PSC Northern Fund
Final Report

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Project Title: Origins of Chinook Salmon Harvested in Southeast Alaska Fisheries, 2019

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Abstract:
U.S. fisheries in Southeast Alaska (SEAK) harvest stocks of Chinook salmon bound for river systems in Alaska, Canada, and the continental U.S. Thus, fisheries in SEAK are managed under the purview of the Pacific Salmon Treaty (PST), in which an aggregate abundance-based management (AABM) framework is used for Chinook fisheries. This requires management to have access to reliable information on stock-specific catch, escapement, and recruitment to forecast indices of abundance in PST fisheries. This project aimed to improve fishery management and provide estimates of stock composition in AY 2019 commercial troll and sport Chinook salmon fisheries in Southeast Alaska, independent of coded wire tag (CWT) recoveries, using genetic mixed stock analysis (MSA, also known as genetic stock identification [GSI]). A total of 12,222 fish were sampled and 7,152 fish were genotyped from sport and commercial fisheries in 2019. Results indicate considerable temporal and spatial variation in the compositions of troll and sport harvests within years and across years. The largest contributors to the Southeast Alaska commercial troll fisheries were diverse with *South Thompson*, *Interior Columbia River Su/Fa*, *Southeast Alaska/TBR*, *Oregon Coast*, and *West Vancouver Island* reporting groups each contributing >10% to the annual harvest. The largest contributors to the Southeast Alaska sport fisheries were the *Southeast Alaska/TBR* and *West Vancouver Island* reporting groups, which accounted for over 60% of the annual harvest with *South Thompson* providing ~10% of the annual harvest. These stock composition estimates provide important information for Chinook salmon fisheries managed under the Pacific Salmon Treaty.

Introduction:
Chinook salmon are harvested throughout the year by commercial and sport fishers in the waters of Southeast Alaska, including in commercial troll fisheries and sport fisheries throughout the region. In these fisheries mixed stocks of Chinook salmon are harvested, including salmon originating from Alaska, British Columbia, and the Lower 48. Thus, these fisheries are under the jurisdiction of the Pacific Salmon Treaty (PST) which established a framework for aggregate abundance-based management (AABM) of the Chinook salmon harvest in Southeast Alaska. Allowable catches are specified by the PSC and rely on catch, escapement, recruitment information, and stock composition estimates to forecast indices of abundance in Treaty fisheries. Since 1999, genetic stock identification has been used to estimate the composition of the commercial troll fishery harvest (Crane et al. 2000; Templin et al. 2011; Gilk-Baumer et al. 2013, 2017a, 2017b, 2018), gillnet and seine harvest (e.g. Gilk-Baumer and Carlile 2012), and sport

fishery harvests (Gilk-Baumer et al. 2017c, 2018). This genetic stock identification program had particularly important benefits in 2019 by incorporating CWT information to provide separate estimates of wild and hatchery SEAK/TBR stocks. This breakout of hatchery and wild SEAK/TBR harvest estimates helped measure the effectiveness of management actions taken to reduce harvest of wild-origin SEAK stocks during the winter and spring commercial troll and sport fisheries (Hagerman, Ehresmann, and Shaul 2019). This project is an integral part of a larger SEAK GSI program, which includes comprehensive coverage of major gillnet, troll, and sport fisheries for Chinook salmon.

Objectives:
The objective of this project is to identify the origins—stock, age, and hatchery or natural origin—of fish harvested in the Southeast Alaska (SEAK) Chinook salmon fisheries in Accounting Year 2019. Project tasks to accomplish this objective are as follows:

1. Assay individual genotypes from a maximum of 7,150 sampled Chinook salmon
2. Estimate the relative stock composition of seasonal fishery harvests in SEAK using genetic mixed stock analysis such that the estimated stock composition is within 5% of the true value 90% of the time:
    a. Troll fishery – seasonal troll fishery harvests from October 2018 through September 2019 (<u>early winter</u>: October to December, <u>late winter</u>: January to March, <u>spring</u>: April to June, <u>summer</u>: July to September).
    b. Sport fishery – harvests between April and September 2019.

Approach:
The stock composition of Chinook salmon harvested in SEAK fisheries were estimated using GSI. Chinook salmon samples were collected from commercial troll landings at processors in SEAK, and in the sport fishery by onboard participants and by creel census samplers.

