Genetic Stock Composition Analysis of Chum Salmon from the Prohibited Species Catch of the 2020 Bering Sea Walleye Pollock Trawl Fishery

Report to the North Pacific Fisheries Management Council

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Executive Summary[1]

We analyzed genetic stock compositions of chum salmon prohibited species catch (PSC), referred to as "bycatch," samples collected from the 2020 walleye pollock (*Gadus chalcogrammus*) fishery in the Bering Sea. Samples were genotyped for 84 single nucleotide polymorphism markers from which stock contributions were estimated using a range-wide chum salmon baseline developed by the Alaska Department of Fish and Game. The chum salmon bycatch was 343,821 fish, up from the 10-year average of 226,304. The timing of the chum salmon bycatch was atypically late in 2020, with 50% of the bycatch encountered by statistical week 35 (average week 33). Environmental covariates (Pacific Decadal Oscillation, Sea surface temperature, warm pool and sea ice extent) were evaluated for correlations with bycatch timing measured as the statistical week by which 50% of the chum salmon bycatch had been caught. Mean sea ice extent from January and February was positively correlated with bycatch timing; however, fishing effort was also delayed, with fewer hauls occurring prior to week 24 than in previous years. The contribution of W Alaska and Up/Mid Yukon fish was smaller than in previous years (9% versus an average of ~20% over the last decade). Even though the total chum salmon bycatch was higher than average, the number of W Alaska and Up/Mid Yukon fish caught was lower (30,908 in 2020 compared to an average of 51,515 from 2011 to 2019). Relative to prior years the contribution of EGOA/PNW stocks was larger than typical (42.5% versus a long-term average of ~28%), which was similar to 2015, when EGOA/PNW stocks comprised 51.4% of the bycatch and bycatch occurred later in the season. Conversely, the contribution from NE Asia stocks was slightly below average (32% vs a long-term average of 36%). In summary, although total chum PSC was higher than average, the contribution of W Alaska and Up/Mid Yukon fish was lower than average, leading to a lower catch of W Alaska and Up/Mid Yukon fish compared to previous years.

[1] *Disclaimer* - These represent preliminary analyses of the 2020 chum salmon genetic data. All estimates are subject to change. Numerous plots in this report display fishery information. All data are non-confidential. Data have been aggregated and any data point with fewer than three unique vessels has been removed.

Catch Summary

Temporal Trends

The chum salmon prohibited species catch, referred to as "bycatch" throughout this report, in the Bering Sea walleye pollock trawl fishery was 343,821 fish in 2020, with 343,014 fish in the B-season (Figure 1). This was 117,517 fish greater than the 10-year average of 226,304 (SD 145,306). As is typical, over 99% of the bycatch of chum salmon occurred in the B-season (between June and October).

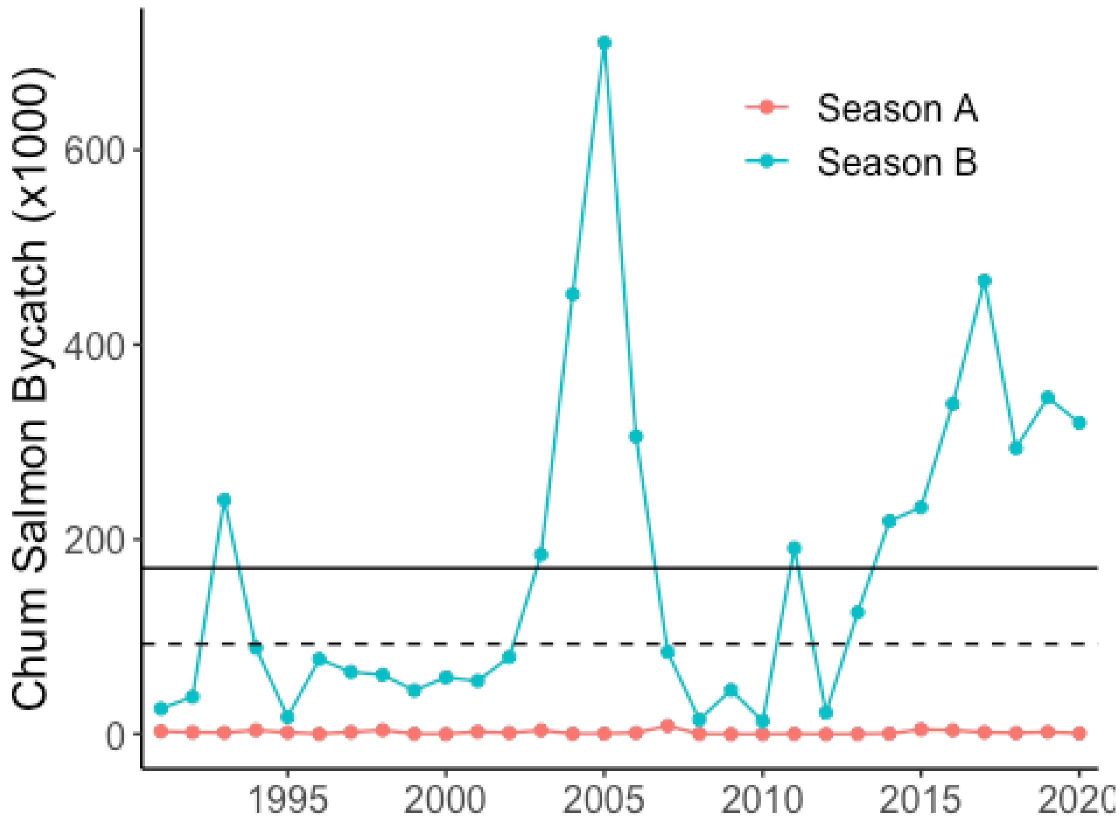

Figure 1: Chum salmon prohibited species catch (PSC) for the A- and B-seasons from the Bering Sea pollock-directed trawl fisheries. The solid horizontal line represents the mean PSC and the dashed line represents the median PSC from 1991 to 2019.

Within the B-season, the chum salmon were caught later than in the previous six years (Figure 2). The chum salmon bycatch did not increase until after the 30th statistical week, when nearly 75% of the bycatch had already occurred in 2017.

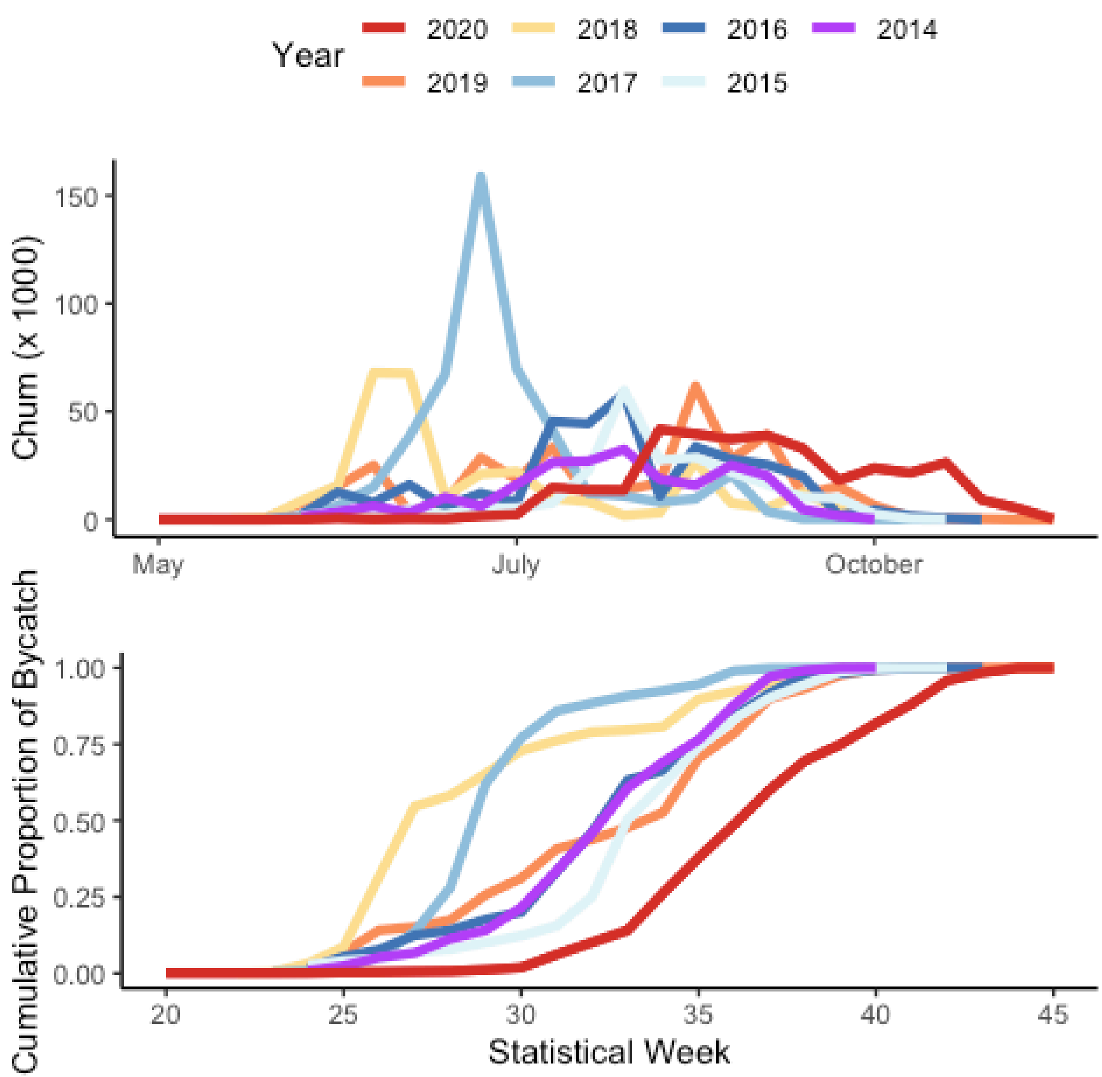

Figure 2: Number of chum salmon caught during the B-season (top) and cumulative proportion of chum salmon catch (bottom) from the Bering Sea pollock trawl fishery by statistical week for years 2015 to 2020.

The timing of the chum salmon bycatch could be the result of the seasonally changing spatial distribution of chum salmon in response to environmental conditions, following prey species that may be responding to environmental conditions, how the fleet allocates fishery effort, or a combination of these and other factors. We explored several environmental covariates with bycatch encounter data. We investigated the correlations between bycatch timing, as measured by when fifty percent of the bycatch was caught, and climate drivers such as sea surface temperature (SST), the Pacific Decadal Oscillation (PDO), sea ice extent, and warm pool extent. Climate data were downloaded from NOAA's Physical Science Laboratory climate indicies data repository. All climate covariates for the time series, except for SST were expressed in anomalies or deviations from the long-term average.

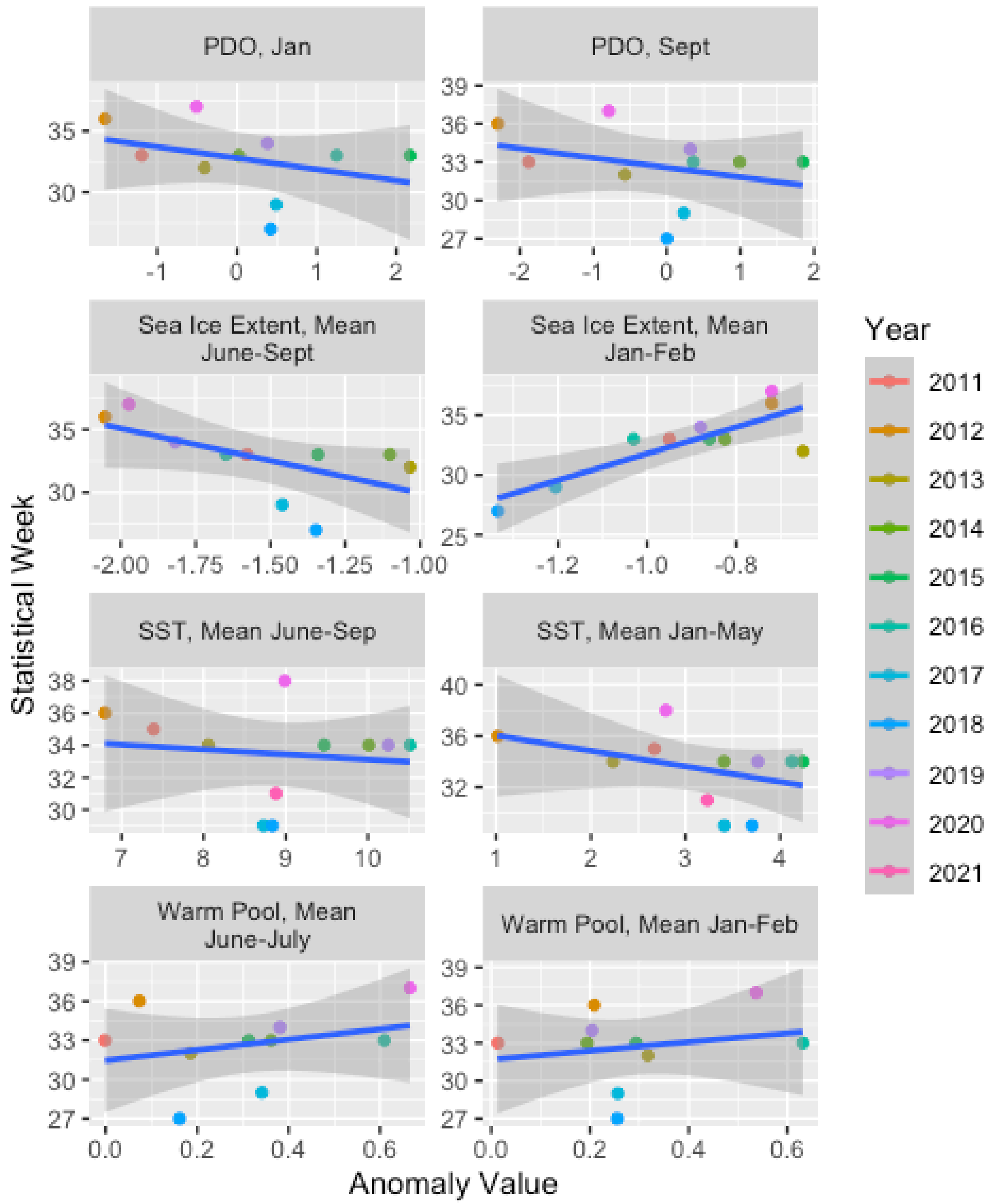

Figure 3: Correlation of climate covariates (PDO, Sea ice extent, SST, and warm pool extent) and the statistical week by which 50% *of the chum salmon PSC were caught.*

