

Yukon River Chinook Subsistence Harvest Genetic Stock Identification, 2016

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Abstract

Residents of over 40 communities located along the Yukon River depend on salmon to help meet their subsistence needs. Subsistence Chinook salmon (*Oncorhynchus tshawytscha*) harvests on the Yukon River were the lowest on record between 2013 and 2015; however, harvest increased substantially in 2016 and is expected to remain strong if the Chinook salmon run improves. Understanding the age, sex, length and stock of origin of Chinook salmon caught in the subsistence fishery is important for making well informed management decisions and for forecasting salmon runs. The objective of this study was to collect representative genetic mixed stock analysis (MSA) information, coupled with age, sex, length (ASL) data, from the Chinook salmon subsistence harvest in Districts 1 through 5. Thirty four subsistence fishermen from 11 communities sampled 1,209 Chinook salmon that were harvested using gillnets, fish wheels, and dip nets,. The age, sex, and length composition of the harvest was 3.1% age-3, 29.1% age-4, 53.7% age-5, 13.6% age-6, 0.6% age-7, 27.4% female, and an average of 688 mm in length. The proportion of the catch that was Canadian-origin ranged from 41% in District 2 to 64% in District 5B; about 57% of the total Chinook salmon subsistence harvest was of Canadian-origin in 2016. The data generated from this project are essential to form the basis of the spawner-recruit models used to estimate past and future run productivity. Due to the variability in Chinook salmon runs, management actions, and harvest, annual monitoring of the subsistence Chinook salmon harvest is needed.

Introduction

Subsistence salmon fisheries within the Yukon River drainage are among the largest in Alaska. Fishing occurs in the Alaskan portion of the Yukon River across distinct fishery management districts and sub-districts (hereafter, districts). Together, the districts span the Yukon River for hundreds of miles; thus, the stock composition of the subsistence harvest varies among these districts because of differences in harvest timing, location, and gear used. Complete information on harvest is critical for creating Canadian-origin Chinook salmon brood year tables and for performing run reconstructions, which form the basis of the spawner-recruit models used to estimate past and future run productivity for Canadian-origin Chinook salmon. These data also help managers understand the effects of management actions and fishing gear on harvest composition. In addition, measuring the total harvest of Canadian-origin Yukon River Chinook salmon is necessary in order to address harvest sharing objectives outlined in the Pacific Salmon Treaty (PST).

Due to conservation concerns for recent poor runs of Chinook salmon, the commercial harvest in Alaska has been greatly reduced or absent since 2008. Therefore, an understanding of the stock composition of subsistence harvests is the remaining critical component necessary to appropriately characterize the stock and age composition of the harvest on the Yukon River. The Alaskan subsistence harvest of Yukon River Chinook salmon also declined from a long term average (1961-2015) of about 34,000 fish per year to a recent average (2011-2015) of about 18,000 fish per year (JTC 2017). As a result, the subsistence harvest sampling programs have been essentially eliminated in the lower and middle Yukon River districts. Since 2013, historical estimates and assumptions about harvest stock compositions have been used to update brood tables and estimate the Canadian-origin component of the harvest. These estimates were considered sufficient for making projections because subsistence harvests were so small. The U.S. subsistence harvest of Chinook salmon increased from about 6,600 fish in 2015 to about 21,000 fish in 2016 due to a relatively strong return of Chinook salmon in 2016. The subsistence harvest of Chinook salmon is expected to increase if run sizes continue to improve in the Yukon River, making understanding the age and stock composition of this component of the harvest critical to understanding the Yukon River Chinook salmon run as a whole.

Harvest patterns have been variable among years as a result of changing management actions aimed at limiting the Chinook salmon harvest. Year-to-year changes in the fishery mean that it is not always possible to use historical harvest composition as a proxy for annual data collection in years with large subsistence harvests. For example, in 2005 under minimal subsistence harvest restrictions, 60% of District 1 subsistence harvest was estimated to be of Canadian origin (DuBois and DeCovich 2008), but under the highly restricted fishery in 2009, the Canadian origin component was down to 36% (DeCovich and Howard 2010). Because of this interannual variation, it is essential to have a comprehensive subsistence harvest monitoring program in place to more accurately assess the true stock composition of the harvest in each year.

The goal of this study was to collect representative genetic mixed stock analysis (MSA) information, coupled with age, sex, length (ASL) data, from the Chinook salmon subsistence harvest in Yukon River districts 1 through 5. This study provided information needed to understand the dynamics of the Yukon River Chinook salmon subsistence harvest, with particular emphasis on the proportion of Canadian-origin fish in the harvest. This study also provides an assessment of stock productivity and long-term trends in the ASL composition for Yukon River Chinook salmon caught in the subsistence fishery.

Objectives

The objectives of this study were as follows:

- Sample up to 400 Chinook salmon caught in the subsistence fishery, per district, within districts 1 through 5.
- Estimate the ASL composition of Chinook salmon harvested in the subsistence fishery.
- Estimate the genetic stock composition of Chinook salmon harvested in the subsistence fishery.

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). 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. The study occurred in villages located along the Yukon River, within districts 1 through 5 (Figure 1).

Methods

Sample Size Consideration

We assumed that the age and stock composition of the subsistence Chinook salmon harvests were a function of the selectivity of the gear, run timing, and location of fishing relative to the total Chinook salmon run through the districts. Given these assumptions, a representative sample required that data be collected proportional to the true distribution of the harvest across gear, time, and location. However, the true distribution was unknown and each of these three elements varied between fishermen and throughout the season, depending on variables such as personal preferences, fish availability (i.e., run timing and abundance), fishing conditions (e.g., turbidity and water level), and regulatory requirements (e.g., gear, time, and area restrictions). Such constraints created practical limits that precluded implementing a true random sampling design. Instead, we used a “grab sample” design (Geiger and Wilbur 1990) and assumed that a well distributed grab sample from volunteer participants resulted in a representative dataset that was “self-weighted” to the actual distribution of harvest across gear, time, and location of harvest.

