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Canadian-Origin Chinook Salmon Rearing in Non-Natal U.S. Tributary Streams of the Yukon River, Alaska, 2006–2007

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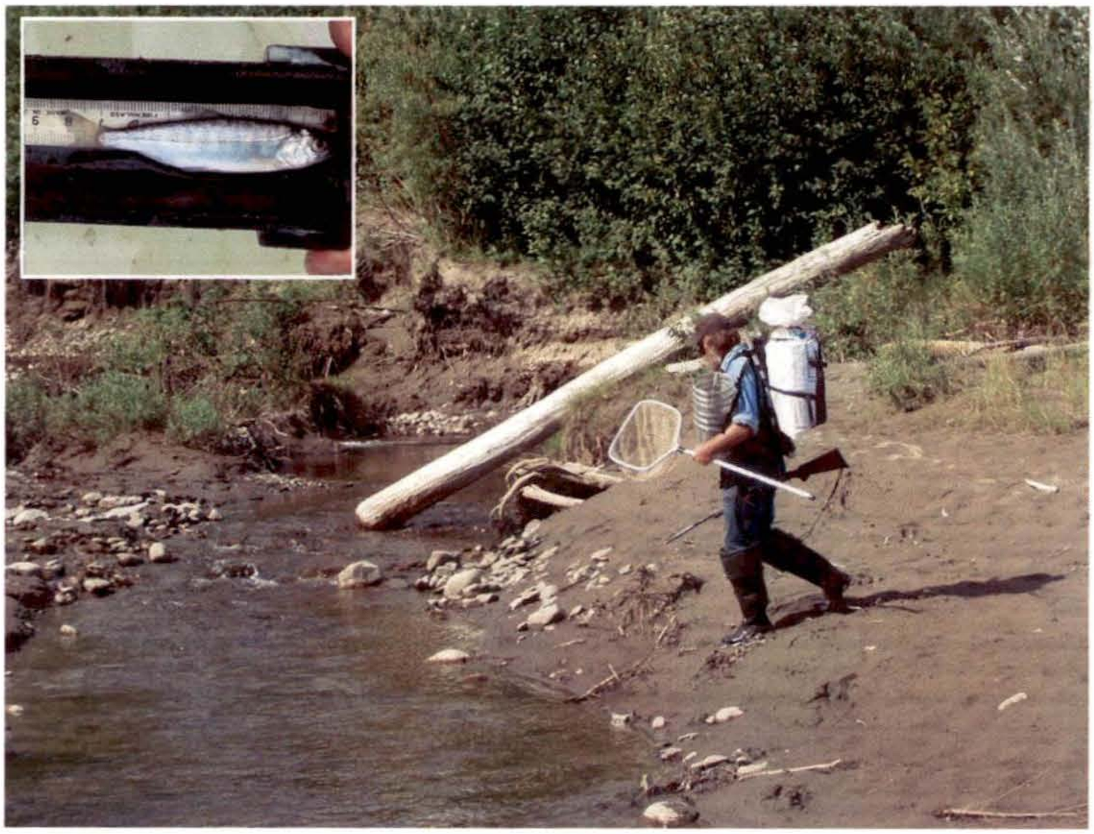

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Canadian-Origin Chinook Salmon Rearing in Non-Natal U.S. Tributary Streams of the Yukon River, Alaska, 2006–2007

David W. Daum and Blair G. Flannery

Abstract

Yukon River Chinook salmon are described as having "stream-type" life histories. After emergence from river gravel, juvenile Chinook salmon feed and grow in tributary streams of the Yukon River throughout their first summer, overwinter in freshwater, and usually leave rearing areas for marine waters during the second spring/summer. In 2006–2007, a study was conducted to document non-natal rearing and genetic-origin of Chinook salmon in downstream U.S. waters. Eight non-natal streams were selected for study; seven located in a 260-km segment between the U.S.–Canada border and Circle, Alaska and one located below the Yukon Flats, 742 rkm downstream from the border. Age-0 juvenile Chinook salmon were captured in all eight streams. Juvenile lengths were generally greatest in the largest watersheds and mean lengths increased throughout the summer. Genetic samples from age-0 Chinook salmon were collected and genetic analyses revealed that captured fish were from Canadian source populations. Stock composition analysis indicated that populations from the Carmacks region contributed 91% to the mixtures in 2006 and 82% in 2007. Simulation and known-origin mixture analyses demonstrated that stock composition and individual assignment estimates derived from the baseline were accurate and precise. Some age-0 Chinook salmon travelled over 1,200 km to reach non-natal rearing areas. Protecting these important rearing habitats is essential for maintaining healthy, self-sustaining Yukon River Chinook salmon populations.

Introduction

The Yukon River drainage encompasses 854,700 km^2 (Brabets et al. 2000) and provides important subsistence and commercial salmon fisheries along most of its 3,200 km length (JTC 2008). Adult Chinook salmon *Oncorhynchus tshawytscha* travel the furthest upstream of the five species of salmon present in the Yukon River, spawning up to 2,900 km from the mouth (Eiler et al. 2006a, 2006b). Approximately 50% of Chinook salmon entering the Yukon River each year are bound for spawning grounds in Canada (Eiler et al. 2004, 2006a, 2006b). The annual contribution of Canadian-origin fish to in-river harvest is also significant, ranging from 47% to 67% of the total harvest in lower Yukon River commercial and subsistence fisheries (Templin et al. 2005). Recent declines in Yukon River salmon runs have led to harvest restrictions, fisheries closures, and some spawning escapements below management goals (JTC 2008). The Yukon River Salmon Agreement (annexed to the Pacific Salmon Treaty between Canada and the USA) recognizes the importance of maintaining high quality salmon spawning and rearing habitats on both sides of the border. Numerous potential threats to freshwater habitat in the upper U.S. portion of the Yukon River Basin include mineral and gravel extraction, oil and gas exploration, hydrokinetic energy development, logging, transportation corridors, and private land

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development (USDOI 1982, 1985; ADNR 1991; FERC 2007). Past commercial gold mining operations in the region (USDOI 1982; Barker 1986; L'Ecuyer 1997; Cameron 2000; Werdon et al. 2004) have also degraded fish habitat by altering natural channel morphology, increasing turbidity and sedimentation, denuding stream banks of vegetation, and altering flow patterns (Madison 1981; USDOI 1982; Bjerklie and LePerriere 1985; Reynolds et al. 1989).

Yukon River Chinook salmon are classified as "stream-type" (Gilbert 1922; Healey 1983; Taylor 1990). After emergence from river gravel, stream-type Chinook salmon typically disperse downstream to suitable rearing habitats, feed and grow throughout the summer, overwinter in freshwater, and usually leave these rearing areas for marine waters during the second or third year (Healey 1983, 1991). Previous life history and distribution studies have shown that some stream-type, age-0 Chinook salmon leave their natal streams and colonize downriver, non-natal habitats for rearing and overwintering (Bjornn 1971; Delaney et al. 1982; Russell et al. 1983; Murray and Rosenau 1989; Levings and Lauzier 1991; Scrivener et al. 1994; Bradford and Taylor 1997; Bradford et al. 2001). The mechanisms that cause some individuals to migrate out of their natal streams while others remain are largely unknown (Healey 1991) but appear to be controlled, at least in part, by some active behavioral response and not solely from passive displacement by river current (Healey 1991; Taylor et al. 1994; Bradford and Taylor 1997). Possible explanations for these behavioral responses include: phenotypic variability among individuals (Bradford and Taylor 1997); competition (Reimers 1968; Stein et al. 1972; Grant and Kramer 1990; Zabel and Achord 2004); and genetic predisposition (Healey 1991).

In the upper Yukon River, displacement of age-0 Chinook salmon out of natal streams and subsequent downstream main-stem movement appears to be delayed compared to smolt outmigration. Juvenile fish studies in the upper, main-stem Yukon River have documented a peak downstream movement of age-0 Chinook salmon from mid-June through mid-July (Brown et al. 1976; Bradford et al. 2008), about four to six weeks after Chinook salmon smolts (mostly age-1) begin their seaward migration (Walker 1976; Bradford et al. 2008). The size of these captured age-0 juveniles suggested that they reared for considerable time in upstream locations before moving downstream past the traps (Bradford et al. 2008). During the summer, dispersed Yukon River age-0 Chinook salmon concentrate in main-stem habitats near clearwater inputs from tributary streams (Howe 2004) and subsequently colonize accessible non-natal streams for rearing (Bradford et al. 2001; Perry et al. 2003; Mossop and Bradford 2004; A. von Finster, Fisheries and Oceans Canada (DFO), personal communication). After colonization, summer movement between tributary streams appears minimal (Bradford et al. 2001), though redistribution between streams has been documented (Daum, unpublished data). During fall, age-0 Chinook salmon may stay in their rearing stream for overwintering (Delaney et al. 1982; Bradford et al. 2001), though movement to other overwintering sites can not be discounted.

A large data gap exists in the upper U.S. portion of the Yukon River drainage since most non-natal stream rearing habitats for juvenile Chinook salmon have not been surveyed or catalogued (Daum 1994; Johnson and Weiss 2006). Without this documentation, the importance of these habitats to juvenile salmon can not be determined and habitat protection or rehabilitation can not be initiated. In sharp contrast, several hundred non-natal streams in the upper Canadian portion of the Yukon River drainage have been found to provide important feeding, and in some cases, overwintering habitat for Chinook salmon juveniles (Brown et al. 1976; Walker 1976; Beacham et al. 1989; Murray et al. 1990; Moodie et al. 2000; Bradford et al. 2001; Perry et al. 2003; Mossop and Bradford 2004, 2006; A. von Finster, DFO, personal communication). Because of this lack of information for U.S. waters, most habitat restoration projects for Yukon River salmon have occurred on the Canadian side of the border (JTC 2007, 2008). In the upper U.S. portion of the Yukon River, stream inventories of non-spawning streams have not been a priority to management agencies. Few records of Chinook salmon spawning exist in the area (Barton 1984; Daum 1994; Johnson and Weiss 2006) and long distance colonization of non-natal U.S. streams by Canadian-origin populations was assumed unlikely.

