Inseason analysis of chum salmon (*Oncorhynchus keta*) bycatch from the shoreside sector of the Bering Sea Aleutian Islands walleye pollock (*Gadus chalcogrammus*) trawl fishery

Results from Statistical Week 29

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Summary

This is the fifth inseason analysis of the 2026 chum salmon *Oncorhynchus keta* bycatch from the shoreside sector of the Bering Sea and Aleutian Islands (BSAI) walleye pollock *Gadus chalcogrammus* trawl fishery. In statistical week 29 there were 1,660 chum salmon caught by the shoreside sector. Of that total catch, 332 were sampled, 332 were selected for genotyping, and 320 (19.3% of the total catch) were successfully genotyped to determine the genetic stock composition of the bycatch. E GOA/PNW comprised the largest proportion of the chum salmon bycatch (43.7%), 725 chum salmon. Western Alaska (Coastal Western Alaska and Upper/Middle Yukon combined) comprised 15.3% of the bycatch (254 fish). Since statistical week 24 a total of 14,516 chum salmon have been caught by the shoreside sector. Of those chum salmon, an estimated 2940 were of Western Alaska (Coastal Western Alaska and Upper/Middle Yukon River) origin.

Chum salmon bycatch from statistical week 29 from the shoreside sector of the BSAI walleye pollock trawl fishery and the cumulative catch over all statistical weeks analyzed from the B season. For individual week estimates see Appendix I.

	Stat Week 29 (PSC = 1,660; n = 320)					B season
Region	Est. num.	Est. CI	Mean	2.5%	97.5%	Est. num.
SE Asia	338	266-416	0.204	0.160	0.251	2093
NE Asia	337	261-420	0.203	0.157	0.253	1599
W Alaska	132	76-195	0.079	0.046	0.118	2029
Up/Mid Yukon	122	72-182	0.074	0.044	0.109	911
SW Alaska	6	0-48	0.003	0.000	0.029	457
E GOA/PNW	725	635-817	0.437	0.383	0.492	7410

Introduction

Chum salmon (*Oncorhynchus keta*) incidental catch occurs within the Federally Managed midwater trawl fishery for walleye pollock (*Gadus chalcogrammus*) in the Bering Sea and Aleutian Islands (BSAI). Salmon are managed as a prohibited species catch (referred to as bycatch) and are highly regulated. The fishery is composed of three distinct processing sectors, each with different operational constraints. Within the shoreside sector, smaller vessels which lack the ability to process hauls at-sea often fish closer to the Alaska Peninsula. Differences in the stock specific distribution of chum salmon within the Bering Sea result in the shoreside sector often catching the largest proportion and number of Western Alaska (Coastal Western Alaska and Upper/Middle Yukon River genetic groups combined) chum salmon bycatch relative to the catcher processor and mothership sectors (Kondzela et al. 2017). Currently, annual estimates of genetic stock composition are produced by the genetics program of NOAA's Alaska Fishery Science Center (AFSC) and presented to the North Pacific Fisheries Management Council (NPFMC) at their April Council meeting (~3 months after the end of the B season). Within the fishery, all chum salmon bycatch is enumerated by the North Pacific Observer Program and 1 in 30 are sampled for length, weight, sex, and a tissue sample and a scale are sent to the AFSC genetics program for analysis. In 2024, a project was initiated by Bristol Bay Science Research Institute (BBSRI) to sample the bycatch from the shoreside sector of the fleet in order to obtain weekly estimates of genetic stock composition. Estimates were produced in both 2024 and 2025, with weekly and annual reports available at https://www.bbsri.org/inseason-chum-genetics. This is the third year for which weekly stock composition estimates have been made in season. This report outlines the results the analysis of the chum salmon bycatch from statistical week 29 (12 Jul - 18 Jul).