The data collected represented a “grab sample” of the total subsistence harvest of Chinook salmon in districts 1 through 5.

For districts where more than one community was sampled, the targeted sample size was 400. This ensured that communities with different fishing methods were adequately represented within the sample. For districts where a single community represented the district, 200 samples were sufficient (Bromaghin 1993). Communities with the largest historical Chinook salmon harvests in the district were chosen for sampling; including, Emmonak and Kotlik in District 1; Mountain Village, St. Mary’s, and Marshall in District 2; Russian Mission in District 3; Kaltag, Nulato, Galena, and Ruby in District 4; and Tanana in District 5 (Figure 1). Fish caught in ADF&G’s Lower Yukon River Test Fishery (LYTF) in Emmonak that were distributed for subsistence use were also sampled to bolster District 1’s sample size. Due to the long-term stock composition dataset that has already been collected by Spearfish Research in Fort Yukon and other neighboring communities, Tanana was the only community sampled in District 5.

Sampling Procedures and Analysis

Community members were recruited and trained on how to take ASL and GSI samples of their subsistence-caught Chinook salmon. Training followed ADF&G’s salmon ASL sampling procedures and were augmented with instructions from the ADF&G Gene Conservation Laboratory. Trainings included verbal, visual, and hands-on activities regarding data collection. Participants were paid \$7 for each fish sampled in order to encourage participation. Local community coordinators were hired in each village to help recruit participants in their community and to serve as a local contact for sampling questions. Community coordinators also assisted with the return of samples from participants to Spearfish Research.

Samples were collected immediately after fish were caught. Participants were asked to sample all Chinook salmon harvested during the 2016 season. Data sheets included capture methods, mesh size, location, harvest date, fish number, scale card number, sampler’s name, and genetic vial numbers. Participants followed collection methods established by ADF&G:

- Sex was determined by cutting the abdomen of the fish and inspecting the gonads, as sex identification from external examination alone has been unreliable (Molyneaux et al. 2010).
- 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 and placed in an individual vial.

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).

Genetic data was collected from the fishery samples as individual multi-locus genotypes for 42 SNPs (Table 1). Genomic DNA was extracted using a DNeasy® 96 Blood & Tissue Kit by QIAGEN® (Valencia, CA). Chinook salmon samples were genotyped using Fluidigm 192.24 Dynamic Array IFCs (Integrated Fluidic Circuit), which systematically combine up to 24 assays and 192 samples into 4,806 parallel reactions. Each reaction was conducted in a 8 nL volume consisting of 20X Fast GT Sample Loading Reagent (Fluidigm), TaqMan® GTXpress™ Master Mix (2X; by Applied Biosystems and consisting of AmpliTaq® Fast DNA Polymerase, UP, dNTPs, Tracking Dye, and ROX™ dye), TaqMan® Custom SNP Genotyping Assay (containing 72 µM of each polymerase chain reaction (PCR) primer and 16 µM of each probe), 2X Assay Loading Reagent (Fluidigm), ROX (50X, Invitrogen), and 60-400ng/µl DNA. Thermal cycling

was performed on a Fluidigm FC1™ Cycler. The Dynamic Array IFCs was read on a BioMark™ after amplification and scored using Fluidigm® SNP Genotyping Analysis Genotyping Analysis software. Genotype data were stored in an Oracle database (LOKI) on a network drive maintained by ADF&G computer services. Quality control measures included 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.

The stock composition of fishery mixtures was estimated using the program BAYES (Pella and Masuda 2001). The Bayesian method of genetic MSA estimated the proportion of stocks caught within each fishery using four pieces of information: 1) a baseline of allele frequencies for each population, 2) the grouping of populations into the reporting groups desired for MSA, 3) prior information about the stock proportions of the fishery, and 4) the genotypes of fish sampled from the fishery. For each fishery mixture, we ran five independent Markov Chain Monte Carlo (MCMC) chains of 40,000 iterations in BAYES with different starting values, discarding the first 20,000 iterations to remove the influence of the initial start values. In order to assess the among-chain convergence, we examined the Gelman-Rubin shrink factors computed for all stock groups (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 the five chains to form the posterior distribution and tabulate mean estimates, 90% credibility intervals, and standard deviations from a total of 100,000 iterations.

When sample sizes were larger than 200, stock composition estimates were reported for reporting groups at 3 hierarchical levels (Table 2): 1) country of origin (*U.S.* and *Canada*), 2) broad scale (*Lower Yukon*, *Middle Yukon*, and *Canada*), and 3) fine scale (*Lower Yukon*, *Middle Yukon*, *Upper U.S. Yukon*, and *Canada*). The *Middle Yukon* reporting group included fish bound for the Koyukuk and Tanana rivers. When sample sizes were between 100 and 200, only the first 2 levels of the hierarchy were reported. When sample sizes were insufficient to provide the desired level of stock apportionment for a particular area stratum, samples were pooled. This strategy allowed all available fish samples to be utilized. This method was also used to pool estimates from different communities to create stock composition estimates for a single district.

