

Genetic Stock Composition Analysis of Chum Salmon from the Prohibited Species Catch of the 2021 Bering Sea Walleye Pollock Trawl Fishery

Report to the North Pacific Fisheries Management Council

P. Barry, C. Kondzela, J. Whittle, J. Watson, K. Karpan, K. D'Amelio, & W. Larson

23 May 2022

Table of Contents

Executive Summary.....	1
Catch Summary.....	2
Temporal Trends.....	2
Spatial Trends.....	3
Bycatch Genotyping Summary.....	5
Genetic Stock Composition.....	6
Overall Trends.....	6
Temporal Trends.....	8
Spatial Trends.....	9
Spatiotemporal Trends.....	10
Age Trends.....	11
Sector Trends.....	12
Excluder Device Experimental Trawls.....	13
Summary for Western Alaska, Upper/Middle Yukon, and SW Alaska stocks.....	15
Acknowledgements.....	15
References.....	16
Appendix I - GSI Estimates.....	17
Appendix II - GSI Methods.....	22

Executive Summary¹

We analyzed genetic stock compositions of chum salmon (*Oncorhynchus keta*) prohibited species catch (PSC) samples collected from the 2021 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 PSC was 546,043 fish, the second highest bycatch number since 1991 and considerably higher than the 10-year average of 257,023. Despite large catches of chum salmon PSC occurring early in the year and relatively close to the Alaska Peninsula where higher proportions of coastal western Alaska fish are expected, the combined proportion of western Alaska and Middle/Upper Yukon fish was 9.4%, which was similar to the proportion in 2020, but substantially less than the recent (10 year) long-term average of 19.9%. The total number of western Alaska and Upper/Middle Yukon chum salmon caught as PSC in the BSAI B-season in 2021 was estimated to be 51,510 fish. Despite the large total PSC in 2021, the number of western Alaska fish caught is similar to the long-term average of 49,290 from 2011 to 2020. We hypothesize that the relatively low proportion of western Alaska fish reflects their recent low run sizes but cannot rule out other factors such as fleet behavior or differences in distribution. Fish from Asia were by far the most numerous stocks in our samples, with NE Asia contributing 55.7% and SE Asia contributing 11.9% for a total of 67.6% of the bycatch. The EGOA/PNW reporting group contribution (20%) was down substantially from the high observed in 2020 (42.5%). Over the last 11 years the contribution of NE Asia and EGOA/PNW stocks has been negatively correlated ($r^2 = 0.86$), with large proportions from Asia coinciding with small proportions from the EGOA/PNW and vice versa. Reporting group stock proportions on finer-scale spatial and temporal strata were generally consistent with prior observations.

¹ *Disclaimer* - These represent preliminary analyses of the 2021 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 (PSC), referred to as “bycatch” throughout this report, in the Bering Sea walleye pollock trawl fishery was 546,043 fish in 2021, with 545,883 from the B-season (Figure 1). This was 273,603 fish more than the 10-year average of 257,023 (SD 126,526). As is typical, over 99% of the bycatch of chum salmon occurred in the B season (between June and October).

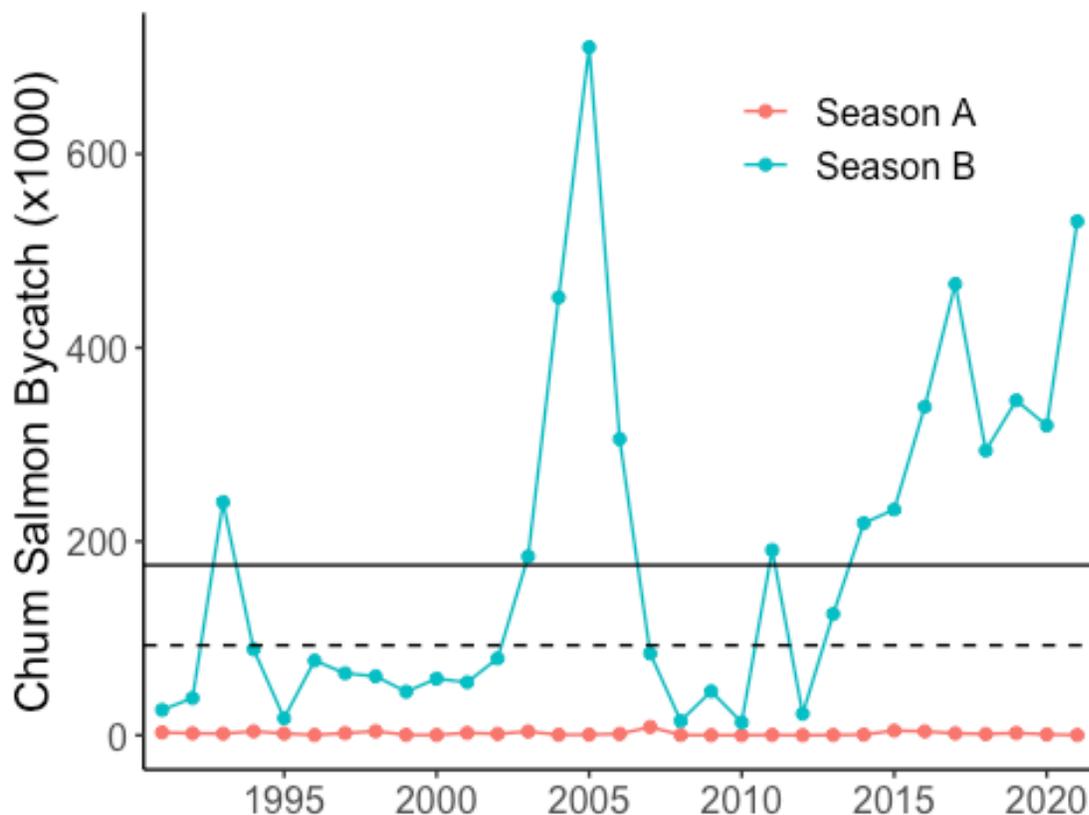


Figure 1: Chum salmon prohibited species catch (PSC) for the A and B seasons from the Bering Sea pollock-directed trawl fisheries. The solid horizontal line represents the mean PSC and the dashed line represents the median PSC from 1991 to 2021.

Within the B season, the chum salmon bycatch was bimodally distributed with peaks occurring in weeks 29 and 32 (Figure 2, top panel). Overall, the timing of the bycatch fell between the early catches in 2017 and 2018 and the later catch in 2020 (Figure 2, bottom panel).

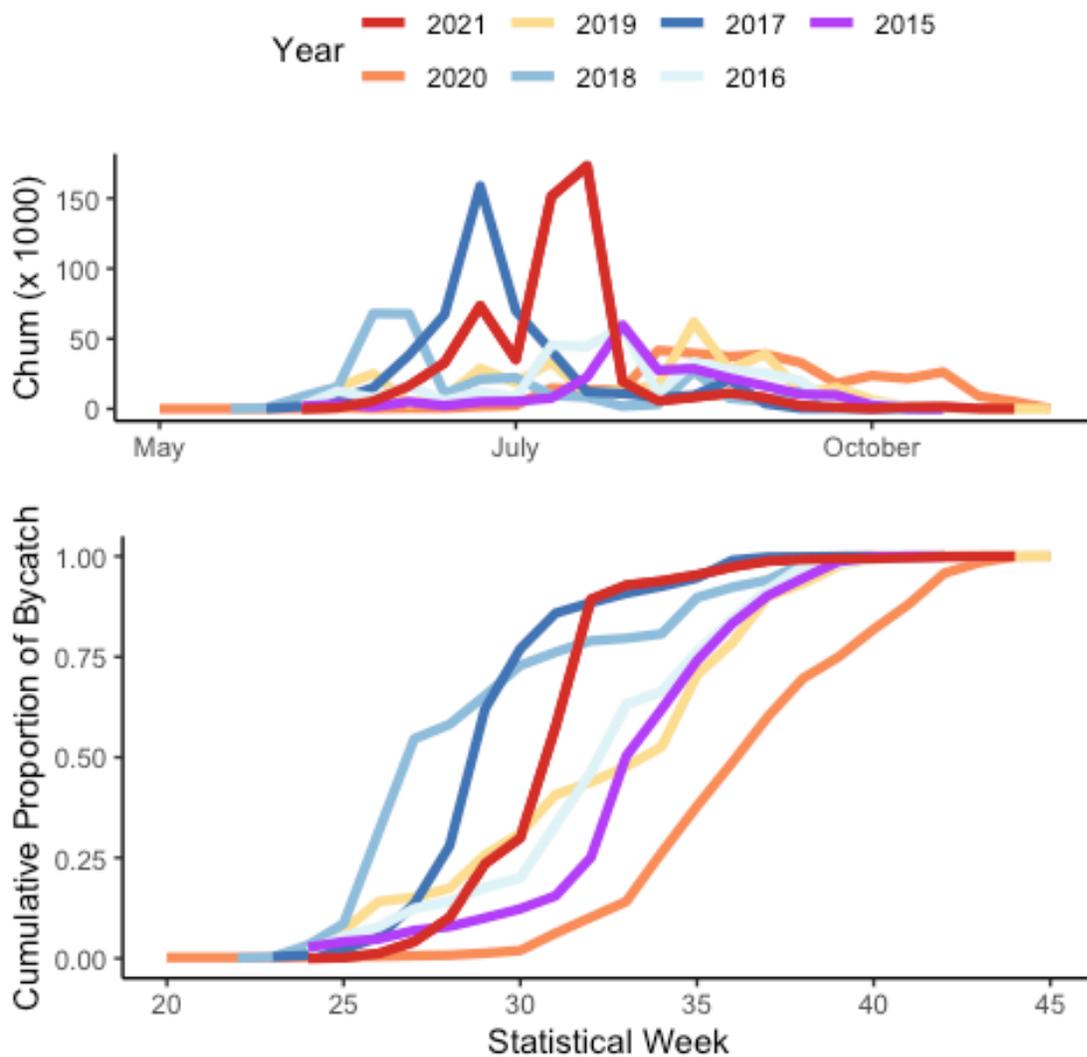


Figure 2: Number of chum salmon caught during the B-season (top) and cumulative proportion of chum salmon catch (bottom) from the Bering Sea pollock trawl fishery by statistical week for years 2016 to 2021.

Spatial Trends

The geographical distribution of the chum salmon bycatch was concentrated closer to the Alaska Peninsula in 2021 relative to prior years (Figure 3). Of the spatial clusters previously defined by the Alaska Fisheries Science Center (AFSC) Auke Bay Laboratory (ABL) Genetics Program the highest rates of PSC occurred in clusters 1 and 2; with the highest bycatch coming from Alaska Department of Fish and Game (ADF&G) statistical area 685530.

