

# Genetic Stock Identification of Pilot Station Chinook Salmon, 2018

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**Symbols and Abbreviations**  
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## ABSTRACT

Knowledge of the inseason stock of origin, age, sex, and length of Chinook salmon *Oncorhynchus tshawytscha* early in their migration up the Yukon River 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 564 Chinook salmon were sampled from the test fishery in 2018. The proportion of the sample by strata that was of Canadian-origin ranged from 29% in strata 4 to 53% in strata 1. About 42% of the total Chinook salmon caught at Pilot Station test fishery was of Canadian-origin. The age and sex composition of the test fishery catch was 0.8% age-3, 12.1% age-4, 49.6% age-5, 36.9% age-6, 0.6% age-7, and 48.2% female. Average length was 735 mm mid eye to tail fork.

Key words Chinook salmon *Oncorhynchus tshawytscha*, Yukon River, Pilot Station, genetic stock composition.

## 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 Interim Management Escapement Goal plus the Canadian harvest share as defined in the Yukon River Salmon Agreement between U.S. and Canada, as outlined in Appendix 2 of Chapter 8 of the Pacific Salmon Treaty. An estimate of the Canadian-origin Chinook salmon run strength and migration timing is vital to ensuring appropriate management actions are taken to meet Alaska-Canada border objectives. A sonar project near Pilot Station, in the lower portion of the Yukon River, provides a valuable platform for generating inseason and total run estimates of Chinook salmon stock composition. Inseason estimates of run size and stock composition are made for distinct pulses of Chinook salmon past the Pilot Station sonar, which are used to guide management. Pulses are identified by an increase in catch per unit effort (CPUE) for a sustained period of 3 to 5 days followed by a substantial decrease in CPUE. Postseason, analysis provides an estimate of stock composition and stock-specific abundance for the entire Chinook salmon run past the Pilot Station sonar.

The ADF&G Gene Conservation Laboratory (GCL) creates inseason stock composition estimates using genotypes of samples from the Pilot Station sonar project test fishery (PSTF) in genetic mixed stock analysis (MSA). This project provides fishery managers an important “first look” at the Canadian-origin Chinook salmon run strength and timing before those fish migrate through most Alaska fisheries. 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 a mainstem sonar project at Eagle, when most 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.

Genetic MSA requires a baseline of allele frequencies. The baseline for Chinook salmon populations in the Yukon River has evolved to include 42 single nucleotide polymorphisms (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. Because this sample size cannot always be met, 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 (CV) 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 has been tested using repeated fishery scenario tests where 200 fish were removed from the baseline in proportions expected in a fishery and then the stock composition of the test mixture was estimated with the baseline of remaining fish. These tests used proportions of 5 groups of populations typically observed in the Pilot Station Test Fishery (*Canada*=45.5%, *Upper U.S.*=5.5%, *Tanana*=21.5%, *Koyukuk*=2%, and *Lower Yukon*=25.5%) and had root mean square errors ranging from 1.0% to 1.7% (mean=1.4%; Alaska Department of Fish and Game, unpublished data).

This report was submitted to the Yukon River Panel in partial fulfillment of grant requirements of the Restoration and Enhancement (R&E) fund. This and past year project reports can be found on the YRP website<sup>1</sup>. Beginning in 2017, annual R&E reports were also published in the ADF&G RIR series to improve accessibility through the ADF&G publications database.

## OBJECTIVES

The objectives of this study were to:

- 1) Estimate the following using genetic MSA such that the estimates of 20% or greater have a coefficient of variation of 20% or less:
  - a. the inseason stock composition of pulses of the Yukon River Chinook salmon run at Pilot Station, and
  - b. the post season stock composition of the total run of Yukon River Chinook salmon at Pilot Station; and
- 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<sup>2</sup>, is the fourth largest drainage basin in North America, and discharges over 200 km<sup>3</sup> 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 5 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).

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<sup>1</sup> <https://www.yukonriverpanel.com/restoration-enhancement-fund/>

# 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 designed to apportion sonar counts by species, used a suite of 8 gillnet mesh sizes ranging from 2.75 inch to 8.5 inch stretch mesh, and was assumed to be representative of the entire run of Chinook salmon that passed upriver from the sonar site. All Chinook salmon caught in the test fishery were sampled. As such, genetic tissue (axillary process), age, sex, and length (ASL) samples were assumed to be collected in proportion to Chinook salmon passage, as estimated by the sonar. Samples were self-weighted because as test fish catches increase, passage at the sonar also increases and vice versa.

