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Genetic Stock Identification of Chinook Salmon Harvest on the Yukon River 2008

by

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Alaska Department of Fish and Game

Divisions of Sport Fish and Commercial Fisheries

Symbols and Abbreviations

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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)

Measures (fisheries)

fork length	FL
mideye to fork	MEF
mideye to tail fork	METF
standard length	SL
total length	TL

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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ABSTRACT

Significant genetic variation exists among populations of Chinook salmon within the Yukon River drainage which has been used to provide estimates of the composition of mixed stock fishery harvests since the early 1990s. In 2008, a single nucleotide polymorphism (SNP) baseline was used to estimate the stock composition of Chinook salmon test fishery catches and harvests in the U.S. portion of the Yukon River. Of the samples collected from test, commercial, and subsistence fisheries, 3,672 individuals were assayed for genetic variation at 26 SNPs. Mixed stock analysis of these samples was used to estimate the stock composition of the harvest at 3 hierarchical levels: country of origin (U.S. and Canada), broad scale (Lower Yukon, Middle Yukon, and Canada), and fine scale (Lower Yukon, Upper U.S. Yukon, Tanana River, Canada Border, Pelly, Carmacks and Takhini). In the Lower Yukon Test Fishery, Canadian stocks contributed between 57% and 32% of the catch over 3 strata representing the main pulses of the run. In the District Y-1 commercial harvest, Canadian stocks of Chinook salmon caught in the first 2 periods of the directed chum salmon fishery contributed 41% and 14% of the run, respectively. The analysis and reporting of results from these 2 fisheries (Lower Yukon Test Fishery and District Y-1 commercial) were done inseason. In the test fishery associated with a sonar project at Pilot Station, Canadian Chinook stocks contributed between 47% and 31% of the catch over the 3 main pulses.

Key words: Chinook salmon, *Oncorhynchus tshawytscha,* genetic stock identification, Yukon River, single nucleotide polymorphism, SNP, commercial fishery, subsistence

INTRODUCTION

Knowing the origin of Chinook salmon (*Oncorhynchus tshawytscha*) harvested in Yukon River commercial fisheries is important for the successful management of these fisheries. Under the Yukon River Salmon Agreement between the United States and Canada, U.S. fishery managers are obligated to pass a specified target range of Chinook salmon into Canada which is comprised of an escapement goal and a harvest share of the total Canadian-origin run. Monitoring the proportion of Canadian-origin Chinook salmon in fishery harvests from U.S. waters of the Yukon River represents an important tool for successfully meeting those obligations. Yukon River fisheries managers consider test fishery and commercial harvest numbers an important indicator of Chinook salmon run size for inseason management, and postseason genetic analyses have been very effective at distinguishing major stock components in the commercial catch since 2004. Past studies on stock compositions of the commercial harvest in Districts Y-1 and Y-2 have shown that the proportion of Canadian-origin fish may vary significantly within a season, with a contribution ranging from 25% to 69% of the harvest (Templin et al. 2006; DeCovich and Templin 2009). Since 2004, the stock composition of Chinook salmon harvests in the subsistence and commercial Chinook salmon fisheries of the Yukon River has been estimated by genetic stock identification (GSI) techniques based on a comprehensive baseline of DNA markers (Smith et al. 2005a; Templin et al. 2005; Beacham and Candy 2006; Templin et al. 2006a-b; Templin et al. 2008; DeCovich and Templin 2009).

Two types of genetic markers, single nucleotide polymorphisms (SNPs) (Smith et al. 2005a; Templin et al. 2006b) and microsatellites (Flannery et al. 2006; Templin et al. 2006a,c; Beacham et al. 2008) have replaced the allozyme baseline developed in the 1990s (Beacham et al. 1989; Wilmot et al. 1992; Templin et al. 2005). The 2004 baseline of 9 SNPs assayed in 23 populations was increased to 17 SNPs (Templin et al. 2006b) and in 2006, the SNP baseline was augmented with additional populations and genetic markers and now consists of 25 populations and 51 SNPs (Templin et al. 2008). A subset of this baseline, consisting of all 25 populations and 26 SNPs, was used to provide the stock composition estimates reported in this study.

This report describes the mixed stock analysis of the Chinook salmon test fishery catches, and commercial and subsistence harvests in the U.S. portion of the Yukon River in 2008. We briefly describe the baseline used, the simulations used to verify the accuracy and precision of estimated stock proportions, and report the results of the mixed stock analysis of fishery samples. The stock contribution estimates are provided for 3 hierarchical sets of reporting groups: 1) country of origin (U.S. and Canada), 2) broad scale (Lower Yukon, Middle Yukon, and Canada), and 3) fine scale (Lower Yukon, Tanana, Upper U.S. Yukon, Canada Border, Pelly, Carmacks and Takhini). In addition, we provide age-specific estimates for the 5- and 6-year old components of the run, the dominant age classes, for selected fisheries.

Funding for this project was provided by three sources. The 2008 Yukon River Panel Restoration and Management Fund, project URM 08-08, provided funding to analyze samples from the commercial harvest in Districts Y-1 and Y-2, as well as subsistence harvests from Districts Y-1 and Y-4. The 2008 Restoration and Enhancement Fund of the Yukon River Panel, project 19N-08, provided funding for the inseason analysis of samples collected from the Lower Yukon Test Fishery (LYTF). This was a pilot study to test the feasibility and application of inseason stock composition estimates for management of Chinook salmon fisheries. The State of Alaska provided funding for analysis of samples from Pilot Station, and the subsistence harvests from Districts Y-3 and Y-5.

OBJECTIVES

The goal of this project was to provide estimates of the stock composition of the Chinook salmon catches in test fisheries, and harvests in commercial and subsistence fisheries on the Yukon River in 2008. To achieve this goal, the following objectives were to be met:

1) Sample individuals from each test, commercial and subsistence fishery in districts Y-1, Y-2, Y-3, Y-4 and Y-5 as follows:
    i. District Y-1 subsistence – 400 individuals
    ii. District Y-1 commercial – 400 individuals per period for directed Chinook salmon fishing periods, 200 individuals per period for incidental harvest in chum salmon fishing periods
    iii. District Y-1 Lower Yukon Test Fishery – Sample as needed in lieu of a directed commercial Chinook salmon fishery
    iv. District Y-2 Pilot Station Test Fishery – 1000 individuals
    v. District Y-2 commercial – 400 individuals per period
    vi. District Y-3 subsistence – 250 individuals
    vii. District Y-4 subsistence – 250 individuals from each subdistrict
    viii. District Y-5 subsistence – 400 individuals.
2) Analyze the first 3 periods of the District Y-1 commercial fishery inseason. If no directed Chinook salmon commercial fishery occurs in 2008, analyze samples from 3 pulses of Chinook salmon from the LYTF after the pulses are identified by the test fishery.
3) Analyze a representative sample of individuals from each district and period for genetic variation at the SNP loci in the baseline.
4) Estimate the relative contribution of stocks to the test, commercial, and subsistence fisheries of the Yukon River.

METHODS

COLLECTIONS

The Chinook salmon baseline collections (Table 1, Figure 1) were assembled as a part of a 3-laboratory collaboration (Alaska Department of Fish and Game [ADF&G], Department of Fisheries and Oceans Canada [DFO], and U.S. Fish and Wildlife Service [USFWS]) to survey genetic variation in the Yukon River drainage (Flannery et al. 2006). The same baseline was used to analyze the fishery samples from Chinook salmon in 2006 (Templin et al. 2008), 2007 (DeCovich and Templin 2009), and 2008 (this study).

Chinook salmon were sampled from the test, commercial, and subsistence fisheries in the U.S. portion of the river (Table 2; Figure 1). Samples were collected randomly during each fishing period during the process of sampling the harvest for age, sex, and length data (DuBois and DeCovich 2008). A fishing period is a designated time during which either subsistence or commercial fishing is allowed. Chinook salmon fishing periods on the U.S. portion of the Yukon River are authorized by ADF&G and the USFWS (Bue and Hayes 2008). The tissues collected were axillary processes and were preserved in ethanol. Samples were collected from test fisheries in Districts Y-1 (LYTF) and Y-2 (Pilot Station), commercial harvests in Districts Y-1 and Y-2, and from subsistence harvests in Districts Y-1, Y-3, Y-4, and Y-5. The subsistence samples from District Y-4 were collected from subdistricts Y-4A (Kaltag and Nulato), Y-4B (Bishop Rock and Galena), and Y-4C (Ruby). The subsistence samples from District Y-5 were collected from subdistricts Y-5B (North bank of the Yukon River at Tanana) and Y-5C (Rapids).

Target sample sizes of 400 individuals per Chinook salmon-directed fishing period were established to allow for levels of precision and accuracy necessary to ensure stock composition estimates within 5% of the true value 90% of the time (Thompson 1987). Larger sample sizes also allow for subsampling by age to provide age-structured estimates. Target sample sizes of 250 individuals were established for subsistence fisheries to account for smaller harvests and greater difficulty in obtaining samples.

Samples from the LYTF were collected over the course of the Chinook salmon run (approximately June 1 to July 15) from 3 mouths of the Yukon River, the south mouth (where the Big Eddy net sites are located) and the middle and north mouths (collectively referred to as Middle Mouth), using set gillnets with 8.5-inch mesh. Samples were flown to the ADF&G Gene Conservation Laboratory (GCL) in Anchorage at the conclusion of each of 3 pulses detected in the LYTF. Pulses are identified by increases in LYTF catch per unit effort (CPUE) for a sustained period of 3–5 days followed by a substantial decrease in CPUE. Samples from each pulse were analyzed and results were reported within 36 hours of receipt at the GCL. For each pulse, separate stock composition estimates were provided for the samples collected at Big Eddy and Middle Mouth. A third, pooled estimate created by combining the samples from both locations was also reported. For this estimate, it is necessary to assume that the samples represent the same proportion of the total Chinook salmon passage at each location.

For both the Pilot Station Test Fishery and District Y-5 subsistence fishery collections, samples were stratified temporally postseason. Sample sets were created in such manner that they created representative catch proportion estimates, while maintaining minimum sample size requirements. The Pilot station samples were stratified to represent the same 3 pulses detected in the LYTF.

Samples were collected in subdistrict Y-4A from Kaltag and Nulato, and in subdistrict Y-4B from Bishop Mountain and Galena. Stock composition estimates were calculated for these fisheries both by location (i.e., Kaltag and Nulato separately) and also by subdistrict (i.e., Kaltag and Nulato pooled). Samples were also collected from a single location in subdistrict Y-4C, Ruby.