The correlations between climate indices and timing of chum salmon catch are not strong (Figure 3), potentially due in part to the substantial variation in the timing of bycatch, particularly in 2017 and 2018 which were very early. We evaluated the relationship between chum salmon bycatch timing and the environmental indicies measured over individual months and aggregated over seasons, but only those periods with the strongest correlations for each index are displayed in this report. The extent of sea ice was the environmental covariate with the strongest correlation (Figure 3, second row down). As the sea ice extent anomaly (between June and September) increases, chum salmon tend to be caught earlier. However, as the sea ice extent anomaly (between January and February) increases, the chum salmon bycatch occurs later, although 2017 and 2018 have high leverages in determining the relationship. The oscillating control hypothesis (OCH) states that when there is early ice retreat, there is a later plankton bloom with warmer waters dominated by smaller copepod species. Alternatively, when the ice retreat is late there is an early bloom associated with colder water and large Calanus copepods dominate (Hunt Jr et al. 2002). In warmer years, when large copepods or euphausiids are not as abundant, we spectulate that chum salmon may delay migrating onto the shelf area where the majority of pollock trawls occur.

We also investigated the fishing behavior of the fleet as chum salmon bycatch encounter timing could be a byproduct of fishing effort occurring either earlier or later in the B season. The number of unique pollock hauls by statistical week was used as a proxy of effort, without accounting for the haul duration (Figure 4). These data are non-confidential and weeks with fewer than three unique vessels have been excluded, which removes the early and late ends of the distributions, but is inconsequential for the general trend.

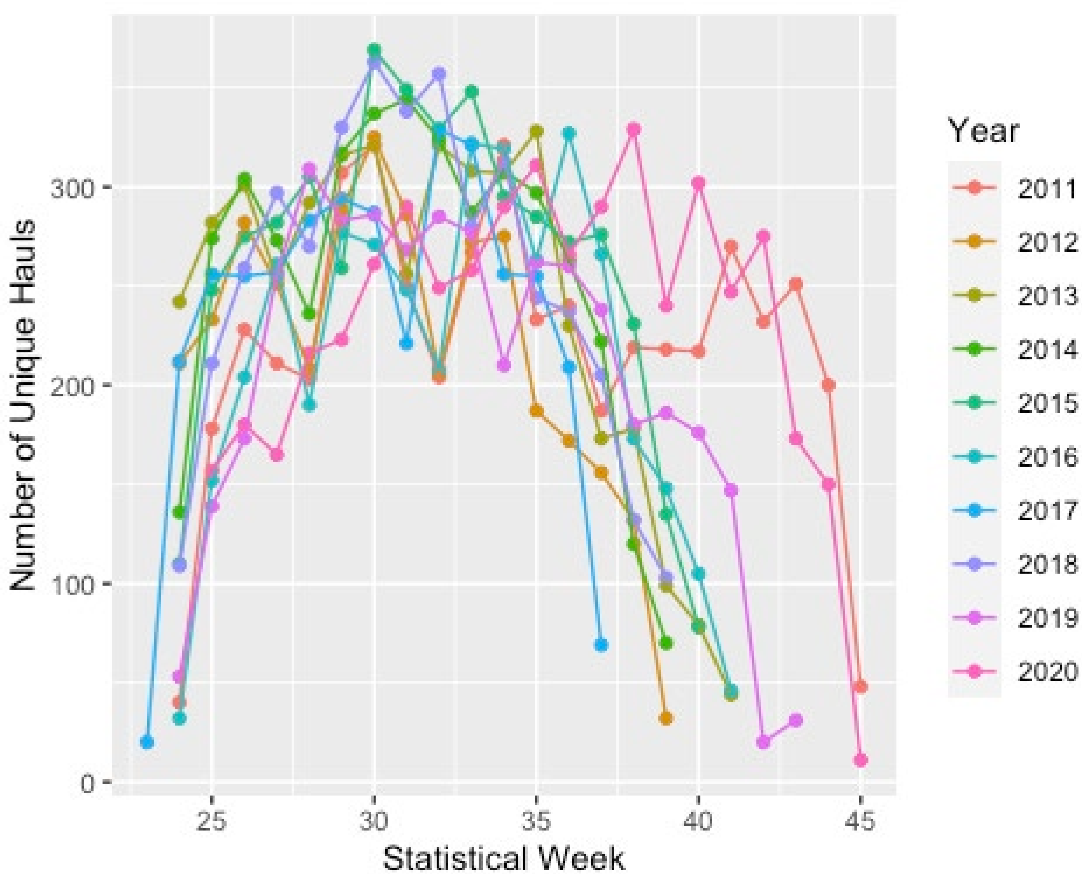

Figure 4: Number of unique hauls per week by pollock trawl vessels fishing in the Bering Sea, B-season.

In 2020 and in 2011, two of the years in which chum salmon bycatch occurred late in the B-season, substantial fishing effort continued later into the season than in other years. In contrast, the 2017 and 2018 B-season were characterized by high bycatch early in the season (Figure 2) with earlier fishing effort (Figure 3).

In summary, there does appear to be a relationship between the timing of chum salmon bycatch and both environmental covariates as well as the timing of fishing effort; however, to disentangle environmental factors and trends in fishing effort a more thorough investigation is required, which is outside the scope of this report.

Spatial Trends in Bycatch

The geographical distribution of the chum salmon bycatch was highly dispersed over the shelf in 2020 (Figure 4), with high rates of bycatch in each of the four spatial clusters previously defined by the Alaska Fisheries Science Center (AFSC) Auke Bay Laboratories (ABL) Genetics Program. This trend is consistent with the observation that in colder years (e.g., 2011 and 2012), typically characterized by lower adult pollock abundance, the fleet is more dispersed with some catcher-processor vessels traveling far to the northwest.

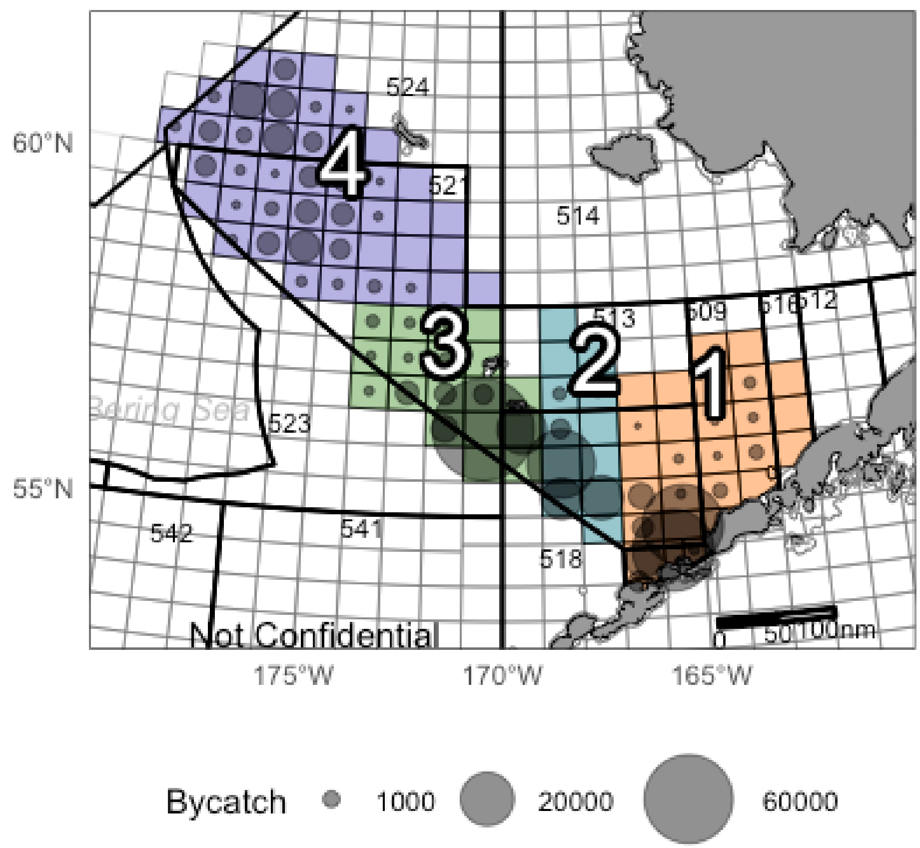

Figure 5: Spatial distribution of chum salmon bycatch caught in the 2020 Bering Sea, B-season pollock fishery. ADF&G groundfish statiscial areas are highlighted based on the four geographic strata assigned in prior genetic analyses.

To evaluate shifts in the distribution of the chum salmon bycatch, the centroid (center of the bycatch) was calculated for each year by sector: Catcher-processor (CP), mothership (M), and shoreside (S). The spatial arrangement of the centroid was investigated for associations with sea surface temperature (not shown) and sea ice extent anomaly. The centroid of the chum salmon bycatch for all sectors was further west than on average. The catcher-processor sector was nearly the most western of the time series (2011-2020), most similar to 2014 and 2019 (Figure 6, CP). It also appeared that in years with negative sea ice extent anomalies (more sea ice), the centroid of the catcher-processor sector is further west than in years with a larger sea ice extent anomaly; however, 2014 had a larger anomaly and was the most western. The 2020 centroid for the mothership sector was similarly farther west than typical (Figure 6, M) and was similar to years 2014 and 2019. The distribution of the shoreside sector centroids was much more concentrated than the CP and M sectors and the 2020 centroid was also the furthest west of the time series.

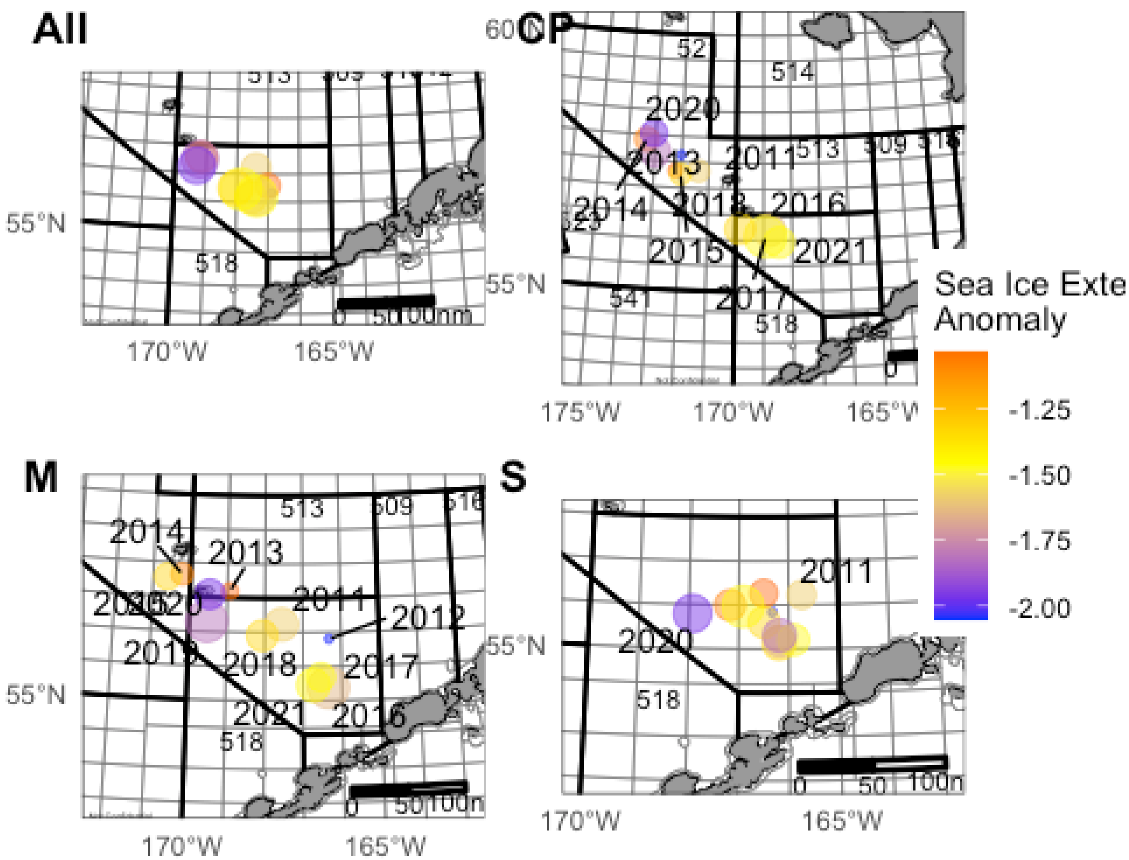

Figure 6: Change in the spatial distribution of chum salmon bycatch as measured by the centroid of the bycatch by sector; catcher-processor (CP), mothership (M) and shoreside (S). Point sizes reflect the relative size of the bycatch and point colors reflect the sea ice extent anomaly.

