

**Fishery Data Series No. 09-39**

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# **Genetic Stock Identification of Chinook salmon Harvest on the Yukon River 2007**

by

**Nicholas A. DeCovich**

and

**William D. Templin**

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July 2009

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Alaska Department of Fish and Game

Divisions of Sport Fish and Commercial Fisheries



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Weights and measures (metric)		General		Measures (fisheries)	
centimeter	cm	Alaska Administrative		fork length	FL
deciliter	dL	Code	AAC	mideye to fork	MEF
gram	g	all commonly accepted		mideye to tail fork	METF
hectare	ha	abbreviations	e.g., Mr., Mrs., AM, PM, etc.	standard length	SL
kilogram	kg			total length	TL
kilometer	km	all commonly accepted			
liter	L	professional titles	e.g., Dr., Ph.D., R.N., etc.	<b>Mathematics, statistics</b> <i>all standard mathematical signs, symbols and abbreviations</i>	
meter	m	at	@		
milliliter	mL	compass directions:			
millimeter	mm	east	E	alternate hypothesis	H <sub>A</sub>
		north	N	base of natural logarithm	<i>e</i>
		south	S	catch per unit effort	CPUE
		west	W	coefficient of variation	CV
		copyright	©	common test statistics	(F, t, $\chi^2$ , etc.)
		corporate suffixes:		confidence interval	CI
		Company	Co.	correlation coefficient	
		Corporation	Corp.	(multiple)	R
		Incorporated	Inc.	correlation coefficient	
		Limited	Ltd.	(simple)	r
		District of Columbia	D.C.	covariance	cov
		et alii (and others)	et al.	degree (angular )	°
		et cetera (and so forth)	etc.	degrees of freedom	df
		exempli gratia		expected value	<i>E</i>
		(for example)	e.g.	greater than	>
		Federal Information		greater than or equal to	≥
		Code	FIC	harvest per unit effort	HPUE
		id est (that is)	i.e.	less than	<
		latitude or longitude	lat. or long.	less than or equal to	≤
		monetary symbols		logarithm (natural)	ln
		(U.S.)	\$, ¢	logarithm (base 10)	log
		months (tables and		logarithm (specify base)	log <sub>2</sub> , etc.
		figures): first three		minute (angular)	'
		letters	Jan,...,Dec	not significant	NS
		registered trademark	®	null hypothesis	H <sub>0</sub>
		trademark	™	percent	%
		United States		probability	P
		(adjective)	U.S.	probability of a type I error	
		United States of		(rejection of the null	
		America (noun)	USA	hypothesis when true)	$\alpha$
		U.S.C.	United States	probability of a type II error	
			Code	(acceptance of the null	
		U.S. state	use two-letter	hypothesis when false)	$\beta$
			abbreviations	second (angular)	"
			(e.g., AK, WA)	standard deviation	SD
				standard error	SE
				variance	
				population	Var
				sample	var
<b>Weights and measures (English)</b>					
cubic feet per second	ft <sup>3</sup> /s				
foot	ft				
gallon	gal				
inch	in				
mile	mi				
nautical mile	nmi				
ounce	oz				
pound	lb				
quart	qt				
yard	yd				
<b>Time and temperature</b>					
day	d				
degrees Celsius	°C				
degrees Fahrenheit	°F				
degrees kelvin	K				
hour	h				
minute	min				
second	s				
<b>Physics and chemistry</b>					
all atomic symbols					
alternating current	AC				
ampere	A				
calorie	cal				
direct current	DC				
hertz	Hz				
horsepower	hp				
hydrogen ion activity	pH				
(negative log of)					
parts per million	ppm				
parts per thousand	ppt, ‰				
volts	V				
watts	W				

***FISHERY DATA SERIES NO. 09-39***

**GENETIC STOCK IDENTIFICATION OF CHINOOK SALMON  
HARVEST ON THE YUKON RIVER 2007**

by  
Nicholas A. DeCovich,  
and  
William D. Templin  
Alaska Department of Fish and Game, Division of Commercial Fisheries  
Gene Conservation Laboratory, Anchorage

Alaska Department of Fish and Game  
Division of Sport Fish, Research and Technical Services  
333 Raspberry Road, Anchorage, Alaska, 99518-1565

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*Nicholas A. DeCovich,  
Alaska Department of Fish and Game, Division of Commercial Fisheries  
333 Raspberry Road, Anchorage, AK 99518-1565*

*and*

*William D. Templin,  
Alaska Department of Fish and Game, Division of Commercial Fisheries  
333 Raspberry Road, Anchorage, AK 99518-1565*

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## ABSTRACT

Significant genetic variation exists among populations of Chinook salmon within the Yukon River drainage and has been used to provide estimates of stock composition of fishery harvests since the early 1990s. In 2007, a single nucleotide polymorphism (SNP) baseline was used to estimate the stock composition of Chinook salmon harvests in the U.S. portion of the Yukon River. Of the samples collected from subsistence and commercial fisheries, 6,852 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 management District Y-1, the portion of harvest attributable to Canadian origin fish ranged from a high of 55% in the first commercial fishing period (June 18–19) to a low of 14% in the eighth period (July 2). In the management District Y-2, Canadian stocks contributed between 69% and 23% of the harvest over the 4 commercial fishing periods.

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

## INTRODUCTION

Knowledge of the origin of Chinook salmon (*Oncorhynchus tshawytscha*) stocks harvested in the subsistence and commercial fisheries on the Yukon River is important for the successful management of these fisheries. The proportion of Canadian-origin Chinook salmon harvested in the U.S. portion of the Yukon River is necessary information for meeting the obligations set forth in the Yukon River Salmon Agreement between the United States (U.S.) and Canada. Since 2004, the stock composition of Chinook salmon harvests in the subsistence and commercial Chinook fisheries of the Yukon River has been estimated by genetic stock identification based on a comprehensive baseline of DNA markers. (Smith et al. 2005a; Templin et al. 2005; Templin et al. 2006a, b, Templin et al. 2008; Beacham and Candy 2006).

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 and used to provide stock composition estimates of the 2004 Chinook harvests in the U.S. portion of the Yukon River drainage (Templin et al. 2006b). 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 harvest in the U.S. portion of the Yukon River in 2007. We describe the baseline used, the simulations used to verify the accuracy and precision of estimated stock proportions, and the stock composition of the subsistence and commercial harvest. 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 6-year old component of the run.

## OBJECTIVES

The goal of this project was to provide estimates of the stock composition of the Chinook salmon harvest in commercial and subsistence fisheries on the Yukon River in 2007. To achieve this goal, the following objectives were to be met:

- 1) Sample individuals from each commercial or subsistence fishery opening in districts Y-1, Y-2, Y-4 and Y-5 as follows:
  - i. District Y-1 subsistence – 400 individuals
  - ii. District Y-1 commercial – 400 individuals per period
  - iii. District Y-2 commercial – 400 individuals per period
  - iv. District Y-4 subsistence – 300 individuals from each sub district
  - v. District Y-5 subsistence – 400 individuals
- 2) Analyze a representative sample of individuals from each district and period for genetic variation at the SNP loci in the baseline.
- 3) Estimate the relative contribution of stocks to the commercial and subsistence fisheries of the Yukon River.
- 4) Augment the baseline through the analysis and inclusion of 400 individuals from unrepresented or under-represented spawning populations.

In 2007, samples from the Pilot Station test fishery were also analyzed as part of a separate, concurrent project. The results of that analysis are reported here.

## 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) and 2007 (this report). Additional samples were also collected in 2007 from Henshaw Creek and the Anvik, Chatanika, Goodpaster, and Kandik rivers in the U.S. portion of the Yukon River. Samples collected in 2007 from Blind Creek and the Klondike, Stewart, Little Salmon, Big Salmon, Teslin, Porcupine, and mainstem Yukon rivers in the Canadian portion of the Yukon River were provided by DFO. These samples are being evaluated for possible inclusion in the current SNP baseline as part of a separate project, URE-11-07, funded by the Yukon River Restoration and Enhancement Fund.

Chinook salmon were sampled from the commercial, subsistence, and test fisheries in the U.S. portion of the river (Table 2; Figure 2). Samples were collected from the commercial harvest in Districts Y-1, Y-2, and Y-5; and from the subsistence harvest in Districts Y-1, Y-3, Y-4, and Y-5. The ADF&G test fishery in District Y-1 at Pilot Station was also sampled. 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-5C (Rapids) and Y-5B (Tanana River-north bank). Samples were collected randomly during each fishing period during the process of sampling the harvest for age,

sex, and length data (DuBois et al. 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. The tissues collected were axillary processes preserved in ethanol.

Target sample sizes of 400 individuals per period were established to allow for levels of precision and accuracy necessary to ensure that stock composition estimates will be within 5% of the true value 90% of the time. Larger sample sizes also allow for subsampling by age for the purpose of providing age-structured estimates. Target sample sizes of 300 individuals were established for subsistence fisheries to account for smaller harvests and greater difficulty obtaining samples. Age-structured estimates were not produced for these samples.

For both the Pilot Station and District Y-5 subsistence fishery collections, samples were pooled temporally postseason. Sample sets were created in such a manner that they created useful catch proportion estimates, while maintaining minimum sample size requirements.

## **LABORATORY METHODS**

Genetic data were collected from the fishery samples as individual multi-locus genotypes for 26 SNPs (Table 3). This reduced set of SNPs, when compared to the original set of 51 SNPs, was also used to provide stock composition estimates in 2006, and was determined to provide acceptable levels of accuracy and precision while enabling substantial cost savings. Samples were arranged into subsets for the purpose of fitting collections (a group of samples taken to represent a single fishing period) onto 384-well reaction plates.

SNP genotyping was performed in 384-well reaction plates, with 4 wells in each plate left empty as negative controls. Each polymerase chain reaction (PCR) was conducted in a 5 $\mu$ L volume consisting of 0.10 $\mu$ L template DNA in 1X TaqMan Universal Buffer (ABI), 900nM each PCR primer, and 200nM each probe. Thermal cycling was performed on a Dual 384-Well GeneAmp PCR System 9700 as follows: an initial denaturizing step of 10 min at 95°C followed by 50 cycles of: 92°C for 1 sec and annealing/extension temperature for 1 min. Cycling was conducted at a ramp speed of 1°C per second. The plates were read on an ABI PRISM 7900HT Sequence Detection System after amplification and scored using Sequence Detection Software 2.2 (ABI).

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 insure the quality and consistency of data produced by laboratory procedures:

- 1) Each individual was assigned a unique accession identifier. When DNA was extracted or 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 the 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**

The same genetic baseline was used in 2006 (Templin et al. 2008) and 2007 (this study). A brief description 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 ( $\alpha=0.05$ ) were adjusted for multiple tests within collections and multiple tests across markers within collection (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 markers and treated them as a single locus in further analyses. Composite haplotypes were used rather than eliminating one of the 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.