LABORATORY METHODS

Genetic data were collected from the fishery samples as individual multi-locus genotypes for 48 SNPs. However, the same version of the baseline with 26 SNPs used in 2006 and 2007 (Templin et al. 2008) was used in 2008, and only genotypes from those SNPs were used to analyze the fishery samples in this study (Table 3). This reduced set of SNPs, when compared to the original set of 51 SNPs assayed in 2006, was determined to provide acceptable levels of accuracy and precision while providing substantial cost savings. More SNPs were assayed in this study because recent advancements in laboratory technology reduced the cost per genotype, and it is no longer cost effective for the GCL to run only 26 SNPs. The current platform supports genotyping either 48 samples and 48 assays or 96 samples and 96 assays, with the lowest cost per genotype obtained when all 48 by 48 or 96 by 96 reactions are performed. Therefore, 48 SNPs were assayed for this study, and an expanded baseline using 48 SNPs will be used for future Yukon River Chinook salmon GSI studies.

Genomic DNA was extracted using a DNeasy® 96 Tissue Kit by QIAGEN® (Valencia, CA).[1] Chinook salmon samples were genotyped using a BioMark 48.48 Dynamic Array (Fluidigm http://www.fluidigm.com/biomark_ genotyping.htm). The BioMark 48.48 Dynamic Array contains a matrix of integrated channels and valves housed in an input frame. On one side of the frame are 48 inlets to accept the sample DNA from each individual fish, and on the other are 48 inlets to accept the assays for each of the SNP markers. Once in the wells, the components are pressurized into the chip using the NanoFlex 4-IFC Controller. The 48 samples and 48 assays are then systematically combined into 2,304 parallel reactions. Each reaction was conducted in a 6.75 nL volume consisting of 1xTaqMan Universal Buffer (Applied Biosystems), 1.5 U AmpliTaq Gold DNA Polymerase (Applied Biosystems), 9 mM of each polymerase chain reaction (PCR) primer, 2 mM of each probe, 1xDA Assay Loading Buffer (Fluidigm), 12.5xROX (Invitrogen), and 0.01% Tween-20. Thermal cycling was performed on a BioMark IFC Cycler as follows: an initial denaturation of 10 min at 95°C followed by 50 cycles of 92° for 15 s and 60° for 1 min. The Dynamic Arrays were read on a BioMark Real-Time PCR System after amplification and scored using BioMark Genotyping Analysis software (Fluidigm).

The SNP data collected were individual diploid genotypes for each locus. Genotype data were stored as output text files on a network drive. The data on this network are backed up nightly. Long term storage of the data is in an Oracle database, *LOKI*, supported and maintained by ADF&G.

QUALITY CONTROL METHODS

The following measures were implemented to ensure the quality and consistency of data produced by laboratory procedures:

1) Each individual was assigned a unique accession identifier. When DNA was extracted

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

and analyzed from each individual, a sample sheet was created that linked each individual's code to a specific well in a uniquely numbered 96-well plate. This sample sheet accompanied the individual through all phases of a project, minimizing the risk of misidentification of samples.

2) Genotypes were assigned to individuals using a double-scoring system. Two researchers designated allele scores for each individual.

3) Approximately 8% of individuals, 8 samples from each 96-well DNA extraction plate, were reanalyzed for all SNPs. This provided a measure of reproducibility and allowed for correcting any errors created during the processing of individual plates.

4) The final data were checked for duplicated multi-locus genotypes for indication of errors caused prior to extraction of the DNA. When duplicate genotypes were found, the genotype was attributed to the first individual, and subsequent individuals with the same genotype were removed from the analysis.

5) The data have been permanently stored in an Oracle database, *LOKI,* administered by ADF&G.

BASELINE ANALYSES

A brief description of the baseline analysis is provided here, but the reader is referred to Templin et al. (2008) for a more complete description. Genotype distributions were tested for deviation from Hardy-Weinberg expectation (H-W), and all pairs of markers were tested for linkage disequilibrium within each collection using GENEPOP (version 3.3; updated version of Raymond and Rousset 1995). Critical values (α=0.05) were adjusted for multiple tests within collections and multiple tests across markers within collections using the sequential Bonferroni approach (Rice 1989). If linkage disequilibrium was significant in more than half of the collections, we produced composite haplotypes for each fish by combining the genotypes from these linked markers and treated them as a single locus in further analyses. Composite haplotypes were used rather than eliminating one of the linked loci because, for some loci, linkage associations between alleles are not consistent across populations. Eliminating a locus would result in the loss of additional information found in the differences in association between alleles. For each fish, if the genotype for either marker was missing, then the composite-haplotype locus was excluded from further analysis.

Baseline collections taken in multiple years from the same location were pooled for further analyses. The log likelihood ratio test (Weir 1990) was used to test for homogeneity among collections taken in multiple years. Comparison of population structure in this baseline of 26 SNPs to previous baselines was performed by first computing the Cavalli-Sforza and Edwards (1967) chord distances between population pairs and then clustering the populations using the unweighted paired group mean algorithm (UPGMA; Sneath and Sokal 1973) to display patterns of interpopulation similarity.

Simulations

Simulations were conducted to evaluate the accuracy and precision of the SNP baseline to provide compositional estimates of mixtures of Chinook salmon harvested in Yukon River fisheries. These simulations were used to help assess whether the baseline of allele frequencies at the 26 SNP markers would provide sufficient information to identify individual stocks or groups of stocks (reporting groups) in mixtures. Reporting groups for genetic stock identification of Yukon River Chinook salmon were defined in previous studies based on a combination of genetic similarity, geographic features, and management applications.

Reporting groups were defined hierarchically into 3 levels: 1) country of origin, 2) broad scale, and 3) fine scale. The broad scale groups (Lower Yukon, Middle Yukon, and Canada) were the same regions previously used for estimating stock composition of the harvest by scale pattern analysis (JTC 1997). Simulations performed using fine-scale reporting groups represent identifiable sets of populations useful for management and research (Table 1). These groups were previously defined in 2004 (Templin et al. 2006b) when SNPs were first used to estimate the stock composition of the harvest.

Simulations were performed using the Statistical Package for Analyzing Mixtures (SPAM version 3.7, Debevec et al. 2000). Mixture genotypes were randomly generated from the baseline allele frequencies assuming Hardy-Weinberg equilibrium. Each simulated mixture (N=400) was composed entirely of the stock or reporting group under study. When a reporting group mixture was simulated, all stocks in the reporting group contributed equally to the mixture. Average estimates of mixture proportions and 90% confidence intervals were derived from 1,000 simulations. Reporting groups with mean correct estimates of 90% or better are considered highly identifiable in fishery applications.

MIXED STOCK ANALYSIS

Chinook salmon stock composition estimates for the stock groups of management interest were generated using the program BAYES (Pella and Masuda 2001). The estimation routine in BAYES was run using 3 chains without thinning with a Markov Chain Monte Carlo sample size of 10,000. Three chains were run beginning with different starting conditions. Inference was based on the posterior distribution based on a combined set of the last 5,000 steps of each chain. The mean of the posterior distribution is reported as the best estimate, and the central 90% of the distribution was reported as the 90% confidence interval. A flat prior was used, where the Dirichlet prior distribution parameters for stock proportions were equal (1/N).

Stock composition estimates were reported for 3 hierarchical levels when sample sizes were ≥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, Tanana, Upper U.S. Yukon, Canada Border, Pelly, Carmacks, and Takhini). When sample sizes were <200, only the first 2 levels of the hierarchy, country of origin and broad scale, were reported. Increasing the resolution to 3 reporting groups in the U.S. (Lower River, Tanana, and Upper Koyukuk/Upper U.S. Yukon) has been supported by simulation studies of the baseline.

RESULTS

COLLECTIONS

During 2008, 4,899 Chinook salmon were sampled as part of 13 collections from test, commercial, and subsistence fisheries in the U.S. portion of the Yukon River drainage (Table 2; Figure 1). Test fishery catches were sampled from the LYTF located in District Y-1 and from the Pilot Station Test Fishery located in District Y-2. Sampling was conducted in 6 commercial fishing periods in District Y-1. In 2008, all lower Yukon River commercial fishing targeted chum salmon, and samples were taken from the incidental harvest of Chinook salmon. Mesh sizes in this fishery were restricted to 6 inches or less for the purpose of targeting chum salmon. Chinook salmon were sampled in one chum salmon-directed commercial fishing period in District Y-2.

Subsistence harvests were sampled in Districts Y-1, Y-3, Y-4, and Y-5. Samples from the District Y-4 subsistence harvest were taken from Kaltag and Nulato (subdistrict Y-4A), Bishop Mountain and Galena (subdistrict Y-4B), and Ruby (subdistrict Y-4C). District Y-5 samples were taken from Tanana (subdistrict Y-5B) and Rapids (District Y-5C).

LABORATORY / QUALITY CONTROL ANALYSIS

Of the fishery samples, a total of 3,672 individuals were analyzed for allelic variation at 26 SNPs. The quality control procedure demonstrated an overall discrepancy rate of 0.26%. This discrepancy rate is based on the re-analysis of 8% of the total number of samples. The overall genotyping failure rate was 1.49%, and ranged from a low of 0.17% for the samples collected at Pilot Station to a high of 3.07% for the samples collected from the District Y-1 commercial fishery harvest. The failure rate represents the number of samples that did not amplify during PCR, averaged over all loci.

BASELINE ANALYSIS

Linkage disequilibrium within each collection yielded significant results in >90% of collections at 2 marker pairs: *Ots_FGF6A* and *Ots_FGF6B*; and *Ots_HSP90B-100* and *Ots_HSP90B-385*. These 2 marker pairs were combined, creating 2 composite-haplotype loci (Table 3).

Simulations

All fine-scale reporting regions had mean correct allocations of >90% for the 100% simulation tests (Table 4). The population structure revealed by this version of the baseline is similar to past versions (Figure 2). The reader is referred to Templin et al. (2008) for a comprehensive discussion of the baseline analysis results.

MIXED STOCK ANALYSIS

Test Fishery

Three pulses of Chinook salmon were detected passing through the LYTF (Table 2; Figure 3). The conclusion of the first pulse was identified by a decline in the daily catch from a high of 122 on June 16 and 358 samples caught through June 17 were flown back to Anchorage and analyzed. To ease reading hereafter, all stock composition estimates will be rounded to the nearest percent. Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the LYTF from June 3 through June 17 was 53%. The estimates for Big Eddy and Middle Mouth for the same period were 50% and 55% respectively (Table 5; Figure 4).

