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by
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U.S. DEPARTMENT OF COMMERCE
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ABSTRACT

A genetic analysis of samples from the Chinook salmon (*Oncorhynchus tshawytscha*) bycatch of the 2014 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 2014, 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 1,385 Chinook salmon bycatch samples collected throughout the 2014 BSAI walleye pollock trawl fishery, Coastal Western Alaska stocks dominated the sample set (49%) with smaller contributions from North Alaska Peninsula (18%), British Columbia (14%), and West Coast U.S. (WA/OR/CA) (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 Coastal Western Alaska, North Alaska Peninsula and Yukon stocks and higher contributions of West Coast U.S. (WA/OR/CA), British Columbia, NW Gulf of Alaska and Coastal Southeast Alaska stocks during the "B" season.

CONTENTS

INTRODUCTION

The Bering Sea and the Gulf of Alaska (GOA) are known feeding habitats for multiple brood years of Chinook salmon (*Oncorhynchus tshawytscha*) originating from many different localities in North America and Asia. Determining the geographic origin and stock composition of 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

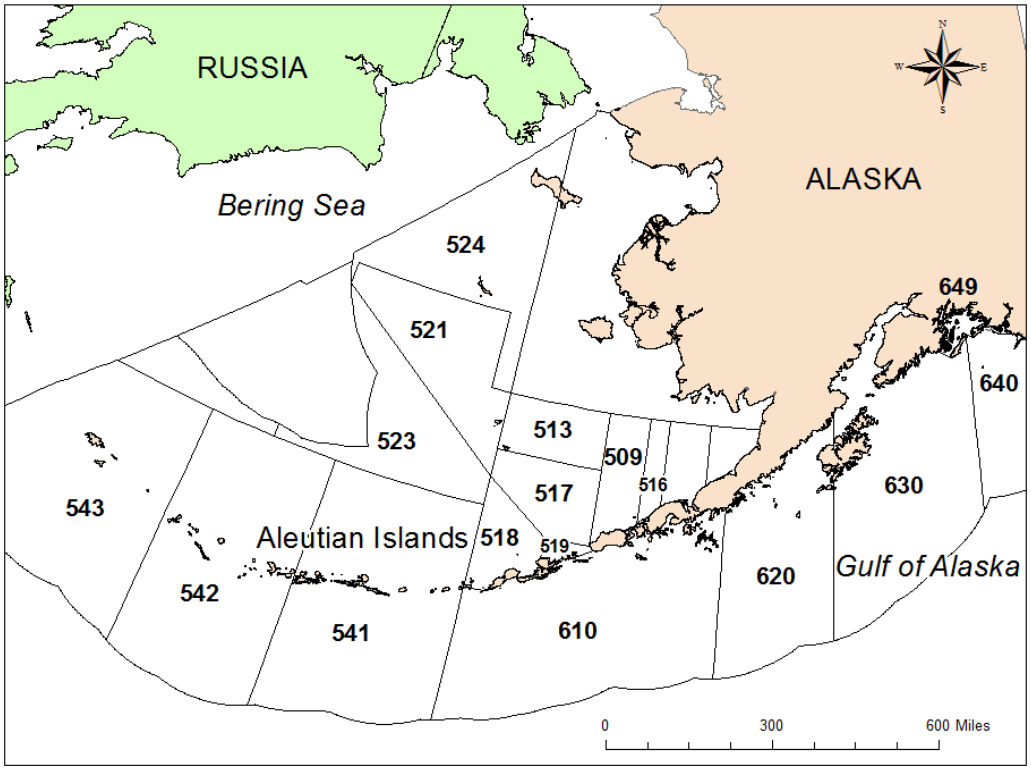

Figure 1. -- NMFS statistical areas associated with the Bering Sea-Aleutian Island (BSAI) and Gulf of Alaska (GOA) groundfish fisheries.

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 2014, 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 2014. 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 2005-2013 Chinook salmon bycatch (NMFS 2009; Guyon et al. 2010a, b; Guthrie et al. 2012, 2013, 2014, and 2015; 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 the NPGOP to collect genetic samples from one out of every 10 Chinook salmon encountered as bycatch in the BSAI pollock fishery. Samples of

Table 1. -- Yearly Chinook salmon bycatch estimates from the BSAI pollock trawl fishery

Year	Total	"A" Season	"B" Season
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

axillary process tissue were collected from the Chinook salmon bycatch throughout 2014. Axillary process tissues were stored in coin envelopes which were labeled, frozen, and shipped to ABL for analysis.

