

# Genetic Stock Identification of Chinook Salmon Harvests on the Yukon River

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### 1. Introduction:

#### *Summary:*

Significant genetic variation exists among populations of Chinook salmon from the Yukon River drainage and use of this variation for providing estimates of stock composition of fishery harvests has been possible since the early 1990's. In 2006, a 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 the subsistence fishery in Districts Y-1, Y-4 and Y-5 and commercial fisheries in Districts Y-1, Y-2, Y-3 and Y-5, 4,977 individuals were assayed for genetic variation at the 26 SNPs. Mixed stock analysis of these samples enabled the estimation of the stock composition of the harvest at three 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 District Y-1 the portion of harvest attributable to Canadian origin fish was consistently near 50% with the exception of one commercial fishing period, when it dropped below 40%. In the District Y-2 harvest, Canadian stocks contributed between 36% and 60% of the harvest over the four commercial fishing periods.

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 in fishery harvests in the U.S. waters of the Yukon River is necessary information for meeting the obligations of the Yukon River Salmon Agreement between the United States (U.S.) and Canada. Until recently, scale pattern analysis was used to estimate stock composition of the harvest, but the recent development of baseline data for Chinook salmon populations in the Yukon River drainage has demonstrated the ability of genetic stock identification to deliver the same information more accurately and more efficiently (Smith et al. 2005a; Templin et al. 2005; Templin et al. 2006a,b, 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. *in review*) have been explored to provide a replacement for the allozyme baseline developed in the 1990's (Beacham et al. 1989; Wilmot et al. 1992; Templin et al. 2005). The baseline of nine SNPs and 23 populations, completed in 2004, 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 this SNP baseline was augmented with the addition of populations and genetic markers; the new version consists of 25 populations

and 26 SNPs. Two collections were added from U.S. populations, the Sheenjek and Kantishna rivers, and one population, Little Salmon River, was added from Canada. One collection previously used in the 2004 baseline, Stoney River, was removed from the 2006 baseline based on recommendations from biologists from Department of Fisheries and Oceans Canada (DFO).

This report describes the mixed stock analysis of the Chinook salmon harvest in the U.S. portion of the Yukon River in 2006. 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 three hierarchical sets of reporting groups: Country, Broad-scale, and Fine-scale. In addition, we provide age-specific estimates for the five- and six-year old components of the run.

### ***Objectives:***

The goal of this project was to provide estimates of the stock composition of Chinook salmon harvest in commercial and subsistence fisheries on the Yukon River in 2006. 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 subdistrict
  - v. District Y-5 subsistence – 400 individuals
- 2) Analyze a representative sample of individuals from each district and period for genetic variation using the SNP 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.

**2. Study Area:** Districts Y-1, Y-2, Y-4 and Y-5 of the Yukon River.

### **3. Methods:**

#### **COLLECTIONS**

Many of the Chinook salmon collections that comprise the baseline (Table 1, Figure 1) were assembled as a part of a three-laboratory collaboration (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). Additional samples were obtained from Mike Turner, a subsistence fisher on the Kantishna River and from a project on the Sheenjek River by the Council of Athabaskan Tribal Governments.

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 randomly each fishing period during the process of sampling the harvest for age, sex, and length data (DuBois et al. 2007). The tissues collected were axillary processes preserved in ethanol.

## LABORATORY METHODS

Genetic data were collected from the fishery samples as individual multi-locus genotypes for 26 SNPs (Table 3). Samples were arranged into subsets for the purpose of fitting collections onto 384-well reaction plates. Samples were omitted only from fishery collections with large sample sizes ( $n \geq 200$ ), and no more than 10% of any collection was omitted.

Baseline individuals were assayed for their genotypes at 26 SNPs (Table 3). SNP genotyping was performed in 384-well reaction plates, with four 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 denaturing 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, eight samples from each 96-well DNA extraction plate, were reanalyzed for all SNPs. This insured that the data are reproducible and any errors created from the processing of individual plates were corrected.
- 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 to insure that any given individual did not appear more than once in the baseline.
- 5) The data are permanently stored in an Oracle database, *LOKI*, administered by ADF&G.

## STATISTICAL ANALYSES

When 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 similarity.

## **SIMULATIONS**

Simulations were conducted to evaluate the accuracy and precision of the enlarged 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 three 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. Another set of simulations was performed using fine-scale reporting groups (Table 1), which represent identifiable sets of populations useful for management and research. These groups were previously defined in 2004 (Templin et al. 2006b) when SNPs were 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 1000 simulations. Reporting groups with mean correct estimates of 90% or better are considered highly identifiable in fishery applications. Reporting groups with mean correct estimates lower than 90% can still be considered identifiable in mixtures, but sources of misallocation should be considered when interpreting the results.

## **MIXED STOCK ANALYSIS**

Stock composition estimates for country-of-origin, the three broad-scale, and the seven 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 percent of the mixture that was removed. Further, we deleted any individual missing data at five 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 1000 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 1000 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. When sample sizes permitted, the stock compositions of the five- and six-year old portions of the harvest were also estimated.

#### **4. Results:**

##### **COLLECTIONS**

The only new baseline tissue samples collected in 2006 that were available for this analysis were 37 individuals collected from the Sheenjek River (Table 1). The Kantishna River samples were collected in 2005 and the Little Salmon River samples were collected in 1987 and 1997, but were not added to the SNP baseline until 2006.

During 2006, 5,090 Chinook salmon were sampled as part of 16 collections from the commercial and subsistence fishery harvests in the U.S. portion of the Yukon River drainage (Table 2). Sampling was conducted in five periods in District Y-1. Chinook salmon were sampled in four out of five commercial fishing periods in District Y-2. No Chinook salmon samples were taken in Period 2 in Y-2 as this fishery was restricted to 6-inch mesh gear and intended to target chum salmon.

##### **LABORATORY ANALYSIS**

For the baseline, a total of 3,649 individuals from 43 collections representing 25 populations were analyzed (Table 1). Of these, 351 individuals representing the Kantishna, Sheenjek and Little Salmon rivers were added to the existing SNP baseline. In addition, the number of SNPs surveyed in the existing baseline increased from 18 to 26 for all populations.

Of the fishery samples, a total of 4,977 individuals were analyzed for allelic variation at 26 SNPs. Because it is more efficient to analyze sets of 95 individuals (rather than 100) in the laboratory, in some cases subsets of collections were used. In general, no more than 10% of a collection was omitted, and individual collections were not reduced below a sample size of 190. Sampling theory (Thompson 1987) shows that this reduction in sample size should have little effect on the precision or accuracy of the estimate. The quality control checks employed demonstrated an overall error rate of less than 1% for baseline samples and 0% for fishery samples.

##### **STATISTICAL ANALYSIS**

Collections taken in multiple years from the same location were pooled for further analyses. After adjusting for the number of tests, no significant differences were found between temporally-spaced collections from the same location.

Genetic distances were calculated between each pair of populations and then used to create a dendrogram of genetic relationships between the populations in the baseline (Figure 3). This clustering analysis demonstrated the geographic structuring of Chinook salmon in the Yukon River. The most distinct group identified in this analysis was the set of Chinook salmon

populations from the lower Yukon River and lower Koyukuk River. The next group contained the populations from the Takhini River. Within the remaining populations, two clusters were found. The first contained the remaining U.S. populations (the Tanana River and upper portions of the Yukon and Koyukuk river drainages) and the second contained the remaining Canadian populations. Within the main Canada cluster, populations also grouped geographically into four smaller regional clusters: populations near the U.S./Canada border, the Pelly and Stewart river drainages, populations from the Tatchun area, and the Whitehorse Hatchery collection.

