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U.S. DEPARTMENT OF COMMERCE
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ABSTRACT

A genetic analysis of samples from the Chinook salmon (*Oncorhynchus tshawytscha*) bycatch of the 2013 Gulf of Alaska (GOA) trawl fisheries for Pacific rockfish (*Sebastes* spp.) and arrowtooth (*Atheresthes stomias)* flounder was undertaken to determine the stock composition of the sample sets. Samples were genotyped for 43 single nucleotide polymorphism (SNP) DNA markers and results were estimated using the Alaska Department of Fish and Game (ADF&G) SNP baseline. In 2013, genetic samples from the bycatch of the GOA rockfish fishery were collected by the fishing industry using a census sampling protocol where every Chinook salmon encountered was sampled. Based on the analysis of 2,029 Chinook salmon bycatch samples collected throughout the 2013 GOA rockfish trawl fishery, West Coast U.S. stocks (WA/OR/CA) represented the largest stock grouping (60%) with smaller contributions from British Columbia (31%), Coastal Southeast Alaska (6%), and Northwest GOA (2%) stocks. Genetic samples were also collected from Chinook salmon taken in the bycatch of the 2013 GOA arrowtooth flounder trawl fisheries. Those samples were collected opportunistically from a single vessel; consequently, the resulting stock composition estimates should be considered as stock compositions of the sample set rather than a representative composition of the overall bycatch. Based on the analysis of 279 Chinook salmon bycatch samples, West Coast U.S. (43%), British Columbia (39%), Coastal Southeast Alaska (14%), and Northwest GOA (3%) stocks comprised the largest stock groups. We also produced a stock composition estimate of Chinook salmon from a single test haul of the salmon excluder device performed in April 2013 in an area near Kodiak Island in Shelikof Strait. Stock composition results showed that the majority of those 95 Chinook salmon originated from West Coast U.S. (79%), British Columbia (17%), and Coastal Southeast Alaska (3%) stocks.

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INTRODUCTION

The Bering Sea and the Gulf of Alaska (GOA) are known feeding habitats for multiple brood years of Chinook salmon (*Oncorhynchus tshawytscha*) originating from many different localities in North America and Asia. Determining the geographic origin and stock composition of salmon caught in federally managed fisheries is essential to understanding whether fisheries management could address conservation concerns. This report provides genetic stock identification results for Chinook salmon bycatch samples collected 1) in the GOA from the rockfish (*Sebastes* spp.) and arrowtooth flounder (*Atheresthes stomias)* trawl fisheries and 2) from a Gulf of Alaska salmon excluder device test.

The goal of this report is to present stock composition estimates for the samples collected from the bycatch of the trawl fisheries and salmon excluder device test. The analysis uses a single nucleotide polymorphism (SNP) baseline provided by the Alaska Department of Fish and Game (ADF&G) (Templin et al. 2011). This baseline was used previously to estimate stock composition of samples from the 2005-2012 Chinook salmon bycatch (NMFS 2009; Guyon et al. 2010a and b; Guthrie et al. 2012, 2013, 2014; Larson et al. 2013). For additional information regarding background and methodology, refer to the Chinook salmon bycatch report prepared previously for the 2008 Bering Sea trawl fishery (Guyon et al. 2010a).

SAMPLE DISTRIBUTION

Gulf of Alaska Rockfish Fishery

Samples were collected from the Chinook salmon bycatch of the federally managed 2013 Alaska GOA rockfish trawl fishery by the Alaska Groundfish Data Bank (AGDB) for analysis at the Alaska Fisheries Science Center’s Auke Bay Laboratories (ABL). Although there was no requirement for sample collection, the AGDB implemented a census approach in 2013 whereby genetic samples (axillary processes) and biological information were collected from every Chinook salmon encountered in the bycatch. Axillary process tissues were stored in coin envelopes which were labeled, frozen, and shipped to the ABL. Between 1 May and 15 November 2013 (week numbers 18-46), genetic samples were collected from 2,079 Chinook salmon. Because samples were taken from the overall bycatch, the sample distribution is considered to be the bycatch distribution. The sample collection area is approximated in Figure 1 and the bycatch enumeration is shown in Figure 2.