Assumptions

1. The ASL and stock compositions of samples were a function of the harvest gear, time, and location.
2. Recruitment of participants was independent of participant preferences for harvest gear, timing, location, and harvest goals (i.e., number of fish).
3. Taken together, participants employed harvest methods (harvest gear, time, and location) that were proportional to the unknown actual distribution of harvest methods used by the collective Chinook salmon subsistence fleet in districts 1 through 5.
4. Samples that were pooled across gear type, time, and area for each district were representative of the actual total age and stock composition of the season total subsistence harvest of that district.

Results

Sixty subsistence fishermen from 12 communities were recruited and trained to sample their subsistence caught Chinook salmon for ASL and genetic tissue in 2016. Of those, 34 people from 11 communities sampled their harvest. The first Chinook salmon sampled in the subsistence fishery was caught using a 6-inch drift gillnet in Emmonak on May 26, 2016. The last Chinook salmon sampled was caught using a 6-inch set gillnet in Tanana on July 21, 2016. Fishermen sampled 1,209 Chinook salmon that were caught using various gear types and gillnet

mesh sizes (Table 3). The number of samples obtained per sampler ranged from 1-200 with an average of 36 Chinook salmon sampled per person. The highest number of samples collected by an individual were collected from Chinook salmon caught in a 6-inch drift gillnet in Kaltag. Only 25 (2%) of the fish sampled were caught using dip nets or fishwheels, while drift and set gillnets accounted for 742 (61%) and 427 (35%) of the Chinook salmon sampled, respectively.

Age, sex, and length were successfully determined for 1,011 (84%) of the Chinook salmon sampled. The ASL composition of the subsistence Chinook salmon harvest varied among communities and gear (Table 4; Figure 2). Overall ASL composition of the harvest was 3.1% age-3, 29.1% age-4, 53.7% age-5, 13.6% age-6, 0.6% age-7, 27.4% female, and an average of 688 mm in length (Table 2). Of the fish caught in gillnets, ages ranged from an average of 4 years old in the 4-inch stretch mesh gillnets to 5 years old in the 7.5-inch stretch mesh gillnets and fish length tended to increase with mesh size (Table 5).

Genetic MSA was successfully performed using 1,032 (85%) of the samples collected in 2016. Over 100 genetic samples were collected in each of Emmonak, Russian Mission, Kaltag, Ruby, and Tanana (Table 6). The proportion of the catch that was Canadian-origin ranged from 42% in Russian Mission and Kaltag to 64% in Tanana (Table 6). After pooling samples from multiple communities, over 100 genetic samples were collected in each of districts 1, 2, 3, 4A-Upper, 4B, 4C, and 5B (Table 7). The proportion of the catch that was Canadian-origin ranged from 41% in District 2 to 64% in District 5B (Table 7). Across all districts and communities, roughly 57% of the Chinook salmon harvest was Canadian-origin. Genetic samples collected from the Lower Yukon Test Fishery (N=201) were used to supplement the low subsistence harvest sample size in Emmonak (District 1).

Discussion

This study's sampling design was developed in the context of both the representativeness of the samples and its effect on the accuracy and precision of the estimate. Precision and accuracy of stock composition estimates are affected primarily by the representativeness of the genetic baseline and the harvest sampling. 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 did not achieve the desired sampling goal of 400 fish from each district. However, we were able to process samples from over 100 fish in all but one district sampled, which allowed us to determine the Canadian and U.S. components of the harvest in those districts. The lower than anticipated sample sizes were due to fishing regulations and issues with sample quality. Quality control screenings occurred throughout the period of data collection and analysis; however, some issues with sample quality still arose. Poorly mounted scales and the collection of regenerated scales attributed to the loss of some age data. The degradation of tissue samples also 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 in the future to keep the loss at a minimum. For example, feedback will be given to repeat samplers on their data quality and additional training will be given as needed. In addition, genetic tissue samples will be stored in ethanol instead of silica beads in the future which will help prevent tissue

degradation. There was not a goal for number of participants; however, the intent was to collect samples from enough participants so that the resulting collection was representative of the overall subsistence harvest, including variation between fishermen in their harvest time, gear selection, and harvest location.

Gillnets were the most commonly used gear among samplers due to their catch efficiency and management actions that required the live release of Chinook salmon from dipnets. Despite these management actions, relatively few fish were sampled from dip nets which indicated that some fishermen may have been unaware that Chinook retention was not allowed from this gear type. These samples provided a unique opportunity to determine if this gear type appeared to be selective for certain age classes. Recognizing that the sample size was low, Chinook salmon caught in dip nets had a similar age composition to those caught in gillnets. Individuals who provided samples from fish caught in dipnets were informed post-season of the requirement to release Chinook salmon alive from that gear type in the future.

The ASL and genetic compositions of Chinook salmon caught in the subsistence fishery differed from those of the Chinook salmon run, as measured at Pilot Station, during 2016. For example, fish caught in the subsistence fishery had a higher proportion of age-3 and age-4 fish and a lower proportion of age-5, age-6, and age-7 fish than those sampled in the test fishery at the Pilot Station sonar. The test fishery at the sonar uses a wide range of mesh sizes and is assumed to be representative of the entire Chinook salmon run (JTC 2017). In addition, the proportion of the subsistence harvest that consisted of female fish (27%) was dramatically lower than the proportion in the test fishery at the Pilot Station sonar (45%). The differences in ASL composition of the harvest and the run are undoubtedly a consequence of the management actions taken in 2016. Fishermen were restricted to relatively small mesh gillnets, which tend to catch higher proportion of younger and male fish. For example, 6-inch or smaller gillnets were used for the majority of the season with minimal opportunity for 7.5-inch gillnets. In addition, the proportion of the subsistence harvest that was of Canadian-origin (54%) was slightly higher than the proportion of the Chinook salmon run that was of Canadian-origin (43%), as indicated by inseason genetic MSA at the Pilot Station sonar. In 2016, subsistence Chinook salmon fishing was liberalized towards the end of the season, when an unusually high proportion (54%) of fish entering the Yukon River were bound for Canada, as indicated by the inseason genetic MSA at the Pilot Station sonar. Similarly, the majority of the U.S. harvest of Chinook salmon occurs in upper river communities which may not have access to lower or middle Yukon River Chinook salmon stocks. Consequently, 61% of the samples collected in 2016 came from districts upriver of District 3.

