Regional Information Report 3A19-08

Genetic Stock Identification of Pilot Station Chinook Salmon, 2017

by

Fred West

and

Tyler H. Dann

October 2019

Alaska Department of Fish and Game **Divisions of Sport Fish and Commercial Fisheries**

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Weights and measures (metric)	
centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)	
cubic feet per second	ft^3/s
foot	ft
gallon	gal
inch	in
mile	mi
nautical mile	nmi
ounce	oz
pound	lb
quart	qt
yard	yd

Time and temperature	
day	d
degrees Celsius	°C
degrees Fahrenheit	°F
degrees kelvin	K
hour	h
minute	min
second	s

Physics and chemistry	
all atomic symbols	
alternating current	AC
ampere	A
calorie	cal
direct current	DC
hertz	Hz
horsepower	hp
hydrogen ion activity (negative log of)	pH
parts per million	ppm
parts per thousand	ppt, ‰
volts	V
watts	W

General	
Alaska Administrative Code	AAC
all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.
all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.
at	@
compass directions:	
east	E
north	N
south	S
west	W
copyright	©
corporate suffixes:	
Company	Co.
Corporation	Corp.
Incorporated	Inc.
Limited	Ltd.
District of Columbia	D.C.
et alii (and others)	et al.
et cetera (and so forth)	etc.
exempli gratia (for example)	e.g.
Federal Information Code	FIC
id est (that is)	i.e.
latitude or longitude	lat or long
monetary symbols (U.S.)	$, ¢
months (tables and figures): first three letters	Jan,...,Dec
registered trademark	®
trademark	™
United States (adjective)	U.S.
United States of America (noun)	USA
U.S.C.	United States Code
U.S. state	use two-letter abbreviations (e.g., AK, WA)

Mathematics, statistics	
all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$\log_{2,}$ etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

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by
Fred West and Tyler H. Dann
Alaska Department of Fish and Game, Division of Commercial Fisheries, Anchorage

Alaska Department of Fish and Game
Division of Commercial Fisheries
333 Raspberry Road, Anchorage, Alaska, 99518-1565

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Fred West and Tyler H. Dann,
Alaska Department of Fish and Game, Division of Commercial Fisheries,
333 Raspberry Rd., Anchorage AK, 99518, USA

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ABSTRACT

Knowledge of the inseason stock of origin, age, sex, and length of Chinook salmon early in their travel 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 613 Chinook salmon were sampled from the test fishery in 2017. The proportion of the sample by stratum that was of Canadian-origin ranged from 41% in stratum 4 to 49% in stratum 2; about 44% of the total Chinook salmon caught at Pilot Station test fishery was of Canadian-origin. The age and sex, 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, and 52.8% female and length averaged 754 mm.

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 about 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 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 are made for distinct pulses, 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. 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 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 over several years 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% 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 has been tested using repeated fishery scenario tests where 200 fish are removed from the baseline in proportions expected in a fishery and then the stock composition of the test mixture is 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%; data on file with the Division of Commercial Fisheries, Kuskokwim 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 project reports can be found on the YRP website[1]. Beginning in 2017, this information was also published in the ADF&G Division of Commercial Fisheries, RIR series (Regional Information Report) as the annual report *Genetic stock identification of Pilot Station Chinook salmon* to improve public accessibility (http://www.adfg.alaska.gov/sf/publications/).

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 (CV) of 20% or less:
    a. the inseason stock composition of pulses of the Yukon River Chinook salmon run at Pilot Station, and
    b. the postseason 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^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). 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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[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 apportioned sonar counts by species, and used a suite of 8 gillnet mesh sizes, ranging from 2.75 inch to 8.5 inch stretch mesh. The test fishery was designed to be representative of the entire run of Chinook salmon that passed upriver from the sonar site. Due to the nature of the test fishery, 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. All Chinook salmon caught in the test fishery were sampled and expected to adequately represent Chinook salmon passing the sonar during each pulse. Samples were self-weighted because as test fishery catches increase, passage at the sonar also increases and vice versa.