Bycatch Genotyping Summary

Data from the AFSC Fisheries Monitoring and Analysis Observer Program (Observer Program), total chum salmon bycatch, and genetic sample information were downloaded from the AFSC schema in the Alaska Fisheries Information Network (AKFIN) database. The ABL Genetics Program received 11,261 genetic samples from the Bering Sea and 104 samples from the Gulf of Alaska (GOA). Because of the small number of samples and restrictions on access to the genetics laboratory during the COVID pandemic, the GOA chum salmon samples were not analyzed. After inventorying the Bering Sea genetic samples, a 1-in-5 subsample was conducted for genotyping. DNA from 2,628, 23.3 % of the total genetic samples collected by the Observer Program, was extracted and amplified for the 84-SNP GTseq panel (See Appendix II Table A1). The subsample exceeded the target of 20% (1-in-5) to obtain sufficient sample sizes for certain temporal and spatial strata (e.g., Cluster 4 Late). Samples that were not genotyped for greater than 80% of the GTseq panel (minimum of 68 loci) were omitted from analyses. Of the 2,628 samples amplified, 2,258 (85.9%) were of adequate quality to include for stock composition analyses (20.1% of the total sample collection).

We re-amplified and re-genotyped 3% of samples in the laboratory for quality control. The allele calls of these quality control samples were compared with the allele calls of the originally genotyped samples to estimate the genotyping error rates. This ensures that the GTseq assay is consistent and that samples were organized correctly, ensuring that the mixtures we analyze contain the correct genetic samples. The average agreement over loci was 99.7% and the average agreement among individuals was also high, 99.1% indicating high genotyping accuracy and correct sample organization.

Genetic Stock Composition

The stock composition analyses for the 2020 chum salmon samples were performed with the Bayesian conditional mixed-stock analysis (MSA) approach with bootstrapping over reporting groups implemented in the R package *rubias* (Moran and Anderson 2019). Mixture genotypes were compared to the WASSIP baseline (DeCovich et al. 2012; See Appendix II Figure A1, Table A2) in which populations were grouped into regional reporting groups that were consistent with prior analyses based on the Fisheries and Oceans Canada (DFO) chum salmon microsatellite baseline (Beacham et al. 2009). The reporting groups for baseline populations were: Southeast Asia (SE Asia), Northeast Asia (NE Asia), Western Alaska (W Alaska), Upper/Middle Yukon (Up/Mid Yukon), Southwest Alaska (SW Alaska), and the Eastern Gulf of Alaska/Pacific Northwest (EGOA/PNW)

Overall Trends

Consistent with prior years, the three Alaska-only reporting groups comprised the smallest contribution (13%) to the chum salmon bycatch in the 2020 Bering Sea, B-season (Figure 7, Table 1). The highest contributions were from SE and NE Asia (44.6%) and EGOA/PNW (42.5%) reporting groups, the latter being considerably higher than the long-term average of ~28% (2011 - 2019). The large estimate from the EGOA/PNW reporting group is not however completely atypical. In 2015, 51.4% of the B-season bycatch was comrpised of EGOA/PNW fish. In both 2015 and 2020 the bycatch occurred late in the season (Figure 2). It is possible that delayed fishing effort results in a larger proportion of EGOA/PNW stocks represented in the bycatch, particularly if the majority of the bycatch occurs in the Eastern Bering Sea, off of the Alaska Peninsula (Figures 5 & 6).

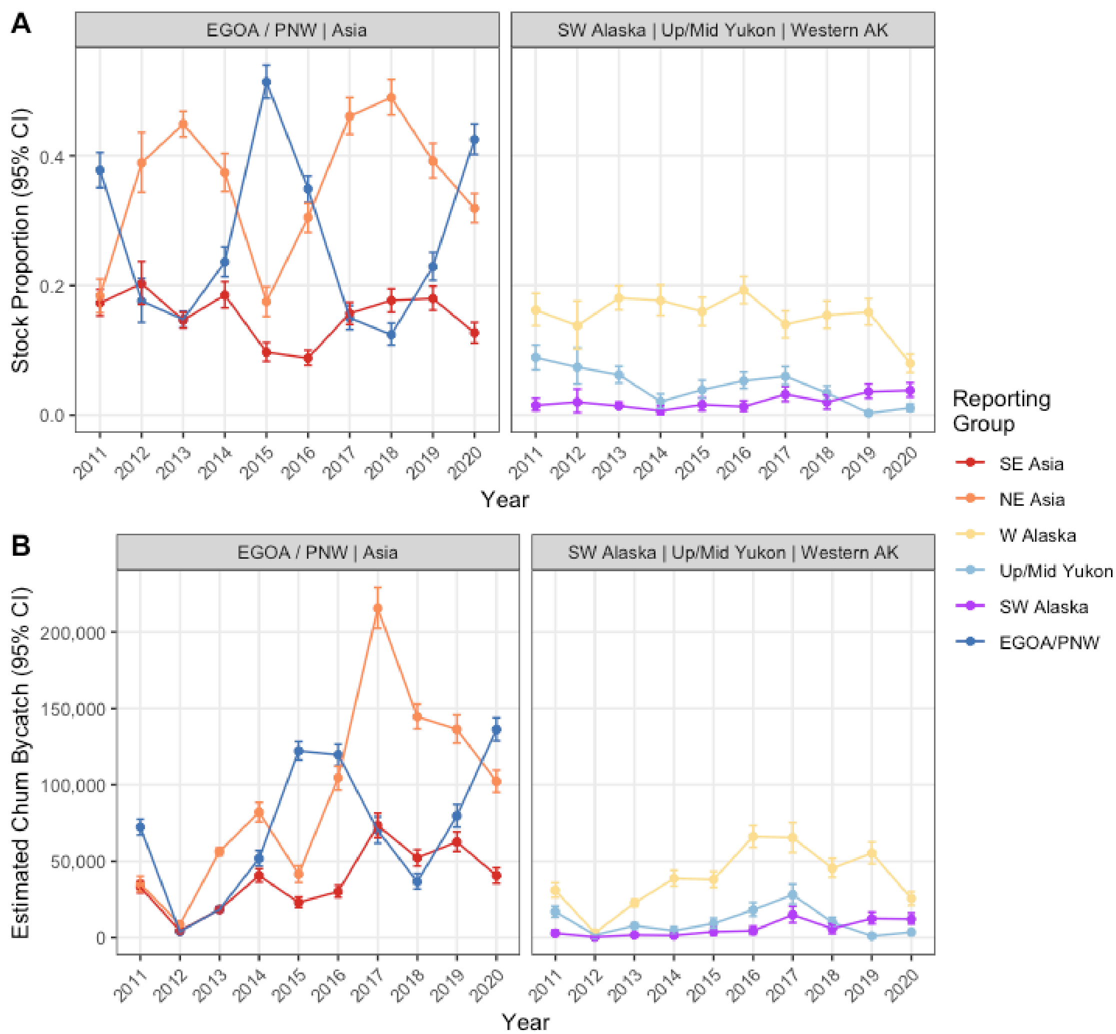

Figure 7: Annual bycatch estimates of B-season chum salmon PSC from 2011 to 2021. (A) stock proportions with 95% credible intervals, (B) Estimated number of chum salmon with 95% credible intervals.

Alternatively, increasing contributions of EGOA/PNW fish may be occurring throughout the B-season. The mean age of bycatch samples has decreased though time which may suggest that EGOA/PNW fish are increasing in relative abundance as chum salmon of southern origin (i.e. Gulf of Alaska and Pacific Northwest populations) mature at younger ages than in the north (i.e. Bering Sea populations) due to the longer growing season in the south than in the north (Sato 1991). Changes in age of the chum salmon bycatch may signify a

Table 1: Regional stock composition estimates of chum salmon from the 2020 Bering Sea, B-season pollock fishery (PSC = 343,014; n = 1816). The estimated number of chum salmon bycatch and mean proportion are provided with standard deviations (SD), 95% credible intervals, median estimate, P = 0 statistic, and the Gelman-Rubin shrink factor.

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0
SE Asia	43,544	0.127	0.008	0.111	0.127	0.143	0.00
NE Asia	109,534	0.319	0.012	0.297	0.319	0.342	0.00
W Alaska	27,295	0.080	0.007	0.066	0.079	0.094	0.00
Up/Mid Yukon	3,613	0.011	0.003	0.006	0.010	0.017	0.00
SW Alaska	13,198	0.038	0.006	0.028	0.038	0.050	0.00
E GOA/PNW	145,827	0.425	0.012	0.402	0.425	0.449	0.00

shift of southern stocks into northern waters; however, the age at maturity of salmon across their range has been decreasing (Oke et al. 2020). The support for these hypotheses is being evaluated with paired age and genetic information from 2005 to 2019 (Ellen Yasumiishi, personal communication).

Temporal Trends

The B-season was divided into Middle (weeks 30-34) and Late (post-week 34) time periods to evaluate if regional group contributions changed through the season. We did not have sufficient sample sizes to run an analysis on the Early (prior to week 30) samples.

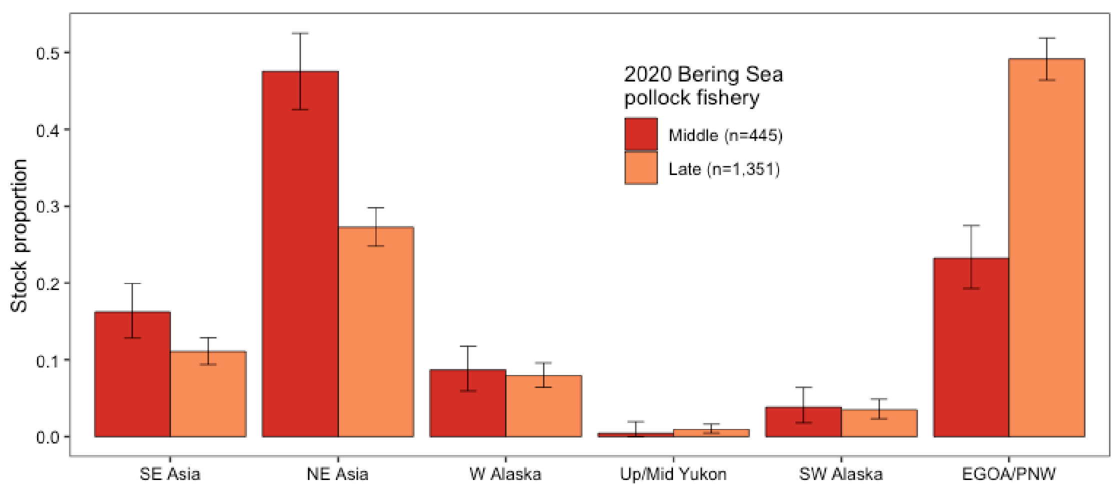

Figure 8: Stock composition estimates from the Middle and Late periods of the Bering Sea, B-season pollock fishery.

For each of the Alaska reporting groups, the Middle and Late stock contributions were similar. However, there was a substantial shift in catch composition between the Middle and Late time periods (Figure 8). The EGOA/PNW reporting group, which increased from 23.23% in the Middle time period to 49.2% in the Late time period, and for the NE Asia reporting group, which had the opposite trend, decreasing from 47.5% in the Middle time period to 27.3% in the Late time period. In 2015, a year with a similarly high contribution of EGOA/PNW fish, there was a similar increase from the Early time period (13%) to the Middle and Late time periods (55%).

Spatial Trends

Typically, more Asian stocks, particularly from SE Asia, are intercepted west of 170°W and Alaskan and EGOA/PNW stocks often have higher contributions east of 170°W. This pattern was generally true for the 2020 chum salmon bycatch. SE Asia contributed more to catches in the west while Western Alaska and Southwest Alaska contributions were higher east of 170°W (Figure 9). However, the EGOA/PNW stocks contributed relatively more west of 170°W.