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. By estimating the total harvest of Canadian-origin fish, managers can assess the effectiveness of management actions aimed at achieving Total Allowable Catch. The results from this study will be used with those from the post-season subsistence harvest survey project, which provides annual estimates of harvest by community within the Alaskan portion of the Yukon. For example, the age and stock composition of the harvest were applied directly to the harvest estimates by community and district. This information ultimately allows managers to better forecast the Chinook salmon run and predict potential Canadian-origin harvests while considering fishing gear and time restrictions in an effort to meet harvest objectives. If the Chinook salmon run in the Yukon River continues to improve, and management actions adjust accordingly, it will be important to continue to sample the subsistence harvest and identify shifts in the ASL and genetic compositions of the harvest.

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Tables and Figures

Table 1. Single Nucleotide Polymorphism (SNP) markers used for this study.

Locus	Source
<i>GTH2B-550</i>	GAPs locus
<i>NOD1</i>	GAPs locus
<i>Ots_E2-275</i>	Smith et al. 2005a
<i>Ots_arf-188</i>	Smith et al. 2005a
<i>Ots_AsnRS-60</i>	Smith et al. 2005a
<i>Ots_ETIF1A</i>	GAPs locus
<i>Ots_FARSLA-220</i>	Smith et al. 2007
<i>Ots_FGF6A</i>	Unpublished
<i>Ots_GH2</i>	Smith et al. 2005b
<i>Ots_GPDH-338</i>	Smith et al. 2005a
<i>Ots_GPH-318</i>	Smith et al. 2007
<i>Ots_GST-207</i>	Smith et al. 2007
<i>Ots_hnRNPL-533</i>	Smith et al. 2007
<i>Ots_HSP90B-100</i>	Smith et al. 2007
<i>Ots_IGF-I.1-76</i>	Smith et al. 2005a
<i>Ots_Ikaros-250</i>	Smith et al. 2005a
<i>Ots_il-1racp-166</i>	Smith et al. 2005a
<i>Ots_LEI-292</i>	Smith et al. 2007
<i>Ots_MHC1</i>	Smith et al. 2005b
<i>Ots_MHC2</i>	Smith et al. 2005b
<i>Ots_ZNF330-181</i>	Smith et al. 2005a
<i>Ots_LWSop-638</i>	Smith et al. 2005a
<i>Ots_SWS1op-182</i>	Smith et al. 2005a
<i>Ots_P450</i>	Smith et al. 2005b
<i>Ots_P53</i>	Smith et al. 2005b
<i>Ots_Prl2</i>	Smith et al. 2005b
<i>Ots_ins-115</i>	Smith et al. 2005a
<i>Ots_SC1kF2R2-135</i>	Smith et al. 2005a
<i>Ots_SERPC1-209</i>	Smith et al. 2007
<i>Ots_RFC2-558</i>	Smith et al. 2005a
<i>Ots_SL</i>	Smith et al. 2005b
<i>Ots_TAPBP</i>	GAPs locus
<i>Ots_Tnsf</i>	Smith et al. 2005b
<i>Ots_u202-161</i>	Smith et al. 2005a
<i>Ots_u211-85</i>	Smith et al. 2005a
<i>Ots_U212-158</i>	Smith et al. 2005a
<i>Ots_u4-92</i>	Smith et al. 2005a
<i>Ots_u6-75</i>	Smith et al. 2005a
<i>Ots_Zp3b-215</i>	Smith et al. 2005a
<i>RAG3</i>	GAPs locus
<i>S7-1</i>	GAPs locus
<i>unkn526</i>	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
<i>U.S.</i>					
	<i>Lower Yukon</i>				
		<i>Lower Yukon</i>			
			Andreafsky River	2003	202
			Anvik River	2007	58
			Nulato River	2012	51
			Kateel River	2002, 2008, 2012	174
			Gisasa River	2001	78
			Tozitna River	2002, 2003	278
	<i>Middle Yukon</i>				
		<i>Middle Yukon</i>			
			S. Fork Koyukuk River	2003	49
			Henshaw Creek	2001, 2007	180
			Kantishna River	2005	187
			Chatanika River	2001, 2007	43
			Chena River	2001	176
			Salcha River	2005	188
			Goodpaster River	2006, 2007, 2011	79
	<i>Upper U.S. Yukon</i>				
			Beaver Creek	1997	91
			Chandalar River	2002, 2003, 2004	162
			Sheenjek River	2002, 2004, 2006, 2011	69
			Colleen River	2011	24
<i>Canada</i>	<i>Canada</i>				
		<i>Canada</i>			
			Kandik River	2007, 2008, 2009, 2010, 2011	56
			Chandindu River	2001	146
			Klondike River	2001, 2003, 2007, 2010, 2011	144
			Porcupine River - Old Crow	2007	127
			Stewart River	1997, 2007	102
			Mayo River	1997, 2003, 2011	72
			Pelly River	1996, 1997	107
			Blind Creek	2003, 2007, 2008	218
			Tin Cup Creek	2003, 2009, 2010, 2011	132
			Mainstem at Minto	2007	97
			Tatchun Creek	1987, 1997, 2002, 2003	160
			Nordenskiold River	2003	55
			Little Salmon	1987, 1997, 2007, 2010	237
			Big Salmon	1987, 1997, 2007	176
			Nisutlin River	1987, 1997	55
			Teslin River	2007, 2009, 2010, 2011	198
			Morley River	1997, 2002, 2003, 2009, 2010	46
			Takhini River	1997, 2003	96
			Whitehorse Hatchery	1985, 1987, 1997, 2010	303
					4616

