Genetic Stock Identification of Pilot Station Chinook Salmon, 2017

Project No. URE-92-17

by

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Abstract

Knowledge of the inseason stock of origin, age, sex, and length of Chinook salmon early in their travel upriver is important for making well informed management decisions. Due to the variability in Chinook salmon runs, management actions, and harvest, annual monitoring of the inseason Chinook salmon run is needed. The objective of this study was to obtain inseason genetic stock composition information and age, sex, and length data from the test fishery at Pilot Station sonar, located in the lower portion of the Yukon River. The data generated from this project are important to assist managers in meeting treaty obligations as outlined in the Yukon River Salmon Agreement between the U.S. and Canada. A total of 613 Chinook salmon were sampled from the test fishery in 2017. The proportion of the sample by strata that was of Canadian-origin ranged from 41% in strata 4 to 49% in strata 2; and about 44% of the total Chinook salmon caught at Pilot Station test fishery was of Canadian-origin. The age, sex, and length composition of the harvest was 0.4% age-3, 9.0% age-4, 53.2% age-5, 35.1% age-6, 2.3% age-7, 52.8% female, and an average of 754 mm in length.

Introduction

Effective management of Yukon River Chinook salmon (*Oncorhynchus tshawytscha*) stocks originating from Canada requires an understanding of the stock composition of the run as it enters the river. Canadian-origin Chinook salmon migrate through approximately 1,900 kilometers of fisheries in the Alaska portion of the drainage. The Alaska Department of Fish and Game (ADF&G) manages harvest of Yukon River Chinook salmon to achieve spawning escapement goals which have been established to ensure sustained yields, for subsistence and other uses. In addition, ADF&G manages the Canadian-origin component of the total run to achieve the Alaska-Yukon border spawning objective plus the midpoint of the Canadian guideline harvest range as defined in the Yukon River Salmon Agreement between U.S. and Canada. An estimate of the Canadian-origin Chinook salmon run strength and migration timing is vital to ensuring appropriate management actions are taken to meet border escapement objectives. This project improves management of Yukon River Chinook salmon by providing inseason estimates of stock composition of Chinook salmon migrating past the mainstem sonar project near Pilot Station in the lower portion of the Yukon River during distinct pulses and contributes to the estimates of total run abundance post-season. The ADF&G Gene Conservation Laboratory (GCL) creates inseason stock composition estimates using genotypes of samples from the sonar project test fishery in mixed stock analysis (MSA).

Genetic MSA of samples from the mainstem sonar project near Pilot Station provides fishery managers an important "first look" at the Canadian-origin Chinook salmon run strength and timing before those fish migrate through the majority of Alaska fisheries. No other assessment project along the Alaska portion of the drainage directly assesses the Canadian-origin stock of the Chinook salmon run on the Yukon River except the mainstem sonar project near the border at Eagle. Without genetic MSA at the mainstem sonar project near Pilot Station, fishery managers lack clear indication of Canadian-origin run strength and timing until fish arrive at Eagle, when the majority of the run has already passed through 1,900 kilometers of fisheries. Knowledge of Canadian-origin Chinook salmon run strength and timing early in the run and lower in the river allows more appropriate and timely management actions to ensure escapement and harvest sharing objectives will be met in a given year.

The baseline of allele frequencies for Chinook salmon populations has evolved over the past several years to include 42 SNPs (Table 1) genotyped in 36 populations (Table 2) throughout the Yukon River drainage. This baseline allows 5 reporting groups to be identified in mixture samples when sample sizes are at least 200 fish. The baseline has been tested using proof tests. In these tests, the genotype data from 200 fish are removed from the baseline, and the stock composition

of this test mixture sample is estimated using the baseline of remaining fish. This test was repeated five times using a random set of individuals drawn from five reporting groups in proportion to what has been historically observed in Pilot Station test fisheries.

Genetic MSA has been conducted since 2005 on the Yukon River and has provided essential information to fishery managers inseason. Due to statewide budget reductions for ADF&G in 2016, there are no funds for further genetic analysis on the Yukon; therefore, this was the second year seeking R&E funding to continue providing essential data for effective inseason management. While historical data could be used to estimate the stock composition of the run each year, inter-annual shifts in stock composition result in inaccurate inseason estimates of Canadian-origin Chinook salmon run strength and timing when assuming historical stock proportions. It is critical to have an annual inseason tool that assesses the Canadian-origin Chinook salmon stock lower in the river in order to most effectively manage this complex fishery for escapement objectives. Furthermore, knowledge of the stock-specific passage of groups of populations on the Alaska side of the Yukon River, combined with estimates of stock-specific harvest in subsistence fisheries (R&E Project No. URE-03-17), may permit the reconstruction of the return to these groups where other means of assessment are not available. As such the ability to estimate stock-specific passage for Alaska groups of populations of Chinook salmon provides additional value when sample sizes and accuracy and precision permit.

