

Genetic Stock Identification of Pilot Station Chinook Salmon, 2019

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ABSTRACT

The objective of this study was to obtain inseason Chinook salmon *Oncorhynchus tshawytscha* 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 managing annual Chinook salmon runs to meet escapement goals in Alaska and treaty obligations as outlined in the Yukon River Salmon Agreement between the U.S. and Canada. A total of 556 Chinook salmon were sampled and selected for genotyping from the test fishery in 2019. The proportion of the sample, by stratum, that was of Canadian-origin ranged from 36% in stratum 3 to 56% in stratum 1. About 45% 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 selected for genotyping was 0.4% age-3, 12.1% age-4, 46.0% age-5, 39.7% age-6, 1.7% age-7, and 49.2% female. Average length was 740 mm mid eye to tail fork.

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

INTRODUCTION

Effective management of Yukon River Chinook salmon *Oncorhynchus tshawytscha* stocks originating from Canada requires an understanding of the proportion of the total run of Yukon River Chinook salmon that is Canadian-origin near the mouth of the Yukon River before substantial inriver harvest occurs. 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 ensure 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 to generate 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. Post season, sample groupings by pulse can be evaluated in context of the entire run and stratified as needed to estimate stock composition estimates for each temporal stratum of the run and the total run past the sonar.

The ADF&G Gene Conservation Laboratory (GCL) uses genetic mixed stock analysis (MSA) methods to create inseason stock composition estimates using genotypes of samples from the Pilot Station sonar project test fishery (PSTF). 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 on the Alaska-Canada border, 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 each year. Postseason, analysis provides an estimate of stock composition and stock-specific abundance for the entire Chinook salmon run past the Pilot Station sonar.

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 (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% or greater have a coefficient of variation (CV) of 20% or less ("JTC 20/20 recommendation"; JTC 1997). Furthermore, if estimator performance is to be assessed using simulation techniques, the JTC recommended that the Relative Root Mean Squared Error (RRMSE) be 20% or less. 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 using 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%; data on file with the Division of Commercial Fisheries, Yukon Research Group, ADF&G, Anchorage).

This report was submitted to the Yukon River Panel (YRP) 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 website¹. 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 as follows:

- 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 selected for genetic MSA at Pilot Station.

STUDY AREA

The Yukon River watershed exceeds 855,000 km², is the fourth largest drainage basin in North America, and discharges over 200 km³ of water per year into the Bering Sea (Brabets et al. 2000). The distance between the mouths of the Yukon River in Alaska and 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. Chinook salmon were sampled at the sonar project near Pilot Station, Alaska, approximately 200 river kilometers inland (Figure 1).

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

METHODS

FISHERY SAMPLING

Sample collection occurred in the District 2 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) and 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:

- All sampled Chinook salmon were released alive whenever possible.
- Sex was determined by visual inspection of external secondary sexual characteristics.
- 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. Pulses were identified inseason by an increase in test fishery catch per unit effort and sonar-based estimates of passage for a sustained period of 3 to 5 days followed by a substantial decrease. Pulse timing was used to determine when to ship samples and associated data to the GCL in Anchorage. Genetic tissue samples sent to the GCL were analyzed and results were reported to fishery managers within 36 hours of receipt. Postseason, sample strata were evaluated in context of the total run. Sample groupings were re-stratified as needed to align with actual pulses, achieve minimum sample requirements, and account for any samples that were not run inseason. ADF&G staff determined the age of samples from scale pattern analysis using standard methods (Eaton, 2015) and recorded using European notation (Koo 1962).

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). Genomic DNA was extracted using a NucleoSpin® 96 Tissue Kit² 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.

² Product names used in this report are included for scientific completeness, but do not constitute a product endorsement.

Genotypic data collected in this study was subject to several quality control checks. Prior to MSA, 2 statistical quality control analyses were conducted to ensure that only quality genotypic data were included to estimate stock compositions using R (R Core Team 2019). Individuals missing genotypes for 20% or more of loci were removed because these individuals may have poor-quality DNA. The inclusion of individuals with poor-quality DNA could introduce genotyping errors and reduce the accuracy and precision of MSA. Then, individuals with duplicate genotypes were identified and 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, to identify laboratory errors, and to 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, 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: 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; Table 2). If sample sizes were smaller than 200 and estimates of stock proportions did not meet the JTC 20/20 recommendation, only the first 2 levels of the hierarchy were reported (DeCovich and Howard 2011). This study primarily focused on the Canada reporting group, because estimates of Canada stock proportions and stock-specific passage were 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 using sonar counts (Dreese and Lozori 2019). 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 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 ($E_{t,y}^{(i)}$).

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 844 Chinook salmon were sampled using various gillnet mesh sizes over 3 strata from June 2 through August 24 (Table 3, Figure 2). Strata were defined by ADF&G staff and resulted in a range of samples per stratum (176 samples in stratum 3 to 438 in stratum 1). The large sample sizes in strata 1 and 2 provided the ability to subsample for genotyping in proportion to daily passage. Strata 1 and 2 each consisted of 190 samples and stratum 3 had 176 samples. Results in this report reflect those 556 fish selected for genotyping.