Chinook salmon were selected for sampling without regard to size, sex, adipose fin-clip, or position in the hold. Axillary process tissue was dissected from sampled fish and placed on Whatman paper grid cards for dry tissue preservation. Along with each individual sampled, basic information was recorded such as size, sex, date, vessel, and age (from scale samples). Scale and tissue samples were taken from each sampled fish in a manner that allows specimens to be tracked to individual fish. Each individual fish sampled was assigned a unique sample number and all associated data were maintained in the ADF&G database. At the end of the fishery, genetic samples were shipped to the ADF&G Gene Conservation Laboratory, Anchorage, for analysis.

Representative sets of individuals for mixture analysis were created by subsampling from the collected samples in proportion to the harvest in quadrants comprising the stratum to be estimated. Target mixture sizes were 200, 300, or 400 individuals to achieve acceptable levels of accuracy and precision. Due to the vagaries of fisheries and fishery sampling, target sample sizes were not available for every time and space stratum. Sample sizes smaller than the target were analyzed, but strata represented by fewer than 100 individuals were pooled into larger groups for analysis.

Samples were assayed for DNA loci developed by the Genetic Analysis of Pacific Salmon (GAPS) group funded by the PSC for use in PST fisheries (Seeb et al. 2007). Laboratory methods are well established and have been described in previous proposals and reports. Briefly, DNA were extracted from tissue and the polymerase chain reaction (PCR) was used to amplify DNA fragments at specified locations in the genome. PCR fragment analysis was done on an AB 3730 capillary DNA sequencer and PCR bands were visualized and separated into bin sets using *AB GeneMapper* software v4.0. All laboratory analyses followed protocols accepted by the CTC. The genetic data collected were individual genotypes for each locus. Genotype data are stored in an *Oracle* database (LOKI) maintained by ADF&G.

Errors which can occur in tissue handling, laboratory processes, genotyping, and data recording can have an effect on the accuracy and precision of stock composition estimates and individual assignments. Several measures were implemented to ensure the quality of data produced, including reanalysis of approximately 8% of the individuals for all loci and genotyping by two observers. Details on quality control methods can be found in Gilk-Baumer et al. (2013).

The stock composition of fishery mixtures was estimated using the program BAYES (Pella and Masuda 2001). Proof tests indicate that a minimum of 26 reporting groups are identifiable at a correct allocation of 90% or better (Table 1). We defined prior parameters for each stock group equal to results from the corresponding estimates generated for the 2018 fisheries, with the prior for each stock group subsequently divided equally to populations within that stock group. We ran five independent Markov Chain Monte Carlo (MCMC) chains of 40,000 iterations with different starting values, and then discarded the first 20,000 iterations to remove the influence of the initial start values. Convergence was tested both within and among chains. The mean and 90% credibility intervals were tabulated from the combined set of the second half of the five chains. This procedure was repeated for each fishery mixture, with the goal of estimating the proportions in the mixtures within 7% of the true value 90% of the time (Thompson 1987).

For SEAK/TBR stocks, Chinook salmon containing CWTs were expanded by the sampling percentage and the mark fraction to estimate the fish of hatchery origin. Within each stock group, the natural origin Chinook salmon was estimated by calculating the difference between the estimated stock total and the estimate of hatchery origin fish.

Table 1. Relationship between populations and reporting groups for Chinook salmon used to report stock composition of Southeast Alaska troll and sport fishery harvests for the coast-wide Chinook salmon baseline. Collection details are available in Seeb et al. 2007 and Moran et al. 2005.

