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Genetic Stock Identification of Chinook salmon Harvest on the Yukon River 2006

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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)

centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)

cubic feet per second	ft^3/s
foot	ft
gallon	gal
inch	in
mile	mi
nautical mile	nmi
ounce	oz
pound	lb
quart	qt
yard	yd

Time and temperature

day	d
degrees Celsius	°C
degrees Fahrenheit	°F
degrees kelvin	K
hour	h
minute	min
second	s

Physics and chemistry

all atomic symbols	
alternating current	AC
ampere	A
calorie	cal
direct current	DC
hertz	Hz
horsepower	hp
hydrogen ion activity (negative log of)	pH
parts per million	ppm
parts per thousand	ppt, ‰
volts	V
watts	W

General

Alaska Administrative Code	AAC
all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.
all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.
at	@
compass directions:	
east	E
north	N
south	S
west	W
copyright	©
corporate suffixes:	
Company	Co.
Corporation	Corp.
Incorporated	Inc.
Limited	Ltd.
District of Columbia	D.C.
et alii (and others)	et al.
et cetera (and so forth)	etc.
exempli gratia (for example)	e.g.
Federal Information Code	FIC
id est (that is)	i.e.
latitude or longitude	lat. or long.
monetary symbols (U.S.)	$, ¢
months (tables and figures): first three letters	Jan,...,Dec
registered trademark	®
trademark	™
United States (adjective)	U.S.
United States of America (noun)	USA
U.S.C.	United States Code
U.S. state	use two-letter abbreviations (e.g., AK, WA)

Measures (fisheries)

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

Mathematics, statistics

all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$\log_{2,}$ etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

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ABSTRACT

Significant genetic variation exists among populations of Chinook salmon 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 1990s. In 2006, a single nucleotide polymorphism 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 and commercial fisheries, 4,977 individuals were assayed for genetic variation at the 26 single nucleotide polymorphisms. Mixed stock analysis of these samples enabled the estimation of 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 was consistently near 50% with the exception of one commercial fishing period, when it dropped below 40%. In the management District Y-2 harvest, Canadian stocks contributed between 36% and 60% of the harvest over the 4 commercial fishing periods.

Key words: Chinook salmon, genetic stock identification, Yukon River, single nucleotide polymorphism, SNP

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 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 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. 2008) 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 9 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 both 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 Creek, was removed from the 2006 baseline based on recommendations from biologists from Department of Fisheries and Oceans Canada. This collection is comprised of juvenile samples and there is evidence it may be a mixture from separate spawning populations.

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 3 hierarchical sets of reporting groups: Country, Broad-scale, and Fine-scale. In addition, we provide age-specific estimates for the 5- and 6-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 (Figure 2) 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.

METHODS

COLLECTIONS

Many of the Chinook salmon collections that comprise the baseline (Table 1, Figure 1) were assembled as a part of a 3-laboratory collaboration (Alaska Department of Fish and Game, Department of Fisheries and Oceans Canada, and U.S. Fish and Wildlife Service) 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 Athabascan 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). 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 the Alaska Department of Fish and Game (ADF&G). The tissues collected were axillary processes preserved in ethanol.

Target sample sizes of 400 individuals per period were established to allow for acceptable levels of precision and accuracy; 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.

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 (a group of samples taken to represent a single fishing period) onto 384-well reaction plates.

Baseline individuals were assayed for their genotypes at 26 SNPs (Table 3). SNP genotyping was performed in 384-well reaction plates, with 4 wells in each plate left empty as negative controls. Each polymerase chain reaction was conducted in a 5μL volume consisting of 0.10μL template DNA in 1X TaqMan Universal Buffer (ABI), 900nM each polymerase chain reaction primer, and 200nM each probe. Thermal cycling was performed on a Dual 384-Well GeneAmp polymerase chain reaction 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 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 have been permanently stored in an Oracle database, *LOKI*, administered by ADF&G.

STATISTICAL ANALYSES

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 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 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. 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 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 (1×10^{-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. When sample sizes permitted, the stock compositions of the 5- and 6-year old portions of the harvest were also estimated.

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. Each of these sets of samples were assayed at 51 SNP loci and added to the baseline as part of this study.

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 5 periods in District Y-1. Chinook salmon were sampled in 4 out of 5 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

The baseline includes a total of 3,649 individuals from 43 collections representing 25 populations (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, 2 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 4 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: Andreafsky 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 3 of the 5 commercial fishing periods (Table 5; Figure 4). The largest portion of the Canadian component 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 2 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 4 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 3 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 the Y-5 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 5- and 6-year-old components for the Y-1 and Y-2 commercial (Appendices 1 and 2; Figures 6 and 7). In the District Y-1 commercial fishery, the Canadian component of 5- and 6-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 6-year old component seen in periods 4 and 5 (July 4, 6). In the District Y-2 commercial fishery, 6-year old Canadian Chinook salmon made up the largest component of the harvest in periods 1 and 3 (June 15 and 24), while the 5- and 6-year-old components were approximately equal in periods 4 and 5 (June 27 and July 2).

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 from the 2006 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 it 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 genetic stock identification 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.

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TABLES

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, 2006.