## **SIMULATIONS**

Reporting groups for mixed stock analysis of Chinook salmon in the Yukon River were defined based on previous studies (Templin et al. 2005; Smith et al. 2005a, Templin et al. 2006b) and supported by the structure revealed in this analysis: 1) Lower Yukon – Andraefsky River, Anvik River, Tozitna River, and Gisasa River, 2) Upper U.S. Yukon – Henshaw Creek, South Fork Koyukuk River, Beaver Creek, Chandalar River, and Sheenjek River, 3) Tanana River – Kantishna River, Chena River, Salcha River, 4) Canada Border – Chandindu River and Klondike River, 5) Pelly – Pelly River, Mayo River, Stewart River, and Blind Creek, 6) Carmacks – Tatchun River, Nisutlin River, Nordenskiold River, Big Salmon River, and Little Salmon River, 7) Takhini – Takhini River and Whitehorse Hatchery. Simulation studies based on this fine-scale structure indicate that these reporting groups are highly identifiable in mixtures. When simulated mixtures composed entirely from a single reporting group were treated as mixtures of unknown origin more than 90% of the mixture was correctly identified to region-of-origin (Table 4). As expected, a higher level of distinction was also seen when simulating mixtures from broad-scale groups (97% correct allocation) and country-of-origin (98% correct allocation).

## **MIXTURE ANALYSIS**

Estimates of stock composition in the commercial harvest in District Y-1 of the Yukon River indicate that Chinook salmon of Canadian origin contributed approximately 50% of the harvest during three of the five commercial fishing periods (Table 5; Figure 4). The largest portion of the Canadian salmon was estimated to be from the Carmacks Region. During periods 3 (June 30) and 4 (July 4) the contribution of Canadian populations in the harvest dropped to 44% and 36%, respectively. These reductions were matched by an increase in the presence of Lower Yukon populations in the harvest (44% and 56% respectively).

Stock composition estimates of the Canadian contribution to the commercial harvest in District Y-2 varied more widely over the two weeks of the fishery (Table 6; Figure 5). The Canadian component of the harvest ranged from a high of 60% in period 1 (June 15) to a low of 36% in period 4 (June 27). The Middle Yukon portion of the harvest dropped over the course of the four periods from 37% to 10%, while the Lower Yukon contribution increased from 3% to 47%.

In the district Y-3 commercial harvest, 54% 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 Canada Border Region with 21% of the harvest, while the largest component of the U.S. harvest came from Tanana River stocks with 22% of the harvest (Table 7).

The stock composition of the commercial harvest in District Y-5 was similar to that in District Y-3 when considering country-of-origin, with 53% of the harvest estimated to be from Canada. Unlike District Y-3, however, the largest component of the Canadian portion of the commercial harvest in District Y-5 was estimated to be from the Carmacks Region, and the largest component of the U.S. portion of the harvest was from the Upper U.S. Region (Table 7).

In the District Y-1 subsistence fishery, 45% of the harvest was comprised of Canadian populations. The Pelly Region contributed the largest component of the Canadian harvest with 23% (Table 7). Of the U.S. contribution, almost half was estimated to be from the Tanana River (25%).

The estimated contribution of Canadian populations to the subsistence harvest in District Y-4 varied from a high of 50% in subdistrict 4-A to a low of 4% in subdistrict 4-C. As with the commercial harvest in District Y-1, the Carmacks Region comprised the greatest portion of the Canadian estimate in District Y-4 in all three subdistricts (Table 8). Estimates for subdistrict 4-A were produced using only individuals sampled in Kaltag and Nulato. A total of 49 individuals were collected from Koyukuk, however the exact collection location for these samples was unknown at the time of this report. These samples will be included in the appropriate mixture once the collection location is established, and this updated estimate will be used by ADF&G to produce estimates of harvest abundance.

The Canadian contribution to the subsistence harvest in District Y-5 was larger than to the commercial harvest; Canadian populations were estimated to contribute 71% of the subsistence harvest. The Upper U.S. populations contributed most of the U.S. portion of the harvest, and the Pelly Region contributed the largest portion of the Canadian harvest (Table 7).

Stock composition of the harvests was also estimated independently by age class. Sufficient samples were available to estimate the composition of the five- and six-year old components for the Y-1 and Y-2 commercial fisheries and the Y-1 subsistence fishery (Appendices 1 and 2; Figures 6 and 7). In the District Y-1 commercial fishery, the Canadian component of five- and six-year old Chinook salmon harvested remained approximately equal in periods 1 through 3 (June 20, 26 and 30), with an increase in the Canadian contribution to the six-year old component seen in periods 4 and 5 (July 4, 6). In the District Y-2 commercial fishery, six-year old Canadian Chinook salmon made up the largest component of the harvest in periods 1 and 3 (June 15 and 24), while the five- and six-year old components were approximately equal in periods 4 and 5 (June 27 and July 2).

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

		Andraefsky 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
			1987, 1997, 2002,	
		Tatchun Creek	2003	169
		Nordenskiold River	2003	56
		Nisutlin River	1987, 1997	56
		Takhini		
		Takhini River	1997, 2003	101
		Whitehorse Hatchery	1985, 1987, 1997	242
		<b>Total</b>		<b>3,649</b>

Table 2. Chinook salmon collections from selected commercial and subsistence fishery harvests in the Yukon River drainage, 2006.

District	Period	Dates	Location	Sample size		
				Collected	Analyzed	
<b>Commercial</b>						
Y1	1	June 20	Emmonak	400	400	
	2	June 26	Emmonak	400	400	
	3	June 30	Emmonak	400	400	
	4	July 4	Emmonak	398	398	
	5	July 6	Emmonak	241	241	
Y2	1	June 15	Saint Marys	293	293	
	3	June 24	Saint Marys	400	400	
	4	June 27	Saint Marys	400	400	
	5	July 2	Saint Marys	400	379	
Y3		June 21		107	107	
Y5		July 8-13	Rampart	500	475	
				<b>Total</b>	<b>3,939</b>	<b>3,893</b>
<b>Subsistence</b>						
Y1		June 7-23	Emmonak	139	139	
Y4A		June 27- July 11	Kaltag/ Nulato/ Koyukuk	420	380	
Y4B		July 5-15	Bishop Rock	200	190	
Y4C		July 7-15	Ruby	90	90	
Y5			Rapids	302	285	
				<b>Total</b>	<b>1,151</b>	<b>1,084</b>
<b>Grand Total</b>				<b>5,090</b>	<b>4,977</b>	

Table 3. Single nucleotide polymorphisms assayed in individuals sampled from the commercial and subsistence harvest of Chinook salmon on the U.S. portion of the Yukon River drainage, 2006.