	Population	Fine-scale	Driver stocks [a]	Broad-scale
1	1	*Situk*	*SEAK/TBR*	*Alaska*
2	2-5	*Alsek*	*SEAK/TBR*	*TBR*
3	6-10	*N Southeast Alaska*	*SEAK/TBR*	*Alaska*
4	11-17	*Taku*	*SEAK/TBR*	*TBR*
5	18-21	*Andrew*	*SEAK/TBR*	*Alaska*
6	22-28	*Stikine*	*SEAK/TBR*	*TBR*
7	29-42	*S Southeast Alaska*	*SEAK/TBR*	*Alaska*
8	43-51	*Nass*	*NCBC*	*Canada*
9	52-78	*Skeena*	*NCBC*	*Canada*
10	79-97	*BC Coast/Haida Gwaii*	*NCBC*	*Canada*
11	98-113	*West Vancouver*	*West Vancouver*	*Canada*
12	114-123	*East Vancouver*	*Other*	*Canada*
13	124-157	*Fraser*	*Other*	*Canada*
14	158-166	*Lower Thompson*	*Other*	*Canada*
15	167-172	*North Thompson*	*Other*	*Canada*
16	173-180	*South Thompson*	*South Thompson*	*Canada*
17	181-212	*Puget Sound*	*Other*	*US South*
18	213-223	*Washington Coast*	*Washington Coast*	*US South*
19	224-226	*West Cascades Sp*	*Other*	*US South*
20	227-240	*Lower Columbia F*	*Other*	*US South*
21	241-246	*Willamette Sp*	*Other*	*US South*
22	247-302	*Columbia Sp*	*Other*	*US South*
23	303-320	*Interior Columbia Su/F*	*Interior Columbia Su/F*	*US South*
24	321-331	*North Oregon Coast*	*Oregon Coast*	*US South*
25	332-339	*Mid Oregon Coast*	*Oregon Coast*	*US South*
26	340-357	*S Oregon/California*	*Other*	*US South*

Note: Population numbers are listed in Appendix A1 of Gilk Baumer et al. 2018. Populations were combined into (1) 26 fine-scale reporting groups, (2) 8 driver stock reporting groups including an "*Other*" group, and (3) 4 broad-scale reporting groups.

[a] Driver stocks are aggregate stocks that consistently comprise a large proportion (>5%) of all Chinook salmon harvested annually in Southeast Alaska fisheries, and thus are important stocks that help drive catch allocations under the Pacific Salmon Treaty.

In addition to making raw data available for outside analyses, summarization of data will be completed through stock composition estimates. This work will assess different parts of the model that currently use CWT information and will provide additional information on stocks or components of stocks not included in the model. In addition, the above analyses could be used in a number of ways including: assessment of differential vulnerabilities of components of different stocks (e.g. different mortality rates between separate age groups for a particular stock); real-time forecasting of Chinook salmon runs (e.g. Hyun et al. 2013); and estimation of terminal run sizes of certain stocks (e.g. Korman et al. 2012, Bernard et al. 2014). This data has already been used to look at the origins of Chinook salmon harvested in SEAK troll and sport fisheries to provide independent estimates of stock composition of wild- versus hatchery-origin stocks.

Results/Findings:

Sampling of harvests of Chinook salmon in Southeast Alaska troll and sport fisheries began in October 2018 and continued until September 30, 2019. Samples from fisheries were returned to the laboratory in January–October 2019, and laboratory analysis was completed in December 2019

(Tables 2). Data analysis was completed in January 2020 to estimate the relative stock composition of CTC Model stocks of interest in Southeast Alaska fisheries using genetic stock identification and applied these estimates to harvest numbers (Figures 1–4).

Table 2. Number of Chinook salmon sampled in the Southeast Alaska commercial troll and sport fisheries between October 201 and September 2019 (AY 2019).

Fishery	Port	Goal	Sampled
Winter Troll: (Early/Late)	Sitka	450/430	164/811
	Juneau	90/70	112/87
	Ketchikan	120/80	64/76
	Craig	100/330	15/214
	Petersburg/Wrangell	70/80	124/84
Spring Troll (subject to fishery openers)	Craig	50	302
	Sitka	300	2509
	Petersburg	100	0
	Wrangell	300	0
	Ketchikan	200	411
	Juneau	200	0
	Yakutat	0	604
Summer Troll: Retention Per (1 / 2+)			
	Pelican/Elfin Cove	80/80	0/0
	Sitka	400/400	432/554
	Hoonah/Juneau	40/40	40/40
	Petersburg	250/180	87/130
	Wrangell	100/120	100/16
	Port Alexander	100/50	0/0
	Craig	550/420	501/300
	Ketchikan	150/200	218/177
	Tender rider	0/0	262/0
	Total	6,130	8,470
Sport	Juneau	600	449
	Haines	15	0
	Skagway	20	0
	Glacier Bay	65	22
	Sitka	1,500	1,563
	Yakutat	75	120
	Elfin Cove	50	171
	Craig	500	602
	Petersburg	450	132
	Wrangell	200	74
	Ketchikan	600	619
	Total	4,075	3,752