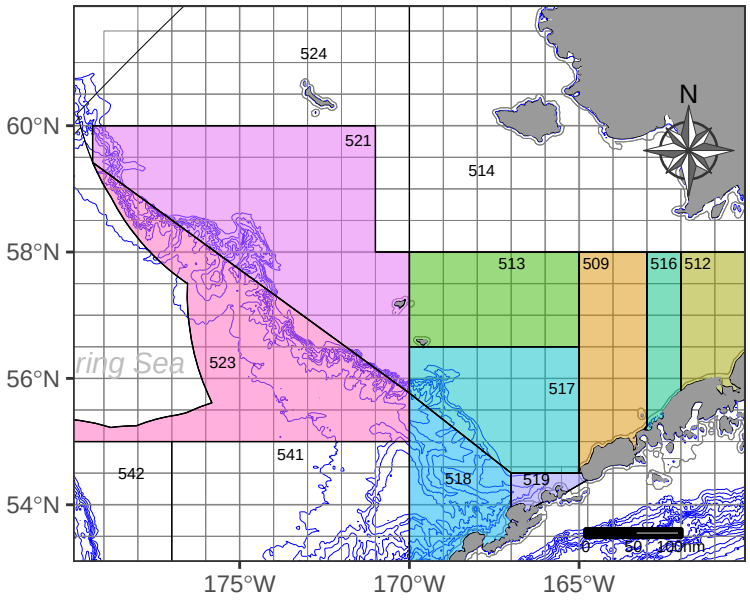

Figure 1: Map of National Marine Fisheries Service management areas within the Bering Sea and Aleutian Islands. Colored areas indicate management areas where chum salmon bycatch has historically occurred.

Methods

Bycatch Sampling

Port samplers, employed by BBSRI, sampled pollock hauls delivered to processing plants in Dutch Harbor and Akutan. The target sampling rate for statistical week 29 was fixed at 1 in 5 chum salmon sampled (Table

1). After NMFS observers had processed the offload, BBSRI technicians took a length measurement, scale sample for age estimation, and a fin clip for genetic analyses. Fin clips were stapled onto a Whatman card labelled with haul-level information from the delivery. Scale samples were mounted on gum cards and stored for post-season analysis. Sampling and genotyping data were sent to the AFSC genetics program for analysis.

Genotyping

All tissue samples collected were sent to the BBSRI staffed genetics laboratory in Dutch Harbor for processing. Genomic DNA was extracted from dried fin clips with Macherey-Nagel (Allentown, PA) NucleoSpin Tissue kits. Extracted DNA was amplified for 96 single nucleotide polymorphism markers (SNPs) with a Fluidigm (San Francisco, CA) BioMark X9 system with 96.96 Dynamic Array integrated fluidic circuit (IFC). Each of the 9,216 parallel reactions consisted of 50–500 $\eta g/\mu l$ DNA, 1X Fast GT Sample Loading Reagent (Fluidigm), 1X TaqMan GTXpress Master Mix (Applied Biosystems), 10X Custom ABI TaqMan SNP Genotyping Assay (Applied Biosystems), 1X Assay Loading Reagent (Fluidigm), and 2.5X ROX Reference Dye (Invitrogen). The temperature profile for amplification was thermal mixing at 60°C for 10 min and 70°C for 30 min followed by "Hot-Start" denaturation at 95°C for 2 min and 40 cycles of amplification (denaturation at 95°C for 2 s and annealing at 60°C for 20 s). After amplification, genotypes were scored with BioMark Genotyping Analysis software.

Genetic Stock Identification

Mixtures were created by grouping sampled fish into temporal groups (statistical week) from non-debriefed observer data provided by the Alaska Regional Office and linked to genetic samples by BBSRI. Individual samples with fewer than 80% of their multilocus genotype scored were dropped from analyses. Additionally, if individuals are identified to have matching multilocus genotypes (>95% similarity) the individuals with fewer scored loci was dropped. Genetic stock identification was performed with the conditional genetic stock identification model in the R package *rubias* (Moran and Anderson 2019) following the methods used in NOAA's annual bycatch reports. Briefly, baseline populations were grouped into seven regions adapted from (2010): Southeast Asia (SE Asia), Northeast Asia (NE Asia), Coastal Western Alaska (W Alaska), Upper/Middle Yukon (Up/Mid Yukon), Southwest Alaska (SW Alaska), and the Eastern GOA/Pacific Northwest (E GOA/PNW). 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, seven separate MCMC chains of 100,000 iterations (burn-in of 50,000) of the non-bootstrapped model were run, with 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 and Rubin 1992) estimated with the gelman.diag function in the coda library (Plummer et al. 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. The estimated number of fish for each genetic group, and associated uncertainty, is estimated as the mean stock proportion and 95% credible intervals multiplied by the total bycatch in a given statistical week.