Samples were collected using the following protocol:

- Sex was determined by visual inspection of external secondary sexual characteristics. All fish were released alive whenever possible.
- Length was measured from mid eye to tail fork (to the nearest mm) using a rigid meter stick.
- From each fish, 3 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.
- From each fish, 1 axillary process was clipped and placed in an individual vial filled with ethanol.
- 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.

For inseason genetic analyses, samples were stratified to represent distinct pulses of Chinook salmon passing the test fishery and analyzed promptly to inform inseason management decisions. A stratum was identified when pulses were grouped together or to include samples before, between or after pulses to obtain the necessary sample size. Once collection for a stratum was completed, all data and samples were shipped to ADF&G in Anchorage 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). Samples sent to the ADF&G Gene Conservation Laboratory (GCL) in Anchorage were analyzed and results were 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 (DeCovich and Howard 2011). These markers have been used by ADF&G for Yukon Chinook projects since 2007 (DeCovich and Templin 2009; DeCovich and Howard 2010, 2011; Templin et al. 2006a, 2006b, 2006c). In short, genomic DNA was extracted using a NucleoSpin® 96 Tissue Kit by Macherey-Nagel (Düren, Germany). Chinook salmon samples were genotyped for 42 SNPs using Taqman chemistry. Genotypic data was stored in an Oracle database 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 2 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 were estimated using the program BAYES (Pella and Masuda 2001). The Bayesian method of MSA estimates the proportion of stocks caught within each fishery using 4 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, 5 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 5 chains was combined to form the posterior distribution and tabulated means, medians, 90% credibility intervals, standard deviations, the probability that the group estimate is equal to zero ( $P=0$ ), and CV from a total of 100,000 iterations.

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*; DeCovich and Howard 2011). When sample sizes were smaller than 200, only the first 2 levels of the hierarchy were reported (DeCovich and Howard 2011). Primarily, this study focused on the *Canada* 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.

## STOCK-SPECIFIC PASSAGE

Estimates of stock-specific passage by the Pilot Station sonar 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 ( $E_t$ ) such that  $E_{t,y} = p_{t,y}E_t$ . 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,  $E_{t,y}^{(i)} = p_{t,y}^{(i)}E_t^{(i)}$ . The distributions of the stock compositions ( $p_{t,y}^{(i)}$ ) were the Bayesian posterior distributions of stock proportions from the MSA described above. Passage was estimated from sonar counts.

The estimate ( $\hat{E}_{t,y}$ ) was determined by the median of the K observations of ( $E_{t,y}^{(i)}$ ). The 90% credibility interval (CI) was determined by 5<sup>th</sup> and 95<sup>th</sup> 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 ( $E_{t,y}^{(i)}$ ).

## 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 564 Chinook salmon were sampled from various gillnet mesh sizes over 4 strata starting June 2 through August 5 (Table 3, Figure 2). Strata were defined by area management and research biologists and resulted in a range of samples per stratum of 89 samples in stratum 1 to 196 in stratum 2.

Age, sex, and length were successfully determined for 512 (91%) of the Chinook salmon sampled. The ASL composition of Chinook salmon caught in the Pilot Station sonar test fishery varied among temporal strata and gillnet mesh size (Tables 4 and 5). Overall ASL composition of the sampled fish was 0.8% age-3, 12.1% age-4, 49.6% age-5, 36.9% age-6, 0.6% age-7, 48.2% female, and an average of 735 mm in length (Table 4). Age by mesh size ranged from an average of 4.0 years old in the 5.75-inch stretch mesh gillnets to 5.5 years old in the 8.50-inch stretch mesh gillnets and fish length tended to increase with mesh size (Table 5).