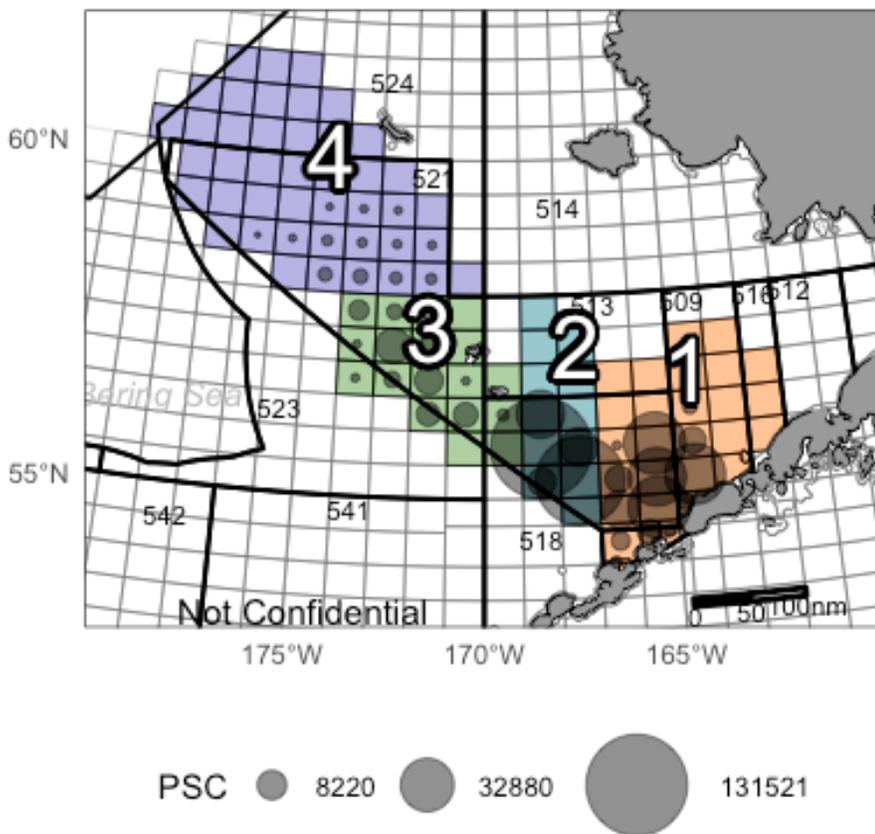


Figure 3: Spatial distribution of chum salmon bycatch caught in the 2021 Bering Sea B-season pollock fishery. ADF&G statistical areas are highlighted based on the four geographic strata assigned in prior genetic analyses.

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 the catcher-processor sector was the most eastern of the time series (Figure 4, CP). It also appears 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. The centroid for the mothership sector was similarly closer to the AK peninsula than typical (Figure 4, M) and was similar to years 2016 and 2017. The distribution of the shoreside sector centroids was much more concentrated than the CP and M sectors and may be influenced less by SST and sea ice extent than the more mobile sectors.

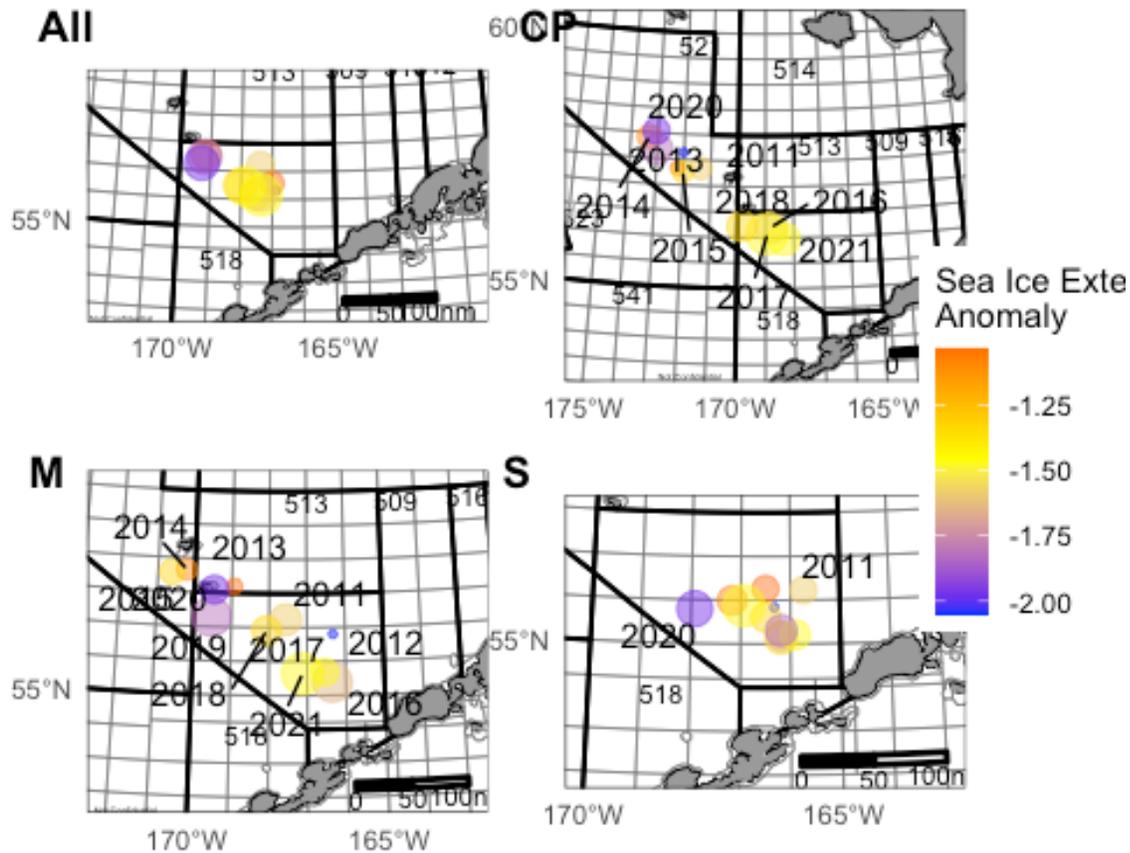


Figure 4: Change in the spatial distribution of chum salmon bycatch as measured by the centroid of the bycatch by sector; catcher-processor (CP), mothership (M) and shoreside (S). Point sizes reflect the relative size of the bycatch and point colors reflect the sea ice extent anomaly.

Bycatch Genotyping Summary

Data from the AFSC Fisheries Monitoring and Analysis North Pacific 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 16,371 genetic samples from the Bering Sea and Aleutian Islands (BSAI) and 244 samples from the Gulf of Alaska (GOA) that were collected by the Observer Program in 2021. Due to the small number of samples and the accelerated time frame of this reporting cycle, the GOA chum salmon samples were not analyzed. Previous reporting indicated that nearly all chum bycatch samples from the GOA are from the EGOA/PNW reporting group. After inventorying the genetic samples, a 1-in-5 sub-sample was conducted for genotyping. DNA from 4,069 genetic samples, 25.0% of the total genetic samples collected by the Observer Program, was extracted and amplified for the 84-SNP locus GTseq panel (See Appendix II Table A1). The subsample exceeded the target of 20% (1-in-5 sub-sample) to obtain adequate 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 4,069 samples amplified, 3,534 were of adequate quality to include (86.3%).

We re-amplified and genotyped 3% of samples for quality control (QC). The scores of these QC samples were compared with the scores from the originally genotyped samples to estimate the genotyping error rates. This ensures that the GTseq assay is consistent and that samples were organized correctly, providing confidence that the mixtures we analyze contain the correct genetic samples. The average agreement over loci was 99.2%, and the average agreement among individuals was also high (98%), indicating high genotyping accuracy and correct sample organization. This ensured that the GTseq assay was consistent and provided confidence that the mixtures we analyzed contained the correct genetic samples.

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

Western Alaska comprised 8.9% of the bycatch which is slightly greater than the contribution in 2020, but remains less than its long-term average of 15.7% (Figure 5, Table 1). Similarly, SW Alaska and the Upper/Middle Yukon comprised relatively minor portions of the bycatch, 2.4% and 0.5% respectively. Consistent with prior years, Asia stocks comprised a substantial fraction (67.5%) of the chum salmon bycatch in 2021. Of the bycatch in the B-season, the contribution from the NE Asia reporting group (55.7%) was the highest since systematic sampling of the bycatch was undertaken in 2011 (Figure 5). The EGOA/PNW reporting group accounted for (20.6%) of the bycatch, which is substantially less than the composition in 2020 (43%) and slightly less than the long-term average of 27.5% (Figure 5).

Table 1: Regional stock composition estimates of chum salmon from the 2021 Bering Sea, B-season pollock fishery (PSC = 545,883; n = 3534). 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	64,692	0.119	0.006	0.107	0.118	0.130	0.00
NE Asia	303,892	0.557	0.009	0.539	0.557	0.574	0.00
W Alaska	48,656	0.089	0.005	0.079	0.089	0.100	0.00
Up/Mid Yukon	2,854	0.005	0.002	0.002	0.005	0.009	0.00
SW Alaska	13,175	0.024	0.004	0.017	0.024	0.032	0.00
EGOA/PNW	112,611	0.206	0.007	0.192	0.206	0.221	0.00