Results

Chum Salmon Bycatch

In statistical week 29 of the BSAI pollock trawl fishery there were 1,660 chum salmon caught by the shoreside sector. The majority of these chum salmon were caught in NMFS area 513. Since statistical week 24 a total of 14,516 chum salmon have been caught by the shoreside sector. Chum have been caught in five statisical areas. The majority of chum salmon caught have come from NMFS area 509 (Figure 2).

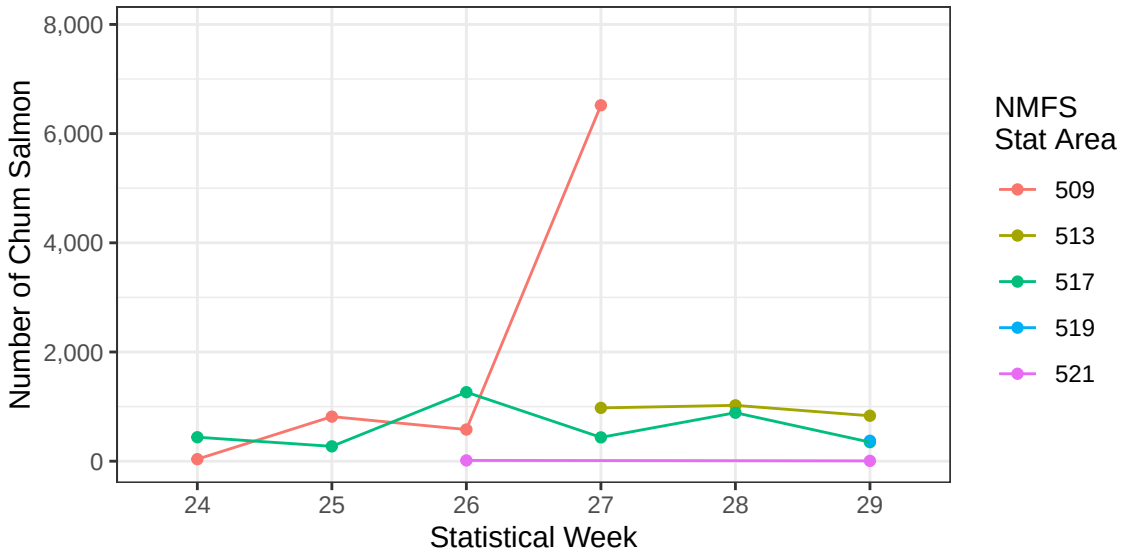

Figure 2: Number of chum salmon caught by the shoreside sector of the Bering Sea pollock trawl fishery by statistical week. Weekly totals for which fewer than 3 vessels made deliveries have been omitted.

Sampling & Genotyping

In statistical week 29, BBSRI technicians sampled hauls delivered to Dutch Harbor and Akutan. A total of 332 chum salmon were sampled for an overall sampling rate of 0.2 or ~1/5. All chum salmon sampled were processed for genotyping with 320 (96.4%) successfully genotyped.

Table 1: Chum salmon bycatch sampling and genotyping information for statistical week 29 for the shoreside processing plants. Sampling is grouped by processing plant and target sampling rate. Chum genotyped is the number of chum that were amplified for the marker panel. Chum analyzed are those chum that were genotyped for at least 80% of the genetic markers after potential duplicate samples were removed.

Plant	Target Sample Rate	Total Chum	Chum Sampled	Sample Rate	Chum Genotyped	Chum Analyzed	Genotype Rate
P1	0.2	301	59	0.196	59	56	0.186
P2	0.2	81	16	0.198	16	16	0.198
P3	0.2	986	198	0.201	198	190	0.193
P4	0.2	246	50	0.203	50	50	0.203
P5	0.2	46	9	0.196	9	8	0.174
Total		1660	332	0.200	332	320	0.193

Stock Specific Catches

In statistical week 29, 6 of the six genetic groups were present in the bycatch. The E GOA/PNW reporting group comprised the largest proportion of the chum salmon bycatch (43.7%), 725 of the total bycatch of 1,660 chum salmon. The second largest contributing regional group to the bycatch was SE Asia with 20.4% or 338 fish. Western Alaska (Coastal Western Alaska and Upper/Middle Yukon combined) comprised 15.3% of the bycatch (254 fish). Asia (NE Asia and SE Asia combined) comprised 40.7% of the bycatch (675 fish).