In 2014, an estimated 15,031 Chinook salmon were taken in the bycatch of BSAI pollock trawl fisheries (NMFS 2015). Of the total bycatch, 11,539 were from the trawl “A” season and 3,492 were from the “B” season. These estimates are similar to the Chinook salmon bycatch estimates from 2012 and 2013, and is 59% below the historical average (36,386) for the Bering

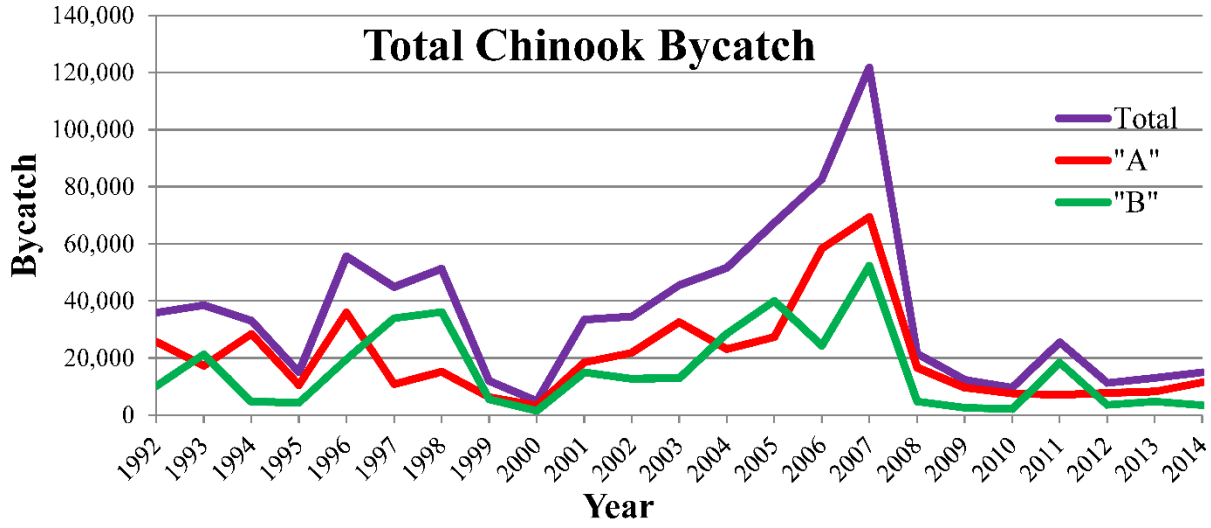

Figure 2. -- Yearly, “A” season, and “B” estimates for the Chinook salmon bycatch from the BSAI pollock trawl fishery (NMFS 2015).

Sea between 1992 and 2014 (Fig. 2). Since 1992, the year with the highest overall Chinook bycatch in the BSAI was 2007 (Fig. 2) when an estimated 121,770 fish were taken in the pollock trawl fisheries. In 2014, 1,455 genetic samples were taken from a BSAI Chinook salmon bycatch of 15,031; of the samples taken 1,385 were successfully genotyped for an effective sampling rate of 9.2% (“A” season, 1,066 fish, 9.2% sampling rate; “B” season, 319 fish, 9.1% sampling rate).

Potential biases associated with the timing of 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 time distributions for the 2014 Chinook salmon bycatch sample sets were compared to the timing of the overall bycatch distributions (Fig. 3).