When baseline collections were taken in multiple years from the same location, all collections 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. 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 stock composition of the harvest.

Simulations were performed using the Statistical Package for Analyzing Mixtures (SPAM version 3.7, Debevec et al. 2000). Baseline and mixture genotypes were randomly generated from the baseline allele frequencies assuming Hardy-Weinberg equilibrium. Each simulated mixture ( $N=400$ ) was composed 100% 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**

Stock composition estimates for country-of-origin, the 3 broad-scale, and the 7 fine-scale stock groups were generated using SPAM. For each estimation procedure, genotypes were removed from the estimation procedure if their probability of occurring was near zero ( $1 \times 10^{-45}$ ). For these cases, the mixture estimates have a group labeled “unknown” containing the proportion of the mixture that was removed. Further, we deleted any individual missing data at 5 or more SNPs. Individual population or stock estimates were first calculated, and then summed into reporting regions. Ninety percent confidence intervals for all group contribution estimates were computed from 1,000 bootstrap resamples of the baseline and mixture genotypes. For each resample, contribution estimates were generated for all populations and summed to the group level. The 1,000 estimates for a group were then sorted from lowest to highest with the 51st and 950th values in the sequence taken respectively as the lower and upper bounds of the 90% confidence interval for that group.

# **RESULTS**

## **COLLECTIONS**

During 2007, 6,852 Chinook salmon were sampled as part of 13 collections from the commercial and subsistence fishery harvests in the U.S. portion of the Yukon River drainage (Table 2). Sampling was conducted in 9 out of 10 commercial periods in District Y-1. In this fishery, the first, third, and fifth periods specifically targeted Chinook salmon and no restrictions were placed on the net mesh size allowed. The remaining periods were restricted to mesh sizes of less than 6 inches to specifically target chum salmon, and the Chinook salmon incidental harvest was sampled. Chinook salmon were sampled in 5 out of 7 commercial fishing periods in District Y-2. As in the Y1 fishery, the first, third, and fifth periods allowed use of nets with unrestricted mesh size.

## **LABORATORY / QUALITY CONTROL ANALYSIS**

Of the fishery samples, a total of 6,815 individuals were analyzed for allelic variation at 26 SNPs. The quality control checks employed demonstrated an overall discrepancy rate of less than

0.01%. This discrepancy rate is based on the re-analysis of 8% of the total number of samples. The overall genotyping failure rate was 3.2%, and ranged from a low of 1.0% for the samples collected at Pilot Station to a high of 5.8% 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).

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 3).

The reader is referred to Templin et al. (2008) for a comprehensive discussion of the baseline analysis results.

## **MIXED STOCK ANALYSIS**

### **Commercial**

Estimates of stock composition in the commercial harvest in District Y-1 of the Yukon River indicate that Chinook salmon of Canadian origin contributed between 55% and 14% of the harvest across all of the commercial fishing periods (Table 5; Figure 4). Periods 9 and 10 were pooled for this analysis due to the small sample size ( $n=63$ ) for period 10. The largest portion of the Canadian component was estimated to be from the Carmacks region for all periods. In general, the proportion of Canadian stocks in the harvest was greatest in the initial fishing period, and decreased as the season went on. There was a reversal in this trend in the final, pooled, restricted fishing period, when the proportion of Canadian stocks increased to 24%.

Stock composition estimates of the Canadian contribution to the commercial harvest in District Y-2 varied more widely over the 2 weeks of the fishery (Table 6; Figure 5). The Canadian component of the harvest ranged from a high of 69% in period 1 (June 15) to a low of 45% in period 2 (June 19). As with the commercial harvest in District Y-1, the Carmacks region represented the largest component of the Canadian contribution of the harvest.

In the District Y-5 commercial fishery, 65% of the harvest was estimated to be of Canadian origin. The largest component of the Canadian portion of the harvest was comprised of stocks from the Pelly region with 27% of the harvest, while the largest component of the U.S. harvest came from Upper U.S. region stocks with 34% of the harvest (Table 7).

### **Test Fishery**

In the Pilot Station test fishery, the Canadian contribution to the Chinook passage ranged from a high of 53% in the first period (June 6–19) to a low of 21% in the third and final period (July 1–17) (Table 8; Figure 6). It is important to remember that the periods described were fabricated postseason for the purpose of pooling estimates into meaningful groups based on collection timing, and therefore do not represent actual management controlled fishing periods.

## **Subsistence**

In the District Y-1 subsistence fishery, 57% of the harvest was comprised of Canadian populations. The Pelly Region contributed the largest component of the Canadian harvest with 25%. Of the U.S. contribution, the largest component was estimated to be from the Tanana River (23%). The harvest from the Y-3 subsistence fishery showed similar proportions, with 61% of the harvest comprised of Canadian populations and the largest component of the U.S. contribution coming from the Tanana River (19%) (Table 9).

Unlike past years, harvest composition estimates in the District Y-4 subsistence fishery were not pooled among locations for individual subdistricts. For example, samples were collected in Subdistrict Y-4A from both Kaltag and Nulato, and these samples were kept separate for the purpose of this analysis. The estimated contribution of Canadian populations to the subsistence harvest in District Y-4 varied from a high of 62% in Bishop Mountain (Subdistrict 4-B) to a low of 17% in Ruby (Subdistrict 4-C). As with the commercial harvest in the lower river, the Carmacks Region comprised the greatest portion of the Canadian estimate in all 3 subdistricts (Table 10). In 2007, exact harvest location information was also available for samples taken in District Y-4. The harvest of Chinook salmon from the south bank of the Yukon River at Bishop Mountain was estimated to have a Tanana River component of 13%. In contrast, the harvest component from the Tanana River for samples taken from the south bank at Ruby, 70 river miles upstream, was 68% (Table 11; Figure 7).

The Canadian contribution to the subsistence harvest in District Y-5, Subdistrict Y-5B, was 76% for the first pooled period (June 27–July 1), and 64% for July 7. The Canadian contribution to the subsistence harvest in Subdistrict Y-5C, was 65% for the first pooled period (June 20–July 8), and 81% for the second pooled period (July 9–31). The Upper U.S. region populations contributed most of the U.S. portion of the harvest. In Subdistrict Y-5B, the Carmacks region component of the Canadian harvest increased from 8% in the first period to 37% in the second period; this trend was accompanied by a decrease in the Pelly region component from 36% in the first period to 23% in the second period. In Subdistrict Y-5C, the Carmacks region component of the harvest decreased from 27% in the first period to 24% in the second period, while the Pelly region component increased from 26% to 31% over the same periods (Table 12). The point estimates involved with each of these trends, with the exception of the increase of the Carmacks region component seen in Subdistrict Y-5B, fall within the margin of error defined by the 90% confidence interval reported for the concordant estimate. However, examination of the lower and upper bounds of the 90% confidence intervals reveals similar trends.

## **Age-class**

Sufficient samples were available to estimate the composition of the 6-year old component for fishing periods allowing nets of unrestricted mesh size in the Y-1 (periods 1, 3 and 5) and Y-2 commercial harvest (periods 1, 3 and 5) (Appendices A and B; Figures 8 and 9). Samples sizes of less than 100 were available to estimate the 6-year old component for each of the 3 time periods used to stratify the Pilot Station samples, therefore harvest components were calculated for country of origin only (Appendix C; Figure 10). In the District Y-1 commercial fishery, the Canadian component of the 6-year old harvest decreased from 53% to 43% over the 3 unrestricted periods. In the District Y-2 commercial fishery, the Canadian component of the 6-year old harvest dropped from 75% to 48% from period 1 to period 3, and increased to 55% in period 5. The Canadian component of 6-year old samples taken from Pilot Station decreased over 3 periods, ranging from 60% in the first period to 32% in the third period.

## DISCUSSION

The stock composition estimates from the 2007 commercial fisheries in District Y-1 show similar patterns to the estimates from 2006. In 2007, the midpoint of the Yukon River Chinook salmon run in District Y-1 was observed on June 22 (JTC 2008). The Canadian proportion of the harvest was estimated to be 45% for the unrestricted fishing period on June 21–22. The midpoint of the run in 2006 for District Y-1 was observed on June 24 (JTC 2007), and the Canadian component of the harvest from the June 26 fishing period, the period closest to the estimated midpoint, was 51%. In 2007, Chinook salmon were sampled from the harvest in the fishing periods restricted to mesh sizes of less than or equal to 6 inches. This was the first year that restricted-mesh fishing periods were sampled. These restricted fishing periods are intended to harvest chum salmon, so Chinook salmon are caught at a lower rate.

In 2007, a general trend of decreasing contributions to the harvest from Canada, matched by an increase in the presence of Lower Yukon populations in the harvest during unrestricted fishing periods was seen in District Y-1. A similar, although more pronounced trend, was seen in the restricted mesh-size fishing periods. A similar pattern was also seen in the commercial harvests in District Y-1 in 2005 and 2006, when only unrestricted fishing periods were sampled. In District Y-2, stock composition trends in the unrestricted fishing periods were similar to those seen in 2006; however, in 2007 the proportions of Canadian Chinook salmon were higher than in 2006. The first unrestricted period in 2007 included a Canadian harvest component of 69%, and the third and final unrestricted period had a Canadian component of 53%. This corresponds to a Canadian component of 60% in the initial fishing period of 2006, and 43% in the fourth and final period. Only 3 fishing periods were sampled in District Y-2 in 2005, making a comparison to following years difficult. It should be mentioned, however, that the Canadian component of the harvest in 2005 for District Y-2 never exceeded 50%, and the initial period sampled had the lowest Canadian component of all periods sampled at 28%. This trend is opposite of that seen in 2006 and 2007.

As in 2005 and 2006, the subsistence harvest in Ruby (Subdistrict Y-4C) had the lowest Canadian harvest component of all District Y-4 subsistence fisheries, and the highest Tanana River component. Exact harvest location data were available in 2007. Estimates were calculated for Chinook salmon harvested from the south bank of the Yukon River at Bishop Mountain, and from the harvest along the south bank at Ruby. The Canadian component decreased from 66% for the Bishop Mountain south bank harvest, to 6% for the Ruby south bank harvest. The proportion of Tanana River Chinook salmon in the harvest increased from 13% for the Bishop Mountain south bank harvest to 68% for the Ruby south bank harvest. The gear type used for the Bishop Mountain south bank harvest was 8.5 inch mesh set gillnet, while the south bank Ruby harvest came from set gill nets of various mesh sizes and fishwheels. A high proportion of Tanana River Chinook salmon were harvested at Ruby in 2007. This was the third year in a row that this phenomenon was observed. One possible reason for this is that these fish are starting to home in on the Tanana River water plume present along the south bank of the Yukon River at Ruby. It is surprising that this high proportion of Tanana River Chinook salmon were not seen in the harvest from the south bank at Bishop Mountain, 70 River miles downstream from Ruby. Additional investigation will be necessary to determine if other factors, such as the effect of fishwheels used at Ruby, contribute to this increased proportion of Tanana River Chinook salmon.