Genetic MSA was successfully completed using 539 (97%) of the samples collected and selected for genotyping at Pilot Station in 2019 (Table 3). Estimates for country of origin, broad scale and fine scale reporting groups were provided, and all met the JTC 20/20 reporting guidelines for MSA (JTC 1997). Chinook salmon that passed Pilot Station from June 2 to June 23 (stratum 1) were an estimated 56% Canadian-origin, based on 184 samples (Table 4, Figure 3). Stratum 1 represented early run fish and the first pulse of Chinook salmon. Chinook salmon that passed Pilot Station from June 24 to June 30 (stratum 2) were an estimated 42 % Canadian-origin, based on 184 samples. Chinook salmon that passed from July 1 to August 24 (stratum 3 and late run fish) were an estimated 36% Canadian-origin, based on 171 samples. Across all strata, 45% of the Chinook salmon samples were Canadian-origin (Table 4, Figure 3).

The weighted estimate of Canadian-origin Chinook salmon based on genetic MSA of fish sampled in the test fishery and passage by stratum at the sonar project near Pilot Station was 99,110 fish (90% CI = 86,202–112,648; Table 4). Stratum 1 estimated total passage at the sonar was 82,035 Chinook salmon and the weighted Canadian-origin passage was an estimated 45,637 fish (90% CI = 36,923–54,602). Stratum 2 estimated total passage was 73,551 Chinook salmon and the weighted Canadian-origin passage was an estimated 30,563 fish (90% CI = 23,274–38,444). Stratum 3 estimated total passage was 64,038 Chinook salmon and the weighted Canadian-origin passage was an estimated 22,910 fish (90% CI = 17,107–29,573).

ASL were successfully determined for 478 (86%) of the Chinook salmon sampled and selected for genotyping. The ASL composition of Chinook salmon caught in the Pilot Station sonar test fishery varied among temporal strata and gillnet mesh size (Tables 5 and 6). Overall ASL composition of the selected fish was 0.4% age-3, 12.1% age-4, 46.0% age-5, 39.7% age-6, 1.7% age-7, 49.2% female, and an average of 737 mm in length (Table 5). Age by mesh size ranged from an average

of 4.5-years-old in the 5.00-inch stretch mesh gillnets to 5.6-years-old in the 8.5-inch stretch mesh gillnets. Fish length tended to increase with mesh size (Table 6).

DISCUSSION

The project objectives were successfully achieved in 2019. Sample collection occurred throughout the season in proportion to Chinook salmon abundance past the Pilot Station sonar. Inseason estimates of stock composition were completed for 3 temporal strata, and MSA results were provided to research and management biologists within 36 hrs of samples being received by the GCL. Stratum 1 and stratum 2 were defined inseason based on pulse timing. The number of samples available for genotyping in each stratum was greater than our desired sample size of 190. Therefore, GCL staff were able to subsample proportional to daily passage. Postseason review indicated re-stratification of strata 1 and 2 was not necessary. As such, inseason results were considered final. The inseason sample size for stratum 3 (n=122) was less than the desired sample size of 190. Strata 3 was reanalyzed postseason to include an additional 51 samples collected from fish captured during the end of Chinook salmon run. As such, a final sample size of 171 fish was used postseason to characterize the stock composition of strata 3.

Precision and accuracy of stock composition estimates are affected primarily by the representativeness of the genetic baseline and sample sizes of mixtures. The baseline used by this study has been shown to meet the JTC criteria for Chinook salmon (JTC 1997) when sample sizes were adequate. The 2019 sample sizes were large enough to achieve the desired objective criteria whereby stock components with stratum estimates of 20% or greater have a coefficient of variation of 20% or less. The 2019 stratum-specific sample sizes allowed for reporting results to each of 3 hierarchical groups (i.e., country, broad scale, and fine scale). Some estimates had CVs that approached the upper limit accepted for reporting by the JTC (Table 4). In Stratum 1, 31% of the sample was estimated as Middle Yukon with a CV of 17%. Also, in Stratum 1, 28% of the sample was estimated as Tanana with a CV of 18%. In Stratum 2, 20% of the sample was estimated as Middle Yukon and the CV was 20%. In all cases where the CV was greater than 20%, the stock composition estimate was less than 20% (Table 4).

Findings from this study were used during the 2019 season to manage the fishery in accordance with the US/Canada Yukon River Salmon Agreement as outlined in Appendix 2 of Chapter 8 of the Pacific Salmon Treaty. Inseason stock composition estimates provided critical information about the relative abundance of Canadian-origin Chinook salmon as the run progressed through the lower Yukon River. ADF&G staff used Pilot Station sonar passage estimates and inseason MSA results to project end-of-season abundance of the Canadian stock past the Pilot Station sonar. Canadian stock run size estimates, allowable harvest, and harvest share expectations were refined inseason as MSA results became available (JTC 2020). The number of Canadian-origin Chinook salmon that were estimated passed the U.S./Canada border was less than expected based on inseason run projections and expectations of U.S. harvest (JTC 2020). It is not certain why the inseason projections and border passage estimates did not align more closely. The observed difference cannot be explained by the combined uncertainty in the Pilot station sonar estimates, MSA results, or U.S harvest estimates. It has been speculated that unmeasured en route mortality of Canadian-origin Chinook salmon, in response to the anomalously warm water temperatures recorded in 2019, may have contributed (JTC 2020).