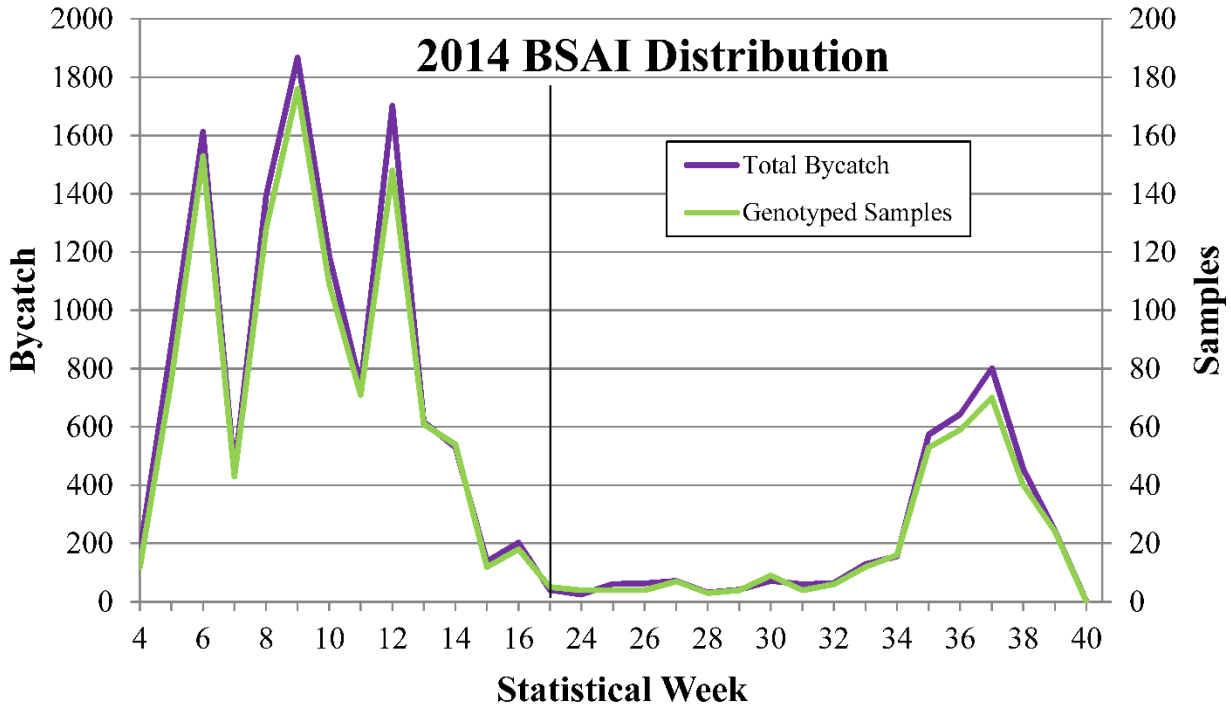

Figure 3. -- Number of Chinook salmon bycatch and genetic samples graphed by statistical week. Distribution of all Chinook salmon caught in the 2014 Bering Sea pollock trawl fishery versus the distribution of the 1,385 genotyped samples from the 2014 bycatch. Weeks 4-17 correspond to the groundfish "A" season, whereas weeks 24-40 correspond to the "B" season, the demarcation of which is a vertical line.

Samples and bycatch have about the same temporal distribution. To evaluate the sample similarity of 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.

2014 was the fourth 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, 2012, and 2013, the sample spatial and temporal distribution was excellent in 2014 compared to

previous years when samples were collected more opportunistically (Guyon et al. 2010a, 2010b; Guthrie et al. 2012, 2013, 2014).