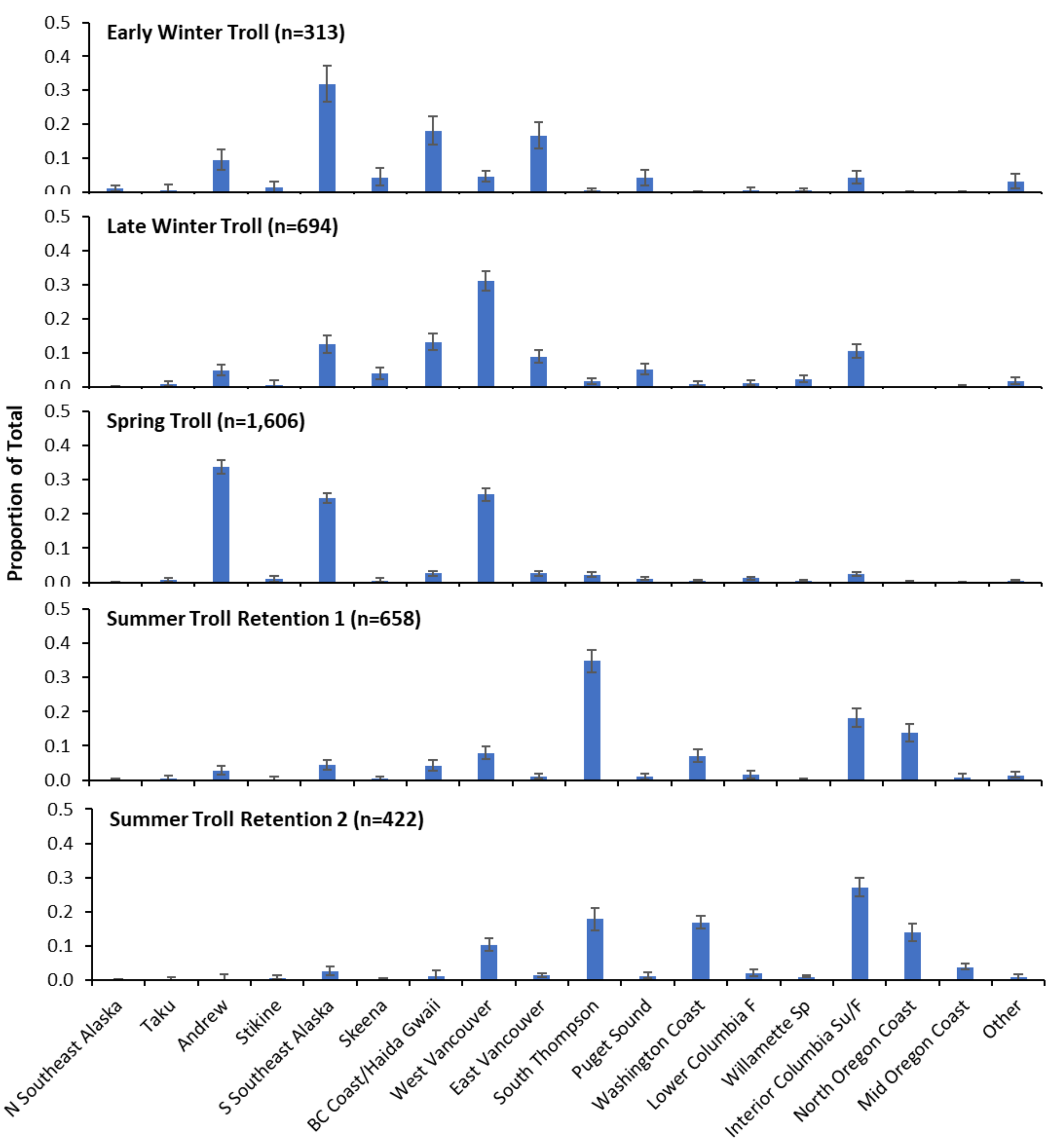