Since 2005, genetic MSA applied to Pilot Station sonar counts has proven to be a reliable and useful inseason tool for informing management of the Canadian stock. Inseason Canadian stock projections, based on sonar and genetic data, typically align with end-of-season estimates past Pilot using the same methods. For example, 90% CIs for 2014–2019 mid-season projections included the end-of-season estimate in all but one year (Figure 4). This demonstrates that inseason projections provided a consistent interpretation of run size before final sonar and genetic information was available, but early enough to be useful for management. However, post season estimates of Canadian run size, used by the JTC, are not based on Pilot Station sonar methods. The post season total run estimate has been produced by summing estimates of Canadian spawning escapement and harvest of Canadian-origin Chinook salmon in Alaska and Canada (JTC 2020). It is important that inseason methods used by ADF&G are comparable to post season methods based on different information. Since 2005, the 90% CIs based on sonar and MSA included the comparable postseason estimate in 9 of 15 years (60%; Figure 5). Of the 6 years with run size estimates that did not align postseason, 3 were larger and 3 were smaller. This demonstrates that sonar and MSA methods are unbiased, albeit imprecise, relative to post season estimation methods. While it is not possible to know which estimate of Canadian run size is most correct, U.S. fishery managers continue to learn how to interpret the sonar and genetic information to improve the likelihood that Treaty obligations will be met. Since 2014, the established Interim Management Escapement Goal for Canadian-origin Chinook salmon and a full Canadian harvest share has been provided or exceeded in each year except 2019.

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TABLES AND FIGURES

Table 1.–Single nucleotide polymorphism (SNP) markers used for genetic MSA in 2019.

Locus	Source	Locus	Source
<i>GTH2B-550</i>	GAPs locus ^a	<i>Ots_LWSop-638</i>	Smith et al. 2005a
<i>NOD1</i>	GAPs locus ^a	<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_Pr12</i>	Smith et al. 2005b
<i>Ots_ETIF1A</i>	GAPs locus ^a	<i>Ots_ins-115</i>	Smith et al. 2005a
<i>Ots_FARSLA-220</i>	Smith et al. 2007	<i>Ots_SC1kF2R2-135</i>	Smith et al. 2005a
<i>Ots_FGF6A</i>	Unpublished	<i>Ots_SERPCI-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 ^a
<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 ^a
<i>Ots_MHC2</i>	Smith et al. 2005b	<i>S7-1</i>	GAPs locus ^a
<i>Ots_ZNF330-181</i>	Smith et al. 2005a	<i>unkn526</i>	GAPs locus ^a

^a 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, 2019.

Country	Reporting groups		Population	Year(s) collected	Sample size
	Broad scale	Fine 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>Koyukuk</i>	S. Fork Koyukuk River	2003	49
			Henshaw Creek	2001, 2007	180
		<i>Tanana</i>	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 stratum and the number and percent (%) of those samples successfully selected for genetic MSA and ASL composition estimation, 2019.

Strata	Dates	N	Number Selected for Genotyping ^a	Genetics		ASL	
				Processed	Percent	Processed	Percent
1	6/02 - 6/23	438	190	184	96.8	169	88.9
2	6/24 - 6/30	230	190	184	96.8	157	82.6
3	7/01 - 8/24	176	176	171	97.2	152	86.4
Total	6/02 - 8/24	844	556	539	96.9	488	86.0

^a Selected samples were randomly chosen and weighted by daily passage.

Table 4.—Stock composition (%) and stock-specific passage (number of fish) of Yukon River Chinook salmon at Pilot Station sonar, by temporal stratum, 2019.