Samples were collected using the following protocol:

- Sex was determined by visual inspection. 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. A sample size greater than 200 was necessary to report 3 hierarchical levels: 1) country of origin (U.S. and Canada), 2) broad scale (Lower Yukon, Middle Yukon and Canada), and 3) fine scale (Lower Yukon, Middle U.S. Yukon, Koyukuk River, Tanana River, Upper U.S. Yukon, and Canada; DeCovich and Howard 2011). Only the first 2 levels included reported sample sizes less than 200 (DeCovich and Howard 2011). Once identified, 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 using European notation (Koo 1962). Samples sent to the ADF&G Gene Conservation Laboratory (GCL) in Anchorage were 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 (DeCovich and Howard 2011). These markers have been used by ADF&G for Yukon Chinook salmon 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 Kit[2] by Macherey-Nagel (Düren, Germany). Chinook salmon samples were genotyped for 42 SNPs using Taqman chemistry. Genotypic data is 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, 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 excluded because these individuals probably 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 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, 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.

In each fishery mixture, 5 independent Markov Chain Monte Carlo (MCMC) chains of 40,000 iterations were run using 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-SPECIFIC PASSAGE

Estimates of stock-specific passage by the Pilot Station sonar counter in 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 using Monte Carlo simulation. Here, K is 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, $E_{t,y}^{(i)} = p_{t,y}^{(i)}E_t^{(i)}$.

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

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

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). If sample sizes were smaller than 200, only the first 2 levels of the hierarchy were reported. This study primarily focused on the Canada reporting group, because management actions in this area were crucial 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 passage rate, gear, and time.

RESULTS

A total of 613 Chinook salmon were sampled using various gillnet mesh sizes over 4 strata from May 31 through August 11 (Table 3, Figure 2). Strata were defined by ADF&G staff and resulted in a range of samples per stratum (103 samples in Stratum 1 to 210 in Stratum 4).

ASL 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 temporal strata and gillnet mesh size (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-years-old in the 5.0-inch stretch mesh gillnets to 5.5-years-old in the 8.5-inch stretch mesh gillnets. Fish length tended to increase with mesh size (Table 5).

Genetic MSA was successfully completed using 586 (96%) of the samples collected at Pilot Station in 2017 (Table 3). Sample sizes for all individual stratums were less than 200. Stock composition estimates were not provided for the fine scale reporting groups because sample sizes did not meet the JTC 20/20 recommendation. Estimates were generated for country of origin and broad scale reporting groups, and all but 2 met the JTC 20/20 recommendation (Canada in Stratum 1, Lower Yukon in Stratum 3). Flexibility applying the JTC 20/20 recommendation was appropriate because stock composition estimates were taken in context of one another and could place these estimates in a historical context. Chinook salmon that passed Pilot Station from May 31 to June 13 (first stratum) were an estimated 43% Canadian-origin, based on 99 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 20 (second stratum) were an estimated 49% Canadian-origin, based on 180 samples. Chinook salmon that passed from

June 21 to June 25 (third stratum) were an estimated 43% Canadian-origin, based on 115 samples. Chinook salmon that passed from June 26 to August 11 (fourth stratum) were an estimated 41% Canadian-origin, based on 192 samples. The fourth pulse represented late run fish and the last pulse. Across all strata, 44% of the Chinook salmon samples were 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 stratum at the sonar project near Pilot Station was 115,917 fish (90% CI = 103,402–128,229). Stratum 1 estimated passage was 30,088 Chinook salmon and the weighted Canadian-origin passage was an estimated 12,857 fish (90% CI = 7,862–17,619). Stratum 2 estimated passage was 79,913 Chinook salmon and the weighted Canadian-origin passage was an estimated 39,929 fish (90% CI = 32,028–45,605). Stratum 3 estimated passage was 69,392 Chinook salmon and the weighted Canadian-origin passage was an estimated 30,121 fish (90% CI = 23,330–37,004). Stratum 4 estimated passage was 83,621 Chinook salmon and the weighted Canadian-origin passage was an estimated 34,008 fish (90% CI = 28,449–39,624; Table 6).