The conclusion of the second pulse was detected by a decline in the daily catch from a high of 117 on June 24 and 327 samples caught between June 18 and June 25 were flown back to GCL and analyzed. Stock composition estimates indicated that the proportion of Canadian-origin Chinook salmon present in the LYTF from June 18 through June 25 had declined to 43%. The estimates for Big Eddy and Middle Mouth for the same period were 52% and 40%, respectively (Table 6; Figure 5).

The end of the third pulse was detected by a decline in the daily catch from a high of 205 on June 27 and 215 samples caught between June 26 and June 29 were flown back to GCL and analyzed. Stock composition estimates showed that the proportion of Canadian-origin Chinook salmon present in the LYTF from June 26 through June 29 was 44%. The estimates for Big Eddy and Middle Mouth for the same period were 57% and 32% respectively, (Table 7; Figure 6).

The estimates for each of the 3 pulses were available within 36 hours of receipt of samples at the GCL.

Samples from the Pilot Station Test Fishery were divided into 3 strata postseason. These strata were intended to characterize the same 3 pulses detected in the LYTF. In the Pilot Station Test Fishery, the Canadian contribution to the Chinook salmon passage ranged from a high of 47% in the first strata (June 7–23) to a low of 31% in the third and final strata (June 30–August 2) (Table 8; Figure 7).

Commercial

Estimates of stock composition in the commercial harvest in District Y-1 of the Yukon River were calculated for Periods 1 and 2 (July 4 and 6, respectively), and Periods 3 through 6 (July 8–14) were pooled for the purpose of achieving an adequate sample size. The Canadian component contributed between 41% and 14% of the harvest across all of the commercial fishing periods (Table 9; Figure 8). The largest portion of the Canadian component was estimated to be from the Carmacks region for all periods.

The Canadian component was estimated at 28% for the District Y-2 commercial fishery period sampled on July 4 (Table 10).

Subsistence

In the District Y-1 subsistence fishery, 54% of the harvest samples were comprised of Canadian populations (Table 11). The Pelly region was the largest contributor to the Canadian component with 25%. Of the U.S. contribution, the largest component was estimated to be from the Tanana River (30%), while the Lower Yukon populations contributed 8% of the harvest. The harvest from the Y-3 subsistence fishery showed a similar proportion of Canadian populations (49%). However, in this fishery, the Lower Yukon component was larger than in District Y-1 (31%). The estimated contribution of Canadian populations to the subsistence harvest in District Y-4 varied from a high of 59% in Bishop Mountain (subdistrict 4-B) to a low of 33% in Galena (subdistrict 4-B; Tables 12–14). As with the commercial harvest in the lower river, the Carmacks region comprised the greatest portion of the Canadian estimate in all 3 subdistricts.

The Canadian contribution to the subsistence harvest in District Y-5, subdistrict Y-5B, was 67%. The Canadian contribution to the subsistence harvest in subdistrict Y-5C, was 78% for the first pooled period (June 17–July 2), and 68% for the second pooled period (July 2–24). The Upper U.S. region populations contributed most of the U.S. portion of the harvest in all District Y-5 subdistricts. The Carmacks region component increased from 4% in the first period (the lower bound of the 90% confidence interval was 0) to 46% in the second period; this trend was accompanied by a decrease in the Pelly region component from 49% in the first period to 16% in the second period (Table 15). This trend of an increasing Carmacks component accompanied by a decreasing Pelly component is significant given the non-overlapping 90% confidence intervals.

Age-class

Sufficient samples were available to estimate the composition of the age-5 and age-6 component for samples collected in the Y-1 subsistence fishery, and for the pooled sample from the subdistrict Y-4A subsistence fishery (Kaltag and Nulato combined) (Appendices A and B). In the District Y-1 subsistence fishery, the Canadian component of the age-5 harvest was 52%, and 56% for the age-6 component. In the subdistrict Y-4A subsistence fishery, the Canadian component of the age-5 harvest was 43%, and 55% for the age-6 component.

DISCUSSION

The 2008 Yukon River Chinook salmon run was well below average. Midway through the season, it was clear that projected Chinook salmon run abundance would not support average subsistence harvests in Alaska (approximately 50,000 Chinook salmon), meet escapement goals in Alaska, and meet the interim management escapement goal (IMEG) of >45,000 fish in Canada agreed to by the Yukon River Panel. In conjunction with low overall run strength estimated at Pilot Station sonar, the inseason genetics information on the Canada-bound proportion of the run highlighted concerns regarding the run's capacity to meet the Canadian border escapement goal, Alaska subsistence harvest needs, and Canadian aboriginal harvest needs.

Based on inseason projections from the LYTF and Pilot Station sonar combined with inseason genetics information, subsistence salmon fishing periods were reduced chronologically upriver during the second and third pulses of Chinook salmon run consistent with the migratory timing as the run progressed in an effort to conserve Chinook salmon. These reductions, beginning June 23 in District Y-1, while unfortunate, were needed to provide adequate numbers of Chinook salmon on the spawning grounds.

This study detected an increasing preference through time for Canadian-origin Chinook salmon entering the south mouth of the river, where the Big Eddy sites are located, as evidenced by declining proportions through time at Middle Mouth and corresponding increases at Big Eddy. The difference in proportions of Canadian-origin Chinook salmon between Big Eddy and Middle Mouth are significant for the third pulse, given that the 90% confidence intervals do not overlap. It is interesting to note that in 2008 the majority of Chinook salmon entered the Yukon River through the Middle Mouth; hence, in the future there is potential to inform fishery management decisions by applying these stock composition estimates to relative abundance data collected at the test fishery (Dani Evenson, Commercial Fisheries Biologist, ADF&G; personal communication). However, interpretation of the pooled LYTF estimates requires the assumption that equal proportions of the total run were sampled at the Big Eddy and Middle Mouth sites.

The pilot study on the potential for inseason analysis demonstrated that rapid production of stock composition estimates is possible for lower Yukon River Chinook salmon fisheries. Frequent flight service from Emmonak enabled timely delivery of samples, and all estimates were provided within 36 hours of receipt at the GCL.

The trend of a declining Canadian component in stock composition was similar through time between the LYTF and the Pilot Station test fishery. In 2008, the midpoint of the Chinook salmon run was June 26, and the midpoint at Pilot Station was June 29 (Hayes and Newland 2008), representing a 3-day travel time of Chinook salmon from the LYTF (rm 24) to Pilot Station (rm 123). In the LYTF, the Canada Border reporting region made up the largest portion of the Canadian component in the first pulse of Chinook salmon entering the Yukon River (24%

overall), while the Tanana region made up the largest portion of the U.S. component (27% overall). During the second pulse, the largest portion of the Canadian component shifted to the Pelly reporting region (20% overall) and the Lower Yukon region made up the largest portion of the U.S. component (29% overall). During the third pulse, the largest portion of the Canadian component was from the Carmacks region (34% overall), and the Lower Yukon region made up an even greater portion of the U.S. component than that observed in the second pulse (33% overall). The samples from the Pilot Station test fishery stratified over the same 3 pulses detected in the LYTF, showed a similar trend of an increasing Lower Yukon proportion and corresponding increase in the Carmacks proportion over the 3 main pulses. In this test fishery, the Lower Yukon region went from 13% during the first pulse to 60% during the third pulse, and the Carmacks region increased from 11% to 22% overall (fine-scale estimates were not provided for the middle strata in this fishery due to insufficient sample sizes). It should be noted that the LYTF uses set gillnets made of 8.5 inch and is intended to assess the relative abundance and run timing of Chinook salmon, while the Pilot Station test fishery uses drift gillnets of multiple mesh sizes and is intended to catch both Chinook and chum salmon for the purpose of speciating Pilot Station sonar estimates. Different catchabilities for Chinook salmon between these 2 test fisheries may have an effect on their estimated stock compositions.

A similar pattern to that seen in the Lower River test fisheries was observed in the samples collected from subsistence fish wheels in subdistrict Y-5C. This fishery is located at Rapids (rm 731), approximately 75 miles upriver of the confluence of the Tanana and Yukon rivers. In this fishery, the Upper U.S. region made up the largest portion of the U.S. component, as expected, with 20% and 24% of the overall proportion over 2 temporal strata. The pattern in the Canadian component was similar to that seen in the Lower Yukon test fisheries, with a decrease in the Pelly portion from 49% to 16%, and a corresponding increase in the Carmacks component from 4% (the lower bound of the 90% CI was zero) to 46%.

Comparisons between 2008 stock proportion estimates and previous years for District Y-1 and Y-2 commercial fisheries are difficult to make due to the limited fishing effort in 2008. The first commercial chum salmon fishing period, from which the incidental harvest of Chinook salmon was sampled, was on July 2 in District Y-1 and July 4 in District Y-2, well past the midpoint of the run which occurred on June 26. However, the higher proportion of U.S. stocks present in these harvests at this point in the run is consistent with previous years, as the first pulse of Chinook salmon entering the Yukon River consistently has the highest Canadian proportion (Templin et al. 2006a,b; Templin et al. 2008; DeCovich and Templin 2009).

As in 2007, harvest locations were available for District Y-4 subsistence samples. However, sample sizes were not large enough to provide stock composition estimates by river bank. The proportions of U.S. and Canadian stocks were similar between subdistricts Y-4A, B, and C. The Canadian proportion varied from a high of 46% in the subdistrict Y-4A pooled sample to a low of 44% in the subdistrict Y-4C pooled sample. These proportions are not appreciably different from each other given the size of the samples.

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TABLES AND FIGURES

Table 1.–Chinook salmon collections from the Yukon River drainage organized hierarchically into reporting groups for mixed stock analysis using genetic stock identification.

Country	Broad scale	Fine scale	Population	Year(s)	Sample size
United States					
	Lower Yukon				
		Lower Yukon			
			Andreafsky River	2003	208
			Anvik River	2002	99
			Tozitna River	2002, 2003	450
			Gisasa River	2001	228
	Middle Yukon				
		Upper U.S. Yukon			
			Sheenjek River	2002, 2004, 2006	51
			Beaver Creek	1997	100
			Chandalar River	2002, 2003, 2004	178
			Henshaw Creek	2001	150
			S. Fork Koyukuk River	2003	56
		Tanana River			
			Kantishna River	2005	200
			Chena River	2001	200
			Salcha River	2005	200
Canada					
	Canada				
		Border			
			Chandindu River	2001	158
			Klondike River	2001, 2003	80
		Pelly			
			Mayo River	1997, 2003	62
			Stewart River	1997	99
			Blind Creek	1997, 2003	139
			Pelly River	1996, 1997	150
		Carmacks			
			Little Salmon	1987, 1997	100
			Big Salmon	1987, 1997	119
			Tatchun Creek	1987, 1997, 2002, 2003	169
			Nordenskiold River	2003	56
			Nisutlin River	1987, 1997	56
		Takhini			
			Takhini River	1997, 2003	101
			Whitehorse Hatchery	1985, 1987, 1997	242
				Total	3,651

Table 2.–Chinook salmon collections from test fishery catches, and commercial and subsistence fishery harvests in the Yukon River drainage, 2008.