Genetic MSA was successfully completed using 553 (98%) of the samples collected at Pilot Station in 2018 (Table 3). Sample sizes for all individual strata were less than 200. Stock composition estimates were not provided for the fine scale reporting groups (1 of 3 hierarchical levels) due to insufficient sample sizes to meet the JTC 20/20 recommendation (JTC 1997). We provided estimates for country of origin and broad scale reporting groups, and all met the JTC 20/20 reporting guidelines for MSA (JTC 1997). Chinook salmon that passed Pilot Station from June 2 to June 13 (first stratum) were estimated to be 53% Canadian-origin, based on 97 samples (Table 6, Figure 3). 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 24 (second stratum) were estimated to be 46.8% Canadian-origin, based on 192 samples collected during the second pulse. Chinook salmon that passed from June 25 to July 3 (third stratum) were estimated to be 41% Canadian-origin, based on 175 samples collected during the third pulse. Finally, the proportion of Chinook salmon that passed from July 4 to August 5 (fourth stratum) were estimated to be 29% Canadian-origin based on 89 samples which represented the fourth pulse and late run fish. Across all strata, 42% of the Chinook salmon sampled in the test fishery were of Canadian-origin (Table 6, Figure 3).

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 67,609 fish (90% interval 56,154–79,365; Table 6). Stratum 1 estimated passage at the sonar was 16,275 Chinook salmon and the weighted Canadian-origin passage was estimated to be 8,621 fish (90% CI = 5,818–11,573). Stratum 2 estimated passage was 56,270 Chinook salmon and the weighted Canadian-



origin passage was estimated to be 26,357 fish (90% CI = 20,012–32,994). Stratum 3 estimated passage was 57,070 Chinook salmon and the weighted Canadian-origin passage was estimated to be 23,227 fish (90% CI = 16,667–30,222). Stratum 4 estimated passage was 32,216 Chinook salmon and the weighted Canadian-origin passage was estimated to be 9,402 fish (90% CI = 3,485–16,104).

## DISCUSSION

This study's sampling design was developed in the context of both the effect of sample size on the accuracy and precision of estimates and the representativeness of samples. Precision and accuracy of stock composition estimates are affected primarily by sample sizes of mixtures and the representativeness of the genetic baseline. 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.

The objective of this project was to estimate stock-specific passage both inseason by pulse and postseason for the year, particularly of Canadian-origin Chinook salmon. We achieved sample sizes greater than 100 in 2 of 4 strata (sample from stratum 1 was 97 fish and sample from stratum 4 was 89 fish) and reported country-of-origin estimates inseason. Although sample sizes were relatively low in 2019, we were able to meet JTC reporting recommendations requiring all estimates representing greater than 20% of the mixture to have CVs less than 20% (JTC 1997). Some estimates had CVs that approached the upper limit accepted for reporting by the JTC, such as in Stratum 1, where 42% of the sample was *Middle Yukon* with a CV of 20%, and in Stratum 4, where 29% of the sample was *Canada* and the CV was 20% (Table 6). In all cases where the CV was greater than 20%, the stock composition estimate was less than 20% (Table 6).

Genetic MSA provided a reasonable estimate of Canadian-origin Chinook salmon that past the Pilot station sonar in 2018. The genetic MSA estimate of 67,609 past Pilot combined with the approximate harvest of Canadian-origin Chinook of 3,200 below the sonar brought the total MSA estimate to approximately 70,800. The official JTC estimate of 76,530, which is the sum of the estimated Canadian spawning escapement, the U.S. harvest of Canadian-origin Chinook salmon and the Canadian harvest, was slightly larger but within the bounds of the 90% confidence interval (56,154–79,365) based on MSA of Pilot Station passage (JTC 2019, Table 6).

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 most Alaska fisheries. Knowing the run strength and timing of Canadian-origin Chinook salmon 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.

## ACKNOWLEDGEMENTS

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## **TABLES AND FIGURES**

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

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

<sup>a</sup> Locus developed for use in the Genetic Analysis of Pacific Salmonids program.

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

Reporting Groups		Population	Year(s) collected	Sample size
Country	Broad scale			
<i>U.S.</i>				
	<i>Lower Yukon</i>			
		<i>Lower Yukon</i>		
		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
	<i>Middle Yukon</i>			
		<i>Middle Yukon</i>		
		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
	<i>Upper U.S. Yukon</i>			
		Beaver Creek	1997	91
		Chandalar River	2002, 2003, 2004	162
		Sheenjek River	2002, 2004, 2006, 2011	69
		Colleen River	2011	24
<i>Canada</i>	<i>Canada</i>			
	<i>Canada</i>			
		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
				4,616

Table 3. Number of Chinook salmon sampled (N) at Pilot Station sonar by strata and the number and percent (%) of those samples successfully used for genetic MSA and ASL composition estimation, 2018.