				Sample size	
District	Period	Dates	Location	Collected	Analyzed
Commercial					
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
			Total	3,939	3,893
Subsistence					
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
			Total	1,151	1,084
			Grand Total	5,090	4,977

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.

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

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 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

	Period 1			Period 2			Period 3			Period 4			Period 5		
	20-Jun			26-Jun			30-Jun			4-Jul			6-Jul		
	N = 396			N = 399			N = 399			N = 397			N = 240		
Reporting Group	P	S.D.	90%CI	P	S.D.	90%CI	P	S.D.	90%CI	P	S.D.	90%CI	P	S.D.	90%CI
Country															
United States	0.463	0.036	(0.402-0.520)	0.493	0.031	(0.439-0.542)	0.564	0.032	(0.514-0.617)	0.646	0.030	(0.597-0.692)	0.470	0.038	(0.408-0.531)
Canada	0.537	0.036	(0.480-0.598)	0.507	0.031	(0.458-0.561)	0.436	0.032	(0.383-0.486)	0.355	0.030	(0.308-0.403)	0.530	0.038	(0.469-0.592)
Broad-scale															
Lower Yukon	0.062	0.019	(0.034-0.098)	0.332	0.032	(0.280-0.383)	0.436	0.033	(0.382-0.487)	0.558	0.030	(0.512-0.612)	0.381	0.037	(0.316-0.435)
Middle Yukon	0.402	0.038	(0.333-0.463)	0.161	0.030	(0.112-0.209)	0.128	0.028	(0.085-0.179)	0.088	0.023	(0.047-0.121)	0.089	0.028	(0.050-0.141)
Canada	0.537	0.036	(0.480-0.598)	0.507	0.031	(0.458-0.561)	0.436	0.032	(0.383-0.486)	0.355	0.030	(0.308-0.403)	0.530	0.038	(0.469-0.592)
Fine-scale															
Lower Yukon	0.062	0.019	(0.034-0.098)	0.332	0.032	(0.280-0.383)	0.436	0.033	(0.382-0.487)	0.558	0.030	(0.512-0.612)	0.381	0.037	(0.316-0.435)
Upper U.S. Yukon	0.195	0.049	(0.102-0.264)	0.058	0.025	(0.019-0.100)	0.034	0.026	(0.002-0.087)	0.069	0.023	(0.024-0.099)	0.061	0.029	(0.015-0.110)
Tanana	0.206	0.042	(0.146-0.289)	0.102	0.027	(0.058-0.149)	0.094	0.026	(0.049-0.132)	0.019	0.014	(0.000-0.046)	0.028	0.022	(0.000-0.074)
Canada Border	0.063	0.023	(0.031-0.106)	0.012	0.016	(0.000-0.050)	0.021	0.013	(0.000-0.044)	0.009	0.010	(0.000-0.031)	0.019	0.015	(0.000-0.049)
Pelly	0.161	0.047	(0.108-0.260)	0.143	0.041	(0.084-0.220)	0.084	0.034	(0.041-0.151)	0.061	0.031	(0.027-0.130)	0.000	0.030	(0.000-0.085)
Carmacks	0.293	0.044	(0.188-0.335)	0.268	0.043	(0.184-0.324)	0.273	0.040	(0.194-0.323)	0.216	0.037	(0.142-0.262)	0.409	0.050	(0.296-0.460)
Takhini	0.021	0.015	(0.004-0.053)	0.085	0.021	(0.051-0.118)	0.059	0.020	(0.032-0.097)	0.069	0.019	(0.035-0.099)	0.103	0.034	(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 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as "unknown" due to low genotype probabilities.

	Period 1			Period 3			Period 4			Period 5		
	15-Jun			24-Jun			27-Jun			2-Jul		
	N = 292			N = 398			N = 397			N = 379		
Reporting Group	P	S.D.	90% CI	P	S.D.	90% CI	P	S.D.	90% CI	P	S.D.	90% CI
Country												
United States	0.398	0.042	(0.337-0.480)	0.473	0.033	(0.412-0.520)	0.644	0.032	(0.588-0.693)	0.573	0.030	(0.523-0.623)
Canada	0.602	0.042	(0.520-0.663)	0.528	0.033	(0.480-0.588)	0.356	0.032	(0.307-0.412)	0.427	0.030	(0.377-0.477)
Broad-scale												
Lower Yukon	0.025	0.015	(0.006-0.055)	0.111	0.022	(0.081-0.154)	0.394	0.030	(0.349-0.446)	0.472	0.032	(0.422-0.526)
Middle Yukon	0.373	0.044	(0.306-0.452)	0.361	0.035	(0.292-0.406)	0.250	0.031	(0.193-0.293)	0.102	0.022	(0.065-0.138)
Canada	0.602	0.042	(0.520-0.663)	0.528	0.033	(0.480-0.588)	0.356	0.032	(0.307-0.412)	0.427	0.030	(0.377-0.477)
Fine-scale												
Lower Yukon	0.025	0.015	(0.006-0.055)	0.111	0.022	(0.081-0.154)	0.394	0.030	(0.349-0.446)	0.472	0.032	(0.422-0.526)
Upper U.S. Yukon	0.129	0.050	(0.067-0.232)	0.178	0.036	(0.107-0.228)	0.093	0.037	(0.054-0.175)	0.033	0.020	(0.003-0.071)
Tanana	0.244	0.042	(0.161-0.300)	0.183	0.035	(0.128-0.246)	0.156	0.035	(0.075-0.190)	0.069	0.021	(0.032-0.102)
Canada Border	0.173	0.036	(0.113-0.231)	0.056	0.025	(0.028-0.112)	0.014	0.010	(0.000-0.033)	0.000	0.004	(0.000-0.012)
Pelly	0.288	0.052	(0.200-0.370)	0.114	0.042	(0.070-0.205)	0.048	0.034	(0.015-0.124)	0.043	0.035	(0.009-0.125)
Carmacks	0.142	0.043	(0.072-0.212)	0.352	0.044	(0.249-0.392)	0.246	0.041	(0.162-0.295)	0.311	0.042	(0.216-0.356)
Takhini	0.000	0.003	(0.000-0.007)	0.007	0.010	(0.000-0.031)	0.048	0.020	(0.016-0.081)	0.073	0.021	(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 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as "unknown" due to low genotype probabilities.