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. Sample sizes greater than 100 were achieved in 3 of 4 strata (Stratum 1 was 99 fish) and reported country-of-origin estimates inseason. However, because about 600 samples were used for annual estimates, stock composition estimates for all strata were incorporated into annual estimates of the 3 broad-scale groups. This resulted in not following the JTC 20/20 recommendation in Stratum 1, where 43% of the catch was Canada with a CV of 23%, or in Stratum 3, where 23% 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 CVs exceeding 20% were also below 20% of the mixture (Table 6).

The genetic MSA estimate of Canadian-origin Chinook salmon (115,917) was larger than the official JTC estimate of 92,622, which was 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 close 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 the difference between the 2 methods could be the large passage of summer chum salmon past Pilot Station sonar in 2017. The run of summer chum salmon in 2017 was the largest since 2006 (JTC 2018) and the third largest since 1995. Even a small underrepresentation of summer chum salmon in the test fishery catch would result in an overestimation of Chinook salmon at the Pilot station sonar, and therefore a higher genetic MSA estimate.

Findings from this study apply directly to implementation of the U.S./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 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 in 2017.

Locus	Source	Locus	Source
GTH2B-550	GAPs locus [a]	*Ots_LWSop-638*	Smith et al. 2005a
NOD1	GAPs locus [a]	*Ots_SWS1op-182*	Smith et al. 2005a
Ots_E2-275	Smith et al. 2005a	*Ots_P450*	Smith et al. 2005b
Ots_arf-188	Smith et al. 2005a	*Ots_P53*	Smith et al. 2005b
Ots_AsnRS-60	Smith et al. 2005a	*Ots_Prl2*	Smith et al. 2005b
Ots_ETIF1A	GAPs locus [a]	*Ots_ins-115*	Smith et al. 2005a
Ots_FARSLA-220	Smith et al. 2007	*Ots_SClkF2R2-135*	Smith et al. 2005a
Ots_FGF6A	Unpublished	*Ots_SERPC1-209*	Smith et al. 2007
Ots_GH2	Smith et al. 2005b	*Ots_RFC2-558*	Smith et al. 2005a
Ots_GPDH-338	Smith et al. 2005a	*Ots_SL*	Smith et al. 2005b
Ots_GPH-318	Smith et al. 2007	*Ots_TAPBP*	GAPs locus [a]
Ots_GST-207	Smith et al. 2007	*Ots_Tnsf*	Smith et al. 2005b
Ots_hnRNPL-533	Smith et al. 2007	*Ots_u202-161*	Smith et al. 2005a
Ots_HSP90B-100	Smith et al. 2007	*Ots_u211-85*	Smith et al. 2005a
Ots_IGF-I.1-76	Smith et al. 2005a	*Ots_U212-158*	Smith et al. 2005a
Ots_Ikaros-250	Smith et al. 2005a	*Ots_u4-92*	Smith et al. 2005a
Ots_il-1racp-166	Smith et al. 2005a	*Ots_u6-75*	Smith et al. 2005a
Ots_LEI-292	Smith et al. 2007	*Ots_Zp3b-215*	Smith et al. 2005a
Ots_MHC1	Smith et al. 2005b	*RAG3*	GAPs locus [a]
Ots_MHC2	Smith et al. 2005b	*S7-1*	GAPs locus [a]
Ots_ZNF330-181	Smith et al. 2005a	*unkn526*	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, 2017.

Reporting groups					Sample
Country	Broad scale	Fine scale	Population	Year(s) collected	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
					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 used for genetic MSA and ASL composition estimation, 2017.

