Genetic Stock Identification of Pilot Station Chinook Salmon, 2016

Project No. URE-92-16

Prepared for the
Yukon River Panel
Restoration and Enhancement Fund

by
Fred West[1], Tyler Dann

September 2017

[1] Alaska Department of Fish and Game, 333 Raspberry Road, Anchorage, AK 99518

TABLE OF CONTENTS

Page

LIST OF TABLES

Table **Page**

LIST OF FIGURES

Figure **Page**

Abstract

Knowledge of the inseason stock of origin, age, sex, and length of Chinook salmon early in their travel upriver is important for making well informed management decisions. The objective of this study was to obtain inseason genetic stock identification information and age, sex, and length data from the test fishery at Pilot Station sonar. A total of 650 Chinook salmon were sampled from the test fishery. The age, sex, and length composition of the harvest was 0.3% age-3, 14.1% age-4, 68.4% age-5, 16.1% age-6, 1.1% age-7, 44.5% female, and an average of 721 mm in length. The proportion of the sample by strata that was of Canadian-origin ranged from 34% in strata 2 to 54% in strata 3; about 43% of the total Chinook Pilot Station test fishery catch was of Canadian-origin in 2016. The data generated from this project are important to assist managers in meeting treaty obligations. Due to the variability in Chinook salmon runs, management actions, and harvest, annual monitoring of the inseason Chinook salmon run is needed.

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, and the Alaska Department of Fish and Game (ADF&G) manages those fisheries with the goals of managing for sustainable yields, providing for subsistence uses, and ultimately to meet or exceed the Alaska-Yukon border spawning objective plus the midpoint of the Canadian guideline harvest range as defined in the Yukon River Salmon Agreement. An estimate of the Canadian-origin Chinook salmon run strength and migration timing is vital to ensuring appropriate management actions are taken to meet border escapement objectives. This project improves management of Yukon River Chinook salmon by providing inseason estimates of stock composition of Chinook salmon migrating past the mainstem sonar project near Pilot Station in the lower portion of the Yukon River during distinct pulses and contributes to the estimates of total run abundance post-season. The ADF&G Gene Conservation Laboratory (GCL) creates inseason stock composition estimates using genotypes of samples from the sonar project test fishery in mixed stock analysis (MSA).

Genetic MSA of samples from the mainstem sonar project near Pilot Station offer fishery managers an important “first look” at the Canadian-origin Chinook salmon run strength and timing before those fish migrate through the majority of Alaska fisheries. No other assessment project along the Alaska portion of the drainage directly assesses the Canadian-origin stock of the Chinook salmon run on the Yukon River except the mainstem sonar project near the border at Eagle. Without genetic MSA at the mainstem sonar project near Pilot Station, fishery managers lack clear indication of Canadian-origin run strength and timing until fish arrive at Eagle, when the majority of the run has already passed through 1,200 miles 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 has been conducted since 2005 on the Yukon River and has provided essential information to fishery managers inseason. Due to statewide budget reductions for ADF&G in 2016, there are no funds for further genetic analysis on the Yukon; therefore, this was the first year seeking R&E funding to continue providing essential data for effective inseason management. While historical data could be used to estimate the stock composition of the run each year, inter-annual shifts in stock composition result in inaccurate inseason estimates of Canadian-origin Chinook salmon run strength and timing when assuming historical stock proportions. It is critical to have an annual inseason tool that assesses the Canadian-origin

Chinook salmon stock lower in the river in order to most effectively manage this complex fishery for escapement objectives.

Objectives

The objective of this study was as follows:

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

Study Area

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

Methods

Fishery Sampling

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

Chinook salmon caught in the test fishery were sampled and axillary processes were collected and stored in individual vials partially filled with silica desiccant beads for drying and preserving the samples. Scales were mounted on gum cards. Data sheets recorded mesh size, date, fish number, scale card number, sampler name, and genetic vial number for each sample. Samples were collected using the following protocol:

- Sex was determined by visual inspection as all fish were released alive whenever possible.
- Length was measured from mid-eye to fork of tail (to the nearest mm) using a rigid meter stick.
- Three scales were collected from the left side of the fish, 2-3 rows of scales above the lateral line, and mounted on pre-printed gum cards.
- One axillary process was clipped from each fish and placed in an individual vial with desiccant beads.