	Y-1 Subsistence			Y-3 Commercial			Y-5 Commerical			Y-5 Subsistence		
	N = 139			N = 106			N = 472			N = 285		
Reporting Group	P	S.D.	90%CI	P	S.D.	90%CI	P	S.D.	90%CI	P	S.D.	90%CI
Country												
United States	0.553	0.053	(0.471-0.645)	0.457	0.077	(0.336-0.586)	0.470	0.037	(0.389-0.512)	0.295	0.044	(0.223-0.365)
Canada	0.448	0.053	(0.355-0.529)	0.543	0.077	(0.414-0.664)	0.530	0.037	(0.488-0.612)	0.705	0.044	(0.635-0.777)
Broad-scale												
Lower Yukon	0.193	0.043	(0.124-0.263)	0.067	0.034	(0.018-0.129)	0.016	0.009	(0.004-0.034)	0.011	0.010	(0.000-0.032)
Middle Yukon	0.360	0.056	(0.270-0.455)	0.390	0.079	(0.268-0.524)	0.454	0.037	(0.371-0.496)	0.284	0.043	(0.213-0.352)
Canada	0.448	0.053	(0.355-0.529)	0.543	0.077	(0.414-0.664)	0.530	0.037	(0.488-0.612)	0.705	0.044	(0.635-0.777)
Fine-scale												
Lower Yukon	0.193	0.043	(0.124-0.263)	0.067	0.034	(0.018-0.129)	0.016	0.009	(0.004-0.034)	0.011	0.010	(0.000-0.032)
Upper U.S. Yukon	0.107	0.061	(0.045-0.244)	0.172	0.081	(0.053-0.317)	0.441	0.043	(0.335-0.474)	0.239	0.046	(0.165-0.312)
Tanana	0.253	0.060	(0.133-0.332)	0.218	0.069	(0.098-0.332)	0.013	0.019	(0.000-0.062)	0.045	0.026	(0.005-0.091)
Canada Border	0.052	0.032	(0.000-0.108)	0.205	0.076	(0.079-0.322)	0.029	0.025	(0.010-0.093)	0.190	0.041	(0.134-0.269)
Pelly	0.234	0.062	(0.118-0.317)	0.185	0.082	(0.048-0.315)	0.198	0.047	(0.137-0.293)	0.294	0.062	(0.170-0.370)
Carmacks	0.106	0.052	(0.037-0.206)	0.150	0.064	(0.056-0.264)	0.287	0.043	(0.201-0.338)	0.198	0.055	(0.125-0.305)
Takhini	0.056	0.028	(0.015-0.106)	0.003	0.013	(0.000-0.037)	0.024	0.011	(0.004-0.052)	0.024	0.015	(0.004-0.052)

Table 8.–Estimated proportional contributions (P) and 90% confidence intervals of Chinook salmon harvested from the subsistence fishery in the 3 subdistricts of District Y-4 of the Yukon River, 2006. 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.