Objectives

The objective of this study was as follows:

1) Estimate the inseason pulse stock composition and post season total run stock composition of Yukon River Chinook salmon at Pilot Station such that estimates of 20 percent or greater have a coefficient of variation (CV) of 20 percent or less.

2) Estimate the age, sex and length composition of Yukon River Chinook salmon at Pilot Station.

Study Area

The Yukon River watershed exceeds 855,000 km^2, is the fourth largest drainage basin in North America, and discharges over 200 km^3 of water per year into the Bering Sea (Brabets et al. 2000). As the longest river in Alaska, the distance between the mouths of the Yukon River to its headwaters in British Columbia, Canada is more than 3,000 km. All five species of Pacific salmon *Oncorhynchus* spp. enter the Yukon River to spawn each year. Genetic tissue samples were collected at the sonar project near Pilot Station, approximately 200 river kilometers inland (Figure 1).

Methods

Fishery Sampling

Sample collection occurred in District 2 in the test fishery at the mainstem sonar project near Pilot Station (Figure 1). The test fishery was used to apportion sonar counts by species and used a suite of 8 gillnet mesh sizes, ranging from 2.75 inch to 8.5 inch stretch mesh, designed to be representative of the entire run of Chinook salmon that passed upriver from the sonar site. Axillary process tissue samples and age sex length (ASL) data were collected in proportion to Chinook salmon passage as estimated by the sonar. Due to the nature of the test fishery, samples are collected in proportion to passage rate. Samples were self-weighted because as test fish catches increase, passage at the sonar also increases and vice versa. All Chinook salmon caught in the test fishery were sampled and expected to adequately represent the Chinook salmon run passing the sonar during each pulse.

Samples were collected using the following protocol:

- Sex was determined by visual inspection as all fish were released alive whenever possible.
- Length was measured from mid-eye to fork of tail (to the nearest mm) using a rigid meter stick.
- Three scales were collected from the left side of the fish, 2-3 rows of scales above the lateral line, and mounted on pre-printed gum cards.
- One axillary process was clipped from each fish and placed in an individual vial with ethanol alcohol.
- Data sheets were used to record sampler name, mesh size, date, fish number, scale card number, sex, length, and genetic vial number for each sample.

All data and samples were shipped to ADF&G for processing. ADF&G staff determined the age of samples from scale pattern analysis using standard methods (Eaton, 2015) and recorded them using European notation (Koo 1962).

For inseason analyses, samples were stratified to represent distinct pulses of Chinook salmon passing the test fishery and analyzed promptly to inform inseason management decisions. Pulses were identified by increases in catch per unit effort (CPUE) for a sustained period of 3 to 5 days followed by a substantial decrease in CPUE. A stratum was identified when pulses were grouped together or to include samples before, between or after pulses in order to obtain the necessary sample size. Samples were flown to the ADF&G Gene Conservation Laboratory (GCL) in Anchorage, analyzed and reported to fishery managers within 36 hours of receipt at the GCL.

Laboratory Analysis

Genetic data was collected from the fishery samples as individual multi-locus genotypes for 42 SNPs (Table 1) following a well-established protocol. These markers have been used by ADF&G for Yukon Chinook projects since 2004 (DeCovich and Templin 2009; DeCovich and Howard 2010, 2011; Templin et al. 2006a, 2006b, 2006c). Genomic DNA was extracted using a NucleoSpin® 96 Tissue Kit by Macherey-Nagel (Düren, Germany). Chinook salmon samples were genotyped for selected SNPs using Taqman chemistry. Genotypic data is stored in an Oracle database (LOKI) on a network drive maintained by ADF&G computer services.

Genotypic data collected by this study was subject to several quality control checks. Prior to MSA, we conducted two statistical quality control analyses to ensure that only quality genotypic data were included in the estimation of stock compositions. First, we excluded individuals missing genotypes for 20% or more of loci, because these individuals likely have poor-quality DNA. The inclusion of individuals with poor-quality DNA could introduce genotyping errors and reduce the accuracy and precision of MSA. Second, individuals identified with duplicate genotypes were removed from further analyses. The individual with the most missing data from each duplicate pair was removed. Laboratory quality control measures included postseason reanalysis of 8% of each collection for all markers to ensure that genotypes were reproducible and to identify laboratory errors and measure rates of inconsistencies during repeated analyses.

Mixed Stock Analysis

Stock compositions of fishery mixtures was estimated using the program BAYES (Pella and Masuda 2001). The Bayesian method of MSA estimates the proportion of stocks caught within each fishery using four pieces of information: 1) a baseline of allele frequencies for each population, 2) the grouping of populations into the reporting groups desired for MSA, 3) prior information about the stock proportions of the fishery, and 4) the genotypes of fish sampled from the fishery.

For each fishery mixture, five independent Markov Chain Monte Carlo (MCMC) chains of 40,000 iterations were run with different starting values and the first 20,000 iterations were discarded to remove the influence of the initial start values. Gelman-Rubin shrink factors were computed for all stock groups in BAYES to assess among-chain convergence (Gelman and Rubin 1992). If a shrink factor for any stock group in a mixture was greater than 1.2, the mixture was reanalyzed with 80,000 iterations. The last 20,000 iterations of each of the five chains was combined to form the posterior distribution and tabulated means, 90% credibility intervals, and standard deviations from a total of 100,000 iterations.