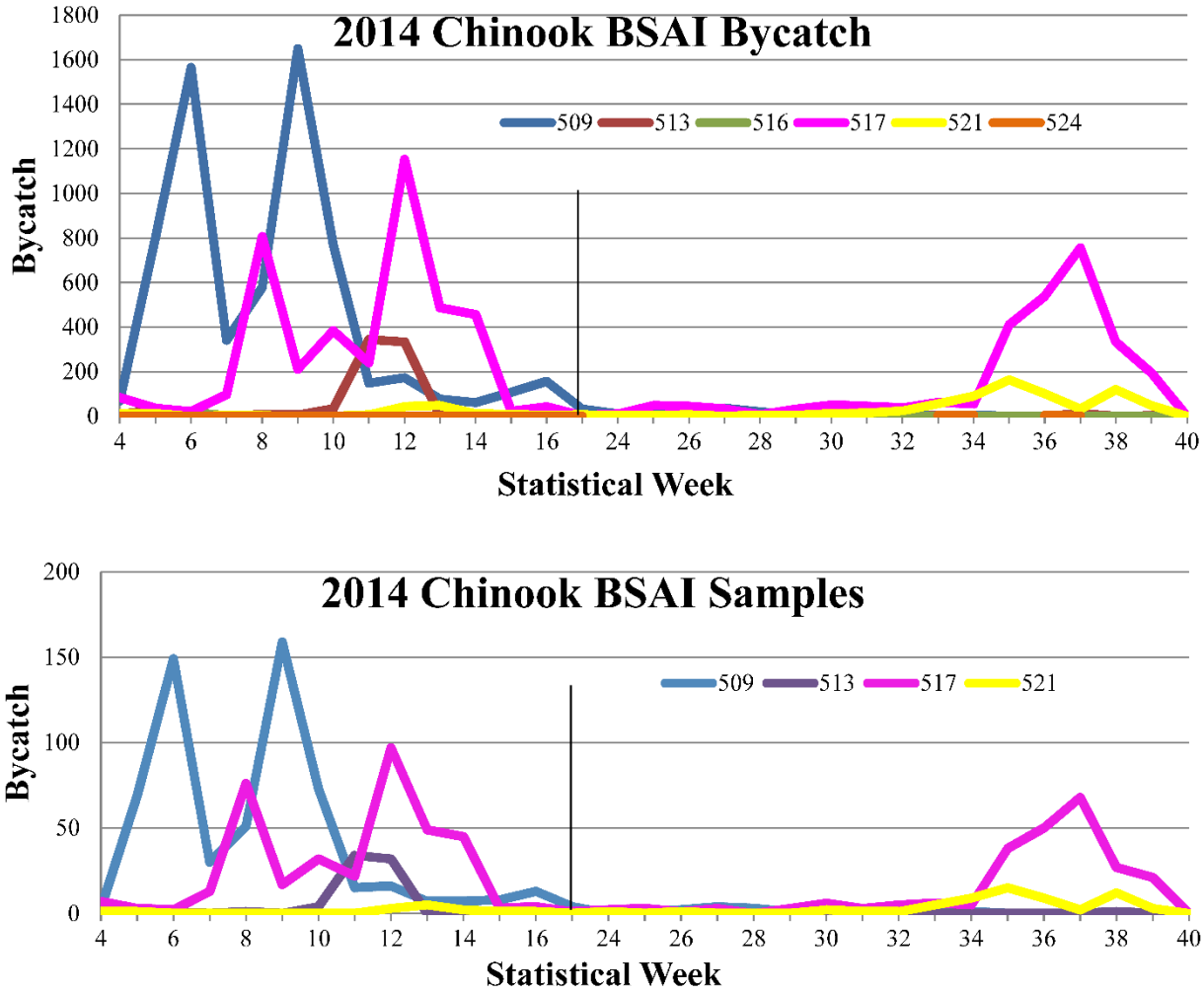

Figure 4. -- Number of Chinook salmon bycatch and genetic samples graphed by statistical week. Distribution of all Chinook salmon caught in the 2014 Bering Sea pollock trawl fishery versus the distribution of the 1,385 genotyped samples from the 2014 bycatch. Weeks 4-17 correspond to the groundfish "A" season, whereas weeks 24-40 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 2005-2013 Chinook bycatch (NMFS 2009; Guyon et al. 2010a, b; Guthrie et al. 2012, 2013, 2014, and 2015). 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 (Life Technologies, Inc.). Concordance rates of 99.8% between the two chemistries for the 2014 controls confirmed the utility and compatibility of both genotyping methods.

From the 2014 Chinook salmon bycatch from the BSAI pollock trawl fishery, a total of 1,455 samples were analyzed of which 1,386 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 95.3%. These genotypes were analyzed using C++ programs written by the ABL's Genetics Program to check for duplicate samples and one was found which was subsequently removed from the analysis. The remaining 1,385 samples had genetic information for an average of 41.5 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 2-4).

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

Results (BAYES) suggest that 85% of the 1,066 samples from the “A” season originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska stock contributing the most (55%), followed by the North Alaska Peninsula (23%), Upper Yukon (4%), and Middle Yukon (3%). The other major contributor was British Columbia (10 %) (Table 2). For the “B” season, over 35% of the 319 samples originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska region contributing the most (32%). This was followed by British Columbia (25%), Northwest GOA (18%), and West Coast U.S. stocks (18%) (Table 3).

Table 2. -- Regional BAYES and SPAM stock composition estimates for the 1066 Chinook salmon samples from the bycatch of the 2014 "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	**0.006**	0.003	0.002	0.006	0.012	**0.007**	0.002
Coast W AK	**0.546**	0.022	0.504	0.546	0.588	**0.556**	0.016
Mid-Yukon	**0.033**	0.012	0.012	0.032	0.059	**0.035**	0.002
Up Yukon	**0.041**	0.008	0.027	0.041	0.058	**0.039**	0.003
N AK Penn	**0.227**	0.016	0.197	0.227	0.259	**0.205**	0.009
NW GOA	**0.001**	0.003	0.000	0.000	0.011	**0.013**	0.001
Copper	**0.000**	0.001	0.000	0.000	0.001	**0.001**	0.001
NE GOA	**0.000**	0.001	0.000	0.000	0.001	**0.000**	0.000
Coast SE AK	**0.006**	0.004	0.000	0.006	0.014	**0.007**	0.000
BC	**0.102**	0.010	0.083	0.101	0.122	**0.108**	0.005
WA/OR/CA	**0.037**	0.006	0.025	0.036	0.050	**0.031**	0.003

Table 3. -- Regional BAYES and SPAM stock composition estimates for the 319 Chinook salmon samples from the bycatch of the 2014 "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	**0.004**	0.005	0.000	0.001	0.017	**0.010**	0.003
Coast W AK	**0.318**	0.031	0.258	0.317	0.379	**0.295**	0.020
Mid-Yukon	**0.017**	0.010	0.001	0.015	0.039	**0.018**	0.003
Up Yukon	**0.016**	0.009	0.003	0.014	0.036	**0.020**	0.003
N AK Penn	**0.001**	0.003	0.000	0.000	0.010	**0.011**	0.001
NW GOA	**0.184**	0.027	0.134	0.183	0.239	**0.169**	0.015
Copper	**0.001**	0.004	0.000	0.000	0.013	**0.012**	0.005
NE GOA	**0.001**	0.003	0.000	0.000	0.011	**0.008**	0.001
Coast SE AK	**0.036**	0.014	0.013	0.034	0.067	**0.037**	0.002
BC	**0.245**	0.026	0.196	0.244	0.297	**0.248**	0.016
WA/OR/CA	**0.179**	0.022	0.138	0.178	0.224	**0.173**	0.012