Strata dates and sample size	Reporting group			Stock composition							Stock-specific passage					
				Country	Broad scale	Fine Scale	Median	90% CI		P=0	Mean	SD	CV	Median	90% CI	
	0.05	0.95	0.05					0.95								
Stratum 1 6/02-6/23 N:184	U.S.				44.2	36.2	53.0	0.00	44.4	5.1	11.5	36,072	28,532	44,880	36,398	4,967
			Lower Yukon		12.9	7.8	19.5	0.00	13.2	3.6	27.1	10,569	6,231	16,139	10,824	3,036
			Middle Yukon		31.0	22.8	40.1	0.00	31.2	5.2	16.8	25,303	18,179	33,481	25,574	4,668
				Koyukuk	0.3	0.0	6.1	0.09	1.4	2.2	162.8	249	-	5,052	1,114	1,825
				Tanana	27.5	19.3	35.8	0.00	27.6	5.0	18.2	22,420	15,434	30,048	22,606	4,446
				Upper U.S.	1.0	0.0	8.2	0.06	2.3	2.9	127.6	820	-	6,746	1,855	2,340
			Canada		55.8	47.0	63.8	0.00	55.6	5.1	9.1	45,579	36,923	54,602	45,637	5,370
												Total		82,035		
Stratum 2 6/24-6/30 N:184	U.S.				58.5	51.1	65.7	0.00	58.4	4.4	7.6	42,767	33,807	52,555	42,988	5,651
			Lower Yukon		38.3	31.9	45.0	0.00	38.3	4.0	10.4	27,978	21,480	35,464	28,194	4,238
			Middle Yukon		20.0	13.7	26.9	0.00	20.1	4.0	20.0	14,595	9,576	20,426	14,794	3,318
				Koyukuk	0.2	0.0	4.6	0.10	1.0	1.7	169.1	121	-	3,459	727	1,255
				Tanana	9.7	5.2	15.2	0.00	9.9	3.1	31.1	7,036	3,713	11,466	7,277	2,386
				Upper U.S.	9.1	3.4	15.7	0.00	9.2	3.7	40.6	6,620	2,524	11,744	6,790	2,844
			Canada		41.5	34.3	48.9	0.00	41.6	4.4	10.6	30,295	23,274	38,444	30,563	4,662
												Total		73,551		
Stratum 3 7/01-8/24 N:171	U.S.				64.3	57.3	71.0	0.00	64.2	4.2	6.5	40,998	32,416	50,230	41,128	5,440
			Lower Yukon		55.0	47.5	62.1	0.00	54.9	4.4	8.1	35,062	27,294	43,570	35,155	4,933
			Middle Yukon		9.0	4.9	14.7	0.00	9.3	3.0	32.3	5,706	3,046	9,663	5,973	2,045
				Koyukuk	0.2	0.0	3.4	0.09	0.8	1.2	161.9	106	-	2,143	494	789
				Tanana	3.3	0.0	9.4	0.02	3.8	3.1	80.5	2,114	2	6,161	2,433	1,982
				Upper U.S.	4.8	0.0	10.4	0.03	4.8	3.4	70.8	3,013	1	6,770	3,045	2,188
			Canada		35.7	29.0	42.7	0.00	35.8	4.2	11.6	22,786	17,107	29,573	22,910	3,761
												Total		64,038		

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Strata dates and sample size	Reporting group			Stock composition							Stock-specific passage				
				90% CI							90% CI				
	Country	Broad scale	Fine Scale	Median	0.05	0.95	P=0	Mean	SD	CV	Median	0.05	0.95	Mean	SD
Total	U.S.			54.8	50.3	59.3	0.00	54.9	2.7	5.0	120,301	105,297	135,757	120,514	9,264
6/02-8/24		Lower Yukon		33.7	29.8	37.9	0.00	33.8	2.5	7.3	73,995	62,664	86,277	74,173	7,188
N:539		Middle Yukon		21.0	17.0	25.4	0.00	21.1	2.5	12.1	46,025	36,586	56,510	46,341	6,070
			Koyukuk	0.8	0.0	3.2	0.00	1.1	1.1	99.4	1,648	49	6,998	2,335	2,324
			Tanana	14.7	10.9	18.7	0.00	14.7	2.4	16.0	32,123	23,776	41,418	32,316	5,397
			Upper U.S.	5.2	2.4	8.7	0.00	5.3	1.9	36.1	11,344	5,232	19,236	11,690	4,281
	Canada			45.2	40.7	49.7	0.00	45.1	2.7	6.0	98,967	86,202	112,648	99,110	8,013
															Total 219,624

Note: 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. 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.

Table 5.—Age, sex, and length (mm) composition of Yukon River Chinook salmon sampled and selected for genotyping in the Pilot Station sonar test fishery, 2019.

Stratum	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	Total
	Brood year	2017	2016	2015	2015	2014	2014	2013	2013	
June 2–June 23	Male n	0	18	53	0	27	0	0	0	98
	Female n	0	1	35	0	33	0	2	0	71
	Total n	0	19	88	0	60	0	2	0	169
	Male %	0.0	10.7	31.4	0.0	16.0	0.0	0.0	0.0	58.0
	Female %	0.0	0.6	20.7	0.0	19.5	0.0	1.2	0.0	42.0
	Total %	0.0	11.2	52.1	0.0	35.5	0.0	1.2	0.0	100.0
	Male mean length		583	705		798				708
	Min of length		450	603		725				450
	Max of length		688	830		910				910
	SD		47	46		47				85
	n	0	18	53	0	27	0	0	0	98
	Female mean length		677	740		823		854		781
	Min of length		677	634		704		818		634
	Max of length		677	846		972		889		972
	SD			48		58		50		68
n	0	1	35	0	33	0	2	0	71	
June 24–June 30	Male n	0	18	36	2	16	0	1	0	73
	Female n	0	0	35	0	45	0	4	0	84
	Total n	0	18	71	2	61	0	5	0	157
	Male %	0.0	11.5	22.9	1.3	10.2	0.0	0.6	0.0	46.5
	Female %	0.0	0.0	22.3	0.0	28.7	0.0	2.5	0.0	53.5
	Total %	0.0	11.5	45.2	1.3	38.9	0.0	3.2	0.0	100.0
	Male mean length		578	679	549	793		960		679
	Min of length		406	553	538	704		960		406
	Max of length		708	780	560	879		960		960
	SD		68	58	16	59				102
	n	0	18	36	2	16	0	1	0	73
	Female mean length			743		811		896		787
	Min of length			660		663		846		660
	Max of length			823		920		936		936
	SD			51		52		37		65
n	0	0	35	0	45	0	4	0	84	