Stock-Specific Passage

Estimates of stock-specific passage by the Pilot Station sonar counter for each reporting group (y) and time stratum (t) were derived by applying the stock-specific composition proportions ($p_{t,y}$) to the stratum passage (E_t).

$$E_{t,y} = p_{t,y} E_t$$

The estimate ($\hat{E}_{t,y}$) and distribution of stock-specific passage were obtained by Monte Carlo simulation. Here, K = 100,000 independent realizations (i) of the reporting group-specific passage ($E_{t,y}^{(i)}$) drawn randomly from the joint distribution of the passage ($E_t^{(i)}$) and stock composition ($p_{t,y}^{(i)}$) for each stratum

$$E_{t,y}^{(i)} = p_{t,y}^{(i)} E_t^{(i)}$$

$$\hat{E}_{t,y} = median\ of\ the\ K\ observations\ of\ E_{t,y}^{(i)}.$$

The 90% credibility interval (CI) was determined by 5th and 95th quantiles of the K observations of ($E_{t,y}^{(i)}$). The median, 90% CI, mean, SD and CV of the stock-specific passage were estimated directly from K observations of ($E_{t,y}^{(i)}$).

Generation of stock-specific passage distributions required an estimate of the distribution of each component. The distributions of the stock compositions ($p_{t,y}^{(i)}$) were the Bayesian posterior distributions of stock proportions from the mixed stock analysis described above. Passage and associated uncertainty was estimated from sonar counts.

Stock composition estimates were reported for 3 hierarchical levels when sample sizes were larger than 200 as follows: 1) country of origin (U.S and Canada), 2) broad scale (Lower Yukon, Middle Yukon, and Canada), and 3) fine scale (Lower Yukon, Koyukuk, Tanana, Upper U.S. Yukon, and Canada). When sample sizes were smaller than 200, only the first 2 levels of the hierarchy were reported. Primarily, this study focused on the country-of-origin reporting group, as this was most crucial for managing to achieve treaty objectives. Broad-scale and fine-scale estimates were given when sample sizes were sufficient.

Assumptions

1. Samples collected at Pilot station are representative of all stocks passing the sonar.

2. The ASL and stock compositions of samples were a function of the passage rate, gear, and time.

Results

A total of 613 Chinook salmon were sampled from various gillnet mesh sizes over four strata starting May 31 through August 11 (Table 3). The number of samples obtained per stratum ranged from 103 in stratum one to 210 in stratum four.

Age, sex, and length were successfully determined for 547 (89%) of the Chinook salmon sampled. The ASL composition of the Pilot Station sonar Chinook salmon in the test fishery varied among strata and gear (Tables 4 and 5). Overall ASL composition of the sampled fish was 0.4% age-3, 9.0% age-4, 53.2% age-5, 35.1% age-6, 2.3% age-7, 52.8% female, and an average of 754 mm in length (Table 4). Age by mesh size ranged from an average of 4.0 years old in the 5.00-inch stretch mesh gillnets to 5.5 years old in the 8.5-inch stretch mesh gillnets and fish length tended to increase with mesh size (Table 5).

Genetic MSA was successfully completed using 586 (96%) of the samples collected in 2017 (Table 3). Chinook salmon that passed Pilot Station from May 31 to June 13 (first stratum) were estimated to be 43% Canadian-origin, based on 99 samples. The first stratum represented early run fish and the first pulse of Chinook salmon. Chinook salmon that passed Pilot Station from June 14 to June 20 (second stratum) were estimated to be 49% Canadian-origin, based on 180 samples collected during the second pulse. Chinook salmon that passed from June 21 to June 25 were estimated to be 43% Canadian-origin, based on 115 samples collected during the third pulse. Finally, the proportion of Chinook salmon that passed from June 26 to August 11 were estimated to be 41% Canadian-origin based on 192 samples which represented the fourth pulse and late run fish. Across all strata, roughly 44% of the Chinook salmon sampled in the test fishery were of Canadian-origin.

The weighted estimate of Canadian-origin Chinook salmon based on genetic MSA of fish sampled in the test fishery and passage by strata at the sonar project near Pilot Station was approximately 115,917 fish (90% interval 103,402-128,229; Table 6). Stratum one estimated passage at the sonar was 30,088 Chinook salmon and the weighted Canadian-origin passage was estimated to be 12,857 fish. Stratum two estimated passage was 79,913 Chinook salmon and the weighted Canadian-origin passage was estimated to be 39,929 fish. Stratum three estimated passage was 69,392 Chinook salmon and the weighted Canadian-origin passage was estimated to be 30,121 fish. Stratum four estimated passage was 83,621 Chinook salmon and the weighted Canadian-origin passage was estimated to be 34,008 fish.