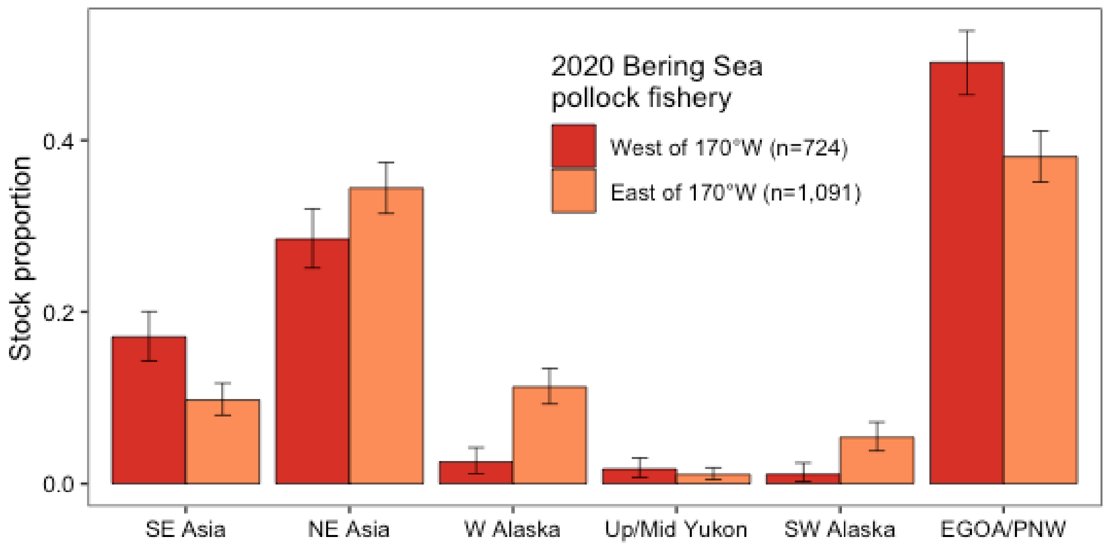

Figure 9: Stock composition estimates for the chum salmon bycatch from the 2020 Bering Sea, B-season pollock fishery from the U.S. waters of the Bering Sea west of 170° W and the southeastern Bering Sea east of 170° W.

The ABL has previously separated the Bering Sea into finer-scale spatial strata (four clusters of ADF&G groundfish statistical areas), and incorporated temporal stratification (Early and Late) to evaluate the spatio-temporal stock specific contributions. The 2020 stock composition estimates were mostly consistent with historic trends. The Asian component decreased from west to east and from Early to Late (Figure 10, left panels). The Alaska reporting group (including W Alaska) contributions increased from west to east (Figure 10, middle panels). And the EGOA/PNW reporting group group increased from Early to Late with the largest contribution in cluster 3 during the Late time period (Figure 10, right panel). Based on the large contribution of EGOA/PNW stocks to the overall B-season bycatch, we might expect greater numbers of hauls and salmon bycatch during the Late time period in cluster 3.

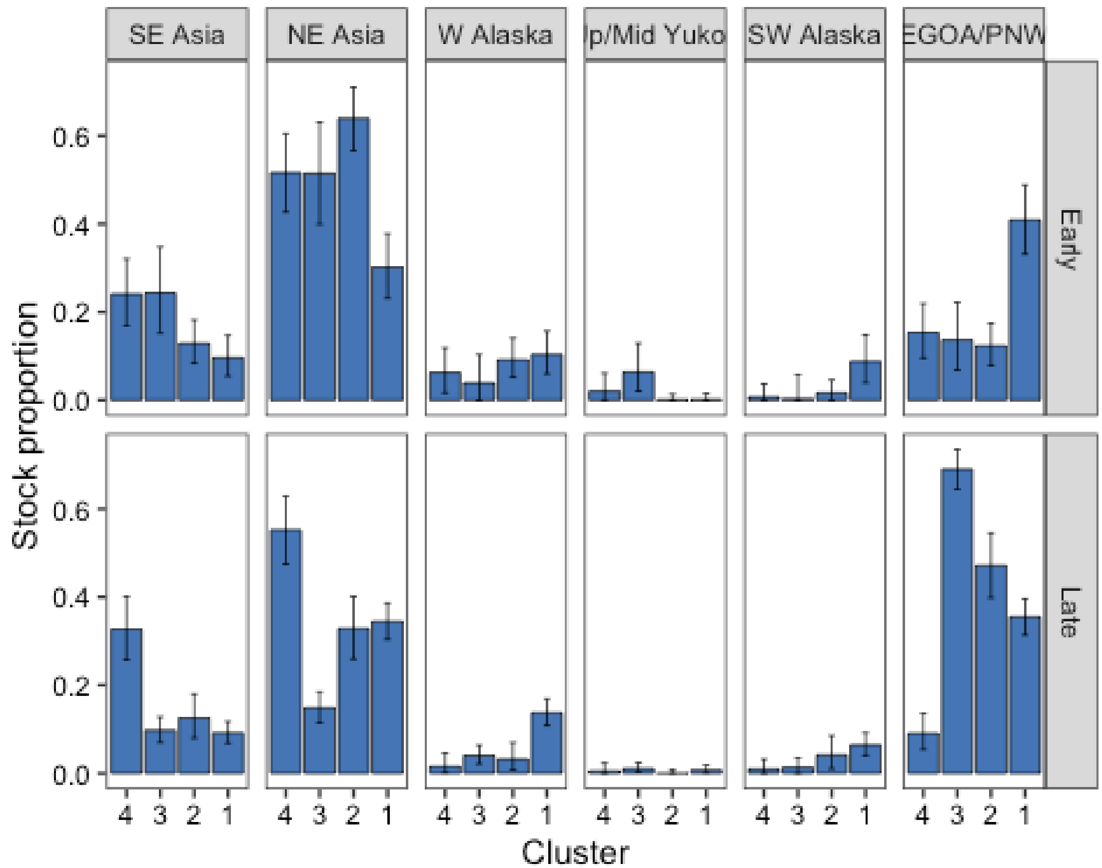

Figure 10: Stock composition estimates for the chum salmon bycatch collected from four spatial clusters along the continental shelf edge during Early (Weeks 24-32) and Late (Weeks 33-43) time periods of the 2020 Bering Sea, B-season pollock fishery. Clusters are ordered from west (cluster 4) to east (cluster 1). See map in Figure 5.

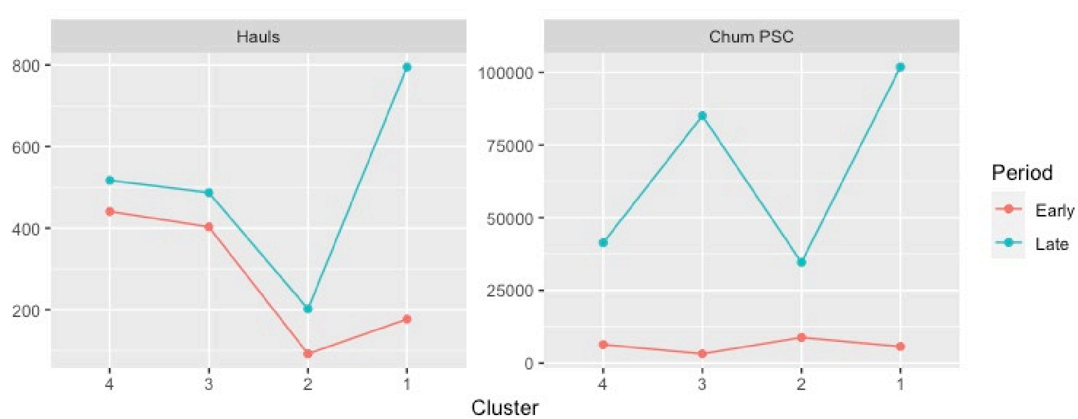

Figure 11: Number of hauls and total chum salmon bycatch from four spatial clusters along the continental shelf edge during Early (Weeks 24-32) and Late (Weeks 33-43) time periods of the 2020 Bering Sea, B-season pollock fishery.

However, the greatest number of hauls and the majority of the chum salmon bycatch were taken in the Late time period in cluster 1. The drop in chum salmon bycatch in cluster 2 during the late period is reflected in the decrease in the number of hauls (Figure 11).

Age Trends

The total age of individual fish was estimated as the number of freshwater and saltwater annuli formed on the scale plus one to account for the winter spent rearing in fresh water. A total of 2,220 chum salmon were aged. Of those, 1,918 had genotypic information and were included in stock composition analyses.

Historically, Age-3 chum salmon are typically dominated by EGOA/PNW stocks while Age-5 chum salmon are overwhelmingly from NE Asian stocks, a pattern supported by maturation at an earlier age in southern stocks and at a later age in northern stocks (Sato1991). In 2020, the data were consistent with historic trends. The EGOA/PNW stocks comprised 48.2% of Age-3 fish and decreased to 6.1% of Age-5 fish, whereas NE Asia stocks comprised 27.2% of Age-3 fish and increased to 62.3% of Age-5 fish (Figure 12). Fish from W Alaska and Up/Mid Yukon stocks did not show any substantial differences in age, with relatively similar representation across age classes. The same was true for SE Asia and SW Alaska stocks.

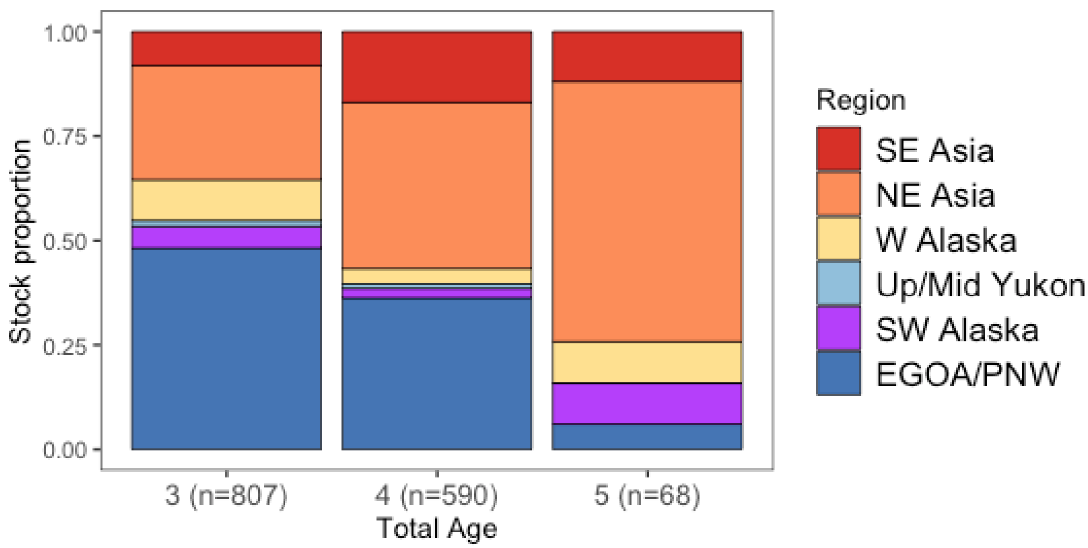

Figure 12: Stock composition estimates for the three predominate ages of chum salmon from the 2020 Bering Sea, B-season pollock fishery.

Sector Trends

Reporting group contributions to chum salmon bycatch from each fishing sector were consistent with historic patterns. The majority of the bycatch from the catcher-processor sector was from Asian stocks and the majority of the bycatch from the shoreside sector was from EGOA/PNW and Alaska stocks (Figure 13). The credible intervals on the mothership estimates reflect greater uncertainty because of small sample size (n = 92) relative to the shoreside and catcher-processor sectors (n = 1,343 and n = 381 respectively).

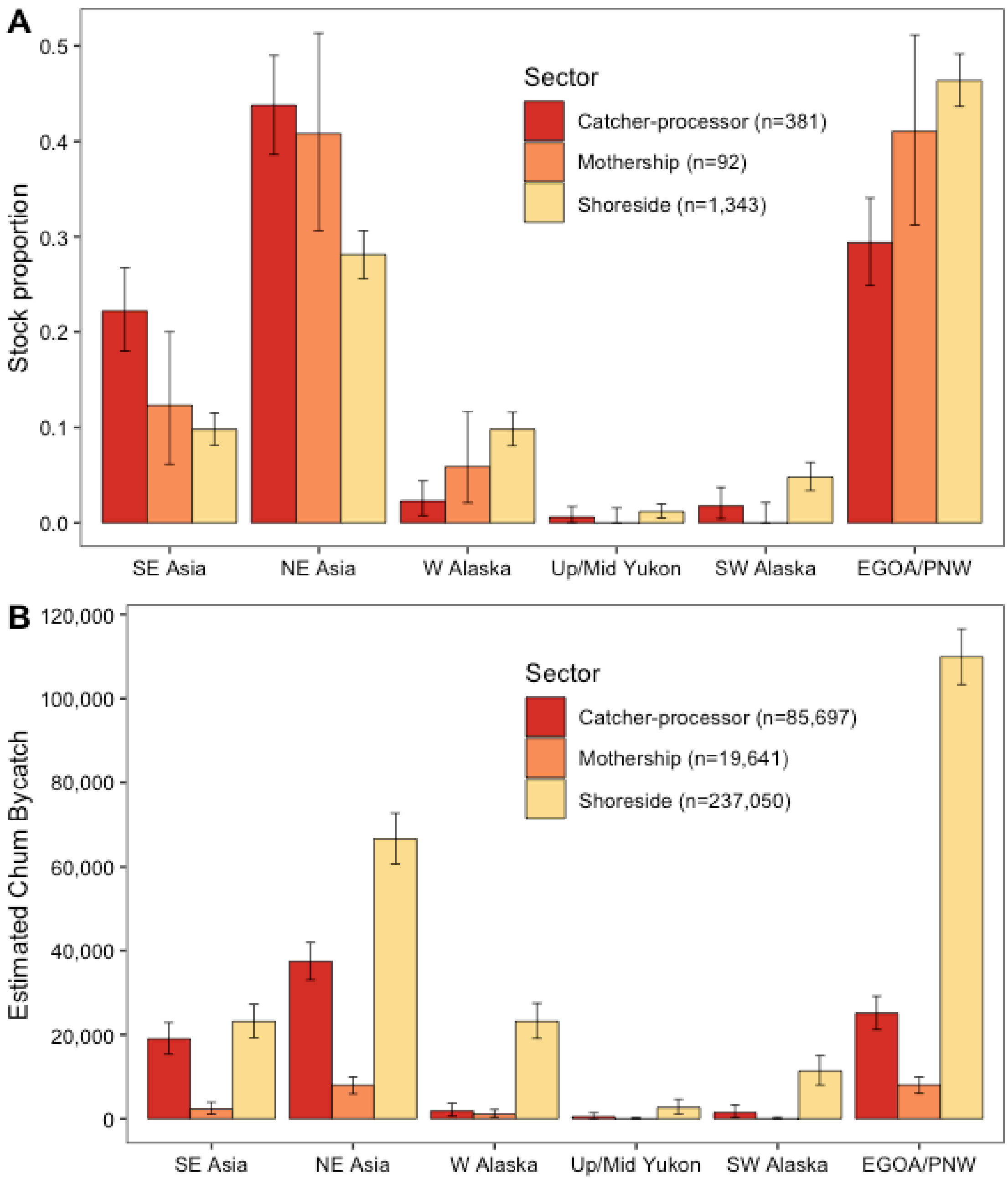

Figure 13: Stock composition estimates for chum salmon bycatch from the 2020 Bering Sea, B-season pollock fishery from the catcher-processor, shoreside, and mothership fishing sectors. (A) reporting group proportions with sample sizes for mixture analysis given in the legend. (B) Estimated number of chum salmon with total bycatch given in the legend.