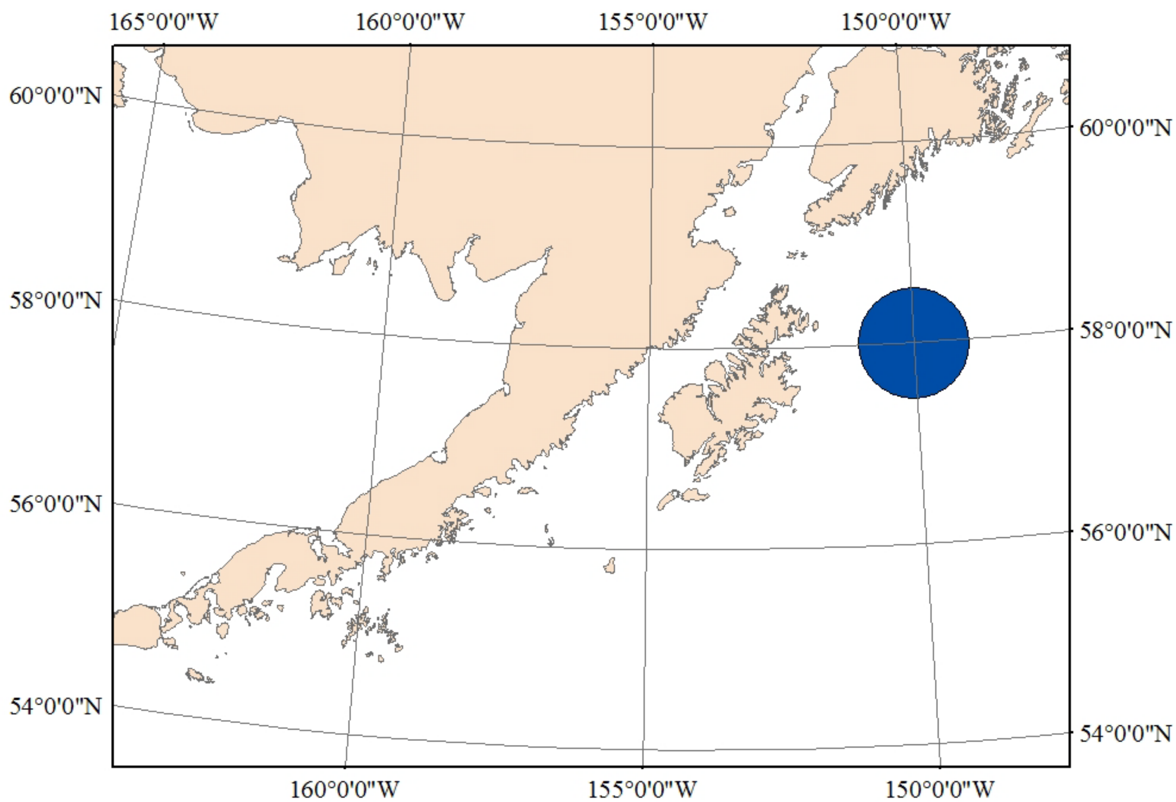

Figure 1. -- Relative location of Chinook salmon bycatch samples collected by the Alaska Groundfish Data Bank in the 2013 Gulf of Alaska rockfish trawl fishery.

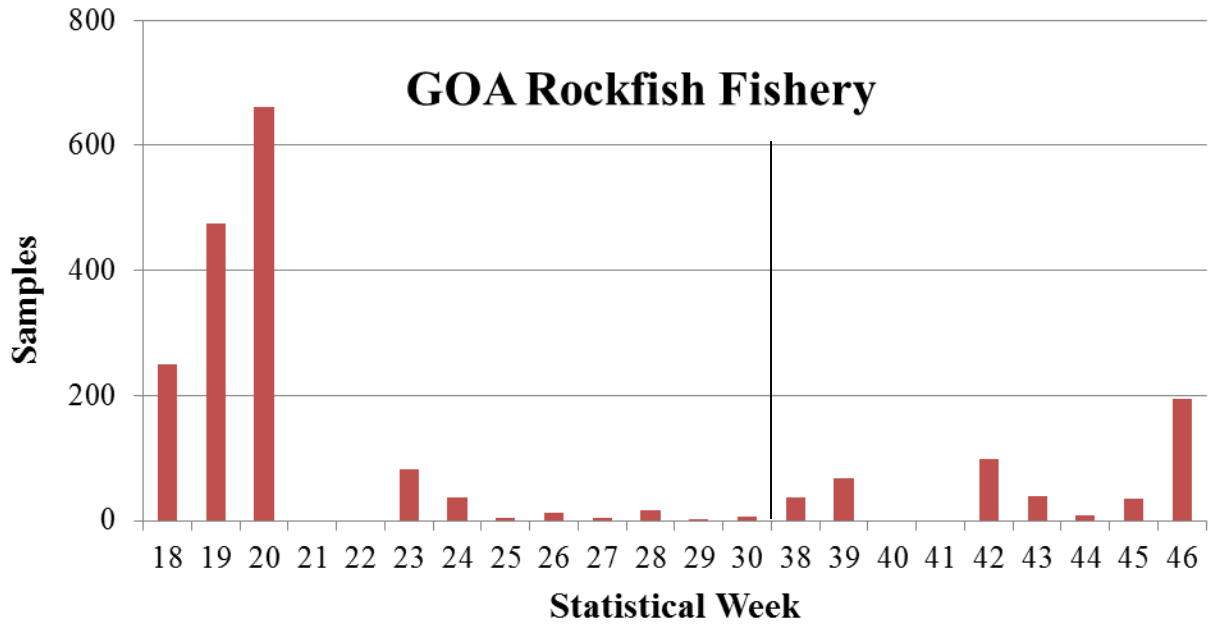

Figure 2. -- Genetic samples collected by the Alaska Groundfish Data Bank from the census of the Chinook salmon bycatch in the 2013 Gulf of Alaska rockfish trawl fishery plotted by statistical week. The line shows the demarcation between weeks 30 and 38 for which no Chinook salmon bycatch was encountered.