As significant portions of the Yukon River Chinook salmon adult escapement and harvest are of Canadian origin (Templin et al. 2005), it would be prudent to identify rearing areas in the U.S. used by Canadian-origin salmon in order to maintain the productivity of this resource. To accomplish this, genetic mixed-stock (MSA) and individual assignment (IA) analyses are effective methods for estimating source origin (Cadrin et al. 2005; Koljonen et al. 2005). Genetic data have been collected for Yukon River Chinook salmon from allozyme (Templin et al. 2005), single nucleotide polymorphism (SNP; Smith et al. 2005), and microsatellite (Flannery et al. 2006; Templin et al. 2006; Beacham et al. 2008) loci. These studies revealed significant genetic divergence among regional population groups suitable for MSA and IA applications. For the 13 standardized microsatellite loci established by the Chinook Technical Committee of the Pacific Salmon Treaty (Seeb et al. 2007), MSA simulations were 94.1%–99.3% accurate to 8 regions of management interest and >99% accurate to country-of-origin (Flannery et al. 2006).

In this study, we sampled eight non-natal Yukon River tributary streams to: 1) document presence and length-weight relationships for captured age-0 Chinook salmon; 2) determine genetic-origin of the captured juveniles using the standardized microsatellite baseline; and 3) describe non-natal stream rearing habitat characteristics for Yukon River Chinook salmon. This work provides an initial assessment of the importance of non-natal streams for rearing by region-specific juvenile Chinook salmon in the upper U.S. portion of the Yukon River drainage. With this much needed information in hand, State and Federal land management agencies can initiate protection of identified Chinook salmon rearing habitats and develop plans to rehabilitate areas that have been disturbed.

Study Area

The eight non-natal streams included in this study were located in the middle Yukon River, between 1,228 and 1,951 river kilometers (rkm) upstream from the Yukon River mouth (Figure 1). Seven of eight streams were located in the upper U.S. portion of the Yukon River, between Circle and the U.S.–Canada border. The most downriver stream sampled was Minook Creek, 742 rkm downstream from the border. The region has a continental subarctic climate characterized by extreme temperatures: –59°C to 37°C (USDOI 1964, 1985). Precipitation ranges from 25 to 38 cm per year, with about half falling as rain in summer months (Brabets et al. 2000). Shade Creek, on the north side of the Yukon River originates in the foothills of the Ogilvie Mountains, while the other seven streams begin in the Yukon-Tanana Uplands to the south. Principal sources of stream water include rainfall, snowmelt, and to a lesser extent, groundwater (USDOI 1982). Most runoff occurs in June from snowmelt and in late summer from rainfall (Brabets et al. 2000). Summer water turbidity is highly variable, depending on rainfall events. Yukon River streams are typically ice-free by early June, and freeze-up occurs from late September to mid-October.

Land status varies throughout the area, with the Yukon-Charley Rivers National Preserve occupying a substantial portion of land (8,650 km^2) in the upper U.S. portion of the drainage

(USDOI 1985). Other land holdings include State of Alaska, Regional and Village Native Corporations, Native allotments, and private lands (USDOI 1985; ADNR 1993). Substantial gold deposits occur along the highly mineralized Tintina Fault resulting in patented and unpatented placer mining claims throughout the region (Barker 1986; Newberry and Clautice 1997). The fault runs in an east/west orientation for over 1,000 km south of the Yukon River corridor, from northwestern Canada to eastern Alaska. All of the study streams to the south, except Trout Creek, have experienced historic placer mining in portions of their drainages, with active claims currently in Minook and Mission creeks and Seventymile River.

Methods

Stream Selection

Eight non-natal Yukon River tributary streams between Rampart, Alaska and the U.S.–Canada border were selected for juvenile Chinook salmon sampling in 2006 and 2007 (Figures 1 and 2). Streams without documented spawning populations were determined based on information provided by Barton (1984); Daum (1994); Eiler et al. (2004, 2006a, 2006b); and Johnson and Weiss (2006). Because of the project's emphasis on detecting Canadian-origin Chinook salmon, sampling was concentrated in the upper U.S. portion of the Yukon River drainage between Circle and the border (seven of the eight streams sampled). Non-natal streams were picked sequentially, beginning above potential U.S. population input (near U.S.–Canada border) and working downstream to incorporate streams with potential U.S. population input. As distance downstream from the border increases and the potential for immigration of fry belonging to small U.S. populations increases, downstream samples may begin to show assemblages with U.S.-origin populations present. The upper three streams sampled (Mission Creek, Shade Creek, and Seventymile River) are upriver of all U.S. spawning populations, while Minook Creek, the furthest downriver stream sampled, is located downstream of three genetically described U.S. spawning populations (Sheenjek and Chandalar rivers and Beaver Creek). River distances for sampled streams and upper U.S. genetic baseline populations were calculated from tributary-main-stem confluence to U.S.–Canada border and to the Yukon River mouth using Barton (1984; Table 1). For Canadian genetic baseline populations, a 1:2 million scale base map (Natural Resources Canada 1985) was imported into ESRI ArcMap (ver. 9.02) and distances from tributary-main-stem confluence to U.S.–Canada border and to Yukon River mouth were estimated using ArcMap digital measuring tool (Table 1).

Stream selection was also influenced by the likelihood of capturing non-natal juvenile Chinook salmon. Streams with intermittent access to the Yukon River main stem were avoided. Streams having high potential fish predator habitat in lower reaches were not selected, i.e., low gradient, deep and turbid water, and low water velocity. Selected streams contained preferred juvenile Chinook salmon rearing habitat as described by Hillman et al. (1987), Healey (1991), and Roper et al. (1994), i.e., riffle-pool stream type, escape and resting habitat, clear water, sufficient gradient and flow, and bottom substrate larger than mud /silt. Only one selected stream, Minook Creek, had previous documentation of juvenile Chinook salmon presence (Townsend 2000; Johnson and Weiss 2006).

Fish Data

Fish sampling. — In 2006, the eight selected streams were sampled for juvenile Chinook salmon (Figures 1 and 2). Seven of the eight streams were revisited in 2007 to increase genetic sample sizes for the upriver sites (Minook Creek excluded). Sampling began after July 15 as determined from downstream migrant studies of age-0 Chinook salmon in the Canadian Yukon River main stem (Brown et al. 1976; Walker 1976; Bradford et al. 2008) and subsequent colonization timing into non-natal streams (Moodie et al. 2000; Bradford et al. 2001). Streams were accessed by motorized canoe and individual stream sampling was conducted on foot, except for Seventymile River (canoe) and Minook Creek (all-terrain vehicle). Sampling began near each stream's confluence with the Yukon River and proceeded upstream depending on accessibility and sampling gear placement constraints. Within-stream sampling stations were combined into one general sample site per stream (Table 2); expressed as the distance between the uppermost station and the mouth. The exception was the Seventymile River where three sampling sites were established 4.5, 10.6, and 25.0 rkm upstream of the Yukon River confluence. Gee-type minnow traps (23 x 45 cm, 0.6 cm wire mesh, 2.5 cm diameter opening), baited with salmon roe, were set overnight in areas associated with Chinook salmon rearing habitat, i.e., log jams, root wads, small pools, and stream banks adjacent to riffles (Hillman et al. 1987; Roper et al. 1994; Mossop and Bradford 2004). Overnight trapping was preferred because of the high variability in daily foraging activity exhibited by juvenile Chinook salmon (Bradford and Higgins 2001). Small beach seines (9.1 x 1.2 m with 0.3 cm Delta mesh) were used when minnow trapping was ineffective, i.e., high turbid water or lack of trapping sites. Catch per unit effort (CPUE) was recorded for minnow trapping as the number of Chinook salmon juveniles captured per trap-day (24-hour) and for seining as juveniles per haul. It should be emphasized that this project was designed to first document occurrence of juvenile Chinook salmon and subsequently maximize sample size for genetic analysis; not to estimate relative abundance or fish density. Caution should be taken when comparing CPUE data of juvenile Chinook salmon between streams, since many factors affecting catch rates were not evaluated, i.e., gear saturation, standardized effort, uniform catch rates, constant catchability, and standardized sampling within specific habitat types (Hubert 1996; Hubert and Fabrizio 2007).

Biological data were collected from captured juvenile Chinook salmon. Other captured fish species were noted by species and life stage (juvenile or adult). Fork length (FL) of juvenile Chinook salmon was measured to the nearest millimeter by placing juveniles in a measuring cradle. In 2007, length measurements were coupled with weight measurements from a subset of captured fish. Weight was measured to the nearest 0.1 g with a handheld, 10 g Pesola spring-type scale. All juvenile Chinook salmon were examined for adipose fin clips (Whitehorse Hatchery releases) and any external abnormalities. Captured juvenile Chinook salmon were not aged, but classified as either age-0 (young-of-year) or age-1 (overwintered one year) based on temporal length distribution data (Duncan and Bradford 2006), i.e., age-0 juveniles measured <93 mm FL for July 17–August 2 sample collections and <105 mm FL for August 14–29 collections. Also, the presence of age-1 juveniles in non-natal streams of the upper Yukon River is unlikely after July 15 (Moodie et al. 2000; Bradford et al. 2001); most age-1 fish have smolted. Five scale samples, three from individuals over 85 mm FL, were digitally photographed using a camera-mounted compound microscope and sent to the Fish Ageing Unit, DFO, for age verification.