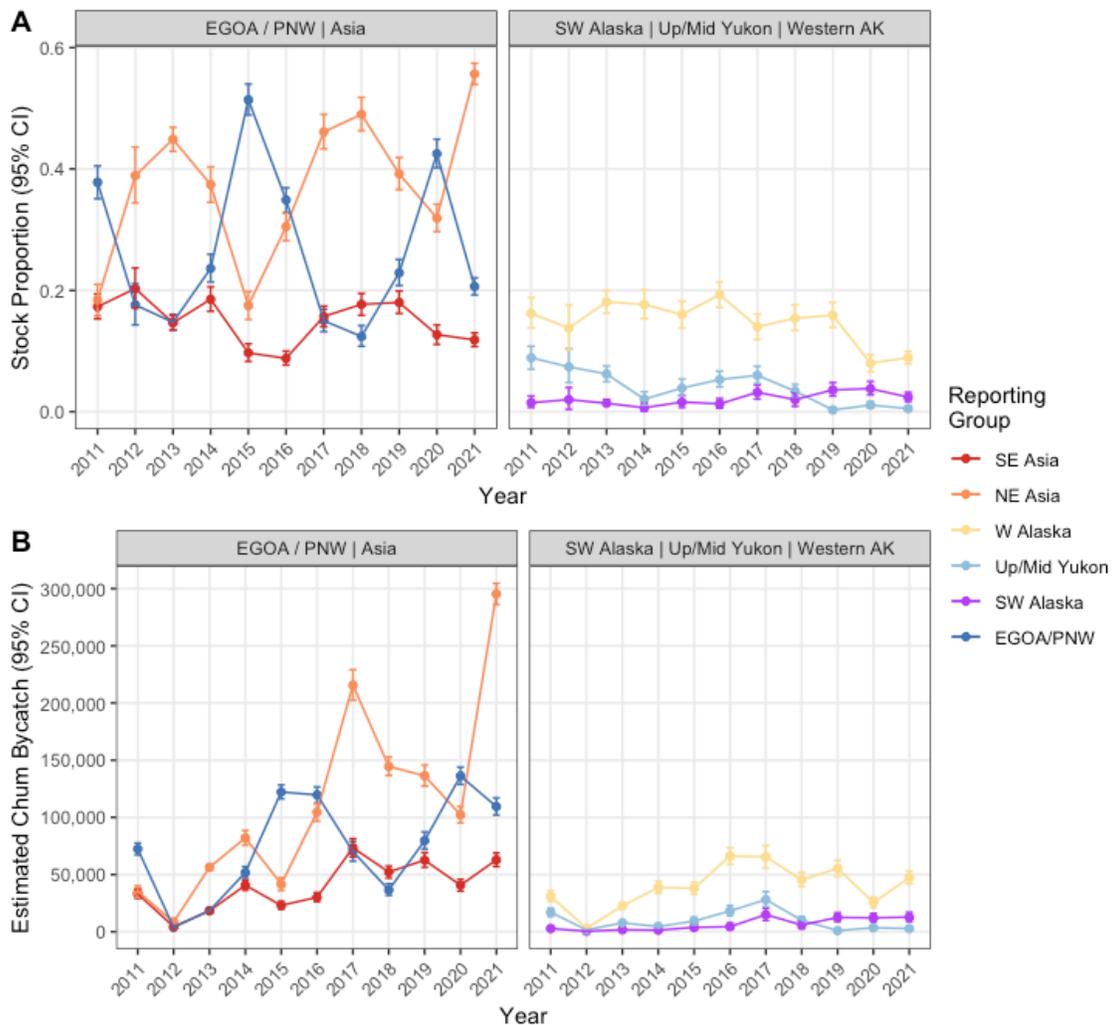


Figure 5: Annual bycatch estimates of B-season chum salmon PSC from 2011 to 2021. (A) stock proportions with 95% credible intervals, (B) Estimated number of chum salmon with 95% credible intervals.

There is a clear cyclical pattern of contribution between the NE Asia and EGOA/PNW reporting groups (Figure 5) with a strong negative correlation (Figure 6; $r^2 = 0.86$). Additionally, the two stocks comprise an increasing proportion of the bycatch through time, starting at a low of 56.2 % in 2011 to a high of 76.3 % in 2021. The recent, large declines in escapement of Western Alaska chum salmon (Technical Committee of the Yukon River U. S./Canada Panel 2022) may have led to a relative increase in the proportion of these two reporting groups; however, there is also evidence that suggests that the NE Asia run sizes are increasing (Ruggerone and Irvine 2018).

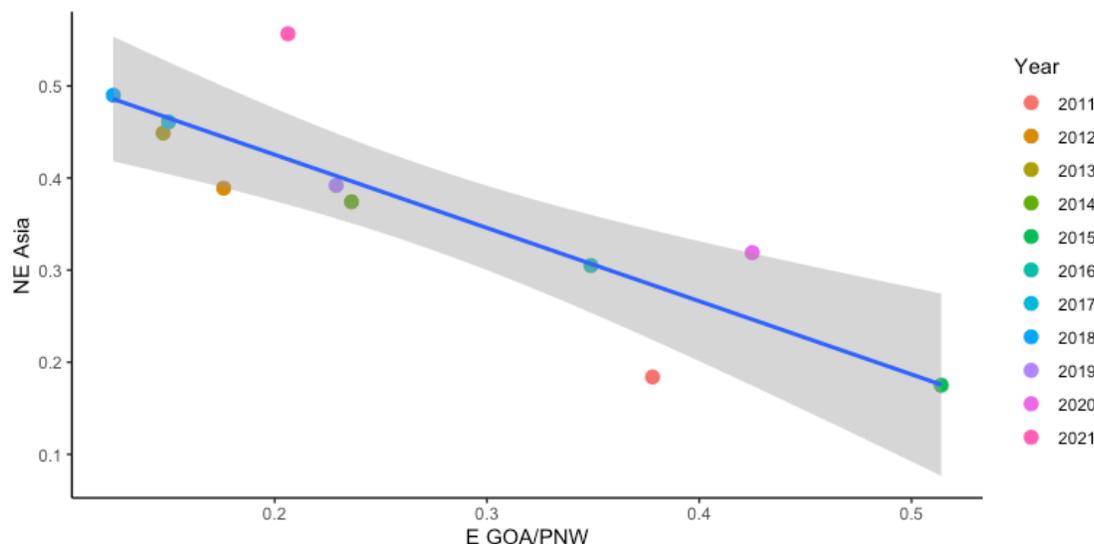


Figure 6: Correlation between NE Asia and EGOA/PNW reporting group mixture proportions for 2011 to 2021 ($r^2 = 0.86$).

Temporal Trends

The B season was divided into Early (pre week 30), Middle (weeks 30-34) and Late (post week 34) time periods to evaluate whether regional group contributions changed through the season.

The catch composition changed among the time periods for some reporting groups (Figure 7). The EGOA/PNW reporting group increased from 21.0% and 19.4% in the Early and Middle time periods respectively, to 29.6% in the Late time period. Since 2011 the average contribution of the GOA/PNW reporting group has increased from 16.1% in the Early period to 24.7% and 34.8% in the Middle and Late periods respectively. The contribution of the NE Asia reporting group peaked in the Middle time period, increasing from 50.1% in the early period to 58.4% in the Middle time period, and declined to a low of 43.7% in the Late time period. The Western Alaska reporting group had no significant temporal pattern; however, historically Western Alaska has contributed more to early catches. Since 2011 the average contribution of the Western Alaska reporting group has decreased from 19.2% to 17.8% and 12.6% in the Early, Middle and Late periods respectively. The Upper/Middle Yukon increased from 1.5% to 3.2% between the Early and Late periods, however the large credible intervals around those estimates suggests that the shift is marginal. This was in

contrast to the long-term historic pattern where the Upper/Middle Yukon reporting group have contributed, on average, more to early catches. Between 2011 and 2020, the average contribution of the Upper/Middle Yukon reporting group has decreased from 6.0% to 3.0% and 3.7% in the Early, Middle, and Late periods respectively. Contributions from the SW Alaska reporting group generally decrease over the season, and this was consistent in 2021 (Figure 7). The SW Alaska reporting group contributed 5.1% to the Early period in 2021 (2.2% long-term average) decreasing to 0.5% (2.2% long-term average) for the Late period.

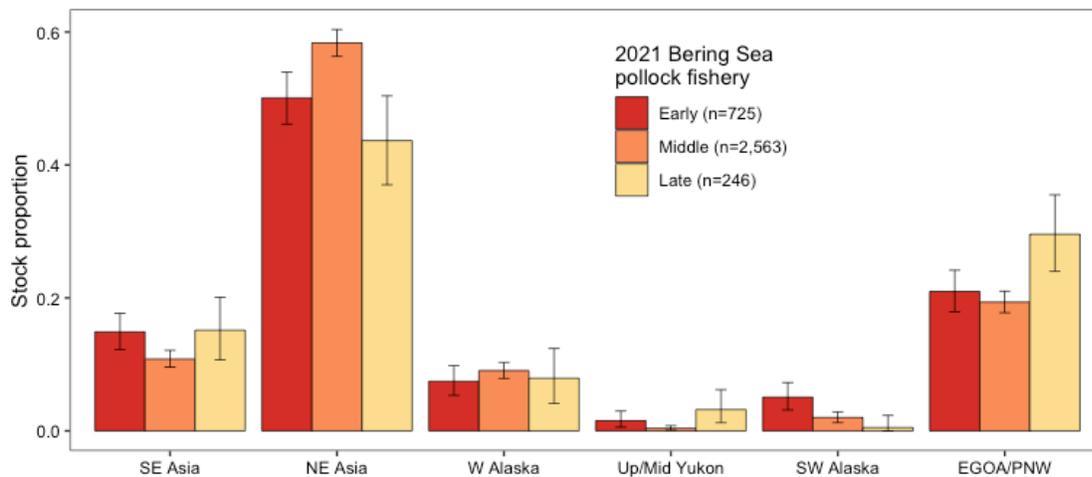


Figure 7: Stock composition estimates for the chum salmon bycatch from the Early, Middle, and Late periods of the 2021 Bering Sea, B-season pollock fishery.

Spatial Trends

Analyses where the bycatch has been divided into mixtures based on longitude, with 170°W as the dividing line, have historically shown that the relative contributions of the Western Alaska, Upper/Mid Yukon, Southwestern Alaska, and EGOA/PNW reporting groups generally increase further southeast closer to the Alaskan Peninsula. In 2021, this was true for the point estimates of the Western Alaska, Southwestern Alaska, and EGOA/PNW reporting groups, although the 95% credible intervals overlapped substantially (Figure 8). Uncharacteristically, the contribution of Upper/Middle Yukon reporting group was higher from bycatch west of 170°W (2.6%) than east of 170°W (0.3%); which was observed in 2013 (9.2% west and 4.8% east of 170°W).

The relative contribution of the Asia reporting groups, alternatively, are generally larger for mixtures west of 170°W. This was true for the SE Asia reporting group; comprising 20% of the bycatch west of 170°W and 11.1% of the bycatch east of 170°W. The NE Asia reporting group contributed slightly more to catches east of 170°W (Figure 8); although the credible intervals around the west of 170°W mean estimate were quite large.