Gulf of Alaska Arrowtooth Flounder Fishery

Samples were collected from the Chinook salmon bycatch of the federally managed 2013 Alaska GOA arrowtooth flounder trawl fishery by the Alaska Seafood Cooperative for analysis at the ABL. Although there was no requirement for sample collection, the Alaska Seafood Cooperative implemented an opportunistic sampling approach in 2013 to collect genetic samples (axillary processes) and biological information from Chinook salmon encountered in the bycatch. Axillary process tissues were stored in coin envelopes which were labeled, frozen, and shipped to the ABL. From 66 tows, 302 Chinook salmon (7.5% of the overall bycatch) were sampled between 28 April and 18 May 2013. Because samples were taken opportunistically from a single vessel, the sample distribution is not considered representative of the entire bycatch but is used to indicate presence/absence of particular Chinook salmon stocks. The sample collection area is approximated in Figure 3.

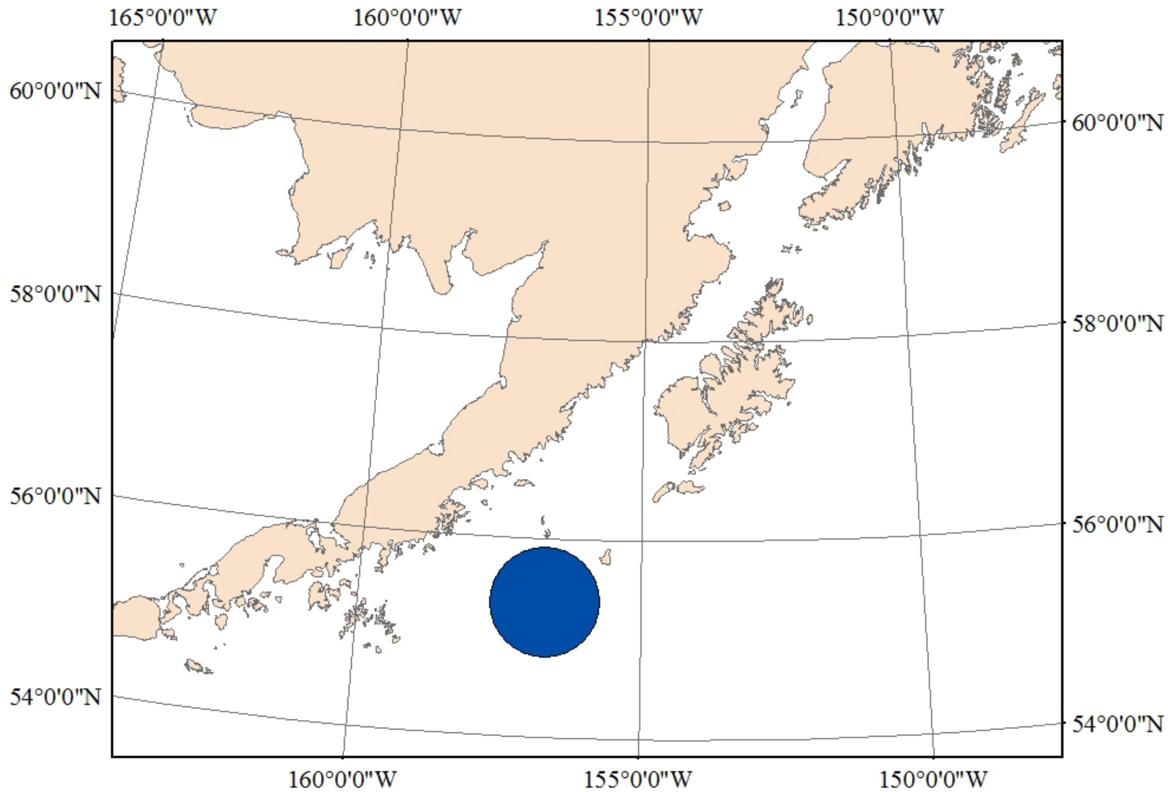

Figure 3. -- Approximate location of Chinook salmon bycatch samples collected by the Alaska Seafood Cooperative in the 2013 Gulf of Alaska arrowtooth flounder trawl fishery.

Excluder Samples

Chinook salmon from excluder tests were genetically sampled in test hauls that had greater than 50 Chinook salmon samples, which in the Spring of 2013, occurred in a single haul aboard the FV *Caravelle*. This unique sample set of 105 samples from a single haul provided an opportunity to continue testing whether Chinook salmon stocks could be aggregated at sea. The location of the sample collection is shown in Figure 4.