District	Period	Dates	Gear Type	Location	Sample size	Number assayed
Commercial						
Y-1	1	7/2	≤6 restricted	Emmonak	175	175
	2	7/5	≤6 restricted		200	200
	3	7/8	≤6 restricted		65	65
	4	7/10	≤6 restricted		72	72
	5	7/12	≤6 restricted		19	19
	6	7/14	≤6 restricted		4	4
				Total Y-1 commercial	535	535
Y-2	1	7/4	≤6 Restricted	Saint Mary's	108	100
				Total Commercial	643	100
Subsistence						
Y-1		6/24–7/7	SGN	Emmonak	472	472
Y-3		6/17–7/14	SGN	Holy Cross	133	133
Y-4A		6/25–7/9	DGN	Kaltag	250	250
Y-4A		6/26–7/15	SGN	Nulato	130	130
Y-4B		7/7–7/22	SGN	Bishop Mountain	103	103
Y-4B		6/20–7/17	SGN/ DGN	Galena	145	145
Y-4C		6/26–7/17	SGN/ FW	Ruby	128	128
				Total Y-4 Subsistence	756	756
Y-5B		6/25–7/6	FW	Tanana	213	200
Y-5C		6/17–7/24	FW	Rapids	1071	400
				Total Subsistence	2,645	1,961
Test Fishery						
Y-1	A	6/3–6/17	SGN	LYTF-Big Eddy	183	183
	B	6/17–6/25	SGN		105	105
	C	6/26–6/29	SGN		112	112
Y-1	A	6/5–6/17	SGN	LYTF-Middle Mouth	175	175
	B	6/17–6/25	SGN		222	222
	C	6/26–6/29	SGN		103	103
				Total LYTF	900	900
Y-2	A	6/7–6/23	DGN	Pilot Station	333	333
	B	6/24–6/29	DGN		155	155
	C	6/30–8/2	DGN		223	223
				Total Pilot Station	711	711
				Total Test Fishery	1,611	1,611
				Grand Total	4,899	3,672

Note: Gear types used were set gillnet (SGN), drift gillnet (DGN), and fish wheels (FW). Commercial fisheries in Districts Y-1 and Y-2 used drift gillnets with <6 inch restricted mesh sizes.

Table 3.–Single nucleotide polymorphisms assayed in individual Chinook salmon sampled in the U.S. portion of the Yukon River drainage, 2008.

Locus	Source
Ots_E2-275	Smith et al. 2005a
Ots_ETIF1A	Unpublished
Ots_FGF6A[1]	Unpublished
Ots_FGF6B[1]	Unpublished
Ots_GH2	Smith et al. 2005b
Ots_GPDH-338	Smith et al. 2005a
Ots_GST-207	Smith et al. 2005a
Ots_hnRNPL-533	Smith et al. 2005a
Ots_HSP90B-100[2]	Smith et al. 2005a
Ots_HSP90B-385[2]	Smith et al. 2005a
Ots_IGF-I.1-76	Smith et al. 2005a
Ots_il-1racp-166	Smith et al. 2005a
Ots_MHC1	Smith et al. 2005b
Ots_MHC2	Smith et al. 2005b
Ots_SWS1op-182	Smith et al. 2005a
Ots_P53	Smith et al. 2005b
Ots_Prl2	Smith et al. 2005b
S7-1	Unpublished
Ots_SClkF2R2-135	Smith et al. 2005a
Ots_SERPC1-209	Smith et al. 2005a
Ots_SL	Smith et al. 2005b
Ots_Tnsf	Smith et al. 2005b
Ots_u202-161	Smith et al. 2005a
Ots_u4-92	Smith et al. 2005a
unkn526	Unpublished
Ots_u6-75	Smith et al. 2005a

Note: Superscripts denote locus pairs that were combined into composite haplotype loci.

Table 4.–Mean reporting group allocations of simulated mixtures of Yukon River Chinook salmon from the baseline of 26 SNPs.

Reporting region		Mean	90% CI
Country			
	United States	0.983	(0.962–0.999)
	Canada	0.987	(0.965–1.000)
Broad-scale			
	Lower Yukon	0.990	(0.975–1.000)
	Middle Yukon	0.971	(0.941–0.994)
	Canada	0.987	(0.965–1.000)
Fine-scale			
	Lower Yukon	0.990	(0.975–1.000)
	Upper US	0.907	(0.840–0.967)
	Tanana	0.940	(0.886–0.980)
	Canada Border	0.968	(0.933–0.993)
	Pelly	0.913	(0.846–0.968)
	Carmacks	0.931	(0.870–0.981)
	Takhini	0.981	(0.956–0.998)

Note: Each set of mixtures (*N*=400) was created from a single reporting region based on allelic frequencies for that region. The results reported are the mean and bounds of the middle 90% (CI) of correct allocations from 1,000 bootstrap iterations (Templin et al. 2008).

Table 5.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of Chinook salmon caught in the Lower Yukon Test Fishery, representing the first pulse (“A”), 2008.

	Lower Yukon Chinook Test Fishery- Pulse "A"								
	Big Eddy June 3–17 *N*=183			Middle Mouth June 5–17 *N*=175			Pooled June 3–17 *N*=358		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI	Est	S.D.	90% CI
Country									
United States	0.505	0.055	(0.413–0.594)	0.450	0.053	(0.365–0.540)	0.468	0.043	(0.399–0.540)
Canada	0.495	0.055	(0.406–0.587)	0.550	0.053	(0.460–0.635)	0.532	0.043	(0.460–0.602)
Broad-scale									
Lower Yukon	0.110	0.028	(0.066–0.160)	0.167	0.034	(0.114–0.224)	0.139	0.022	(0.104–0.177)
Middle Yukon	0.395	0.058	(0.301–0.490)	0.283	0.052	(0.202–0.375)	0.328	0.044	(0.259–0.405)
Canada	0.495	0.055	(0.406–0.587)	0.550	0.053	(0.460–0.635)	0.532	0.043	(0.460–0.602)
Fine-scale	*Insufficient samples*			*Insufficient samples*					
Lower Yukon							0.139	0.022	(0.104–0.177)
Upper U.S. Yukon							0.063	0.050	(0.000–0.150)
Tanana							0.265	0.038	(0.204–0.328)
Canada Border							0.235	0.041	(0.170–0.304)
Pelly							0.168	0.061	(0.071–0.271)
Carmacks							0.128	0.045	(0.058–0.202)
Takhini							0.001	0.002	(0.000–0.004)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 6.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of Chinook salmon caught in the Lower Yukon Test Fishery, representing the second pulse ("B"), 2008.

	Lower Yukon Chinook Test Fishery- Pulse "B"								
	Big Eddy June 18–25 *N*=105			Middle Mouth June 18–25 *N*=222			Pooled June 18–25 *N*=327		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI	Est	S.D.	90% CI
Country									
United States	0.485	0.062	(0.384–0.588)	0.602	0.045	(0.530–0.676)	0.568	0.037	(0.507–0.628)
Canada	0.515	0.062	(0.412–0.616)	0.398	0.045	(0.324–0.471)	0.432	0.037	(0.372–0.493)
Broad-scale									
Lower Yukon	0.210	0.047	(0.136–0.290)	0.332	0.038	(0.271–0.397)	0.290	0.030	(0.242–0.341)
Middle Yukon	0.276	0.060	(0.179–0.379)	0.270	0.047	(0.197–0.350)	0.278	0.037	(0.217–0.340)
Canada	0.515	0.062	(0.412–0.616)	0.398	0.045	(0.324–0.471)	0.432	0.037	(0.372–0.493)
Fine-scale	*Insufficient samples*								
Lower Yukon				0.332	0.038	(0.271–0.397)	0.290	0.030	(0.242–0.341)
Upper U.S. Yukon				0.059	0.050	(0.000–0.149)	0.069	0.041	(0.002–0.140)
Tanana				0.211	0.046	(0.137–0.286)	0.208	0.037	(0.148–0.271)
Canada Border				0.073	0.034	(0.021–0.132)	0.065	0.029	(0.020–0.116)
Pelly				0.231	0.072	(0.116–0.353)	0.201	0.057	(0.111–0.298)
Carmacks				0.092	0.055	(0.001–0.184)	0.165	0.049	(0.088–0.247)
Takhini				0.003	0.006	(0.000–0.016)	0.002	0.005	(0.000–0.012)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 7.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of Chinook salmon caught in the Lower Yukon Test Fishery, representing the third pulse ("C"), 2008.

	Lower Yukon Chinook Test Fishery- Pulse "C"								
	Big Eddy June 26–29 *N*=112			Middle Mouth June 26–29 *N*=103			Pooled June 26–29 *N*=215		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI	Est	S.D.	90% CI
Country									
United States	0.433	0.059	(0.337–0.531)	0.679	0.065	(0.567–0.780)	0.556	0.045	(0.481–0.629)
Canada	0.567	0.059	(0.469–0.663)	0.322	0.065	(0.220–0.433)	0.444	0.045	(0.371–0.519)
Broad-scale									
Lower Yukon	0.267	0.049	(0.190–0.351)	0.394	0.063	(0.294–0.501)	0.332	0.040	(0.267–0.400)
Middle Yukon	0.166	0.052	(0.086–0.256)	0.284	0.074	(0.160–0.404)	0.224	0.043	(0.156–0.296)
Canada	0.567	0.059	(0.469–0.663)	0.322	0.065	(0.220–0.433)	0.444	0.045	(0.371–0.519)
Fine-scale									
Lower Yukon	*Insufficient samples*			*Insufficient samples*			0.332	0.040	(0.267-0.400)
Upper U.S. Yukon							0.166	0.055	(0.082–0.262)
Tanana							0.058	0.042	(0.000–0.128)
Canada Border							0.006	0.014	(0.000–0.036)
Pelly							0.046	0.045	(0.000–0.130)
Carmacks							0.339	0.057	(0.245–0.433)
Takhini							0.053	0.026	(0.013–0.100)

Note: The estimated group proportions are given for each of 3 hierarchical levels.

Table 8.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of Chinook salmon caught during 3 periods in the Pilot Station Test Fishery, 2008.