	Subdistrict A			Subdistrict B			Subdistrict C		
	N = 378			N = 188			N = 89		
Reporting Group	P	S.D.	90%CI	P	S.D.	90%CI	P	S.D.	90%CI
Country									
United States	0.484	0.036	(0.418-0.551)	0.523	0.046	(0.443-0.593)	0.956	0.033	(0.887-0.999)
Canada	0.516	0.036	(0.449-0.582)	0.477	0.046	(0.407-0.557)	0.044	0.033	(0.001-0.113)
Broad-scale									
Lower Yukon	0.036	0.016	(0.018-0.077)	0.104	0.037	(0.055-0.175)	0.174	0.055	(0.095-0.279)
Middle Yukon	0.448	0.038	(0.368-0.512)	0.419	0.053	(0.316-0.490)	0.781	0.062	(0.663-0.868)
Canada	0.516	0.036	(0.449-0.582)	0.477	0.046	(0.407-0.557)	0.044	0.033	(0.001-0.113)
Fine-scale									
Lower Yukon	0.036	0.016	(0.018-0.077)	0.104	0.037	(0.055-0.175)	0.174	0.055	(0.095-0.279)
Upper U.S. Yukon	0.196	0.044	(0.120-0.277)	0.212	0.058	(0.112-0.303)	0.082	0.072	(0.004-0.240)
Tanana	0.252	0.039	(0.171-0.309)	0.207	0.050	(0.118-0.282)	0.699	0.085	(0.512-0.798)
Canada Border	0.057	0.024	(0.021-0.103)	0.002	0.014	(0.000-0.040)	0.011	0.016	(0.000-0.043)
Pelly	0.121	0.043	(0.053-0.211)	0.112	0.056	(0.034-0.219)	0.000	0.022	(0.000-0.057)
Carmacks	0.308	0.043	(0.214-0.371)	0.319	0.064	(0.194-0.401)	0.034	0.023	(0.000-0.074)
Takhini	0.030	0.016	(0.007-0.066)	0.044	0.032	(0.004-0.112)	0.000	0.002	(0.000-0.000)

FIGURES

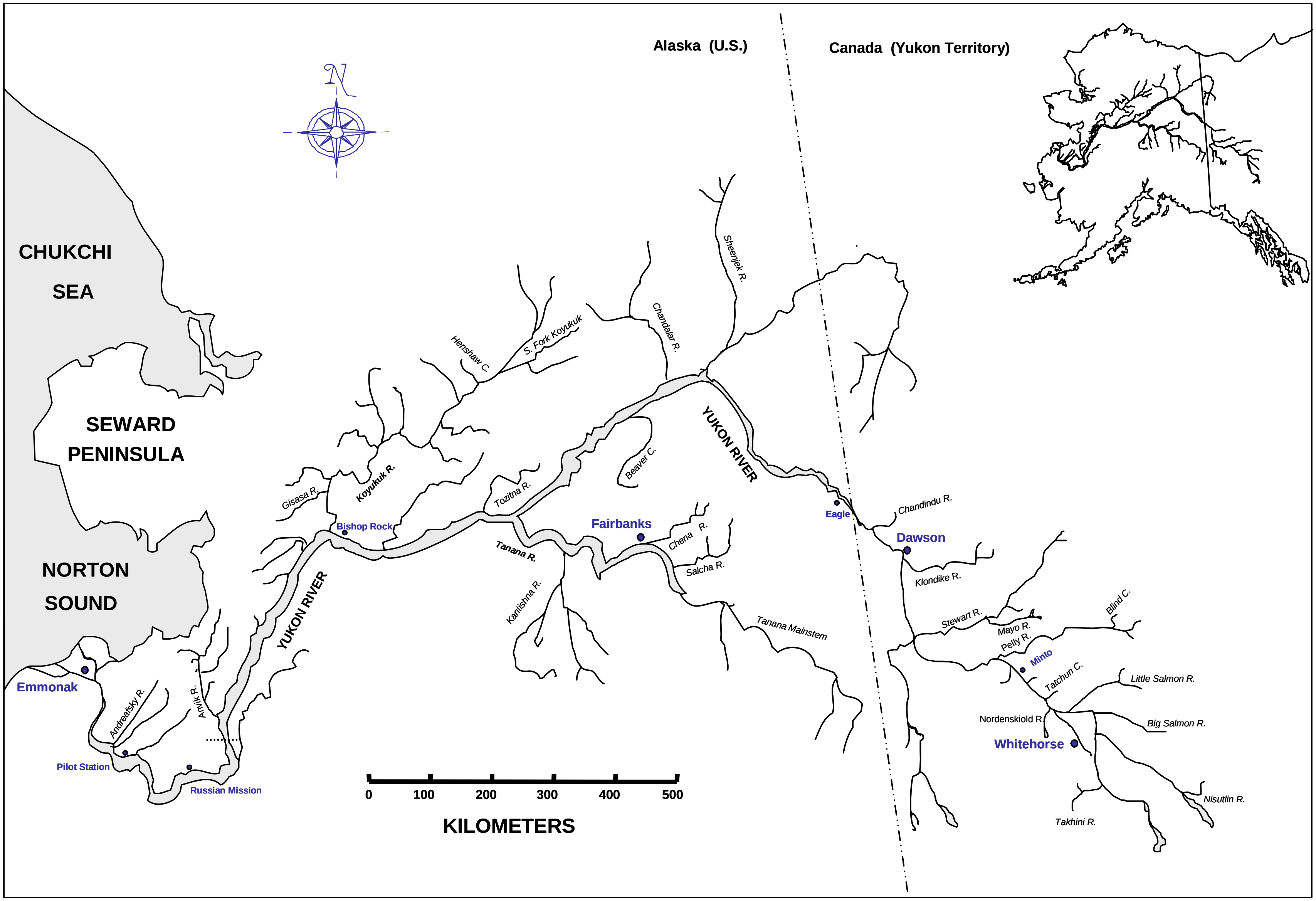

Figure 1.–Map of the locations of Chinook salmon collections in the Yukon River drainage.