Discussion

This study's sampling design was developed in the context of both the representativeness of samples and the effect of sample size on the accuracy and precision of estimates. Precision and accuracy of stock composition estimates are affected primarily by sample sizes of mixtures and the representativeness of the genetic baseline. The Yukon River Panel's Joint Technical Committee's (JTC) Subcommittee on Stock Identification recommended specific criteria for the precision and accuracy of stock composition estimates used for the management of Yukon River Chinook salmon. The JTC recommended that stock composition estimates of 20 percent or greater have a coefficient of variation of 20% or less and if estimator performance is to be assessed using simulation techniques, it was recommended that the Relative Root Mean Squared Error (RRMSE) be 20% or less ("JTC 20/20 recommendation"; JTC 1997). The baseline used by this study met these criteria for Chinook salmon when samples sizes were adequate. The ability of a genetic baseline to discriminate stocks in MSA was critical to the success of this project. Similar criteria are also used for genetic MSA studies on trans-boundary rivers in southeast Alaska and British Columbia.

The objective of this project was to estimate stock-specific passage both inseason by pulse and post-season for the year, particularly of Canadian-origin Chinook salmon. We achieved sample sizes greater than 100 in three of four strata (sample from stratum 1 was 99 fish) and reported country of origin estimates inseason. However, since ~600 samples were used for annual estimates, here we report stock composition estimates for all strata incorporated into annual estimates to the three broad-scale groups. This resulted in not following the JTC 20/20 recommendation in Stratum 3, where 22.9% of the catch was Lower Yukon and the CV was 23% (Table 6). Despite sample sizes below 200 in other strata, the JTC 20/20 recommendation was met because the only estimates with CV's exceeding 20% were below 20% of the mixture (Table 6).

The genetic MSA estimate of Canadian-origin Chinook salmon was larger than the official estimate of 92,622, which is the sum of the estimated Canadian spawning escapement, the U.S. harvest of Canadian-origin Chinook salmon and the Canadian harvest. (JTC 2018). The official estimate was more similar to, but still less than, the lower bound of the 90% confidence interval (103,402-128,229) based on MSA of Pilot Station passage. One possible explanation for overestimating the number of Chinook salmon based on genetics is the large passage of summer chum salmon past the Pilot station sonar in 2017. The Yukon summer chum salmon run in 2017 was the largest since 2006 (JTC 2018) and the third largest since 1995. Even a small misallocation of summer chum salmon to Chinook salmon based on catches in the test fishery would result in an overestimation of Chinook salmon at the Pilot station sonar.

Findings from this study apply directly to implementation of the US/Canada Yukon River Salmon Agreement management regime as outlined in Appendix 2 of Chapter 8 of the Pacific Salmon Treaty. Genetic MSA of samples from the mainstem sonar project near Pilot Station provided fishery managers an important early indicator of the Canadian-origin Chinook salmon run strength and timing before those fish migrated through the majority of Alaska fisheries. Knowing the Canadian-origin Chinook salmon run strength and timing early in the run and near the mouth of the river allowed for more informed and timely management actions to ensure escapement and harvest sharing objectives were met.

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Tables and Figures

Table 1. Single nucleotide polymorphism (SNP) markers used for this study.

Locus	Source
GTH2B-550	GAPs locus
NOD1	GAPs locus
Ots_E2-275	Smith et al. 2005a
Ots_arf-188	Smith et al. 2005a
Ots_AsnRS-60	Smith et al. 2005a
Ots_ETIF1A	GAPs locus
Ots_FARSLA-220	Smith et al. 2007
Ots_FGF6A	Unpublished
Ots_GH2	Smith et al. 2005b
Ots_GPDH-338	Smith et al. 2005a
Ots_GPH-318	Smith et al. 2007
Ots_GST-207	Smith et al. 2007
Ots_hnRNPL-533	Smith et al. 2007
Ots_HSP90B-100	Smith et al. 2007
Ots_IGF-I.1-76	Smith et al. 2005a
Ots_Ikaros-250	Smith et al. 2005a
Ots_il-1racp-166	Smith et al. 2005a
Ots_LEI-292	Smith et al. 2007
Ots_MHC1	Smith et al. 2005b
Ots_MHC2	Smith et al. 2005b
Ots_ZNF330-181	Smith et al. 2005a
Ots_LWSop-638	Smith et al. 2005a
Ots_SWS1op-182	Smith et al. 2005a
Ots_P450	Smith et al. 2005b
Ots_P53	Smith et al. 2005b
Ots_Prl2	Smith et al. 2005b
Ots_ins-115	Smith et al. 2005a
Ots_SClkF2R2-135	Smith et al. 2005a
Ots_SERPC1-209	Smith et al. 2007
Ots_RFC2-558	Smith et al. 2005a
Ots_SL	Smith et al. 2005b
Ots_TAPBP	GAPs locus
Ots_Tnsf	Smith et al. 2005b
Ots_u202-161	Smith et al. 2005a
Ots_u211-85	Smith et al. 2005a
Ots_U212-158	Smith et al. 2005a
Ots_u4-92	Smith et al. 2005a
Ots_u6-75	Smith et al. 2005a
Ots_Zp3b-215	Smith et al. 2005a
RAG3	GAPs locus
S7-1	GAPs locus
unkn526	GAPs locus

Table 2. Chinook salmon collections from the Yukon River drainage organized hierarchically into reporting groups for genetic mixed stock analysis.