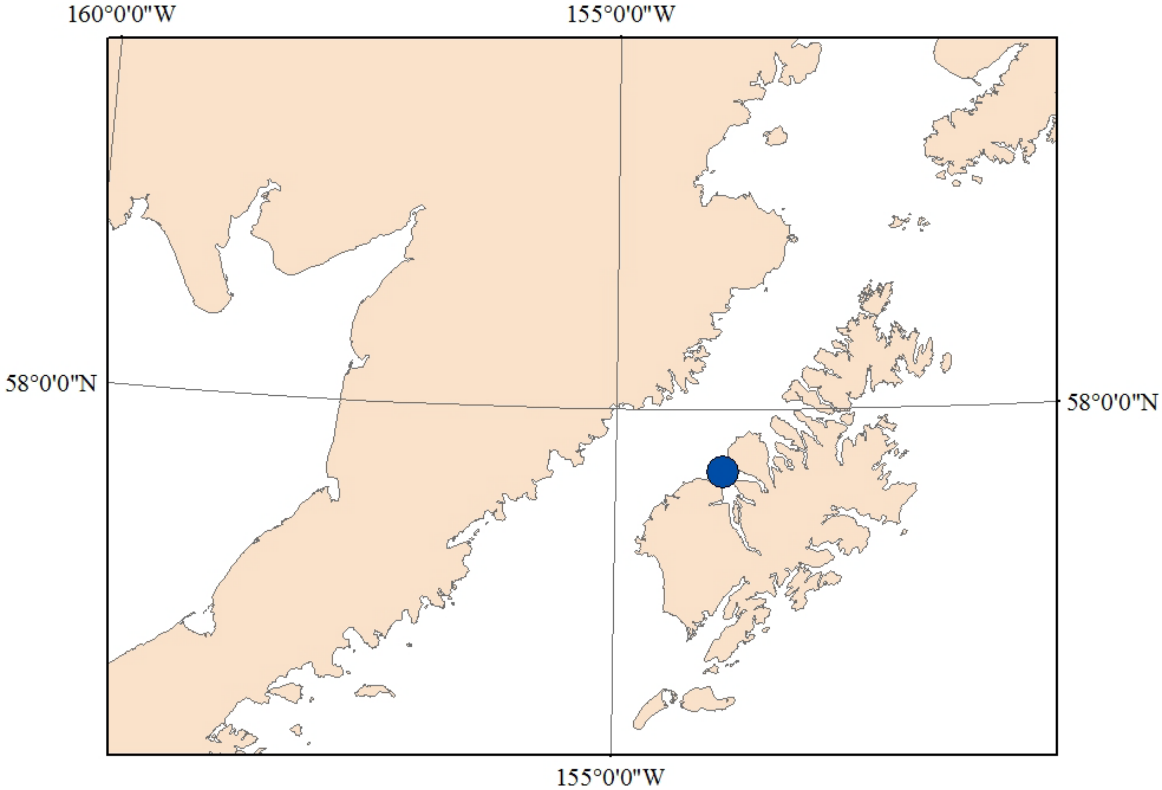

Figure 4. -- Location of samples collected in the 2013 salmon excluder device test. Plotted is the position of the single haul from the FV *Caravelle* where 105 Chinook salmon genetic samples were collected.

GENETIC STOCK COMPOSITION

Genotyping

DNA was extracted from axillary process tissue and matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) genotyping was performed as described previously (Guyon et al. 2010a) using a Sequenom MassARRAY iPLEX platform (Gabriel et al. 2009) to genotype 43 SNP DNA markers represented in the Chinook salmon baseline (Templin et al. 2011). The SNP baseline contains genetic information for 172 populations of Chinook salmon grouped into 11 geographic regions. This baseline was used previously for the genetic analysis of the 2005-2012 Chinook bycatch (NMFS 2009; Guyon et al. 2010a, b; Guthrie et al.

2012, 2013, and 2014). In addition to internal MALDI-TOF chip controls, 10 previously genotyped samples were included on each chip during the analyses and resulting genotypes were compared to those from ADF&G, which used TaqMan chemistries (Life Technologies, Inc.). Concordance rates of 99.8% between the two chemistries for the 2013 controls confirmed the utility and compatibility of both genotyping methods.

From the Chinook salmon bycatch of the 2013 GOA rockfish trawl fishery, a total of 2,070 samples were analyzed of which 2,030 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 98%. These genotypes were analyzed using C++ programs written by the ABL's Genetics Program to check for duplicate samples and one was found and subsequently removed for a final sample set of 2,029. Those remaining samples had genetic information for an average of 42.3 of 43 markers.

From the Chinook salmon bycatch of the 2013 GOA arrowtooth trawl fishery, a total of 302 samples were analyzed of which 279 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 92%. These genotypes were analyzed to check for duplicate samples and none were found. The 279 samples had genetic information for an average of 41.5 of 43 markers.

From the Chinook salmon sampled in the GOA from the 2013 salmon excluder device test, a total of 105 samples were analyzed of which 95 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 90%. These genotypes were analyzed to check for duplicate samples and none were found. The 95 samples had genetic information for an average of 40.4 of 43 markers.