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

Community	Samplers	N	Genetics		ASL	
			Processed	Percent	Processed	Percent
Kotlik	3	67	33	49	60	90
Emmonak	5	44	32	73	42	95
Mountain Village	3	38	33	87	33	87
St. Mary's	2	88	69	78	72	82
Marshall	1	8	4	50	8	100
Russian Mission	4	135	109	81	129	96
Galena	3	84	81	96	79	94
Kaltag	3	330	280	85	281	85
Nulato	2	85	79	93	44	52
Ruby	4	128	126	98	110	86
Tanana	4	202	186	92	153	76
Total	34	1,209	1,032	85	1,011	84

Table 4. Age, sex, and length (mm) composition of Yukon River Chinook salmon sampled in the subsistence fishery by community, 2016.

Village/City	Sample Size	Brood Year Age	2014	2013	2012	2012	2011	2011	2010	2010	Total
			1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	
Emmonak	42	Male n	0	6	20	0	1	0	0	0	27
		Female n	0	2	11	0	2	0	0	0	15
		Total n	0	8	31	0	3	0	0	0	42
		Male %	0.0	14.3	47.6	0.0	2.4	0.0	0.0	0.0	64.3
		Female %	0.0	4.8	26.2	0.0	4.8	0.0	0.0	0.0	35.8
		Total %	0.0	19.1	73.8	0.0	7.2	0.0	0.0	0.0	100.0
		Male Mean Length		568	674		640				
		SD		56	55		0				
		Range		500-650	590-780		640-640				
		n	0	6	20	0	1	0	0	0	
		Female Mean Length		605	712		760				
		SD		7	71		14				
Range		600-610	580-840		750-770						
n	0	2	11	0	2	0	0	0			
Kotlik	60	Male n	0	18	21	0	2	0	0	0	41
		Female n	0	3	5	0	10	1	0	0	19
		Total n	0	21	26	0	12	1	0	0	60
		Male %	0.0	30.0	35.0	0.0	3.3	0.0	0.0	0.0	68.3
		Female %	0.0	5.0	8.3	0.0	16.7	1.7	0.0	0.0	31.7
		Total %	0.0	35.0	43.3	0.0	20.0	1.7	0.0	0.0	100.0
		Male Mean Length		627	710		712				
		SD		70	95		117				
		Range		484-773	563-975		629-794				
		n	0	18	21	0	2	0	0	0	
		Female Mean Length		728	787		839	811			
		SD		16	53		65	0			
Range		710-740	720-860		740-920	811-811					
n	0	3	5	0	10	1	0	0			

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Table 4. Page 2 of 6.

Village/City	Sample Size	Brood Year Age	2014	2013	2012	2012	2011	2011	2010	2010	Total	
			1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4		
Marshall	8	Male n	0	0	4	0	0	0	0	1	5	
		Female n	0	0	2	0	1	0	0	0	3	
		Total n	0	0	6	0	1	0	0	1	8	
		Male %	0.0	0.0	50.0	0.0	0.0	0.0	0.0	0.0	12.5	62.5
		Female %	0.0	0.0	25.0	0.0	12.5	0.0	0.0	0.0	0.0	37.5
		Total %	0.0	0.0	75.0	0.0	12.5	0.0	0.0	0.0	12.5	100.0
		Male Mean Length				749					804	
		SD				65					0	
		Range				664-814					804-804	
		n			0	0	4	0	0	0	0	1
		Female Mean Length					746		828			
		SD					12		0			
		Range					738-755		828-828			
n			0	0	2	0	1	0	0	0		
Mountain	33	Male n	0	12	13	1	1	0	0	0	27	
		Female n	0	0	5	0	1	0	0	0	6	
		Total n	0	12	18	1	2	0	0	0	33	
		Male %	0.0	36.4	39.4	3.0	3.0	0.0	0.0	0.0	81.8	
		Female %	0.0	0.0	15.2	0.0	3.0	0.0	0.0	0.0	18.2	
		Total %	0.0	36.4	54.6	3.0	6.0	0.0	0.0	0.0	100.0	
		Male Mean Length			526	683	548	638				
		SD			134	38	0	0				
		Range			310-686	633-766	548-548	638-638				
		n			0	12	13	1	1	0	0	0
		Female Mean Length					678		920			
		SD					46		0			
		Range					644-758		920-920			
n			0	0	5	0	1	0	0	0		

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Table 4. Page 3 of 6.