Country	Broad scale	Fine scale	Population	Year(s)	Sample size
U.S.					
	Lower Yukon				
		Lower Yukon			
			Andreafsky River	2003	202
			Anvik River	2007	58
			Nulato River	2012	51
			Kateel River	2002, 2008, 2012	174
			Gisasa River	2001	78
			Tozitna River	2002, 2003	278
	Middle Yukon				
		Middle Yukon			
			S. Fork Koyukuk River	2003	49
			Henshaw Creek	2001, 2007	180
			Kantishna River	2005	187
			Chatanika River	2001, 2007	43
			Chena River	2001	176
			Salcha River	2005	188
			Goodpaster River	2006, 2007, 2011	79
		Upper U.S. Yukon			
			Beaver Creek	1997	91
			Chandalar River	2002, 2003, 2004	162
			Sheenjek River	2002, 2004, 2006, 2011	69
Canada			Colleen River	2011	24
	Canada				
		Canada			
			Kandik River	2007, 2008, 2009, 2010, 2011	56
			Chandindu River	2001	146
			Klondike River	2001, 2003, 2007, 2010, 2011	144
			Porcupine River - Old Crow	2007	127
			Stewart River	1997, 2007	102
			Mayo River	1997, 2003, 2011	72
			Pelly River	1996, 1997	107
			Blind Creek	2003, 2007, 2008	218
			Tin Cup Creek	2003, 2009, 2010, 2011	132
			Mainstem at Minto	2007	97
			Tatchun Creek	1987, 1997, 2002, 2003	160
			Nordenskiold River	2003	55
			Little Salmon	1987, 1997, 2007, 2010	237
			Big Salmon	1987, 1997, 2007	176
			Nisutlin River	1987, 1997	55
			Teslin River	2007, 2009, 2010, 2011	198
			Morley River	1997, 2002, 2003, 2009, 2010	46
			Takhini River	1997, 2003	96
			Whitehorse Hatchery	1985, 1987, 1997, 2010	303
					4616

Table 3. Number of Chinook salmon sampled (N) by strata and the number and percent (%) of those samples that were successfully used for genetics and ASL composition estimation, 2017.

Strata	Dates	N	Genetics		ASL	
			Processed	Percent	Processed	Percent
1	5/31 - 6/13	103	99	96.1	79	76.7
2	6/14 - 6/20	183	180	98.4	167	91.3
3	6/21 - 6/25	117	115	98.3	109	93.2
4	6/26 - 8/11	210	192	91.4	192	91.4
Total	5/31 - 8/11	613	586	95.6	547	89.2

Table 4. Age, sex, and length (mm) composition of Yukon River Chinook salmon sampled in the Pilot Station sonar test fishery, 2017.

Strata	Brood Year	2015	2014	2013	2013	2012	2012	2011	2011	
	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	Total
May 31 - June 13	Male n	0	5	21	0	8	0	0	2	36
	Female n	0	2	28	0	11	1	0	1	43
	Total n	0	7	49	0	19	1	0	3	79
	Male %	0.0	6.3	26.6	0.0	10.1	0.0	0.0	2.5	45.6
	Female %	0.0	2.5	35.4	0.0	13.9	1.3	0.0	1.3	54.4
	Total %	0.0	8.9	62.0	0.0	24.1	1.3	0.0	3.8	100.0
	Male Mean Length		581	744		829			858	746
	Min of Length		542	612		718			790	542
	Max of Length		614	843		955			925	955
	SD		34	60		72			95	98
	n	0	5	21	0	8	0	0	2	36
	Female Mean Length		604	747		831	728		874	764
	Min of Length		595	650		754	728		874	595
	Max of Length		612	860		898	728		874	898
	SD		12	58		55				76
	n	0	2	28	0	11	1	0	1	43
Strata	Brood Year	2015	2014	2013	2013	2012	2012	2011	2011	
	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	Total
June 14 - June 20	Male n	0	11	47	0	21	0	0	1	80
	Female n	0	3	49	0	33	1	0	1	87
	Total n	0	14	96	0	54	1	0	2	167
	Male %	0.0	6.6	28.1	0.0	12.6	0.0	0.0	0.6	47.9
	Female %	0.0	1.8	29.3	0.0	19.8	0.6	0.0	0.6	52.1
	Total %	0.0	8.4	57.5	0.0	32.3	0.6	0.0	1.2	100.0
	Male Mean Length		596	747		824			788	747
	Min of Length		550	545		624			788	545
	Max of Length		640	840		956			788	956
	SD		30	59		73				91
	n	0	11	47	0	21	0	0	1	80
	Female Mean Length		616	767		817	737		786	781
	Min of Length		572	630		690	737		786	572
	Max of Length		668	887		947	737		786	947
	SD		48	55		76				74
	n	0	3	49	0	33	1	0	1	87

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Table 4. Page 2 of 3.