Table 4. -- Regional BAYES and SPAM stock composition estimates for the 1,385 Chinook salmon samples from the bycatch of the 2014 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	**0.006**	0.002	0.003	0.006	0.012	**0.007**	0.001
Coast W AK	**0.487**	0.018	0.452	0.487	0.522	**0.494**	0.013
Mid-Yukon	**0.032**	0.009	0.015	0.032	0.051	**0.031**	0.001
Up Yukon	**0.038**	0.007	0.026	0.037	0.051	**0.034**	0.003
N AK Penn	**0.177**	0.014	0.152	0.177	0.204	**0.161**	0.007
NW GOA	**0.042**	0.010	0.024	0.041	0.063	**0.051**	0.003
Copper	**0.000**	0.001	0.000	0.000	0.003	**0.003**	0.001
NE GOA	**0.000**	0.001	0.000	0.000	0.002	**0.001**	0.000
Coast SE AK	**0.014**	0.004	0.006	0.014	0.023	**0.013**	0.000
BC	**0.136**	0.010	0.117	0.136	0.157	**0.141**	0.005
WA/OR/CA	**0.067**	0.008	0.052	0.067	0.083	**0.063**	0.004

For the entire year, 73% 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 (49%), trailed by the North Alaska Peninsula (18%), Upper Yukon (4%) and Middle Yukon (3%). Other contributors were British Columbia (14%), West Coast U.S. (7%), and Northwest GOA (4%) (Table 4).

To investigate how stock compositions might change for over smaller time and area intervals, estimates were developed for the following three strata with the largest number of samples: area 509 “A” season (604 samples), 517-early “A” season (371 samples), and 517 “B” season (241 samples). For areas 509 and 517, the resulting stock compositions showed that the largest contributing stocks in the spring fishery were from Coastal Western Alaska (55% for 509 “A”, 54% for 517 “A”) and North Alaska Peninsula (23% for 509 “A”, 25% for 517 “A”) although differences were apparent in smaller contributing stocks including the Upper Yukon

(0% for 509 “A”, 7% for 517 “A”), British Columbia (13% for 509 “A”, 8% for 517 “A”), and West Coast US (5% for 509 “A”, 2% for 517 “A”) (Tables 5 and 6; Fig. 5). Larger stock differences were seen when comparing earlier time area compositions from the later. For example, in area 517, the stock composition from the salmon bycatch in the “B” season included a smaller proportion of fish from river drainages flowing into the Bering Sea (Coastal Western Alaska, North Alaska Peninsula, Middle Yukon, Upper Yukon) and a higher proportion of fish from river drainages flowing into the Gulf of Alaska and Pacific Ocean (British Columbia, West Coast US, Northwest GOA, and Coastal Southeast Alaska) (Tables 5, 6, and 7; Fig. 5).

Table 5. -- Regional BAYES and SPAM stock composition estimates for the 604 Chinook salmon samples from the bycatch of the 2014 BSAI pollock trawl fishery from “A” season in area 509. 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	**0.004**	0.003	0.001	0.004	0.012	**0.005**	0.003
Coast W AK	**0.546**	0.024	0.498	0.546	0.593	**0.537**	0.024
Mid-Yukon	**0.028**	0.011	0.010	0.027	0.053	**0.030**	0.010
Up Yukon	**0.002**	0.004	0.000	0.000	0.014	**0.007**	0.004
N AK Penn	**0.233**	0.021	0.194	0.233	0.275	**0.212**	0.019
NW GOA	**0.001**	0.004	0.000	0.000	0.013	**0.020**	0.009
Copper	**0.000**	0.001	0.000	0.000	0.003	**0.003**	0.003
NE GOA	**0.000**	0.001	0.000	0.000	0.001	**0.000**	0.000
Coast SE AK	**0.003**	0.004	0.000	0.000	0.014	**0.006**	0.004
BC	**0.133**	0.014	0.106	0.133	0.163	**0.140**	0.015
WA/OR/CA	**0.050**	0.009	0.033	0.049	0.070	**0.040**	0.009

Table 6. -- Regional BAYES and SPAM stock composition estimates for the 371 Chinook salmon samples from the bycatch of the 2014 BSAI pollock trawl fishery from "A" season in area 517. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

Region	BAYES	SD	2.5%	Median	97.5%	SPAM	SD
Russia	**0.011**	0.006	0.003	0.010	0.025	**0.013**	0.003
Coast W AK	**0.535**	0.031	0.474	0.535	0.594	**0.527**	0.026
Mid-Yukon	**0.026**	0.013	0.005	0.024	0.054	**0.037**	0.002
Up Yukon	**0.070**	0.015	0.044	0.069	0.102	**0.074**	0.009
N AK Penn	**0.248**	0.026	0.199	0.247	0.301	**0.237**	0.018
NW GOA	**0.003**	0.006	0.000	0.000	0.020	**0.006**	0.001
Copper	**0.000**	0.001	0.000	0.000	0.003	**0.000**	0.000
NE GOA	**0.000**	0.001	0.000	0.000	0.003	**0.000**	0.000
Coast SE AK	**0.013**	0.008	0.002	0.012	0.033	**0.010**	0.001
BC	**0.076**	0.015	0.049	0.075	0.107	**0.080**	0.007
WA/OR/CA	**0.019**	0.007	0.007	0.018	0.035	**0.017**	0.005