<b>Locus</b>	<b>Source</b>
<i>Ots_E2-275</i>	Smith et al. 2005a
<i>Ots_ETIF1A</i>	Unpublished
<i>Ots_FGF6A</i>	Unpublished
<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_hmRNPL-533</i>	Smith et al. 2005a
<i>Ots_HSP90B-100</i>	Smith et al. 2005a
<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_SC1kF2R2-135</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

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

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	(0.933-0.993)
Carmacks	0.931	(0.870-0.981)
Takhini	0.981	(0.956-0.998)

Table 5. Estimated proportional contributions (P) and 90% confidence intervals of Chinook salmon harvested from the commercial fishery in District Y-1 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Reporting Group	Period 1		Period 2		Period 3		Period 4		Period 5	
	June 20		June 26		June 30		July 4		July 6	
	N =	396	N =	399	N =	399	N =	397	N =	240
	<b>P</b>	<b>90%CI</b>								
<b>Country</b>										
United States	0.463	(0.402-0.520)	0.493	(0.443-0.547)	0.564	(0.514-0.617)	0.646	(0.597-0.692)	0.470	(0.408-0.531)
Canada	0.537	(0.480-0.598)	0.507	(0.453-0.557)	0.436	(0.383-0.486)	0.355	(0.308-0.403)	0.530	(0.469-0.592)
<b>Broad-scale</b>										
Lower Yukon	0.062	(0.034-0.098)	0.332	(0.281-0.384)	0.436	(0.382-0.487)	0.558	(0.512-0.612)	0.381	(0.316-0.435)
Middle Yukon	0.402	(0.333-0.463)	0.161	(0.112-0.209)	0.128	(0.085-0.179)	0.088	(0.047-0.121)	0.089	(0.050-0.141)
Canada	0.537	(0.480-0.598)	0.507	(0.453-0.557)	0.436	(0.383-0.486)	0.355	(0.308-0.403)	0.530	(0.469-0.592)
<b>Fine-scale</b>										
Lower Yukon	0.062	(0.034-0.098)	0.332	(0.281-0.384)	0.436	(0.382-0.487)	0.558	(0.512-0.612)	0.381	(0.316-0.435)
Upper U.S. Yukon	0.195	(0.102-0.264)	0.058	(0.017-0.097)	0.034	(0.002-0.087)	0.069	(0.024-0.099)	0.061	(0.015-0.110)
Tanana	0.206	(0.146-0.289)	0.102	(0.056-0.146)	0.094	(0.049-0.132)	0.019	(0.000-0.046)	0.028	(0.000-0.074)
Canada Border	0.063	(0.031-0.106)	0.012	(0.000-0.023)	0.021	(0.000-0.044)	0.009	(0.000-0.031)	0.019	(0.000-0.049)
Pelly	0.161	(0.108-0.260)	0.143	(0.067-0.203)	0.084	(0.041-0.151)	0.061	(0.027-0.130)	0.000	(0.000-0.085)
Carmacks	0.293	(0.188-0.335)	0.268	(0.211-0.352)	0.273	(0.194-0.323)	0.216	(0.142-0.262)	0.409	(0.296-0.460)
Takhini	0.021	(0.004-0.053)	0.085	(0.051-0.118)	0.059	(0.032-0.097)	0.069	(0.035-0.099)	0.103	(0.051-0.162)

Table 6. Estimated proportional contributions (P) and 90% confidence intervals of Chinook salmon harvested from the commercial fishery in District Y-2 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Reporting Group	Period 1		Period 3		Period 4		Period 5	
	June 15		June 24		June 27		July 2	
	N =	292	N =	398	N =	397	N =	379
	P	90% CI						
Country								
United States	0.398	(0.337-0.480)	0.473	(0.412-0.520)	0.644	(0.588-0.693)	0.573	(0.523-0.623)
Canada	0.602	(0.520-0.663)	0.528	(0.480-0.588)	0.356	(0.307-0.412)	0.427	(0.377-0.477)
Broad-scale								
Lower Yukon	0.025	(0.006-0.055)	0.111	(0.081-0.154)	0.394	(0.349-0.446)	0.472	(0.422-0.526)
Middle Yukon	0.373	(0.306-0.452)	0.361	(0.292-0.406)	0.250	(0.193-0.293)	0.102	(0.065-0.138)
Canada	0.602	(0.520-0.663)	0.528	(0.480-0.588)	0.356	(0.307-0.412)	0.427	(0.377-0.477)
Fine-scale								
Lower Yukon	0.025	(0.006-0.055)	0.111	(0.081-0.154)	0.394	(0.349-0.446)	0.472	(0.422-0.526)
Upper U.S. Yukon	0.129	(0.067-0.232)	0.178	(0.107-0.228)	0.093	(0.054-0.175)	0.033	(0.003-0.071)
Tanana	0.244	(0.161-0.300)	0.183	(0.128-0.246)	0.156	(0.075-0.190)	0.069	(0.032-0.102)
Canada Border	0.173	(0.113-0.231)	0.056	(0.028-0.112)	0.014	(0.000-0.033)	0.000	(0.000-0.012)
Pelly	0.288	(0.200-0.370)	0.114	(0.070-0.205)	0.048	(0.015-0.124)	0.043	(0.009-0.125)
Carmacks	0.142	(0.072-0.212)	0.352	(0.249-0.392)	0.246	(0.162-0.295)	0.311	(0.216-0.356)
Takhini	0.000	(0.000-0.007)	0.007	(0.000-0.031)	0.048	(0.016-0.081)	0.073	(0.040-0.111)

Table 7. Estimated proportional contributions (P) and 90% confidence intervals of Chinook salmon harvested from the subsistence fisheries in District Y-1 and Y5, and the commercial fishery in District Y-3 and Y-5 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Reporting Group	Y-1 Subsistence		Y-3 Commercial		Y-5 Commercial		Y-5 Subsistence	
	N =	139	N =	106	N =	472	N =	285
	P	90%CI	P	90%CI	P	90%CI	P	90%CI
Country								
United States	0.553	(0.471-0.645)	0.457	(0.336-0.586)	0.470	(0.389-0.512)	0.295	(0.223-0.365)
Canada	0.448	(0.355-0.529)	0.543	(0.414-0.664)	0.530	(0.488-0.612)	0.705	(0.635-0.777)
Broad-scale								
Lower Yukon	0.193	(0.124-0.263)	0.067	(0.018-0.129)	0.016	(0.004-0.034)	0.011	(0.000-0.032)
Middle Yukon	0.360	(0.270-0.455)	0.390	(0.268-0.524)	0.454	(0.371-0.496)	0.284	(0.213-0.352)
Canada	0.448	(0.355-0.529)	0.543	(0.414-0.664)	0.530	(0.488-0.612)	0.705	(0.635-0.777)
Fine-scale								
Lower Yukon	0.193	(0.124-0.263)	0.067	(0.018-0.129)	0.016	(0.004-0.034)	0.011	(0.000-0.032)
Upper U.S. Yukon	0.107	(0.045-0.244)	0.172	(0.053-0.317)	0.441	(0.335-0.474)	0.239	(0.165-0.312)
Tanana	0.253	(0.133-0.332)	0.218	(0.098-0.332)	0.013	(0.000-0.062)	0.045	(0.005-0.091)
Canada Border	0.052	(0.000-0.108)	0.205	(0.079-0.322)	0.029	(0.010-0.093)	0.190	(0.134-0.269)
Pelly	0.234	(0.118-0.317)	0.185	(0.048-0.315)	0.198	(0.137-0.293)	0.294	(0.170-0.370)
Carmacks	0.106	(0.037-0.206)	0.150	(0.056-0.264)	0.287	(0.201-0.338)	0.198	(0.125-0.305)
Takhini	0.056	(0.015-0.106)	0.003	(0.000-0.037)	0.024	(0.004-0.052)	0.024	(0.004-0.052)