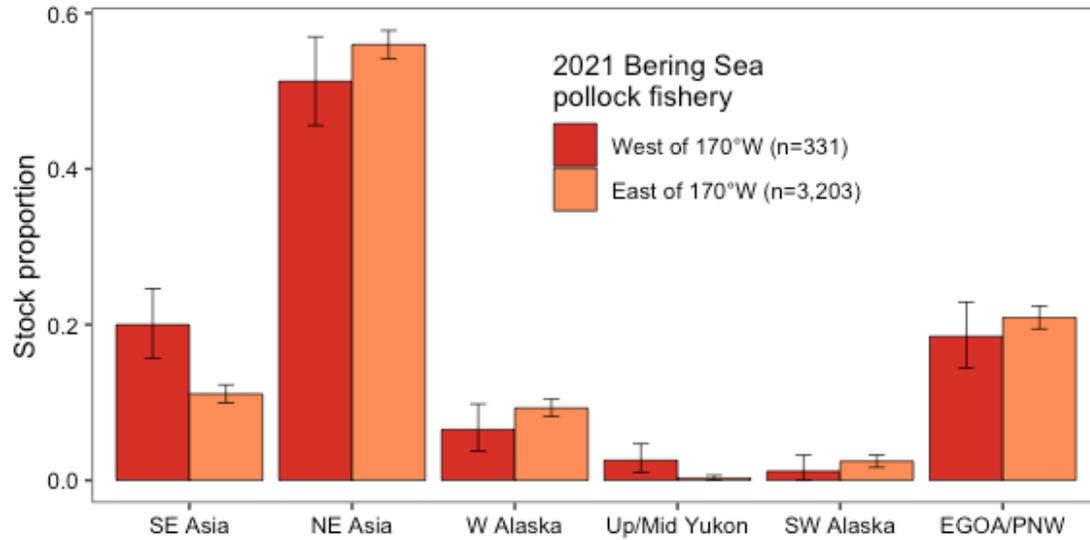


Figure 8: Stock composition estimates for the chum salmon bycatch from the 2021 Bering Sea, B-season pollock fishery from the U.S. waters of the Bering Sea west of 170° W and the southeastern Bering Sea east of 170° W.

Spatiotemporal Trends

The ABL genetics program has previously separated the Bering Sea into finer-scale spatial strata (4 clusters of ADF&G statistical areas), and incorporated temporal stratification (Early and Late) to evaluate the spatio-temporal stock specific contributions. Because the bycatch distribution was more geographically contracted in 2021, sufficient samples to facilitate analysis were not available from cluster 4 (Figure 9). Additionally, an insufficient number of samples were available to perform an analysis on the late time period for cluster 2.

Stock composition estimates were mostly consistent with historic trends. The Asian component primarily decreases from west to east and from early to late (Figure 9, left panels). The Western Alaska contribution was similar across spatial clusters in the Early period, but displayed a higher proportion in cluster 1 than 3 in the Late time period. The EGOA/PNW stock group shows an increase from Early to Late and west to east with the largest contribution in cluster 1, which is close to the Alaska Peninsula (Figure 9, right panel).

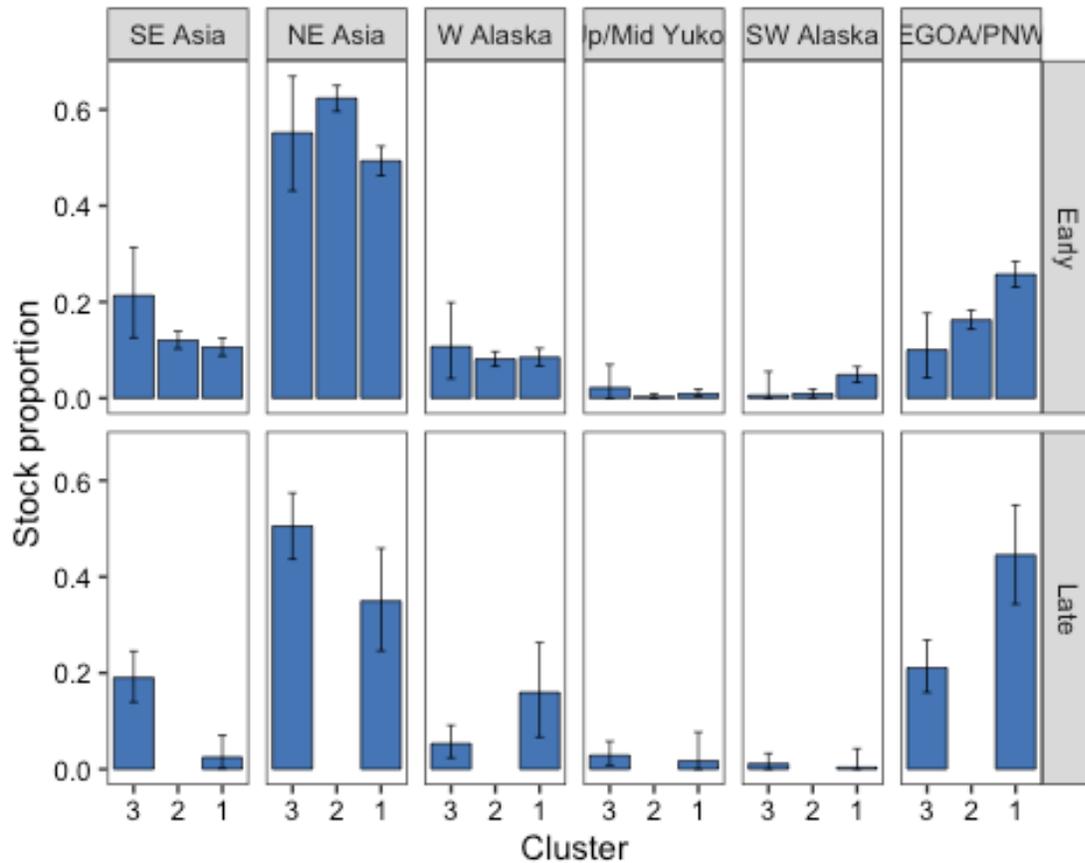


Figure 9: Stock composition estimates for the chum salmon collected from four spatial clusters along the continental shelf edge during Early (Weeks 24-32) and Late (Weeks 33-43) time periods of the 2021 Bering Sea, B-season pollock fishery. Clusters are ordered from west (cluster 3) to east (cluster 1). See map in Figure 3.

Age Trends

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 3,459 chum salmon were aged. Of those, 3,028 had genotypic information and were included in GSI analyses.

Historically, Age-3 mixtures are typically dominated by GOA/PNW stocks while the Age-4 and Age-5 mixtures are overwhelmingly made up of NE Asian stocks. This may be due to the fact that stocks in the southern range typically mature at an earlier age than northern stocks.

In 2021, W Alaska comprised an average of 9.4% of age-3 and age-4 fish, but only 3.6% of age-5 fish. The Up/Mid Yukon stocks had relatively similar representation across age classes (0.8%). The most common age for fish from Southwest Alaska was age-4, with much less representation in other age classes. SE Asia contributed an equal proportion to age-3 and age-5 mixtures (19.7%). The GOA/PNW stocks comprised 41.1% of Age-3 fish

compared to 11.2% of Age-4 fish and 15.1% of Age-5 fish. NE Asia comprised 29.2% of Age-3 fish and increased to 67.4% and 59.2% of Age-4 and Age-5 fish respectively (Figure 10).

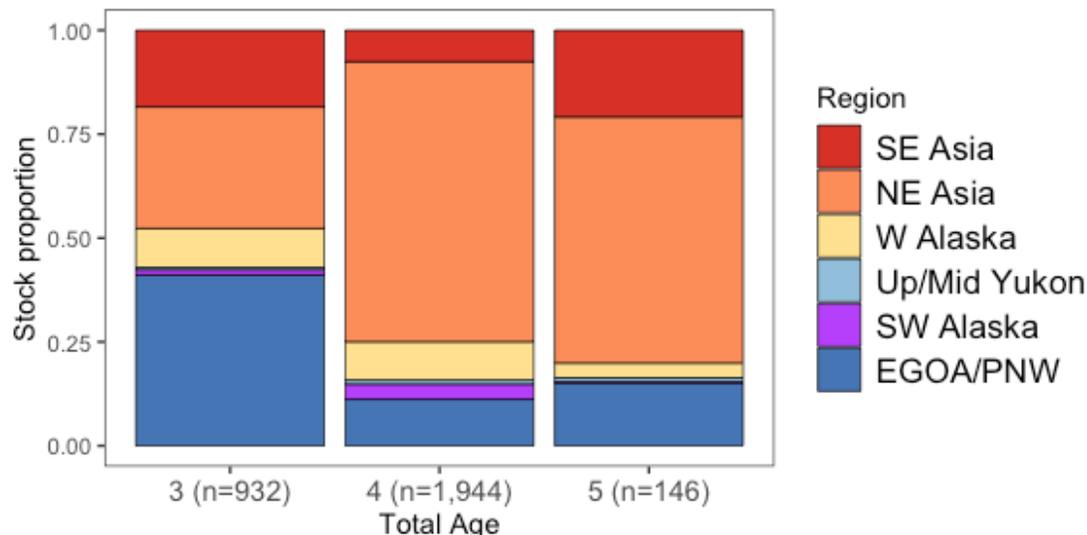


Figure 10: Stock composition estimates for the three predominate ages of chum salmon bycatch from the 2021 Bering Sea, B-season pollock fishery.

Sector Trends

Reporting group contributions to the 2021 chum salmon bycatch from each fishing sector were generally consistent with historic patterns. The three Alaska reporting group stock contributions were low, and within each reporting group, similar by fishing sector. The NE Asia stocks comprised the majority of the chum salmon bycatch (>50%) from all three fishing sectors (Figure 11). The three fishing sectors had similar (<14%) stock contributions from the SE Asia reporting group. The catcher-processor sector had a lower contribution of EGOA/PNW stocks than the shoreside and mothership sectors.