Table 7. -- Regional BAYES and SPAM stock composition estimates for the 241 Chinook salmon samples from the bycatch of the 2014 BSAI pollock trawl fishery from "B" season in area 517. 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	**0.010**	0.007	0.001	0.009	0.027	**0.013**	0.005
Coast W AK	**0.290**	0.034	0.226	0.289	0.357	**0.257**	0.022
Mid-Yukon	**0.002**	0.005	0.000	0.000	0.017	**0.009**	0.002
Up Yukon	**0.005**	0.005	0.000	0.003	0.019	**0.007**	0.001
N AK Penn	**0.000**	0.002	0.000	0.000	0.005	**0.000**	0.000
NW GOA	**0.182**	0.029	0.129	0.181	0.242	**0.181**	0.017
Copper	**0.002**	0.005	0.000	0.000	0.018	**0.017**	0.008
NE GOA	**0.001**	0.004	0.000	0.000	0.013	**0.006**	0.001
Coast SE AK	**0.048**	0.018	0.018	0.046	0.090	**0.051**	0.003
BC	**0.261**	0.031	0.202	0.260	0.323	**0.264**	0.019
WA/OR/CA	**0.200**	0.027	0.150	0.199	0.254	**0.195**	0.015

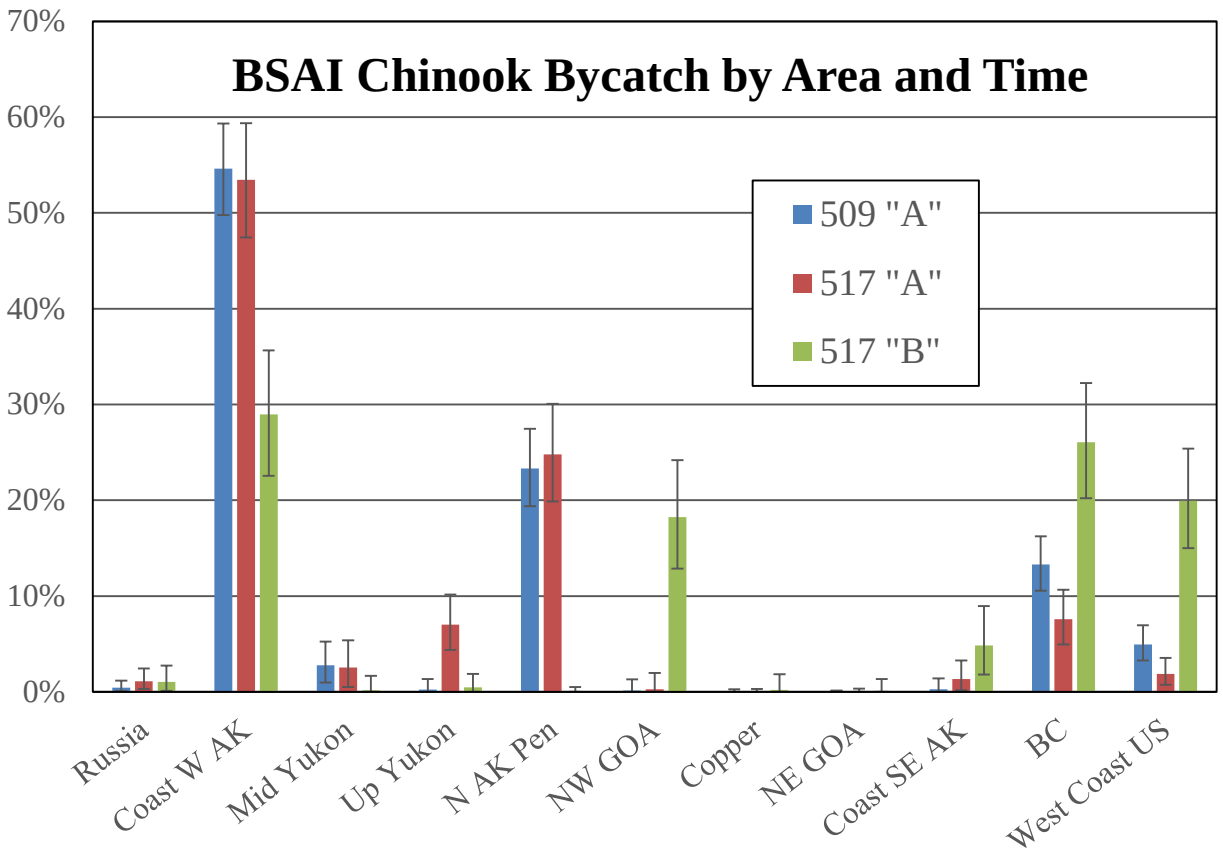

Figure 5. -- Comparison of area and time stock composition estimates from the 2014 BSAI Chinook salmon bycatch for NMFS Area 509 “A” (604 samples), Area 517 “A” (371 samples), and Area 517 “B” (241 samples). BAYES 95% credible intervals are plotted for yearly estimates.