Stock Composition Methods

Stock composition estimates were derived using both BAYES (Bayesian analysis) and SPAM Ver. 3.7 (maximum likelihood analysis) software (Tables 1-3). BAYES software uses a Bayesian algorithm to produce stock composition estimates and can account for missing alleles in the baseline (Pella and Masuda 2001). In contrast, SPAM uses a conditional maximum likelihood approach in which the mixture genotypes are compared directly with the baseline although an option was used within SPAM to allow Bayesian modeling of baseline allele frequencies (ADF&G 2003). Convergence of the SPAM estimates was monitored with the "Percent of Maximum" value and all exceeded the 90% guaranteed percent achievement of the maximal likelihood. For each BAYES analysis, 11 Monte Carlo chains starting at disparate values of stock proportions were configured such that 95% of the stocks came from one designated region with weights equally distributed among the stocks of that region. The remaining 5% was equally distributed among remaining stocks from all other regions. For all estimates, a flat prior of 0.005814 (calculated as 1/172) was used for all 172 baseline populations. The analyses were completed for a chain length of 10,000 with the first 5,000 deleted during the burn-in phase when determining overall stock compositions. Convergence of the chains to posterior distributions of stock proportions was determined with Gelman and Rubin shrink statistics, which were 1.17 or less for all the estimates, conveying strong convergence to a single posterior distribution (Pella and Masuda 2001).

Stock Composition Results – 2013 Gulf of Alaska Rockfish Trawl Bycatch

The BAYES results estimate that almost all of the 2,029 Chinook salmon samples from the bycatch of the 2013 GOA rockfish trawl fishery originated from GOA/Pacific coastal regions, with the West Coast U.S. (WA/OR/CA) contributing the most (60%), followed by British Columbia (BC, 31%), Coastal Southeast Alaska (Coast SE AK, 6%), and Northwest GOA (NW GOA, 2%) (Table 1).

Stock Composition Results – 2013 Gulf of Alaska Arrowtooth Flounder Trawl Bycatch

The BAYES results estimate that almost all of the 279 Chinook salmon samples from the bycatch of the 2013 GOA arrowtooth flounder trawl fishery originated from GOA/Pacific coastal regions, with the West Coast U.S. contributing the most (43%), followed by British Columbia (39%), Coastal Southeast Alaska (14%), and Northwest GOA (3%) (Table 2).

Table 1. -- Regional BAYES and SPAM Ver. 3.7 stock composition estimates for the 2,029 Chinook salmon samples from the bycatch of the 2013 Gulf of Alaska rockfish trawl fishery. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

Region	BAYES	SD	2.5%	Median	97.5%	SPAM	SD
Russia	**0.000**	0.000	0.000	0.000	0.000	**0.000**	0.000
Coast W AK	**0.000**	0.001	0.000	0.000	0.002	**0.000**	0.001
Mid-Yukon	**0.000**	0.000	0.000	0.000	0.000	**0.000**	0.000
Up Yukon	**0.000**	0.000	0.000	0.000	0.001	**0.000**	0.000
N AK Penn	**0.000**	0.000	0.000	0.000	0.000	**0.000**	0.000
NW GOA	**0.022**	0.004	0.016	0.022	0.030	**0.021**	0.004
Copper	**0.003**	0.001	0.001	0.002	0.006	**0.003**	0.001
NE GOA	**0.000**	0.001	0.000	0.000	0.003	**0.002**	0.002
Coast SE AK	**0.064**	0.007	0.050	0.063	0.078	**0.061**	0.007
BC	**0.313**	0.014	0.285	0.313	0.339	**0.325**	0.012
WA/OR/CA	**0.599**	0.013	0.573	0.598	0.624	**0.588**	0.012

Table 2. -- Regional BAYES and SPAM Ver. 3.7 stock composition estimates for the 279 Chinook salmon samples from the bycatch of the 2013 GOA arrowtooth flounder trawl fishery. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

Region	BAYES	SD	2.5%	Median	97.5%	SPAM	SD
Russia	**0.001**	0.002	0.000	0.000	0.008	**0.000**	0.000
Coast W AK	**0.001**	0.002	0.000	0.000	0.007	**0.000**	0.000
Mid-Yukon	**0.000**	0.001	0.000	0.000	0.002	**0.000**	0.000
Up Yukon	**0.000**	0.001	0.000	0.000	0.003	**0.000**	0.000
N AK Penn	**0.000**	0.001	0.000	0.000	0.002	**0.000**	0.000
NW GOA	**0.032**	0.012	0.013	0.031	0.058	**0.034**	0.012
Copper	**0.002**	0.003	0.000	0.000	0.011	**0.004**	0.004
NE GOA	**0.001**	0.003	0.000	0.000	0.008	**0.004**	0.005
Coast SE AK	**0.144**	0.026	0.096	0.143	0.198	**0.130**	0.025
BC	**0.385**	0.034	0.321	0.385	0.452	**0.397**	0.034
WA/OR/CA	**0.434**	0.031	0.374	0.434	0.496	**0.433**	0.032

Table 3. -- Regional BAYES and SPAM Ver. 3.7 stock composition estimates for the 95 Chinook salmon samples from the 2013 test in the GOA of the salmon excluder device. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrap resamplings of the mixture.