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Stratum	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	Total	
	Brood year	2017	2016	2015	2015	2014	2014	2013	2013		
July 1–August 24	Male n	2	21	34	0	14	1	0	0	72	
	Female n	0	0	25	0	54	0	1	1	80	
	Total n	2	21	59	0	68	1	1	1	152	
	Male %	1.3	13.2	22.5	0.0	9.3	0.7	0.0	0.0	47.0	
	Female %	0.0	0.0	16.6	0.0	35.8	0.0	61.7	0.7	53.0	
	Total %	1.3	13.2	39.1	0.0	45.0	0.7	61.7	0.7	100.0	
	Male mean length	406	575	723		801	745			685	
	Min of length	392	460	610		755	745			392	
	Max of length	419	680	832		890	745			890	
	SD	19	57	61		38				110	
	n	2	21	34	0	13	1	0	0	71	
	Female mean length			744		822		848	785	798	
	Min of length			654		708		848	785	654	
	Max of length			860		955		848	785	955	
	SD			48		58				66	
	n	0	0	25	0	54	0	1	1	80	
	Total	Male n	2	57	123	2	57	1	1	0	243
		Female n	0	1	95	0	132	0	6	1	235
		Total n	2	58	218	2	189	1	7	1	478
Male %		0.4	11.9	25.7	0.4	11.9	0.2	0.2	0.0	50.8	
Female %		0.0	0.2	19.9	0.0	27.6	0.0	1.3	0.2	49.2	
Total %		0.4	12.1	45.6	0.4	39.5	0.2	1.5	0.2	100.0	
Male mean length		406	579	702	549	797	745	960		693	
Min of length		392	406	553	538	704	745	960		392	
Max of length		419	708	832	560	910	745	960		960	
SD		19	57	56	16	48				99	
n		2	57	123	2	56	1	1		242	
Female mean length			677	742		819		882	785	789	
Min of length			677	634		663		818	785	634	
Max of length			677	860		972		936	785	972	
SD				49		56		42		66	
n			1	95		132		6	1	235	

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 6.—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 selected for genotyping, by mesh size, 2019.

Mesh	N	Length		Age		Percent female
		Mean	SD	Mean	SD	
2.75	13	636	96	4.8	0.7	15.4
4.00	30	682	131	4.9	0.9	36.7
5.00	4	629	98	4.5	1.0	25.0
5.25	40	647	116	4.8	0.7	22.5
5.75	5	721	90	5.2	0.8	20.0
6.50	127	733	86	5.3	0.7	44.1
7.50	176	754	82	5.4	0.6	57.4
8.50	83	788	68	5.6	0.6	65.1
Total	478	737	97	5.3	0.7	49.2