The catcher-processor sector had higher proportions of Asian fish than the shoreside sector, which is likely due at least in part to the high proportion of catcher-processor vessels that fished in the northwestern area of the fishery where Asian fish are more prevalent.

General trends for W Alaska and Mid/Up Yukon stocks

Chum salmon bycatch occurred later and further west than in previous years. Additionally, the total chum salmon bycatch was higher than average. Despite high variation in the timing and spatial distribution of chum salmon bycatch across years, the average contributions of W Alaska and Up/Mid Yukon stocks had been relatively consistent, with an average of ~20%. However, the contribution of W Alaska and Up/Mid Yukon stocks was much lower than average in 2020 (9%). Additionally, even though chum salmon bycatch was higher than average, the number of W Alaska and Up/Mid Yukon chum salmon that were caught was lower than average. We hypothesize that the lower-than-average contribution of W Alaska and Up/Mid Yukon stocks may be correlated with the low recent returns of chum salmon to western Alaska. It is important to note that although contributions from W Alaska and Up/Mid Yukon stocks were lower than average, there were still strata with relatively high contributions from these stocks. For example, the easternmost cluster (cluster 1) in the Late strata contained nearly 20% W Alaska fish. Research to better understand spatiotemporal trends for W Alaska and Up/Mid Yukon stocks with the goal of reducing interception rates for these stocks is ongoing.

Acknowledgements

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Appendix I - GSI Estimates

Regional stock composition estimates of chum salmon samples from the 2020 Bering Sea, B-season pollock trawl fishery. Note that total PSC was tabulated from the AKFIN database with observer records and is slightly smaller than the AKRO mortality estimate for the B-season.

West of 170° (PSC = 144,086; n = 724)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	24,635	0.171	0.015	0.143	0.171	0.200	0.00	1.00
NE Asia	41,049	0.285	0.018	0.251	0.285	0.320	0.00	1.00
W Alaska	3,662	0.025	0.008	0.012	0.025	0.042	0.00	1.00
Up/Mid Yukon	2,478	0.017	0.006	0.007	0.017	0.030	0.00	1.00
SW Alaska	1,600	0.011	0.006	0.002	0.010	0.024	0.00	1.00
E GOA/PNW	70,658	0.490	0.019	0.453	0.490	0.527	0.00	1.00

East of 170° (PSC = 198,305; n = 1091)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	19,362	0.098	0.009	0.080	0.097	0.117	0.00	1.00
NE Asia	68,241	0.344	0.015	0.315	0.344	0.375	0.00	1.00
W Alaska	22,329	0.113	0.011	0.093	0.112	0.134	0.00	1.00
Up/Mid Yukon	2,136	0.011	0.004	0.005	0.010	0.019	0.00	1.00
SW Alaska	10,721	0.054	0.009	0.038	0.054	0.072	0.00	1.00
E GOA/PNW	75,513	0.381	0.015	0.351	0.381	0.411	0.00	1.00

Middle (PSC = 85,910; n = 445)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	13,954	0.162	0.018	0.128	0.162	0.199	0.00	1.00
NE Asia	40,839	0.475	0.025	0.426	0.475	0.525	0.00	1.00
W Alaska	7,476	0.087	0.015	0.060	0.086	0.118	0.00	1.00
Up/Mid Yukon	365	0.004	0.006	0.000	0.002	0.020	0.28	1.00
SW Alaska	3,312	0.039	0.012	0.018	0.038	0.064	0.00	1.00
E GOA/PNW	19,960	0.232	0.021	0.193	0.232	0.275	0.00	1.00

Late (PSC = 252,850; n = 1351)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	28,071	0.111	0.009	0.094	0.111	0.129	0.00	1.00
NE Asia	69,003	0.273	0.013	0.248	0.273	0.298	0.00	1.00
W Alaska	20,114	0.080	0.008	0.064	0.079	0.096	0.00	1.00
Up/Mid Yukon	2,432	0.010	0.003	0.005	0.009	0.016	0.00	1.00
SW Alaska	8,890	0.035	0.006	0.023	0.035	0.049	0.00	1.00
E GOA/PNW	124,337	0.492	0.014	0.464	0.492	0.519	0.00	1.00

Catcher-processor (PSC = 85,697; n = 381)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	19,037	0.222	0.022	0.180	0.222	0.268	0.00	1.00
NE Asia	37,486	0.437	0.027	0.386	0.437	0.490	0.00	1.00
W Alaska	1,950	0.023	0.009	0.007	0.022	0.044	0.00	1.00
Up/Mid Yukon	510	0.006	0.004	0.000	0.005	0.017	0.01	1.00
SW Alaska	1,540	0.018	0.009	0.004	0.017	0.037	0.00	1.00
E GOA/PNW	25,171	0.294	0.023	0.248	0.293	0.341	0.00	1.00

Shoreside (PSC = 237,050; n = 1343)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	23,188	0.098	0.008	0.082	0.098	0.115	0.00	1.00
NE Asia	66,616	0.281	0.013	0.256	0.281	0.307	0.00	1.00
W Alaska	23,197	0.098	0.009	0.081	0.098	0.116	0.00	1.00
Up/Mid Yukon	2,754	0.012	0.004	0.005	0.011	0.020	0.00	1.00
SW Alaska	11,366	0.048	0.008	0.034	0.048	0.063	0.00	1.00
E GOA/PNW	109,926	0.464	0.014	0.436	0.464	0.492	0.00	1.00

Mothership (PSC = 19,641; n = 92)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	2,415	0.123	0.036	0.061	0.120	0.200	0.00	1.00
NE Asia	8,013	0.408	0.053	0.307	0.407	0.514	0.00	1.00
W Alaska	1,153	0.059	0.025	0.021	0.055	0.116	0.00	1.00
Up/Mid Yukon	0	0.000	0.005	0.000	0.000	0.016	0.78	1.00
SW Alaska	0	0.000	0.006	0.000	0.000	0.021	0.78	1.00
E GOA/PNW	8,059	0.410	0.051	0.312	0.410	0.512	0.00	1.00

Age-3 (PSC = 170,270; n = 807)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	13,868	0.081	0.010	0.062	0.081	0.102	0.00	1.00
NE Asia	46,375	0.272	0.017	0.240	0.272	0.305	0.00	1.00
W Alaska	16,689	0.098	0.013	0.075	0.098	0.123	0.00	1.00
Up/Mid Yukon	2,570	0.015	0.007	0.004	0.014	0.030	0.00	1.00
SW Alaska	8,634	0.051	0.010	0.033	0.050	0.071	0.00	1.00
E GOA/PNW	82,131	0.482	0.018	0.446	0.482	0.518	0.00	1.00

Age-4 (PSC = 140,349; n = 590)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	23,816	0.170	0.016	0.139	0.169	0.203	0.00	1.00
NE Asia	55,811	0.398	0.021	0.356	0.398	0.439	0.00	1.00
W Alaska	5,054	0.036	0.009	0.021	0.035	0.054	0.00	1.00
Up/Mid Yukon	1,440	0.010	0.005	0.003	0.010	0.022	0.00	1.00
SW Alaska	3,455	0.025	0.008	0.011	0.024	0.042	0.00	1.00
E GOA/PNW	50,770	0.362	0.020	0.323	0.362	0.402	0.00	1.00

Age-5 (PSC = 17,582; n = 68)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	2,104	0.120	0.041	0.052	0.116	0.209	0.00	1.00
NE Asia	10,948	0.623	0.061	0.500	0.624	0.739	0.00	1.00
W Alaska	1,741	0.099	0.037	0.040	0.095	0.182	0.00	1.00
Up/Mid Yukon	0	0.000	0.005	0.000	0.000	0.018	0.78	1.00
SW Alaska	1,723	0.098	0.041	0.030	0.094	0.189	0.00	1.00
E GOA/PNW	1,064	0.061	0.031	0.015	0.056	0.135	0.00	1.00

Cluster 1 Early (PSC = 5,643; n = 170)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	541	0.096	0.024	0.055	0.094	0.146	0.00	1.00
NE Asia	1,704	0.302	0.038	0.231	0.301	0.378	0.00	1.00
W Alaska	585	0.104	0.025	0.060	0.102	0.156	0.00	1.00
Up/Mid Yukon	6	0.001	0.004	0.000	0.000	0.015	0.66	1.00
SW Alaska	495	0.088	0.028	0.039	0.086	0.148	0.00	1.00
E GOA/PNW	2,309	0.409	0.040	0.332	0.409	0.489	0.00	1.00

Cluster 1 Late (PSC = 101,893; n = 558)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	9,317	0.091	0.013	0.068	0.091	0.117	0.00	1.00
NE Asia	35,116	0.345	0.021	0.304	0.344	0.386	0.00	1.00
W Alaska	13,977	0.137	0.016	0.108	0.137	0.169	0.00	1.00
Up/Mid Yukon	755	0.007	0.004	0.001	0.007	0.018	0.00	1.00
SW Alaska	6,578	0.065	0.013	0.041	0.064	0.091	0.00	1.00
E GOA/PNW	36,146	0.355	0.021	0.314	0.355	0.397	0.00	1.00

Cluster 2 Early (PSC = 8,780; n = 184)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	1,129	0.129	0.025	0.083	0.127	0.182	0.00	1.00
NE Asia	5,617	0.640	0.037	0.566	0.640	0.711	0.00	1.00
W Alaska	802	0.091	0.023	0.051	0.090	0.141	0.00	1.00
Up/Mid Yukon	7	0.001	0.004	0.000	0.000	0.013	0.69	1.00
SW Alaska	141	0.016	0.012	0.000	0.014	0.046	0.04	1.00
E GOA/PNW	1,081	0.123	0.024	0.079	0.122	0.175	0.00	1.00

Cluster 2 Late (PSC = 34,620; n = 185)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	4,356	0.126	0.026	0.080	0.124	0.180	0.00	1.00
NE Asia	11,371	0.328	0.036	0.259	0.328	0.401	0.00	1.00
W Alaska	1,118	0.032	0.016	0.008	0.030	0.070	0.00	1.00
Up/Mid Yukon	0	0.000	0.003	0.000	0.000	0.008	0.78	1.00
SW Alaska	1,440	0.042	0.019	0.011	0.039	0.085	0.00	1.00
E GOA/PNW	16,333	0.472	0.037	0.398	0.472	0.546	0.00	1.00

Cluster 3 Early (PSC = 3,141; n = 81)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	763	0.243	0.050	0.152	0.241	0.348	0.00	1.00
NE Asia	1,616	0.515	0.059	0.399	0.515	0.631	0.00	1.00
W Alaska	122	0.039	0.027	0.000	0.035	0.103	0.03	1.00
Up/Mid Yukon	199	0.064	0.028	0.020	0.060	0.129	0.00	1.00
SW Alaska	8	0.003	0.016	0.000	0.000	0.057	0.68	1.00
E GOA/PNW	429	0.137	0.039	0.069	0.134	0.222	0.00	1.00

Cluster 3 Late (PSC = 85,085; n = 443)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	8,267	0.097	0.015	0.070	0.097	0.128	0.00	1.00
NE Asia	12,601	0.148	0.018	0.115	0.147	0.185	0.00	1.00
W Alaska	3,451	0.041	0.011	0.021	0.040	0.064	0.00	1.00
Up/Mid Yukon	903	0.011	0.006	0.002	0.010	0.024	0.00	1.00
SW Alaska	1,116	0.013	0.009	0.000	0.012	0.035	0.04	1.00
E GOA/PNW	58,744	0.690	0.023	0.644	0.691	0.735	0.00	1.00

Cluster 4 Early (PSC = 6,318; n = 133)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	1,521	0.241	0.039	0.169	0.239	0.321	0.00	1.00
NE Asia	3,264	0.517	0.045	0.427	0.517	0.605	0.00	1.00
W Alaska	395	0.063	0.026	0.017	0.061	0.119	0.00	1.00
Up/Mid Yukon	125	0.020	0.017	0.000	0.016	0.061	0.00	1.00
SW Alaska	44	0.007	0.011	0.000	0.003	0.037	0.33	1.00
E GOA/PNW	967	0.153	0.032	0.096	0.152	0.219	0.00	1.00

Cluster 4 Late (PSC = 41,370; n = 182)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	13,520	0.327	0.037	0.257	0.326	0.400	0.00	1.00
NE Asia	22,861	0.553	0.040	0.475	0.553	0.630	0.00	1.00
W Alaska	631	0.015	0.012	0.002	0.013	0.045	0.00	1.00
Up/Mid Yukon	217	0.005	0.007	0.000	0.003	0.023	0.23	1.00
SW Alaska	397	0.010	0.009	0.000	0.008	0.032	0.12	1.00
E GOA/PNW	3,741	0.090	0.021	0.054	0.089	0.136	0.00	1.00

Appendix II - GSI Methods

Sequencing libraries are prepared using the Genotyping-in-Thousands by Sequencing (GT-seq) protocol (Campbell 2015). PCR is performed on extracted DNA with primers that amplify 84 SNP loci in the WASSIP chum panel (DeCovich et al. 2012). These PCR products are then indexed in a barcoding PCR, normalized using SequalPrep plates (Invitrogen) and each 96 well plate is subsequently pooled. Next, a double-sided bead size selection is performed using AMPure XP beads (Beckman Coulter), using ratios of beads to library of 0.5x to remove non-target larger fragments and then 1.2x to retain the desired amplicon. Libraries are sequenced on a MiSeq (Illumina) using a single 150-cycle lane run with 2×75 bp paired-end (PE) chemistry. PE reads for each individual are joined with FLASH2 (Magoč & Salzberg, 2011; https://github.com/dstreett/FLASH2). Merged reads are are genotyped with the R package GTscore (McKinney; https://github.com/gjmckinney/GTscore). Individuals with low quality multilocus genotypes (<80% of loci scored) are discarded. We re-genotype 3% of all project individuals as quality control measures.