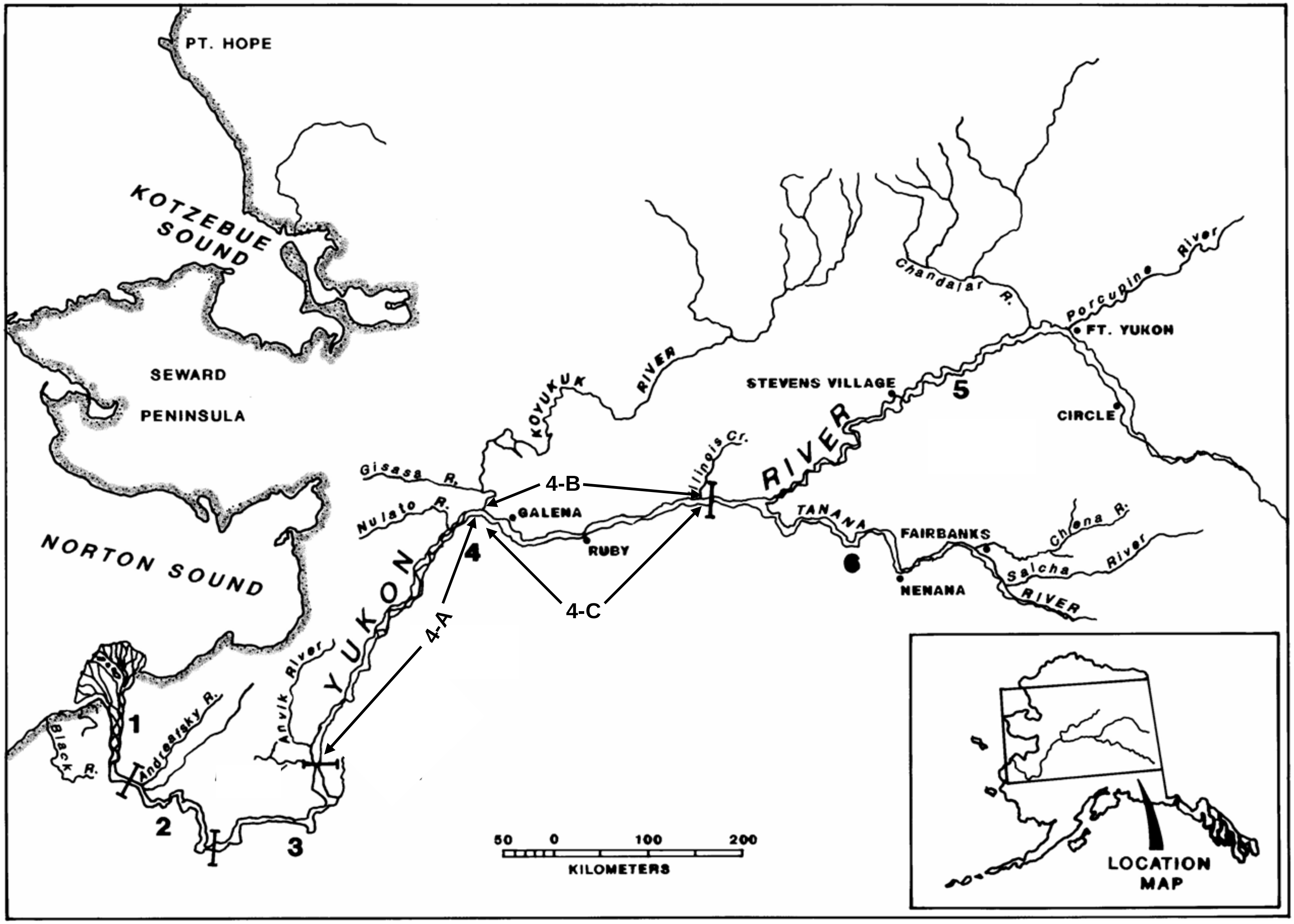

Figure 2.–Location of the fishing districts (and District Y-4 subdistricts) used for management of salmon fisheries in the United States portion of the Yukon River drainage.