	Pilot Station Test Fishery 2008								
	Period A June 7–23 *N*=333			Period B June 24–29 *N*=155			Period C June 30–Aug 2 *N*=223		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI	Est	S.D.	90% CI
Country									
United States	0.528	0.039	(0.465–0.592)	0.672	0.038	(0.609–0.732)	0.694	0.039	(0.628–0.757)
Canada	0.473	0.039	(0.408–0.535)	0.328	0.038	(0.268–0.391)	0.306	0.039	(0.243–0.372)
Broad-scale									
Lower Yukon	0.134	0.025	(0.096–0.176)	0.484	0.037	(0.424–0.545)	0.597	0.040	(0.532–0.663)
Middle Yukon	0.394	0.040	(0.329–0.461)	0.188	0.036	(0.130–0.248)	0.097	0.029	(0.053–0.148)
Canada	0.473	0.039	(0.408–0.535)	0.328	0.038	(0.268–0.391)	0.306	0.039	(0.243–0.372)
Fine-scale									
Lower Yukon	0.134	0.025	(0.096–0.176)	*Insufficient samples*			0.597	0.040	(0.532-0.663)
Upper U.S. Yukon	0.026	0.034	(0.000–0.097)				0.071	0.039	(0.001–0.134)
Tanana	0.368	0.043	(0.295–0.437)				0.026	0.030	(0.000–0.086)
Canada Border	0.189	0.035	(0.134–0.250)				0.001	0.004	(0.000–0.009)
Pelly	0.171	0.061	(0.073–0.275)				0.043	0.037	(0.000–0.112)
Carmacks	0.111	0.048	(0.030–0.191)				0.222	0.048	(0.145–0.301)
Takhini	0.001	0.003	(0.000–0.008)				0.040	0.028	(0.000–0.089)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 9.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested from 3 periods in the commercial fishery in District Y-1 of the Yukon River, 2008.

	Yukon Y-1 Commercial								
	Period 1 July 2 *N*=175			Period 2 July 6 *N*=200			Periods 3 - 6 July 8–14 *N*=161		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI	Est	S.D.	90% CI
Country									
United States	0.589	0.045	(0.515–0.663)	0.865	0.029	(0.815–0.911)	0.727	0.039	(0.662–0.790)
Canada	0.411	0.045	(0.337–0.485)	0.136	0.029	(0.089–0.185)	0.273	0.039	(0.211–0.338)
Broad-scale									
Lower Yukon	0.511	0.045	(0.438–0.586)	0.819	0.031	(0.766–0.869)	0.685	0.040	(0.618–0.750)
Middle Yukon	0.078	0.033	(0.030–0.137)	0.046	0.019	(0.018–0.081)	0.043	0.021	(0.013–0.080)
Canada	0.411	0.045	(0.337–0.485)	0.136	0.029	(0.089–0.185)	0.273	0.039	(0.211–0.338)
Fine-scale									
Lower Yukon	*Insufficient samples*			0.819	0.031	(0.766-0.869)	*Insufficient samples*		
Upper U.S. Yukon				0.008	0.014	(0.000–0.038)			
Tanana				0.038	0.019	(0.009–0.072)			
Canada Border				0.001	0.003	(0.000–0.005)			
Pelly				0.007	0.014	(0.000–0.037)			
Carmacks				0.122	0.031	(0.073–0.174)			
Takhini				0.005	0.010	(0.000–0.027)			

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 10.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (N) of Chinook salmon harvested in the commercial fishery in District Y-2 of the Yukon River, 2008.

	Y-2 Commercial		
	July 4		
	N=100		
Reporting Group	Est	S.D.	90% CI
Country			
	0.718	0.054	(0.626-0.803)
United States	0.282	0.054	(0.197-0.374)
Canada			

Note: The estimated group proportions are given for country-of-origin.

Table 11.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the District Y-1 and Y-3 subsistence fisheries, 2008.

	Y-1 Subsistence			Y-3 Subsistence		
	Emmonak *N*=472			Holy Cross *N*=133		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI
Country						
United States	0.465	0.039	(0.401–0.529)	0.507	0.051	(0.422–0.591)
Canada	0.535	0.039	(0.471–0.599)	0.493	0.051	(0.409–0.578)
Broad-scale						
Lower Yukon	0.077	0.018	(0.049–0.109)	0.313	0.046	(0.240–0.390)
Middle Yukon	0.389	0.041	(0.322–0.456)	0.193	0.045	(0.123–0.271)
Canada	0.535	0.039	(0.471–0.599)	0.493	0.051	(0.409–0.578)
Fine-scale						
Lower Yukon	0.077	0.018	(0.049–0.109)	*Insufficient samples*		
Upper U.S. Yukon	0.093	0.060	(0.000–0.191)			
Tanana	0.295	0.047	(0.219–0.374)			
Canada Border	0.162	0.032	(0.111–0.218)			
Pelly	0.254	0.040	(0.191–0.323)			
Carmacks	0.109	0.034	(0.054–0.165)			
Takhini	0.010	0.009	(0.000–0.027)			

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 12.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the subsistence fishery in District Y-4, subdistrict A, 2008.

	Y-4A Subsistence								
	Kaltag *N*=250			Nulato *N*=130			Pooled (Kaltag and Nulato) *N*=380		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI	Est	S.D.	90% CI
Country									
United States	0.519	0.044	(0.447–0.591)	0.583	0.058	(0.486–0.677)	0.537	0.035	(0.479–0.595)
Canada	0.481	0.044	(0.409–0.553)	0.417	0.058	(0.323–0.514)	0.463	0.035	(0.405–0.521)
Broad-scale									
Lower Yukon	0.082	0.029	(0.037–0.132)	0.174	0.053	(0.091–0.266)	0.129	0.025	(0.090–0.171)
Middle Yukon	0.438	0.047	(0.360–0.515)	0.409	0.067	(0.301–0.521)	0.408	0.037	(0.348–0.470)
Canada	0.481	0.044	(0.409–0.553)	0.417	0.058	(0.323–0.514)	0.463	0.035	(0.405–0.521)
Fine-scale									
Lower Yukon	0.082	0.029	(0.037–0.132)		*Insufficient samples*		0.129	0.025	(0.090-0.171)
Upper U.S. Yukon	0.144	0.046	(0.072–0.223)				0.142	0.038	(0.082–0.208)
Tanana	0.293	0.043	(0.225–0.366)				0.266	0.036	(0.209–0.327)
Canada Border	0.025	0.023	(0.000–0.069)				0.030	0.020	(0.000–0.067)
Pelly	0.253	0.057	(0.159–0.348)				0.227	0.050	(0.148–0.306)
Carmacks	0.166	0.053	(0.084–0.257)				0.175	0.044	(0.108–0.251)
Takhini	0.036	0.018	(0.010–0.070)				0.031	0.016	(0.008–0.059)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

Table 13.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the subsistence fishery in District Y-4B, 2008.

	Y-4B Subsistence								
	Bishop Mountain *N*=103			Galena *N*=145			Pooled *N*=248		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI	Est	S.D.	90% CI
Country									
United States	0.412	0.074	(0.290–0.535)	0.675	0.048	(0.593–0.752)	0.546	0.047	(0.469–0.625)
Canada	0.588	0.074	(0.465–0.710)	0.325	0.048	(0.248–0.407)	0.454	0.047	(0.375–0.531)
Broad-scale									
Lower Yukon	0.068	0.032	(0.023–0.126)	0.152	0.053	(0.064–0.241)	0.118	0.034	(0.067–0.180)
Middle Yukon	0.344	0.075	(0.224–0.469)	0.523	0.063	(0.422–0.628)	0.428	0.055	(0.338–0.523)
Canada	0.588	0.074	(0.465–0.710)	0.325	0.048	(0.248–0.407)	0.454	0.047	(0.375–0.531)
Fine-scale									
Lower Yukon	*Insufficient samples*			*Insufficient samples*			0.118	0.034	(0.067-0.180)
Upper U.S. Yukon							0.094	0.064	(0.000–0.204)
Tanana							0.334	0.049	(0.255–0.415)
Canada Border							0.095	0.030	(0.050–0.147)
Pelly							0.102	0.058	(0.003–0.202)
Carmacks							0.254	0.055	(0.163–0.345)
Takhini							0.004	0.010	(0.000–0.024)

Note: The estimated group proportions are given for each of 3 hierarchical levels.

Table 14.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (N) of Chinook salmon harvested in the subsistence fishery in District Y-4C, 2008.

	Y-4C Subsistence		
	Ruby *N*=128		
Reporting Group	Est	S.D.	90%CI
Country			
United States	0.562	0.063	(0.458–0.667)
Canada	0.438	0.063	(0.333–0.542)
Broad-scale			
Lower Yukon	0.083	0.038	(0.030–0.153)
Middle Yukon	0.479	0.069	(0.365–0.592)
Canada	0.438	0.063	(0.333–0.542)

Note: The estimated group proportions are given for each of broad-scale and country-of-origin reporting groups.

Table 15.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of Chinook salmon harvested in the subsistence fishery in District Y-5, subdistricts B and C, 2008.

	Y-5B Subsistence			Y-5C Subsistence					
	Tanana			Stratum 1 - Rapids June 17–July 2			Stratum 2 - Rapids July 2–July 24		
	N=199			*N*=200			*N*=200		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI	Est	S.D.	90% CI
Country									
United States	0.335	0.052	(0.250–0.421)	0.222	0.061	(0.129–0.329)	0.319	0.046	(0.245–0.395)
Canada	0.665	0.052	(0.579–0.750)	0.778	0.061	(0.671–0.871)	0.681	0.046	(0.605–0.755)
Broad-scale									
Lower Yukon	0.053	0.027	(0.015–0.102)	0.003	0.007	(0.000–0.016)	0.032	0.021	(0.002–0.070)
Middle Yukon	0.282	0.053	(0.196–0.372)	0.219	0.061	(0.125–0.325)	0.287	0.045	(0.215–0.365)
Canada	0.665	0.052	(0.579–0.750)	0.778	0.061	(0.671–0.871)	0.681	0.046	(0.605–0.755)
Fine-scale									
Lower Yukon		*Insufficient samples*		0.003	0.007	(0.000-0.016)	0.032	0.021	(0.002-0.070)
Upper U.S. Yukon				0.196	0.071	(0.081–0.317)	0.243	0.051	(0.160–0.328)
Tanana				0.023	0.032	(0.000–0.092)	0.044	0.036	(0.000–0.107)
Canada Border				0.243	0.062	(0.144–0.349)	0.048	0.035	(0.000–0.109)
Pelly				0.490	0.079	(0.350–0.611)	0.163	0.065	(0.060–0.275)
Carmacks				0.042	0.049	(0.000–0.141)	0.464	0.066	(0.355–0.572)
Takhini				0.003	0.006	(0.000–0.017)	0.006	0.012	(0.000–0.034)

Note: The estimated group proportions are given for each of 3 hierarchical levels when possible.