Mixtures were created by separating sampled fish into spatial and temporal groups from observer data from the AKFIN database. Genetic stock identification was performed with the conditional genetic stock identification model in the R package rubias (Moran and Anderson 2019). As described previously (Gray 2010), with minor changes to regional group names, baseline populations were grouped into six regions: Southeast Asia (SE Asia), Northeast Asia (NE Asia), Western Alaska (W Alaska), Upper/Middle Yukon (Up/Mid Yukon), Southwest Alaska (SW Alaska), and the Eastern Gulf of Alaska/Pacific Northwest (EGOA/PNW; Figure A1). For all estimates, the Dirichlet prior parameters for the stock proportions were defined by region to be $1/(GC_g)$, where C_g is the number of baseline populations in region g, and G is the number of regions. To ensure convergence to the posterior distribution, six separate MCMC chains of 100,000 iterations (burn-in of 50,000) of the non-bootstrapped model were run, in which each chain starting at disparate values of stock proportions; configured such that for each chain 95% of the mixture came from a single designated reporting group (with probability equally distributed among the populations within that reporting group) and the remaining 5% equally distributed among remaining reporting groups.The convergence of chains for each reporting group estimate was assessed with the Gelman-Rubin statistic (Gelman 1992) estimated with the gelman.diag function in the coda library (Plummer 2006) within R. Once chain convergence was confirmed, inference was conducted with the conditional genetic stock identification model with bootstrapping over reporting groups (MCMC chains of 100,000 iterations, burn-in of 50,000, 100 bootstrap iterations).

The stock composition estimates were summarized by the mean, standard deviation, median, 95% credible interval (2.5th and 97.5th percentile of the MCMC iterates in the posterior output), and $P = 0$, which is the probability that a stock composition estimate is effectively zero (Munro et al. 2012). The $P = 0$ statistic is the frequency of the last half of the MCMC iterates of each chain for which the individual regional contribution to the mixture was less than a threshold of $0.5E^{-6}$. This statistic may be more useful than the credible interval for assessing the presence or absence of minor stocks.

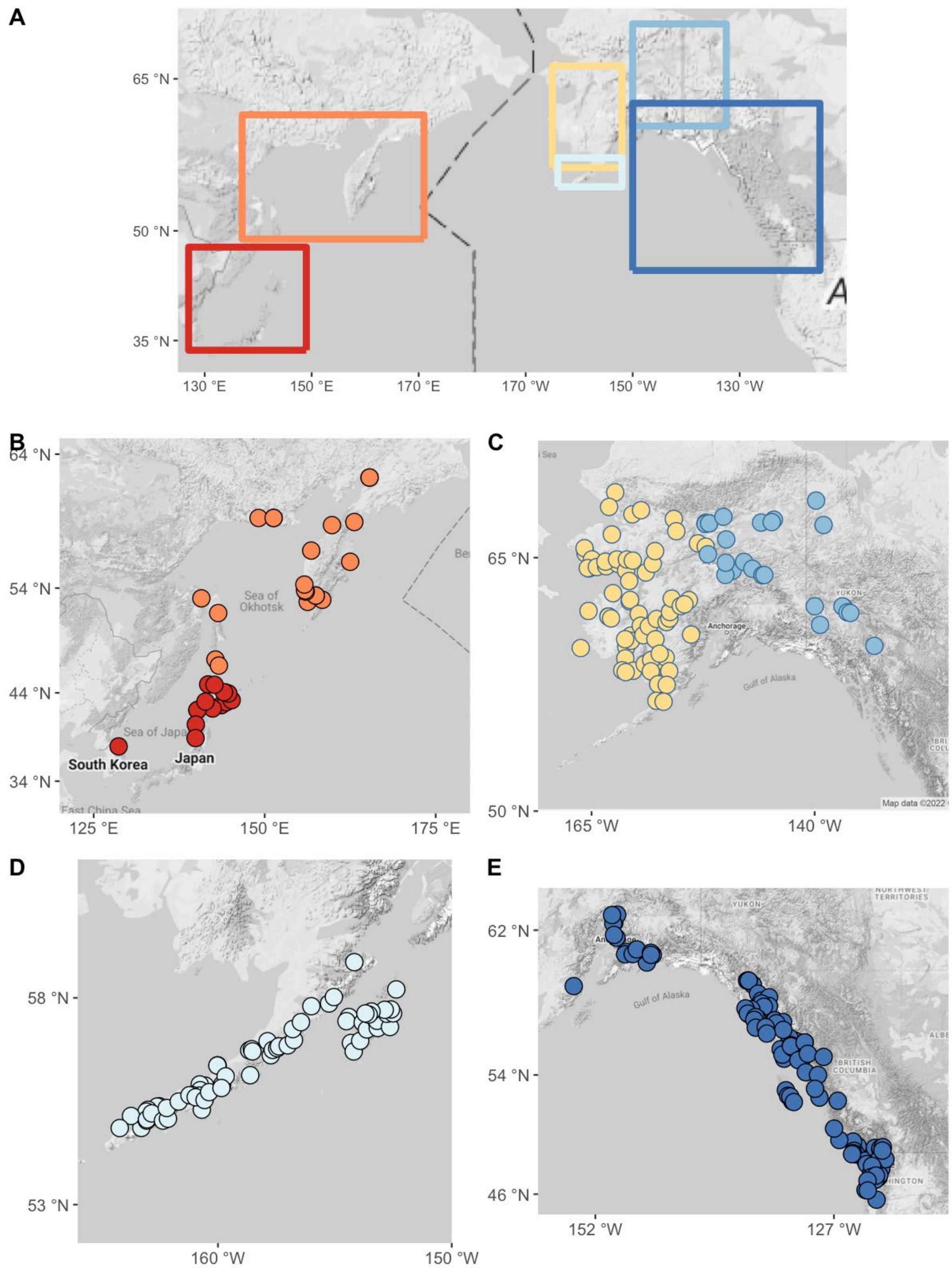

Figure A1: Six reporting groups of baseline chum salmon populations used in this report, circles represent individual populations represented in the baseline. (A) Range wide distribution of the six reporting groups. (B) SE Asia (red) and NE Asia (orange), (C) W Alaska (Yellow) and Up/Mid Yukon (Mid Blue), (D) SW Alaska (light blue), and (E) EGOA/PNW (dark blue) reporting groups.

Appendix II Table A1: Single nucleotide polymorphisms included in the 84-SNP panel used for stock composition analysis for the 2020 Bering Sea, B-season analyses.

Locus	Ploidy	SNPpos	Allele1	Allele2	Probe1	Probe2	Primer	Primer Conc. (uM)
Oke_ACOT-100	2	1	C	G	CTTCCGCTCTCTACTCC	TTCCGCTCTGTACTCC	TCAGGGACGATAAAGGGATCATCTT	0.2000
Oke_ATP5L-105	2	1	C	G	AGTATATTGAGATGAATCCCAC	ATATTGAGATGAATGCCAC	GTGCACACCAATCCATTTCTGAAT	0.2500
Oke_AhR1-78	2	1	G	A	CAGCCTCGGTGCCAT	TCAGCCTCAGTGCCAT	AGCAGAACCAGCACCTACAG	0.2000
Oke_CATB-60	2	1	C	T	CAGGAACGGGTATGAG	CAGGAACGAGTATGAG	GCTTCTATGGGTCCTACTACCGTAT	0.2500
Oke_CD81-108	2	1	G	T	TCCGGCATGTCCCAG	TCCGGCATTTCCCAG	CAGTATCATCATACAGCACAGATACAACA	0.2500
Oke_CD81-173	2	1	A	C	CAGTCACAGAGAGTCAC	AGTCACAGCGAGTCAC	GATGACTGGAGTCAGCTTGCA	0.2000
Oke_CKS-389	2	1	G	A	AAATGAATGATAATGTGTTCTG	AAATGAATGATAATATGTTCTG	GGGCCATTCTCTGAGTTCAGT	0.2500
Oke_CKS1-94	2	1	G	T	TCTGGATAAATTTGTGTATTC	TTCTGGATAAATTTTTGTATTC	TCTTCGACATGTTTAATCGAACAGAAGT	0.2500
Oke_DCXR-87	2	1	A	T	CCTGTTTGTTGAAACCGTA	CCTGTTTGTTGTAACCGTA	GTCACCCAGAACAATAGAATGAGTCT	0.2500
Oke_FANK1-166	2	1	C	T	CTACAGCCCGGCTGTG	CTACAGCCCAGCTGTG	ACTCACGTGTGGTAGAGACAGA	0.2500
Oke_FBXL5-61	2	1	G	A	TCTGAGGGAAACTGC	TCTGAGGAAAACTGC	TGGTGTGTAACGTCAGTGACTTAAG	0.3000
Oke_GHII-3129	2	1	G	A	CAGGGCGACTCTAT	ACAGGGCAACTCTAT	GTCAAGCTGATACCACTCAAATCTCA	0.3000
Oke_GPDH-191	2	1	T	A	CGGAGCCACTTCCAGTA	CGGAGCCACTACCAGTA	CCTGTACCTATAGGGCAACTTCAC	0.2000
Oke_GPH-105	2	1	T	G	CCAGTAATTGGTATTTTGA	CCAGTAATTGGTCTTTTGA	CAGATCAACCCTGGAAAAATATCTGATGT	0.2500
Oke_HP-182	2	1	A	C	AGAAAAGGTGAGCTAGTATG	AAAAGGTGAGCTCGTATG	CCGATGACTCCAAAGAAGTTGCT	0.2500
Oke_IL8r2-406	2	1	T	G	AAACACAAAACCCC	AAACACAAACCCCC	GGATGGACATTCACAGTCTGGTT	0.2000
Oke_KPNA2-87	2	1	T	A	ACAGAACAGAAACAGTG	AACAGAACAGTAACAGTG	AGGCAGCCAGGTAAGTCAGTA	0.1875
Oke_LAMP2-186	2	1	A	G	CTAACTTTACAAAGACACTGC	AACTTTACAAAGGCACTGC	TTCTAGCCATGACCCAATGAAAGG	0.2500
Oke_MLRN-63	2	1	G	A	CTGGTGATTGACGATCC	CTGGTGATTAACGATCC	CCATTTCAGCATTGCCAGATTTGAAA	0.2500
Oke_Moesin-160	2	1	T	G	CATTTTGTAATTCTAATTTTAAGC	ATTTTGTAATTCTAATGTTAAGC	TTTCAGCAAATGAAGAGAACATCAAACTG	0.2500
Oke_NUPR1-70	2	1	G	T	CTATGAGGACGGGTCACA	ACTATGAGGACTGGTCACA	AGACGGTGAACTCTGCTGTAGA	0.3000
Oke_PPA2-635	2	1	C	T	TTGCCTCCCCCGCTC	TTATTGCCTCTCCCGCTC	ACACAACTGACCATATTGACTTTCGA	0.2500
Oke_RFC2-618	2	1	G	A	CAGCTCCTGGACTCA	CAGCTCCTAGACTCA	GACAATGTGTTAGTGTAGGCTTCACT	0.2000
Oke_RH1op-245	2	1	C	T	AGTGGTGAAGCCTC	TAGTGGTAAAGCCTC	TGGCCGATCTCTTCATGGTAATC	0.2500
Oke_RS27-81	2	1	G	A	TGTCCAGGCGTCATGA	TGTCCAGGCATCATGA	GCAACAAAGTGGACTATCACATTGAA	0.3000
Oke_RSPRY1-106	2	1	A	T	TAGTCTCTTTACATAATCTC	TAGTCTCTTTACTTAATCTC	GTCCTCCCTATTCTTCCACTTACCT	0.2500
Oke_TCP1-78	2	1	A	G	ATACTGCTCCAGAGACG	CTGCTCCAGGGACG	CTCCAGGGCATCAGCAAATG	0.2000
Oke_Tf-278	2	1	C	A	ATTTTACAGTTGACATTCAA	TTTTACAGTTGAAATTCAA	GCCACAATTGTAATTCTAGATCCAGAGT	0.2500
Oke_U1008-83	2	1	A	G	CCGTTCTCTTCTTGGACAC	CGTTCTCTTCCTGGACAC	GTCACCAAACATCCTGCGAATG	0.3000
Oke_U1010-251	2	1	A	G	ATAGAGGTGAGCATTGACAT	TAGAGGTGAGCACTGACAT	CACCTCAATCAATCAAATGTATTTATAAAGCCA	0.1875
Oke_U1012-241	2	1	C	G	ATGGAAAAAGAACTGTTTACT	ATGGAAAAAGAACTCTTTACT	GCAGAGGTTATACCCATTTTAGATGCA	0.2500
Oke_U1015-255	2	1	A	G	CAAACACACACAGAGCC	AACACACGCAGAGCC	CAGAGTGCAGAGTAATACGCATACA	0.2500
Oke_U1016-154	2	1	C	T	CCATGTTTGCGGTATGT	CCATGTTTGCAGTATGT	GCAGGTTGCTAAGTCATGTTACACA	0.3000
Oke_U1017-52	2	1	C	T	AGAGAGTTGTCGTTCATC	AGAGAGTTGTCATTCATC	TGGCAATGGGATGTCAAGTTATGA	0.3000
Oke_U1018-50	2	1	C	T	CTGGGCACGTACAGCT	CTGGGCACATACAGCT	TCCAGGTTGCTGACAATGTAAAAGT	0.3000
Oke_U1022-139	2	1	A	G	CTGGAACATGAAGCAAA	TGGAACATGGAGCAAA	AACATTAAAACTGTGGTTTTGACCTCTTG	0.2500
Oke_U1023-147	2	1	A	C	CATCAGGGAAAGCCTACAAA	AGGGAAAGCCGACAAA	TCTTAAAATGGAGAGAGCGATTAATGAAGG	0.2500
Oke_U1024-113	2	1	A	G	CCAGAAACAACTTAATTAT	CAGAAACAACTCAATTAT	CATGCTGGTGAATTATTGGACAATGT	0.2500
Oke_U1025-135	2	1	G	T	ACTTAGTCTATTTGTAACTTT	ACTTAGTCTATTTTTAACTTT	GGCTAGGGTTCTATTTGGACCAT	0.2500
Oke_U2007-190	2	1	C	G	CTAAAAGCTGAGAATAAAT	AAAGCTGACAATAAAT	ACAGGCTGTGATGAGTTAACAATGTAAA	0.2500
Oke_U2011-107	2	1	G	T	TTCTGTGAGAGATTTAG	TTTCTGTGAGATATTTAG	CCGTTTCTGTCAGACTCTGGTAAA	0.1250
Oke_U2015-151	2	1	C	T	AATTGATCACGATCATTC	ATTGATCACAATCATTC	GCATTTTATCCTCAAACTTTTCAACTGACA	0.2500