Village/City	Sample Size	Brood Year Age	2014	2013	2012	2012	2011	2011	2010	2010	Total
			1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	
St. Mary's	72	Male n	0	24	25	1	3	0	0	0	53
		Female n	0	4	11	0	4	0	0	0	19
		Total n	0	28	36	1	7	0	0	0	72
		Male %	0.0	33.3	34.7	1.4	4.2	0.0	0.0	0.0	73.6
		Female %	0.0	5.6	15.3	0.0	5.6	0.0	0.0	0.0	26.5
		Total %	0.0	38.9	50.0	1.4	9.8	0.0	0.0	0.0	100.0
		Male Mean Length		612	722	520	757				
		SD		76	75	0	85				
		Range			510-830	590-870	520-520	660-820			
		n		0	24	25	1	3	0	0	0
		Female Mean Length			626	728		792			
		SD			74	87		49			
		Range			540-700	520-815		730-840			
n		0	4	11	0	4	0	0	0		
Russian Mission	129	Male n	30	39	30	0	1	2	0	0	102
		Female n	1	10	13	0	3	0	0	0	27
		Total n	31	49	43	0	4	2	0	0	129
		Male %	23.3	30.2	23.3	0.0	0.8	1.6	0.0	0.0	79.2
		Female %	0.8	7.8	10.1	0.0	2.3	0.0	0.0	0.0	21.0
		Total %	24.1	38.0	33.4	0.0	3.1	1.6	0.0	0.0	100.0
		Male Mean Length		411	573	687		745	606		
		SD		60	51	92		0	0		
		Range		330-650	470-700	400-810		745-745	606-606		
		n		30	39	30	0	1	2	0	0
		Female Mean Length		390	535	771		862			
		SD		0	49	42		49			
		Range		390-390	465-610	701-880		807-900			
n		1	10	13	0	3	0	0	0		

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Table 4. Page 4 of 6.

Village/City	Sample Size	Brood Year Age	2014	2013	2012	2012	2011	2011	2010	2010	Total
			1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	
Galena	79	Male n	0	9	34	0	7	2	1	0	53
		Female n	0	1	19	0	4	1	0	1	26
		Total n	0	10	53	0	11	3	1	1	79
		Male %	0.0	11.4	43.0	0.0	8.9	2.5	1.3	0.0	67.1
		Female %	0.0	1.3	24.1	0.0	5.1	1.3	0.0	1.3	33.1
		Total %	0.0	12.7	67.1	0.0	14.0	3.8	1.3	1.3	100.0
		Male Mean Length		602	702		808	634	855		
		SD		64	46		71	30	0		
		Range		536-714	608-794		709-938	612-655	855-855		
		n		0	9	34	0	7	2	1	0
		Female Mean Length		719	739		815	740	856		
		SD		0	43		32	0	0		
		Range		719-719	669-843		788-853	740-740	856-856		
		n		0	1	19	0	4	1	0	1
Ruby	110	Male n	0	33	54	0	6	1	0	0	94
		Female n	0	0	11	0	4	0	1	0	16
		Total n	0	33	65	0	10	1	1	0	110
		Male %	0.0	30.0	49.1	0.0	5.5	0.9	0.0	0.0	85.5
		Female %	0.0	0.0	10.0	0.0	3.6	0.0	0.9	0.0	14.5
		Total %	0.0	30.0	59.1	0.0	9.1	0.9	0.9	0.0	100.0
		Male Mean Length		607	695		786	645			
		SD		33	59		58	0			
		Range		520-675	540-891		700-869	645-645			
		n		0	33	54	0	6	1	0	0
		Female Mean Length			736		828	890			
		SD			48		50	0			
		Range			653-798		773-876	890-890			
		n		0	0	11	0	4	0	1	0

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Table 4. Page 5 of 6.

Village/City	Sample Size	Brood Year Age	2014	2013	2012	2012	2011	2011	2010	2010	Total
			1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	
Kaltag	281	Male n	0	58	94	2	12	3	0	0	169
		Female n	0	10	59	0	40	2	0	1	112
		Total n	0	68	153	2	52	5	0	1	281
		Male %	0.0	20.6	33.5	0.7	4.3	1.1	0.0	0.0	60.2
		Female %	0.0	3.6	21.0	0.0	14.2	0.7	0.0	0.4	39.9
		Total %	0.0	24.2	54.5	0.7	18.5	1.8	0.0	0.4	100.0
		Male Mean Length		600	709	580	823	728			
		SD		31	49	21	50	35			
		Range		535-690	605-870	565-595	760-910	690-760			
		n	0	58	94	2	12	3	0	0	
		Female Mean Length		635	753		843	680		785	
		SD		55	53		41	85		0	
		Range		570-740	600-870		740-910	620-740		785-785	
		n	0	10	59	0	40	2	0	1	
Nulato	44	Male n	0	16	17	2	2	0	0	0	37
		Female n	0	0	4	0	2	1	0	0	7
		Total n	0	16	21	2	4	1	0	0	44
		Male %	0.0	36.4	38.6	4.5	4.5	0.0	0.0	0.0	84.0
		Female %	0.0	0.0	9.1	0.0	4.5	2.3	0.0	0.0	15.9
		Total %	0.0	36.4	47.7	4.5	9.0	2.3	0.0	0.0	100.0
		Male Mean Length		589	707	596	808				
		SD		29	44	26	32				
		Range		527-635	595-765	578-615	785-830				
		n	0	16	17	2	2	0	0	0	
		Female Mean Length			754		791	777			
		SD			13		37	0			
		Range			742-772		765-817	777-777			
		n	0	0	4	0	2	1	0	0	

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Table 4. Page 6 of 6.