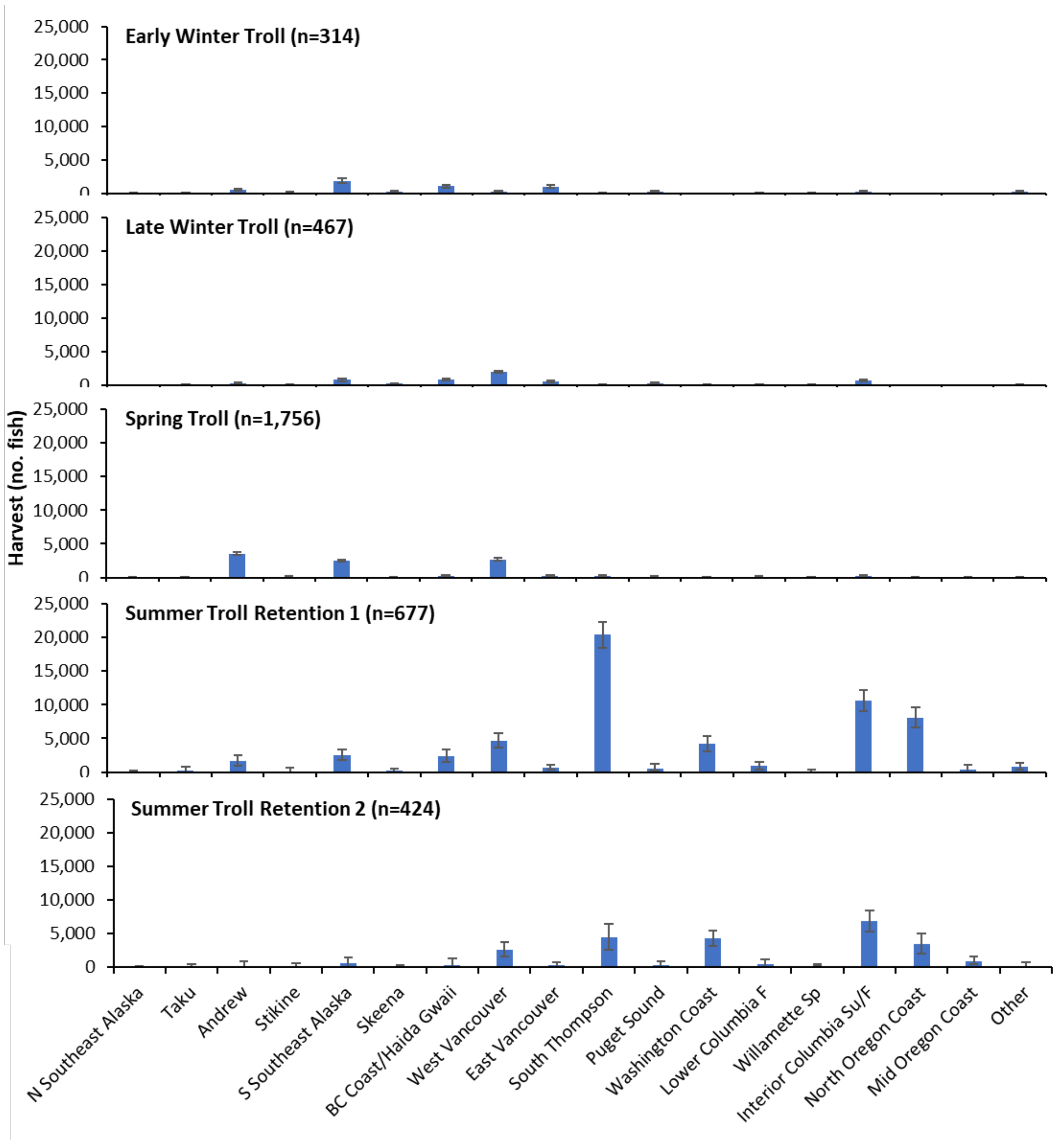