In the District Y-1 commercial fishery, the Canadian component of the 6-year old harvest decreased throughout the fishing season. This was also the case in 2005 and 2006, with the exception of the final fishing period in 2006, when the proportion increased to 61% from 40% in the previous period. In District Y-2, this component was more variable, and this variability was also seen in 2005 and 2006 (see Templin et. al 2006a,c and 2008). In the Pilot Station test fishery, there was a decreasing trend in this component over the 3 time strata used in this report. The 6-year old component predominated the Chinook salmon run on the Yukon River in 2007 (Dani Evenson, Fishery Biologist, ADF&G, personal communication) and sample sizes for the 5-year-old component were below 100 for all fishing periods and districts sampled. For this reason, estimates for the 5-year-old component are not provided in this report.

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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.

Country	Broad scale	Fine scale	Population	Year(s)	Sample size
United States					
	Lower Yukon				
		Lower Yukon			
			Anvik River	2002	99
			Andreafsky River	2003	208
			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					3,649

Table 2.–Chinook salmon collections from selected commercial and subsistence fishery harvests in the Yukon River drainage, 2007.

District	Period	Dates	Gear type	Location	Sample size
Commercial					
Y-1	1	18-19 Jun	Unrestricted	Emmonak	400
	2	20 Jun	≤6 Restricted	Emmonak	0
	3	21-22 Jun	Unrestricted	Emmonak	400
	4	22 Jun	≤6 Restricted	Emmonak	115
	5	25-26 Jun	Unrestricted	Emmonak	400
	6	27 Jun	≤6 Restricted	Emmonak	139
	7	30 Jun	≤6 Restricted	Emmonak	200
	8	2 Jul	≤6 Restricted	Emmonak	169
	9	6 Jul	≤6 Restricted	Emmonak	138
	10	9-10 July	≤6 Restricted	Emmonak	63
					2,024
Y-2	1	15 Jun	Unrestricted	Saint Marys	322
	2	19 Jun	≤6 Restricted	Saint Marys	158
	3	20 Jun	Unrestricted	Saint Marys	400
	4	21 Jun	≤6 Restricted	Saint Marys	0
	5	24 Jun	Unrestricted	Saint Marys	400
	6	26 Jun	≤6 Restricted	Saint Marys	0
	7	28 Jun	≤6 Restricted	Saint Marys	140
					1,420
Y-5	4-11 Jul		Mixed <sup>a</sup>	Rampart	400
	Total commercial				3,844
Test Fishery					
Y-1	6 Jun - 29 July		DGN	Pilot Station	550
Subsistence					
Y-1	6-11 Jun		SGN	Emmonak	242
Y-3	13-22 Jun		DGN, SGN	Holy Cross	204
Y-4A	27 Jun - 14 Jul		DGN	Kaltag	250
Y-4A	26 Jun - 12 Jul		DGN	Nulato	99
Y-4B	25 Jun - 7 Jul		SGN	Bishop Mountain	200
Y-4B	21 Jun - 17 Jul		SGN, FW	Galena	145

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District	Period	Dates	Gear type	Location	Sample size
Subsistence					
Y-4C		28 Jun - 19 Jul	SGN, FW	Ruby	213
					907
Y-5B		27 Jun - 7 Jul	FW	Tanana North Bank	319
Y-5C		20 Jun - 31 Jul	FW	Rapids	786
					1105
				Total Subsistence	2,458
				Grand Total	6,852

*Note:* Gear types used were set gillnet (SGN), drift gillnet (DGN), and fishwheels (FW). Commercial Fisheries in Districts Y-1 and Y-2 used drift gillnets with either unrestricted or <6 inch restricted mesh sizes.

<sup>a</sup> Information on exact gear types used was not available.



Table 3.–Single nucleotide polymorphisms assayed in individuals sampled from the commercial and subsistence harvest of Chinook salmon in the U.S. portion of the Yukon River drainage, 2007.

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

Table 5.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of Chinook salmon harvested from the commercial fishery in District Y-1 of the Yukon River, 2007.

Reporting Group	Period 1 - Unrestricted			Period 3 - Unrestricted			Period 4 - Restricted			Period 5 - Unrestricted		
	June 18-19			June 21-22			June 22			June 25-26		
	N =	393		N =	399		N =	100		N =	399	
	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country												
United States	0.451	0.035	(0.390-0.507)	0.549	0.033	(0.489-0.600)	0.623	0.062	(0.511-0.711)	0.580	0.032	(0.520-0.629)
Canada	0.549	0.035	(0.493-0.610)	0.451	0.033	(0.400-0.511)	0.377	0.062	(0.289-0.489)	0.420	0.032	(0.372-0.480)
Broad-scale												
Lower Yukon	0.126	0.022	(0.089-0.162)	0.150	0.025	(0.112-0.193)	0.315	0.054	(0.224-0.403)	0.234	0.027	(0.191-0.280)
Middle Yukon	0.325	0.035	(0.265-0.380)	0.399	0.035	(0.336-0.456)	0.309	0.063	(0.198-0.401)	0.346	0.036	(0.283-0.398)
Canada	0.549	0.035	(0.493-0.610)	0.451	0.033	(0.400-0.511)	0.377	0.062	(0.289-0.489)	0.420	0.032	(0.372-0.480)
Fine-scale												
Lower Yukon	0.126	0.022	(0.089-0.162)	0.150	0.025	(0.112-0.193)	0.315	0.054	(0.224-0.403)	0.234	0.027	(0.191-0.280)
Upper U.S. Yukon	0.142	0.039	(0.092-0.220)	0.263	0.037	(0.195-0.318)	0.167	0.068	(0.055-0.282)	0.216	0.044	(0.142-0.289)
Tanana	0.183	0.032	(0.120-0.227)	0.136	0.033	(0.090-0.196)	0.142	0.058	(0.045-0.234)	0.130	0.033	(0.071-0.177)
Canada Border	0.057	0.021	(0.029-0.097)	0.019	0.016	(0.000-0.053)	0.029	0.033	(0.000-0.103)	0.027	0.016	(0.000-0.058)
Pelly	0.222	0.046	(0.155-0.308)	0.173	0.042	(0.107-0.247)	0.107	0.067	(0.010-0.234)	0.041	0.034	(0.012-0.126)
Carmacks	0.259	0.045	(0.159-0.312)	0.252	0.042	(0.171-0.309)	0.204	0.071	(0.077-0.309)	0.313	0.040	(0.221-0.353)
Takhini	0.011	0.015	(0.000-0.048)	0.008	0.012	(0.000-0.038)	0.036	0.026	(0.000-0.085)	0.040	0.017	(0.015-0.072)

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Reporting Group	Period 6 - Restricted			Period 7 - Restricted			Period 8 - Restricted			Period 9-10 - Restricted		
	June 27			June 30			July 2			July 6-10		
	N =	139		N =	198		N =	168		N =	199	
	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country												
United States	0.660	0.053	(0.580-0.758)	0.811	0.034	(0.751-0.867)	0.864	0.032	(0.813-0.919)	0.759	0.039	(0.694-0.823)
Canada	0.340	0.053	(0.243-0.420)	0.189	0.034	(0.133-0.249)	0.136	0.032	(0.081-0.187)	0.241	0.039	(0.177-0.306)
Broad-scale												
Lower Yukon	0.464	0.056	(0.371-0.557)	0.671	0.042	(0.607-0.741)	0.787	0.039	(0.713-0.845)	0.634	0.040	(0.562-0.696)
Middle Yukon	0.196	0.055	(0.122-0.306)	0.140	0.037	(0.078-0.207)	0.077	0.033	(0.034-0.146)	0.125	0.036	(0.073-0.191)
Canada	0.340	0.053	(0.243-0.420)	0.189	0.034	(0.133-0.249)	0.136	0.032	(0.081-0.187)	0.241	0.039	(0.177-0.306)
Fine-scale												
Lower Yukon	0.464	0.056	(0.371-0.557)	0.671	0.042	(0.607-0.741)	0.787	0.039	(0.713-0.845)	0.634	0.040	(0.562-0.696)
Upper U.S. Yukon	0.102	0.056	(0.032-0.218)	0.078	0.036	(0.025-0.141)	0.054	0.028	(0.012-0.105)	0.065	0.040	(0.018-0.152)
Tanana	0.095	0.044	(0.020-0.169)	0.062	0.032	(0.010-0.116)	0.023	0.024	(0.000-0.075)	0.060	0.032	(0.000-0.107)
Canada Border	0.068	0.034	(0.019-0.131)	0.000	0.005	(0.000-0.013)	0.000	0.011	(0.000-0.031)	0.039	0.020	(0.000-0.066)
Pelly	0.025	0.035	(0.000-0.102)	0.049	0.028	(0.001-0.096)	0.000	0.008	(0.000-0.020)	0.028	0.032	(0.000-0.104)
Carmacks	0.229	0.055	(0.120-0.293)	0.112	0.039	(0.049-0.175)	0.127	0.035	(0.048-0.163)	0.162	0.041	(0.082-0.214)
Takhini	0.017	0.020	(0.000-0.059)	0.028	0.022	(0.000-0.068)	0.009	0.016	(0.000-0.047)	0.013	0.015	(0.000-0.045)

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Table 6.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of Chinook salmon harvested from the commercial fishery in District Y-2 of the Yukon River, 2007.

