

PSC Northern Fund Final Report

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Project Title: Mixed Stock Analysis of US Districts 108 and 111 Chinook Salmon Fisheries 2018

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Abstract:

The Stikine and Taku rivers in Southeast Alaska support Chinook salmon runs important for various commercial, sport, and aboriginal fisheries in both Alaska and Canada. This project continues the use of genetic stock identification (GSI) of Chinook salmon harvested in the 2018 commercial gillnet and sport fisheries in Districts 108 and 111 by screening 13 microsatellite genetic markers in 412 salmon. The mixed stock analysis results indicated that commercial and sport fisheries in Districts 108 and 111 largely targeted enhanced Andrew Creek Chinook salmon and mostly avoided wild-origin Taku and Stikine Chinook salmon. In the District 108 commercial gillnet fishery, less than 1% of the Chinook salmon harvest was of wild-origin Stikine fish. In the District 111 commercial gillnet fishery, ~12% of the Chinook salmon harvest was of wild-origin Taku fish with the remainder comprised of enhanced Andrew Creek fish. In the District 111 sport fishery, 99% of the Chinook salmon harvest was of enhanced Andrew Creek fish. There was no sport fishery in District 108 during the TBR reporting period. Overall these results show that management actions were largely successful in focusing harvest of enhanced Chinook salmon and avoiding harvest of wild-origin TBR stocks.

Introduction:

The Stikine and Taku rivers in Southeast Alaska (SEAK) support Chinook salmon runs important for various commercial, aboriginal, and recreational fisheries in both the United States (U.S.) and Canada. Included in these are U.S. commercial gillnet fisheries in Alaskan Districts 108 and 111, as well as sport fisheries near Wrangell, Petersburg, and Juneau. U.S. fisheries in these areas harvest stocks of Chinook salmon bound for SEAK and for tributaries in the transboundary Stikine and Taku rivers. Catches of Stikine and Taku river Chinook salmon stocks are subject to a harvest sharing agreement, in which the U.S. and Canada are each given an Allowable Catch (AC) according to provisions outlined in the Transboundary Annex (Annex IV) of the Pacific Salmon Treaty (PST). Allowable catches are specified by the Pacific Salmon Commission (PSC) and rely on catch, escapement, recruitment information, and stock composition estimates to forecast indices of abundance in PST fisheries.

Until 2006, stock composition of harvests was estimated primarily using coded-wire tags, however, only a small portion of the out-migrating Chinook salmon are annually coded wire tagged leading to subsequent harvest estimates that lack the level of precision needed for management. Genetic stock identification (GSI) provides a complementary set of accurate, precise, and reliable

stock composition estimates necessary to meet the needs of the abundance-based management regime for Chinook salmon in these fisheries. Since 1999, GSI has been successfully used to estimate the composition of the commercial troll fishery harvest (Crane et al. 2000; Gilk-Baumer et al. 2013; Templin et al. 2011), gillnet and seine harvest (e.g. Gilk-Baumer and Carlile 2012), and sport fishery harvests (Gilk-Baumer et al. in prep). In addition, the Transboundary Technical Committee has been using GSI estimates from Districts 108 and 111 for post-season analyses calculating harvest-share estimates for more than five years.

This project extended GSI of Chinook salmon harvested in drift gillnet fisheries and sport fisheries in Districts 108 and 111 through 2018. These data are also used to determine Chinook salmon exclusions from the all-gear limits in place for the SEAK AABM fishery, and to estimate actual contributions of above-border Stikine and Taku Chinook salmon to the sport and commercial fisheries in Districts 108 and 111. This project addresses Goal 1 of the Northern Fund: “Development of improved information for resource management, including better stock assessment, data acquisition and improved understanding of limiting factors affecting salmon production in the freshwater and marine environments.”

Objectives:

The objective of this project was to estimate the stock composition of Southeast Alaska Chinook salmon fisheries in Districts 108 and 111 in 2018 such that the estimates are within 10% of the true value 90% of the time. This will be accomplished through the following tasks:

- Representatively sampling of Chinook salmon from commercial and sport fishery harvests relevant to Annex IV, Chapter 1 (Transboundary Rivers) of the Pacific Salmon Treaty.
 - Commercial gillnet fisheries – sample large fish ($MEF \geq 660\text{mm}$) harvests from the commercial drift gillnet fisheries operating in Districts 108 and 111 between statistical weeks 1729, 2018.
 - Sport fishery – sample large fish ($MEF \geq 660\text{mm}$) harvests from the sport fishery in Districts 108 and 111 between statistical weeks 1729, 2018.
- Assay up to 800 individuals for genotypes from sampled Chinook salmon at the loci in the current PSC baseline of genetic markers.
- Estimate the relative stock contributions of above-border Stikine and Taku Chinook salmon to the sport and commercial fisheries in Districts 108 and 111.

Approach:

Fishery Sampling

Chinook salmon were collected from commercial gillnet landings at processors in Southeast Alaska, and in the sport fishery by onboard participants and by creel census samplers. During sampling, Chinook salmon were selected without regard to size, sex, adipose fin-clip, or position in the hold. Axillary process tissue was dissected from sampled fish and dried onto Whatman paper. Along with each individual sampled, matched information was recorded such as size, sex, date, vessel, and age (from scale samples). At the end of the fishery, samples were transported back to the ADF&G Gene Conservation Laboratory, Anchorage, for analysis. Associated data is archived as part of the ASL database maintained by ADF&G.