Figure 1. Estimated proportional contributions of a subset of 18 reporting groups of Chinook salmon to the harvest during the Southeast Alaska troll fisheries in AY 2019. Minor contributing reporting groups are combined into an *Other* group for ease of interpretation. Estimates are given for all quadrants combined for each fishery.



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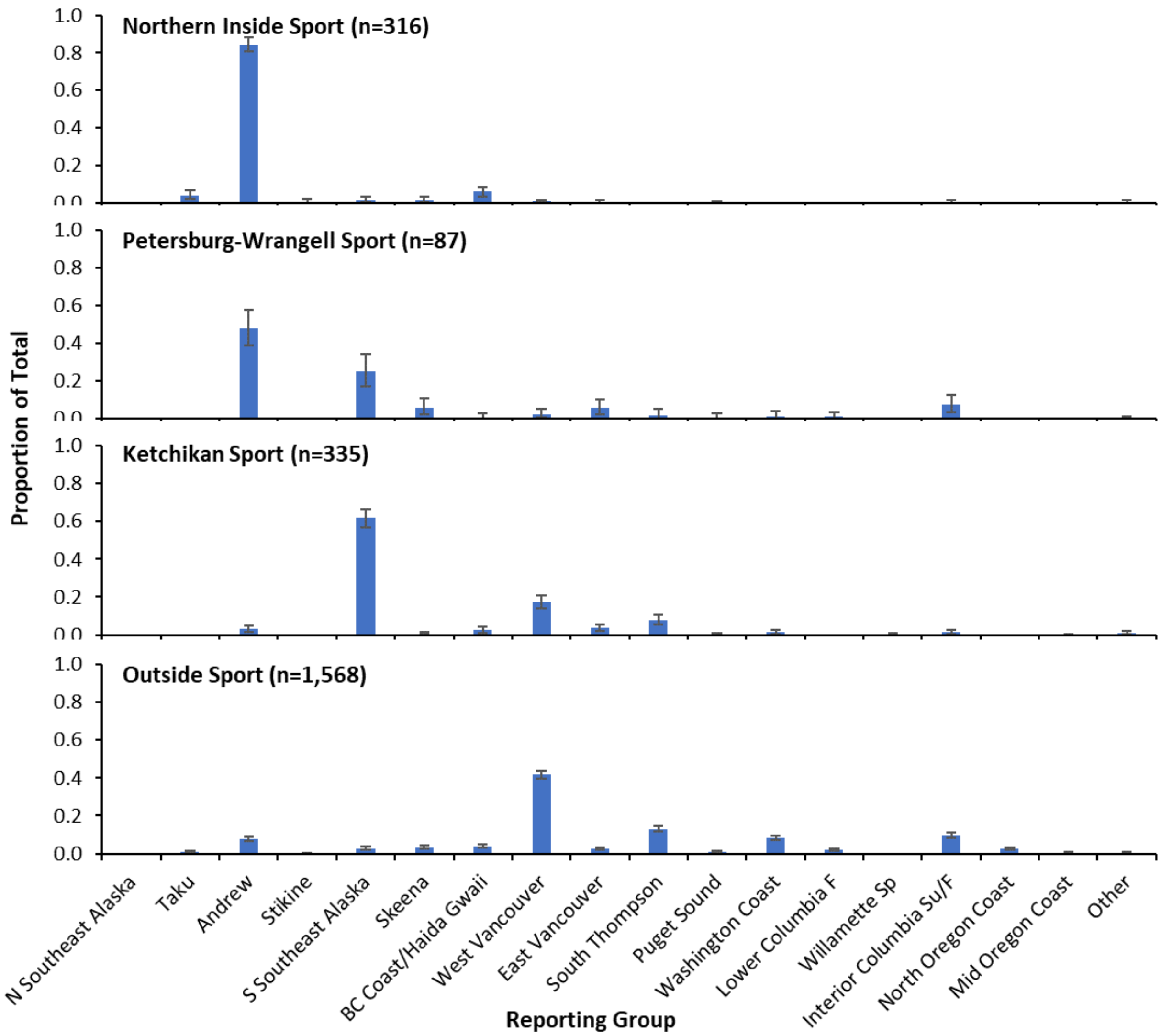

Figure 3. Estimated proportional contributions of a subset of 18 reporting groups of Chinook salmon to the harvest during the Southeast Alaska sport fisheries in AY 2019. Minor contributing reporting groups are combined into an *Other* group for ease of interpretation.