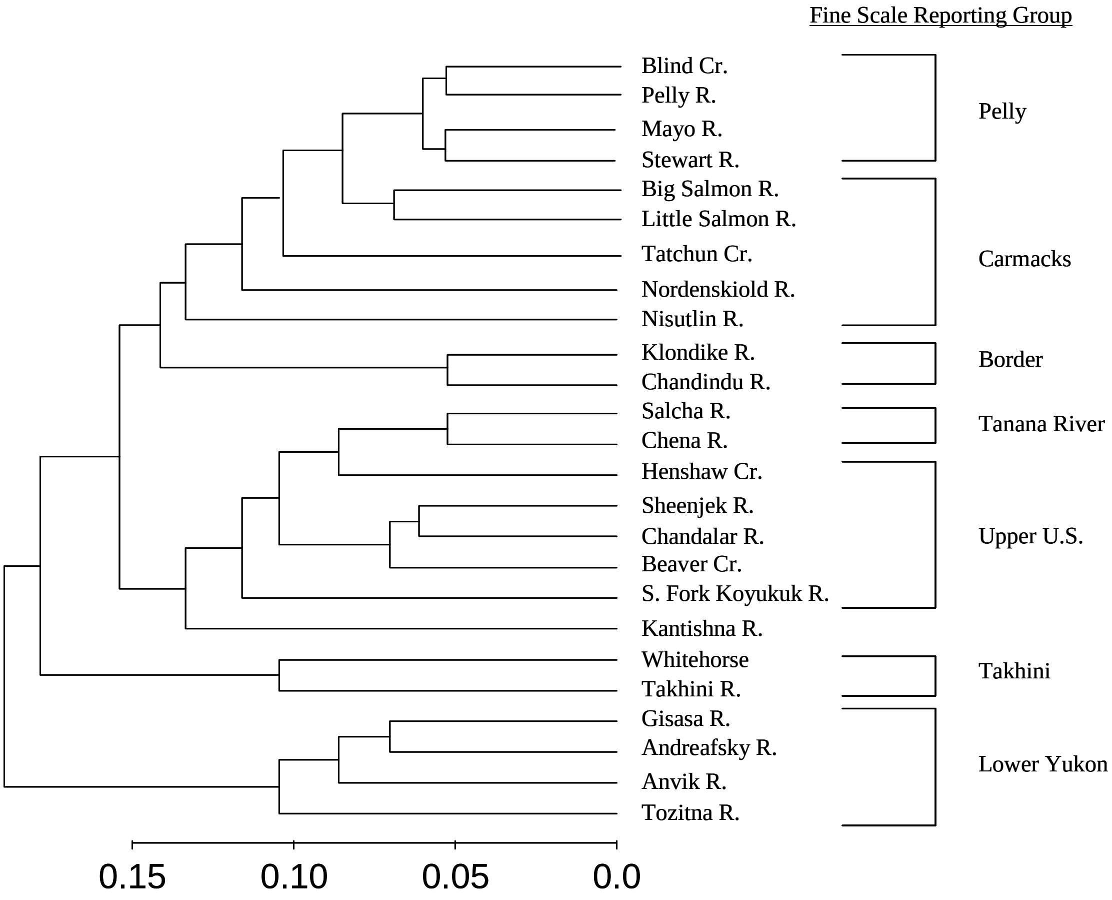

Figure 3.–Unweighted paired group-mean clustering tree based on genetic distances between pairs of Chinook salmon populations in the Yukon River drainage. Population membership in the fine-scale reporting groups from Table 1 is indicated in the right margin.

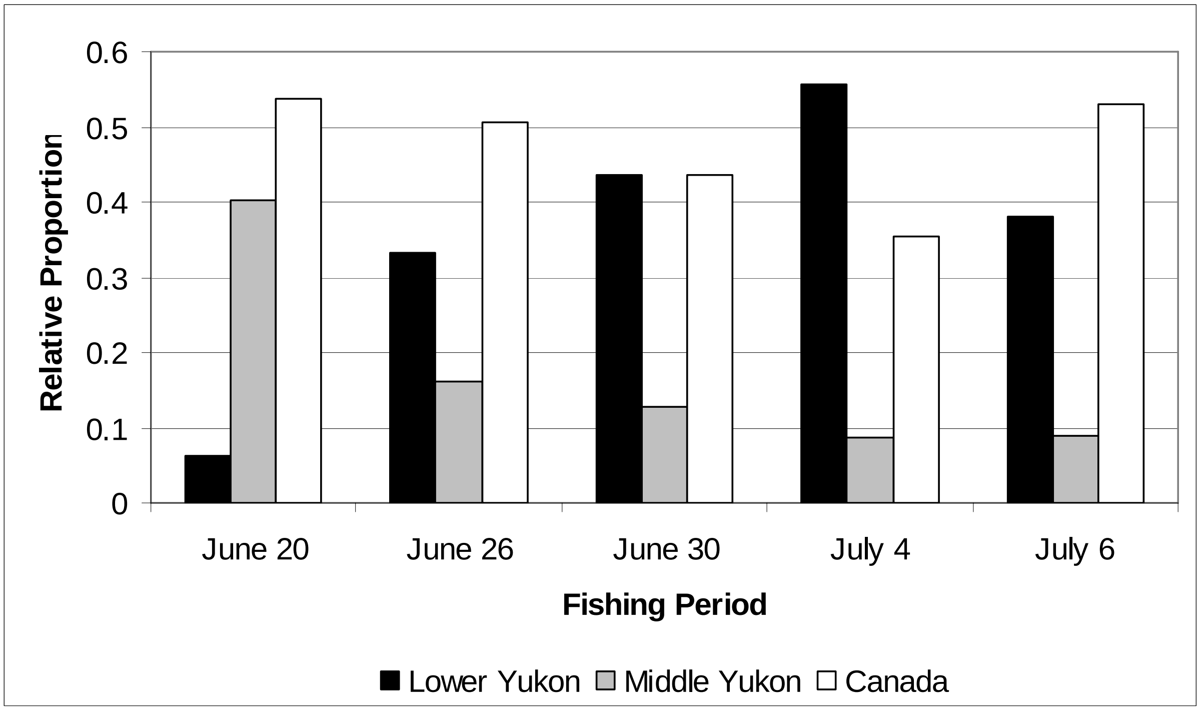

Figure 4.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon harvest during the 5 commercial fishery periods in District Y-1, 2006.