Region	BAYES	SD	2.5%	Median	97.5%	SPAM	SD
Russia	**0.000**	0.002	0.000	0.000	0.003	**0.000**	0.000
Coast W AK	**0.002**	0.004	0.000	0.000	0.013	**0.000**	0.000
Mid-Yukon	**0.001**	0.002	0.000	0.000	0.006	**0.000**	0.000
Up Yukon	**0.001**	0.003	0.000	0.000	0.009	**0.000**	0.000
N AK Penn	**0.000**	0.002	0.000	0.000	0.004	**0.000**	0.000
NW GOA	**0.001**	0.004	0.000	0.000	0.012	**0.000**	0.000
Copper	**0.005**	0.010	0.000	0.000	0.035	**0.010**	0.010
NE GOA	**0.001**	0.003	0.000	0.000	0.007	**0.000**	0.000
Coast SE AK	**0.028**	0.019	0.003	0.025	0.075	**0.011**	0.011
BC	**0.172**	0.041	0.100	0.169	0.257	**0.180**	0.041
WA/OR/CA	**0.790**	0.043	0.699	0.792	0.868	**0.799**	0.043

Stock Composition Results – 2013 GOA Excluder Test

The BAYES results estimate that almost all of the 95 Chinook salmon samples from the 2013 GOA salmon excluder device test originated from GOA/Pacific coastal regions, with the West Coast U.S. contributing the most (79%), followed by British Columbia (17%) and Coastal Southeast Alaska (3%) (Table 3).

ESTIMATE COMPARISONS

While differences in collection protocols between the three sample sets necessitate caution in comparing the different analyses, all show an abundance of southern stock groups (British Columbia, West Coast U.S., and Coastal Southeast Alaska) and some contribution from NW Gulf of Alaska stocks (Fig. 5). These results are generally similar to previous analyses of Chinook salmon bycatch sample sets from the 2010-2012 GOA pollock trawl fishery (Guthrie et al. 2014; Guyon et al. 2014) and suggest that most commonly encountered salmon were from Pacific Ocean and Gulf of Alaska spawning tributaries.

Of the three sample sets, the salmon excluder set was the most homogeneous with approximately 79% of the samples estimated from the West Coast U.S. stock grouping although differences in gear (i.e, mesh size) or location (inshore vs. offshore) could influence the results. In addition, since samples from the salmon excluder device test were all derived from a single haul, it's possible that this could represent some type of aggregation effect in which stocks of similar origin could be encountered as part of a group. Interestingly, the average size of the Chinook salmon encountered in the excluder device test (51 cm +/- 4) was smaller than those encountered in the rockfish fishery (60 cm +/- 8) or the arrowtooth flounder fishery (55 cm

+/- 5). This could reflect changes in growth between the sampling periods, whereas uniformity in size (lowest size standard deviation for the excluder samples) could support of some type of schooling activity.

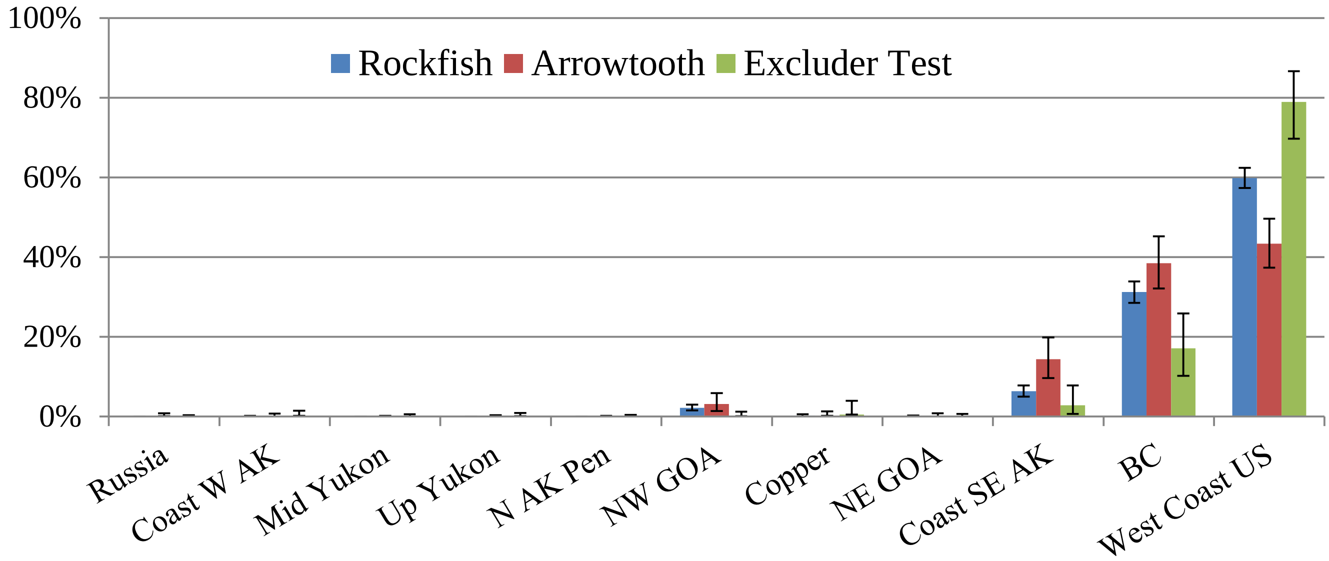

Figure 5. -- Comparison of the GOA stock composition estimates for samples from the 2013 federal rockfish trawl fishery, arrowtooth flounder trawl fishery, and the 2013 GOA salmon excluder device test. Shown are the BAYES 95% credible intervals.