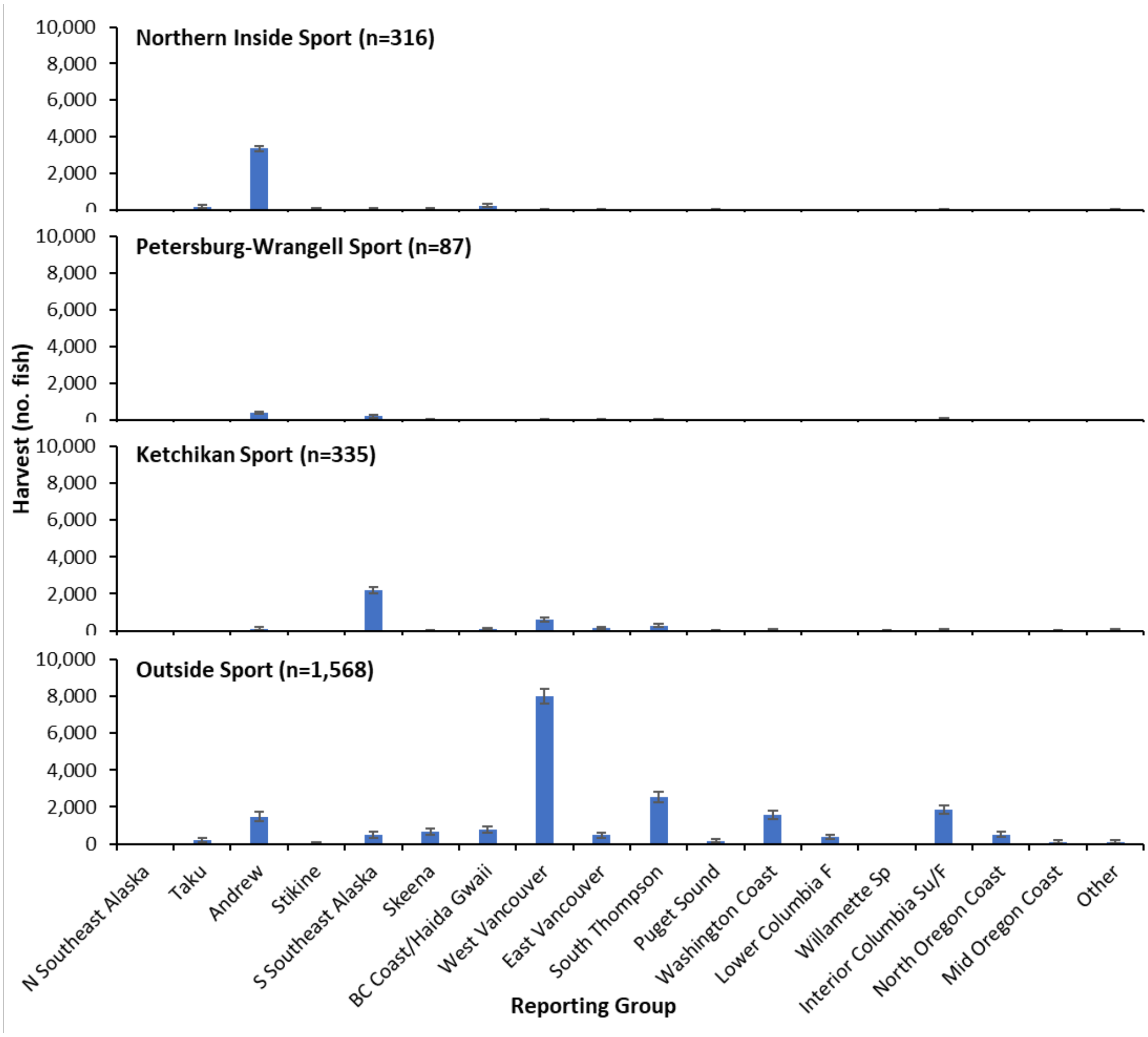

Figure 4. Harvest numbers of a subset of 18 reporting groups of Chinook salmon to the harvest during the Southeast Alaska sport fisheries in AY 2019. Minor contributing reporting groups are combined into an *Other* group for ease of interpretation. *Note* the y-axis scale is different from Figure 2.

Evaluation:

We accomplished the following:

- A total of 12,222 fish were sampled and 7,152 fish were genotyped from Southeast Alaska sport and commercial Chinook fisheries in 2019.
- All samples from were assayed for genotypes for the 13 microsatellite loci and quality control procedures revealed a low rate of inconsistencies.
- Mixture analyses estimated the contributions of 18 reporting groups of CTC interest.
- Mixture analyses indicate considerable temporal and spatial variation in the compositions of troll and sport harvests within years and across years. Similar to AY 2018, largest contributors to the Southeast Alaska troll fisheries were from a very diverse group of driver stocks with *South Thompson*, *Interior Columbia River Su/Fa*, *Southeast Alaska/TBR*, *Oregon Coast*, and *West Vancouver Island* reporting groups each contributing >10% to the

annual harvest. The largest contributors to the Southeast Alaska sport fisheries were the *Southeast Alaska/TBR* and *West Vancouver Island* reporting groups, which accounted for over 60% of the annual harvest with *South Thompson* providing ~10% of the annual harvest.

Project Products:
Results from this project have been presented to ADF&G management staff and have been made available to bilateral PSC committees and panels. A multi-year report published in the ADF&G Fishery Data Series is expected in 2021.

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