Reporting Group	Period 1 - Unrestricted			Period 2 - Restricted			Period 3 - Unrestricted			Period 5 - Unrestricted			Period 7 - Restricted		
	June 15			June 19			June 20			June 24			June 28		
	N =	321		N =	155		N =	398		N =	394		N =	88	
	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country															
United States	0.308	0.039	(0.254-0.383)	0.553	0.054	(0.461-0.637)	0.537	0.035	(0.482-0.600)	0.467	0.033	(0.413-0.522)	0.771	0.056	(0.664-0.850)
Canada	0.692	0.039	(0.617-0.746)	0.447	0.054	(0.364-0.539)	0.463	0.035	(0.401-0.518)	0.533	0.033	(0.478-0.587)	0.229	0.056	(0.150-0.336)
Broad-scale															
Lower Yukon	0.027	0.016	(0.002-0.058)	0.192	0.039	(0.128-0.258)	0.284	0.029	(0.236-0.332)	0.150	0.027	(0.102-0.190)	0.618	0.067	(0.497-0.721)
Middle Yukon	0.281	0.041	(0.225-0.364)	0.361	0.055	(0.268-0.444)	0.253	0.036	(0.195-0.315)	0.318	0.034	(0.266-0.378)	0.153	0.055	(0.060-0.248)
Canada	0.692	0.039	(0.617-0.746)	0.447	0.054	(0.364-0.539)	0.463	0.035	(0.401-0.518)	0.533	0.033	(0.478-0.587)	0.229	0.056	(0.150-0.336)
Fine-scale															
Lower Yukon	0.027	0.016	(0.002-0.058)	0.192	0.039	(0.128-0.258)	0.284	0.029	(0.236-0.332)	0.150	0.027	(0.102-0.190)			
Upper U.S. Yukon	0.104	0.046	(0.037-0.192)	0.061	0.049	(0.007-0.165)	0.104	0.036	(0.059-0.176)	0.167	0.036	(0.116-0.237)			
Tanana	0.177	0.037	(0.118-0.244)	0.300	0.053	(0.189-0.365)	0.149	0.031	(0.089-0.190)	0.150	0.031	(0.095-0.199)			
Canada Border	0.160	0.033	(0.103-0.213)	0.044	0.029	(0.000-0.095)	0.034	0.021	(0.000-0.071)	0.027	0.019	(0.000-0.065)			
Pelly	0.300	0.053	(0.203-0.379)	0.087	0.059	(0.021-0.215)	0.182	0.045	(0.111-0.258)	0.149	0.043	(0.084-0.225)			
Carmacks	0.232	0.043	(0.162-0.304)	0.306	0.064	(0.174-0.383)	0.213	0.045	(0.139-0.286)	0.274	0.047	(0.187-0.343)			
Takhini	0.000	0.006	(0.000-0.015)	0.010	0.018	(0.000-0.053)	0.034	0.017	(0.009-0.064)	0.083	0.024	(0.047-0.127)			

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Table 7.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of Chinook salmon harvested from the commercial fishery in District Y-5 of the Yukon River, 2007.

		Y5 Commercial Rampart		
Reporting Group		N =	395	
		Est	S.D.	90%CI
Country				
	United States	0.349	0.037	(0.283-0.401)
	Canada	0.651	0.037	(0.599-0.717)
Broad-scale				
	Lower Yukon	0.000	0.003	(0.000-0.007)
	Middle Yukon	0.349	0.037	(0.283-0.400)
	Canada	0.651	0.037	(0.599-0.717)
Fine-scale				
	Lower Yukon	0.000	0.003	(0.000-0.007)
	Upper U.S. Yukon	0.343	0.041	(0.255-0.386)
	Tanana	0.006	0.018	(0.000-0.054)
	Canada Border	0.124	0.037	(0.079-0.199)
	Pelly	0.269	0.053	(0.184-0.358)
	Carmacks	0.216	0.044	(0.144-0.287)
	Takhini	0.042	0.017	(0.015-0.072)

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Table 8.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of Chinook salmon caught during 3 periods in the Pilot Station Test Fishery, 2007.

		Period A June 6-19 N = 214			Period B June 20-30 N = 138			Period C July 1-17 N = 188		
Reporting Group		Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country										
	United States	0.468	0.050	(0.386-0.550)	0.626	0.051	(0.534-0.701)	0.794	0.035	(0.738-0.852)
	Canada	0.532	0.050	(0.450-0.614)	0.374	0.051	(0.299-0.467)	0.206	0.035	(0.148-0.262)
Broad-scale										
	Lower Yukon	0.062	0.020	(0.030-0.098)	0.285	0.047	(0.215-0.368)	0.745	0.037	(0.677-0.800)
	Middle Yukon	0.407	0.052	(0.318-0.489)	0.342	0.055	(0.240-0.423)	0.050	0.024	(0.018-0.099)
	Canada	0.532	0.050	(0.450-0.614)	0.374	0.051	(0.299-0.467)	0.206	0.035	(0.148-0.262)
Fine-scale										
	Lower Yukon	0.062	0.020	(0.030-0.098)	0.285	0.047	(0.215-0.368)	0.745	0.037	(0.677-0.800)
	Upper U.S. Yukon	0.173	0.062	(0.069-0.271)	0.199	0.062	(0.078-0.284)	0.035	0.023	(0.000-0.074)
	Tanana	0.233	0.053	(0.149-0.328)	0.143	0.053	(0.068-0.243)	0.015	0.019	(0.000-0.059)
	Canada Border	0.211	0.045	(0.133-0.283)	0.035	0.025	(0.000-0.080)	0.000	0.008	(0.000-0.022)
	Pelly	0.106	0.054	(0.048-0.227)	0.017	0.054	(0.000-0.171)	0.016	0.027	(0.000-0.082)
	Carmacks	0.215	0.051	(0.106-0.276)	0.322	0.061	(0.171-0.373)	0.174	0.039	(0.093-0.223)
	Takhini	0.000	0.006	(0.000-0.016)	0.000	0.014	(0.000-0.038)	0.016	0.015	(0.000-0.047)

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Table 9.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of Chinook salmon harvested from the subsistence fisheries in District Y-1 and Y-3 of the Yukon River, 2007.

Reporting Group		Y-1 Subsistence Emmonak			Y-3 Subsistence Holy Cross		
		N = Est	235 S.D.	90%CI	N= Est	204 S.D.	90%CI
Country							
	United States	0.434	0.050	(0.364-0.527)	0.388	0.053	(0.303-0.474)
	Canada	0.566	0.050	(0.473-0.637)	0.612	0.053	(0.526-0.697)
Broad-scale							
	Lower Yukon	0.068	0.025	(0.037-0.120)	0.036	0.019	(0.003-0.066)
	Middle Yukon	0.366	0.051	(0.287-0.454)	0.352	0.054	(0.270-0.445)
	Canada	0.566	0.050	(0.473-0.637)	0.612	0.053	(0.526-0.697)
Fine-scale							
	Lower Yukon	0.068	0.025	(0.037-0.120)	0.036	0.019	(0.003-0.066)
	Upper U.S. Yukon	0.133	0.053	(0.066-0.239)	0.162	0.059	(0.068-0.263)
	Tanana	0.234	0.046	(0.149-0.301)	0.191	0.045	(0.121-0.269)
	Canada Border	0.179	0.043	(0.105-0.246)	0.136	0.040	(0.073-0.203)
	Pelly	0.249	0.055	(0.132-0.318)	0.258	0.065	(0.156-0.376)
	Carmacks	0.127	0.046	(0.067-0.219)	0.217	0.054	(0.118-0.298)
	Takhini	0.011	0.011	(0.000-0.037)	0.001	0.011	(0.000-0.030)

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.



Table 10.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of Chinook salmon harvested from the subsistence fishery in 5 communities/locations in District Y-4 of the Yukon River, 2007.

	Y-4 A - Kaltag			Y-4 A - Nulato			Y-4 B - Bishop Mountain			Y-4 B - Galena			Y4 C - Ruby		
	N = 250			N = 98			N = 198			N = 145			N = 212		
Reporting Group	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country															
United States	0.501	0.044	(0.417-0.565)	0.541	0.070	(0.422-0.649)	0.381	0.048	(0.305-0.464)	0.782	0.050	(0.684-0.844)	0.834	0.036	(0.765-0.882)
Canada	0.499	0.044	(0.435-0.583)	0.459	0.070	(0.352-0.578)	0.619	0.048	(0.536-0.695)	0.218	0.050	(0.156-0.316)	0.166	0.036	(0.118-0.235)
Broad-scale															
Lower Yukon	0.029	0.021	(0.008-0.079)	0.107	0.048	(0.024-0.187)	0.058	0.026	(0.016-0.100)	0.093	0.034	(0.044-0.156)	0.089	0.040	(0.037-0.167)
Middle Yukon	0.472	0.046	(0.373-0.526)	0.434	0.076	(0.313-0.561)	0.323	0.050	(0.245-0.410)	0.689	0.055	(0.580-0.760)	0.745	0.050	(0.638-0.800)
Canada	0.499	0.044	(0.435-0.583)	0.459	0.070	(0.352-0.578)	0.619	0.048	(0.536-0.695)	0.218	0.050	(0.156-0.316)	0.166	0.036	(0.118-0.235)
Fine-scale															
Lower Yukon	0.029	0.021	(0.008-0.079)				0.058	0.026	(0.016-0.100)	0.093	0.034	(0.044-0.156)	0.089	0.040	(0.037-0.167)
Upper U.S. Yukon	0.235	0.054	(0.136-0.319)				0.213	0.059	(0.126-0.321)	0.206	0.069	(0.083-0.320)	0.219	0.066	(0.106-0.328)
Tanana	0.237	0.048	(0.146-0.306)				0.110	0.044	(0.035-0.179)	0.482	0.067	(0.368-0.585)	0.526	0.063	(0.413-0.622)
Canada Border	0.018	0.024	(0.000-0.077)				0.045	0.031	(0.001-0.102)	0.065	0.035	(0.013-0.124)	0.008	0.014	(0.000-0.041)
Pelly	0.085	0.050	(0.024-0.187)				0.255	0.068	(0.115-0.345)	0.027	0.044	(0.000-0.140)	0.034	0.034	(0.000-0.110)
Carmacks	0.355	0.057	(0.233-0.425)				0.311	0.065	(0.219-0.432)	0.126	0.045	(0.036-0.182)	0.111	0.037	(0.031-0.157)
Takhini	0.042	0.022	(0.012-0.087)				0.008	0.014	(0.000-0.041)	0.000	0.005	(0.000-0.014)	0.013	0.012	(0.000-0.038)

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Table 11.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of Chinook salmon harvested from the south bank only from the subsistence fishery at Bishop Mountain (Subdistrict B) and Ruby (Subdistrict C) of District Y-4 of the Yukon River, 2007.

Reporting Group	Y-4 B Bishop Mountain			Y-4 C Ruby		
	South bank only			South bank only		
	N=	125		N=	165	
	Est	S.D.	90%CI	Est	S.D.	90%CI
Country						
United States	0.343	0.063	(0.237-0.450)	0.944	0.026	(0.891-0.979)
Canada	0.657	0.063	(0.550-0.763)	0.056	0.026	(0.022-0.109)
Broad-scale						
Lower Yukon	0.064	0.029	(0.022-0.115)	0.082	0.041	(0.026-0.156)
Middle Yukon	0.279	0.066	(0.168-0.384)	0.863	0.047	(0.767-0.923)
Canada	0.657	0.063	(0.550-0.763)	0.056	0.026	(0.022-0.109)
Fine-scale						
Lower Yukon	0.064	0.029	(0.022-0.115)	0.082	0.041	(0.026-0.156)
Upper U.S. Yukon	0.153	0.072	(0.056-0.298)	0.180	0.070	(0.082-0.320)
Tanana	0.126	0.051	(0.027-0.194)	0.682	0.070	(0.535-0.770)
Canada Border	0.110	0.050	(0.022-0.187)	0.000	0.006	(0.000-0.014)
Pelly	0.316	0.093	(0.160-0.474)	0.033	0.025	(0.000-0.077)
Carmacks	0.232	0.076	(0.111-0.366)	0.015	0.020	(0.000-0.061)
Takhini	0.000	0.011	(0.000-0.030)	0.007	0.008	(0.000-0.023)

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Table 12.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of Chinook salmon harvested from 2 periods in the subsistence fishery in District Y-5, Subdistricts B and C of the Yukon River, 2007.