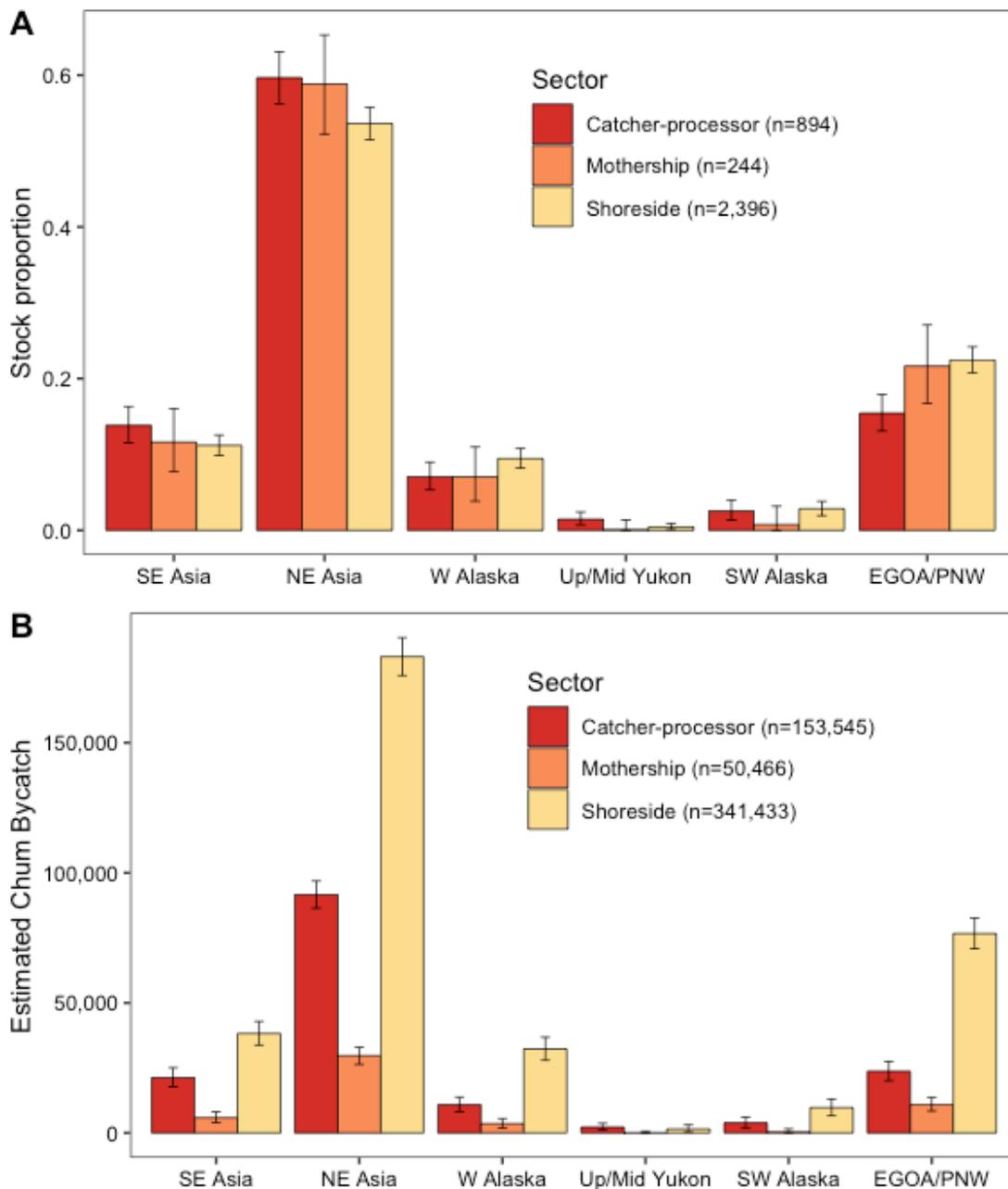


Figure 11: Stock composition estimates for the chum salmon bycatch from the 2021 Bering Sea, B-season pollock fishery from the catcher-processor, shoreside, and mothership fishing sectors. Sample sizes for mixture analysis given in legend. Proportions in top panel; numbers of fish in bottom panel.

Excluder Device Experimental Trawls

In July of 2021, three experimental trips were conducted with a trawl equipped with an excluder device. A total of seven tows were made with a total of 499 chum salmon genetic samples collected. We conducted mixed stock analysis from the samples from each trip, combining all tows within trip, as well as on individual tows provided we had greater than

70 genetic samples for a given tow. These analyses provide insight on whether individual hauls are typically comprised of a single stock group, or are mixtures or reporting groups and more reflective of the stock composition in a given area and time. Of the 499 genetic samples collected, 445 were successfully genotyped (89.2%). We were able to analyze each of the three trips (Cruise 1, Cruise 3, and Cruise 4), and had sufficient sample sizes to individually analyze a single tow in Cruise 1, three tows in Cruise 3, and three tows in Cruise 4. While the sample size from each of the three tows in Cruise 3 were too small to analyze individually, the three tows in Cruise 4 were analyzed individually. The stock composition estimates from these Cruises and individual tows were compared with the most similar spatial and temporal strata available from analysis of observer collected samples. Cruise 1 and Cruise 3 were compared with Cluster 1 Early, while Cruise 4 and all associated tows were compared with Cluster 2 Early.

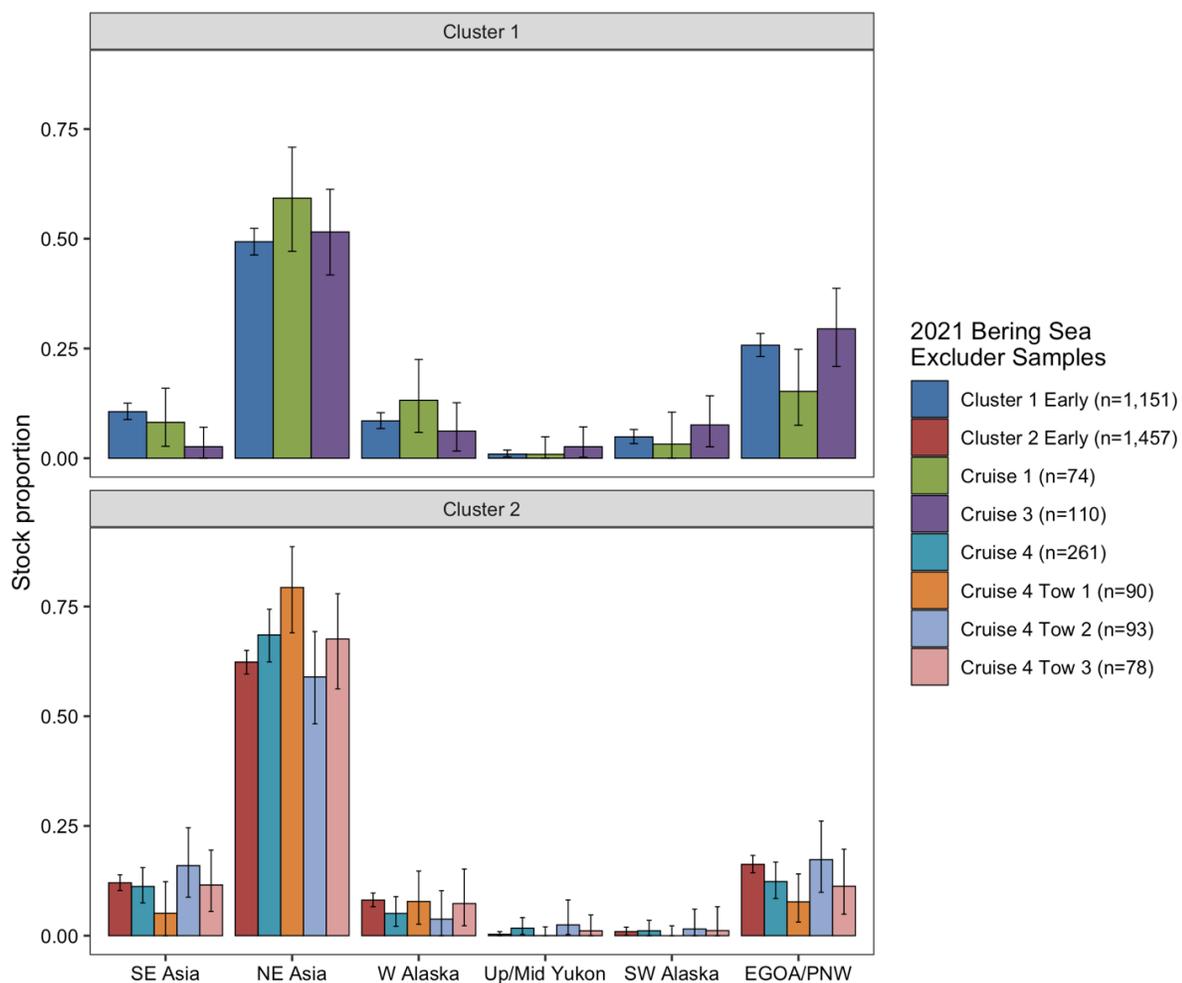


Figure 12: Stock composition estimates for salmon excluder experimental cruises from 2021 Bering Sea. Sample sizes for mixture analysis given in legend. Individual tows and cruises, aggregated over tows, were analyzed. Stock composition estimates were compared with results from the most similar spatial and temporal strata analyzed (Cluster 1 and Cluster 2, See map in Figure 3).

Estimates from experimental cruises and individual tows were generally reflective of the overall mixtures from larger aggregations of fishery hauls over spatial and temporal areas. Cruise 1 and Cruise 3 occurred near the Alaska Peninsula in Cluster 1 five days apart. Mean estimates were similar for all reporting groups with nearly all 95% credible intervals overlapping (Figure 12, Top Panel). Cruise 4 occurred further west than Cruises 1 and 3, within Cluster 2 (*See map in Figure 3*). While there was some variation in the mean estimate for each reporting group across tows, nearly all 95% credible intervals overlapped. From this dataset of four individual tows and three cruises, it appears that tows are typically well mixed and are not comprised of a single reporting group. That is, individual tows generally reflected larger stock composition patterns and were comparable to the most closely associated spatiotemporal strata from observer collected samples. This means that stock-specific bycatch avoidance measures likely would not benefit from trying to optimize stock-specific catch rates at the individual tow level.

Summary for Western Alaska, Upper/Middle Yukon, and SW Alaska stocks

The chum salmon bycatch was the second highest since 1991, occurred in two pulses during statistical weeks 29 and 32 and occurred predominately in the eastern portion of the pollock fishing grounds. Despite the proximity to the Alaska Peninsula, the relative contribution of the Western Alaska, Upper/Middle Yukon, and Southwestern Alaska reporting groups was relatively low, with a combined contribution of 11.9%, which when multiplied by the total bycatch expands to 64,685 fish. Thus, while the amount of chum salmon bycatch in 2021 was high, the number of fish caught as bycatch from Western Alaska, Upper/Middle Yukon, and Southwestern Alaska stocks was average or below average.

Acknowledgements

We are grateful for the help from the AFSC's Fisheries Monitoring and Analysis Division, and the many participating observers who provided genetic samples. Thanks to Rob Ames, Camille Kohler, and Bob Ryznar for developing AKFIN Answer reports that helped us develop new strata for genetic analyses and tabulate strata specific PSC numbers. We also appreciate the work of Bev Agler, Jodi Neil and the rest of the MTA Lab staff for conducting age analysis accurately and efficiently, and Dave Nicolls at ABL for mounting and pressing the scales. We are grateful to Katie Howard, Dani Evenson, and Tyler Dann of ADF&G for their thoughtful reviews of this report.

References

Beacham, T. D., J. R. Candy, K. D. Le, and M. Wetklo. 2009. "Population Structure of Chum Salmon (*Oncorhynchus Keta*) Across the Pacific Rim, Determined from Microsatellite Analysis." *Fishery Bulletin* 107 (2): 244–60.

<https://www.scopus.com/inward/record.uri?eid=2-s2.0-66449109194&partnerID=40&md5=d8c61db8fb8c005dd23c77e9ec439f4c>.

Campbell, S. A., N. R. AND Harmon. 2015. "Genotyping-in-Thousands by Sequencing (GT-Seq): A Cost Effective SNP Genotyping Method Based on Custom Amplicon Sequencing." *Molecular Ecology Resources*, 15 (4): 855–867.