Strata	Dates	N	Genetics		ASL	
			Processed	Percent	Processed	Percent
1	6/02 - 6/13	98	97	99.0	86	87.8
2	6/14 - 6/24	196	192	98.0	180	91.8
3	6/25 - 7/03	179	175	97.8	162	90.5
4	7/03 - 8/05	91	89	97.8	84	92.3
Total	6/02 - 8/05	564	553	98.0	512	90.8

Table 4. Age, sex, and length (mm) composition of Yukon River Chinook salmon sampled in the Pilot Station sonar test fishery, 2018.

Strata	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	Total
	Brood year	2016	2015	2014	2014	2013	2013	2012	2012	
June 2 - June 13	Male n	0	8	29	0	14	0	0	0	51
	Female n	0	2	13	0	20	0	0	0	35
	Total n	0	10	42	0	34	0	0	0	86
	Male %	0.0	9.3	33.7	0.0	16.3	0.0	0.0	0.0	59.3
	Female %	0.0	2.3	15.1	0.0	23.3	0.0	0.0	0.0	40.7
	Total %	0.0	11.6	48.8	0.0	39.5	0.0	0.0	0.0	100.0
	Male mean length		579	709		806				715
	Min of length		467	575		625				467
	Max of length		654	817		948				948
	SD		57	58		83				97
	n	0	8	29	0	14	0	0	0	51
	Female mean length		613	744		852				798
	Min of length		590	687		777				590
	Max of length		635	817		989				989
	SD		32	45		63				88
	n	0	2	13	0	20	0	0	0	35
June 14 - June 24	Male n	1	20	47	0	14	0	0	0	82
	Female n	0	4	39	0	54	0	1	0	98
	Total n	1	24	86	0	68	0	1	0	180
	Male %	0.6	11.1	26.1	0.0	7.8	0.0	0.0	0.0	45.6
	Female %	0.0	2.2	21.7	0.0	30.0	0.0	0.6	0.0	54.4
	Total %	0.6	13.3	47.8	0.0	37.8	0.0	0.6	0.0	100.0
	Male mean length	384	599	696		734				675
	Min of length	384	494	500		367				367
	Max of length	384	650	837		912				912
	SD		35	67		145				98
	n	1	20	47	0	14	0	0	0	82
	Female mean length		783	744		823		708		788
	Min of length		638	615		658		708		615
	Max of length		928	918		953		708		953
	SD		118	61		56				72
	n	0	4	39	0	54	0	1	0	98

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Table 4. Page 2 of 3.

Strata	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	Total
	Brood Year	2016	2015	2014	2014	2013	2013	2012	2012	
June 25 – July 3	Male n	1	12	49	2	16	1	0	0	81
	Female n	0	1	32	0	46	0	1	1	81
	Total n	1	13	81	2	62	1	1	1	162
	Male %	0.6	7.4	30.2	1.2	9.9	0.6	0.0	0.0	50.0
	Female %	0.0	0.6	19.8	0.0	28.4	0.0	0.6	0.6	50.0
	Total %	0.6	8.0	50.0	1.2	38.3	0.6	0.6	0.6	100.0
	Male mean length	377	579	696	587	756	713			684
	Min of length	377	485	610	494	640	713			377
	Max of length	377	645	776	680	850	713			850
	SD		57	50	132	57				83
	n	1	12	49	2	16	1	0	0	81
	Female mean length		660	730		828		848	853	787
	Min of length		660	632		713		848	853	632
	Max of length		660	817		917		848	853	917
	SD			40		48				67
	n	0	1	32	0	46	0	1	1	81
	July 4 - August 5	Male n	2	15	25	0	9	0	0	0
Female n		0	0	18	0	15	0	0	0	33
Total n		2	15	43	0	24	0	0	0	84
Male %		2.4	17.9	29.8	0.0	10.7	0.0	0.0	0.0	60.7
Female %		0.0	0.0	21.4	0.0	17.9	0.0	0.0	0.0	39.3
Total %		2.4	17.9	51.2	0.0	28.6	0.0	0.0	0.0	100.0
Male mean length		422	552	716		837				690
Min of length		405	443	647		674				390
Max of length		439	705	820		950				891
SD		24	66	43		73				102
n		2	15	25	0	9	0	0	0	90
Female mean length				746		804				772
Min of length				680		731				680
Max of length				817		878				878
SD				48		44				54
n		0	0	18	0	15	0	0	0	33