Table 8. Estimated proportional contributions (P) and 90% confidence intervals of Chinook salmon harvested from the subsistence fishery in the three subdistricts of District Y-4 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Reporting Group	Subdistrict A		Subdistrict B		Subdistrict C	
	N =		N =		N =	
	P	90%CI	P	90%CI	P	90%CI
<b>Country</b>						
United States	0.484	(0.418-0.551)	0.523	(0.443-0.593)	0.956	(0.887-0.999)
Canada	0.516	(0.449-0.582)	0.477	(0.407-0.557)	0.044	(0.001-0.113)
<b>Broad-scale</b>						
Lower Yukon	0.036	(0.018-0.077)	0.104	(0.055-0.175)	0.174	(0.095-0.279)
Middle Yukon	0.448	(0.368-0.512)	0.419	(0.316-0.490)	0.781	(0.663-0.868)
Canada	0.516	(0.449-0.582)	0.477	(0.407-0.557)	0.044	(0.001-0.113)
<b>Fine-scale</b>						
Lower Yukon	0.036	(0.018-0.077)	0.104	(0.055-0.175)	0.174	(0.095-0.279)
Upper U.S. Yukon	0.196	(0.120-0.277)	0.212	(0.112-0.303)	0.082	(0.004-0.240)
Tanana	0.252	(0.171-0.309)	0.207	(0.118-0.282)	0.699	(0.512-0.798)
Canada Border	0.057	(0.021-0.103)	0.002	(0.000-0.040)	0.011	(0.000-0.043)
Pelly	0.121	(0.053-0.211)	0.112	(0.034-0.219)	0.000	(0.000-0.057)
Carmacks	0.308	(0.214-0.371)	0.319	(0.194-0.401)	0.034	(0.000-0.074)
Takhini	0.030	(0.007-0.066)	0.044	(0.004-0.112)	0.000	(0.000-0.000)

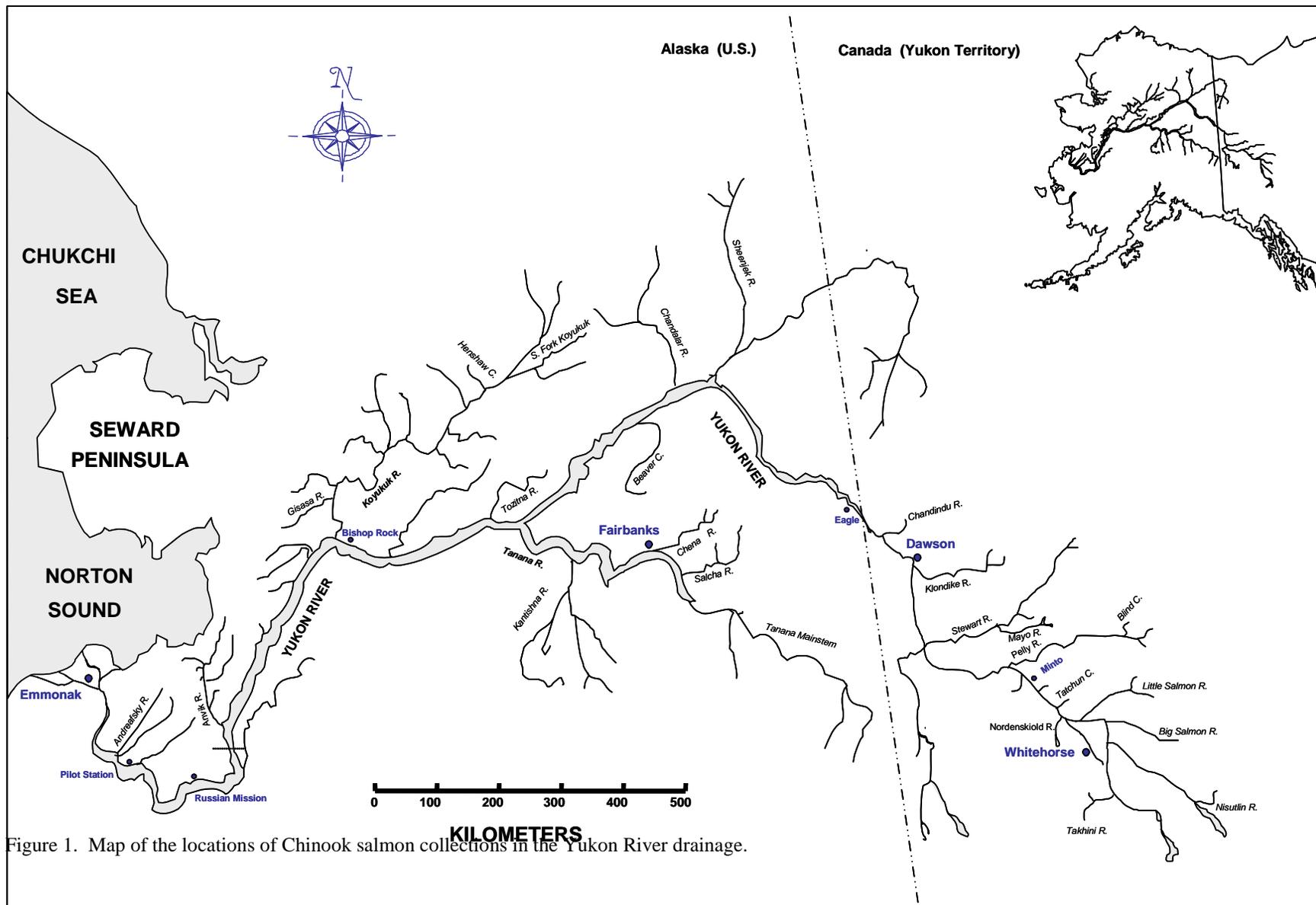


Figure 1. Map of the locations of Chinook salmon collections in the Yukon River drainage.