Length and weight analysis. — Length frequency distributions were plotted for captured age-0 Chinook salmon by stream, sample site, and year. Length can be used to determine growth of juvenile Chinook salmon (Delany et al. 1982; Bradford et al. 2001) and to compare size differences among populations (Walker 1976; Beacham et al. 1989; Isely and Grabowski 2007). A one-way analysis of variance (ANOVA) was used to test the null hypothesis that mean lengths of age-0 Chinook salmon captured from different streams during similar sampling periods were equal ($\alpha = 0.05$). If differences among groups were found, a Tukey multiple comparison test was used to determine the relative position of the groups (family error rate of 0.05). Temporal differences in mean length of age-0 Chinook salmon between the early and late sample periods (Table 2) by year and between the 2006 and 2007 sample by individual streams were tested using two-sample *t* tests ($\alpha = 0.05$).

Condition indices are indicators of fitness or well-being of a population or subgroup. Fish condition is a short-term indicator of fish health status and, in juvenile fish, is primarily influenced by resource availability (Pope and Kruse 2007). Fulton's condition factor (K) was used to estimate the fitness of age-0 Chinook salmon in each sample stream. Fulton's K was calculated by dividing fish weight by the cube of the length and multiplying by 10^5 (Anderson and Neumann 1996). An ANOVA was used to test the null hypothesis that mean condition (K) among age-0 Chinook salmon captured from different streams during 2007 were equal ($\alpha = 0.05$). If differences among groups were found, a Tukey multiple comparison test was used to determine the relative position of the groups (family error rate of 0.05). Condition was not estimated for the 2006 samples since fish were not weighed. All statistical tests were conducted with Minitab 15 version 1.1.0.

Genetics

Genetic profiles were collected for each age-0 juvenile Chinook salmon from 13 microsatellite loci and compared to a genetic baseline representing 34 major spawning populations of Yukon River Chinook salmon (Table 3; Figure 3) to determine source origination. First, the ability of the baseline to estimate source origination was evaluated. The baseline samples were analyzed for Hardy-Weinberg and gametic phase equilibrium to assess whether they represented randomly mating, Mendelian populations. Because the DNA baseline is not comprehensive, the baseline population structure was visualized in a neighbor-joining tree in order to help define regions (stocks) for assigning fishery mixtures. Simulated and real known-origin fishery mixtures were then analyzed to assess the accuracy and precision of stock composition and individual assignment estimates. Finally, an analysis to assess whether the baseline was missing significant stocks was conducted.

Sample collection and laboratory analysis.— Anal fin tissue was removed from captured age-0 Chinook salmon and stored in 100% ethanol in 2-ml vials. The anal fin tissue was chosen for collection because of its tendency to regenerate quickly (Johnsen and Ugedal 1988) and removal would least affect swimming performance (Webb 1975). Collections were spread out over a large spatial area (>>100 m) to decrease the potential of sampling families (Hansen et al. 1997).

The samples were genotyped using the following methods. Total genomic DNA was extracted from anal fin tissue (~25 mg) using proteinase K with the Dneasy™ DNA isolation kit (Qiagen Inc. Valencia, CA). The amount of DNA was quantified by fluorometry and diluted to 30 ng/µl. The following 13 standardized micosatellite loci used by the Genetic Analysis of Pacific Salmonids group (GAPS; Seeb et al. 2007) were assayed for genetic variation: *Ots201b*, *Ots208b*, *Ots211*, *Ots212*, *Ots213*, (Grieg et al. 2003); *Ots3M*, *Ots9* (Banks et al. 1999); *OtsG474* (Williamson et al. 2002); *Ogo2*, *Ogo4* (Olsen et al. 1998); *Omm1080* (Rexroad et al. 2001); *Ssa408* (Cairney et al. 2000); and *Oki100* (K. Miller, DFO, unpublished data). Polymerase chain reaction (PCR) DNA amplification was done in 10 µl volumes; general conditions were: 2.5 mM $MgCl_2$, 1X PCR buffer (20 mM Tris-HCl pH 8.0, 50 mM KCl); 200 µM of each dNTP; 0.40 µM fluorescently labeled forward primer; 0.40 µM unlabeled reverse primer; 0.008 units Taq polymerase; and 1 µl of DNA (30 ng/µl). An MJResearch DNA Engine® thermal cycler was used to perform PCR. Standard thermal cycling conditions included an initial denaturation cycle of 94°C for 3 min; followed by 30 cycles of 94°C for 1 min, 50-62°C for 1 min (locus-specific annealing temperature), 72°C for 1 min; and a final single cycle of 72°C for 10 min. One µl of PCR product was electrophoresed and visualized with the Applied Biosystems 3730 Genetic Analyzer utilizing a polymer denaturing capillary system. The sizes of bands were estimated and scored by the computer program GENEMAPPER® version 4.0. Applied Biosystems GeneScan™-600 LIZ® size standards, 20-600 bases, were loaded in all lanes to ensure consistency of allele scores. All scores were verified manually. Alleles were scored by two independent researchers, with any discrepancies being resolved by re-running the samples in question and repeating the double scoring process until scores matched. Because of the difficulty in visually distinguishing between Chinook and coho *O. kisutch* salmon juveniles, all collected tissue were genetically confirmed to species using diagnostic loci with non overlapping allele size distributions before proceeding with the data analysis.

Baseline data analysis. — Since development of the initial 19 population Yukon River Chinook salmon genetic baseline (Flannery et al. 2006; Templin et al. 2006; Beacham et al. 2008), 15 new populations and additional sample collections have been added (Table 3; Figure 3). Therefore, the baseline data were checked for duplicated genotypes using the program MICROSATELLITE TOOLKIT (Park 2001), with any duplicates removed. The populations and loci were analyzed for Hardy-Weinberg and gametic phase equilibrium using the program FSTAT 2.9.3 (Goudet 1995) and GENETIX 4.05 (Belkhir et al. 2004), respectively. Using PHYLIP 3.57 (Felsenstein 1993), replicate population pairwise chord distance (CSE) matrices (Cavalli-Sforza and Edwards 1967) were calculated from allele frequencies by bootstrapping over loci 1,000 times, from which a consensus neighbor-joining (Saitou and Nei 1987) dendrogram was produced. Regional stock groups were established for apportioning fishery mixtures based on the neighbor-joining results, geography, and management goals.

Simulation and known-origin mixture analyses were used to evaluate the accuracy and precision of stock composition and individual assignment estimates derived from the baseline. Using the program cBAYES (Neaves et al. 2005), artificially simulated mixtures ($n = 100$) representing 100% of each individual population or region were created from baseline allele frequencies under assumptions of Hardy-Weinberg and gametic phase equilibrium. These mixtures were analyzed for stock composition using a Bayesian method (Pella and Masuda 2001) with cBAYES and a conditional maximum likelihood method (Pella and Milner 1987) with SPAM 3.7b (Debevec et al. 2000). Mean stock composition and standard deviation were estimated from 1,000 bootstrap iterations of the baseline and mixture for SPAM 3.7b and from eight 20,000 iteration Markov chain Monte Carlo (MCMC) simulations for cBAYES. Each Markov chain was iteratively sampled a sufficient number of times, with the first 19,000 iterations discarded as a burn-in, to satisfy convergence under the Raftery and Lewis (1996) and Gelman and Rubin (1992) diagnostics. All stock composition priors, estimated quantiles of stock composition, accuracy of estimated quantiles, and probability of attaining estimated quantiles were set at the recommended values (Pella and Masuda 2001). After convergence was confirmed, the mean stock composition estimates and associated variances were calculated from the combined MCMC sample chains, minus the burn-in. For cBAYES, individual assignment accuracy was evaluated for the individual population simulated mixtures. Simulated individuals were assigned to stocks if their posterior source probabilities were ≥ 95%; otherwise, they were classified as unknown. For comparative purposes, assignment accuracy results were also presented for individuals with < 95% posterior source probabilities.

Simulated multi-region mixtures, with sample sizes and region proportions set to those from the radio-telemetry study (Eiler et al. 2006a, 2006b), were analyzed for stock composition using cBAYES and SPAM 3.7b. Finally, real known-origin mixtures were created by randomly sampling without replacement individual genotypes from the baseline using the sample sizes and region proportions from the radio-telemetry study and by compiling 52 samples from populations not currently in the baseline. The known-origin mixtures were analyzed for stock composition by both programs and for individual assignment by cBAYES using a baseline independent of the mixtures.

The baseline was then tested to determine if significant stocks were not represented, which may bias stock composition estimates. Using the program HWLER (Pella and Masuda 2006), the juvenile samples were compared to the baseline, and the probability of an extra-baseline stock was estimated by running a Gibbs and split-merge MCMC sampler, which partitioned mixture samples into Hardy-Weinberg and linkage equilibrium subsets and identified those that originated from extra-baseline stocks. The HWLER program was run and convergence of MCMC chain assessed as recommended by Pella and Masuda (2006).

Juvenile Chinook salmon stock composition and individual assignment analyses.—The age-0 Chinook salmon samples were analyzed using cBAYES and the baseline data. Details of the cBAYES analysis follow methods listed above. Stock compositions and individual assignments were estimated for region and country. Samples were analyzed by collection year, with individual assignments also compiled by collection site. The lack of a comprehensive baseline prevented stock composition estimation for individual populations.