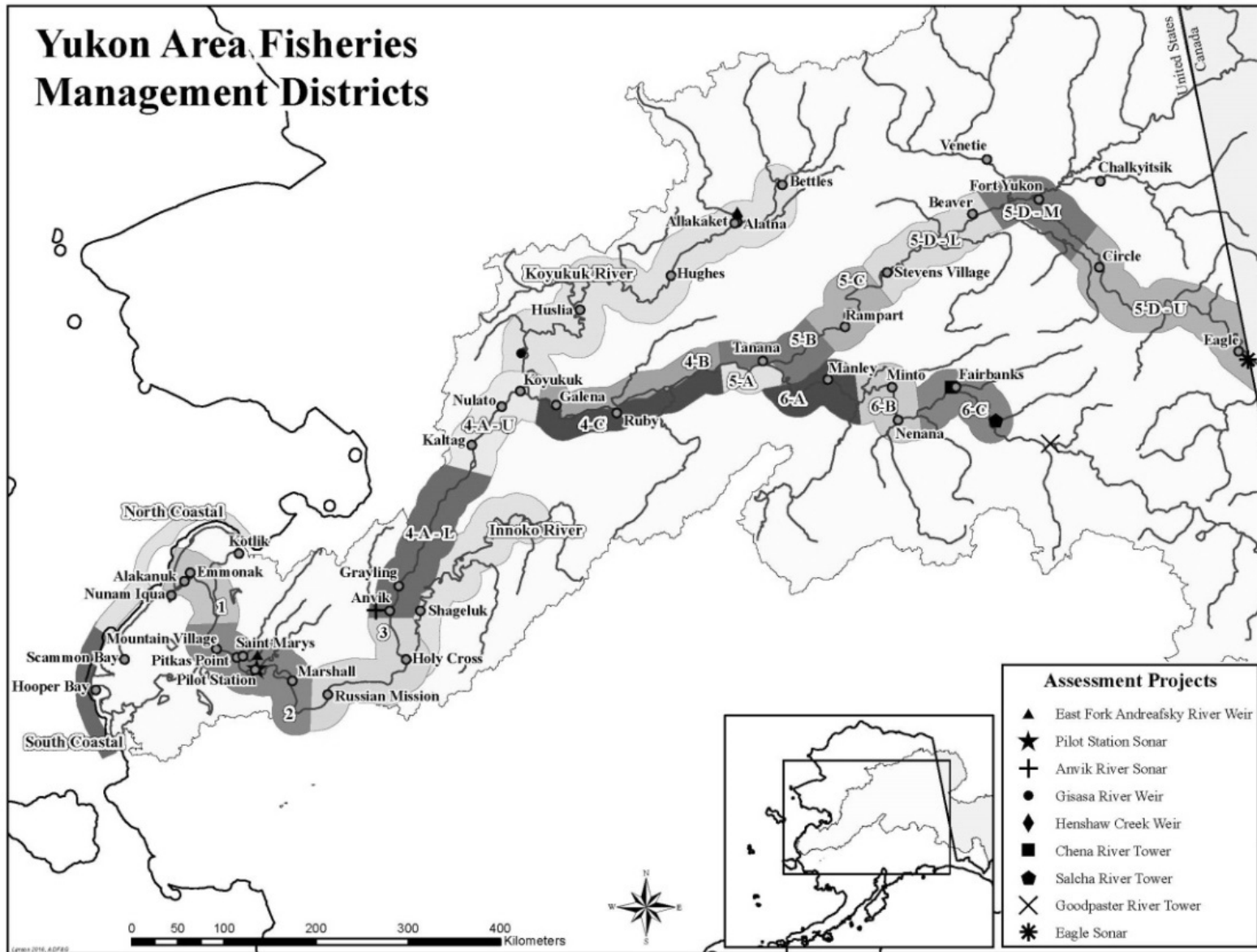


Figure 1.—The Alaska portion of Yukon River with location of assessment projects and fishing districts.

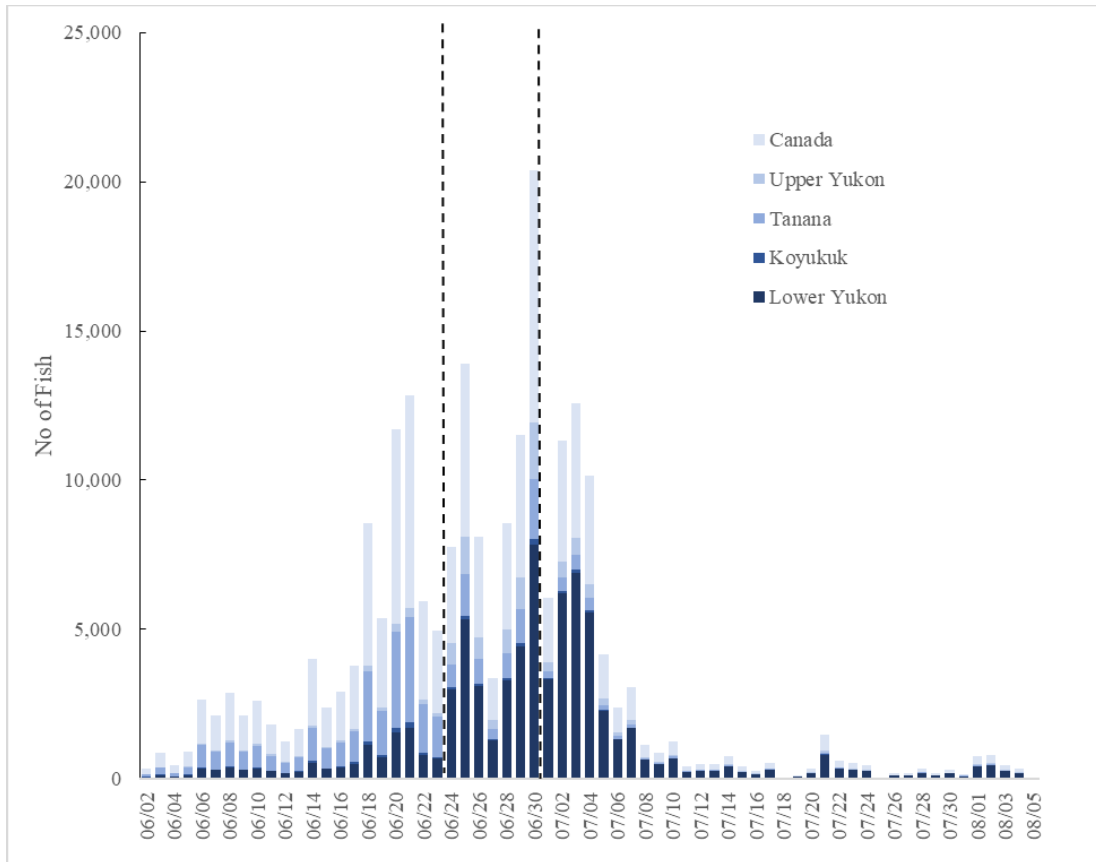


Figure 2.—Daily Chinook salmon passage estimates at the sonar near Pilot Station, 2019.