Table 2: Chum salmon bycatch from statistical week 29 of the shoreside sector BSAI trawl fishery (PSC = 1,660; n = 320)

Region	Est. num.	Est. CI	Mean	2.5%	97.5%	P=0	SF
SE Asia	338	266-416	0.204	0.160	0.251	0.00	1.00
NE Asia	337	261-420	0.203	0.157	0.253	0.00	1.00
W Alaska	132	76-195	0.079	0.046	0.118	0.00	1.00
Up/Mid Yukon	122	72-182	0.074	0.044	0.109	0.00	1.00
SW Alaska	6	0-48	0.003	0.000	0.029	0.59	1.00
E GOA/PNW	725	635-817	0.437	0.383	0.492	0.00	1.00

Of the 14,516 chum salmon caught by the shoreside sector since statistical week 24, the largest contributing genetic group to the bycatch has been the E GOA/PNW, with a point estimate of 7,410 chum salmon. Since the start of the B season, the Coastal Western Alaska (W Alaska) group has comprised an average of 14.8% of the bycatch, with the shoreside sector having caught a total of 2,029 chum salmon from this genetic group. The Southwest Alaska (SW Alaska) regional group made up an average of 2.1% of the bycatch over the 6 weeks, with a total of 457 chum salmon harvested to date. The Upper/Middle Yukon (Up/Mid Yukon) group accounted for an average of 6.5% of the chum salmon bycatch, with 911 fish harvested since statistical week 24-25.