Habitat Measurements

Physical stream characteristics were described for the eight sampled streams in the study. Stream order was assigned based on Strahler (1957). Watershed area (km^2) for each stream was calculated by first importing the 1:24,000 scale Yukon Basin National Hydrography Dataset (NHD) Flowline data layer (USGS 2006) into ESRI ArcMap (ver. 9.02) and then measuring watershed area with ArcMap digital measuring tool. Stream type was described using the Rosgen (1996) classification system. Stream gradient (%) of the lower stream reach was determined from U.S. Geological Survey 1:63,360 scale topographic maps (McMahon et al. 1996). Due to the short sample distance and steep gradient of Shade and Trout creeks, slope was estimated in the field using a surveyor's level (Leica Model NA724) and stadia rod (Hamilton and Bergersen 1984). The dominant stream bottom substrate for each lower stream reach was assigned using substrate classification according to Platts et al. (1983). Seasonal accessibility to the tributary stream from the main-stem Yukon River was estimated using direct observations. Digital photographs were taken of each sample site and outlet area. Any streams or parts of drainages found to contain juvenile Chinook salmon not previously reported in the Alaska Anadromous Waters Catalog (Johnson and Weiss 2006) were nominated for inclusion. A handheld global positioning system (geographic coordinate datum NAD 83) was used to record the upper extent of juvenile Chinook salmon distribution for each stream.

Water quality measurements for each study stream were collected during fish sampling periods (Table 2). Measurements were taken from near each stream's mouth and included water temperature, river stage, and water clarity. Water temperature was taken using a handheld, pocket case thermometer, standardized with a NIST traceable thermometer. River stage and water clarity were described qualitatively. In 2007, pH and conductivity of each sampled stream were measured with a Hach multi-meter, Model HQ40D. The multi-meter was calibrated and periodically checked with a standard during field measurements.

Results

Fish Data

Fish sampling. – Juvenile Chinook salmon were captured in all eight non-natal streams and at all three upstream sample sites on the Seventymile River (farthest site 25 rkm upstream from Yukon River confluence). All captured juvenile Chinook salmon were classified as age-0 based on measured length. Minnow trapping (170 trap-days) and seining (74 hauls) yielded 931 age-0 Chinook salmon (Table 4). Age-0 Chinook salmon had colonized all streams by the beginning sample dates, though the farthest downriver stream, Minook Creek, had very low catch rates on July 17–18 (0.3 fish per trap-day) compared to August 29, 2006 (11.1 fish per trap-day). An extreme rain event on August 13, 2007 and ensuing high turbid stream levels influenced minnow trapping efficiency during the fall sampling period for Sam, Coal, and Thanksgiving creeks. Subsequent high seine catch rates of juvenile fish species near creek confluences with the main-stem Yukon River suggested that fish were flushed out of these drainages during the high flows. Minnow trapping was very effective in capturing age-0 Chinook salmon for all streams when water conditions were favorable. The highest catch rate in 2006 was in Shade Creek (13.3 fish per trap-day) and in 2007 in Trout Creek (20.2 fish per trap-day). Fork length ranged from 52 to 92 mm for the early period (late July–early August) and from 54 to 96 mm for the late period (mid to late August). The five scale samples taken for age verification were from age-0 Chinook salmon, three fish ≥ 86 mm FL (Figure 4).

Ten fish species were captured from the eight sample streams (Table 5). These species included Chinook salmon, Arctic grayling *Thymallus arcticus*, burbot *Lota lota*, chum salmon *O. keta*, lake chub *Couesius plumbeus*, longnose sucker *Catostomus catostomus*, northern pike *Esox lucius*, round whitefish *Prosopium cylindraceum*, slimy sculpin *Cottus cognatus*, and trout-perch *Percopsis omiscomaycus*. Most fish captured were juveniles. Chinook salmon, Arctic grayling, lake chub, longnose sucker, and slimy sculpin were the most common species captured. Species diversity was similar to previous studies on larger rivers in the region using similar gear types (Daum 1994). One spawned-out female chum salmon was found in Thanksgiving Creek on August 17, 2006.

Length and weight analysis. – Mean lengths of age-0 Chinook salmon captured from different streams during similar sampling periods were generally different ($P < 0.05$). For the early sample period in 2006 (Table 6; Figure 5), the mean length of Seventymile River age-0 Chinook salmon was greater than mean length of fish from Mission, Shade, and Trout creeks. Excluding the Seventymile River, length distributions of Chinook salmon were unimodal with modes between 68-71 mm. Length frequency plots for the three Seventymile River sample sites showed a strong bimodal distribution for the two uppermost sites, with modes at 68–71 and 78–85 mm (Figure 6). For the late sample period in 2006, the mean lengths of age-0 Chinook salmon were similar from Sam, Coal, and Thanksgiving creeks, and the mean length of Minook Creek fish was greater than Thanksgiving Creek. For the early sample period in 2007 (Table 6; Figure 7), the mean length of age-0 Chinook salmon from Mission Creek was greater than Shade and Trout creeks, and Trout Creek mean fish length was greater than Shade Creek. For the late sample period in 2007, the mean length of age-0 Chinook salmon from Thanksgiving Creek was greater than Coal Creek ($P = 0.007$).

Mean lengths of age-0 Chinook salmon from Shade and Coal creeks were significantly greater in 2006 than 2007 ($P = 0.003$ and 0.016, respectively; Table 6). Shade Creek Chinook salmon averaged 66.8 mm in 2006 and 63.5 mm in 2007, while Coal Creek fish averaged 76.5 mm in 2006 verses 71.2 mm in 2007. The other streams sampled during both years (Mission, Trout, and Thanksgiving creeks) had similar mean lengths between years. Mean lengths of captured fish (all streams combined) were greater during the late sampling period than the early period in 2006 and 2007 ($P < 0.0005$; Table 6). Mean length increased from 67.3 to 76.2 mm in 2006 and from 66.5 to 72.5 mm in 2007. The Seventymile River sample was excluded from temporal comparisons between streams because of its unusual bimodal length distribution (Figure 5).

The condition indices (Fulton's K) for age-0 Chinook salmon from the five sampled creeks in 2007 were significantly different ($P = 0.001$). Thanksgiving Creek Chinook salmon had an average K value (1.08) that was significantly greater than Trout (1.01) and Coal (1.02) Creek values (Table 6). Age-0 Chinook salmon from Mission and Shade creeks had intermediate K-values of 1.05 and 1.04, respectively.

Genetics

Sample collection and laboratory analysis. — Of the 827 genetic tissue samples collected from age-0 Chinook salmon in 2006 and 2007, 683 samples (83%) were successfully genotyped (Table 7). Trout Creek yielded the most genotyped individuals ($n = 222$) and Sam Creek yielded the least ($n = 4$). All genotyped samples were genetically confirmed as Chinook salmon, i.e., no coho salmon were identified.

Baseline data analysis. — Significant Hardy-Weinberg disequilibrium was observed in only 2 out of 442 tests (0.5%), less than expected due to chance alone. Significant gametic phase disequilibrium was observed in 16 out of 2,617 tests (0.6%), again less than expected due to chance. None of the significant tests were common to any locus or population, so all loci and populations were deemed to be in Hardy-Weinberg and gametic phase equilibrium.

Neighbor-joining analysis of CSE distances among the populations revealed a spatial component to the distribution of genetic diversity (Figure 8). Populations were broadly aligned along the following geographic regions: lower U.S., middle U.S., upper U.S., lower Canada, middle Canada, and upper Canada. Within these broad scale regions, populations were further subdivided, with greater than 50% bootstrap support observed for many of the nodes. Taking into account the neighbor-joining results, geography, and management goals, 10 regions were defined for apportioning mixtures (Table 3).

Accuracies of stock composition estimates from individual population mixture simulations ranged from 71–100% (SD 0.01–0.09) for SPAM 3.7b and 98–99% (SD 0.01–0.04) for cBAYES (Table 8). Overall, misallocation occurred among geographically proximate and genetically similar populations, precluding the need for an exhaustive baseline for regional based stock composition and individual assignment analyses (Beacham et al. 2003). Individual assignment accuracies for individual population mixture simulations ranged from 99–100%. All simulated individuals were assigned, with posterior source probabilities ranging from 99–100%.

Accuracies of stock composition estimates from regional mixture simulations ranged from 93–100% (SD 0.01–0.04) for SPAM 3.7b and 98–99% (SD 0.01–0.02) for cBAYES (Table 9). Simulated multi-region mixture stock composition estimates were within 4% of expected for SPAM 3.7b and 3% of expected for cBAYES (Table 10). Real known-origin mixture stock composition estimates for regions were within 15% of expected for SPAM 3.7b and 10% of expected for cBAYES (Table 11). When using the 95% probability criterion, 39% of the individuals from the known-origin mixtures were assigned to regions with an accuracy of 96% (61% classified as unknown), whereas 78% of the individuals were assigned to country with an accuracy of 100% (21% classified as unknown). When no probability criterion was used, individual assignment accuracy was 71% to regions and 93% to country. No significant stocks were determined to be missing from the baseline in the analysis by HWLER (Table 12). There was a 70% and 93% probability that no extra baseline stocks were present in 2006 and 2007, respectively.

