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Final Report

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Project Title: Mixed stock analysis of U.S. Districts 108 and 111 Chinook fisheries, 2017

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Abstract:
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. This project continued the use of genetic stock identification (GSI) of Chinook salmon harvested in directed drift gillnet fisheries and sport fisheries in Districts 108 and 111 in 2017 by screening 13 microsatellite genetic markers in 634 salmon. Mixed stock analysis results indicated that the stock composition of commercial and sport fisheries in districts 108 and 111 varied by fishery. The District 108 directed gillnet fishery and District 111 sport fishery primarily targeted enhanced Andrew Creek Chinook salmon (92% and 96%, respectively). The District 108 sport fishery harvested a variety of stocks, but was also dominated by enhanced Andrew Creek fish (31%) as well as stocks originating outside the region (29%). There were insufficient samples to generate an estimate for District 111 gillnet fisheries in 2017.

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, 2017a, 2017b; Templin et al. 2011), gillnet and seine harvest (e.g. Gilk-Baumer and Carlile 2012), and sport fishery harvests (Gilk-Baumer et al. 2017c). 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 directed drift gillnet fisheries and sport fisheries in districts 108 and 111 through 2017. 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.

Objectives:

The objective of this project is to estimate the stock composition of Southeast Alaska Chinook salmon fisheries in districts 108 and 111 in 2017 such that the estimates are within 10% of the true value 90% of the time. This was accomplished through the following tasks:

- Representatively sample Chinook salmon from commercial and sport fishery harvests relevant to Annex IV, Chapter 1 (Transboundary Rivers) of the Pacific Salmon Treaty.
  - Directed fisheries – sample harvests from the commercial drift gillnet fisheries operating in Districts 108 and 111 between May and August 2017.
  - Sport fishery – sample the sport fishery harvests in districts 108 and 111 between April and August 2017.
- Assay up to 1,600 individual 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 SEAK, and in the sport fishery by onboard participants and by creel census samplers. 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 placed in alcohol in 2ml cryovials. Along with each individual sampled, basic information was recorded such as size, sex, date, vessel, and age (from scale samples). At the end of the fisheries, genetic samples were transported back to the ADF&G Gene Conservation Laboratory, Anchorage for analysis. Associated data was archived as part of the ASL database maintained by ADF&G.

Representative tissue collections of individuals for mixture analysis were 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, only large Chinook salmon were included in the analysis. Target mixture sample sizes will be 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 always 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. Because directed gillnet fisheries

did not occur in 2017, commercial fishery samples were obtained by sampling Chinook salmon caught incidentally in sockeye salmon 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 Treaty 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 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 of the PSC. The data collected was individual genotypes for each locus. Genotype data are stored in an *Oracle* database (*LOKI*) on a network drive maintained by ADF&G computer services.

Several measures were implemented to ensure the quality of data produced.

I. Sample sheets which contain information for each plate of extracted DNA (95 individuals per plate) in the lab were created in a standard format. Once DNA was extracted a file was created containing sample information for each well on that plate. This sample sheet followed the plate through all phases of a project, minimizing the risk of misidentification of samples through human error.
II. Genotypes were assigned to individuals using a system in which two observers scored the genotype data. Discrepancies between the scores were then resolved with one of three possible outcomes: 1) one score was accepted and the other rejected, 2) both scores were rejected and the score was blanked, or 3) the sample was rerun.
III. Approximately 8% of the individuals, 8 samples from every 95 individuals per extraction plate, were reanalyzed for all loci. This ensured that the data are reproducible and any errors created from the processing of individual plates were corrected.

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 2016 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 2017 fisheries: District 108 gillnet, District 108 sport, and District 111 sport. Insufficient samples were obtained from

Chinook salmon collected in the District 111 sockeye gillnet fisheries to produce an estimate within the precision and accuracy guidelines specified by the TTC.

Results/Findings:

Fishery sampling

A total of 634 Chinook salmon were sampled in districts 108 and 111 commercial and sport fisheries. In District 108, 253 fish were sampled as part of the commercial sockeye gillnet fishery and 182 fish were sampled in the sport fishery during the treaty period. In District 111, 51 Chinook salmon were sampled in the commercial sockeye gillnet fishery and 148 were sampled in the sport fishery.

Laboratory analyses

Of the samples collected in districts 108 and 111 commercial gillnet and sport fisheries, all samples were genotyped at 13 microsatellite genetic markers. During quality control procedures a total of 68 samples were reanalyzed at all 13 markers for a total of 884 comparisons. The average failure rate was ~3.8%. No inconsistencies were found across all comparisons.

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), except for the District 111 gillnet fishery. This estimate was not provided.

Mixture composition varied by fishery and location (Table 2). The largest component of the District 108 directed gillnet fishery and District 111 sport fishery was the *Andrew* reporting group (92% and 96%, respectively), almost all of which are likely enhanced (i.e. hatchery-origin). In contrast, both the *Andrew* and *Other* reporting groups were large contributors to the District 108 sport fishery ((31% and 29%, respectively). Also important in this fishery were the *Southern Southeast Alaska (SSEAK)* and *Stikine* reporting groups (19% and 17%, respectively). Insufficient samples were available to provide estimates for the District 111 gillnet fishery.

Evaluation:

We accomplished the following:

- A total of 634 samples were collected from large (> 600mm MEF) Chinook harvested between statistical week 17–29 in commercial gillnet, troll, and sport fisheries in Districts 108 and 111.
- 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 5 reporting groups including *Taku*, *Andrew* (mostly hatchery-origin), *Stikine*, *SSEAK*, and *Other*.
- Mixture analyses estimate the seasonal stock composition for the District 108 commercial gillnet and troll fisheries, the District 108 sport fishery, and the District 111 sport fishery. Insufficient samples were collected to generate an estimate for the District 111 commercial gillnet fishery.

- Results were incorporated into harvest estimates for PST purposes by the Transboundary Technical Committee (TTC 2019).

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. A multi-year report published in the ADF&G Fishery Data Series is expected in 2020.

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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).

		Sample Size			
District	Fishery	Genotyped	Missing	Duplicate	Final
108	Gillnet	253	7	0	246
108	Sport	182	0	0	182
111	Gillnet	51	3	0	48
111	Sport	148	1	0	147

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

				5 Reporting Groups				
District	Fishery	Sample Size		*Taku*	*Andrew*	*Stikine*	*SSEAK*	*Other*
108	Gillnet	246	Estimate	0.001	0.917	0.007	0.074	0.001
			SD	0.004	0.023	0.009	0.022	0.003
			Lo	0.000	0.876	0.000	0.041	0.000
			Hi	0.007	0.952	0.026	0.112	0.004
108	Sport	182	Estimate	0.038	0.312	0.173	0.185	0.291
			SD	0.036	0.042	0.047	0.046	0.043
			Lo	0.000	0.244	0.096	0.116	0.220
			Hi	0.106	0.383	0.251	0.268	0.361
111	Sport	147	Estimate	0.030	0.955	0.000	0.000	0.014
			SD	0.017	0.020	0.003	0.001	0.010
			Lo	0.008	0.919	0.000	0.000	0.002
			Hi	0.062	0.983	0.000	0.000	0.032