Note: Dashed lines indicate breaks in strata.

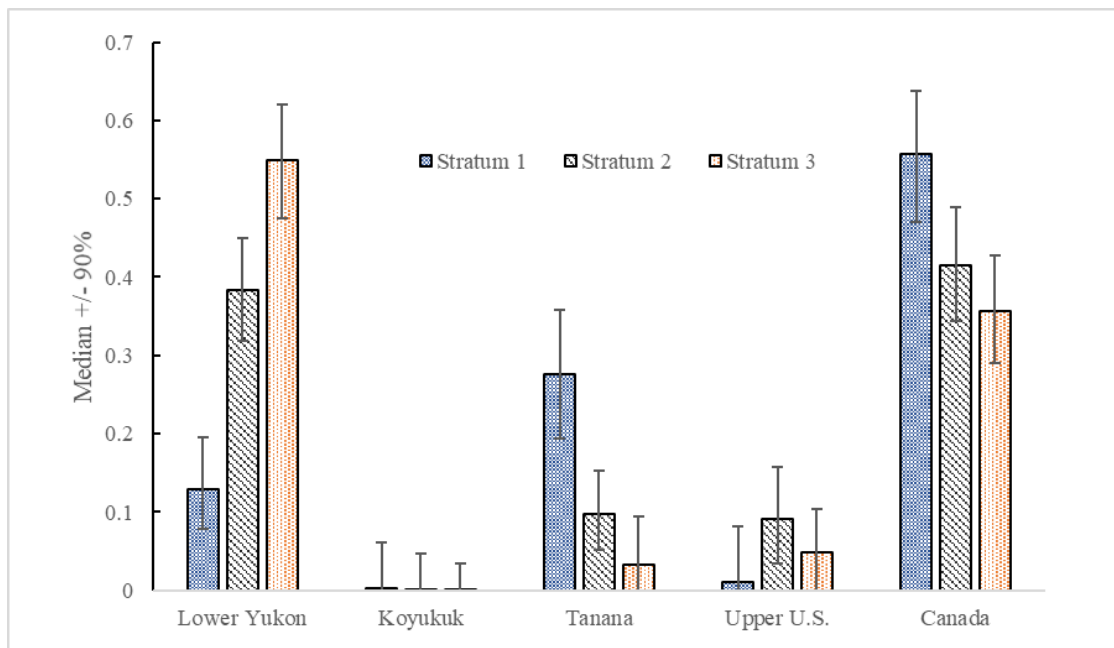
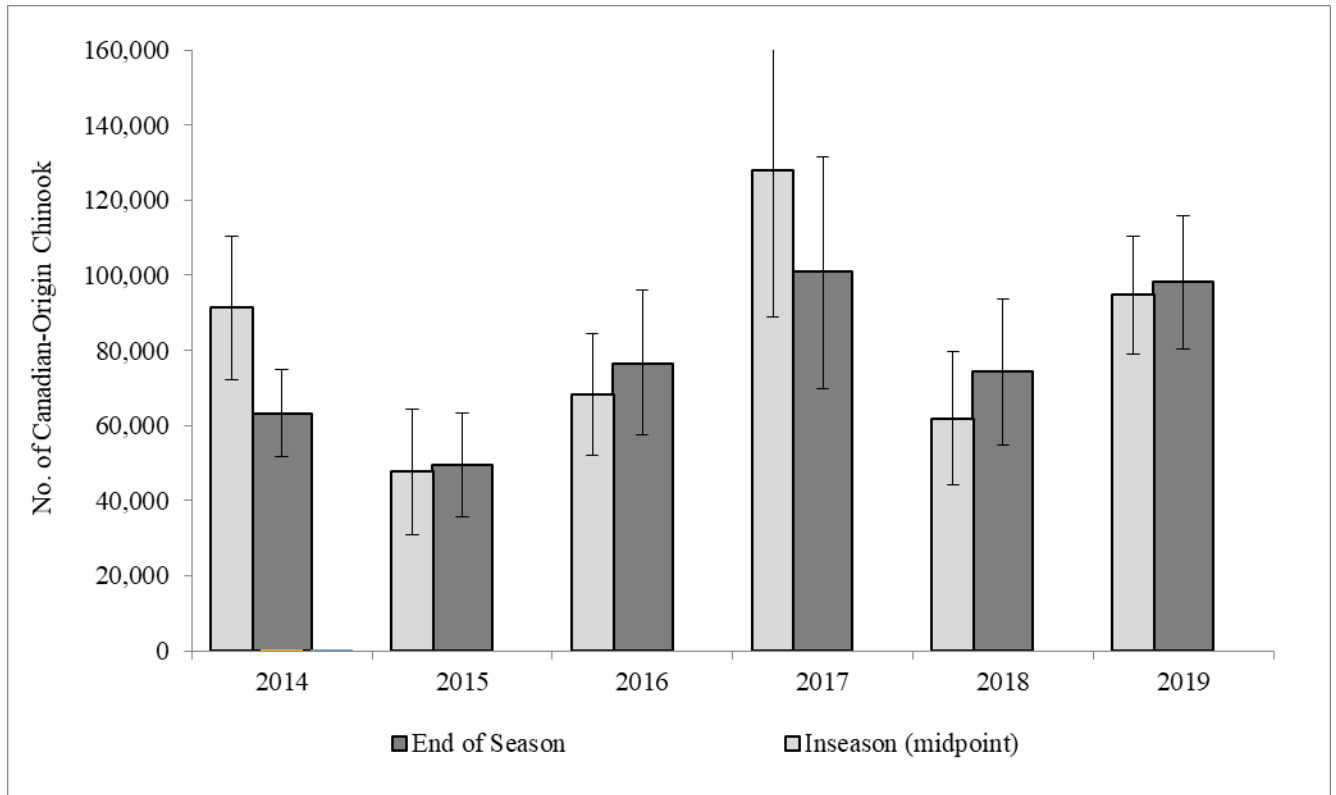