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

For inseason analyses, samples were grouped in strata to represent distinct pulses of Chinook salmon passing through the test fisheries and analyzed promptly to inform inseason management decisions. Pulses were identified by increases in catch per unit effort (CPUE) for a sustained

period of 3 to 5 days followed by a substantial decrease in CPUE. A stratum was identified when pulses were grouped together or to include samples before, between or after pulses in order to obtain the necessary sample size. Samples were flown to the ADF&G Gene Conservation Laboratory (GCL) in Anchorage, analyzed and reported to fishery managers within 36 hours of receipt at the GCL.

Laboratory Analysis

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

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

Mixed Stock Analysis

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

The baseline of allele frequencies for Chinook salmon populations has evolved over the past several years to include 36 populations (Table 2) genotyped at the 42 SNPs used by this study. This baseline allows 5 reporting groups to be identified in mixture samples when sample sizes are at least 200 fish. The baseline has been tested using proof tests. In these tests, the genotype data from 200 fish are removed from the baseline, and the stock composition of this test mixture sample is estimated using the baseline of remaining fish. We repeated this test five times using a random set of individuals drawn from five reporting groups in proportion to what has been historically observed in Pilot Station test fisheries.

For each fishery mixture, we ran five independent Markov Chain Monte Carlo (MCMC) chains of 40,000 iterations with different starting values and discarded the first 20,000 iterations to remove the influence of the initial start values. In order to assess among-chain convergence, we examined the Gelman-Rubin shrink factors computed for all stock groups in BAYES (Gelman and Rubin 1992). If a shrink factor for any stock group in a mixture is greater than 1.2, we reanalyzed the mixture with 80,000 iterations. We combined the last 20,000 iterations of each of the five chains to form the posterior distribution and tabulated means, 90% credibility intervals, and standard deviations 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). When sample sizes were smaller than 200, only the first 2 levels of the hierarchy were reported. Primarily, this study focused on the country-of-origin reporting group, as this is most crucial for obtaining treaty objectives. The broad-scale and fine-scale estimates were given when sample sizes were sufficient. We incorporated each sample in post-season estimates of run reconstruction by weighting each set of stock composition estimates by the passage estimate for that pulse.

Assumptions

1. Samples collected at Pilot station are representative of all of the mixed 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 650 Chinook salmon were sampled from various gillnet mesh sizes over three strata starting May 30 through July 6 (Table 3). The number of samples obtained per stratum ranged from 126 in stratum three to 331 in stratum two.

Age, sex, and length were successfully determined for 580 (89%) of the Chinook salmon sampled. The ASL composition of the Pilot Station sonar Chinook salmon in the test fishery varied among strata and gear (Tables 4 and 5). Overall ASL composition of the sampled fish was 0.3% age-3, 14.1% age-4, 68.4% age-5, 16.0% age-6, 1.0% age-7, 44.5% female, and an average of 721 mm in length (Table 4). Age by mesh size ranged from an average of 4.3 years old in the 2.75-inch stretch mesh gillnets to 5.3 years old in the 8.5-inch stretch mesh gillnets and fish length tended to increase with mesh size (Table 5).

Genetic MSA was successfully completed using 577 (89%) of the samples collected in 2016 Table 3). Genetic MSA on the first stratum (including early fish and the first pulse) of Chinook salmon, based on 178 samples (May 30 to June 14), estimated 52% of the sampled fish were of Canadian-origin (Table 6, Figures 2 and 3). Genetic MSA on the second stratum (including most of the second and third pulse) of Chinook salmon (June 15-25), based on a sample size of 288 fish, estimated 34% of the sampled fish were of Canadian-origin. Genetic MSA on the third strata (fourth pulse and late fish) of Chinook salmon (June 26-July 6), based on a sample size of 111 fish, estimated 54% of the sampled fish were of Canadian-origin. Across all strata, roughly 43% of the Chinook salmon sampled in the test fishery were of Canadian-origin.

The weighted estimate of Canadian-origin Chinook salmon based on genetic MSA of fish sampled in the test fishery and passage by strata at the sonar project near Pilot Station was approximately 76,700 fish (Table 7). Stratum one estimated passage at the sonar was 37,511 Chinook and the weighted Canadian-origin passage was estimated to be 19,356 fish. Stratum two estimated passage was 86,622 Chinook and the weighted Canadian-origin passage was estimated to be 29,105 fish. Stratum 3 estimated passage was 52,765 Chinook and the weighted Canadian-origin passage was estimated to be 28,282 fish.