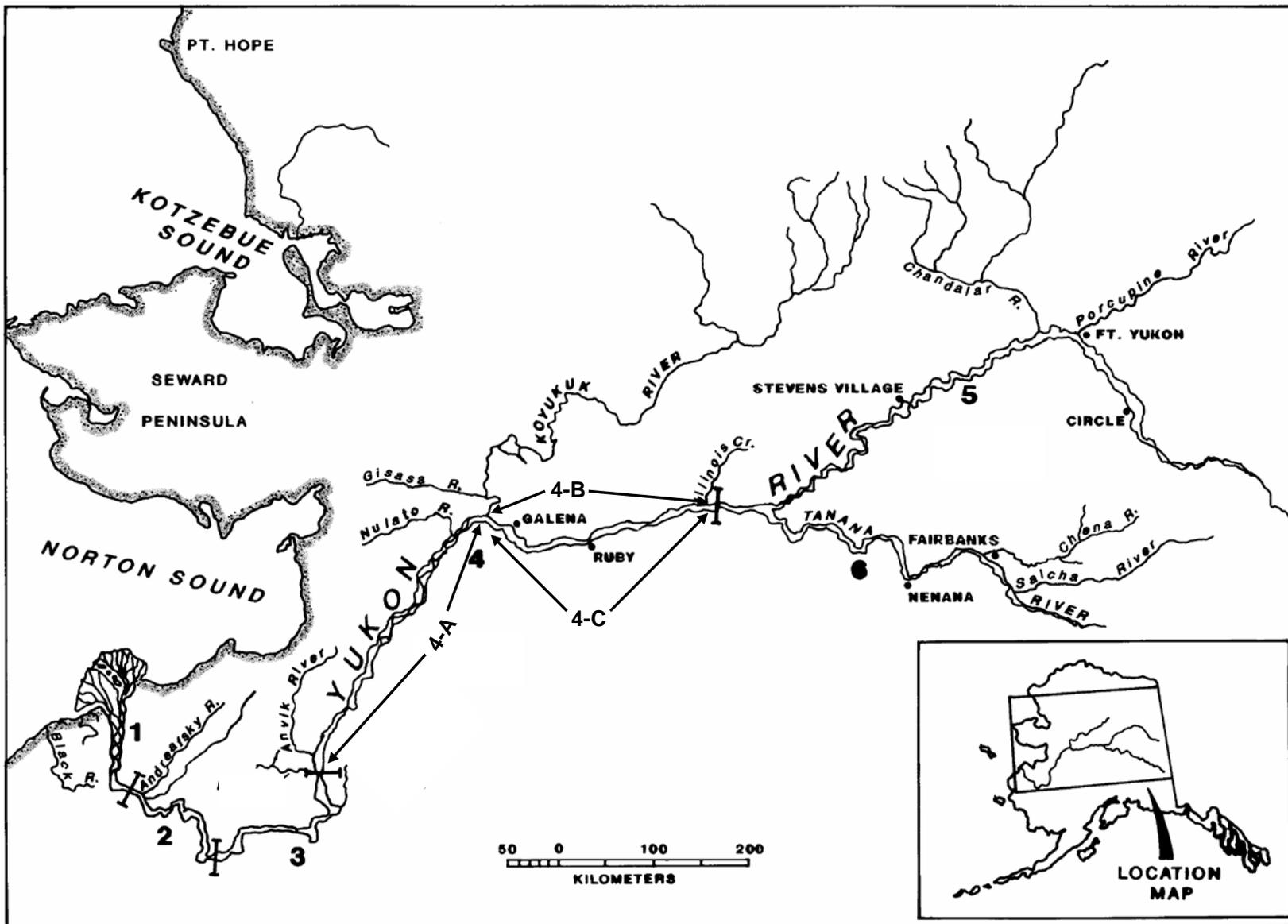


Figure 2. Location of the fishing districts (and District Y-4 subdistricts) used for management of salmon fisheries in the United States portion of the Yukon River drainage.

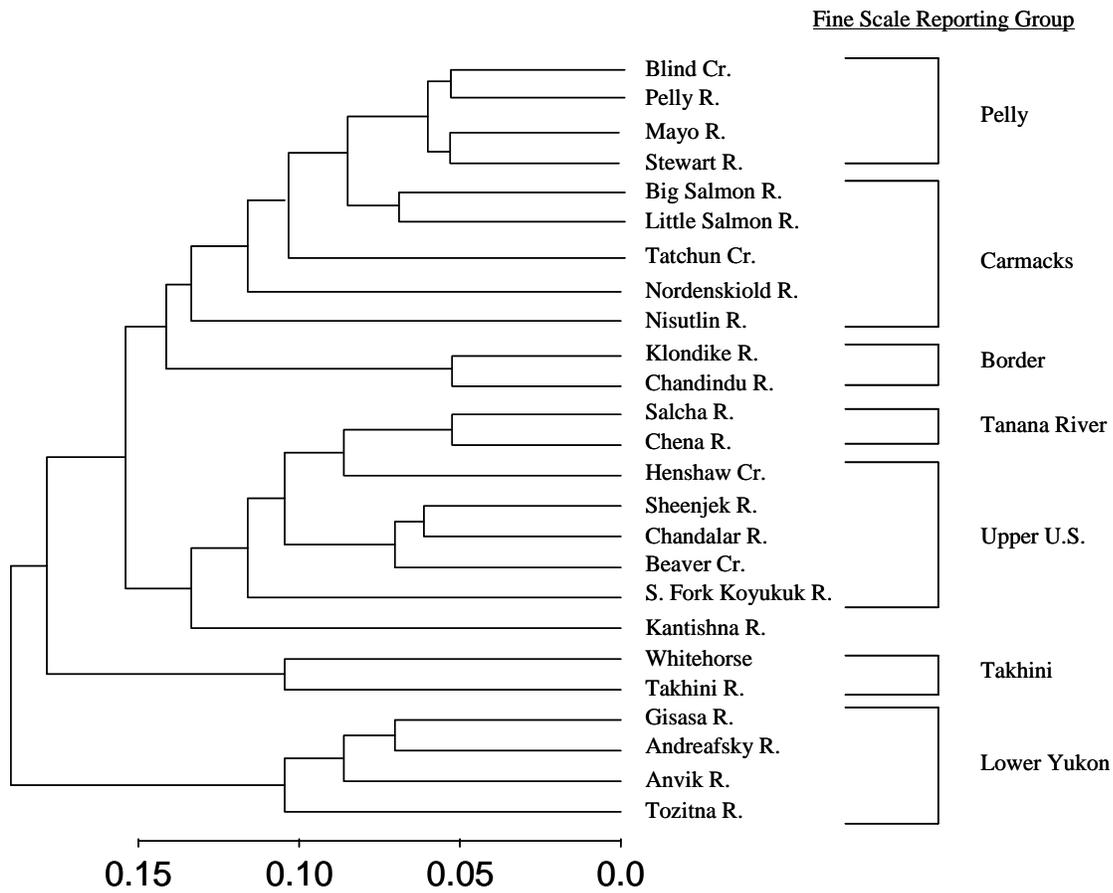


Figure 3. Unweighted paired group-mean clustering tree based on genetic distances between pairs of Chinook salmon populations in the Yukon River drainage. Population membership in the fine-scale reporting groups from Table 1 is indicated in the right margin.

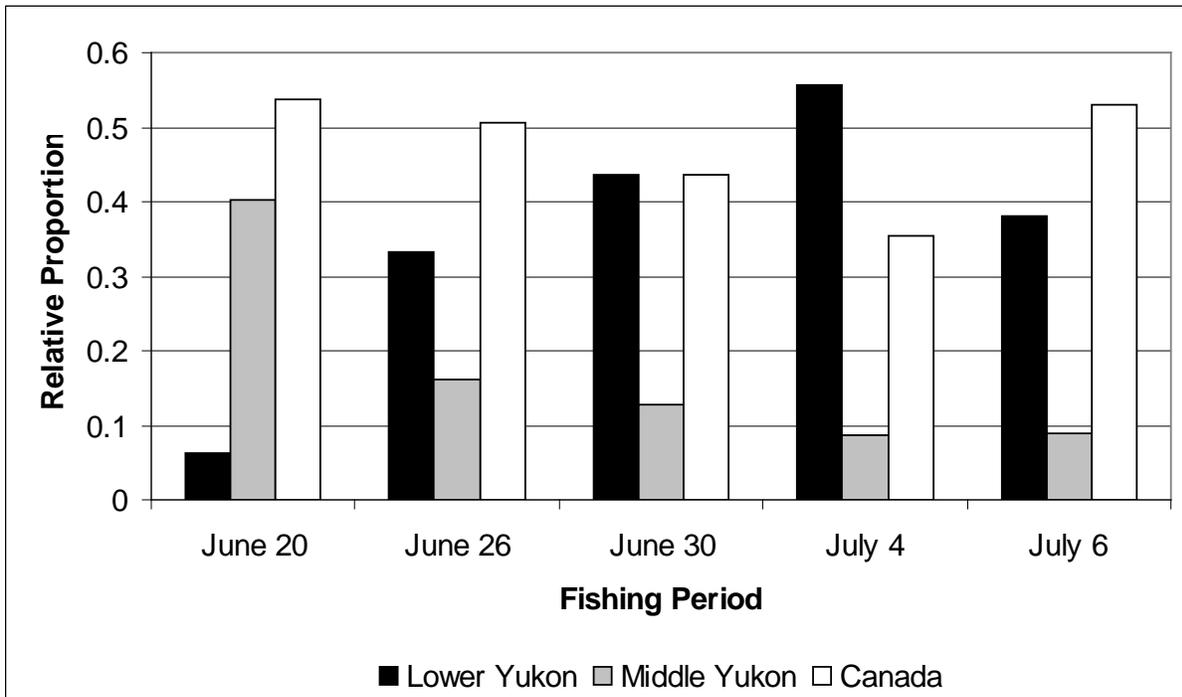


Figure 4. Relative stock composition of three broad-scale reporting groups in the Chinook salmon harvest during the five commercial fishery periods in District Y-1, 2006.