			Genetics		ASL	
Stratum	Dates	N	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.

	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	
Stratum	Brood year	2015	2014	2013	2013	2012	2012	2011	2011	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	6.3	26.6	0	10.1	0	0	2.5	45.6
	Female %	0	2.5	35.4	0	13.9	1.3	0	1.3	54.4
	Total %	0	8.9	62	0	24.1	1.3	0	3.8	100
	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
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	6.6	28.1	0	12.6	0	0	0.6	47.9
	Female %	0	1.8	29.3	0	19.8	0.6	0	0.6	52.1
	Total %	0	8.4	57.5	0	32.3	0.6	0	1.2	100
	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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	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	
Stratum	Brood year	2015	2014	2013	2013	2012	2012	2011	2011	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	3.7	28.4	0	12.8	0	0	1.8	46.8
	Female %	0	0	18.3	0	32.1	0	0.9	1.8	53.2
	Total %	0	3.7	46.8	0	45	0	0.9	3.7	100
	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
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	11.5	21.9	0.5	12	0.5	0	0	47.4
	Female %	0	1	27.1	0	24	0	0	0.5	52.6
	Total %	1	12.5	49	0.5	35.9	0.5	0	0.5	100
	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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	Age	1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	
Stratum	Brood year	2015	2014	2013	2013	2011	2011	2011	2011	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	0.2	0.9	47.2
	Female %	0	1.3	27.2	0	22.9	0.2	0.4	0.9	52.8
	Total %	0.4	9	53	0.2	34.9	0.2	0.5	1.8	100
	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

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.

		Length		Age		
Mesh	N	Mean	SD	Mean	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 stratum 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 to August 11, 2017.

			Stock composition							Stock-specific passage				
	Reporting group			90% CI							90% CI			
Strata dates and sample size	Country	Broad scale	Median	0.05	0.95	*P* = 0	Mean	SD	CV	Median	0.05	0.95	Mean	SD
Stratum 1	U.S.		57.1	41.4	73.9	0.00	57.3	9.9	17.3	17,186	12,469	22,226	17,231	2,983
5/31-6/13		Lower Yukon	0.3	0.0	5.0	0.09	1.2	1.8	150.0	88	0	1,510	352	540
N:99		Middle Yukon	55.9	40.2	72.9	0.00	56.1	10.0	17.8	16,818	12,095	21,928	16,879	3,008
	Canada		42.9	26.1	58.6	0.00	42.7	9.9	23.2	12,902	7,862	17,619	12,857	2,983
												Total	30,088	
Stratum 2	U.S.		51.2	42.9	59.9	0.00	51.3	5.2	10.1	40,900	34,308	47,885	40,984	4,121
6/14-6/20		Lower Yukon	9.6	5.5	14.9	0.00	9.8	2.9	29.6	7,688	4,409	11,905	7,861	2,293
N:180		Middle Yukon	41.3	32.9	50.4	0.00	41.4	5.3	12.8	33,025	26,315	40,300	33,123	4,236
	Canada		48.8	40.1	57.1	0.00	48.7	5.2	10.7	39,013	32,028	45,605	38,929	4,121
												Total	79,913	
Stratum 3	U.S.		56.6	46.7	66.4	0.00	56.6	6.0	10.6	39,285	32,388	46,062	39,271	4,156
6/21-6/25		Lower Yukon	22.9	14.8	32.4	0.00	23.2	5.4	23.3	15,918	10,297	22,512	16,087	3,726
N:115		Middle Yukon	33.2	23.4	44.1	0.00	33.4	6.3	18.9	23,050	16,221	30,610	23,184	4,376
	Canada		43.4	33.6	53.3	0.00	43.4	6.0	13.8	30,107	23,330	37,004	30,121	4,156
												Total	69,392	
Stratum 4	U.S.		59.3	52.6	66.0	0.00	59.3	4.1	6.8	49,625	43,997	55,172	49,613	3,393
6/26-8/11		Lower Yukon	36.8	30.4	43.6	0.00	36.9	4.0	10.8	30,795	25,428	36,466	30,853	3,351
N:192		Middle Yukon	22.3	16.8	28.6	0.00	22.4	3.6	16.1	18,636	14,040	23,903	18,760	3,000
	Canada		40.7	34.0	47.4	0.00	40.7	4.1	10.1	33,996	28,449	39,624	34,008	3,393
												Total	83,621	