Discussion

This study's sampling design was developed in the context of both the representativeness of samples and the effect of sample size on the accuracy and precision of estimates. Precision and accuracy of stock composition estimates are affected primarily by the representativeness of the genetic baseline and sample sizes. The Yukon River Panel's Joint Technical Committee's (JTC)

Subcommittee on Stock Identification recommended specific criteria for the precision and accuracy of stock composition estimates used for the management of Yukon River Chinook salmon. The JTC recommended that stock composition estimates of 20 percent or greater have a coefficient of variation of 20% or less and if estimator performance is to be assessed using simulation techniques, it was recommended that the Relative Root Mean Squared Error (RRMSE) be 20% or less (JTC 1997). The baseline used by this study met these criteria for Chinook salmon. The ability of a genetic baseline to discriminate stocks in MSA was critical to the success of this project. Similar criteria are also used for GSI studies on trans-boundary rivers in southeast Alaska and British Columbia.

We only achieved the desired sampling goal of 200 fish per stratum once. However, we were able to process samples from over 100 fish in strata one and three which allowed the ability to provide country of origin and broad scale reporting group estimates for all three strata but fine scale estimates for only the second stratum. In addition, samples from stratum two included fish from pulse two and three in order to reach the desired number of samples. The lower than anticipated sample sizes were due to a low return of Chinook salmon and issues with data quality. Quality control screenings occurred throughout the period of data collection and analysis; however, some issues with data quality still arose. The degradation of tissue samples occurred and, as a result, not all tissue samples were included in genetic MSA. While some loss of samples during ASL and tissue collection in the field is expected, steps will be taken to keep the loss at a minimum. In 2017, genetic tissue samples will be stored in ethanol instead of silica beads to prevent tissue degradation.

The genetic MSA results from Pilot station performed well in estimating the abundance of Canadian origin Chinook salmon in 2016. The genetic MSA estimate of Canadian-origin Chinook was approximately 76,700 fish, which was similar to the actual total Canadian-origin estimate of 83,140 based on the Eagle sonar estimate and Canadian harvest above and below the sonar (Table 7, JTC 2017). The Eagle sonar estimate was contained in 90% credible intervals of the stratified MSA estimates (68,133-85,022).

The main objective of this project is to identify country of origin from samples collected from the test fishery at Pilot Station sonar to inform management decisions. Even though we were able to break results down to broad scale reporting groups, for the purposes of this report, only country of origin was reported

Findings from this study apply directly to improving and implementing the US/Canada Yukon River Salmon Agreement management regime in order to address harvest sharing agreements 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 offered fishery managers an important early indication of the Canadian-origin Chinook salmon run strength and timing before those fish migrated through the majority of Alaska fisheries. Knowing the Canadian-origin Chinook salmon run strength and timing early in the run and lower in the river allowed for more appropriate and timely management actions to ensure escapement and harvest sharing objectives were met.

Literature Cited

Brabets, T. P., B. Wang, and R. H. Meade. 2000. Environmental and hydrologic overview of the Yukon River Basin, Alaska and Canada. US Department of the Interior, US Geological Survey.

Bromaghin, J.F. 2004. An evaluation of candidate net selectivity models for 1990-2003 Yukon River sonar gill-net catch data. US Fish and Wildlife Service, Alaska Fisheries Technical Report Number 75.

Debevec, E. M., R. B. Gates, M. Masuda, J. Pella, J. Reynolds, and L. W. Seeb. 2000. SPAM (Version 3.2): Statistics program for analyzing mixtures. Journal of Heredity 91:509-511.

DeCovich, N. A., and K. G. Howard. 2011. Genetic stock identification of Chinook Salmon harvest on the Yukon River 2010. Alaska Department of Fish and Game, Fishery Data Series 11-65, Anchorage.

DeCovich, N. A., and K. G. Howard. 2010. Genetic stock identification of Chinook salmon harvest on the Yukon River 2009. Alaska Department of Fish and Game, Fishery Data Series No. 10-58, Anchorage.

DeCovich, N. A., and W. D. Templin. 2009. Genetic stock identification of Chinook salmon harvest on the Yukon River 2007. Alaska Department of Fish and Game, Fishery Data Series No. 09-39, Anchorage.