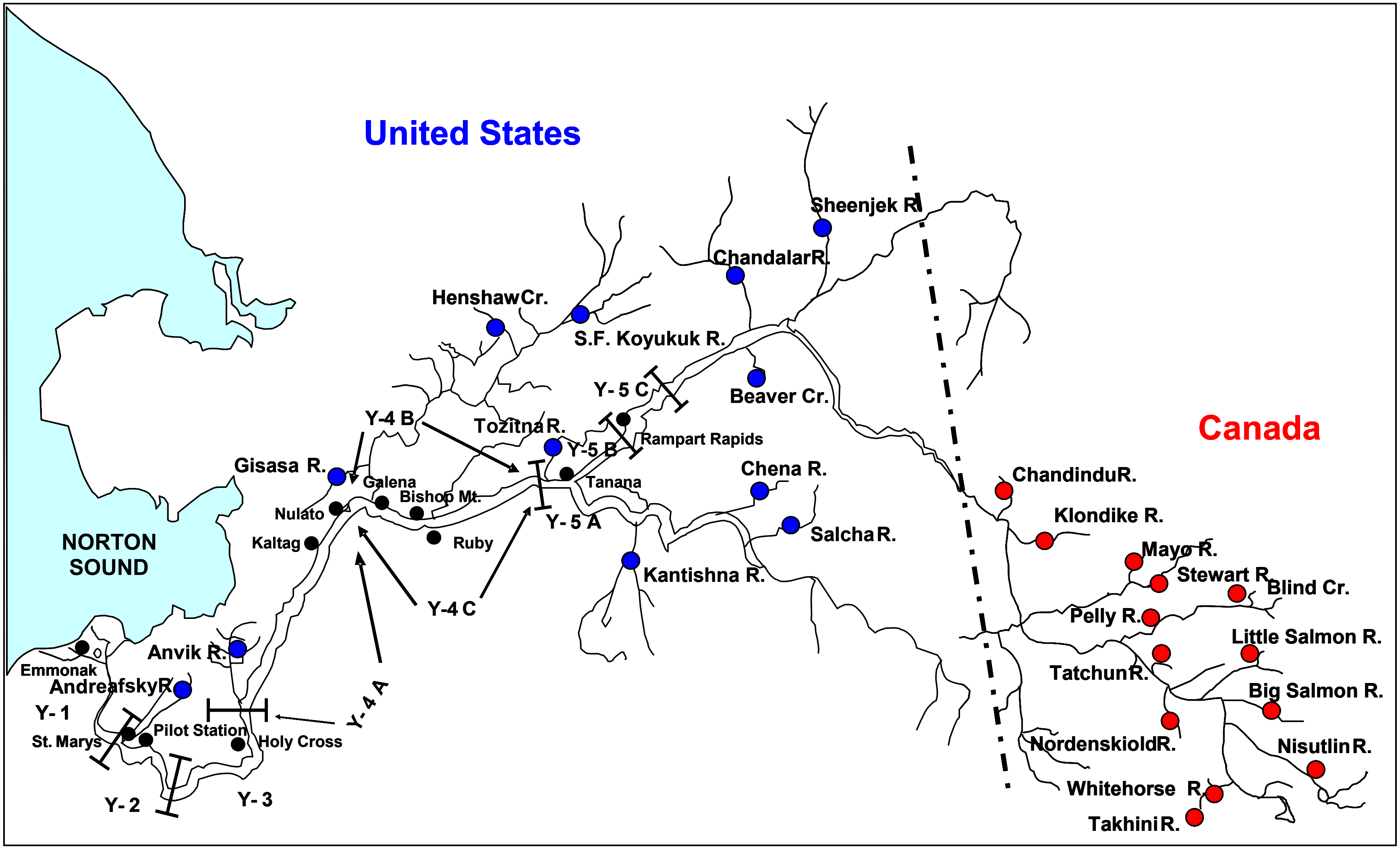
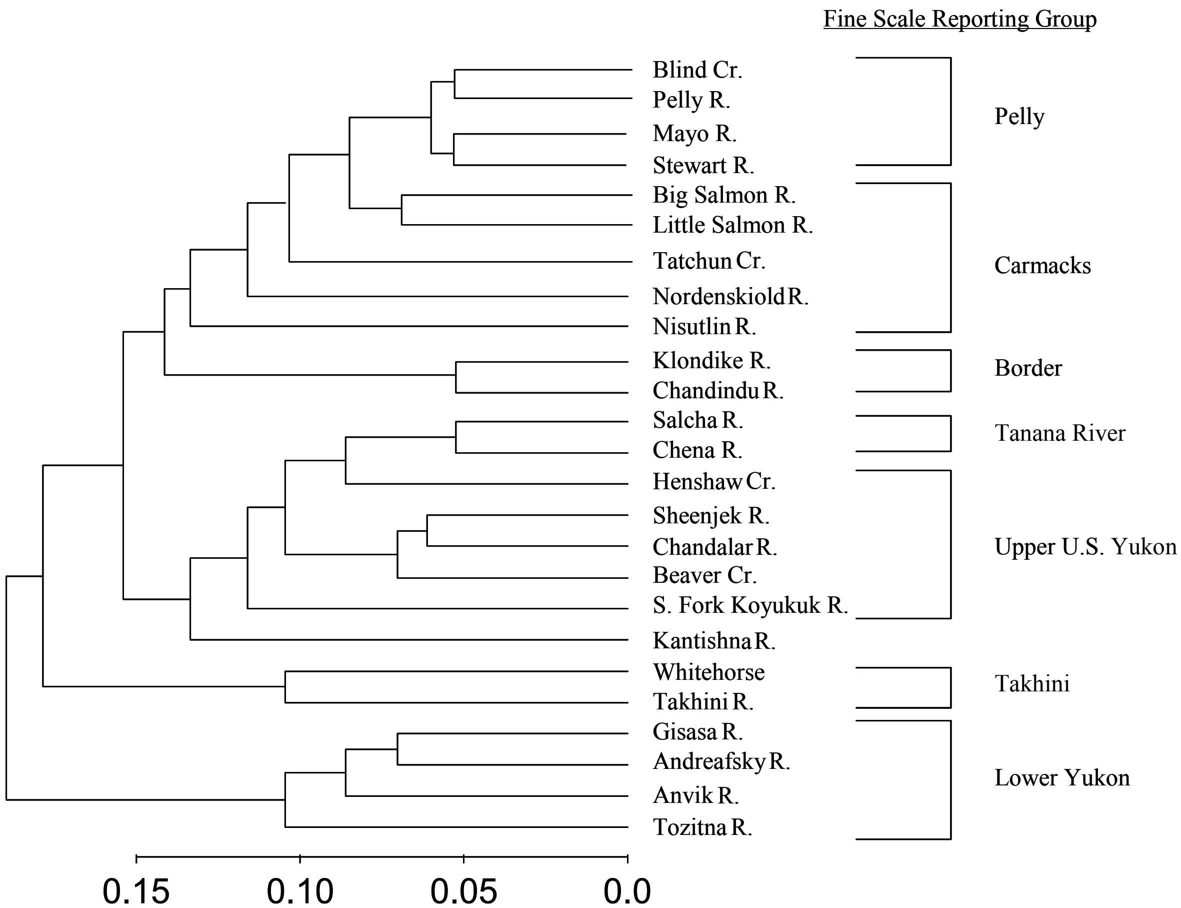
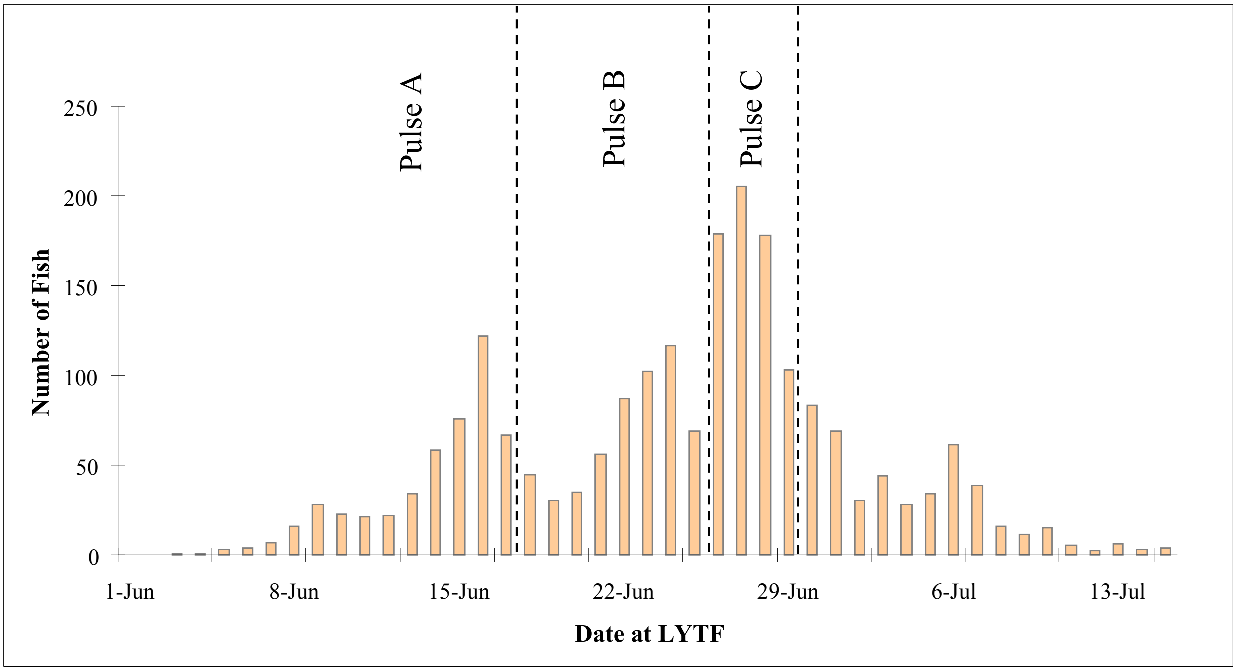


Figure 1.–Baseline collection locations and the fishing districts (and District Y-4 subdistricts) used for management of salmon fisheries in the United States portion of the Yukon River drainage.