Juvenile Chinook salmon stock composition and individual assignment analyses.— Stock composition analysis of age-0 Chinook salmon in the 2006 and 2007 samples indicated that Canadian-origin Chinook salmon contributed 99% to the mixtures, with fish from the Carmacks region contributing 91% in 2006 and 82% in 2007 (Table 13). Individual assignment analysis indicated that 100% of the assigned samples were of Canadian origin and that the majority originated from the Carmacks region (Table 14). The farthest downriver stream (Minook Creek, 742 rkm downstream from the U.S.–Canada border) had 100% of age-0 Chinook salmon samples individually assigned to the Carmacks region in 2006. In contrast, the farthest upriver stream (Mission Creek, 19 rkm downstream from the border) had 86% (2006) and 88% (2007) of the samples assigned to the Carmacks region with small percentages identified from the lower Canada and upper Canada regions. Five of the 10 Yukon River regions were represented in the individual assignment analysis, with no regions downstream from the sampled streams represented in the individually assigned samples. Using the 95% probability criterion for assigning samples, 61% of the individuals were assigned to specific regions and 97% were assigned to country.

Habitat Measurements

Physical characteristics varied substantially between the eight study streams (Table 15). Stream order varied from second to fourth order, with Shade Creek being the lowest. Watershed area varied from 34 km^2 for Shade Creek to 1,694 km^2 for the Seventymile River. Gradient also varied considerably, with the smallest drainage (Shade Creek) having the highest gradient (2.6%) and the largest drainage (Seventymile River) having the lowest gradient (0.3%). Dominate substrate in the lower reaches varied from sand/gravel on the Seventymile River to large cobble on Shade and Thanksgiving creeks. Stream classification (Rosgen 1996) ranged from B4 stream type (Shade Creek) with fairly steep slope, entrenched floodplain, numerous pools, and large cobble substrate to C4 designation (Mission, Sam, Coal, and Minook creeks and Seventymile River) with moderate slope, slightly meandering, moderate pool spacing, and gravel to small cobble substrate. Coal Creek had extensive modification to its original stream channel from historic placer gold mining (Barker 1986). In 2006 and 2007, all study stream mouths were open to the Yukon River throughout the summer providing unrestricted access for juvenile main-stem migrants. Two of the eight study streams were accessible through side-channel habitat. All study streams, except previously registered Minook Creek, were nominated and accepted for inclusion into the Alaska Anadromous Waters Catalog for rearing Chinook salmon. Uppermost capture location for age-0 Chinook salmon (location coordinates) within each stream are given in Table 2.

Water quality measurements were highly variable among streams and between years (Table 16). The highest water temperature (14.2°C) was recorded in Seventymile River and the lowest temperature (6.0°C) was measured in Shade, Sam, and Minook creeks. River stage during sampling was between low and medium/high for all sampling periods except for the late period in 2007. Severe rain during mid-August in 2007 caused Sam, Coal, and Thanksgiving creeks to flood, depositing large amounts of sediment at creek mouths, eroding away stream banks, and creating highly turbid conditions for the duration of the sampling period. At all other sampling times, water clarity for sampled streams ranged from clear to tannic stained. Conductivity and pH were measured for only the early sampling period in 2007 (Table 16). Conductivity ranged from 166 µS/cm in Seventymile River to 603 µS/cm in Shade Creek and pH varied from 7.04 in Seventymile River to 8.14 in Mission Creek.

Discussion

This study documents the presence of Canadian-origin, age-0 juvenile Chinook salmon in non-natal streams of the upper U.S. portion of the Yukon River. Fish were found to travel downstream long distances from their natal origins. Moreover, the study emphasizes the importance of these distant non-natal rearing habitats to the overall health and productivity of Canadian Chinook salmon and that measures should be implemented to identify and protect these areas.

Age-0 Chinook salmon from the Carmacks region made up the vast majority of captures in downstream non-natal tributary streams of the Yukon River. Estimates of adult returns apportioned to the different regional spawning groups (JTC 2006, 2007) were disproportionately represented in the downstream juvenile captures. For the 2005 brood year, 36% of the total Canadian adult escapement was from the Carmacks region, compared to 91% of the downstream age-0 samples in 2006 (Table 17). In 2006, Carmacks-region adult Chinook salmon spawners comprised 43% of the total escapement into Canada and represented 82% of the non-natal stream colonizers in 2007. The largest Canadian river systems (Stewart, Pelly, and Teslin rivers) were significantly underrepresented in the non-natal stream samples.

The mechanisms that cause this disproportionate number of Carmacks area, age-0 Chinook salmon to leave their natal streams are largely unknown. Larger river systems may contain sufficient rearing habitat to "hold" dispersing fish within the drainage, while some smaller spawning streams may be more susceptible to emigration because of limited rearing habitat. The delayed dispersal timing of downstream migrating age-0 juveniles captured on the main-stem Yukon River (Bradford et al. 2008) coupled with an apparent mixture of different stock groups in downstream main-stem catches (Walker et al. 1974; Walker 1976) suggests a complex interaction of density-dependent factors, quantity and quality of rearing habitats, environmental variables, timing of emergence, and perhaps the greater propensity for some populations to disperse.

The simulation and known-origin mixture analyses indicated that the Yukon River genetic baseline for Chinook salmon can provide accurate and precise estimates of regional and country source origination. Therefore, the genetic estimates of region and country origination for age-0 Chinook salmon captured in this study are considered to be accurate. This is further supported by the allocation of the majority of the age-0 Chinook salmon samples to the Carmacks region. Because of the geographic structure of the genetic relationships, if the baseline was misallocating, it would be presumed that allocations would mostly be to geographically proximate locations to the sampled non-natal streams, i.e., the upper U.S. and lower Canada regions.

At present, five spawning populations of Chinook salmon are used to define the Carmacks region in the upper Yukon River (Table 1) where the majority of downstream migrants in this study originated. A main-stem spawning population is included in the baseline for this region, but without a comprehensive, population-specific genetic baseline, the contributions of this and other populations to the overall downstream dispersal remain uncertain. Until the baseline is expanded, many important ecological and mechanistic questions relating to population-specific differences and similarities may remain unanswered.

This study records the longest downstream dispersal distances in published literature for stream-type, Chinook salmon into non-natal streams during the first summer's rearing period. The longest migratory distances were from the Carmacks regional group colonizing Minook Creek, between 1,211 and 1,330 rkm downstream from natal origins (Table 1). Previously, Bradford and Taylor (1997) described stream-type juveniles dispersing up to 100 km downstream in the upper Fraser River. The downstream movement was described as short-lived, decreasing within the first 2 weeks after emergence. In contrast, migrating upper Yukon River age-0 Chinook salmon delay long distance dispersal until mid-June through mid-July, long after emergence (Brown et al. 1976; Bradford et al. 2008). Whether this long distance dispersal mechanism is initiated after a period of rearing in the migrant's natal stream, main-stem Yukon River, or other nearby habitat type is unknown.

Large numbers of age-0 Chinook salmon, along with many other juvenile fish species, were captured at mouths of Yukon River tributary streams after heavy rainfall events, with some streams witnessing extreme bedload movement and scouring. This 'flush-out" of juvenile fishes into the main-stem Yukon River may redistribute some individuals to downstream tributary streams, though some Yukon River non-natal streams retain fish throughout the summer rearing period (Bradford et al. 2001). Subsequent to this study, redistribution of age-0 Chinook salmon between non-natal streams has been documented (Daum, unpublished data). Future research is needed to define the stream-specific mechanisms that "hold" fish in some non-natal streams throughout the first summer feeding season while redistributing them in others.

Size of age-0 Chinook salmon increased throughout the summer and did not decrease with increased distance downstream from natal origin. This suggests that these long-distance migrating juveniles were feeding as they travelled downriver, either by making short sojourns into tributary streams, or feeding along main-stem Yukon River margins. Suspended-sediment concentrations in the main-stem Yukon River below the White River (referenced as Tincup, Figure 3) can be quite high in the summer months, averaging 200 mg/L with peaks of over 2,000 mg/L (Brabets et al. 2000). Main-stem habitats in large, turbid rivers have been described as largely inhospitable to fish during the open-water period and are primarily used as migratory corridors (Junk et al. 1989; Durst 2001; Bradford et al. 2008). But Murphy et al. (1989) found stream-type, age-0 Chinook salmon in channel edges of the main-stem, glacier-fed Taku River, with growth increasing throughout the summer months. Juvenile Chinook salmon densities were highest in channel edge habitat, followed by mouths of tributary streams.

The importance of main-stem channel edges for feeding and rearing by dispersed Yukon River age-0 Chinook salmon is largely unknown. However, tributary stream confluences with the main-stem Yukon River have been described as important habitat for age-0 Chinook salmon and other juvenile fish species in the lower Canadian section of the Yukon River main stem (Howe 2004). During our study, observations of large schools of lake chub surface-feeding on aquatic insects along the Yukon River main-stem margin throughout the summer suggest that this shoreline habitat may also offer feeding opportunities for migrating juvenile Chinook salmon. While it is clear that non-natal clearwater streams offer important rearing habitat for downstream dispersing age-0 Chinook salmon in the upper Yukon River, the significance of main-stem habitats remains unknown.

In summary, this study documents the use of non-natal U.S. streams in the upper Yukon River drainage for summer rearing by Canadian-origin, age-0 Chinook salmon. These juveniles have the ability to colonize rearing habitats at great distances from their natal origins. The majority of downstream colonizers originate from the most productive Canadian region (Carmacks) which underscores the potential importance of these habitats to the overall health and productivity of Yukon River Chinook salmon. Studies are needed to identify and protect these habitats and to further define the importance of this life history strategy to Yukon River Chinook salmon. The uniqueness of these northern, glacially influenced river systems and the fish that have developed there, offer exciting opportunities for future study.