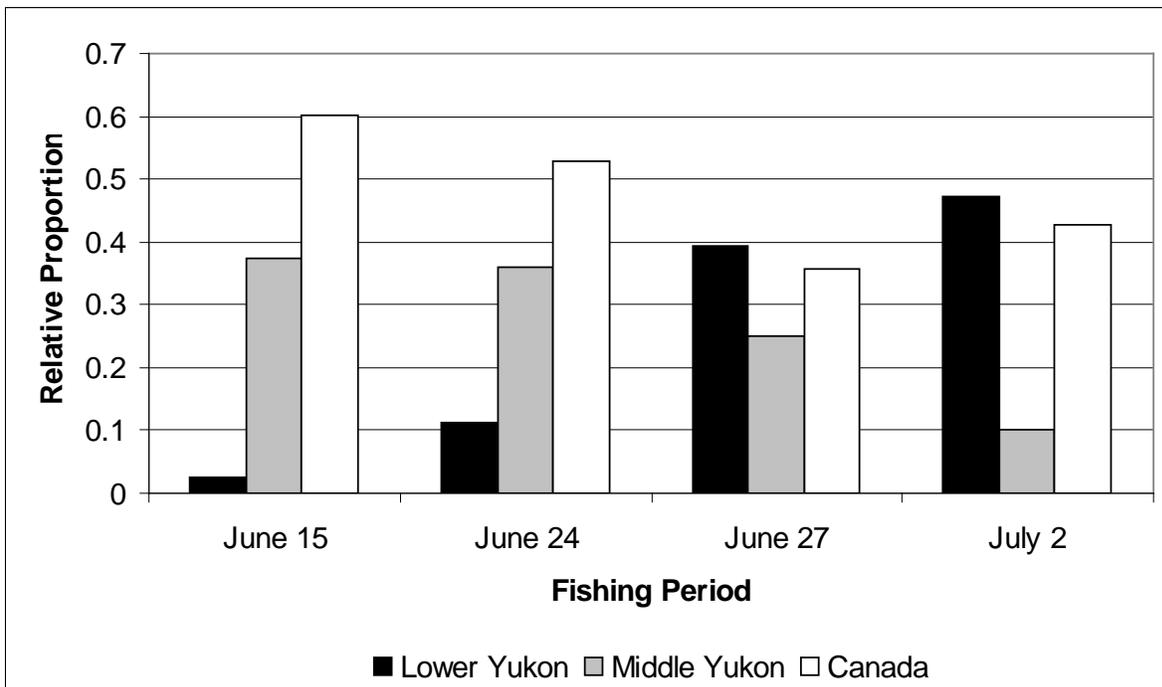


Figure 5. Relative stock composition of three broad-scale reporting groups in the Chinook salmon harvest during the four commercial fishery periods in District Y-2, 2006.

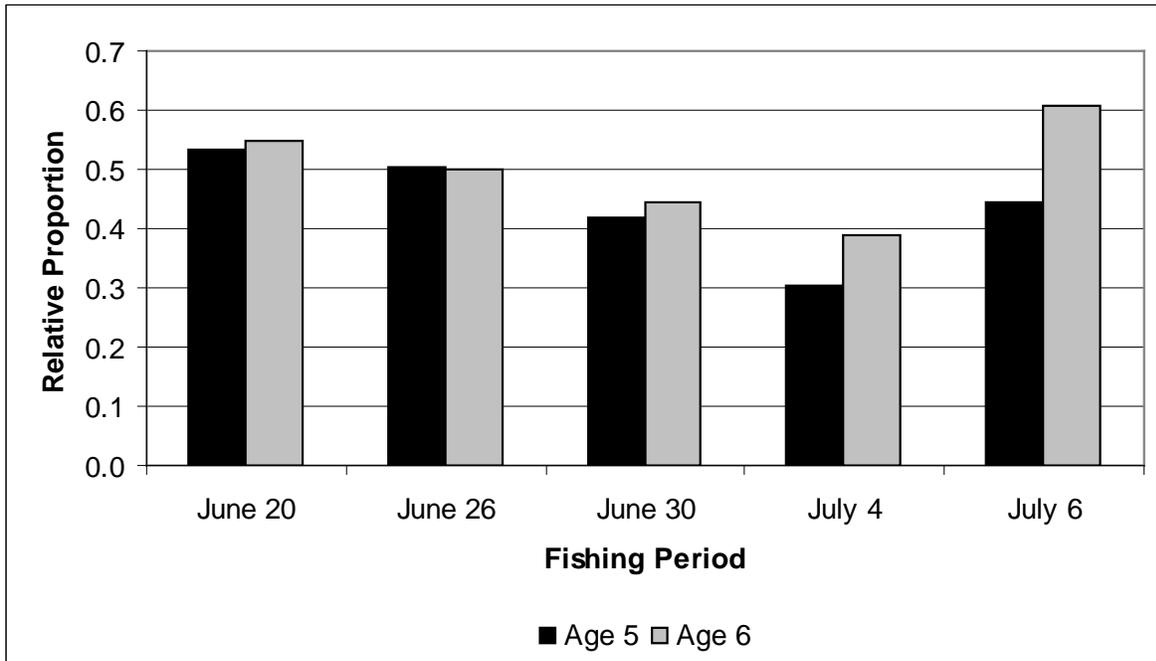


Figure 6. Relative proportion of Canada stocks in the five- and six-year old Chinook salmon harvested during the five commercial fishery periods in District Y-1, 2006.

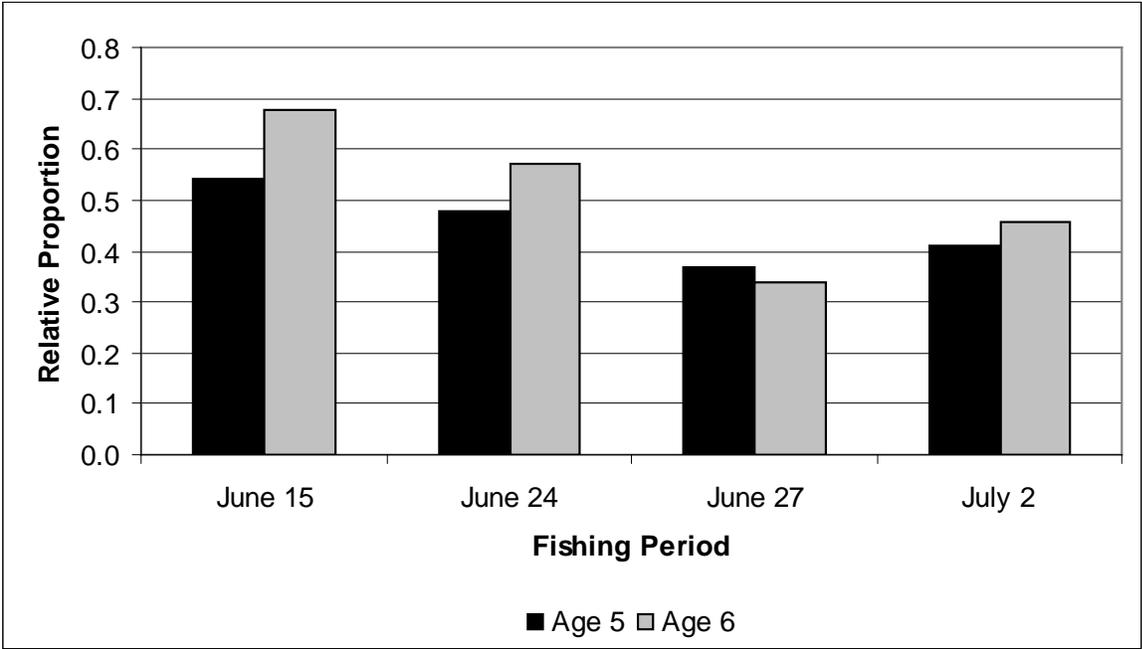


Figure 7. Relative proportion of U.S. stocks in the five- and six-year old Chinook salmon harvested during the four commercial fishery periods in District Y-2, 2006.