Village/City	Sample Size	Brood Year Age	2014	2013	2012	2012	2011	2011	2010	2010	Total
			1.1	1.2	1.3	2.2	1.4	2.3	1.5	2.4	
Tanana	153	Male n	0	49	66	0	9	1	1	0	126
		Female n	0	0	19	0	7	1	0	0	27
		Total n	0	49	85	0	16	2	1	0	153
		Male %	0.0	32.0	43.1	0.0	5.9	0.7	0.7	0.0	82.4
		Female %	0.0	0.0	12.4	0.0	4.6	0.7	0.0	0.0	17.7
		Total %	0.0	32.0	55.5	0.0	10.5	1.4	0.7	0.0	100.1
		Male Mean Length		605	723		851	634	810		
		SD		52	75		53	0	0		
		Range		508-780	530-880		782-924	634-634	810-810		
		n		0	49	66	0	9	1	1	0
		Female Mean Length				796		893	700		
		SD				55		50	0		
		Range				709-910		833-955	700-700		
n		0	0	19	0	7	1	0	0		
Total All Villages	1,011	Male n	30	264	378	6	44	9	2	1	734
		Female n	1	30	159	0	78	6	1	2	277
		Total n	31	294	537	6	122	15	3	3	1,011
		Male %	3.0	26.1	37.4	0.6	4.4	0.9	0.2	0.1	72.7
		Female %	0.1	3.0	15.7	0.0	7.7	0.6	0.1	0.2	27.4
		Total %	3.1	29.1	53.1	0.6	12.1	1.5	0.3	0.3	100.0
		Male Mean Length	411	596	705	570	801	660	832	804	
		SD	60	59	65	34	74	57	32		
		Range	330-650	310-830	400-975	520-615	629-938	606-760	810-855	804-804	
		n	30	264	378	6	44	9	2	1	
		Female Mean Length	390	611	751		840	731	890	820	
		SD		80	59		51	66		50	
		Range	390-390	465-740	520-910		730-955	620-811	890-890	785-856	
n	1	30	159	0	78	6	1	2			

Table 5. Total number of samples (N), mean length (mm) with standard deviation (SD), mean total age, and percent female (%) for Chinook salmon caught in drift and set gillnets, broken out by mesh size, 2016.

Mesh	N	Length	SD	Age	Percent Female
4.00	111	539.6	117.1	4	13.6
5.50	86	661.0	84.1	5	22.1
5.75	15	690.7	113.8	5	26.7
5.88	60	702.7	89.2	5	53.3
6.00	758	703.8	94.3	5	26.7
6.38	33	677.7	106.4	5	18.2
6.50	35	676.9	76.8	5	-
7.00	4	707.5	34.0	5	0.0
7.50	67	751.7	79.7	5	40.3

Table 6. Results from genetic Mixed-Stock-Analysis performed on Yukon River Chinook salmon sampled in the subsistence fishery by community, 2016.

Community	N	Reporting		90% Confidence Interval	
		Group	Estimate	Lower	Upper
Emmonak	231	Lower Yukon	26.8%	21.3%	32.6%
		Middle Yukon	21.0%	14.8%	27.6%
		Upper Yukon	10.6%	5.1%	16.9%
		Canada	52.3%	45.2%	59.2%
Russian Mission	109	Lower Yukon	17.9%	10.8%	26.0%
		Middle Yukon	40.0%	28.6%	52.5%
		Upper Yukon	-	-	-
		Canada	42.0%	30.3%	53.3%
Kaltag	280	Lower Yukon	21.3%	16.2%	26.8%
		Middle Yukon	37.0%	28.0%	45.4%
		Upper Yukon	6.5%	0.0%	13.8%
		Canada	41.8%	33.6%	50.9%
Ruby	126	Lower Yukon	17.8%	10.5%	26.1%
		Middle Yukon	29.1%	20.4%	38.6%
		Upper Yukon	-	-	-
		Canada	53.1%	43.7%	62.2%
Tanana	186	Lower Yukon	10.7%	6.5%	15.6%
		Middle Yukon	24.9%	15.2%	35.2%
		Upper Yukon	-	-	-
		Canada	64.4%	54.0%	74.3%

Note: En-dash indicates that the sample size was not sufficient to produce an estimate. Emmonak samples also include 201 tissue samples collected from the Lower Yukon Test Fishery.

Table 7. Results from genetic Mixed-Stock-Analysis performed on Yukon River Chinook salmon sampled in the subsistence fishery by district, 2016.

District	N	Reporting		90% Confidence Interval	
		Group	Estimate	Lower	Upper
1	264	Lower Yukon	27.3%	22.0%	32.7%
		Middle Yukon	21.3%	15.7%	27.3%
		Upper Yukon	8.3%	3.6%	14.0%
		Canada	51.5%	44.9%	57.9%
2	106	Lower Yukon	23.7%	16.3%	31.8%
		Middle Yukon	35.4%	24.8%	47.0%
		Upper Yukon	-	-	-
		Canada	41.0%	30.0%	51.7%
3	109	Lower Yukon	17.9%	10.8%	26.0%
		Middle Yukon	40.0%	28.6%	52.5%
		Upper Yukon	-	-	-
		Canada	42.0%	30.3%	53.3%
4-A Upper	359	Lower Yukon	18.6%	14.2%	23.4%
		Middle Yukon	39.7%	32.0%	47.2%
		Upper Yukon	6.5%	0.1%	12.9%
		Canada	41.6%	34.5%	49.2%
4-C	126	Lower Yukon	17.8%	10.5%	26.1%
		Middle Yukon	29.1%	20.4%	38.6%
		Upper Yukon	-	-	-
		Canada	53.1%	43.7%	62.2%
5-B	186	Lower Yukon	10.7%	6.5%	15.6%
		Middle Yukon	24.9%	15.2%	35.2%
		Upper Yukon	-	-	-
		Canada	64.4%	54.0%	74.3%

Note: En-dash indicates that the sample size was not sufficient to produce an estimate. Samples were also collected in district 4-B (Galena); however, too few samples were collected to perform genetic MSA for that district. District 1 samples also include 201 tissue samples collected from the Lower Yukon Test Fishery.

