	3,457	33.6	1.78	(30.2,37.2)	3,177	48.6	2.49	(43.7,53.4)	548	13.6	2.30	(9.3,18.3)
Mid Yukon	28	0.3	0.22	(0.0,0.8)	258	3.9	0.96	(2.3,6.0)	14	0.3	0.64	(0.0,2.2)
Up Yukon	1	0.0	0.04	(0.0,0.1)	401	6.1	1.14	(4.1,8.5)	12	0.3	0.36	(0.0,1.3)
N AK Pen	1,227	11.9	1.28	(9.5,14.6)	1,567	24.0	2.10	(19.9,28.2)	63	1.6	0.92	(0.2,3.7)
NW GOA	87	0.9	0.77	(0.0,2.7)	14	0.2	0.41	(0.0,1.4)	252	6.2	1.87	(3.0,10.3)
Copper	5	0.1	0.12	(0.0,0.4)	1	0.0	0.06	(0.0,0.2)	74	1.8	0.80	(0.6,3.7)
NE GOA	4	0.0	0.13	(0.0,0.5)	1	0.0	0.10	(0.0,0.2)	2	0.0	0.22	(0.0,0.5)
Coast SE AK	494	4.8	1.03	(2.9,7.0)	220	3.4	0.98	(1.6,5.5)	277	6.9	1.85	(3.7,10.9)
BC	3,567	34.7	1.79	(31.2,38.3)	708	10.8	1.42	(8.2,13.8)	1,541	38.2	2.98	(32.4,44.1)
West Coast US	1,295	12.6	1.22	(10.3,15.1)	195	3.0	0.76	(1.7,4.6)	1,241	30.8	2.64	(25.7,36.1)
Total Catch	10,277				6,541				4,034			

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