DeCovich, N., T. H. Dann, S. D. Rogers Olive, H. L. Liller, E. K. C. Fox, J. R. Jasper, E. L. Chenoweth, C. Habicht, and W. D. Templin. 2012. "Chum Salmon Baseline for the Western Alaska Salmon Stock Identification Program." Special Publication 12-26. Alaska Department of Fish; Game.

Gelman, AND Rubin, A. 1992. "Inference from Iterative Simulation Using Multiple Sequences." *Statistical Science* 7: 457–511.

Gray, A. AND C. Marvin AND C. Kondzela AND T. McCraney AND J. R. Guyon. 2010. "Genetic Stock Composition Analysis of Chum Salmon Bycatch Samples from the 2009 Bering Sea Trawl Fisheries." Report to the North Pacific Fishery Management Council. 605 W. 4th Ave., Anchorage, Alaska, 99510: NOAA.

Moran, B. M., and E. C. Anderson. 2019. "Bayesian Inference from the Conditional Genetic Stock Identification Model." *Canadian Journal of Fisheries and Aquatic Sciences* 76 (4): 551–60. <https://doi.org/10.1139/cjfas-2018-0016>.

Plummer, N. AND Cowles, M. AND Best. 2006. "CODA: Convergence Diagnosis and Output Analysis for MCMC." *R News* 6: 7–11.

Ruggerone, Gregory T., and James R. Irvine. 2018. "Numbers and Biomass of Natural- and Hatchery-Origin Pink Salmon, Chum Salmon, and Sockeye Salmon in the North Pacific Ocean, 1925–2015." *Marine and Coastal Fisheries* 10 (2): 152–68. <https://doi.org/https://doi.org/10.1002/mcf2.10023>.

Technical Committee of the Yukon River U. S./Canada Panel), JTC (Joint. 2022. "Yukon River Salmon 2021 Season Summary and 2022 Season Outlook." Regional Information Report No. 3A22-01. Anchorage, Alaska: Alaska Department of Fish; Game, Division of Commercial Fisheries.

Appendix I - GSI Estimates

Regional stock composition estimates of chum salmon samples from the 2021 Bering Sea, B-season pollock trawl fishery. Note that total PSC was tabulated from the AKFIN database with observer records and exceeds the AKRO mortality estimate slightly.

East of 170° (PSC = 502,053; n = 3203)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	55,715	0.111	0.006	0.100	0.111	0.123	0.00	1.00
NE Asia	280,909	0.560	0.009	0.541	0.560	0.578	0.00	1.00
W Alaska	46,590	0.093	0.006	0.082	0.093	0.104	0.00	1.00
Up/Mid Yukon	1,548	0.003	0.002	0.001	0.003	0.007	0.01	1.00
SW Alaska	12,283	0.024	0.004	0.017	0.024	0.033	0.00	1.00
E GOA/PNW	105,006	0.209	0.008	0.195	0.209	0.224	0.00	1.00

West of 170° (PSC = 45,508; n = 331)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	9,100	0.200	0.023	0.157	0.199	0.246	0.00	1.00
NE Asia	23,319	0.512	0.029	0.456	0.512	0.570	0.00	1.00
W Alaska	2,970	0.065	0.016	0.038	0.064	0.098	0.00	1.00
Up/Mid Yukon	1,172	0.026	0.009	0.010	0.025	0.047	0.00	1.00
SW Alaska	533	0.012	0.009	0.000	0.010	0.032	0.05	1.00
E GOA/PNW	8,411	0.185	0.022	0.144	0.184	0.229	0.00	1.00

Early (PSC = 128,904; n = 725)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	19,192	0.149	0.014	0.123	0.149	0.177	0.00	1.00
NE Asia	64,560	0.501	0.020	0.462	0.501	0.540	0.00	1.00
W Alaska	9,620	0.075	0.011	0.053	0.074	0.098	0.00	1.00
Up/Mid Yukon	1,971	0.015	0.006	0.005	0.014	0.030	0.00	1.00
SW Alaska	6,537	0.051	0.011	0.032	0.050	0.073	0.00	1.00
E GOA/PNW	27,021	0.210	0.016	0.179	0.209	0.242	0.00	1.00

Middle (PSC = 384,865; n = 2563)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	41,605	0.108	0.007	0.096	0.108	0.121	0.00	1.00
NE Asia	224,571	0.584	0.010	0.563	0.584	0.604	0.00	1.00
W Alaska	34,917	0.091	0.006	0.079	0.091	0.103	0.00	1.00
Up/Mid Yukon	1,496	0.004	0.002	0.001	0.004	0.008	0.00	1.00
SW Alaska	7,722	0.020	0.004	0.012	0.020	0.029	0.00	1.01
E GOA/PNW	74,552	0.194	0.008	0.178	0.194	0.210	0.00	1.00

Late (PSC = 33,792; n = 246)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	5,117	0.151	0.024	0.107	0.151	0.201	0.00	1.00
NE Asia	14,753	0.437	0.034	0.370	0.436	0.504	0.00	1.00
W Alaska	2,676	0.079	0.021	0.041	0.078	0.124	0.00	1.00
Up/Mid Yukon	1,083	0.032	0.013	0.012	0.030	0.062	0.00	1.00
SW Alaska	166	0.005	0.007	0.000	0.003	0.023	0.28	1.00
E GOA/PNW	9,995	0.296	0.030	0.240	0.295	0.355	0.00	1.00

Catcher-processor (PSC = 153,545; n = 894)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	21,250	0.138	0.012	0.115	0.138	0.163	0.00	1.00
NE Asia	91,618	0.597	0.017	0.563	0.597	0.631	0.00	1.00
W Alaska	10,836	0.071	0.009	0.053	0.070	0.090	0.00	1.00
Up/Mid Yukon	2,238	0.015	0.004	0.007	0.014	0.024	0.00	1.00
SW Alaska	3,894	0.025	0.007	0.013	0.025	0.040	0.00	1.00
E GOA/PNW	23,705	0.154	0.012	0.131	0.154	0.179	0.00	1.00

Mothership (PSC = 50,466; n = 244)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	5,860	0.116	0.021	0.078	0.115	0.160	0.00	1.00
NE Asia	29,694	0.588	0.033	0.522	0.589	0.653	0.00	1.00
W Alaska	3,555	0.070	0.018	0.038	0.069	0.110	0.00	1.00
Up/Mid Yukon	48	0.001	0.004	0.000	0.000	0.014	0.68	1.00
SW Alaska	378	0.008	0.009	0.000	0.006	0.032	0.26	1.00
E GOA/PNW	10,928	0.217	0.026	0.167	0.216	0.271	0.00	1.00

Shoreside (PSC = 341,433; n = 2396)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	38,246	0.112	0.007	0.099	0.112	0.126	0.00	1.00
NE Asia	183,120	0.536	0.011	0.515	0.536	0.558	0.00	1.00
W Alaska	32,256	0.094	0.007	0.082	0.094	0.108	0.00	1.00
Up/Mid Yukon	1,478	0.004	0.002	0.001	0.004	0.009	0.01	1.00
SW Alaska	9,699	0.028	0.005	0.019	0.028	0.038	0.00	1.00
E GOA/PNW	76,631	0.224	0.009	0.207	0.224	0.242	0.00	1.00

Age-3 (PSC = 171,597; n = 932)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	31,676	0.185	0.013	0.159	0.184	0.211	0.00	1.00
NE Asia	50,162	0.292	0.016	0.262	0.292	0.324	0.00	1.00
W Alaska	16,197	0.094	0.010	0.075	0.094	0.115	0.00	1.00
Up/Mid Yukon	875	0.005	0.003	0.001	0.005	0.012	0.00	1.00
SW Alaska	2,113	0.012	0.005	0.004	0.012	0.023	0.00	1.00
E GOA/PNW	70,571	0.411	0.016	0.379	0.411	0.443	0.00	1.00

Age-4 (PSC = 348,894; n = 1944)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	26,362	0.076	0.006	0.064	0.075	0.088	0.00	1.00
NE Asia	235,174	0.674	0.011	0.651	0.674	0.696	0.00	1.00
W Alaska	32,376	0.093	0.007	0.079	0.093	0.108	0.00	1.00
Up/Mid Yukon	3,251	0.009	0.003	0.005	0.009	0.016	0.00	1.00
SW Alaska	12,693	0.036	0.006	0.026	0.036	0.048	0.00	1.00
E GOA/PNW	39,035	0.112	0.008	0.097	0.112	0.127	0.00	1.00

Age-5 (PSC = 26,119; n = 146)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	5,446	0.209	0.035	0.144	0.207	0.280	0.00	1.00
NE Asia	15,466	0.592	0.043	0.507	0.593	0.674	0.00	1.00
W Alaska	941	0.036	0.019	0.006	0.034	0.080	0.00	1.00
Up/Mid Yukon	232	0.009	0.010	0.000	0.005	0.036	0.00	1.00
SW Alaska	96	0.004	0.008	0.000	0.000	0.029	0.49	1.00
E GOA/PNW	3,936	0.151	0.030	0.097	0.149	0.213	0.00	1.00

Cluster 1 Early (PSC = 189,688; n = 1151)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	20,120	0.106	0.010	0.088	0.106	0.125	0.00	1.00
NE Asia	93,568	0.493	0.016	0.463	0.493	0.524	0.00	1.00
W Alaska	16,129	0.085	0.009	0.068	0.085	0.104	0.00	1.00
Up/Mid Yukon	1,789	0.009	0.004	0.003	0.009	0.019	0.00	1.00
SW Alaska	9,226	0.049	0.008	0.033	0.048	0.065	0.00	1.00
E GOA/PNW	48,853	0.258	0.013	0.232	0.257	0.284	0.00	1.00

Cluster 1 Late (PSC = 12,145; n = 92)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	302	0.025	0.019	0.001	0.021	0.071	0.01	1.00
NE Asia	4,244	0.349	0.054	0.246	0.348	0.459	0.00	1.00
W Alaska	1,939	0.160	0.050	0.067	0.158	0.263	0.00	1.00
Up/Mid Yukon	205	0.017	0.022	0.000	0.007	0.077	0.00	1.00
SW Alaska	42	0.004	0.012	0.000	0.000	0.043	0.59	1.00
E GOA/PNW	5,409	0.445	0.053	0.343	0.445	0.549	0.00	1.00

Cluster 2 Early (PSC = 226,750; n = 1457)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	27,308	0.120	0.009	0.103	0.120	0.139	0.00	1.00
NE Asia	141,358	0.623	0.014	0.596	0.623	0.650	0.00	1.00
W Alaska	18,391	0.081	0.008	0.066	0.081	0.097	0.00	1.00
Up/Mid Yukon	710	0.003	0.002	0.000	0.003	0.009	0.01	1.00
SW Alaska	2,108	0.009	0.005	0.001	0.009	0.019	0.01	1.00
E GOA/PNW	36,871	0.163	0.010	0.143	0.162	0.183	0.00	1.00