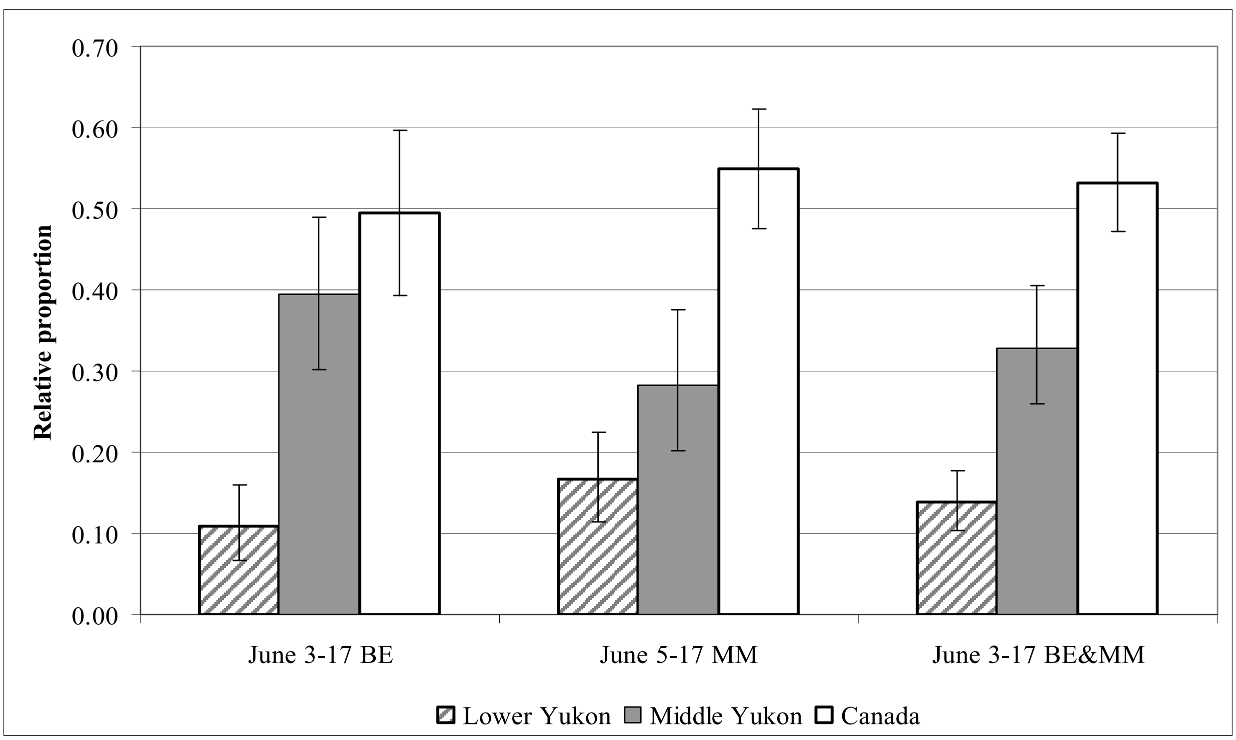
Note: Genetic distances are calculated from allele frequency differences from 26 SNPs. Population membership in the fine-scale reporting groups from Table 1 is indicated in the right margin (Templin et al. 2008).

Figure 2.–Unweighted paired group-mean clustering tree based on genetic chord distances between pairs of Chinook salmon populations in the Yukon River drainage.



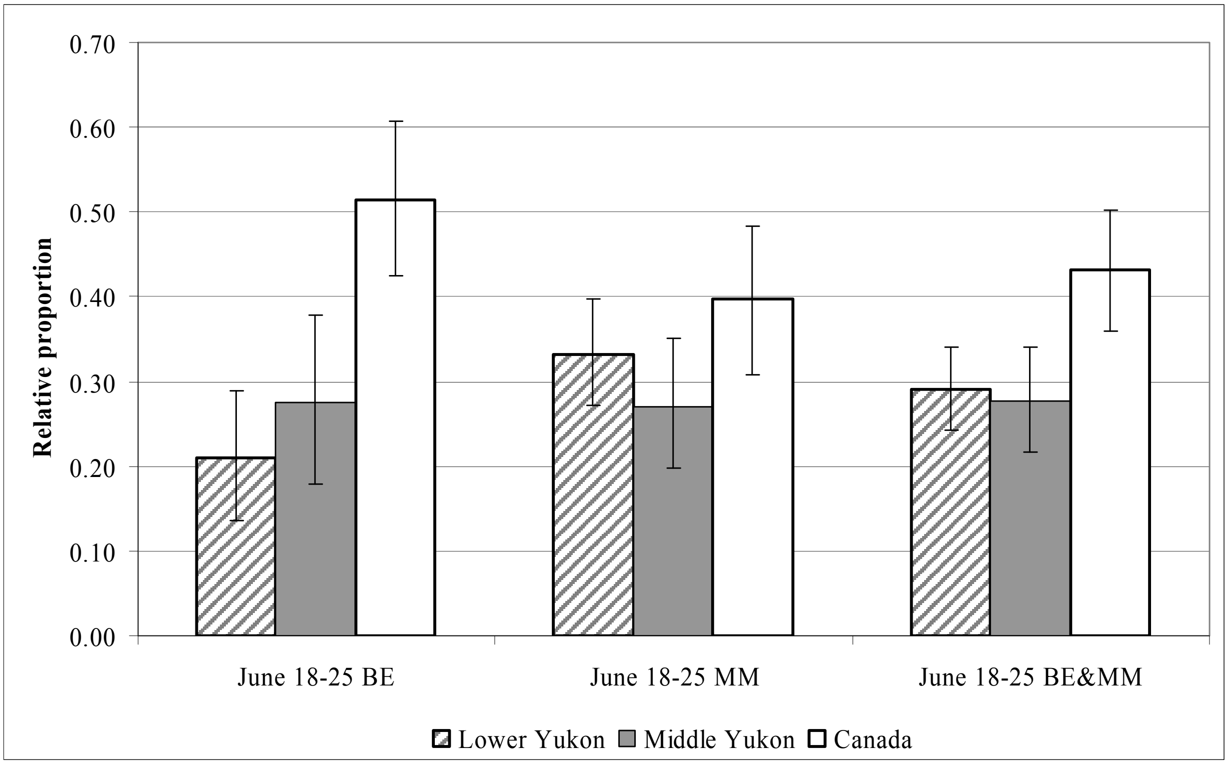
Note: Vertical dashed lines denote the temporal separation of collections for the purpose of sampling 3 distinct pulses of Chinook salmon through the fishery.

Figure 3.–Daily catch of Chinook salmon in the Lower Yukon Test Fishery (LYTF), 2008.



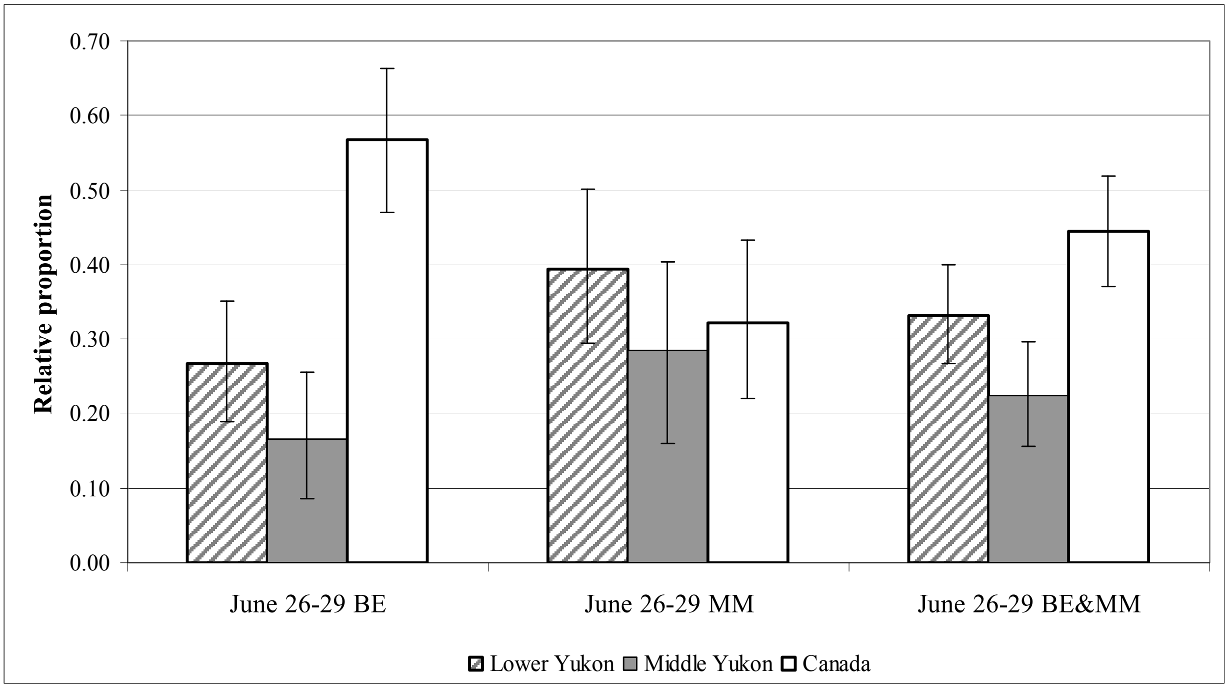
Note: Error bars denote the bounds of the 90% bootstrap confidence interval.

Figure 4.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in the Lower Yukon Test Fishery at Big Eddy (BE) and Middle Mouth (MM), representing the first pulse ("A"), 2008.