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Strata	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	Total
	Brood Year	2016	2015	2014	2014	2013	2013	2012	2012	
Total	Male n	4	55	150	2	53	1	0	0	265
	Female n	0	7	102	0	135	0	2	1	247
	Total n	4	62	252	2	188	1	2	1	512
	Male %	0.8	10.7	29.3	0.4	10.4	0.2	0.0	0.0	51.8
	Female %	0.0	1.4	19.9	0.0	26.4	0.0	0.4	0.2	48.2
	Total %	0.8	12.1	49.2	0.4	36.7	0.2	0.4	0.2	100.0
	Male mean length	401	579	702	587	777	713			686
	Min of length	377	443	500	494	367	713			367
	Max of length	439	705	837	680	950	713			950
	SD	28	55	57	132	101				100
	n	4	55	150	2	53	1	0	0	265
	Female mean length		717	740		827		778	853	787
	Min of length		590	615		658		708	853	590
	Max of length		928	918		989		848	853	989
	SD		119	51		54		99		71
	n	0	7	102	0	135	0	2	1	247

Note: ages are presented in European notation, where the number of years spent in fresh and saltwater is presented separated by a period. Total age is the sum of the 2 numbers plus 1, to account for time in the gravel.

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, 2018.

Mesh	N	Length		Age		Percent female
		Mean	SD	Mean	SD	
2.75	5	658	93	5.2	0.8	20.0
4.00	42	684	142	5.0	1.0	38.6
5.00	2	640	278	5.0	1.4	50.0
5.25	44	662	120	4.8	0.9	25.0
5.75	1	561		4.0		0.0
6.50	134	715	82	5.2	0.7	47.1
7.50	177	747	80	5.3	0.6	53.4
8.50	108	792	77	5.5	0.6	56.8
Total	513	734	99	5.2	0.7	48.4

Table 6. Stock composition (%) and stock-specific passage (number of fish) of Yukon River Chinook salmon at Pilot Station sonar by temporal strata. Median, mean, standard deviation (SD), and 90% credibility interval of the stock specific passage is shown. The probability that the group estimate is equal to zero (P=0), mean, median, standard deviation (SD) and coefficient of variation (CV, %) of the stock composition is shown. The number of samples (N) used to estimate stock composition is provided for each stratum.

Strata Dates and Sample Size	Reporting Group		Stock Composition							Stock-specific Passage				
			Median	90% CI		P=0	Mean	SD	CV	Median	90% CI		Mean	SD
				0.05	0.95						0.05	0.95		
Stratum 1 6/02-6/13 N:97	U.S.	Broad scale	46.7	34.2	61.0	0.00	47.0	8.1	17.3	7,535	5,103	10,575	7,654	1,677
		Lower Yukon	4.1	0.2	10.4	0.01	4.5	3.2	70.3	655	21	1,762	735	534
		Middle Yukon	42.2	29.3	57.0	0.00	42.5	8.4	19.7	6,833	4,468	9,902	6,918	1,655
	Canada	53.3	39.0	65.8	0.00	53.0	8.1	15.3	8,528	5,818	11,573	8,621	1,754	
												Total	16,275	
Stratum 2 6/14-6/24 N:192	U.S.	Broad scale	53.2	44.6	61.8	0.00	53.2	5.2	9.8	29,686	23,135	36,951	29,913	4,194
		Lower Yukon	11.4	6.9	16.9	0.00	11.6	3.0	26.1	6,366	3,737	9,791	6,523	1,854
		Middle Yukon	41.5	32.9	50.5	0.00	41.6	5.4	12.9	23,227	17,497	29,957	23,390	3,822
	Canada	46.8	38.2	55.4	0.00	46.8	5.2	11.2	26,088	20,012	32,994	26,357	3,965	
												Total	56,270	
Stratum 3 6/25-7/03 N:175	U.S.	Broad scale	59.4	51.8	66.6	0.00	59.3	4.5	7.6	33,732	25,515	42,872	33,843	5,237
		Lower Yukon	32.4	25.3	40.0	0.00	32.5	4.5	13.8	18,311	12,990	24,767	18,524	3,563
		Middle Yukon	26.7	19.3	34.8	0.00	26.8	4.7	17.6	15,083	10,084	21,467	15,319	3,471
	Canada	40.6	33.4	48.2	0.00	40.7	4.5	11.1	23,035	16,667	30,222	23,227	4,089	
												Total	57,070	
Stratum 4 7/04-8/05 N:89	U.S.	Broad scale	70.9	61.1	80.1	0.00	70.8	5.7	8.1	22,728	9,412	36,662	22,814	8,264
		Lower Yukon	61.5	52.0	70.6	0.00	61.4	5.7	9.2	19,486	8,095	32,106	19,781	7,316
		Middle Yukon	9.0	3.1	17.2	0.00	9.4	4.3	45.8	2,684	643	6,397	3,033	1,807
	Canada	29.1	19.9	38.9	0.00	29.2	5.7	19.7	9,034	3,485	16,104	9,402	3,871	
												Total	32,216	