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Table 6.–Page 2 of 2.

Strata dates and sample size	Reporting group		Stock composition							Stock-specific passage				
				90% CI							90% CI			
	Country	Broad scale	Median	0.05	0.95	*P*=0	Mean	SD	CV	Median	0.05	0.95	Mean	SD
Total	U.S.		55.9	51.3	60.6	0.00	55.9	2.8	5.1	147,085	134,905	159,464	147,099	7,451
5/31-8/11		Lower Yukon	20.9	17.3	24.9	0.00	21.0	2.3	11.0	55,001	45,592	65,366	55,175	5,988
N:586		Middle Yukon	34.9	30.2	39.9	0.00	34.9	2.9	8.3	91,747	79,463	104,943	91,922	7,746
	Canada		44.1	39.3	48.8	0.00	44.1	2.9	6.6	115,940	103,402	128,229	115,917	7,531
												Total	263,014	

Note: Annual estimates of stock-specific passage are weighted by each stratum-specific passage estimate. Stock composition means may not sum to 100% and stock-specific passage means may not sum to the total passage due to rounding error.

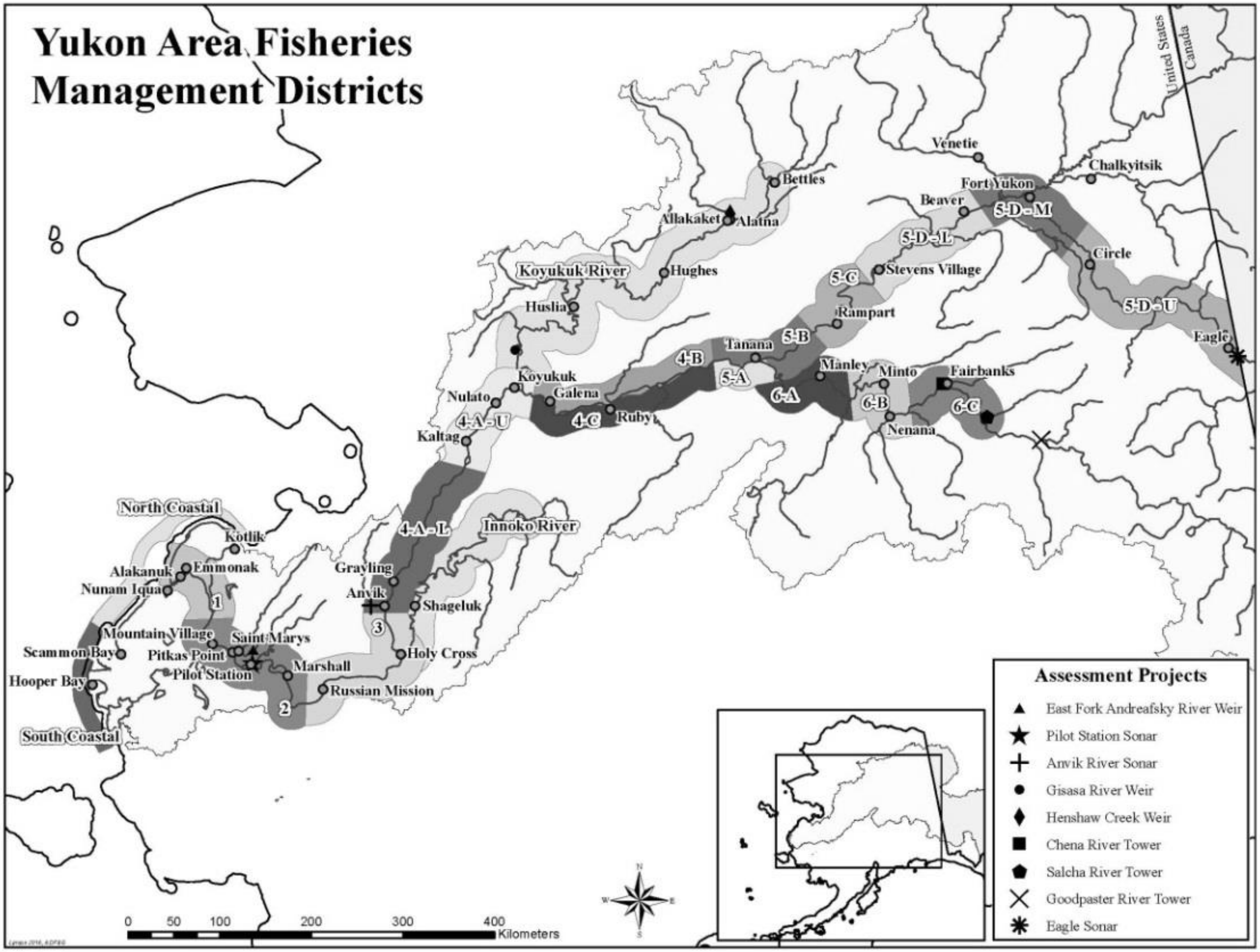

Figure 1.–The Alaska portion of Yukon River with location of assessment projects and fishing districts, 2017.