COMPARISON WITH PREVIOUS ESTIMATES

Stock compositions from the analysis of the 2014 “A” season Chinook salmon bycatch samples were in general agreement with the 2011-13 “A” season estimates. For example, most samples continued to be from stocks originating from river systems directly flowing into the Bering Sea. The Upper and Middle Yukon estimated contribution in 2011, 2013, and 2014 were at similar levels with 2012 being slightly lower (Fig. 6). The 2014 “A” Coastal Western Alaska stock contribution was similar to 2011 and 2013, but all were lower than 2012 (Fig. 6).

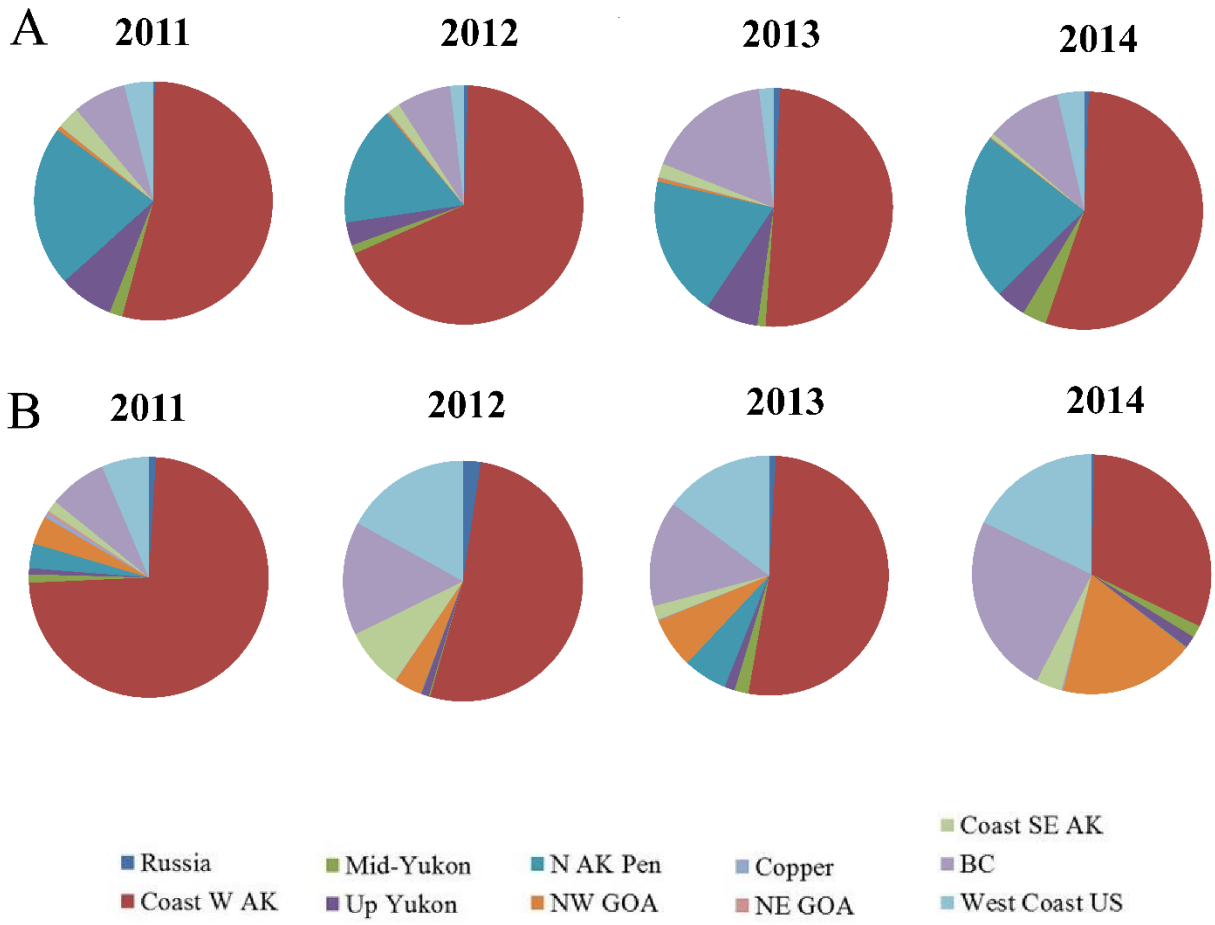

Figure 6. -- A. Comparison of "A" season genetic stock composition estimates for 2011-14 from the BSAI Chinook salmon bycatch. B. Comparison of "B" season genetic stock composition estimates for 2011-14 stock composition estimates from the BSAI "B" season Chinook salmon bycatch. The same genetic baseline and regional groupings were used in all analyses.