Eaton, S. M. 2015. Salmon age, sex, and length (ASL) procedures for the Arctic-Yukon-Kuskokwim Region. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report No. 3A15-04, Anchorage.

Gelman, A., and D. B. Rubin. 1992. Inference from iterative simulation using multiple sequences. Statistical Science 7:457–511.

Groot, C., and L. Margolis, editors. 1991. Pacific salmon life histories. University of British Columbia Press, Vancouver, Canada.

JTC (Joint Technical Committee of the Yukon River U.S./Canada Panel). 2017. Yukon River salmon 2016 season summary and 2017 season outlook. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 3A17-01, Anchorage.

JTC (Joint Technical Committee). 1997. Review of stock identification studies on the Yukon River. The United States and Canada Yukon River Joint Technical Committee, Whitehorse, Yukon Territory.

Pella, J., and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. Fishery Bulletin 99: 151-167.

R Development Core Team. 2010. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900071-70-0.

Smith, C. T., W. D. Templin, J. E. Seeb, and L.W. Seeb. 2005a. Single nucleotide polymorphisms (SNPs) provide rapid and accurate estimates of the proportions of U.S. and Canadian Chinook salmon caught in Yukon River fisheries. North American Journal of Fisheries Management 25:944-953.

Smith C. T., J. E. Seeb, P. Schwenke, L.W. Seeb. 2005b. Use of the 5'-nuclease reaction for SNP genotyping in Chinook salmon. Transactions of the American Fisheries Society 134:207-217.

Smith C. T., A. Antonovich, W. D. Templin, C. M. Elfstom, S. R. Narum, and L. W. Seeb. 2007. Impacts of marker class bias relative to locus-specific variability on population inferences in Chinook salmon; a comparison of SNPs to STRs and allozymes. Transactions of the American Fisheries Society. 136:1647-1687.

Templin, W. D., N. A. DeCovich, and L. W. Seeb. 2006a. Yukon River Chinook salmon genetic baseline: Survey of Pacific Salmon Commission loci for U.S. populations. Alaska Department of Fish and Game, Fishery Data Series No. 06-46, Anchorage.

Templin, W. D., J. M. Berger, N. A. DeCovich, and L. W. Seeb. 2006b. Genetic stock identification of Chinook salmon harvest on the Yukon River in 2004. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 3A06-06, Anchorage.

Templin, W. D., N. A. DeCovich, and L. W. Seeb. 2006c. Genetic stock identification of Chinook salmon harvest on the Yukon River, 2005. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 3A06-05, Anchorage.

Tables and Figures

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

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

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

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

Table 3. Number of Chinook salmon sampled (N) by strata and the number and percent (%) of those samples that were successfully used for genetics and ASL composition estimation, 2016.

			Genetics		ASL	
Stratum	Dates	N	Processed	Percent	Processed	Percent
1	5/31 - 6/14	193	178	92.2	173	89.6
2	6/15 - 6/25	331	288	87.0	290	87.6
3	6/26 - 7/06	126	111	88.1	117	92.9
Total	5/31 - 7/06	650	577	88.8	580	89.2

Table 4. Age, sex, and length (mm) composition of Yukon River Chinook salmon sampled in the Pilot Station sonar test fishery, 2016.