Appendix II Table A1 continued

Locus	Ploidy	SNPpos	Allele1	Allele2	Probe1	Probe2	Primer	Primer Conc. (uM)
Oke_U2025-86	2	1	G	A	ACTTTTTTGTCGTTTTTTT	ACTTTTTTGTCATTTTTTT	AAATCCCCATGGAGAAACACAATGA	0.2000
Oke_U2029-79	2	1	C	T	AGGTGTACTGAAGAGAC	AGGTGTACTAAAGAGAC	GGTTTGATTTCGTCGCGATTTGA	0.2500
Oke_U2032-74	2	1	G	A	CAATAAAGTGCTAGGTGTCC	CAATAAAGTGCTAAGTGTCC	GCTATTCCAATGTAAATCCTGTACTGTGT	0.2000
Oke_U2034-55	2	1	C	T	ATGTCAAATCACGCTGATG	ATGTCAAATCACACTGATG	GGGAAGAAAAGCCTACCATAAACAG	0.2500
Oke_U2035-54	2	1	G	A	CACCAATAACGTCCTAATC	CACCAATAACATCCTAATC	CGCCAATAACGCTCCAACAAC	0.2500
Oke_U2041-84	2	1	G	T	CAGATCCGGTGTATGC	ACAGATCCTGTGTATGC	CCAGACCATGTGCTTGTTTGTCATA	0.2500
Oke_U2043-51	2	1	G	A	TCTGGAGGCGTATTGG	CTGGAGGCATATTGG	CACAAACCTACTACAGACAGCAGTT	0.2000
Oke_U2048-91	2	1	A	C	CAGCCTCATAAGATGTTTA	CAGCCTCATAAGCTGTTTA	AGTTGGGTCTTAAAGATGATCATTTGCT	0.2000
Oke_U2050-101	2	1	C	T	AATTGATCTACAGCTGCACG	AATTGATCTACAACTGCACG	CTCTGAGTGTCACAATCACATATCGT	0.2000
Oke_U2053-60	2	1	C	T	CACACATATGAGATGCC	CACACATATAAGATGCC	TCTGCTTTTGTCGTCTCACCAA	0.1875
Oke_U2054-58	2	1	C	T	ATGCCCAATTACGTCAGCA	TGCCCAATTACATCAGCA	CGTCTCATTCAGCTCTTTGATGTC	0.2000
Oke_U2056-90	2	1	G	T	CGAAGTGATGAAGGTGACAA	CGAAGTGATGAATGTGACAA	CCATCACGTCACCATTACACTGT	0.1875
Oke_U2057-80	2	1	A	G	CACGTTTTCTCTTTTCTC	ACGTTTTCTCCTTTCTC	GCAGTTGTCATGGCAGTAAGG	0.2500
Oke_U212-87	2	1	C	A	CTTGTGACATTCCTCTCT	CTTGTGACATTACTCTCT	TTGATTCATACTCAAGGTGAGCAGATT	0.2500
Oke_U302-195	2	1	C	A	TTGTCAAAGGAATCATTT	TGTCAAAGGAATAATTT	GACCCTCAGCTATTTTAAGAACCTCAA	0.2500
Oke_U504-228	2	1	A	G	TGGCTCAAACTTG	TTGGCTCGAACTTG	CTTAACTCAGTCACACCAACTCACT	0.2500
Oke_U506-110	2	1	C	T	TTGTAAGTTGTGGCTAAAA	TTGTAAGTTGTGACTAAAA	CGTGGTTGGTTTCATTGACTCTCA	0.2000
Oke_U507-286	2	1	T	G	CTGCTGTTCATAAAAGTA	CTGCTGTTCATACAAGTA	TGGTCATAGCTTGCACTGTACAAA	0.3000
Oke_U509-219	2	1	C	T	CCTCTCTGCAGGGCT	CCCTCTCTACAGGGCT	GCACCCCACCTGGCTT	0.1250
Oke_arf-319	2	1	T	C	CTGTGTGAATTGCCTC	CTGTGTGAACTGCCTC	TGCAGAAACTGATCATTGGTAGTGG	0.1875
Oke_azin1-90	2	1	C	T	CCTTTATCTGAGGAACTG	CCTTTATCTGAAGAACTG	GGGAATAGTGTCATTTGGGATGCAT	0.2500
Oke_brd2-118	2	1	C	T	ATGACGAAGCTCTCC	ATGACGAAACTCTCC	CTCAAGCCCTCCACACTCA	0.2000
Oke_brp16-65	2	1	C	T	ACGTTGCCTGTCCAC	ACGTTGCCTATCCAC	TCCACGTCACTCAGCATGATG	0.2500
Oke_ccd16-77	2	1	A	C	CCAGCCCCCTCTGAAA	AGCCCCCGCTGAAA	TGTCTTCAGAATCCAATGCTTTCCT	0.1875
Oke_e2ig5-50	2	1	C	T	CATCTTTGTATCTGTGCCATT	TCATCTTTGTATCTATGCCATT	GCACTGCTCATTCTGTCACATG	0.2500
Oke_eif4g1-43	2	1	G	T	CTGAGATTCTTCATCTTTTAC	TGAGATTCTTCATATTTTAC	GCACCCAACAGTTCATCATGTAAGT	0.2500
Oke_f5-71	2	1	C	T	CAGGTGCGTGCAGTAA	TCAGGTGCATGCAGTAA	CTCAAATTTCCCTTTGACATCAATTCATCA	0.2500
Oke_gdh1-62	2	1	C	T	TTCTGTGTCCCGTGACCT	CTGTGTCCCATGACCT	CCACGTGATACAGGGAGATGTG	0.2000
Oke_glrx1-78	2	1	C	T	TGGGCATTTAGAGTTTATT	TGGGCATTTAGAATTTATT	CGCTCCGTCCAGTGATGTC	0.2500
Oke_il-1racp-67	2	1	G	A	CGTACGAGATGTAGATGT	CGTACGAGATATAGATGT	AATTGCTCCTCCTCGCTATTTCTC	0.2000
Oke_mgll-49	2	1	A	T	ATTTATGGGTGTTCCCC	TTATGGGAGTTCCCC	ACATTGTAATCTGTATTAGTCCAATGCAGAC	0.2500
Oke_nc2b-148	2	1	A	C	TTTAGTTCTAGTCAAAAGTAG	TAGTTCTAGTCCAAAGTAG	CCAGCCTATTTCCTTTAGTGCATATGA	0.2500
Oke_pgap-111	2	1	C	T	AGCTAGCAGGCTAAAG	AGCTAGCAAGCTAAAG	TGCAGATCTCAATTTGAACGACCTAT	0.2000
Oke_psmd9-57	2	1	C	T	CATTGGCGGTGTAACG	TCATTGGCAGTGTAACG	ACTGTAGTGACTGCATTTCATATTGCT	0.2000
Oke_rab5a-117	2	1	C	T	CAGCTGTTTTTCTTGTAGCCT	AGCTGTTTTTCTTATAGCCT	GGGAATAACAGTCATTGCAGCATTT	0.2000
Oke_ras1-249	2	1	T	G	CACCAAGGTAAAAAT	CCAAGGGAAAAAT	GGATGACTAAGAGCGACTGTATGTG	0.2500
Oke_serpin-140	2	1	A	T	CAAGAACTGACCTTAGACAC	AAGAACTGACCTTTGACAC	TCCACAGTGAGTAATAAAGTTGCACAT	0.2000
Oke_slc1a3a-86	2	1	C	T	CCCAACGCGGTGATG	CCCAACGCAGTGATG	TGTCTTCATCTGTGGACTCCTACA	0.3000
Oke_sylc-90	2	1	A	T	ATATCTTTGAGACTAGATTAA	CTTTGAGACAAGATTAA	TTGAGGAAACCACTGGTCTTACAAG	0.1875
Oke_thic-84	2	1	C	T	ATGGAATGACAGCAATGT	ATGGAATGACAACAATGT	GCTGCTGTCTTAAACCACATTCTACA	0.2500
Oke_u200-385	2	1	G	T	CATTATCTCCCTGAATGTA	CATTATCTCCATGAATGTA	CCCATAATTTTGCAACCCTAGTCACA	0.2000
Oke_u217-172	2	1	T	C	CACTCTTACAAAAACA	CACTCTTACGAAAACA	GGATGGAAGAAGTTAGTTGTGTCAGA	0.3000

Appendix II Table A2: Chum salmon populations in the Alaska Department of Fish and Game (ADF&G) single nucleotide baseline grouped by six reporting groups used in the analyses of this report.