Representative tissue collections of individuals for mixture analysis was created by subsampling up to 800 large (≥ 660 mm mid-eye-to-fork length) individuals harvested between statistical weeks

17–29 from the collected samples. Because the PST applies to large Chinook salmon for transboundary management, only large Chinook salmon were included in the analysis. Target mixture sample sizes was 200 individuals per mixture 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 stratum. Sample sizes smaller than the target were analyzed, but strata represented by fewer than 100 individuals would be pooled into larger groups for analysis. Since directed Chinook salmon gillnet fisheries did not occur in 2018, commercial fishery samples were obtained by sampling Chinook salmon caught incidentally in sockeye gillnet fisheries in Districts 108 and 111.

Laboratory Analysis

Samples were assayed for DNA loci developed by the Genetic Analysis of Pacific Salmon (GAPS) group funded by the Pacific Salmon Commission (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 was extracted from fin and muscle tissue and the polymerase chain reaction (PCR) was used to label 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 of the PSC. The data collected were individual genotypes for each locus. Genotype data are stored in an Oracle database (LOKI) on a network drive maintained by ADF&G computer services.

Mixture Analysis

Stock composition estimates for stock groups were generated using the BAYES (Pella and Masuda 2001) software package. The estimation was run using five chains without thinning with MCMC sample sizes of 40,000. Inference was based on the combined distributions of the last 20,000 samples of each chain. We defined prior parameters for each stock group to be equal to results from the corresponding estimates generated for the 2017 fisheries, with the prior for each stock group subsequently divided equally to populations within that stock group. Individual population or stock estimates were calculated and then summed into reporting regions. The mean of the regional compositions in the posterior distribution were reported as the best estimate and the 90% credibility intervals for all group contribution estimates were computed from the posterior distribution. The goal was to report estimates that fall within the precision and accuracy guidelines set by the TTC in April 2013 (to estimate the proportions of stocks within 10% of the true mixture proportions 90% of the time).

A total of 3 seasonal stock composition estimates were made for the 2018 fisheries.

Results/Findings:

Fishery sampling

A total of 412 Chinook salmon were sampled in districts 108 and 111 commercial gillnet and sport fisheries. In District 108 114 fish were sampled in the commercial gillnet fishery and 0 fish were sampled in the sport fishery during the treaty period. In district 111 101 fish were sampled in the commercial gillnet fishery and 193 were sampled in the sport fishery.

Laboratory analyses

Of the 412 total samples collected in District 108 and 111 commercial gillnet and sport fisheries, all samples were genotyped at 13 microsatellite genetic markers. During quality control procedures a total of 34 samples were reanalyzed at all 13 markers for a total of 442 comparisons. The average failure rate was ~4%. No inconsistencies were found across all comparisons. During quality assurance procedures, a total of 20 fish were removed due to incomplete genotypes, leaving a total of 392 fish for final mixture analysis (Table 1).

Mixture analysis

Mixtures of fish representing catches by fishery and district were analyzed. Stock composition estimates can be found in Table 2. All estimates meet the minimum criteria for precision and accuracy accepted by the Pacific Salmon Commission (PSC) Transboundary Technical Committee (within 10% of the true mixture 90% of the time).

The largest component of each fishery mixture was Andrew Creek-origin fish, almost all of which are likely enhanced (i.e. hatchery-origin). The only fishery that had a stock composition of wild-origin TBR fish > 1% was the District 111 commercial gillnet fishery (Taku ~12%).

Evaluation:

We accomplished the following:

- A total of 412 samples were collected from large (> 600mm MEF) Chinook harvested between statistical week 17–29 in commercial gillnet and sport fisheries in District 108 and 111.
- All 412 samples from were assayed for genotypes for the 13 microsatellite loci and quality control procedures revealed a low rate of inconsistencies. The genotypes for 392 samples were used in mixture analysis.
- Mixture analyses estimated the contributions of 5 reporting groups including Taku, Andrew (mostly hatchery-origin), Stikine, Southern Southeast Alaska (SSEAK), and Other.
- Mixture analyses estimate the seasonal stock composition for the District 108 commercial gillnet fishery and the District 111 commercial gillnet and sport fisheries.
- Results will be incorporated into harvest estimates for PST purposes by the Transboundary Technical Committee (TTC *in prep*).

Project Products:

Results from this project have been presented both to ADF&G Commercial Fisheries management staff and to the bilateral PSC Transboundary Technical Committee.

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Table 1. Sample sizes for each mixture indicating the number of fish genotyped and samples removed in the quality assurance process (missing > 20% of genotypes or duplicate individuals).

District	Fishery	Sample Size			Final
		Genotyped	Missing	Duplicate	
108	Gillnet	118	4	0	114
108	Sport	0	0	0	0
111	Gillnet	101	1	0	100
111	Sport	193	15	0	178

Table 2. Stock composition for each mixture the mean estimate, standard deviation and 90% credibility interval (Lo = 5% and Hi = 95%).

District	Fishery	Sample Size		5 Reporting Groups				
				Taku	Andrew	Stikine	SSEAK	Other
108	Gillnet	114	Estimate	0.002	0.821	0.005	0.166	0.007
			SD	0.006	0.043	0.014	0.042	0.011
			Lo	0.000	0.747	0.000	0.101	0.000
			Hi	0.013	0.887	0.034	0.238	0.030
111	Gillnet	100	Estimate	0.117	0.849	0.000	0.007	0.026
			SD	0.038	0.042	0.002	0.013	0.017
			Lo	0.061	0.776	0.000	0.000	0.005
			Hi	0.184	0.913	0.000	0.036	0.059
111	Sport	178	Estimate	0.007	0.987	0.000	0.000	0.006
			SD	0.010	0.012	0.002	0.001	0.006
			Lo	0.000	0.962	0.000	0.000	0.000
			Hi	0.029	1.000	0.000	0.000	0.018