Cluster 3 Early (PSC = 11,158; n = 77)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	2,380	0.213	0.048	0.126	0.211	0.314	0.00	1.00
NE Asia	6,154	0.552	0.061	0.431	0.552	0.669	0.00	1.00
W Alaska	1,195	0.107	0.041	0.041	0.103	0.199	0.00	1.00
Up/Mid Yukon	242	0.022	0.019	0.000	0.017	0.070	0.02	1.00
SW Alaska	65	0.006	0.016	0.000	0.000	0.055	0.54	1.00
E GOA/PNW	1,120	0.100	0.035	0.043	0.097	0.177	0.00	1.00

Cluster 3 Late (PSC = 30,400; n = 225)

Region	Est. num.	Mean	SD	2.5%	Median	97.5%	P=0	SF
SE Asia	5,785	0.190	0.027	0.140	0.189	0.246	0.00	1.00
NE Asia	15,362	0.505	0.035	0.436	0.505	0.574	0.00	1.00
W Alaska	1,617	0.053	0.017	0.024	0.052	0.091	0.00	1.00
Up/Mid Yukon	872	0.029	0.013	0.009	0.027	0.058	0.00	1.00
SW Alaska	349	0.012	0.009	0.000	0.010	0.033	0.05	1.00
E GOA/PNW	6,412	0.211	0.028	0.160	0.210	0.268	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 SequelPrep 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 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.

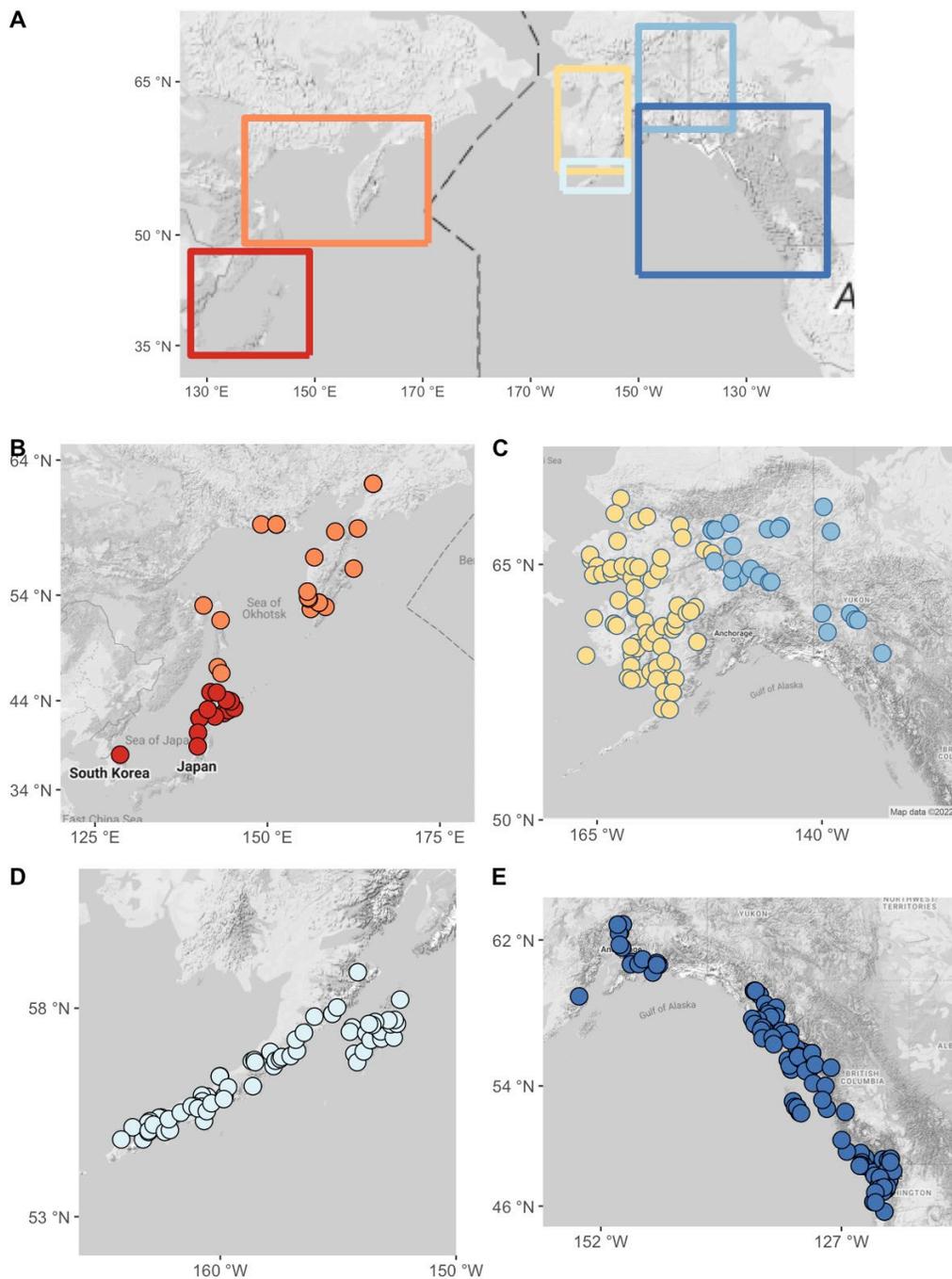


Figure A1: Six reporting groups of baseline chum salmon populations used in this report, circles represent individual populations represented in the baseline. (A) Range wide distribution of the six reporting groups. (B) SE Asia (red) and NE Asia (orange), (C) W Alaska (Yellow) and Up/Mid Yukon (Mid Blue), (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 2021 Bering Sea, B-season analyses.