Population	Reporting Group	Samples	Population	Reporting Group	Samples
Abashiri River	SE Asia	80	Pymta	NE Asia	147
Chitose River - early	SE Asia	80	Tauy	NE Asia	41
Gakko River - early	SE Asia	78	Tym River	NE Asia	53
Kushiro River	SE Asia	79	Udarnitza River	NE Asia	44
Namdae River	SE Asia	90	Vorovskaya	NE Asia	101
Nishibetsu River	SE Asia	79	Agiapuk River	W Alaska	94
Sasanai River	SE Asia	77	Alagnak River	W Alaska	92
Shari River	SE Asia	75	American River	W Alaska	86
Shinzunai River	SE Asia	78	West Fork Andreafsky River	W Alaska	85
Teshio River	SE Asia	80	Andreafsky River - East Fork weir	W Alaska	94
Tokachi River	SE Asia	78	Aniak River	W Alaska	92
Tokoro River	SE Asia	69	Yellow River - Anvik	W Alaska	80
Tokushibetsu River	SE Asia	80	Otter Creek - Anvik	W Alaska	156
Yurappu River - early	SE Asia	80	Big River	W Alaska	94
Yurappu River - late	SE Asia	75	Black River	W Alaska	93
Amur River - summer run	NE Asia	60	Big Creek - Naknek River	W Alaska	69
Bistraya River	NE Asia	66	Chulinak	W Alaska	92
Bolshaya River	NE Asia	93	Clear Creek	W Alaska	94
Hairusova River	NE Asia	85	Eldorado River	W Alaska	89
Kamchatka River	NE Asia	49	Fish River	W Alaska	92
Kanchalan	NE Asia	77	George River	W Alaska	95
Kol River	NE Asia	123	Gisasa River	W Alaska	95
Magadan	NE Asia	77	Goodnews River	W Alaska	137
Naiba	NE Asia	98	Henshaw Creek - early	W Alaska	94
Oklan River	NE Asia	75	Holokuk River	W Alaska	103
Ola River - Hatchery	NE Asia	78	Huslia River, Koyukuk - Set B	W Alaska	95
Ossora	NE Asia	87	Inmachuk River	W Alaska	91
Ozerki Hatchery	NE Asia	93	Iowithla River	W Alaska	95
Palana River	NE Asia	90	Kaltag River	W Alaska	92
Paratunka River	NE Asia	94	Kanektok River weir	W Alaska	94
Penzhina	NE Asia	43	Kasigluk River	W Alaska	55

Appendix II Table A2 continued

Population	Reporting Group	Samples	Population	Reporting Group	Samples
Kelly Lake - Noatak River	W Alaska	95	Stony River	W Alaska	150
Kobuk River - at Kiana	W Alaska	95	Stuyahok River	W Alaska	86
Kisaralik River - (Set F)	W Alaska	93	Sunshine Creek	W Alaska	47
Klutuspak Creek	W Alaska	70	Takotna River - 2 mile above Takotna Village	W Alaska	94
Kobuk - Salmon River (Mile 4)	W Alaska	99	Tatlawiksuk River weir	W Alaska	95
Kogrukluk River weir	W Alaska	95	Togiak River	W Alaska	175
Kokwok River	W Alaska	131	Tozitna River	W Alaska	92
Koyuk River	W Alaska	43	Tubutulik River	W Alaska	93
Kwethluk River	W Alaska	143	Tuluksak River Weir	W Alaska	92
Kwiniuk River	W Alaska	94	Unalakleet	W Alaska	188
Mekoryuk River	W Alaska	104	Ungalik River	W Alaska	144
Melozitna River	W Alaska	91	Wandering Creek - tributary of Dog Salmon River	W Alaska	50
Mulchatna River - Upper Nushagak River	W Alaska	91	Whale Mountain Creek, (King Salmon River, Egegik Bay)	W Alaska	189
Necons River	W Alaska	95	Windy Fork Kuskokwim	W Alaska	93
Niukluk River	W Alaska	93	Innoko River (Yukon A)	W Alaska	85
Noatak River - above hatchery	W Alaska	92	American River	SW Alaska	95
Nome River	W Alaska	94	Foster Creek - Balboa Bay	SW Alaska	182
Nulato River	W Alaska	189	Dog Bay	SW Alaska	95
Nunsatuk River - (Set A)	W Alaska	92	Kizhuyak River	SW Alaska	174
Upper Nushagak	W Alaska	97	Peterson Lagoon	SW Alaska	181
Osviak River	W Alaska	88	Uganik River	SW Alaska	175
Pikmiktalik River	W Alaska	95	Alligator Hole	SW Alaska	183
Pilgrim River	W Alaska	75	Main Creek - Amber Bay	SW Alaska	85
Pumice Creek	W Alaska	95	Barling Bay Creek	SW Alaska	92
Salmon River	W Alaska	95	Belkovski River	SW Alaska	87
Selby Slough	W Alaska	90	Big River (Hallo Bay)	SW Alaska	95
South Fork Koyukuk River - Early	W Alaska	90	Big Sukhoi	SW Alaska	189
South Fork Kuskokwim - fall	W Alaska	95	Canoe Bay	SW Alaska	186
Shaktoolik River	W Alaska	94	Chichagof Bay	SW Alaska	180
Snake River	W Alaska	90	Chiginagak Bay River	SW Alaska	159
Solomon River	W Alaska	62	Coal Valley	SW Alaska	94

Appendix II Table A2 continued

Population	Reporting Group	Samples	Population	Reporting Group	Samples
Coleman Creek	SW Alaska	95	Russell Creek	SW Alaska	185
Coxcomb Creek	SW Alaska	89	Russian River	SW Alaska	185
Deadman River	SW Alaska	95	Sandy Cove	SW Alaska	186
Deer Valley	SW Alaska	91	Sitkinak Island	SW Alaska	93
Delta Creek (Cold Bay)	SW Alaska	95	Spiridon River - Upper	SW Alaska	89
Dry Bay River	SW Alaska	71	St. Catherine Cove	SW Alaska	171
Eagle Harbor	SW Alaska	94	Big River - Stepovak Bay	SW Alaska	143
Frosty Creek	SW Alaska	190	Stepovak River	SW Alaska	94
Gull Cape Creek	SW Alaska	186	Sturgeon River	SW Alaska	109
Three Hills River	SW Alaska	49	Traders Cove	SW Alaska	76
Ivanof River	SW Alaska	181	Volcano Bay (Cold Bay)	SW Alaska	95
Joshua Green	SW Alaska	92	Bear Bay Creek	SW Alaska	187
Karluk Lagoon	SW Alaska	83	North Fork Creek, Aniakchak River	SW Alaska	94
Kialagvik Creek (Wide Bay)	SW Alaska	177	Alagogshak River	SW Alaska	94
Kitoi Hatchery	SW Alaska	194	Portage Creek	SW Alaska	190
Lawrence Valley Creek	SW Alaska	190	North Fork Creek, Kujulik Bay	SW Alaska	164
Little John Lagoon	SW Alaska	172	Wiggly Creek - Cinder	SW Alaska	177
Meshik River	SW Alaska	78	West Kiliuda Creek	SW Alaska	87
Braided Creek (Meshik River)	SW Alaska	94	Zachary Bay	SW Alaska	76
Moffet Creek	SW Alaska	95	Zachar River	SW Alaska	66
Nakililock River	SW Alaska	95	17 Mile Slough (Nenana) - fall run	Up/Mid Yukon	90
North of Cape Seniavin	SW Alaska	96	Big Creek - Canadian Mainstem (Yukon)	Up/Mid Yukon	100
Northeast Creek	SW Alaska	94	Black River	Up/Mid Yukon	95
Sapsuk River, Nelson Lagoon	SW Alaska	144	Bluff Cabin	Up/Mid Yukon	99
Ocean Bay	SW Alaska	78	Big Salt River	Up/Mid Yukon	69
Pass Creek - Wide Bay	SW Alaska	94	Chandalar River	Up/Mid Yukon	92
Plenty Bear Creek (Meshik River)	SW Alaska	138	Chena River	Up/Mid Yukon	77
NE Portage - Alitak	SW Alaska	94	Delta River - Fairbanks	Up/Mid Yukon	149
Right Hand Moller Bay	SW Alaska	94	Donjek River	Up/Mid Yukon	60
Rough Creek	SW Alaska	77	Fishing Branch	Up/Mid Yukon	90
Ruby's Lagoon (Cold Bay)	SW Alaska	92	Henshaw Creek - late	Up/Mid Yukon	60

Appendix II Table A2 continued

Population	Reporting Group	Samples	Population	Reporting Group	Samples
Henshaw Creek - late	Up/Mid Yukon	60	Dosewallips River - summer run	EGOA/PNW	86
Jim River	Up/Mid Yukon	146	Dry Bay Creek	EGOA/PNW	94
Kantishna River	Up/Mid Yukon	94	Ecstall	EGOA/PNW	50
Kluane River	Up/Mid Yukon	114	Elwha River	EGOA/PNW	93
Minto Slough	Up/Mid Yukon	91	Fish Creek - early	EGOA/PNW	131
Old Crow - Porcupine River	Up/Mid Yukon	92	DIPAC Hatchery	EGOA/PNW	281
Pelly River	Up/Mid Yukon	84	Fish Creek - late	EGOA/PNW	49
Salcha River	Up/Mid Yukon	83	Ford Arm Lake - fall	EGOA/PNW	95
South Fork Koyukuk River - Late	Up/Mid Yukon	92	Goldstream River	EGOA/PNW	95
Sheenjek River	Up/Mid Yukon	93	Grays River - fall run	EGOA/PNW	93
Tanana River Mainstem	Up/Mid Yukon	95	Hamma Hamma River - summer	EGOA/PNW	108
Tatchun Creek	Up/Mid Yukon	92	Hamma Hamma River	EGOA/PNW	94
Teslin River	Up/Mid Yukon	92	Harding River	EGOA/PNW	45
Toklat River - Geiger Ck. (Set A) -Mainstream	Up/Mid Yukon	95	Herman Creek - Chilkat River	EGOA/PNW	94
Keta Creek	EGOA/PNW	95	Hidden Falls Hatchery	EGOA/PNW	95
Admiralty Creek	EGOA/PNW	64	Hidden Inlet	EGOA/PNW	82
Aloutte River	EGOA/PNW	95	I-205 Seeps - fall run	EGOA/PNW	72
Bag Harbor	EGOA/PNW	49	Inch Creek	EGOA/PNW	181
Beartrap Creek	EGOA/PNW	582	Jimmy Creek - summer run	EGOA/PNW	92
Big Qualicum River	EGOA/PNW	72	Johns Creek - summer run	EGOA/PNW	92
Big Mission Creek Fall Run	EGOA/PNW	55	Kalama Creek - winter run	EGOA/PNW	54
Carmen Lake	EGOA/PNW	67	Karta River	EGOA/PNW	56
Carroll River	EGOA/PNW	85	Kitasoo Creek	EGOA/PNW	169
Chilkat - mainstem	EGOA/PNW	76	Kitimat River	EGOA/PNW	104
Chunilna River	EGOA/PNW	83	Kitwanga River	EGOA/PNW	74
Constantine Creek	EGOA/PNW	594	Klahini River	EGOA/PNW	50
Conuma River	EGOA/PNW	96	Klehini River - Chilkat River	EGOA/PNW	92
Dewatto River - fall chum	EGOA/PNW	74	Lagoon Creek - fall run	EGOA/PNW	166
Diru Creek - Tribal Hatchery	EGOA/PNW	45	Little Creek - fall run	EGOA/PNW	92
Disappearance Creek - fall run	EGOA/PNW	162	Lilliwaup River - summer run	EGOA/PNW	45
Disappearance Creek	EGOA/PNW	143	Lilliwaup River - fall run	EGOA/PNW	92

Appendix II Table A2 continued

Population	Reporting Group	Samples	Population	Reporting Group	Samples
Long Bay	EGOA/PNW	159	Sarita River	EGOA/PNW	63
Little Qualicum River	EGOA/PNW	98	Satsop River	EGOA/PNW	95
Lower Skagit River - fall run	EGOA/PNW	91	Sawmill Creek - Berners Bay	EGOA/PNW	95
Little Susitna River weir	EGOA/PNW	95	Sedgewick	EGOA/PNW	50
McNeil River Lagoon	EGOA/PNW	108	Sherwood Creek - fall run	EGOA/PNW	87
Medvejie Hatchery	EGOA/PNW	119	Sherwood Creek - summer run	EGOA/PNW	88
Mill Creek - fall run	EGOA/PNW	80	Sisters Lake	EGOA/PNW	86
Nahmint River	EGOA/PNW	95	Siwash Creek	EGOA/PNW	362
Nakat Inlet - summer	EGOA/PNW	95	Skamokawa Creek - fall run	EGOA/PNW	76
Nakwasina River	EGOA/PNW	93	Skykomish River - fall run	EGOA/PNW	87
North Arm Creek	EGOA/PNW	97	Snootli Creek	EGOA/PNW	190
North Creek - fall run	EGOA/PNW	93	Snoqualmie River	EGOA/PNW	84
Neets Bay - fall	EGOA/PNW	95	Sooke River	EGOA/PNW	50
Neets Bay - Summer	EGOA/PNW	145	Spink Creek	EGOA/PNW	44
Nimpkish River	EGOA/PNW	187	Stagoo	EGOA/PNW	49
Nisqually River Hatchery	EGOA/PNW	94	Sugsaw River	EGOA/PNW	60
Nitinat River	EGOA/PNW	113	Surprise	EGOA/PNW	50
Norrish Creek	EGOA/PNW	91	Susitna River (Slough 11)	EGOA/PNW	94
Pallant Creek	EGOA/PNW	209	Swan Cove Creek	EGOA/PNW	88
Prospect Creek	EGOA/PNW	89	Taku River - fall	EGOA/PNW	93
Puntledge River	EGOA/PNW	99	Talkeetna River	EGOA/PNW	50
Olsen Creek (PWS) - Set A	EGOA/PNW	94	Traitors Cove Creek	EGOA/PNW	91
Quilcene - summer run	EGOA/PNW	63	Union River - summer	EGOA/PNW	109
Ralph's Creek	EGOA/PNW	95	Upper Sauk River - fall run	EGOA/PNW	86
Saginaw Creek	EGOA/PNW	41	West Arm Creek	EGOA/PNW	186
Salmon Creek - summer run	EGOA/PNW	82	West Crawfish	EGOA/PNW	92
Salmon River	EGOA/PNW	47	Weaver Creek	EGOA/PNW	96
Saltery Bay	EGOA/PNW	48	Wells River	EGOA/PNW	597
Sample Creek	EGOA/PNW	74	Wells Bridge	EGOA/PNW	46
Sanborn Creek	EGOA/PNW	94	Wally Noerenberg Hatchery	EGOA/PNW	385
Saook Bay	EGOA/PNW	94	Willow Creek	EGOA/PNW	89