Strata	Brood Year Age	2015 1.1	2014 1.2	2013 1.3	2013 2.2	2012 1.4	2012 2.3	2011 1.5	2011 2.4	Total
June 21 - June 25	Male n	0	4	31	0	14	0		2	51
	Female n	0		20	0	35	0	1	2	58
	Total n	0	4	51	0	49	0	1	4	109
	Male %	0.0	3.7	28.4	0.0	12.8	0.0	0.0	1.8	46.8
	Female %	0.0	0.0	18.3	0.0	32.1	0.0	0.9	1.8	53.2
	Total %	0.0	3.7	46.8	0.0	45.0	0.0	0.9	3.7	100.0
	Male Mean Length		581	740		757			845	724
	Min of Length		550	598		537			821	537
	Max of Length		606	833		892			868	892
	SD		28	58		91			33	86
	n	0	4	20	0	14	0	0	2	51
	Female Mean Length			740		811		979	804	789
	Min of Length			598		712		979	794	598
	Max of Length			833		915		979	813	979
	SD			58		47			13	65
	n	0	0	20	0	35	0	1	2	58

Strata	Brood Year Age	2015 1.1	2014 1.2	2013 1.3	2013 2.2	2012 1.4	2012 2.3	2011 1.5	2011 2.4	Total
June 26 - August 11	Male n	2	22	42	1	23	1	0	0	91
	Female n	0	2	52	0	46	0	0	1	101
	Total n	2	24	94	1	69	1	0	1	192
	Male %	1.0	11.5	21.9	0.5	12.0	0.5	0.0	0.0	47.4
	Female %	0.0	1.0	27.1	0.0	24.0	0.0	0.0	0.5	52.6
	Total %	1.0	12.5	49.0	0.5	35.9	0.5	0.0	0.5	100.0
	Male Mean Length	395	584	711		777	700			690
	Min of Length	390	495	616		525	700			390
	Max of Length	400	795	800		891	700			891
	SD	7	64	45		81	0			102
	n	2	22	42	0	23	1	0	0	90
	Female Mean Length		616	770		811			768	786
	Min of Length		582	645		709			768	582
	Max of Length		650	900		900			768	900
	SD		48	55		54				62
	n	0	2	52		46	0	0	1	101

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Strata	Brood Year	2015	2014	2013	2013	2011	2011	2011	2011	
	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	Total
Total	Male n	2	42	141	1	66		1	5	258
	Female n		7	149		125	1	2	5	289
	Total n	2	49	290	1	191	1	3	10	547
	Male %	0.4	7.7	25.8	0.2	12.1	0.0	0.2	0.9	47.2
	Female %	0.0	1.3	27.2	0.0	22.9	0.2	0.4	0.9	52.8
	Total %	0.4	9.0	53.0	0.2	34.9	0.2	0.5	1.8	100.0
	Male Mean Length	395	587	730		794	700		838	722
	Min of Length	390	495	545		525	700		788	390
	Max of Length	400	795	843		956	700		925	956
	SD	7	50	59		83			58	98
	n	2	42	141	0	66	1	0	5	257
	Female Mean Length		612	761		814	733	979	807	782
	Min of Length		572	598		690	728	979	768	572
	Max of Length		668	900		947	737	979	874	979
	SD		35	57		59	6		41	69
	n	0	7	149	0	125	2	1	5	289

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Table 5. Total number of samples (N), mean length (mm) with standard deviation (SD), mean age with standard deviation (SD), and percent female (%) for Chinook salmon caught in test drift gillnets, by mesh size, 2017.

Mesh	N	Length	SD	Age	SD	Percent Female
2.75	8	701	78.0	4.8	0.5	45.5
4.00	36	715	130.4	5.2	0.9	40.0
5.00	3	575	22.7	4.0	0.0	33.3
5.25	28	702	94.1	4.8	0.7	43.3
5.75	2	709	0.7	5.5	0.7	50.0
6.50	127	733	92.1	5.2	0.7	48.3
7.50	234	769	71.5	5.4	0.6	53.1
8.50	109	784	81.0	5.5	0.6	58.1
Total	547	754	88.9	5.3	0.7	51.4

Table 6. Yukon River, Pilot Station sonar estimates by strata of stock composition (%) and stock-specific passage (number of fish) including median, 90% credibility interval, the probability that the group estimate is equal to zero (P=0), mean, standard deviation (SD) and coefficient of variation (CV), May 30-August 11, 2017. Note that annual estimates of stock-specific passage are weighted by and incorporate uncertainty associated with each stratum-specific passage estimate.

