

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 24-25

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Summary

This is the first inseason analysis of chum salmon *Oncorhynchus keta* bycatch from the shoreside sector of the Bering Sea and Aleutian Islands walleye pollock *Gadus chalcogrammus* trawl fishery report of 2025. In statistical week 24-25 of the Bering Sea Aleutian Islands (BSAI) walleye pollock trawl fishery there were 855 chum salmon caught by the shoreside sector. Of that total catch, 172 were sampled, 172 were selected for genotyping, and 169 (19.8% of the total catch) were successfully genotyped to determine the genetic stock composition of the bycatch. SE Asia comprised the largest proportion of the chum salmon bycatch (28.4%), 243 chum salmon. Western Alaska (Coastal Western Alaska and Upper/Middle Yukon combined) comprised 25.2% of the bycatch (216 fish).

Stat Week 24-25 (PSC = 855; n = 169)

Region	Est. num.	Est. CI	Mean	2.5%	97.5%	P=0	SF
Up/Mid Yukon	91	50-143	0.106	0.059	0.167	0.00	1.00
W Alaska	125	72-184	0.146	0.084	0.215	0.00	1.00
E GOA/PNW	222	167-281	0.260	0.195	0.329	0.00	1.00
NE Asia	158	108-216	0.185	0.126	0.252	0.00	1.00
SE Asia	243	185-305	0.284	0.216	0.357	0.00	1.00
SW Alaska	16	0-47	0.018	0.000	0.054	0.06	1.00

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, Yukon Fall run, and Kotzebue Sound 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. This report outlines the results the analysis of the chum salmon bycatch from statistical week 24-25 (11 Jun - 21 Jun).

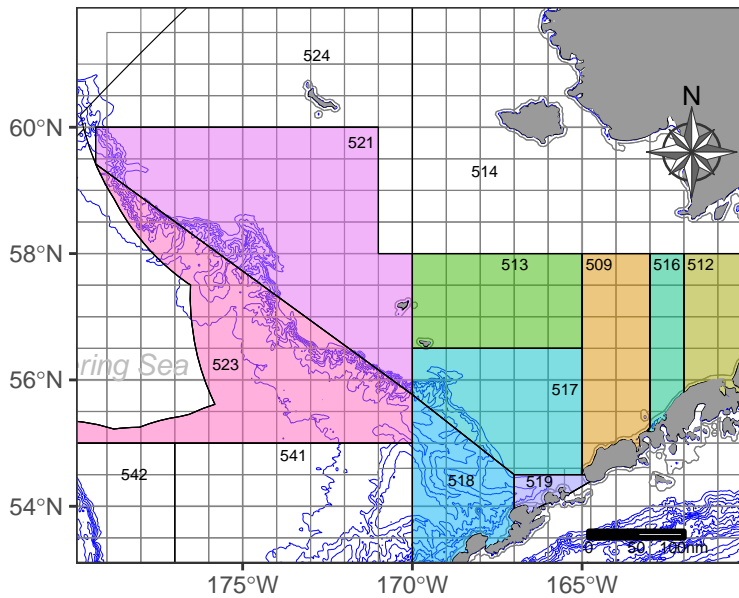


Figure 1: Map of National Marine Fisheries Service management areas within the Bering Sea and Aleutian Islands. Colored areas indicate management areas where chum salmon bycatch has historically occurred.

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 24-25 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), Kotzebue Sound, 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

Sampling & Genotyping

In statistical week 24-25, BBSRI technicians sampled hauls delivered to Dutch Harbor and Akutan. A total of 172 chum salmon were sampled for an overall sampling rate of 0.2 or $\sim 1/5$. All chum salmon sampled were processed for genotyping with 169 (19.8%) successfully genotyped.

Table 1: Chum salmon bycatch sampling and genotyping information for statistical week 24-25 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	120	25	0.208	25	25	0.208
P2	0.2	134	25	0.187	25	24	0.179
P3	0.2	503	102	0.203	102	101	0.201
P4	0.2	86	18	0.209	18	17	0.198
P5	0.2	12	2	0.167	2	2	0.167
Total		855	172	0.200	172	169	0.198

Stock Specific Catches

In statistical week 24-25, 6 of the six genetic groups were present in the bycatch. The SE Asia reporting group comprised the largest proportion of the chum salmon bycatch (28.4%), 243 of the total bycatch of 855 chum salmon. The second largest contributing regional group to the bycatch was E GOA/PNW with 26% or 222 fish. Western Alaska (Coastal Western Alaska and Upper/Middle Yukon combined) comprised 27.1% of the bycatch (232 fish). Asia (NE Asia and SE Asia combined) comprised 46.9% of the bycatch (401 fish).

Table 2: Chum salmon bycatch from statistical week 24-25 of the BSAI trawl fishery (PSC = 855; n = 169)

Region	Est. num.	Est. CI	Mean	2.5%	97.5%	P=0	SF
SE Asia	243	185-305	0.284	0.216	0.357	0.00	1.00
NE Asia	158	108-216	0.185	0.126	0.252	0.00	1.00
W Alaska	125	72-184	0.146	0.084	0.215	0.00	1.00
Up/Mid Yukon	91	50-143	0.106	0.059	0.167	0.00	1.00
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E GOA/PNW	222	167-281	0.260	0.195	0.329	0.00	1.00

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