SUMMARY

Many communities are dependent on Chinook salmon for subsistence and commercial purposes. Recent decreasing Chinook salmon returns have caused hardships in Alaska communities and led to fisheries disaster declarations for Yukon River Chinook salmon in 2010 and 2012 by the U.S. Secretary of Commerce (Locke 2010, Blank 2012), and in the Kuskokwim Rivers, and Cook Inlet in 2012 (Blank 2012). Salmon-dependent communities have expressed concern regarding the numbers of salmon caught as bycatch in the federal trawl fisheries

(Gisclair 2009). The incidental harvest of Chinook salmon in the GOA from the non-pollock federal groundfish fisheries averaged 7,333 salmon per year during 1991-2013, with a peak of 30,455 in 1991 (NMFS 2014). The GOA Chinook salmon bycatch in the non-pollock federal fisheries was above the 23-year average in 2013 at 10,386 Chinook salmon.

Stock composition estimates of the Chinook salmon bycatch are needed for groundfish and salmon fishery managers to understand the biological effects of the incidental take of salmon in the trawl fishery. This report provides stock composition analysis of genetic sample sets from the 1) Chinook bycatch of the 2013 GOA rockfish and arrowtooth flounder fisheries and 2) a single haul from the 2013 test of the salmon excluder device. In agreement with previous stock composition analyses of the Chinook salmon bycatch from the Gulf of Alaska pollock trawl fishery, bycatch samples from both the 2013 GOA rockfish and arrowtooth flounder fisheries show an abundance of southern stock groups (British Columbia, West Coast U.S., and Coastal Southeast Alaska) with some contribution from NW Gulf of Alaska stocks (Fig. 5).

Stock composition estimates for the GOA Chinook salmon bycatch from the 2013 federal rockfish trawl fishery were performed using representative samples; consequently, the reported stock composition estimate provided is for the overall 2013 rockfish trawl bycatch. Opportunistic sampling used to derive the arrowtooth flounder 2013 GOA estimates limit the application of those estimates to presence of stock group.

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APPENDIX

Chinook salmon populations in the ADF&G SNP baseline with the regional designations used in the analyses of this report. S.= South, R.= River, H.= Hatchery, and L.= Lake.

Population name	Reg num.	Region name	Population name	Reg num.	Region name
Bistraya River	1	Russia	Henshaw Creek	3	Mid Yukon
Bolshaya River	1	Russia	Kantishna River	3	Mid Yukon
Kamchatka River late	1	Russia	Salcha River	3	Mid Yukon
Pakhatcha River	1	Russia	Sheenjek River	3	Mid Yukon
Andreafsky River	2	Coast W AK	S. Fork Koyukuk River	3	Mid Yukon
Aniak River	2	Coast W AK	Big Salmon River	4	Up Yukon
Anvik River	2	Coast W AK	Blind River	4	Up Yukon
Arolik River	2	Coast W AK	Chandindu River	4	Up Yukon
Big Creek	2	Coast W AK	Klondike River	4	Up Yukon
Cheeneetnuk River	2	Coast W AK	Little Salmon River	4	Up Yukon
Eek River	2	Coast W AK	Mayo River	4	Up Yukon
Gagaryah River	2	Coast W AK	Nisutlin River	4	Up Yukon
George River	2	Coast W AK	Nordenskiold River	4	Up Yukon
Gisasa River	2	Coast W AK	Pelly River	4	Up Yukon
Golsovia River	2	Coast W AK	Stewart River	4	Up Yukon
Goodnews River	2	Coast W AK	Takhini River	4	Up Yukon
Kanektok River	2	Coast W AK	Tatchun Creek	4	Up Yukon
Kisaralik River	2	Coast W AK	Whitehorse Hatchery	4	Up Yukon
Kogrukluk River	2	Coast W AK	Black Hills Creek	5	N AK Pen
Kwethluk River	2	Coast W AK	King Salmon River	5	N AK Pen
Mulchatna River	2	Coast W AK	Meshik River	5	N AK Pen
Naknek River	2	Coast W AK	Milky River	5	N AK Pen
Nushagak River	2	Coast W AK	Nelson River	5	N AK Pen
Pilgrim River	2	Coast W AK	Steelhead Creek	5	N AK Pen
Salmon R. -Pitka Fork	2	Coast W AK	Anchor River	6	NW GOA
Stony River	2	Coast W AK	Ayakulik River	6	NW GOA
Stuyahok River	2	Coast W AK	Benjamin Creek	6	NW GOA
Takotna River	2	Coast W AK	Chignik River	6	NW GOA
Tatlawiksuk River	2	Coast W AK	Crescent Creek	6	NW GOA
Togiak River	2	Coast W AK	Crooked Creek	6	NW GOA
Tozitna River	2	Coast W AK	Deception Creek	6	NW GOA
Tuluksak River	2	Coast W AK	Deshka River	6	NW GOA
Unalakleet River	2	Coast W AK	Funny River	6	NW GOA
Beaver Creek	3	Mid Yukon	Juneau Creek	6	NW GOA
Chandalar River	3	Mid Yukon	Karluk River	6	NW GOA
Chena River	3	Mid Yukon	Kasilof River mainstem	6	NW GOA