| Strata Dates | | Stock Composition | | | | | | | Stock-specific Passage | | | | |
| | | | 90% CI | | | | | | | 90% CI | | | |
and Sample Size	Reporting Group	Median	5%	95%	P=0	Mean	SD	CV	Median	5%	95%	Mean	SD
Stratum 1	Lower Yukon	0.3	0	5	0.09	1.2	1.8	150%	88	0	1,510	352	540
5/31-6/13	Middle Yukon	55.9	40.2	72.9	0	56.1	10	18%	16,818	12,095	21,928	16,879	3,008
N:99	Canada	42.9	26.1	58.6	0	42.7	9.9	23%	12,902	7,862	17,619	12,857	2,983
											Total	30,088	
Stratum 2	Lower Yukon	9.6	5.5	14.9	0	9.8	2.9	30%	7,688	4,409	11,905	7,861	2,293
6/14-6/20	Middle Yukon	41.3	32.9	50.4	0	41.4	5.3	13%	33,025	26,315	40,300	33,123	4,236
N:180	Canada	48.8	40.1	57.1	0	48.7	5.2	11%	39,013	32,028	45,605	38,929	4,121
											Total	79,913	
Stratum 3	Lower Yukon	22.9	14.8	32.4	0	23.2	5.4	23%	15,918	10,297	22,512	16,087	3,726
6/21-6/25	Middle Yukon	33.2	23.4	44.1	0	33.4	6.3	19%	23,050	16,221	30,610	23,184	4,376
N:115	Canada	43.4	33.6	53.3	0	43.4	6	14%	30,107	23,330	37,004	30,121	4,156
											Total	69,392	
Stratum 4	Lower Yukon	36.8	30.4	43.6	0	36.9	4	11%	30,795	25,428	36,466	30,853	3,351
6/26-8/11	Middle Yukon	22.3	16.8	28.6	0	22.4	3.6	16%	18,636	14,040	23,903	18,760	3,000
N:192	Canada	40.7	34	47.4	0	40.7	4.1	10%	33,996	28,449	39,624	34,008	3,393
											Total	83,621	
Total	Lower Yukon	20.9	17.3	24.9	0	21	2.3	11%	55,001	45,592	65,366	55,175	5,988
5/31-8/11	Middle Yukon	34.9	30.2	39.9	0	34.9	2.9	8%	91,747	79,463	104,943	91,922	7,746
N:586	Canada	44.1	39.3	48.8	0	44.1	2.9	7%	115,940	103,402	128,229	115,917	7,531
											Total	263,014	

Note: Stock composition means may not sum to 100% and stock-specific passage means may not sum to the total passage due to rounding error.
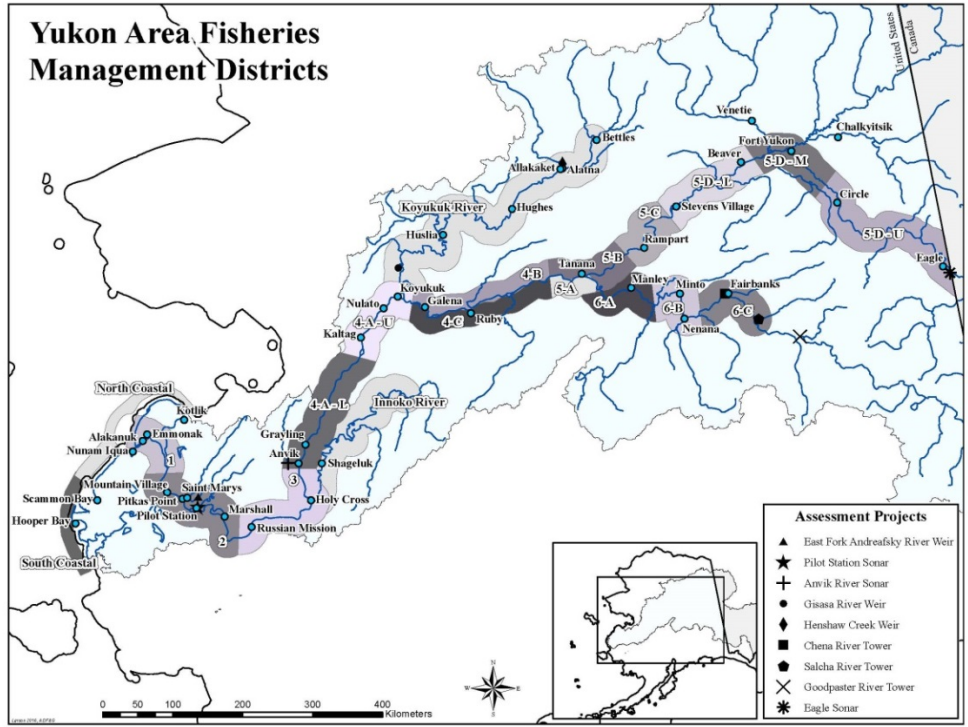
Figure 1. The Alaska portion of Yukon River with location of assessment projects and fishing districts.
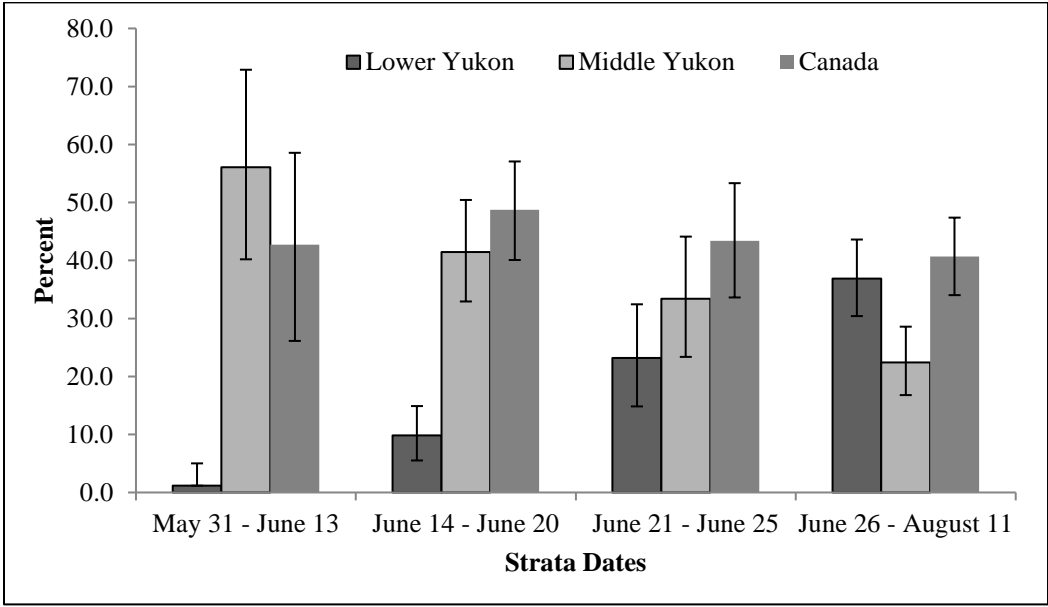