	Brood Year	2014	2013	2012	2011	2011	2010	2010	
Strata	Age	1.1	1.2	1.3	1.4	2.3	1.5	2.4	Total
May 30 - June 14	Male n	0	17	70	9	2	1	0	99
	Female n	0	5	49	17	1	2	0	74
	Total n	0	22	119	26	3	3	0	173
	Male %	0.0	9.8	40.5	5.2	1.2	0.6	0.0	57.2
	Female %	0.0	2.9	28.3	9.8	0.6	1.2	0.0	42.8
	Total %	0.0	12.7	68.8	15.0	1.7	1.7	0.0	100.0
	Male Mean Length		612	723	743	708	932		707
	Min of Length		495	570	660	697	932		495
	Max of Length		670	837	868	718	932		932
	SD		37	60	61	15			74
	n	0	17	70	9	2	1	0	99
	Female Mean Length		657	731	822	710	875		750
	Min of Length		601	590	713	710	857		590
	Max of Length		798	894	900	710	892		900
	SD		81	53	54		25		73
	n	0	5	49	17	1	2	0	74
	Brood Year	2014	2013	2012	2011	2011	2010	2010	
Strata	Age	1.1	1.2	1.3	1.4	2.3	1.5	2.4	Total
June 15 - June 25	Male n	0	46	101	8	1	0	1	157
	Female n	0	6	94	27	4	2	0	133
	Total n	0	52	195	35	5	2	1	290
	Male %	0.0	15.9	34.8	2.8	0.3	0.0	0.3	54.1
	Female %	0.0	2.1	32.4	9.3	1.4	0.7	0.0	45.9
	Total %	0.0	17.9	67.2	12.1	1.7	0.7	0.3	100.0
	Male Mean Length		619	698	730	663		678	676
	Min of Length		430	364	575	663		678	364
	Max of Length		903	875	841	663		678	903
	SD		77	77	84				85
	n	0	46	101	8	1	0	1	157
	Female Mean Length		723	746	810	783	841		760
	Min of Length		550	638	649	698	781		550
	Max of Length		864	906	915	852	900		915
	SD		121	55	64	76	84		67
	n	0	6	94	27	4	2	0	133

-continued-

Table 4. Page 2 of 2.

Strata	Brood Year / Age	2014 1.1	2013 1.2	2012 1.3	2011 1.4	2011 2.3	2010 1.5	2010 2.4	Total
June 26 - July 6	Male n	2	8	44	12	0	0	0	66
	Female n	0	0	39	12	0	0	0	51
	Total n	2	8	83	24	0	0	0	117
	Male %	1.7	6.8	37.6	10.3	0.0	0.0	0.0	56.4
	Female %	0.0	0.0	33.3	10.3	0.0	0.0	0.0	43.6
	Total %	1.7	6.8	70.9	20.5	0.0	0.0	0.0	100.0
	Male Mean Length	348	564	722	788				703
	Min of Length	320	482	632	692				320
	Max of Length	376	604	857	960				960
	SD	40	43	51	80				104
	n	2	8	44	12	0	0	0	66
	Female Mean Length			757	807				769
	Min of Length			628	725				628
	Max of Length			843	890				890
	SD			49	52				54
	n	0	0	39	12	0	0	0	51
Strata	Brood Year / Age	2014 1.1	2013 1.2	2012 1.3	2011 1.4	2011 2.3	2010 1.5	2010 2.4	Total
Total	Male n	2	71	215	29	3	1	1	322
	Female n		11	182	56	5	4		258
	Total n	2	82	397	85	8	5	1	580
	Male %	0.3	12.2	37.1	5.0	0.5	0.2	0.2	55.5
	Female %	0.0	1.9	31.4	9.7	0.9	0.7	0.0	44.5
	Total %	0.3	14.1	68.4	14.7	1.4	0.9	0.2	100.0
	Male Mean Length	348	611	711	758	693	932	678	691
	Min of Length	320	430	364	575	663	932	678	320
	Max of Length	376	903	875	960	718	932	678	960
	SD	40	68	68	77	28			87
	n	2	71	215	29	3	1	1	322
	Female Mean Length		693	744	813	768	813		759
	Min of Length		550	590	649	698	649		550
	Max of Length		864	906	915	852	915		915
	SD		106	54	58	73	58		67
	n	0	11	182	56	5	56	0	258

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, 2016.

Mesh	N	Length	SD	Age	SD	Percent Female
2.75	4	602	192.4	4.3	1.0	50.0
4.00	20	649	107.2	4.9	0.6	20.0
5.25	39	634	76.5	4.5	0.6	24.4
6.50	193	706	82.1	5.0	0.7	42.2
7.50	236	734	72.1	5.1	0.5	49.4
8.50	88	779	65.1	5.3	0.5	50.0
Total	580	721	86.0	5.0	0.6	44.3

Table 6. Results from genetic mixed stock analysis of Yukon River Chinook salmon sampled in the test fishery from the sonar project near Pilot Station, 2016.