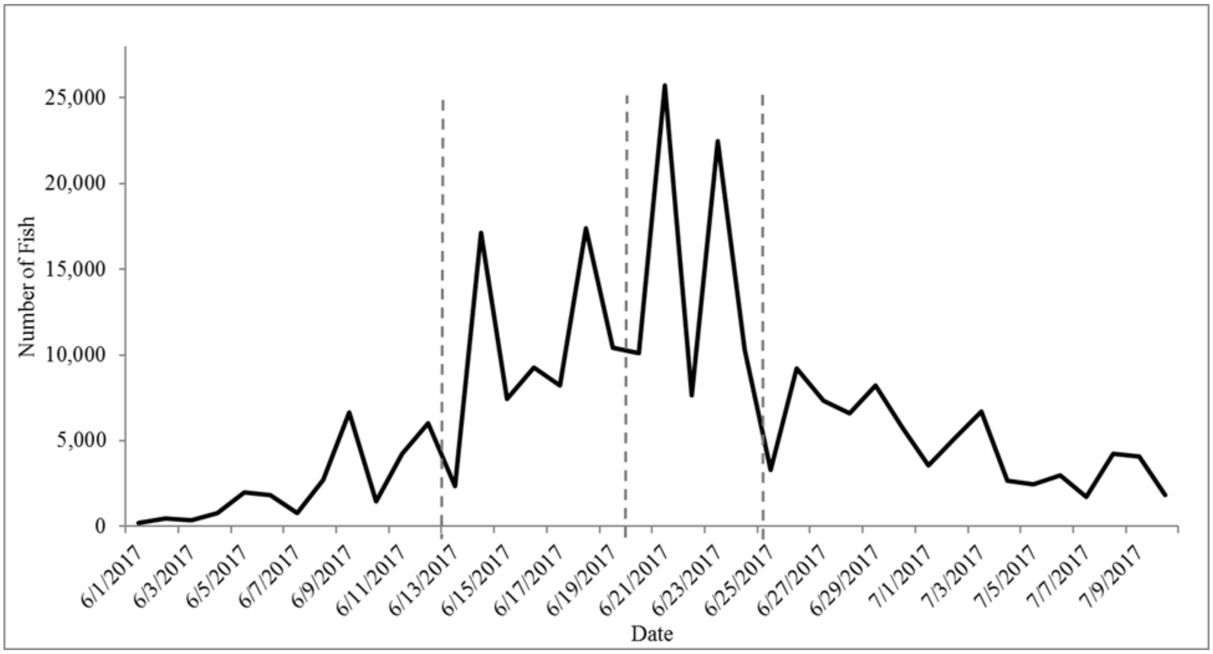

Figure 2.–Daily Chinook salmon passage estimates at the sonar near Pilot Station, 2017.

Note: Dashed lines indicate breaks in strata.

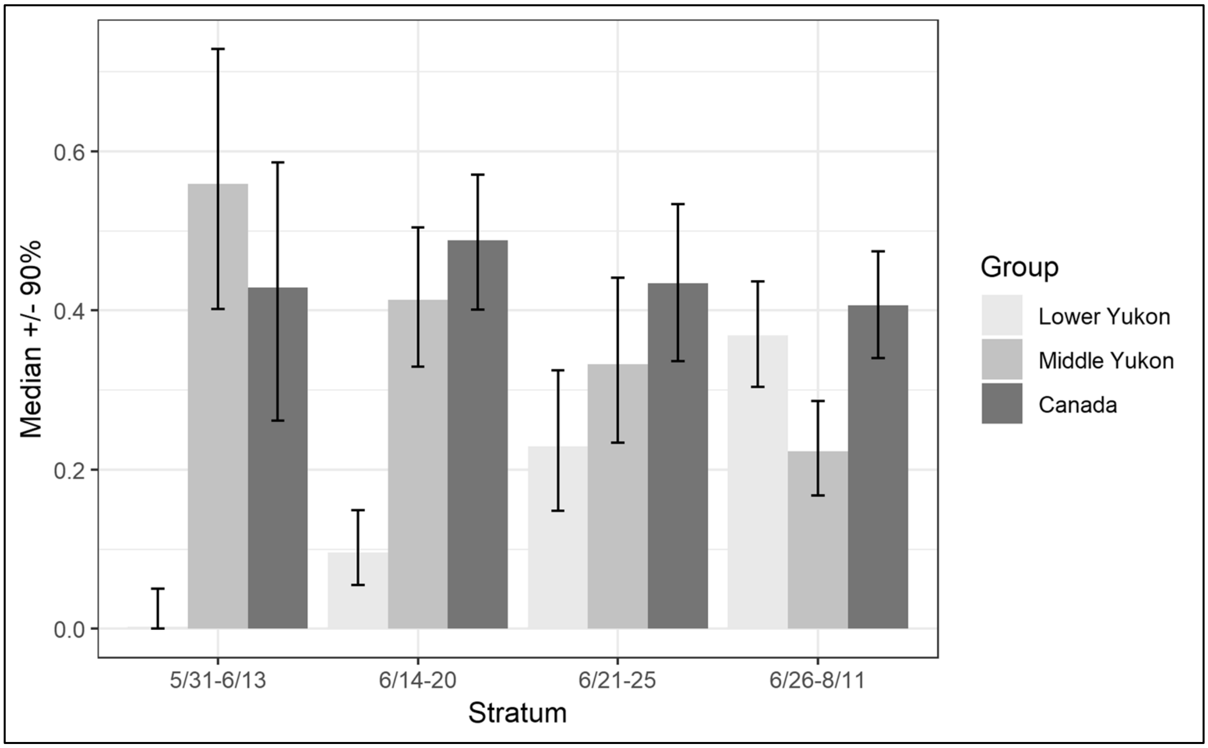

Figure 3.–Stock composition (median and 90% credibility intervals) of Chinook salmon sampled from the Pilot Station test fishery, by temporal stratum, for 3 broad scale reporting groups, 2017.