Reporting Group	Y-5 B Tanana						Y-5 C Rapids					
	June 27-July 1			July 7			June 20-July 8			July 9-July 31		
	N=	156		N=	161		N=	383		N=	227	
	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country												
United States	0.244	0.060	(0.167-0.361)	0.359	0.056	(0.252-0.437)	0.353	0.034	(0.299-0.412)	0.191	0.045	(0.110-0.262)
Canada	0.756	0.060	(0.639-0.833)	0.641	0.056	(0.563-0.748)	0.647	0.034	(0.588-0.701)	0.809	0.045	(0.738-0.890)
Broad-scale												
Lower Yukon	0.000	0.007	(0.000-0.019)	0.007	0.018	(0.000-0.053)	0.026	0.015	(0.006-0.055)	0.002	0.004	(0.000-0.012)
Middle Yukon	0.244	0.060	(0.162-0.360)	0.352	0.059	(0.236-0.426)	0.327	0.035	(0.269-0.384)	0.189	0.045	(0.109-0.258)
Canada	0.756	0.060	(0.639-0.833)	0.641	0.056	(0.563-0.748)	0.647	0.034	(0.588-0.701)	0.809	0.045	(0.738-0.890)
Fine-scale												
Lower Yukon	0.000	0.007	(0.000-0.019)	0.007	0.018	(0.000-0.053)	0.026	0.015	(0.006-0.055)	0.002	0.004	(0.000-0.012)
Upper U.S. Yukon	0.223	0.064	(0.136-0.348)	0.352	0.061	(0.222-0.416)	0.312	0.039	(0.236-0.367)	0.182	0.048	(0.085-0.243)
Tanana	0.021	0.022	(0.000-0.064)	0.000	0.019	(0.000-0.054)	0.015	0.021	(0.000-0.063)	0.007	0.021	(0.000-0.060)
Canada Border	0.304	0.064	(0.184-0.398)	0.032	0.030	(0.000-0.095)	0.029	0.021	(0.002-0.072)	0.267	0.050	(0.196-0.367)
Pelly	0.360	0.078	(0.214-0.476)	0.226	0.071	(0.122-0.357)	0.257	0.051	(0.162-0.326)	0.307	0.074	(0.193-0.444)
Carmacks	0.084	0.054	(0.003-0.187)	0.374	0.068	(0.246-0.472)	0.271	0.051	(0.191-0.351)	0.235	0.061	(0.122-0.315)
Takhini	0.008	0.016	(0.000-0.045)	0.009	0.014	(0.000-0.040)	0.091	0.025	(0.053-0.135)	0.000	0.009	(0.000-0.025)

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

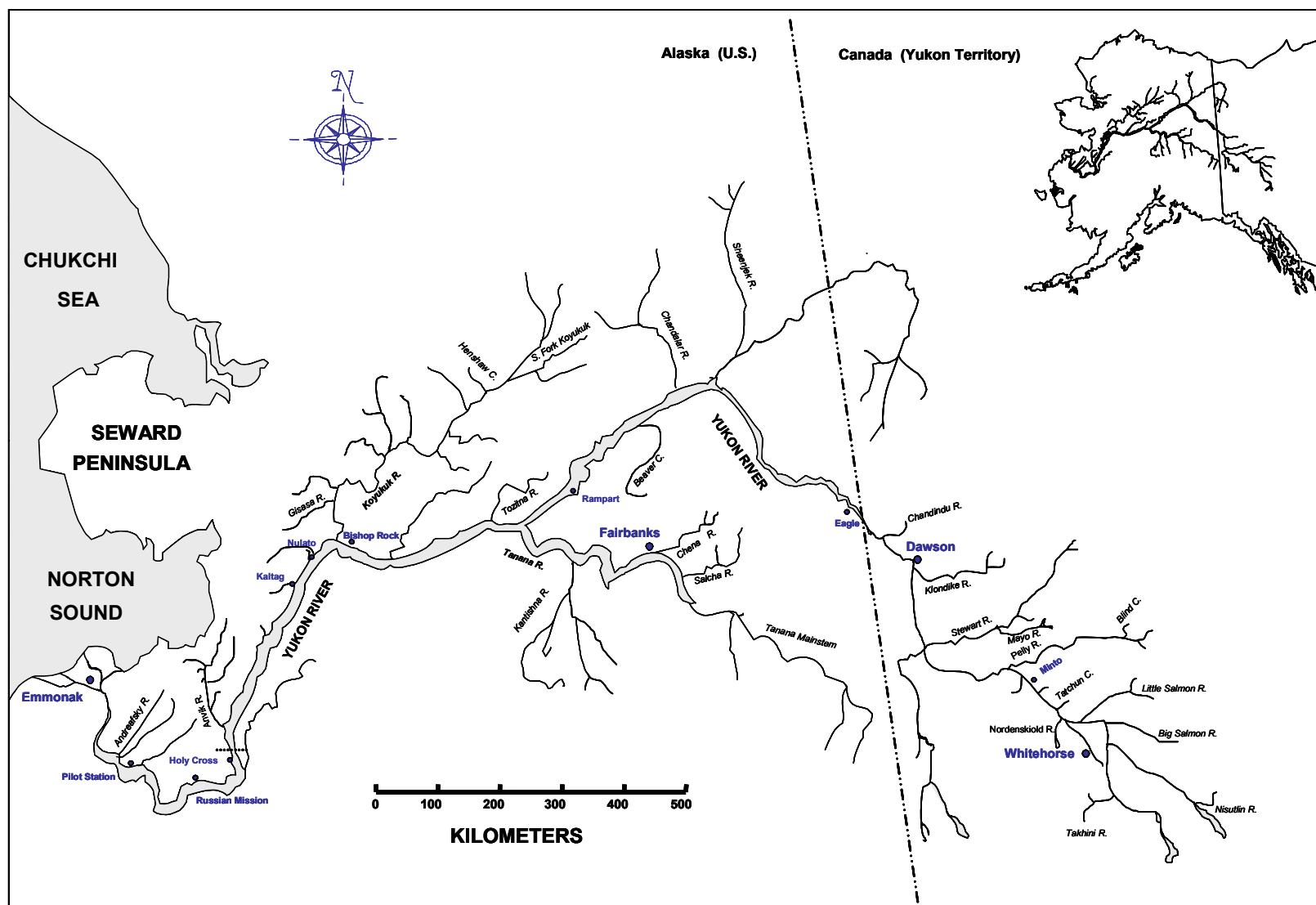


Figure 1.—Map of the locations of Chinook salmon collections in the Yukon River drainage.