Strata	Dates	N	Reporting Group	Estimate	90% Confidence Interval	
					Lower	Upper
1	May 30 - June 14	178	U.S.	48.4	40.6	56.4
			Canada	51.6	43.6	59.4
2	June 15 - June 25	288	U.S.	66.4	59.5	73.8
			Canada	33.6	26.2	40.5
3	June 26 - July 6	111	U.S.	46.4	37.2	55.7
			Canada	53.6	44.3	62.8
Total	May 30 - July 6	577	U.S.	56.6	51.9	61.5
			Canada	43.4	38.5	48.1

Table 7. Estimated Canadian-origin Chinook based on genetic Mixed-Stock-Analysis of fish sampled in the test fishery from the sonar project near Pilot Station, 2016.

Strata	Passage	Stratum	Canadian Estimate		Proportion	Canadian
Dates	Estimates	Weight	Proportion	S.E.	U.S.	origin
5/30-6/14	37,511	0.21	51.6	0.00359	48.4	19,356
6/15-6/25	86,622	0.49	33.6	0.00256	66.4	29,105
6/26-8/24	52,765	0.30	53.6	0.00534	46.4	28,282
Total	176,898	1.00	43.4	0.00120	56.6	76,713

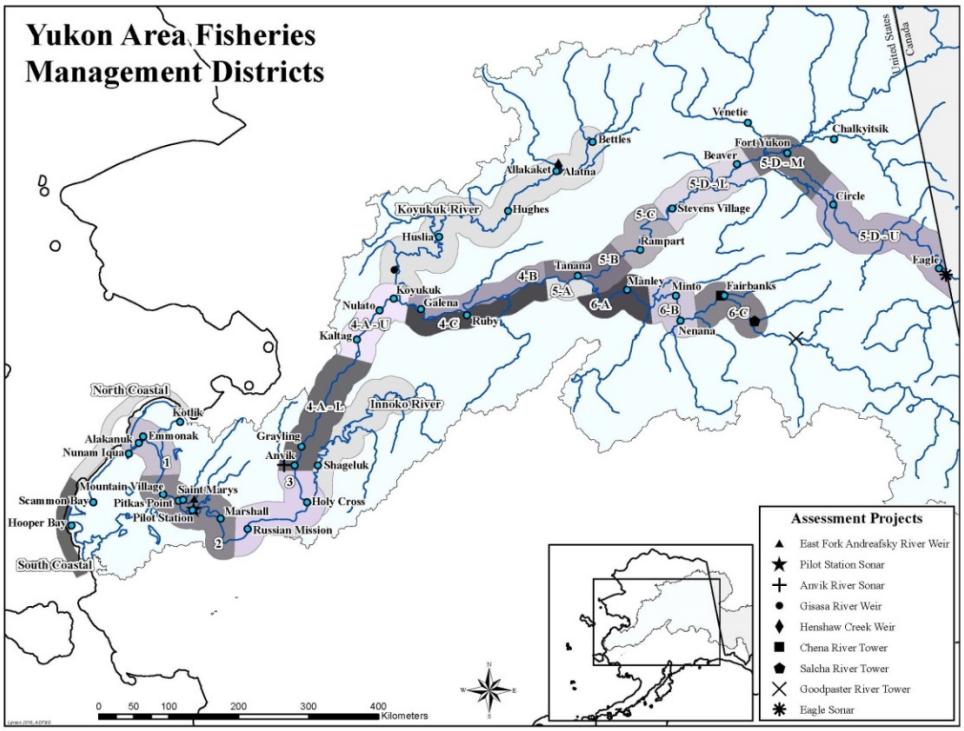

Figure 1. The Alaska portion of Yukon River with location of assessment projects and fishing districts.