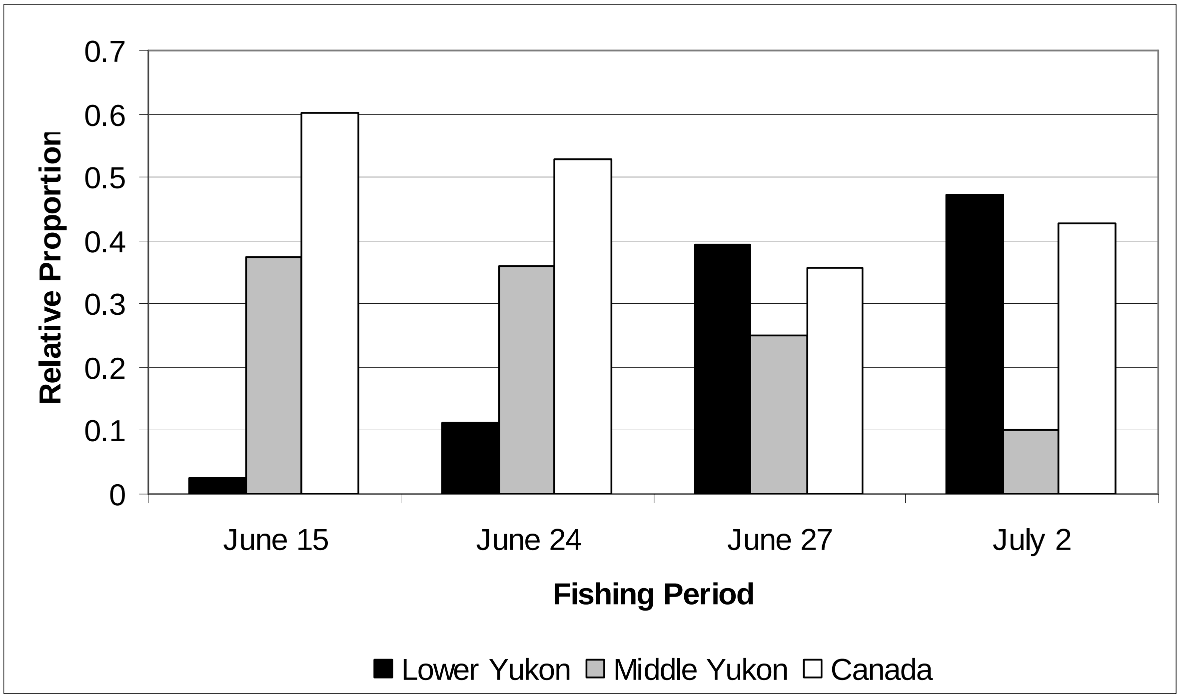

Figure 5.–Relative stock composition of 3 broad-scale reporting groups in the Chinook salmon harvest during the 4 commercial fishery periods in District Y-2, 2006.

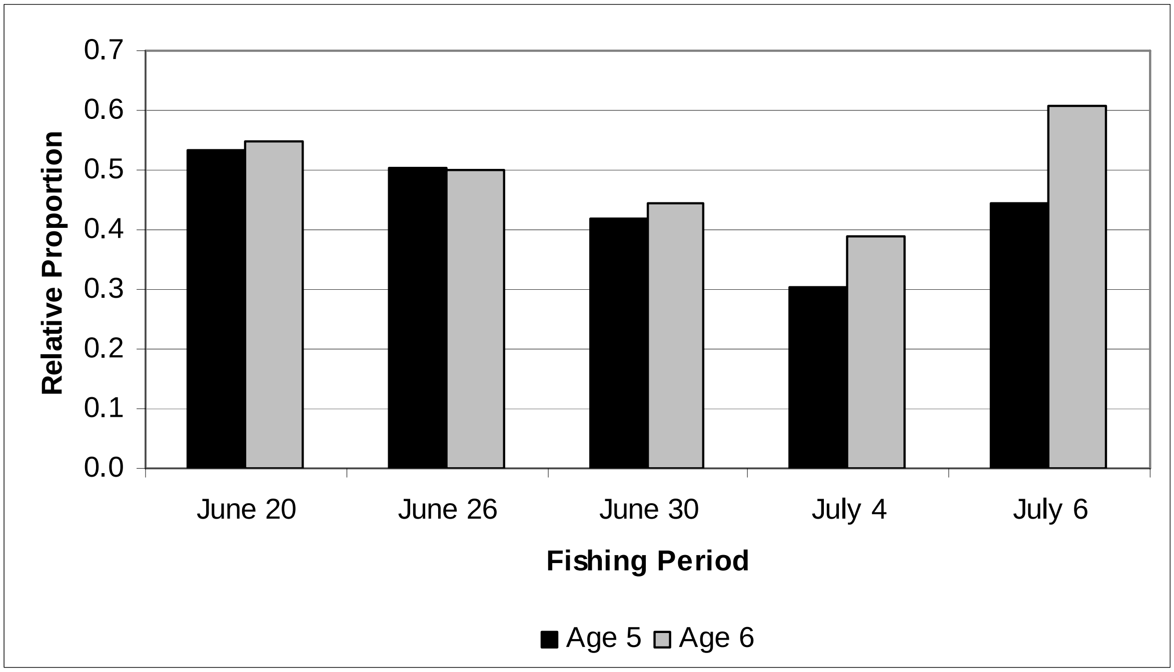

Figure 6.–Relative proportion of Canada stocks in the 5- and 6-year old Chinook salmon harvested during the 5 commercial fishery periods in District Y-1, 2006.