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Table 1. Distances (rkm) from the confluence of each tributary to Yukon River mouth and U.S.–Canada border are presented for genetic baseline populations and study streams (2006-2007) for the upper Yukon River drainage.

Regional groups/populations	Rkm from mouth	Rkm from U.S.-Canada border
Upper U.S.		
Beaver Creek	1,436	534
Chandalar River	1,580	390
Sheenjek River	1,696	441
U.S.–Canada Border	1,970	0
Lower Canada		
Chandindu River	2,068	98
Klondike River	2,100	130
Stewart		
Stewart River	2,196	226
Mayo River	2,426	456
White		
Tincup Creek	2,489	519
Pelly		
Pelly River	2,356	386
Big Kalza River	2,481	511
Little Kalza River	2,486	516
Earn River	2,526	556
Glenlyon River	2,581	611
Blind Creek	2,641	671
Carmacks		
Tatchun River	2,439	469
Yukon main stem (above Tatchun River)	2,439	469
Little Salmon River	2,510	540
Big Salmon River	2,558	588
Nordenskiold River	2,467	497
Upper Canada		
Takhini River	2,701	731
Whitehorse	2,719	749
Wolf Creek	2,732	762
Michie Creek	2,774	804
Teslin		
Nisutlin River	2,830	860
Morley River	2,832	862
Sampled streams		
Minook Creek	1,228	742
Thanksgiving Creek	1,769	201
Coal Creek	1,791	179
Sam Creek	1,806	164
Trout Creek	1,885	85
Seventymile River	1,922	48
Shade Creek	1,938	32
Mission Creek	1,951	19

Table 2. Sample sites, sample dates, sample period, and fishing gear used during juvenile Chinook salmon sampling from eight tributary streams of the Yukon River, 2006 and 2007. Sample site coordinates (datum NAD 83) are from the uppermost sample station within each site.

Stream	Sample site (coordinates)	Sample dates	Sample period	Fishing gear
Mission Creek	Lower 2.4 km	Jul 27, 2006	Early	Minnow trap
	(64.80333N, –141.24167W)	Jul 26–Aug 02, 2007	Early	Minnow trap, seine
Shade Creek	Lower 1.0 km	Aug 02, 2006	Early	Minnow trap
	(64 89194N, –141.10889W)	Jul 27, 2007	Early	Minnow trap
Seventymile River	Site 1: 4.5 km	Jul 30, 2006	Early	Minnow trap, seine
	(64.90611N, –141 27833W)			
	Site 2: 25.0 km	Jul 31, 2006	Early	Minnow trap
	(64.89472N, –141 49028W)			
	Site 3: 10.6 km	Aug 1, 2006	Early	Minnow trap
	(64.88333N, –141.33611W)			
Trout Creek	Lower 1.0 km	Jul 29, 2006	Early	Minnow trap
	(65.11694N, –141.67361W)	Jul 29, 2007	Early	Minnow trap
Sam Creek	Lower 0.6 km	Aug 16, 2006	Late	Minnow trap
	(65.31139N, –142.87417W)	Aug 16, 2007	Late	Minnow trap
Coal Creek	Lower 2.8 km	Aug 16–17, 2006	Late	Minnow trap
	(65 32778N, –143.11667W)	Aug 14–18, 2007	Late	Minnow trap, seine
Thanksgiving Creek	Lower 0.4 km	Aug 17, 2006	Late	Minnow trap
	(65.42370N, –143.63545W)	Aug 17–19, 2007	Late	Minnow trap, seine
Minook Creek	Lower 7.0 km	Jul 17–18, 2006	Early	Minnow trap
	(65.48333N, –150.09944W)	Aug 29, 2006	Late	Minnow trap

Table 3. Genetic baseline collections by sampled population, region, collection years, and number of fish sampled (*n*) from 34 Yukon River Chinook salmon populations. See map in Figure 3 for stream locations.

Population	Region	Sample year	*n*
Andreafsky	Lower U.S.	2003	208
Anvik	Lower U.S.	2002	94
Gisasa	Lower U.S.	2001	188
Henshaw	Upper U.S.	2001	147
South Fork Koyukuk	Upper U.S.	2003	56
Tozitna	Lower U.S.	2003	190
Kantishna	Tanana	2005	187
Chena	Tanana	2001	189
Salcha	Tanana	2003, 2004	133
Beaver	Upper U.S.	1997	100
Chandalar	Upper U.S.	2002, 2003	113
Sheenjek	Upper U.S.	2002, 2004, 2006	51
Chandindu	Lower Canada	1998, 2000, 2001, 2003, 2004	566
Klondike	Lower Canada	1995, 1999, 2001, 2002, 2003	102
Stewart	Stewart	1996, 1997	110
Mayo	Stewart	1992, 1997, 2003	195
Tincup	White	2003	32
Pelly	Pelly	1996, 1997	125
Big Kalzas	Pelly	2003	22
Little Kalzas	Pelly	2003, 2004	40
Earn	Pelly	2003, 2004	54
Glenlyon	Pelly	2003	23
Blind	Pelly	1997, 2003, 2004	161
Tatchun	Carmacks	1987, 1996, 1997, 2002, 2003	366
Yukon main stem	Carmacks	1987, 2002	27
Little Salmon	Carmacks	1987, 1997	100
Big Salmon	Carmacks	1987, 1997	116
Nordenskiold	Carmacks	2003	99
Takhini	Upper Canada	1997, 2002, 2003	167
Whitehorse	Upper Canada	1985, 1987, 1997	241
Wolf	Upper Canada	1995, 2003	59
Michie	Upper Canada	1994	47
Nisutlin	Teslin	1987, 1997	56
Morley	Teslin	1997, 2002, 2003	28

Table 4. Age-0 Chinook salmon catch (*n*) from eight tributary streams of the Yukon River, 2006 and 2007. Catch-per-unit-effort (CPUE) for minnow traps (MT) are expressed as fish per trap-day and for seining (S) as fish per haul.

Stream	Site	Sample dates	Gear	Effort	*n*	CPUE
Mission Creek	Lower 2.4 km	Jul 27, 2006	MT	11.1 d	48	4 3 /d
		Jul 26–Aug 02, 2007	MT	28.8 d	19	0.7 /d
		Jul 27, 2006	S	6 hauls	7	1.2 /haul
Shade Creek	Lower 1.0 km	Aug 02, 2006	MT	7.5 d	100	13.3 /d
		Jul 27, 2007	MT	6.6 d	31	4.7 /d
Seventymile River	Site 1: 4.5 km	Jul 30, 2006	MT	4.6 d	8	4.9 /d
		Aug 1, 2006	S	5 hauls	0	0.0 /haul
	Site 2: 25.0 km	Jul 31, 2006	MT	7.5 d	72	9.6 /d
	Site 3: 10.6 km	Aug 1, 2006	MT	8.0 d	53	6.6 /d
Trout Creek	Lower 1.0 km	Jul 29, 2006	MT	10.0 d	29	2.9 /d
		Jul 29, 2007	MT	15.3 d	309	20.2 /d
Sam Creek	Lower 0.6 km	Aug 16, 2006	MT	4.1 d	5	1.2 /d
		Aug 16, 2007	MT	3.1 d	0	0.0 /d
		Aug 15, 2007	S	5 hauls	0	0.0 /haul
Coal Creek	Lower 2.8 km	Aug 16–17, 2006	MT	9.6 d	14	1.5 /d
		Aug 14–18, 2007	MT	21.4 d	14	0.7 /d
		Aug 14–18, 2007	S	40 hauls	64	1.6 /haul
Thanksgiving Creek	Lower 0.4 km	Aug 17, 2006	MT	5.8 d	10	1.7 /d
		Aug 17–19, 2007	MT	10.6 d	8	0.8 d
		Aug 17–18, 2007	S	18 hauls	34	1.9 /haul
Minook Creek	Lower 7.0 km	Jul 17–18, 2006	MT	6.7 d	2	0.3 /d
		Aug 29, 2006	MT	9.3 d	104	11.1 /d

Table 5. Species list and life stage of fish captured and observed from eight tributary streams of the Yukon River, 2006 and 2007. Life stage indicated by letter "j" for juvenile and "a" for adult.

Stream	Site	Species[1]
Mission Creek	Lower 2.4 km	AGj, KSj, LNSj, RWFj, SSja
Shade Creek	Lower 1.0 km	AGj, KSj, LNSj, SSja
Seventymile River	Site 1: 4.5 km	AGj, BBj, KSj, LCHa, LNSj, RWFj, SSja
	Site 2: 25.0 km	BBj, KSj, LCHa, SSja
	Site 3: 10.6 km	BBj, KSj, LCHa, SSja
Trout Creek	Lower 1.0 km	AGj, KSj, LNSj, RWFj, SSja
Sam Creek	Lower 0.6 km	AGj, KSj, SSj
Coal Creek	Lower 2.8 km	AGj, BBj, KSj, LCHa, LNSj, NPj, RWFj, SSja, TPj
Thanksgiving Creek	Lower 0.4 km	AGj, CSa (spawned-out female), KSj, LCHa, LNSj, SSja
Minook Creek	Lower 7.0 km	AGj, KSj, LNSj, RWFj, SSj

[1] AG=Arctic grayling, BB=Burbot, CS=chum salmon, KS=Chinook salmon, LCH=lake chub, LNS=longnose sucker, NP=northern pike, RWF=round whitefish, SS=slimy sculpin, TP=trout-perch

Table 6. Sample statistics for length and weight analyses of age-0 Chinook salmon from eight tributary streams of the Yukon River, 2006 and 2007. Not all captured juveniles (Table 4) were measured.