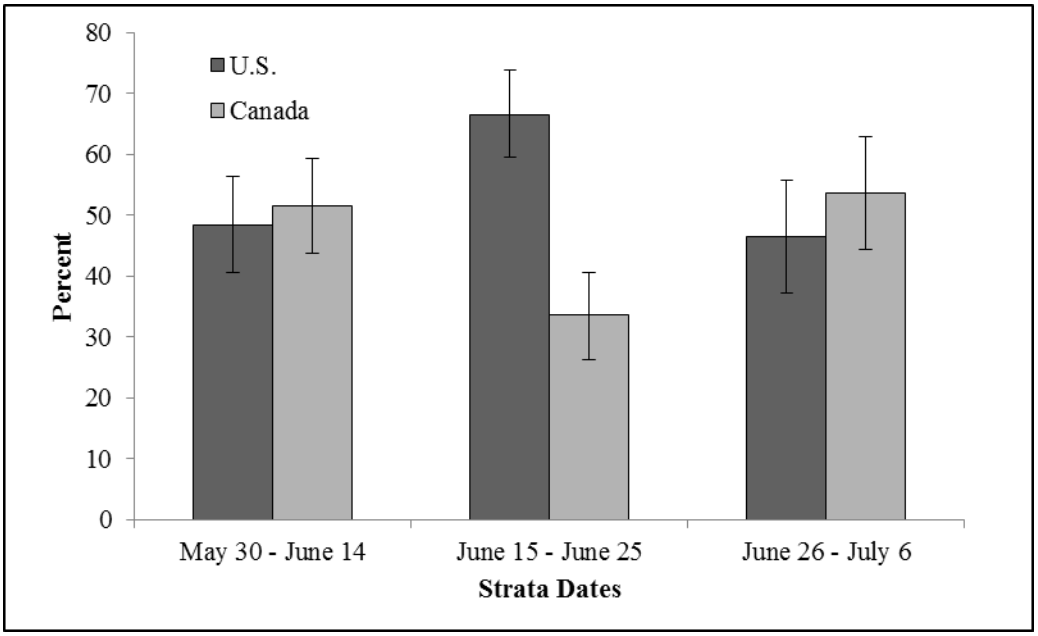

Figure 2. Results of the genetic MSA of Chinook salmon by stratum. Error bars represent 90% confidence intervals.

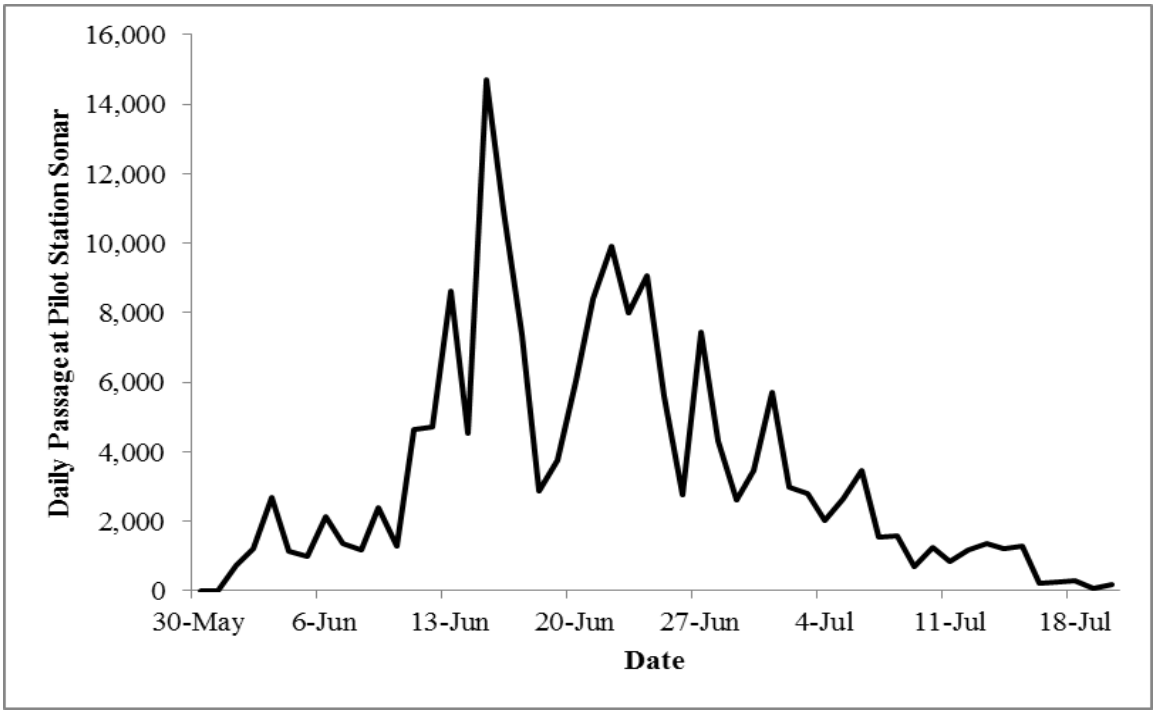

Figure 3. Daily Chinook salmon passage estimates at the sonar near Pilot Station, 2016.