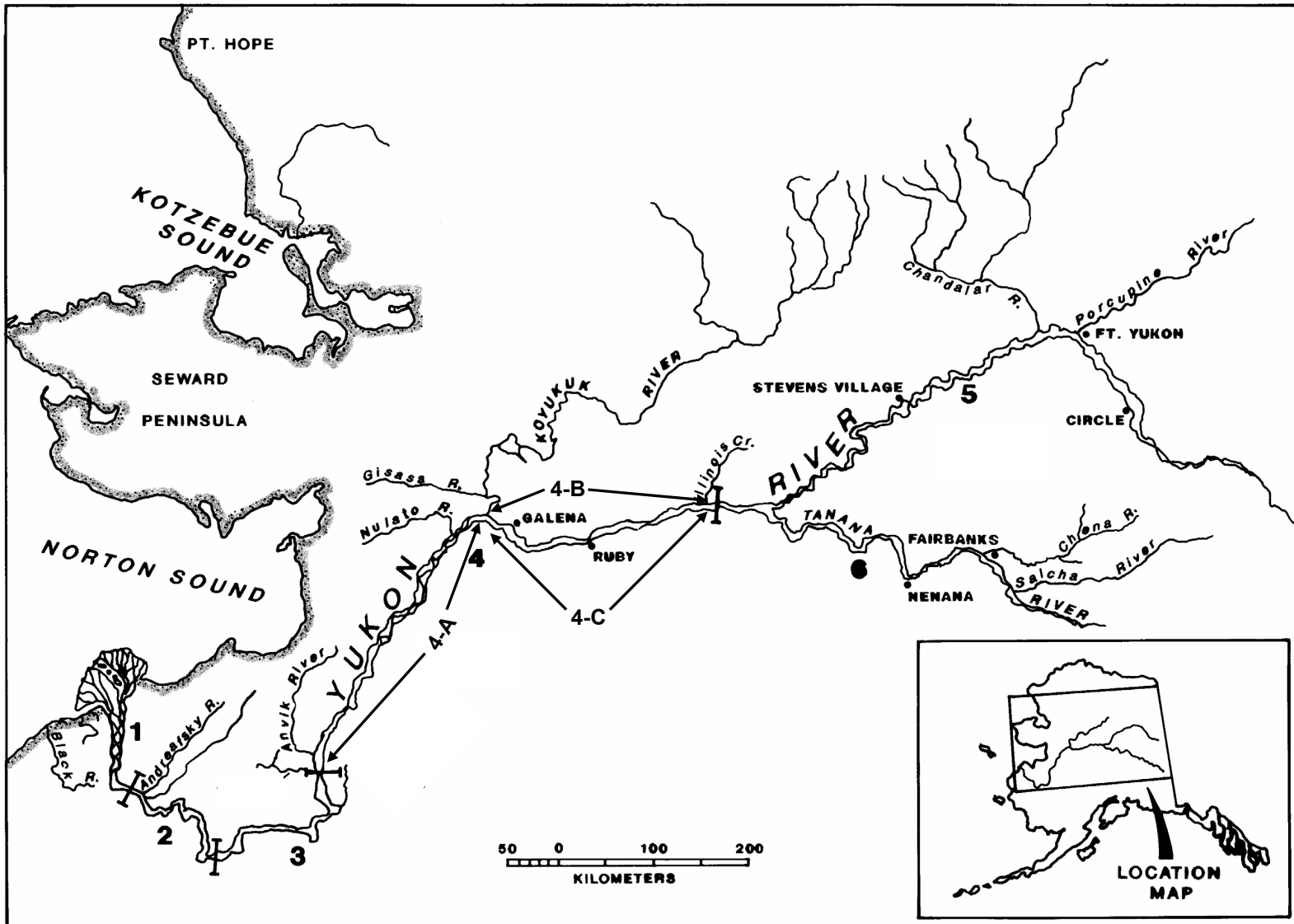
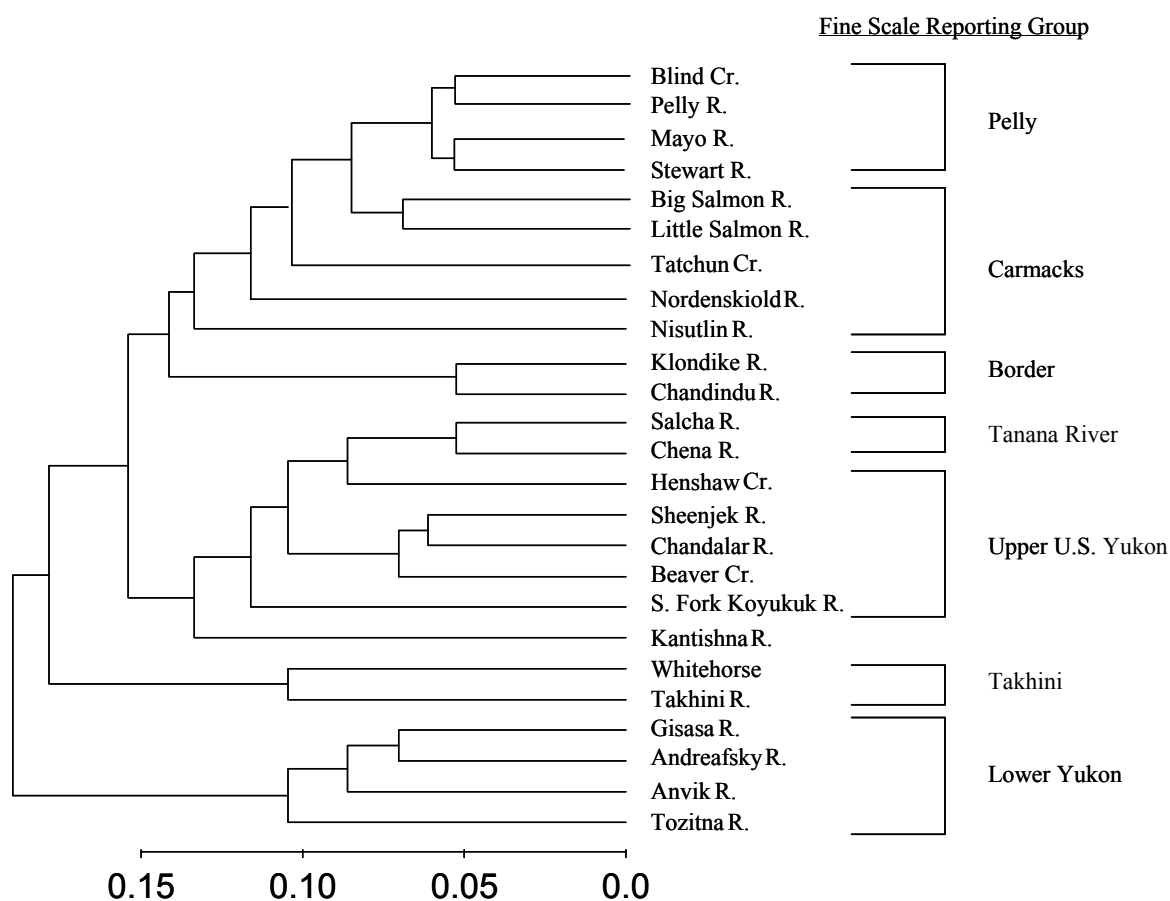
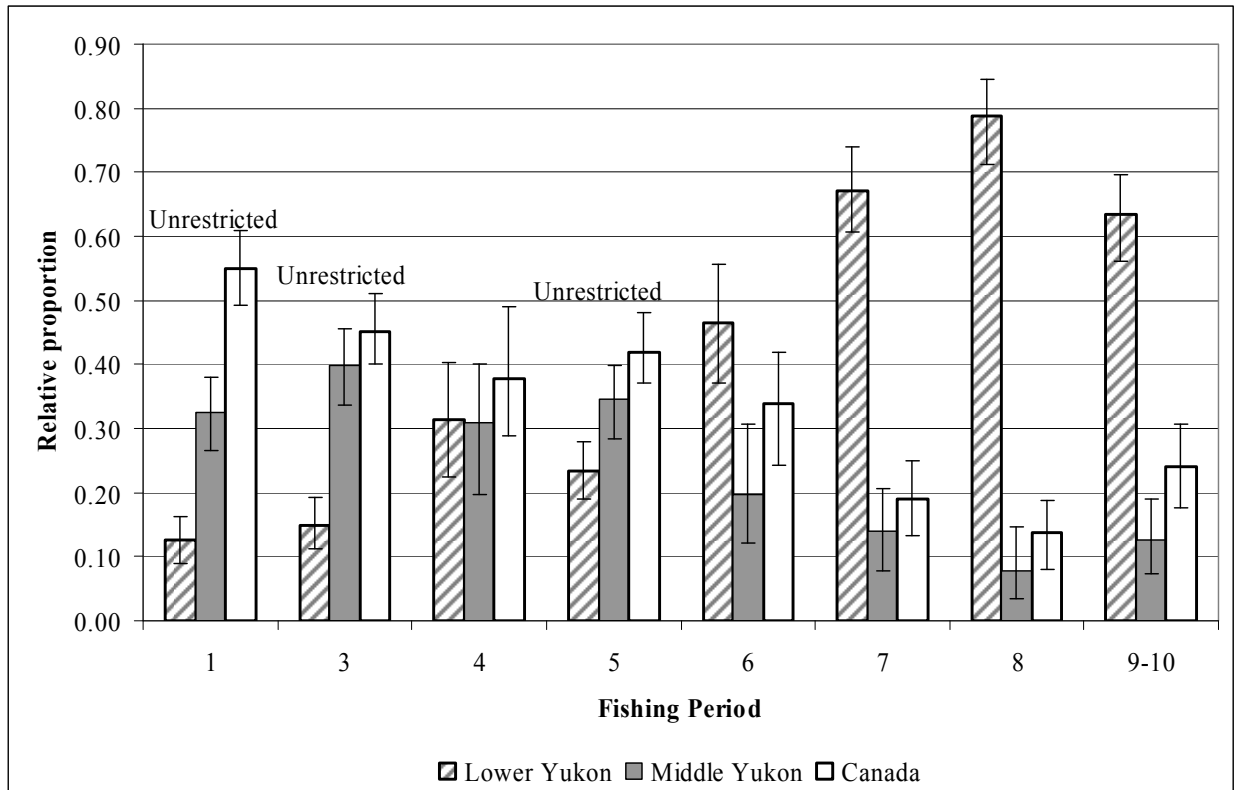


Figure 2.—Location of the fishing districts (and District Y-4 Subdistricts) used for management of salmon fisheries in the United States portion of the Yukon River drainage.



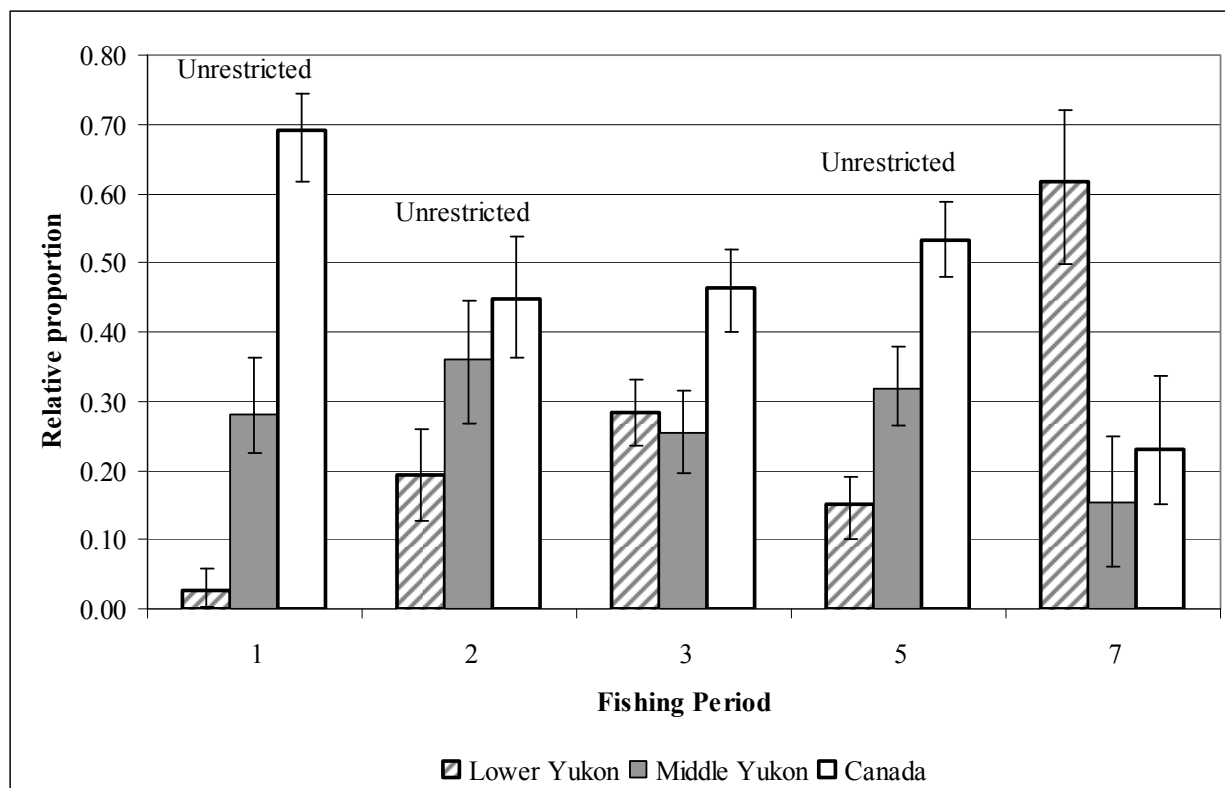
*Note:* Genetic distances are calculated from allele frequency differences from 26 SNPs. Population membership in the fine-scale reporting groups from Table 1 is indicated in the right margin.

Figure 3.—Unweighted paired group-mean clustering tree based on genetic distances between pairs of Chinook salmon populations in the Yukon River drainage.



*Note:* Periods which allowed unrestricted (>6 inch) net mesh sizes are labeled “Unrestricted”. Error bars denote the bounds of the 90% bootstrap confidence interval.