## **5. Discussion:**

In 2006, the stock composition of the Chinook salmon harvest in the Yukon River was estimated using a baseline of 26 SNPs from 25 populations. Due to the differences in marker type, loci and populations used in this baseline, the fine-scale reporting groups for 2006 are not the same as those used in either 2004 (SNPs) or 2005 (microsatellites). However, the country-of-origin and broad-scale reporting groups remain unchanged. Both clustering-based methods and simulations indicate that these reporting groups are supported by the data and are adequately identifiable in mixtures.

The stock composition estimates in the commercial fisheries in District Y-1 show similar patterns to the estimates from 2004 and 2005. In 2006, the Canadian component of the District Y-1 commercial fishery was near 50% in all periods except period 4 (July 4) when is dropped to 36%. A similar pattern was seen in 2004, when estimates of the Canadian component in this fishery were near 50% except for a drop in period 3 (37% on June 24-25) and period 6 (25% on July 2-3). In 2005, the Canadian component of this fishery was lowest during period 3 (43% on June 30-July 1).

In both districts Y-1 and Y-2 there is a general trend of decreasing contributions to the harvest from Canada and the Middle Yukon matched by an increase in the presence of Lower Yukon populations in the harvest. A similar pattern was seen in the commercial harvests in District Y-1 in 2005 and District Y-2 in 2004.

A large difference in the Canadian component of the harvest was seen in the District Y-4 subsistence fishery. Canadian stocks contributed 52% of the harvest in subdistrict 4-A, 48% in subdistrict 4-B, and only 4% in subdistrict 4-C. This decrease in the Canadian component in subdistrict 4-C was accompanied by an increase in the Tanana River component (25%, 21% and 70% in subdistricts 4-A, B and C, respectively). A similar pattern was also seen in the stock contribution estimates for the subsistence fisheries in District Y-4 in 2005 (ADF&G Unpublished data).

The Canadian component of the District Y-5 commercial fishery was 53%. This is the lowest percentage of the Canadian component seen in this fishery since 2004, when GSI was first used to estimate the stock composition of the harvest. Canadian populations contributed 85% of the harvest in 2004 and 77% in 2005. The contribution of Canadian populations to the commercial harvest in District Y-5 can be compared to the estimated contribution to the subsistence fishery (71%). This was the first year that the subsistence harvest in District Y-5 was sampled.

## **Acknowledgements:**

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and from the Sheenjek River by the Council of Athabaskan Tribal Governments. Laboratory analysis was performed with the assistance of Andy Barclay, Zac Grauvogel, Gina Johnston, Beth McLain, and Heather Hoyt. Carita Elfstrom and Judy Berger assisted with project and sample coordination. Funding for this project was provided by the 2006 Yukon River Panel River Panel Restoration and Management Fund (Project URM 16-06) under Agreement No. 70181-6-G400.

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**Appendices:**

Appendix 1.A Estimated proportional contributions (P) and 90% confidence intervals of five-year old Chinook salmon harvested from the commercial fishery in District Y-1 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Reporting Group	Period 1		Period 2		Period 3		Period 4		Period 5	
	June 20		June 26		June 30		July 4		July 6	
	N =		N =		N =		N =		N =	
	P	90%CI								
Country										
United States	0.467	(0.377-0.542)	0.496	(0.420-0.592)	0.583	(0.506-0.662)	0.698	(0.629-0.762)	0.557	(0.462-0.644)
Canada	0.533	(0.458-0.623)	0.504	(0.409-0.581)	0.417	(0.338-0.495)	0.302	(0.238-0.371)	0.443	(0.356-0.538)
Broad-scale										
Lower Yukon	0.034	(0.007-0.089)	0.306	(0.231-0.375)	0.413	(0.344-0.493)	0.616	(0.553-0.693)	0.442	(0.347-0.540)
Middle Yukon	0.433	(0.332-0.506)	0.190	(0.126-0.280)	0.171	(0.100-0.241)	0.082	(0.027-0.122)	0.114	(0.036-0.193)
Canada	0.533	(0.458-0.623)	0.504	(0.409-0.581)	0.417	(0.338-0.495)	0.302	(0.238-0.371)	0.443	(0.356-0.538)
Fine-scale										
Lower Yukon	0.034	(0.007-0.089)	0.306	(0.231-0.375)	0.413	(0.344-0.493)	0.616	(0.553-0.693)	0.442	(0.347-0.540)
Upper U.S. Yukon	0.241	(0.115-0.340)	0.156	(0.083-0.236)	0.055	(0.000-0.139)	0.082	(0.014-0.110)	0.114	(0.032-0.190)
Tanana	0.191	(0.114-0.285)	0.035	(0.000-0.095)	0.115	(0.037-0.178)	0.000	(0.000-0.044)	0.000	(0.000-0.026)
Canada Border	0.075	(0.033-0.144)	0.009	(0.000-0.061)	0.024	(0.000-0.070)	0.006	(0.000-0.038)	0.017	(0.000-0.055)
Pelly	0.112	(0.053-0.245)	0.123	(0.045-0.229)	0.110	(0.037-0.211)	0.044	(0.000-0.132)	0.000	(0.000-0.135)
Carmacks	0.334	(0.190-0.383)	0.285	(0.165-0.355)	0.265	(0.151-0.330)	0.214	(0.112-0.280)	0.336	(0.169-0.440)
Takhini	0.012	(0.000-0.065)	0.086	(0.041-0.142)	0.017	(0.000-0.059)	0.039	(0.000-0.081)	0.091	(0.008-0.180)

Appendix 1.B Estimated proportional contributions (P) and 90% confidence intervals of five-year old Chinook salmon harvested from the commercial fishery in District Y-2 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Reporting Group	Period 1		Period 3		Period 4		Period 5	
	June 15		June 24		June 27		July 2	
	N =	180	N =	209	N =	220	N =	175
	P	90% CI						
<b>Country</b>								
United States	0.460	(0.373-0.558)	0.521	(0.429-0.585)	0.633	(0.566-0.699)	0.589	(0.525-0.668)
Canada	0.541	(0.442-0.628)	0.479	(0.415-0.571)	0.367	(0.301-0.434)	0.411	(0.332-0.476)
<b>Broad-scale</b>								
Lower Yukon	0.018	(0.000-0.053)	0.114	(0.065-0.167)	0.380	(0.312-0.451)	0.472	(0.413-0.560)
Middle Yukon	0.441	(0.345-0.537)	0.408	(0.310-0.476)	0.253	(0.183-0.322)	0.117	(0.059-0.171)
Canada	0.541	(0.442-0.628)	0.479	(0.415-0.571)	0.367	(0.301-0.434)	0.411	(0.332-0.476)
<b>Fine-scale</b>								
Lower Yukon	0.018	(0.000-0.053)	0.114	(0.065-0.167)	0.380	(0.312-0.451)	0.472	(0.413-0.560)
Upper U.S. Yukon	0.243	(0.145-0.376)	0.328	(0.188-0.391)	0.099	(0.049-0.201)	0.050	(0.000-0.108)
Tanana	0.198	(0.100-0.277)	0.080	(0.026-0.183)	0.154	(0.058-0.203)	0.067	(0.017-0.120)
Canada Border	0.137	(0.071-0.218)	0.068	(0.028-0.145)	0.010	(0.000-0.036)	0.000	(0.000-0.024)
Pelly	0.299	(0.170-0.399)	0.137	(0.069-0.258)	0.084	(0.021-0.168)	0.082	(0.022-0.185)
Carmacks	0.104	(0.024-0.187)	0.260	(0.137-0.326)	0.205	(0.112-0.293)	0.306	(0.185-0.372)
Takhini	0.000	(0.000-0.010)	0.013	(0.000-0.046)	0.068	(0.020-0.116)	0.022	(0.000-0.060)