Figure 3.—Stock composition (median and 90% credibility intervals) of Chinook salmon sampled from the Pilot Station test fishery, by temporal stratum, for 5 fine scale reporting groups, 2019.



Note: Inseason projections (light grey bars) are provided as an example. The examples shown use only information available to U.S. fishery managers at the midpoint of the Chinook salmon run past the Pilot Station sonar, such as: cumulative sonar passage estimate, genetic results from the first pulse, prior year genetic results by pulse, and historical run timing scenarios. End of season estimates are based on Pilot Station end of season total passage estimate and annual genetic results by pulse.

Figure 4.— Comparison of inseason projected total run with 90% CI of Canadian-origin Chinook salmon past Pilot Station versus end of season estimate of total run based on sonar and genetic mixed stock analysis, 2014-2019.

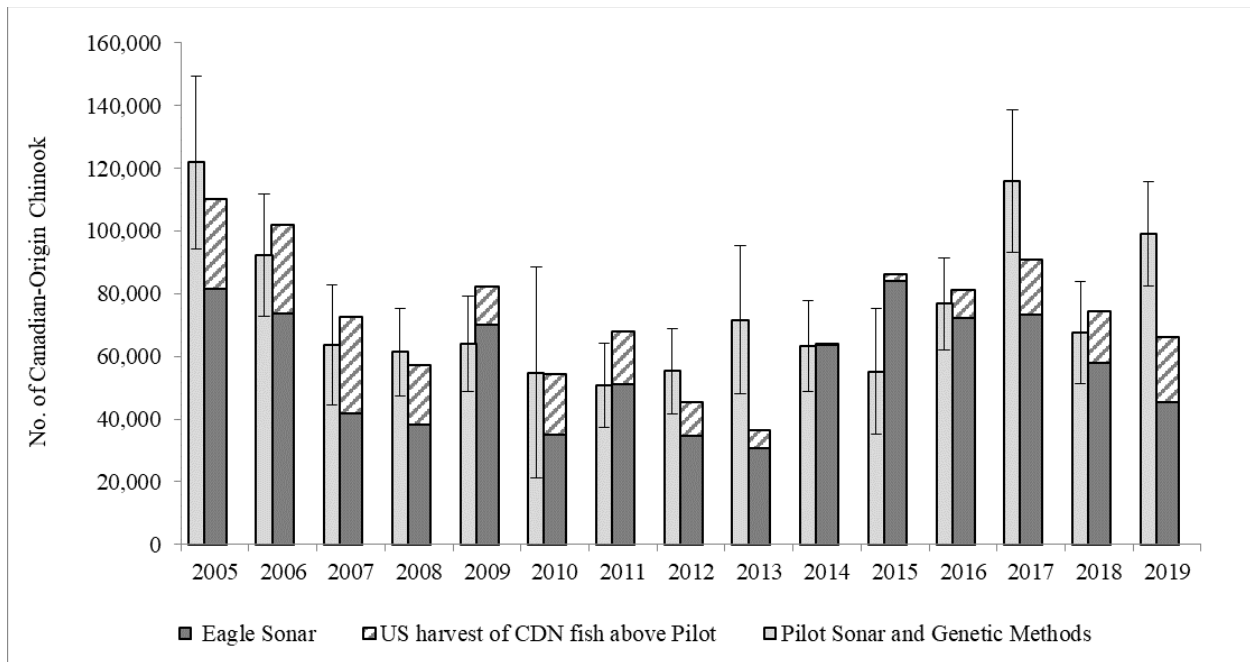


Figure 5.— Estimated number of Canadian-origin Chinook (CDN) salmon using genetic mixed stock analysis of fish sampled from the test fishery at Pilot Station sonar (light grey bars) compared to sum of U.S. harvest of Canadian-origin fish between Pilot Sonar and Eagle Sonar and the estimated passage at Eagle sonar, 2005–2019. Canadian genetic MSA 90% credible interval shown.