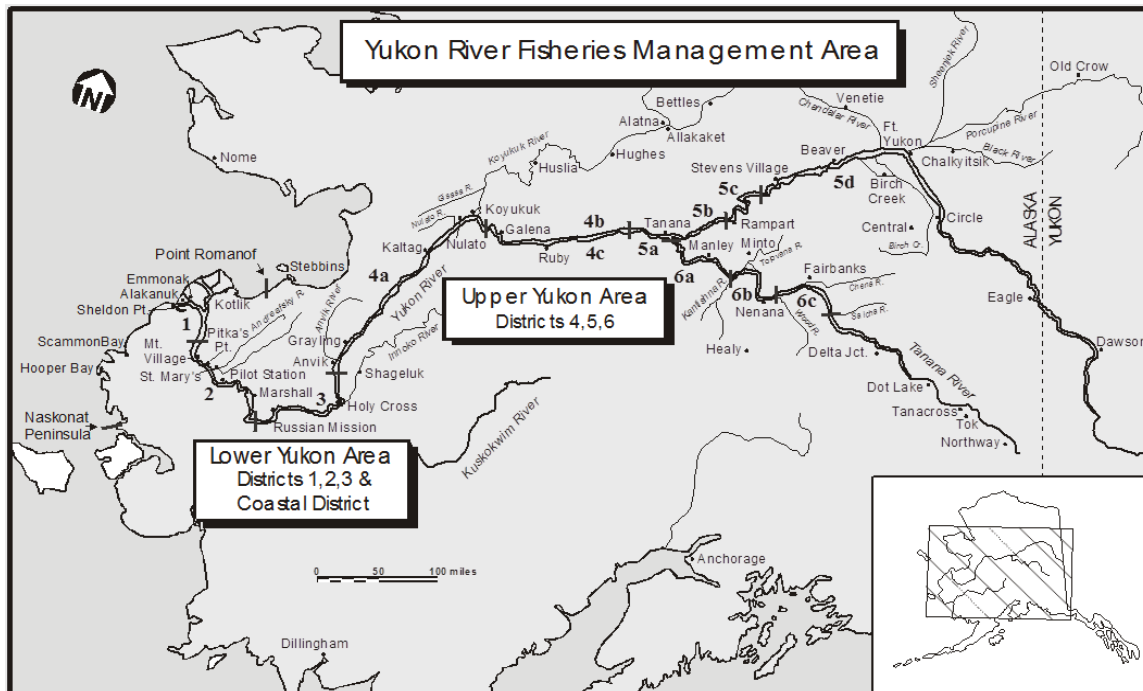


Figure 1. The Alaska portion of Yukon River with location of communities and fishing districts.

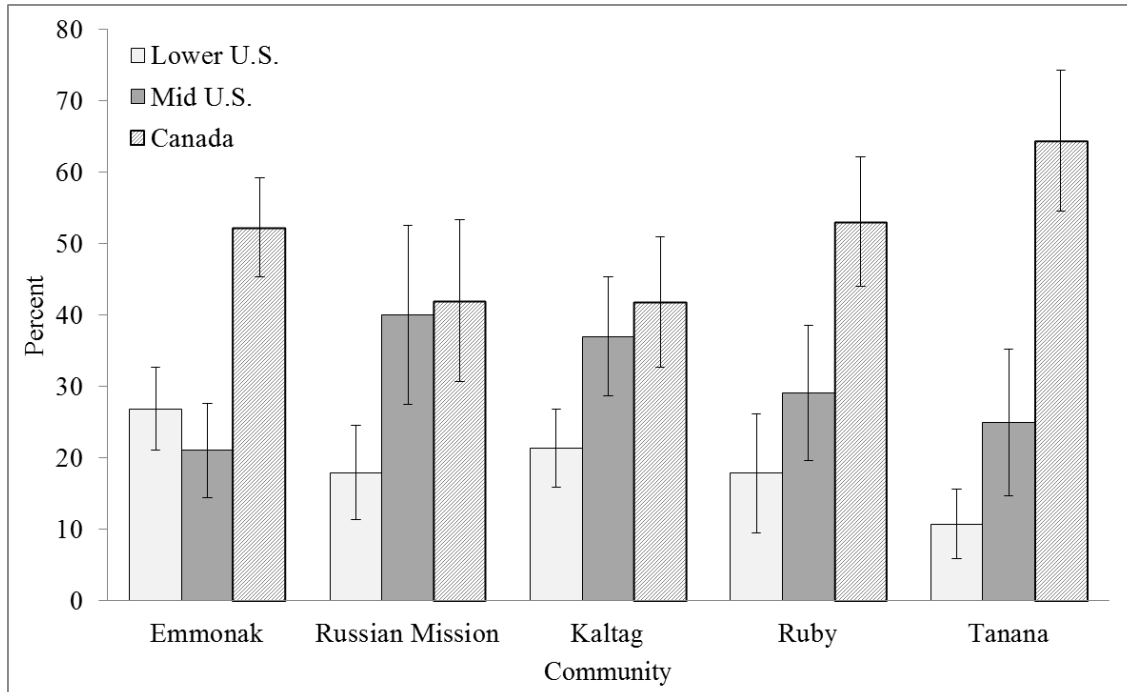


Figure 2. Results of the genetic MSA of Chinook salmon caught in subsistence fisheries in villages where over 100 tissue samples were collected. Error bars represent 90% confidence intervals.