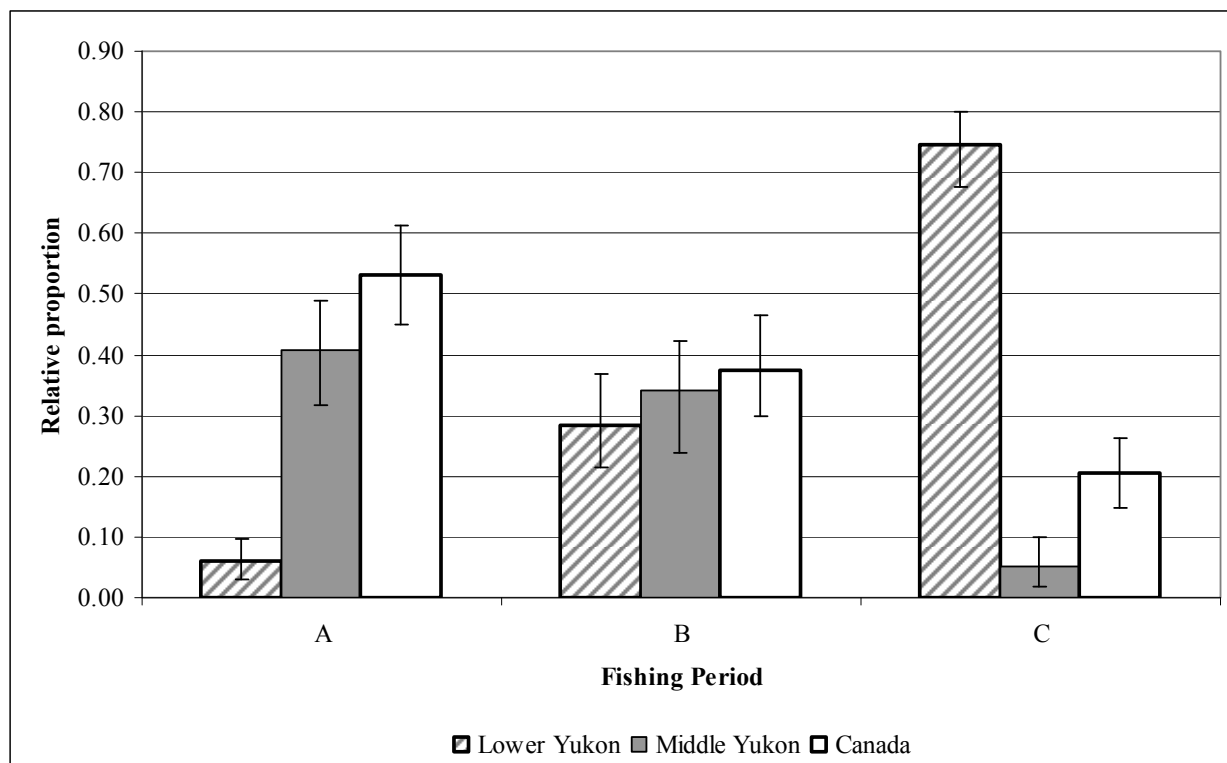
Figure 4.—Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon harvest during 8 commercial fishery periods in District Y-1, 2007.



*Note:* Periods which allowed unrestricted (> 6 inch) net mesh sizes are labeled “Unrestricted”. 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 harvest during 5 fishery periods in District Y-2, 2007.





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

Figure 6.—Relative broad-scale proportion of Chinook salmon caught during 3 periods in the Pilot Station test fishery, 2007.

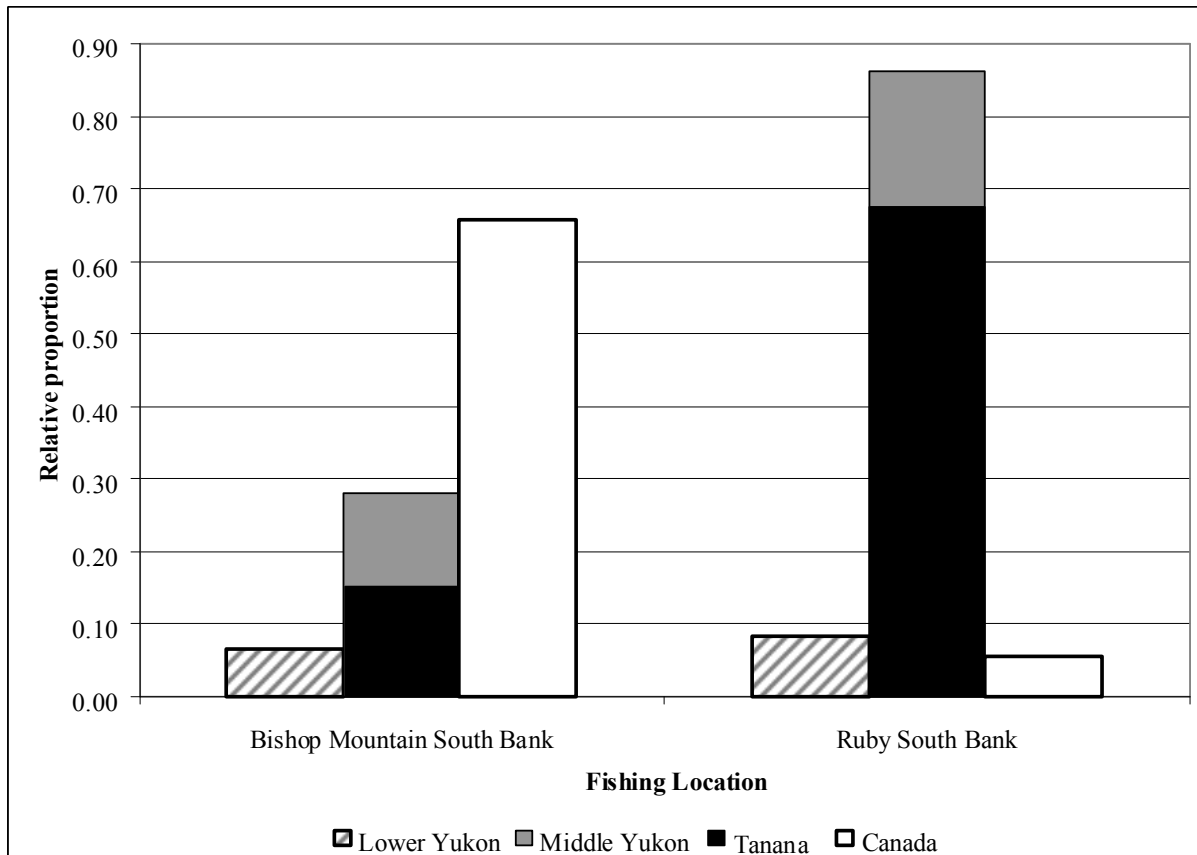
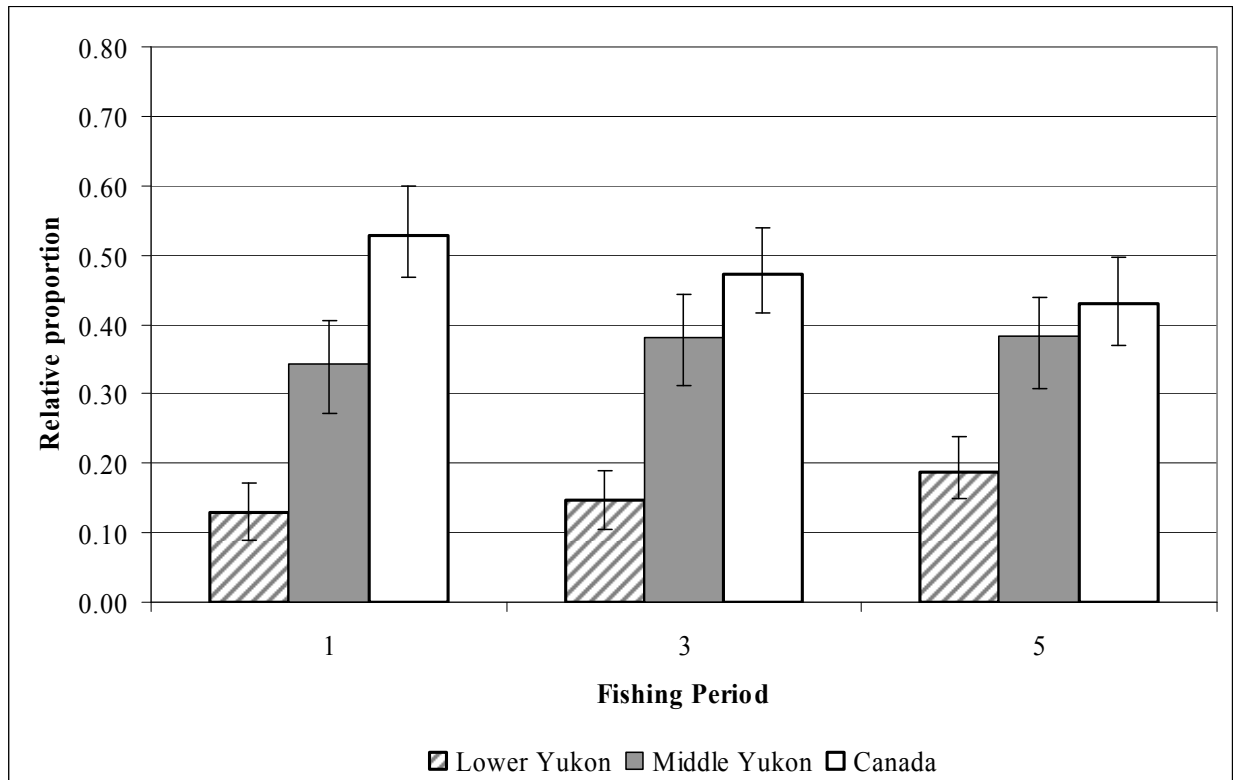
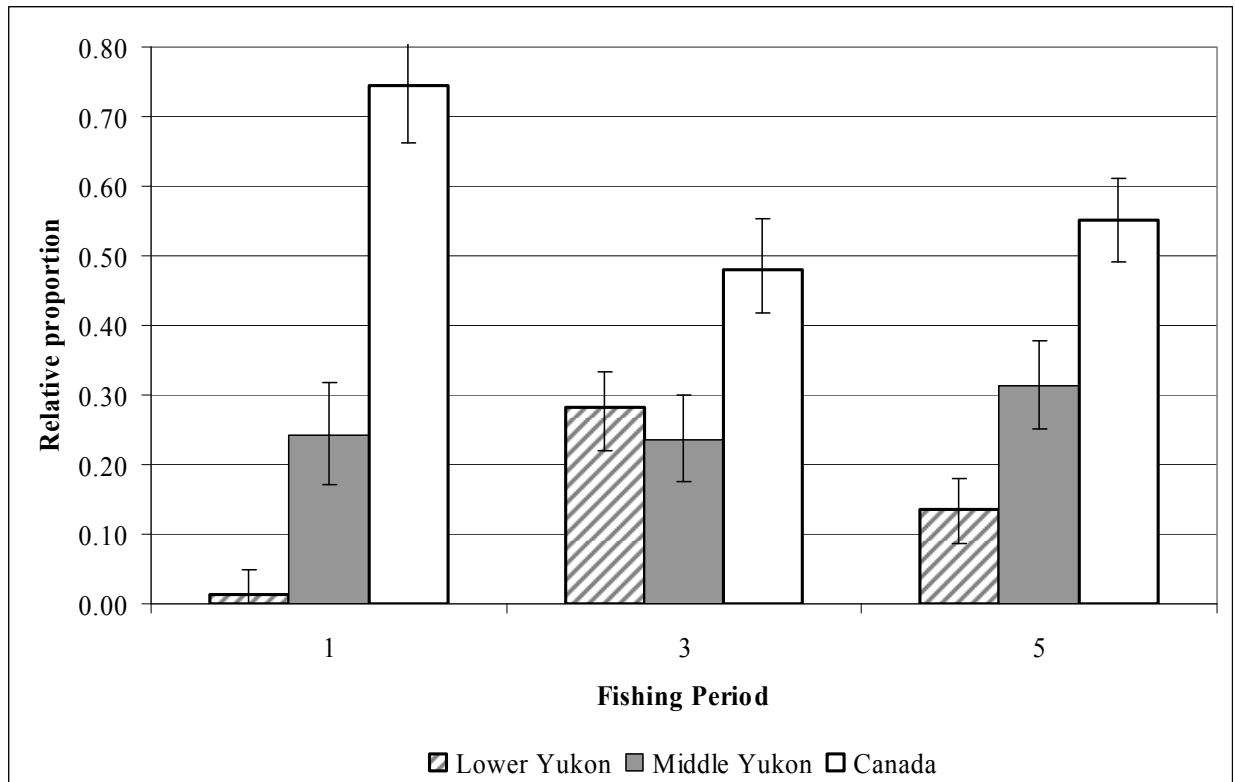