Appendix 1.C Estimated proportional contributions (P) and 90% confidence intervals of five-year old Chinook salmon harvested from the subsistence fisheries in District Y-1 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

		Y-1 Subsistence	
		N =	75
<b>Reporting Group</b>		<b>P</b>	<b>90%CI</b>
Country			
	United States	0.537	(0.417-0.649)
	Canada	0.464	(0.352-0.583)
Broad-scale			
	Lower Yukon	0.159	(0.084-0.244)
	Middle Yukon	0.378	(0.248-0.491)
	Canada	0.464	(0.352-0.583)
Fine-scale			
	Lower Yukon	0.159	(0.084-0.244)
	Upper U.S. Yukon	0.175	(0.048-0.354)
	Tanana	0.203	(0.042-0.310)
	Canada Border	0.078	(0.002-0.170)
	Pelly	0.200	(0.086-0.323)
	Carmacks	0.150	(0.052-0.273)
	Takhini	0.036	(0.000-0.093)

Appendix 2.A Estimated proportional contributions (P) and 90% confidence intervals of six-year old Chinook salmon harvested from the commercial fishery in District Y-1 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Reporting Group	Period 1		Period 2		Period 3		Period 4		Period 5	
	June 20		June 26		June 30		July 4		July 6	
	N =		N =		N =		N =		N =	
	<b>P</b>	<b>90%CI</b>								
<b>Country</b>										
United States	0.453	(0.371-0.548)	0.498	(0.432-0.571)	0.557	(0.487-0.627)	0.611	(0.537-0.677)	0.393	(0.316-0.484)
Canada	0.547	(0.452-0.629)	0.502	(0.429-0.568)	0.443	(0.373-0.513)	0.389	(0.323-0.463)	0.608	(0.516-0.684)
<b>Broad-scale</b>										
Lower Yukon	0.065	(0.018-0.112)	0.353	(0.285-0.427)	0.460	(0.377-0.519)	0.518	(0.441-0.579)	0.308	(0.222-0.388)
Middle Yukon	0.388	(0.305-0.486)	0.145	(0.086-0.209)	0.097	(0.050-0.172)	0.093	(0.042-0.155)	0.085	(0.043-0.151)
Canada	0.547	(0.452-0.629)	0.502	(0.429-0.568)	0.443	(0.373-0.513)	0.389	(0.323-0.463)	0.608	(0.516-0.684)
<b>Fine-scale</b>										
Lower Yukon	0.065	(0.018-0.112)	0.353	(0.285-0.427)	0.460	(0.377-0.519)	0.518	(0.441-0.579)	0.308	(0.222-0.388)
Upper U.S. Yukon	0.166	(0.069-0.281)	0.000	(0.000-0.040)	0.032	(0.000-0.097)	0.059	(0.015-0.125)	0.001	(0.000-0.087)
Tanana	0.222	(0.128-0.321)	0.145	(0.081-0.202)	0.065	(0.019-0.125)	0.034	(0.000-0.072)	0.084	(0.014-0.120)
Canada Border	0.049	(0.000-0.091)	0.025	(0.000-0.063)	0.018	(0.000-0.041)	0.020	(0.000-0.047)	0.020	(0.000-0.060)
Pelly	0.160	(0.083-0.308)	0.180	(0.093-0.279)	0.051	(0.013-0.138)	0.058	(0.011-0.163)	0.000	(0.000-0.122)
Carmacks	0.316	(0.176-0.387)	0.211	(0.103-0.299)	0.283	(0.187-0.344)	0.212	(0.117-0.283)	0.482	(0.319-0.541)
Takhini	0.022	(0.000-0.066)	0.086	(0.040-0.133)	0.091	(0.046-0.145)	0.099	(0.052-0.143)	0.106	(0.038-0.176)

Appendix 2.B Estimated proportional contributions (P) and 90% confidence intervals of six-year old Chinook salmon harvested from the commercial fishery in District Y-2 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

Reporting Group	Period 1		Period 3		Period 4		Period 5	
	June 15		June 24		June 27		July 2	
	N =	180	N =	209	N =	220	N =	175
	<b>P</b>	<b>90% CI</b>						
<b>Country</b>								
United States	0.323	(0.252-0.437)	0.431	(0.364-0.506)	0.662	(0.584-0.732)	0.543	(0.470-0.612)
Canada	0.677	(0.563-0.748)	0.570	(0.494-0.636)	0.339	(0.268-0.416)	0.457	(0.388-0.530)
<b>Broad-scale</b>								
Lower Yukon	0.037	(0.000-0.090)	0.117	(0.073-0.182)	0.422	(0.338-0.491)	0.445	(0.371-0.514)
Middle Yukon	0.286	(0.201-0.400)	0.314	(0.237-0.386)	0.240	(0.168-0.327)	0.099	(0.055-0.157)
Canada	0.677	(0.563-0.748)	0.570	(0.494-0.636)	0.339	(0.268-0.416)	0.457	(0.388-0.530)
<b>Fine-scale</b>								
Lower Yukon	0.037	(0.000-0.090)	0.117	(0.073-0.182)	0.422	(0.338-0.491)	0.445	(0.371-0.514)
Upper U.S. Yukon	0.000	(0.000-0.126)	0.062	(0.014-0.127)	0.068	(0.023-0.196)	0.031	(0.000-0.093)
Tanana	0.286	(0.171-0.368)	0.251	(0.169-0.316)	0.171	(0.055-0.241)	0.068	(0.013-0.109)
Canada Border	0.189	(0.104-0.275)	0.034	(0.000-0.090)	0.019	(0.000-0.047)	0.000	(0.000-0.022)
Pelly	0.275	(0.148-0.389)	0.066	(0.006-0.183)	0.046	(0.000-0.149)	0.014	(0.000-0.122)
Carmacks	0.214	(0.105-0.315)	0.455	(0.324-0.518)	0.254	(0.146-0.320)	0.317	(0.187-0.377)
Takhini	0.000	(0.000-0.001)	0.015	(0.000-0.046)	0.020	(0.000-0.057)	0.126	(0.069-0.189)

Appendix 2.C Estimated proportional contributions (P) and 90% confidence intervals of six-year old Chinook salmon harvested from the subsistence fisheries in District Y-1 of the Yukon River, 2006. The estimated group proportions are given for each of three hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

		Y-1 Subsistence	
		N =	75
<b>Reporting Group</b>		<b>P</b>	<b>90%CI</b>
Country			
	United States	0.554	(0.436-0.690)
	Canada	0.446	(0.310-0.564)
Broad-scale			
	Lower Yukon	0.275	(0.130-0.387)
	Middle Yukon	0.279	(0.176-0.455)
	Canada	0.446	(0.310-0.564)
Fine-scale			
	Lower Yukon	0.275	(0.130-0.387)
	Upper U.S. Yukon	0.074	(0.000-0.258)
	Tanana	0.205	(0.066-0.339)
	Canada Border	0.000	(0.000-0.095)
	Pelly	0.299	(0.058-0.383)
	Carmacks	0.076	(0.005-0.259)
	Takhini	0.071	(0.005-0.158)