		Fork length (mm)		Weight (g)		Fulton K	
Stream	Sample period	*n*	Mean (SE)	*n*	Mean (SE)	*n*	Mean (SE)
Mission Creek	Early 2006	55	67.9 (0.8)				
	Early 2007	19	69.8 (1.1)	19	3.6 (0.2)	19	1.05 (0.01)
Shade Creek	Early 2006	100	66.8 (0.6)				
	Early 2007	31	63.5 (0.9)	31	2.7 (0.1)	31	1.04 (0.01)
Seventymile River	Early 2006	133	71.5 (0.6)				
Trout Creek	Early 2006	29	67.8 (1.0)				
	Early 2007	209	66.6 (0.4)	30	3.1 (0.2)	30	1.01 (0.01)
Sam Creek	Late 2006	5	71.4 (1.0)				
Coal Creek	Late 2006	14	76.5 (1.8)				
	Late 2007	78	71.2 (0.8)	78	3.8 (0.1)	78	1.02 (0.01)
Thanksgiving Creek	Late 2006	10	71.5 (1.4)				
	Late 2007	42	75.0 (1.2)	40	4.8 (0.3)	40	1 08 (0.01)
Minook Creek	Late 2006	104	76.9 (0.5)				

Table 7. Genetic field collection data and number genotyped for age-0 Chinook salmon sampled from eight tributary streams of the Yukon River, 2006 and 2007. Not all captured juveniles (Table 4) were sampled for genetics.

Stream	Sample site	Sample dates	Field collected (*n*)	Genotyped (*n*)
Mission Creek	Lower 2.4 km	Jul 27, 2006	55	47
		Jul 26–Aug 02, 2007	19	19
Total			74	66
Shade Creek	Lower 1.0 km	Aug 02, 2006	100	86
		Jul 27, 2007	31	30
Total			131	116
Seventymile River	Site 1: 4.5 km	Jul 30, 2006	8	8
	Site 2: 25.0 km	Jul 31, 20006	72	51
	Site 3: 10.6 km	Aug 1, 2006	51	39
Total			131	98
Trout Creek	Lower 1.0 km	Jul 29, 2006	29	18
		Jul 29, 2007	209	204
Total			238	222
Sam Creek	Lower 0.6 km	Aug 16, 2006	5	4
Coal Creek	Lower 2.8 km	Aug 16–17, 2006	14	11
		Aug 14–18, 2007	78	78
Total			92	89
Thanksgiving Creek	Lower 0.4 km	Aug 17, 2006	10	7
		Aug 17–19, 2007	42	33
Total			52	40
Minook Creek	Lower 7.0 km	Aug 29, 2006	104	48
Total (2006)			448	319
Total (2007)			379	364
Total (both years)			827	683

Table 8. Estimated stock compositions for 100% single population mixtures. Each baseline population was used to simulate a mixture of 100 fish. Mean stock composition and standard deviation were estimated from 1,000 bootstrap iterations of the baseline and mixture for SPAM 3.7b and from eight 20,000 iteration Markov chain Monte Carlo simulations for cBAYES. Individual assignment accuracy (IA) and the probability of assignment were also derived for cBAYES.

	SPAM 3.7b		cBAYES			
Stock	Estimate	SD	Estimate	SD	IA	Probability
Andreafsky	0.98	0.02	0.99	0.01	1.000	1.00
Anvik	0.87	0.07	0.98	0.02	1.000	1.00
Beaver	0.96	0.02	0.99	0.02	1.000	1.00
Big Kalzas	0.98	0.02	0.99	0.01	1.000	1.00
Big Salmon	0.87	0.05	0.98	0.02	1.000	1.00
Blind	0.96	0.03	0.99	0.02	1.000	1.00
Chandalar	0.96	0.03	0.98	0.02	1.000	1.00
Chandindu	0.99	0.02	0.99	0.02	1.000	1.00
Chena	0.96	0.03	0.99	0.01	1.000	1.00
Earn	0.91	0.05	0.99	0.02	1.000	1.00
Gisasa	0.96	0.03	0.99	0.02	1.000	1.00
Glenlyon	0.98	0.02	0.99	0.01	1.000	1.00
Henshaw	0.98	0.02	0.98	0.02	0.990	0.99
Kantishna	0.99	0.01	0.99	0.01	1.000	1.00
Klondike	0.71	0.09	0.98	0.04	1 000	1.00
Little Kalzas	0.96	0.03	0.99	0.01	1.000	1.00
Little Salmon	0.90	0.05	0.98	0.03	0.990	0.99
Mayo	0.94	0.03	0.98	0.03	1.000	0.99
Michie	0.87	0.07	0.99	0.01	1.000	1.00
Morley	0.93	0.05	0.99	0.02	1.000	1.00
Nisutlin	0.98	0.02	0.99	0.02	1.000	1.00
Nordenskiold	0.98	0.02	0.99	0.01	1.000	1 00
Pelly	0.93	0.04	0.98	0.03	1.000	0.99
Salcha	0.88	0.06	0.98	0.03	1 000	1.00
South Fork Koyukuk	0.93	0.04	0.99	0.02	1.000	1.00
Sheenjek	0.93	0.04	0.99	0.02	1.000	1.00
Stewart	0.85	0.06	0.98	0.03	1 000	1.00
Takhini	0.99	0.01	0.99	0.01	1.000	1.00
Tatchun	0.98	0.02	0.99	0.02	1.000	1.00
Tincup	1.00	0.01	0.99	0.01	1.000	1.00
Tozitna	0.97	0.03	0.99	0.02	1.000	1.00
Whitehorse	0.99	0.02	0.99	0.01	1.000	1.00
Wolf	0.88	0.06	0.99	0.02	1.000	1.00
Yukon main stem	0.84	0.07	0.99	0.02	1.000	1.00

Table 9. Estimated stock compositions for 100% regional mixtures. Each simulated mixture (n = 100) was composed of equal proportions of populations within the region. Mean stock composition and standard deviation were estimated from 1,000 bootstrap iterations of the baseline and mixture for SPAM 3.7b and from eight 20,000 iteration Markov chain Monte Carlo simulations for cBAYES.

	SPAM 3.7b		cBAYES	
Regional group	Estimate	SD	Estimate	SD
Lower U.S.	0.99	0.01	0 99	0.01
Tanana	0.96	0.03	0.99	0.01
Upper U.S.	0.95	0.03	0.99	0.01
Lower Canada	1.00	0.01	0.99	0.01
Stewart	0.93	0.04	0.98	0.02
White	1.00	0.01	0.99	0.01
Pelly	0.96	0.03	0.99	0.01
Carmacks	0.94	0.03	0.98	0.02
Upper Canada	0.98	0.02	0.99	0.01
Teslin	0.94	0.04	0.99	0.01

Table 10. Estimated stock compositions of simulated multi-region mixtures ($n = 100$) that may be encountered in a Yukon River fishery. Each region in the mixtures was composed of equal proportions of populations within the region. Mean stock composition and standard deviation were estimated from 1,000 bootstrap iterations of the baseline and mixture for SPAM 3.7b and from eight 20,000 iteration Markov chain Monte Carlo simulations for cBAYES.

		SPAM 3.7b		cBAYES	
Regional group	Expected	Mean	SD	Mean	SD
	Mixture 1 (Eiler et al. 2006a)				
Lower U.S.	0.12	0.13	0.01	0.12	0.01
Tanana	0.19	0.17	0.02	0.18	0.02
Upper U.S.	0.13	0.14	0.02	0.15	0.02
Lower Canada	0.08	0.08	0.01	0 07	0.01
Stewart	0.05	0.08	0.01	0.05	0.01
White	0.01	0.01	0.00	0.02	0.01
Pelly	0.11	0.13	0.02	0.13	0.01
Carmacks	0.25	0.22	0.02	0.23	0.02
Upper Canada	0.02	0.01	0.00	0.01	0.00
Teslin	0.04	0.03	0.01	0 05	0.01
U.S.	0.44	0.44	0.02	0.45	0.02
Canada	0.56	0.56	0.02	0.55	0.02
	Mixture 2 (Eiler et al. 2006b)				
Lower U S.	0.18	0.19	0 02	0.17	0.02
Tanana	0.26	0.26	0.02	0.27	0.02
Upper U.S.	0.08	0.09	0.01	0.09	0.01
Lower Canada	0.04	0.04	0.01	0.04	0.01
Stewart	0.05	0.07	0.02	0.04	0.01
White	0.00	0.00	0.00	0.00	0.00
Pelly	0.11	0.11	0.02	0.11	0.02
Carmacks	0.22	0.18	0.02	0.19	0.02
Upper Canada	0.00	0.00	0.00	0.00	0.00
Teslin	0.06	0.06	0.01	0.08	0.01
U.S.	0.52	0.54	0.02	0.54	0.02
Canada	0.48	0.46	0.02	0.46	0.02

Table 11. Stock composition analysis of real samples of known origin. Mean stock composition and standard deviation were estimated from 1,000 bootstrap iterations of the baseline and mixture for SPAM 3.7b and from eight 20,000 iteration Markov chain Monte Carlo simulations for cBAYES. Differences in expected values for Table 10 and 11 result from selected individuals being dropped because of incomplete genotype data in the known-origin mixture analysis.