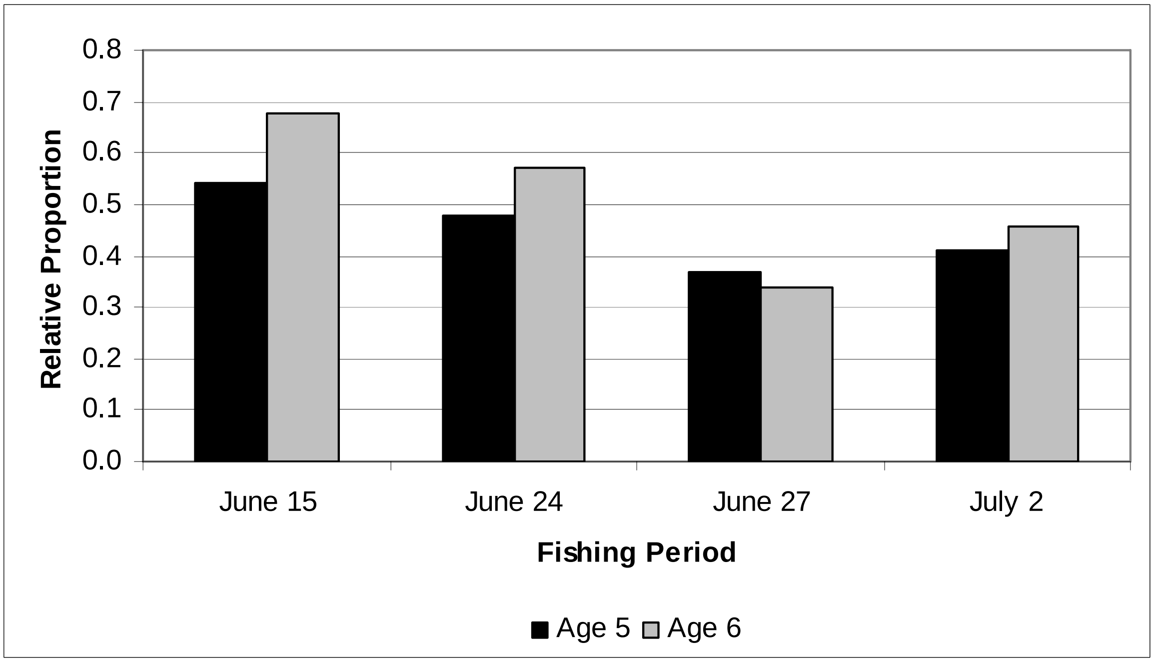

Figure 7.–Relative proportion of Canada stocks in the 5- and 6-year old Chinook salmon harvested during the 4 commercial fishery periods in District Y-2, 2006.

APPENDIX

Appendix 1A.–Estimated proportional contributions (P) and 90% confidence intervals of 5-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 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as "unknown" due to low genotype probabilities.

	Period 1		Period 2		Period 3		Period 4		Period 5	
	June 20		June 26		June 30		July 4		July 6	
	N =	207	N =	168	N =	189	N =	165	N =	100
Reporting Group	P	90%CI	P	90%CI	P	90%CI	P	90%CI	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 1B.–Estimated proportional contributions (P) and 90% confidence intervals of 5-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 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as "unknown" due to low genotype probabilities.

		Period 1		Period 3		Period 4		Period 5	
		June 15		June 24		June 27		July 2	
		N =	180	N =	209	N =	220	N =	175
Reporting Group		P	90% CI	P	90% CI	P	90% CI	P	90% CI
Country									
	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)
Broad-scale									
	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)
Fine-scale									
	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 2A.–Estimated proportional contributions (P) and 90% confidence intervals of 6-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 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as "unknown" due to low genotype probabilities.

	Period 1		Period 2		Period 3		Period 4		Period 5	
	June 20		June 26		June 30		July 4		July 6	
	N =	207	N =	168	N =	189	N =	165	N =	100
Reporting Group	P	90%CI	P	90%CI	P	90%CI	P	90%CI	P	90%CI
Country										
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)
Broad-scale										
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)
Fine-scale										
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 2B.–Estimated proportional contributions (P) and 90% confidence intervals of 6-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 3 hierarchical levels. Estimates may not sum to 1.0, because some genotypes are classed as “unknown” due to low genotype probabilities.

		Period 1		Period 3		Period 4		Period 5	
		June 15		June 24		June 27		July 2	
		N =	180	N =	209	N =	220	N =	175
Reporting Group		P	90% CI	P	90% CI	P	90% CI	P	90% CI
Country									
	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)
Broad-scale									
	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)
Fine-scale									
	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)