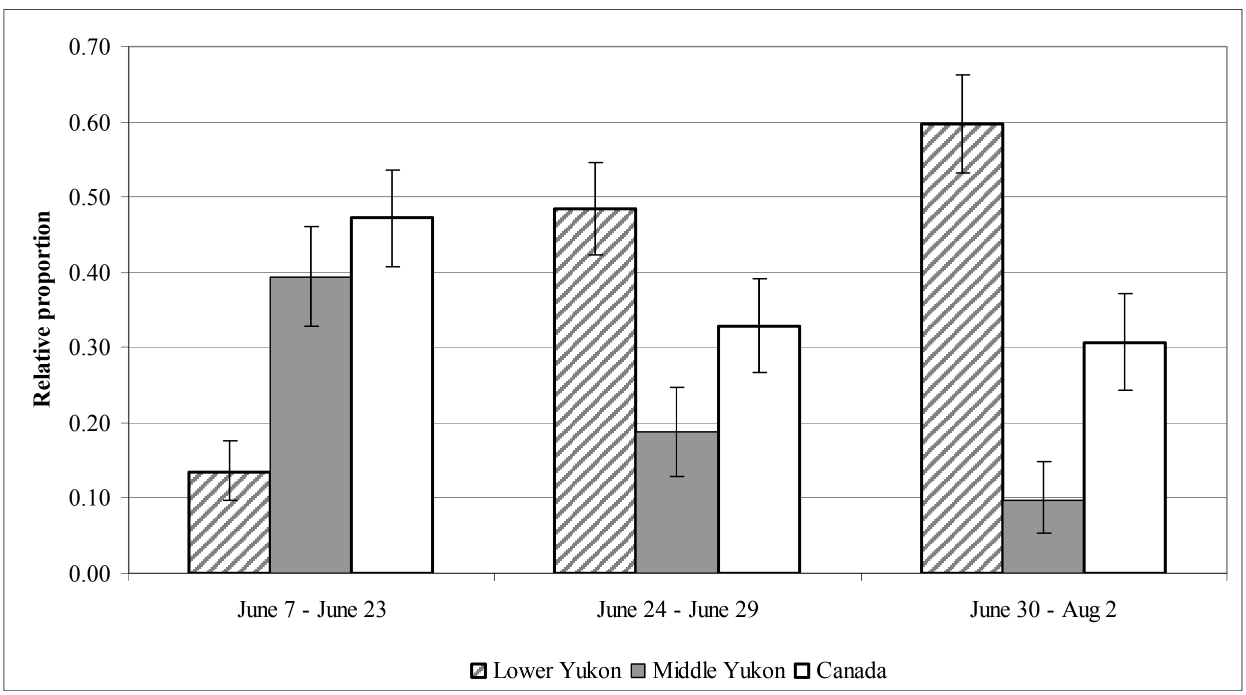
Note: Error bars denote the bounds of the 90% bootstrap confidence interval.

Figure 5.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in the Lower Yukon Test Fishery at Big Eddy (BE) and Middle Mouth (MM), representing the second pulse (“B”), 2008.



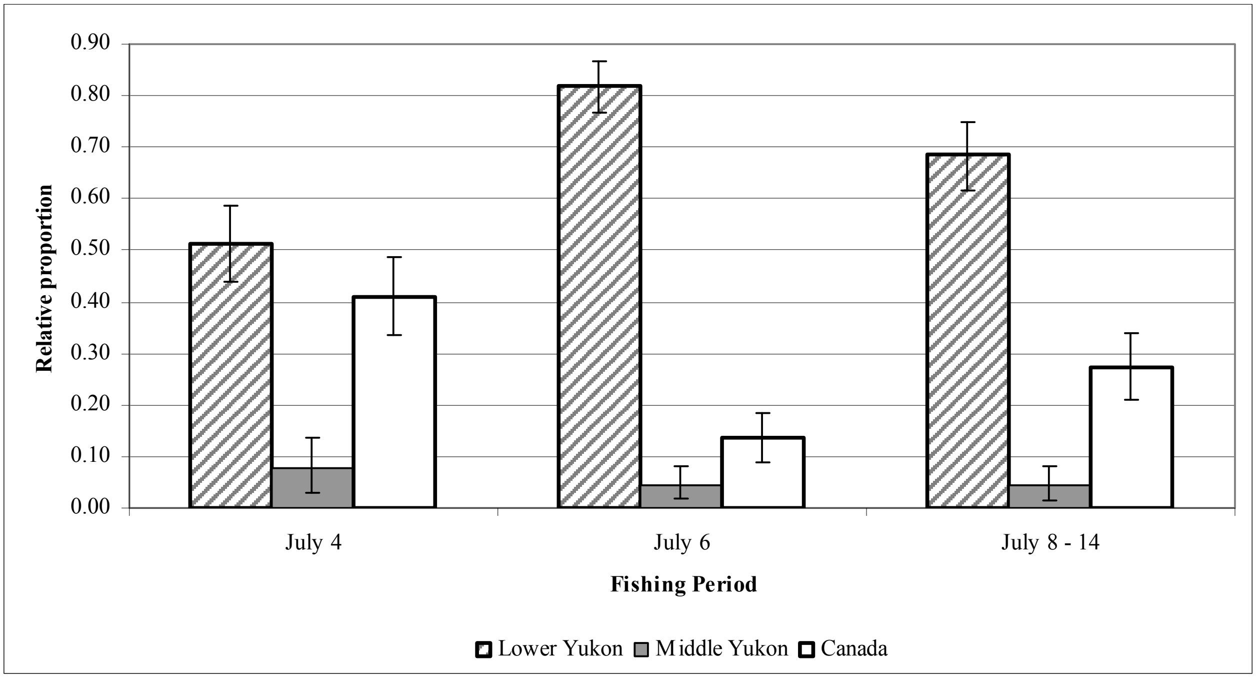
Note: Error bars denote the bounds of the 90% bootstrap confidence interval.

Figure 6.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in the Lower Yukon Test Fishery at Big Eddy (BE) and Middle Mouth (MM), representing the third pulse (“C”), 2008.



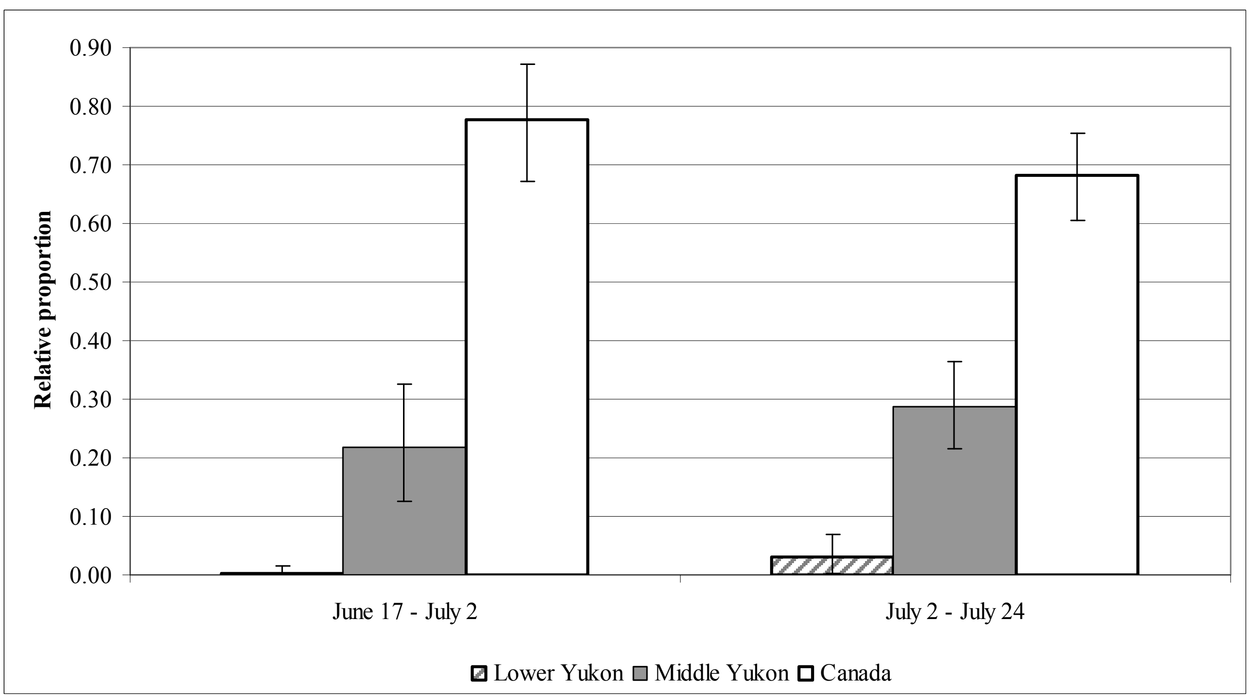
Note: Error bars denote the bounds of the 90% bootstrap confidence interval.

Figure 7.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon caught in the Pilot Station Test Fishery, representing 3 pulses, 2008.



Note: Error bars denote the bounds of the 90% bootstrap confidence interval.

Figure 8.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon harvested from 3 periods in the commercial fishery in District Y-1 of the Yukon River, 2008.



Note: Error bars denote the bounds of the 90% bootstrap confidence interval.

Figure 9.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon harvested during 2 periods in the District Y-5C subsistence fishery at Rapids, 2008.

APPENDIX A

Appendix A.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of age 5 and 6 Chinook salmon harvested in the District Y-1 subsistence fishery, 2008.

	Y-1 Subsistence					
	Age 5 *N*=243			Age 6 *N*=135		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI
Country						
United States	0.481	0.048	(0.404–0.564)	0.441	0.062	(0.339–0.543)
Canada	0.519	0.048	(0.436–0.596)	0.559	0.062	(0.457–0.661)
Broad-scale						
Lower Yukon	0.102	0.026	(0.062–0.147)	0.016	0.018	(0.000–0.051)
Middle Yukon	0.379	0.050	(0.301–0.468)	0.425	0.063	(0.321–0.529)
Canada	0.519	0.048	(0.436–0.596)	0.559	0.062	(0.457–0.661)
Fine-scale						
Lower Yukon	0.102	0.026	(0.062–0.147)	*Insufficient samples*		
Upper U.S. Yukon	0.048	0.058	(0.000–0.169)			
Tanana	0.331	0.054	(0.239–0.416)			
Canada Border	0.170	0.042	(0.103–0.240)			
Pelly	0.263	0.060	(0.167–0.364)			
Carmacks	0.075	0.049	(0.000–0.160)			
Takhini	0.011	0.013	(0.000–0.037)			

APPENDIX B

Appendix B.–Estimated proportional contributions (Est), standard deviations (S.D.), 90% confidence intervals (CI), and analyzed sample size (*N*) of age 5 and 6 Chinook salmon harvested in the District Y-4A subsistence fishery, 2008.

	Y4-A Subsistence Pooled (Kaltag and Nulato)					
	Age 5			Age 6		
	N=171			*N*=136		
Reporting Group	Est	S.D.	90% CI	Est	S.D.	90% CI
Country						
United States	0.575	0.053	(0.488-0.660)	0.454	0.057	(0.360-0.547)
Canada	0.425	0.053	(0.340-0.512)	0.546	0.057	(0.453-0.640)
Broad-scale						
Lower Yukon	0.176	0.039	(0.114-0.242)	0.052	0.031	(0.009-0.110)
Middle Yukon	0.399	0.057	(0.305-0.494)	0.402	0.058	(0.307-0.499)
Canada	0.425	0.053	(0.340-0.512)	0.546	0.057	(0.453-0.640)

Note: The estimated group proportions are given for 2 hierarchical levels.