Figure 7.—Relative broad-scale proportion of Chinook salmon harvested by south bank-oriented fishing gear in the Y-4 subsistence fisheries at Bishop Mountain and Ruby, 2007.



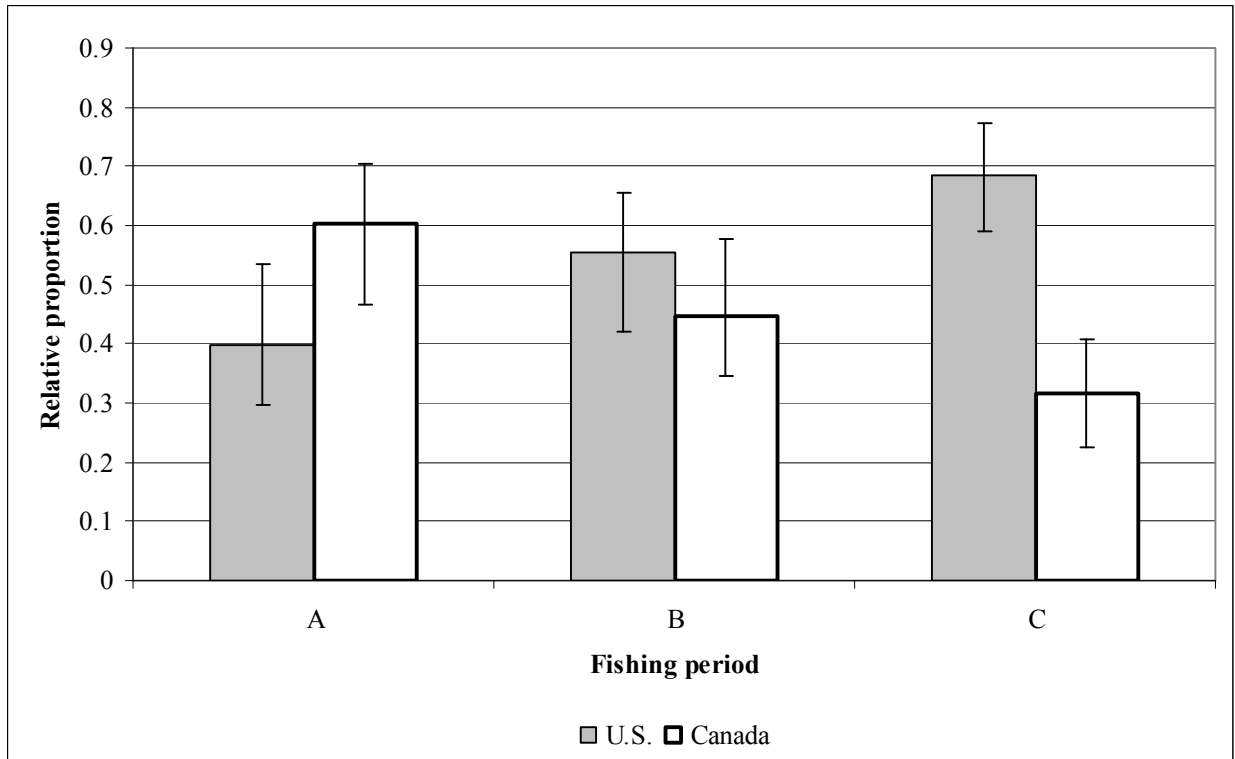
*Note:* Error bars denote the bounds of the 90% bootstrap confidence interval.

Figure 8.—Relative broad-scale proportion of 6-year old Chinook salmon harvested during the 3 unrestricted mesh size commercial fishery periods in District Y-1, 2007.



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

Figure 9.—Relative broad-scale proportion of 6-year old Chinook salmon harvested during the 3 unrestricted mesh size commercial fishery periods in District Y-2, 2007.



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

Figure 10.—Relative proportion of Canada stocks in 6-year old Chinook salmon harvested during 3 periods at Pilot Station, 2007.



## **APPENDICES**

Appendix A1.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of 6-year-old Chinook salmon harvested from the commercial fishery in District Y-1 of the Yukon River, 2007.

Reporting Group	Period 1 - Unrestricted			Period 3 - Unrestricted			Period 5 - Unrestricted		
	June 18-19			June 21-22			June 25-26		
	N = 294			N = 337			N = 326		
	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country									
United States	0.472	0.040	(0.401-0.533)	0.527	0.037	(0.460-0.584)	0.570	0.038	(0.502-0.629)
Canada	0.528	0.040	(0.467-0.600)	0.473	0.037	(0.416-0.540)	0.430	0.038	(0.371-0.498)
Broad-scale									
Lower Yukon	0.130	0.025	(0.090-0.172)	0.147	0.026	(0.104-0.190)	0.188	0.027	(0.150-0.238)
Middle Yukon	0.342	0.041	(0.271-0.405)	0.380	0.040	(0.313-0.444)	0.382	0.039	(0.309-0.438)
Canada	0.528	0.040	(0.467-0.600)	0.473	0.037	(0.416-0.540)	0.430	0.038	(0.371-0.498)
Fine-scale									
Lower Yukon	0.130	0.025	(0.090-0.172)	0.147	0.026	(0.104-0.190)	0.188	0.027	(0.150-0.238)
Upper U.S. Yukon	0.170	0.047	(0.107-0.262)	0.258	0.042	(0.186-0.323)	0.262	0.049	(0.180-0.340)
Tanana	0.172	0.036	(0.097-0.215)	0.122	0.032	(0.073-0.177)	0.120	0.036	(0.059-0.179)
Canada Border	0.050	0.023	(0.018-0.091)	0.012	0.017	(0.000-0.052)	0.026	0.018	(0.000-0.058)
Pelly	0.209	0.052	(0.145-0.318)	0.187	0.047	(0.110-0.263)	0.053	0.036	(0.013-0.138)
Carmacks	0.262	0.050	(0.150-0.320)	0.261	0.047	(0.173-0.335)	0.313	0.043	(0.224-0.371)
Takhini	0.007	0.015	(0.000-0.045)	0.013	0.015	(0.000-0.044)	0.038	0.019	(0.011-0.073)

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.



Appendix B1.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of 6-year-old Chinook salmon harvested from the commercial fishery in District Y-2 of the Yukon River, 2007.

Reporting Group	Period 1 - Unrestricted			Period 3 - Unrestricted			Period 5 - Unrestricted		
	June 15			June 20			June 24		
	N =	227		N =	281		N =	300	
	Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
Country									
United States	0.255	0.043	(0.192-0.338)	0.519	0.040	(0.448-0.581)	0.449	0.037	(0.388-0.508)
Canada	0.745	0.043	(0.663-0.808)	0.481	0.040	(0.419-0.552)	0.551	0.037	(0.492-0.612)
Broad-scale									
Lower Yukon	0.014	0.015	(0.000-0.049)	0.283	0.035	(0.221-0.333)	0.136	0.028	(0.087-0.181)
Middle Yukon	0.241	0.044	(0.171-0.319)	0.236	0.038	(0.175-0.301)	0.313	0.038	(0.252-0.379)
Canada	0.745	0.043	(0.663-0.808)	0.481	0.040	(0.419-0.552)	0.551	0.037	(0.492-0.612)
Fine-scale									
Lower Yukon	0.014	0.015	(0.000-0.049)	0.283	0.035	(0.221-0.333)	0.136	0.028	(0.087-0.181)
Upper U.S. Yukon	0.109	0.049	(0.018-0.184)	0.110	0.038	(0.057-0.180)	0.166	0.041	(0.106-0.242)
Tanana	0.133	0.042	(0.077-0.215)	0.126	0.034	(0.065-0.174)	0.147	0.035	(0.089-0.201)
Canada Border	0.139	0.036	(0.084-0.202)	0.003	0.015	(0.000-0.041)	0.026	0.021	(0.000-0.066)
Pelly	0.361	0.064	(0.251-0.455)	0.186	0.053	(0.106-0.281)	0.153	0.047	(0.086-0.239)
Carmacks	0.243	0.052	(0.159-0.325)	0.253	0.053	(0.154-0.330)	0.288	0.052	(0.192-0.366)
Takhini	0.002	0.010	(0.000-0.025)	0.039	0.019	(0.012-0.076)	0.084	0.027	(0.042-0.129)

*Note:* The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Appendix C1.—Estimated proportional contributions (Est) and 90% confidence intervals (CI) of 6-year-old Chinook salmon harvested from the Pilot Station test fishery of the Yukon River, 2007.

Reporting	Region	Period A			Period B			Period C		
		June 6-19			June 20-30			July 1-17		
		N =	81		N =	69		N =	90	
Country		Est	S.D.	90%CI	Est	S.D.	90%CI	Est	S.D.	90%CI
	United States	0.397	0.071	(0.297-0.535)	0.554	0.071	(0.422-0.655)	0.685	0.055	(0.591-0.774)
	Canada	0.603	0.071	(0.465-0.703)	0.446	0.071	(0.346-0.578)	0.315	0.055	(0.227-0.409)

*Note:* Due to insufficient sample sizes, estimates are only provided for country of origin components. The estimated group proportions are given for each of 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.