Population name	Reg num.	Region name	Population name	Reg num.	Region name
Kenai River mainstem	6	NW GOA	Kowatua River	9	Coast SE AK
Killey Creek	6	NW GOA	Little Tatsemenie River	9	Coast SE AK
Ninilchik River	6	NW GOA	Macaulay Hatchery	9	Coast SE AK
Prairie Creek	6	NW GOA	Medvejie Hatchery	9	Coast SE AK
Slikok Creek	6	NW GOA	Nakina River	9	Coast SE AK
Talachulitna River	6	NW GOA	Tahltan River	9	Coast SE AK
Willow Creek	6	NW GOA	Unuk R.-Deer Mountain H.	9	Coast SE AK
Bone Creek	7	Copper	Unuk River - LPW	9	Coast SE AK
E. Fork Chistochina River	7	Copper	Upper Nahlin River	9	Coast SE AK
Gulkana River	7	Copper	Big Qualicum River	10	BC
Indian River	7	Copper	Birkenhead River spring	10	BC
Kiana Creek	7	Copper	Bulkley River	10	BC
Manker Creek	7	Copper	Chilko River summer	10	BC
Mendeltna Creek	7	Copper	Clearwater River summer	10	BC
Otter Creek	7	Copper	Conuma River	10	BC
Sinona Creek	7	Copper	Damdochax Creek	10	BC
Tebay River	7	Copper	Ecstall River	10	BC
Tonsina River	7	Copper	Harrison River	10	BC
Big Boulder Creek	8	NE GOA	Kateen River	10	BC
Kelsall River	8	NE GOA	Kincolith Creek	10	BC
King Salmon River	8	NE GOA	Kitimat River	10	BC
Klukshu River	8	NE GOA	Klinaklini River	10	BC
Situk River	8	NE GOA	Kwinageese Creek	10	BC
Tahini River	8	NE GOA	Louis River spring	10	BC
Tahini River - Pullen Creek H.	8	NE GOA	Lower Adams River fall	10	BC
Andrews Creek	9	Coast SE AK	Lower Atnarko River	10	BC
Blossom River	9	Coast SE AK	Lower Kalum River	10	BC
Butler Creek	9	Coast SE AK	Lower Thompson River fall	10	BC
Chickamin River	9	Coast SE AK	Marble Creek	10	BC
Chickamin River-LPW	9	Coast SE AK	Middle Shuswap R. summer	10	BC
Chickamin R.Whitman L. H.	9	Coast SE AK	Morkill River summer	10	BC
Clear Creek	9	Coast SE AK	Nanaimo River	10	BC
Cripple Creek	9	Coast SE AK	Nechako River summer	10	BC
Crystal Lake Hatchery	9	Coast SE AK	Nitinat River	10	BC
Dudidontu River	9	Coast SE AK	Oweegee Creek	10	BC
Genes Creek	9	Coast SE AK	Porteau Cove	10	BC
Hidden Falls Hatchery	9	Coast SE AK	Quesnel River summer	10	BC
Humpy Creek	9	Coast SE AK	Quinsam River	10	BC
Kerr Creek	9	Coast SE AK	Robertson Creek	10	BC
Keta River	9	Coast SE AK	Salmon River summer	10	BC
King Creek	9	Coast SE AK	Sarita River	10	BC

Population name	Reg num.	Region name	Population name	Reg num.	Region name
Stuart River summer	10	BC	Lower Deschutes R. fall	11	West Coast US
Sustut River	10	BC	Lyons Ferry H. summer/fall	11	West Coast US
Torpy River summer	10	BC	Makah National Fish H. fall	11	West Coast US
Wannock River	10	BC	McKenzie River spring	11	West Coast US
Alsea River fall	11	West Coast US	Sacramento River winter	11	West Coast US
Carson Hatchery spring	11	West Coast US	Siuslaw River fall	11	West Coast US
Eel River fall	11	West Coast US	Soos Creek Hatchery fall	11	West Coast US
Forks Creek fall	11	West Coast US	Upper Skagit River summer	11	West Coast US
Hanford Reach	11	West Coast US			
Klamath River	11	West Coast US			

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