The 2014 "B" season stock composition estimates from Coastal Western Alaska were lower compared to the 2011-13 estimates (Fig. 6). The 2014 "B" season estimates, continued the trend of larger contributions from British Columbia, West Coast U.S. and Coastal Southeast Alaska stocks (Fig. 6). The estimated relative contribution from the Northwest GOA was more than double the amount from 2011-13 (Fig. 6). In contrast to 2011 and similar to most other

previous years studied, most of the Chinook salmon bycatch occurred in 2014 during the "A" season.

As in previous years since 2011, systematic random sampling was employed in 2014, 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, the Coastal Western Alaska stock contribution trended downward between 2008 and 2010 but increased in 2011, and trended downward through 2014 (Fig. 7). The North Alaska Peninsula stock contribution has remained consistent since 2009 composing 18% of the bycatch in 2014 (Fig. 7). The upper and middle Yukon River contribution continued to be low in 2014, while contributions from the Gulf of Alaska and Pacific Ocean migrating stocks have generally trended upward (Fig. 7).

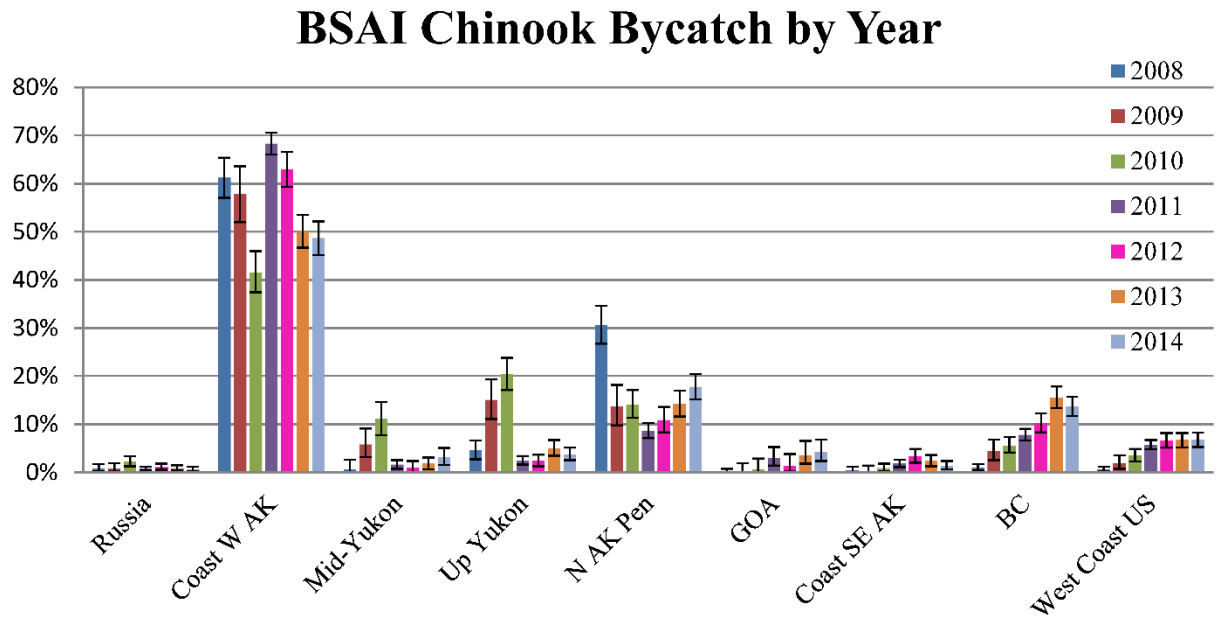

Figure 7. -- Comparison of yearly stock composition estimates (2008-2014) from the BSAI Chinook salmon bycatch. Estimates from 2011-14 are overall bycatch estimates whereas earlier compositions are of available sample sets. The same genetic baseline and general regional groupings were used in all analyses. 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 36,386 salmon per year between 1992-2014, 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 15,031 Chinook salmon in 2014, a number which is 11,355 fish below the 24-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 2014 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, 2014 is the fourth 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 final Chinook salmon Bering Sea bycatch sample set was 1,385 corresponding to an overall sampling rate in 2014 of 9.2%.

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 2014 “A” season differed from the 2014 “B” season, demonstrating temporal differences in the stocks intercepted. This was especially apparent in the Coastal Western Alaska (55% vs. 32%), North Alaska Peninsula (23% vs. 0%), NW GOA (0% vs. 18%), British Columbia (10% vs. 24%), and West Coast U.S. (4% vs. 18%) 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 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 2014 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.

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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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