Figure 2. Results of the genetic MSA of Chinook salmon by stratum. Error bars represent 90% confidence intervals.
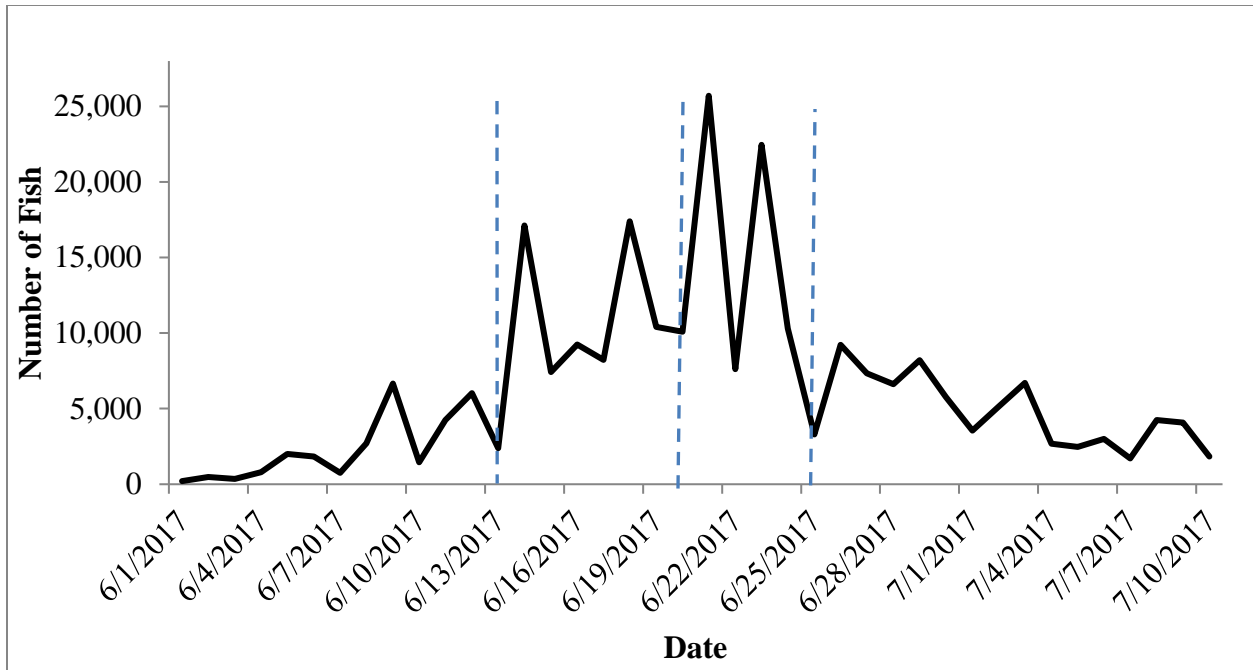
Figure 3. Daily Chinook salmon passage estimates at the sonar near Pilot Station, 2017. Dashed lines indicate breaks in Stratums.