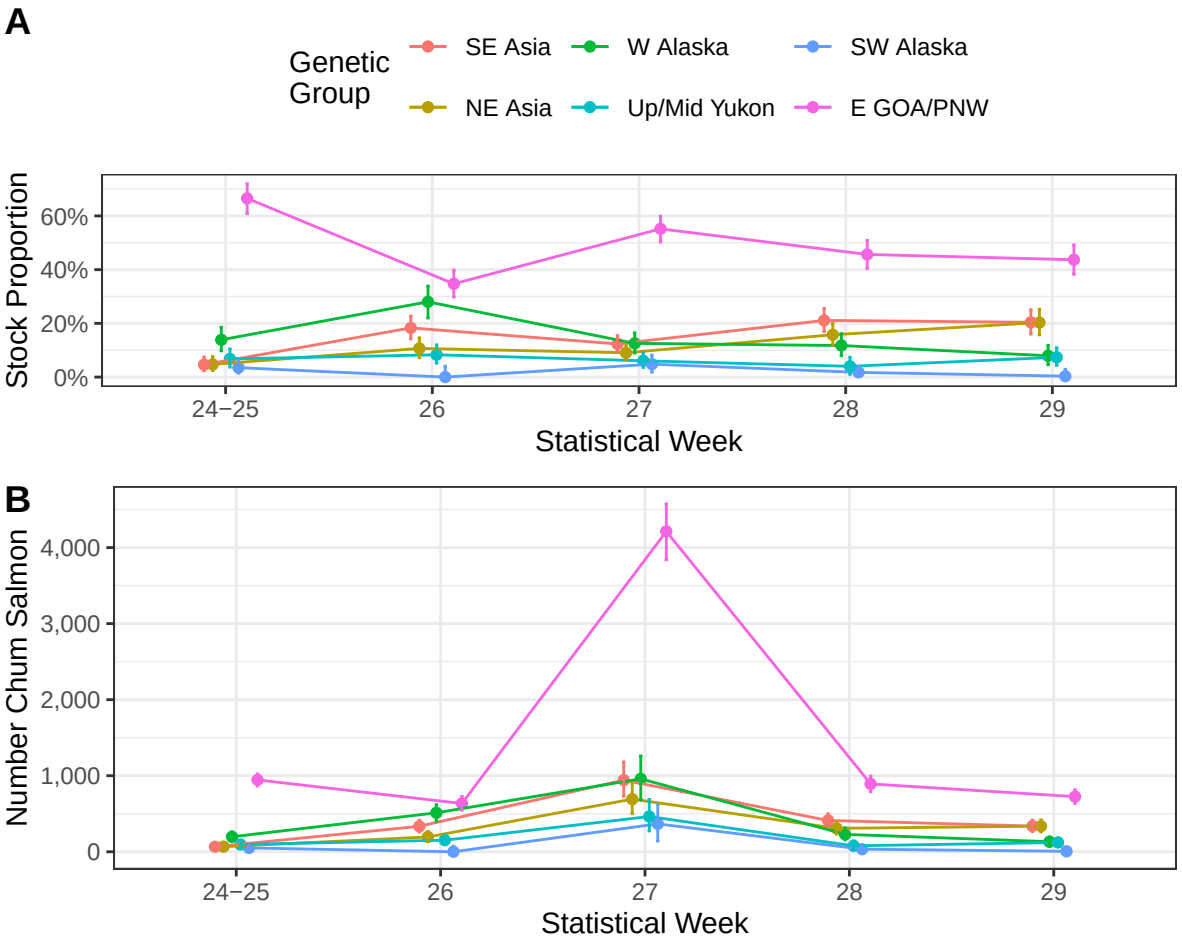

Figure 3: Chum salmon bycatch proportion (A) and total number of fish (B) for the B season of the shoreside sector pollock trawl fishery. Error bars represent 95% credible intervals.

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Appendix I - 2026 GSI Results

Prior week stock composition estimates of chum salmon bycatch from the 2026 shoreside sector's Bering Sea and Aleutian Islands, B-season pollock trawl fishery.

Stat Week 24-25 (PSC = 1,421; n = 279)

Region	Est. num.	Est. CI	Mean	2.5%	97.5%	P=0	SF
SE Asia	66	33-106	0.046	0.023	0.075	0.00	1.00
NE Asia	67	34-109	0.047	0.024	0.076	0.00	1.00
W Alaska	197	139-264	0.139	0.098	0.186	0.00	1.00
Up/Mid Yukon	96	53-149	0.068	0.037	0.105	0.00	1.00
SW Alaska	50	21-88	0.035	0.015	0.062	0.00	1.00
E GOA/PNW	945	864-1,023	0.665	0.608	0.720	0.00	1.00

Stat Week 26 (PSC = 1,829; n = 356)

Region	Est. num.	Est. CI	Mean	2.5%	97.5%	P=0	SF
SE Asia	335	260-415	0.183	0.142	0.227	0.00	1.00
NE Asia	195	132-267	0.107	0.072	0.146	0.00	1.00
W Alaska	512	403-619	0.280	0.220	0.339	0.00	1.01
Up/Mid Yukon	152	95-220	0.083	0.052	0.120	0.00	1.00
SW Alaska	0	0-74	0.000	0.000	0.040	0.69	1.05
E GOA/PNW	635	546-728	0.347	0.298	0.398	0.00	1.00

Stat Week 27 (PSC = 7,636; n = 516)

Region	Est. num.	Est. CI	Mean	2.5%	97.5%	P=0	SF
SE Asia	942	729-1,180	0.123	0.095	0.154	0.00	1.00
NE Asia	692	502-908	0.091	0.066	0.119	0.00	1.00
W Alaska	959	684-1,259	0.126	0.090	0.165	0.00	1.00
Up/Mid Yukon	463	274-689	0.061	0.036	0.090	0.00	1.00
SW Alaska	367	140-626	0.048	0.018	0.082	0.00	1.00
E GOA/PNW	4,213	3,840-4,575	0.552	0.503	0.599	0.00	1.00

Stat Week 28 (PSC = 1,953; n = 367)

Region	Est. num.	Est. CI	Mean	2.5%	97.5%	P=0	SF
SE Asia	412	332-499	0.211	0.170	0.255	0.00	1.00
NE Asia	308	233-389	0.158	0.119	0.199	0.00	1.00
W Alaska	229	156-316	0.117	0.080	0.162	0.00	1.00
Up/Mid Yukon	78	20-144	0.040	0.010	0.074	0.00	1.00
SW Alaska	34	8-79	0.017	0.004	0.041	0.00	1.00
E GOA/PNW	892	790-994	0.457	0.404	0.509	0.00	1.00