Locus	Ploidy	SNPpos	Allele1	Allele2	Probe1	Probe2	Primer	Primer Conc. (uM)
Oke_ACOT-100	2	1	C	G	CTTCCGCTCTCTACTCC	TTCGCTCTGTACTCC	TCAGGGACGATAAAGGGATCATCTT	0.2000
Oke_ATP5L-105	2	1	C	G	AGTATATTGAGATGAATCCCAC	ATATTGAGATGAATGCCAC	GTGCACACCAATCCATTTCTGAAT	0.2500
Oke_AhR1-78	2	1	G	A	CAGCCTCGGTGCCAT	TCAGCCTCAGTGCCAT	AGCAGAACCCAGCACCTACAG	0.2000
Oke_CATB-60	2	1	C	T	CAGGAACGGGTATGAG	CAGGAACGAGTATGAG	GCTTCTATGGTCTCTACTACCGTAT	0.2500
Oke_CD81-108	2	1	G	T	TCCGGCATGTCCAG	TCCGGCATTCCCCAG	CAGTATCATCATAACAGCACAGATACAACA	0.2500
Oke_CD81-173	2	1	A	C	CAGTACAGAGAGTAC	AGTCACAGCGAGTAC	GATGACTGGAGTCAGCTTGCA	0.2000
Oke_CKS-389	2	1	G	A	AAATGAATGATAATGTGTCTG	AAATGAATGATAATATGTTCTG	GGGCCATTCTCTGAGTTCAGT	0.2500
Oke_CKS1-94	2	1	G	T	TCTGGATAAATTTGTGTATTC	TTCTGGATAAATTTTGTATTC	TCTTCGACATGTTTATCGAACAGAGAAGT	0.2500
Oke_DCXR-87	2	1	A	T	CCTGTTTGTGAAACCGTA	CCTGTTTGTGTAACCGTA	GTCAACCCAGAACAAATAGAATGAGTCT	0.2500
Oke_FANK1-166	2	1	C	T	CTACAGCCCAGCTGTG	CTACAGCCCAGCTGTG	ACTCACGTGTGGTAGAGACAGA	0.2500
Oke_FBXL5-61	2	1	G	A	TCTGAGGGAACCTGC	TCTGAGGGAACCTGC	TGGTGTGTAACGTGACTTAAG	0.3000
Oke_GHII-3129	2	1	G	A	CAGGGCGACTCTAT	ACAGGGCAACTCTAT	GTCAGCTGATACCACTCAAATCTCA	0.3000
Oke_GPDH-191	2	1	T	A	CGGAGCCACTTCCAGTA	CGGAGCCACTACCAGTA	CCTGTACTTATAGGGCAACTTCCAC	0.2000
Oke_GPH-105	2	1	T	G	CCAGTAATTGGTATTTTGA	CCAGTAATTGGTCTTTTGA	CAGATCAACCCTGGAAAAATATCTGATGT	0.2500
Oke_HP-182	2	1	A	C	AGAAAAGGTGAGCTAGTATG	AAAAGGTGAGCTCGTATG	CCGATGACTCCAAGAAAGTTGCT	0.2500
Oke_IL8r2-406	2	1	T	G	AAACACAAAACCCC	AAACACAAAACCCC	GGATGGACATTCACAGTCTGGTT	0.2000
Oke_KPN2-87	2	1	T	A	ACAGAACAGAAACAGTG	AACAGAACAGTAACAGTG	AGGCAGCCAGGTAAGTCAGTA	0.1875
Oke_LAMP2-186	2	1	A	G	CTAACTTTACAAAGACACTGC	AACTTTACAAAGGCCTGC	TTCAGCCATGACCAATGAAAGG	0.2500
Oke_MLRN-63	2	1	G	A	CTGGTGATTGACGATCC	CTGGTGATTGACGATCC	CCATTTGAGCATTGCCAGATTTGAAA	0.2500
Oke_Moesin-160	2	1	T	G	CATTTTGTAAATCTAATTTTAAAGC	ATTTTGTAAATCTAATGTTAAAGC	TTTCAGCAAATGAAGAGAATCAAACTG	0.2500
Oke_NUPR1-70	2	1	G	T	CTATGAGGACGGGTACAC	ACTATGAGGACTGGTCACA	AGACGGTGAACCTCTGCTGTAGA	0.3000
Oke_PPA2-635	2	1	C	T	TTGCCTCCCCGCTC	TTATTGCTCTCCCCGCTC	ACACAACCTGACCATATTGACTTTCGA	0.2500
Oke_RFC2-618	2	1	G	A	CAGCTCCTGGACTCA	CAGCTCCTGACTCA	GACAATGTGTTAGTGTAGGCTTCACT	0.2000
Oke_RH1op-245	2	1	C	T	AGTGGTGAAGCCTC	TAGTGGTAAAGCCTC	TGGCCGATCTCTTCATGGTAAATC	0.2500
Oke_RS27-81	2	1	G	A	TGTCCAGGCATCATGA	TGTCCAGGCATCATGA	GCAACAAAAGTGGACTATCACATTGAA	0.3000
Oke_RSPRY1-106	2	1	A	T	TAGTCTCTTTACATAATCTC	TAGTCTCTTTACTTAATCTC	GTCCTCCCTATCTTCCACTTACCT	0.2500
Oke_TCP1-78	2	1	A	G	ATACTGCTCAGAGACG	CTGCTCCAGGACG	CTCCAGGCATCAGCAAATG	0.2000
Oke_Tf-278	2	1	C	A	ATTTTACAGTTGACATTCAA	TTTTACAGTTGAAATTCAA	GCCACAATTTGTAATTTCTAGATCCAGAGT	0.2500
Oke_U1008-83	2	1	A	G	CGTCTCTCTTGGACAC	CGTCTCTCTTGGACAC	GTCACCAACATCCTGCGAATG	0.3000
Oke_U1010-251	2	1	A	G	ATAGAGGTGAGCATTGACAT	TAGAGGTGAGCACTGACAT	CACCTCAATCAATCAAATGTATTTATAAGCCCA	0.1875
Oke_U1012-241	2	1	C	G	ATGGAAAAGAAGCTGTTACT	ATGGAAAAGAAGCTTACT	GCAGAGGTATATCCATTTTAGATGCA	0.2500
Oke_U1015-255	2	1	A	G	CAAACACACAGAGGCC	AACACACGAGAGGCC	CAGAGTGCAGAGTAATACGCATACA	0.2500
Oke_U1016-154	2	1	C	T	CCATGTTTGGGTATGT	CCATGTTTGCAGTATGT	GCAGGTTGCTAAGTCAATGTTACACA	0.3000
Oke_U1017-52	2	1	C	T	AGAGAGTTGTGCTTTCATC	AGAGAGTTGTCTTTCATC	TGGCAATGGGATGTCAAGTTATGA	0.3000
Oke_U1018-50	2	1	C	T	CTGGGCACGTACAGCT	CTGGGCACGTACAGCT	TCCAGGTTGCTGACAATGTAAGT	0.3000
Oke_U1022-139	2	1	A	G	CTGGAACATGAGCAAAA	TGGAACATGAGCAAAA	AACATTAACAACTGTGGTTTTGACCTCTTG	0.2500
Oke_U1023-147	2	1	A	C	CATCAGGGAAAGCCTACAAA	AGGGAAAGCCGACAAA	TCTTAAAAATGGAGAGCGCATTAATGAAGG	0.2500
Oke_U1024-113	2	1	A	G	CCAGAAAACAACCTAATTAT	CAGAAAACAACCTAATTAT	CATGCTGGTGAATTTGGACAATGT	0.2500
Oke_U1025-135	2	1	G	T	ACTTAGTCTATTTGTAACCTT	ACTTAGTCTATTTTAACTTT	GGCTAGGTTCTATTTGGACCAT	0.2500
Oke_U2007-190	2	1	C	G	CTAAAAGCTGAGAATAAAT	AAAGCTGACAATAAAT	ACAGGCTGTGATGAGTTAAACAATGTA	0.2500
Oke_U2011-107	2	1	G	T	TTCTGTGAGATTTAG	TTCTGTGAGATTTAG	CCGTTTCTGTACAGACTCTGGTAAA	0.1250
Oke_U2015-151	2	1	C	T	AATTGATCAGCATCATT	ATTGATCACATCATT	GCATTTTATCCTCAAACCTTTCACTGACA	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	ACTTTTTTGTGCTGTTTTTTT	ACTTTTTTGTGCTTTTTTTT	AAATCCCCATGGAGAAAACACAATGA	0.2000
Oke_U2029-79	2	1	C	T	AGGTGTACTGAAGAGAC	AGGTGTACTAAAGAGAC	GGTTTTGATTTTCGTCCGATTTGA	0.2500
Oke_U2032-74	2	1	G	A	CAATAAAGTGCTAGGTGTCC	CAATAAAGTGCTAAGTGTCC	GCTATTCCAATGTAATCCCTGTACTGTGT	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	CCAGACCATGTGCTTGTFTGTATA	0.2500
Oke_U2043-51	2	1	G	A	TCTGGAGGCGTATTGG	CTGGAGGCATATTGG	CACAAACCTACTACAGACAGCAGTT	0.2000
Oke_U2048-91	2	1	A	C	CAGCCTCATAAGATGTTTA	CAGCCTCATAAGCTGTTTA	AGTTGGGTCTTAAAGATGATCATTGGCT	0.2000
Oke_U2050-101	2	1	C	T	AATTGATCTACAGCTGCACG	AATTGATCTACAACCTGCACG	CTCTGAGTGTCACAATCACATATCGT	0.2000
Oke_U2053-60	2	1	C	T	CACACATATGAGATGCC	CACACATAAAGATGCC	TCTGCTTTTGTGCTCTACCAA	0.1875
Oke_U2054-58	2	1	C	T	ATGCCCAATTACGTCAGCA	TGCCCAATTACATCAGCA	CGTCTCATTACGCTCTTTGATGTC	0.2000
Oke_U2056-90	2	1	G	T	CGAAGTGATGAAGGTGACAA	CGAAGTGATGAATGTGACAA	CCATCACGTCACCATTACACTGT	0.1875
Oke_U2057-80	2	1	A	G	CACGTTTTCTCTTTTCTC	ACGTTTTCTCTTTTCTC	GCAGTTGTCATGGCAGTAAGG	0.2500
Oke_U212-87	2	1	C	A	CTTGTGACATTCTCTCT	CTTGTGACATTACTCTCT	TTGATTCATACTCAAGGTGAGCAGATT	0.2500
Oke_U302-195	2	1	C	A	TTGTCAAAGGAATCAATT	TGTCAAAGGAATAAATT	GACCCCTCAGCTATTTAAGAACCTCAA	0.2500
Oke_U504-228	2	1	A	G	TGGCTCAAACCTTG	TTGGCTCGAACCTTG	CTTAACTCAGTCACACCAACTCACT	0.2500
Oke_U506-110	2	1	C	T	TTGTAAGTTGTGGCTAAAA	TTGTAAGTTGTGACTAAAA	CGTGGTTGGTTTCATTGACTCTCA	0.2000
Oke_U507-286	2	1	T	G	CTGCTGTTTCATAAAGTA	CTGCTGTTTCATACAAGTA	TGGTCATAGCTTGCCTGTACAAA	0.3000
Oke_U509-219	2	1	C	T	CCTCTCTGCAGGGCT	CCCTCTCTACAGGGCT	GCACCCACCTGGCTT	0.1250
Oke_arf319	2	1	T	C	CTGTGTGAATTGGCTC	CTGTGTGAACCTGCCTC	TGCAGAAACTGATCATTTGGTAGTGG	0.1875
Oke_azin1-90	2	1	C	T	CCTTTATCTGAGGAACCTG	CCTTTATCTGAAGAACCTG	GGGAATAGTGTCAATTTGGGATGCAT	0.2500
Oke_brd2-118	2	1	C	T	ATGACGAAGCTCTCC	ATGACGAAACTCTCC	CTCAAGCCCTCCACACTCA	0.2000
Oke_brp16-65	2	1	C	T	ACGTTGCCTGTCCAC	ACGTTGCCTATCCAC	TCCACGTCACCTCAGCATGATG	0.2500
Oke_ced16-77	2	1	A	C	CCAGCCCCCTCTGAAA	AGCCCCCGCTGAAA	TGCTTTCAGAATCCAATGCTTTCTC	0.1875
Oke_e2ig5-50	2	1	C	T	CATCTTTGTATCTGTGCCATT	TCATCTTTGTATCTATGCCATT	GCAGCTCATTTCTGTACATG	0.2500
Oke_eif4g1-43	2	1	G	T	CTGAGATTCTTCATCTTTTAC	TGAGATTCTTCATATTTTAC	GCACCCAACAGTTTCATCATGTAAGT	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_glr1-78	2	1	C	T	TGGGCATTTAGAGTTTATT	TGGGCATTTAGAAATTATT	CGTCCGTCCAGTGATGTC	0.2500
Oke_il-1racp-67	2	1	G	A	CGTACGAGATGTAGATGT	CGTACGAGATATAGATGT	AATTGCTCCTCCTCGCTATTTCTC	0.2000
Oke_mgl1-49	2	1	A	T	ATTTATGGGTGTTCCCC	TTATGGGAGTTCCCC	ACATTGTAATCTGTATTAGTCCAATGCAGAC	0.2500
Oke_nc2b-148	2	1	A	C	TTTAGTTCTAGTCAAAAAGTAG	TAGTTCTAGTCAAAAAGTAG	CCAGCCTATTTCCCTTTAGTGATATGA	0.2500
Oke_pgap-111	2	1	C	T	AGCTAGCAGGCTAAAG	AGCTAGCAAGCTAAAG	TGCAGATCTCAATTTGAACGACCTAT	0.2000
Oke_psm9-57	2	1	C	T	CATTGGCGGTGTAACG	TCATTGGCAGTGTAACG	ACTGTAGTACTGCATTTTATATTGCT	0.2000
Oke_rab5a-117	2	1	C	T	CAGCTGTTTTCTTTAGCCT	AGCTGTTTTCTTTAGCCT	GGGAATAACAGTCAATGCAGCATTT	0.2000
Oke_ras1-249	2	1	T	G	CACCAAGGTAAAAAT	CCAAGGAAAAAT	GGATGACTAAGAGCGACTGTATGTG	0.2500
Oke_serpin-140	2	1	A	T	CAAGAAGCTGACCTTAGACAC	AAGAAGCTGACCTTAGACAC	TCCACAGTGAGTAATAAAGTTGCACAT	0.2000
Oke_slc1a3a-86	2	1	C	T	CCCAACGCGGTGATG	CCCAACGCGAGTATG	TGCTTTCATCTGTGGACTCTTACA	0.3000
Oke_syle-90	2	1	A	T	ATATCTTTGAGACTGATTA	CTTTGAGACAAGATTA	TTGAGGAAACCACTGGTCTTACAAG	0.1875
Oke_thic-84	2	1	C	T	ATGGAATGACAGCAATGT	ATGGAATGACAACAATGT	GCTGCTGTCTTAAACCAATTTTACA	0.2500
Oke_u200-385	2	1	G	T	CATTATCTCCCTGAATGTA	CATTATCTCCATGAATGTA	CCCATAATTTTGCAACCTAGTCACA	0.2000
Oke_u217-172	2	1	T	C	CACTCTTACAAAAACA	CACTCTTACGAAAAACA	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
Kogrukluq 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
Numsatuk 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