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Strata dates and sample size	Reporting group		Stock composition							Stock-specific passage				
			Median	90% CI		<i>P</i> =0	Mean	SD	CV	Median	90% CI		Mean	SD
				0.05	0.95						0.05	0.95		
Total	U.S.	Broad scale	58.2	53.3	63.0	0.00	58.2	0.0	0.1	94,118	76,680	111,773	94,222	10,712
6/02-8/05		Lower Yukon	28.0	22.4	33.5	0.00	28.0	3.4	12.1	45,190	31,933	59,507	45,562	8,347
N:553		Middle Yukon	30.1	25.1	35.7	0.00	30.2	3.2	10.7	48,514	39,658	58,180	48,660	5,686
	Canada		41.8	36.8	46.8	0.00	41.8	3.0	7.2	67,206	56,154	79,365	67,609	7,071
													Total	161,831

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. Annual estimates of stock-specific passage are weighted by and incorporate uncertainty associated with each stratum-specific passage estimate.

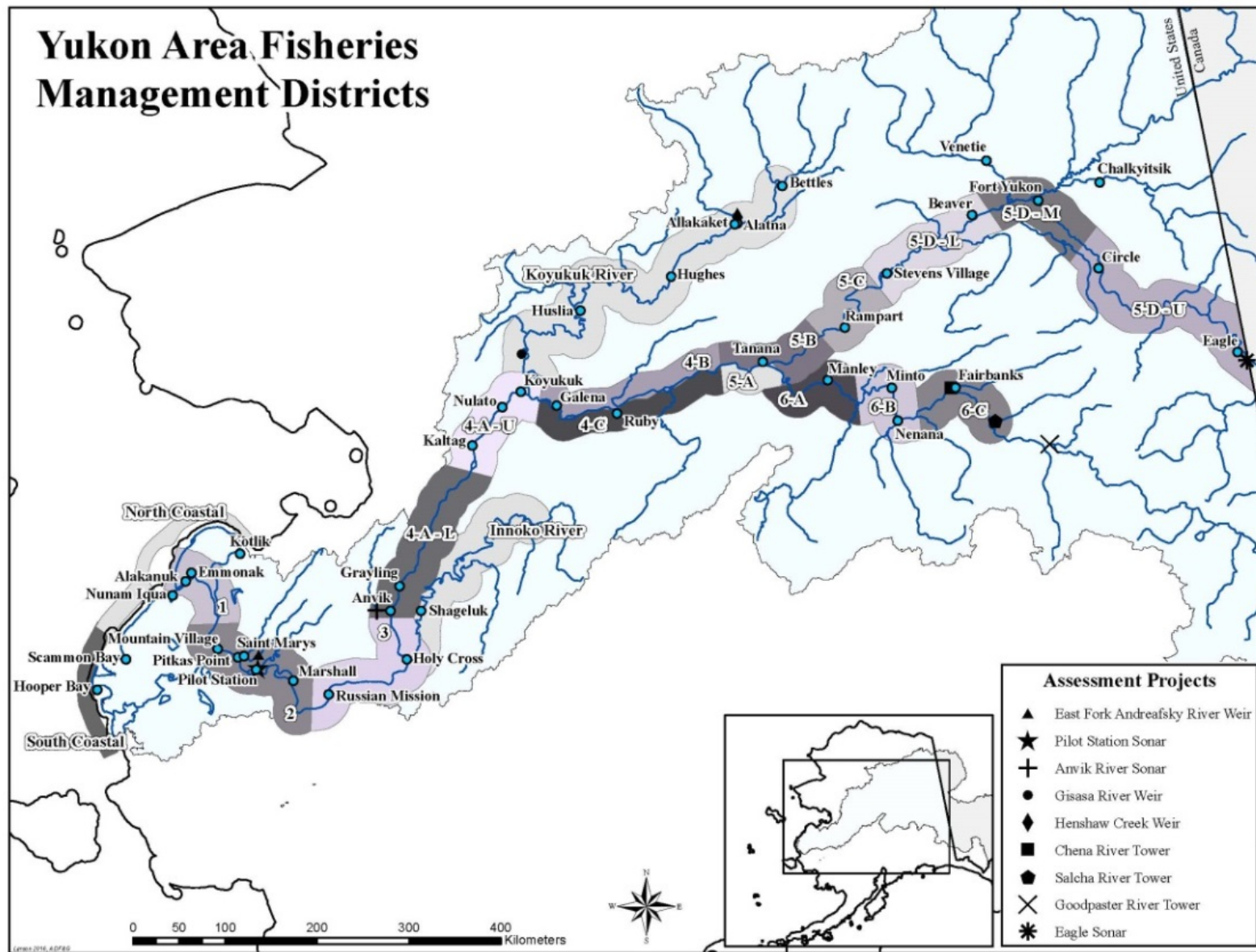


Figure 1. The Alaska portion of Yukon River with location of assessment projects and fishing districts.

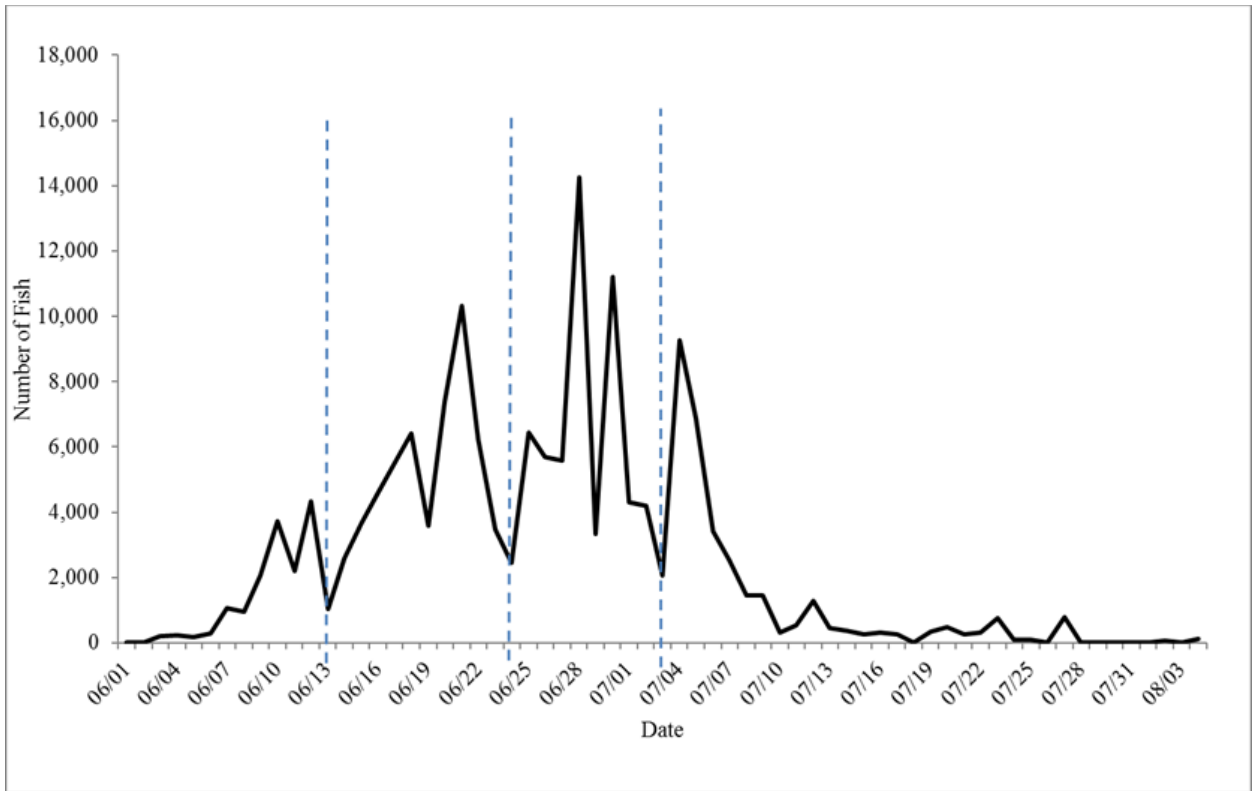


Figure 2. Daily Chinook salmon passage estimates at the sonar near Pilot Station, 2018. Dashed lines indicate breaks in Stratums.

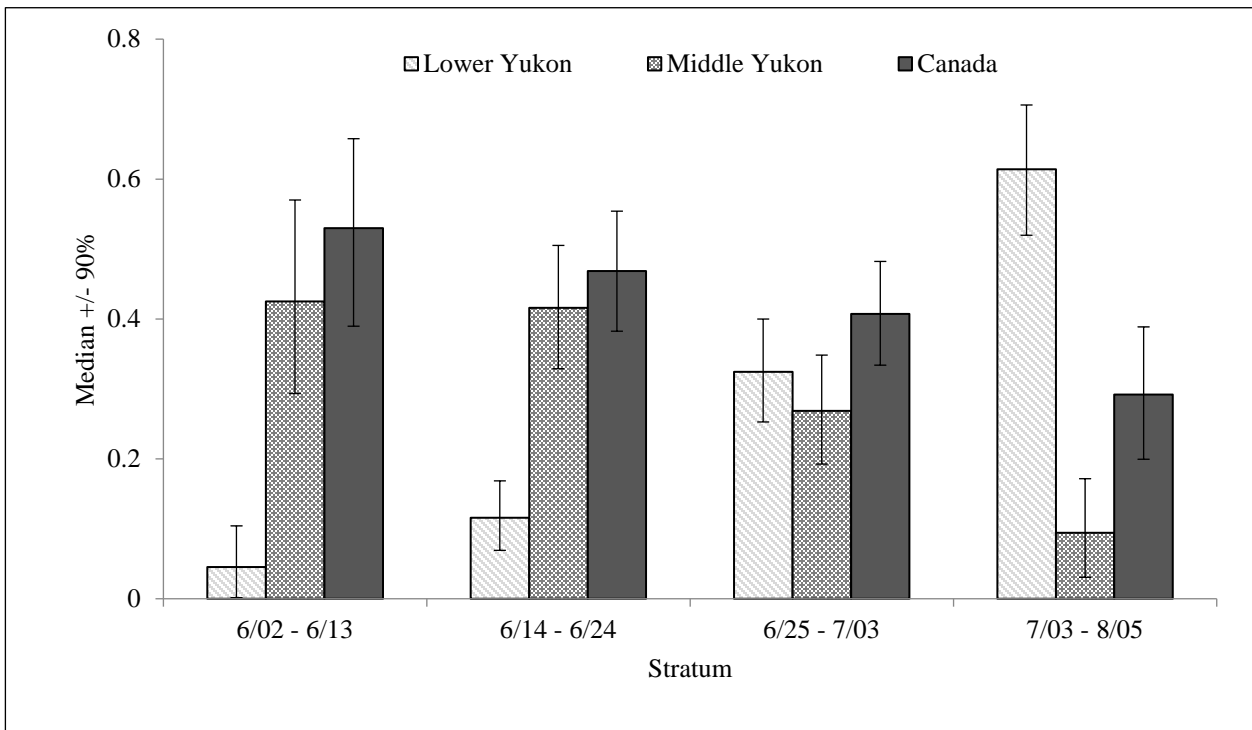


Figure 3. Stock composition (median and 90% credibility intervals) of Chinook salmon sampled from the 2018 Pilot Station test fishery by temporal stratum for 3 broad scale reporting groups.