		SPAM 3.7b		cBAYES	
Regional group	Expected	Mean	SD	Mean	SD
	Mixture 1 (Eiler et al. 2006a; *n*=540)				
Lower U.S.	0.13	0.19	0.02	0.13	0.02
Tanana	0.16	0.14	0.02	0.16	0.02
Upper U.S.	0.15	0.10	0.02	0.15	0.02
Lower Canada	0.10	0.14	0.02	0.11	0.01
Stewart	0.01	0.16	0.02	0.07	0.02
White	0.01	0.00	0.00	0.01	0.01
Pelly	0.11	0.11	0.02	0.11	0.02
Carmacks	0.26	0.11	0.02	0.16	0.03
Upper Canada	0.02	0.03	0.01	0.03	0.01
Teslin	0.05	0.01	0.01	0.06	0.02
U.S.	0.44	0.44	0.02	0.44	0.02
Canada	0.56	0.56	0.02	0.56	0.02
	Mixture 2 (Eiler et al. 2006b; *n*=401)				
Lower U.S.	0.22	0.28	0.03	0.24	0.02
Tanana	0.22	0.17	0.02	0.22	0.02
Upper U.S.	0.09	0.07	0.02	0.06	0.02
Lower Canada	0.05	0.08	0.02	0.07	0.01
Stewart	0 01	0.10	0.02	0.00	0.00
White	0.00	0.00	0.00	0.00	0.00
Pelly	0.10	0.12	0.02	0.09	0.02
Carmacks	0.24	0.16	0.03	0.21	0.03
Upper Canada	0.00	0.02	0.01	0.02	0.01
Teslin	0.07	0.02	0.01	0.08	0.02
U.S.	0.52	0.52	0.03	0.53	0.03
Canada	0.48	0.48	0.03	0.47	0.03
	Mixture 3 (individuals from populations not in baseline; *n*=52)				
Lower U.S.	0.00	0.02	0.02	0.01	0.01
Tanana	0.00	0.00	0.01	0.00	0.01
Upper U.S.	0.00	0.01	0.01	0.00	0.01
Lower Canada	0.29	0.27	0.07	0.26	0.07
Stewart	0.17	0.18	0.08	0.16	0.08
White	0.00	0.00	0.00	0.00	0.00
Pelly	0.17	0.20	0.07	0 24	0.09
Carmacks	0 23	0.26	0.08	0.24	0.08
Upper Canada	0.06	0.06	0.03	0.06	0.03
Teslin	0.08	0.00	0.01	0.02	0.03
U.S.	0.00	0.03	0.03	0.01	0.02
Canada	1.00	0.97	0.03	0.99	0.02

Table 12. The posterior probabilities of the number of extra-baseline stocks (*K*) for the 2006 and 2007 juvenile Chinook salmon genetic samples.

		K			
Year	*n*	0	1	2	3
2006	319	0.700	0.275	0.023	0.002
2007	364	0.925	0.072	0.003	0 000

Table 13. Age-0 Chinook salmon stock composition estimates (2006, *n* = 319 and 2007, *n* = 364) with associated standard deviations and 95% confidence intervals (CI). Mean stock compositions, standard deviations, and 95% confidence intervals were estimated from eight 20,000 iteration Markov chain Monte Carlo simulations using cBAYES.

	2006				2007			
Regional group	Estimate	SD	95% CI		Estimate	SD	95% CI	
Lower U.S.	0.003	0.006	0.000	0.022	0.001	0.001	0.000	0.004
Tanana	0.003	0.004	0.000	0.014	0.001	0.001	0.000	0.004
Upper U.S.	0.002	0.004	0.000	0.014	0.013	0.009	0.000	0.034
Lower Canada	0.047	0 014	0.022	0.078	0.002	0.004	0.000	0.015
Stewart	0.012	0.020	0.000	0.067	0.052	0.020	0.017	0.096
White	0.000	0.001	0.000	0.002	0.012	0.007	0.002	0.029
Pelly	0.006	0.009	0.000	0.032	0.039	0.015	0.015	0.073
Carmacks	0.912	0.030	0.840	0.958	0.824	0.036	0.747	0.888
Upper Canada	0.013	0.011	0.000	0.041	0.032	0.014	0.009	0.062
Teslin	0.003	0.007	0.000	0.027	0.026	0.025	0.000	0.083
U.S.	0.007	0.008	0.000	0.030	0.014	0.009	0.001	0.035
Canada	0.993	0.008	0.970	1.000	0.986	0.009	0.965	0.999

Table 14. The 2006 and 2007 age-0 Chinook salmon were individually assigned by stream to region and country using cBAYES, with eight 20,000 iteration Markov chain Monte Carlo simulations. Individuals were assigned if their source probabilities were at least 95%. The difference in total individuals assigned between region and country results from some cases where individuals could not be assigned to region but could be assigned to country. Streams were sequentially ordered, beginning with stream farthest downstream from U.S.–Canada border.

	2006		2007	
Regional group	Absolute no.	Relative no.	Absolute no.	Relative no.
		Minook Creek		
Lower U.S.	0	0.000	No data	
Tanana	0	0.000		
Upper U.S.	0	0.000		
Lower Canada	0	0.000		
Stewart	0	0.000		
White	0	0.000		
Pelly	0	0 000		
Carmacks	40	1.000		
Upper Canada	0	0.000		
Teslin	0	0.000		
U.S.	0	0.000		
Canada	46	1.000		
		Thanksgiving Creek		
Lower U.S.	0	0.000	0	0.000
Tanana	0	0.000	0	0.000
Upper U.S.	0	0.000	0	0.000
Lower Canada	0	0.000	0	0.000
Stewart	0	0.000	0	0.000
White	0	0.000	0	0.000
Pelly	0	0.000	0	0.000
Carmacks	6	1.000	15	0.938
Upper Canada	0	0.000	1	0.063
Teslin	0	0 000	0	0.000
U.S.	0	0.000	0	0.000
Canada	6	1.000	31	1.000
		Coal Creek		
Lower U.S.	0	0.000	0	0.000
Tanana	0	0.000	0	0.000
Upper U.S.	0	0.000	0	0.000
Lower Canada	0	0.000	0	0.000
Stewart	0	0.000	1	0.030
White	0	0.000	1	0.030
Pelly	0	0.000	1	0.030
Carmacks	11	1.000	29	0.879
Upper Canada	0	0.000	1	0.030
Teslin	0	0.000	0	0.000
U.S.	0	0.000	0	0.000
Canada	11	1.000	76	1.000

Table 14. continued.

	2006		2007	
Regional group	Absolute no.	Relative no.	Absolute no.	Relative no.
		Sam Creek		
Lower U.S.	0	0.000	No data	
Tanana	0	0.000		
Upper U.S.	0	0.000		
Lower Canada	0	0.000		
Stewart	0	0.000		
White	0	0.000		
Pelly	0	0.000		
Carmacks	4	1.000		
Upper Canada	0	0.000		
Teslin	0	0.000		
U.S.	0	0.000		
Canada	4	1.000		
		Trout Creek		
Lower U.S.	0	0.000	0	0.000
Tanana	0	0.000	0	0.000
Upper U.S.	0	0.000	0	0.000
Lower Canada	0	0.000	0	0.000
Stewart	0	0.000	0	0.000
White	0	0.000	1	0.009
Pelly	0	0.000	1	0.009
Carmacks	9	1.000	104	0.981
Upper Canada	0	0.000	0	0.000
Teslin	0	0.000	0	0.000
U.S.	0	0.000	0	0.000
Canada	17	1.000	200	1.000
		Seventymile River		
Lower U.S.	0	0.000	No data	
Tanana	0	0.000		
Upper U.S.	0	0.000		
Lower Canada	0	0 000		
Stewart	0	0.000		
White	0	0.000		
Pelly	0	0.000		
Carmacks	70	1.000		
Upper Canada	0	0.000		
Teslin	0	0.000		
U.S.	0	0.000		
Canada	95	1.000		

Table 14. continued.

Regional group	2006 Absolute no.	2006 Relative no.	2007 Absolute no.	2007 Relative no.
		Shade Creek		
Lower U.S.	0	0.000	0	0.000
Tanana	0	0.000	0	0.000
Upper U.S.	0	0.000	0	0.000
Lower Canada	2	0.029	0	0.000
Stewart	0	0.000	0	0 000
White	0	0.000	0	0.000
Pelly	0	0.000	0	0.000
Carmacks	67	0.971	15	1.000
Upper Canada	0	0.000	0	0.000
Teslin	0	0.000	0	0.000
U.S.	0	0.000	0	0.000
Canada	85	1.000	29	1.000
		Mission Creek		
Lower U.S.	0	0.000	0	0.000
Tanana	0	0.000	0	0.000
Upper U S.	0	0.000	0	0.000
Lower Canada	4	0.138	0	0.000
Stewart	0	0.000	0	0.000
White	0	0.000	0	0.000
Pelly	0	0.000	0	0.000
Carmacks	25	0.862	7	0.875
Upper Canada	0	0.000	1	0.125
Teslin	0	0.000	0	0.000
U.S.	0	0.000	0	0.000
Canada	47	1.000	16	1.000

Table 15. Selected physical characteristics for eight tributary streams of the Yukon River, 2006 and 2007. Gradient, substrate, and Rosgen stream type determined from lower stream reach. Yukon access describes location of tributary stream confluence in relation to Yukon River main stem.

Stream	Stream order	Watershed (km^2)	Gradient (%)	Dominate substrate	Rosgen stream type	Yukon access
Mission Creek	4	602	0 5	Small cobble	C4	Main channel
Shade Creek	2	34	2.6	Large cobble	B4	Main channel
Seventymile River	4	1,694	0.3	Sand/gravel	C4	Main channel
Trout Creek	3	75	1.1	Small cobble	C3	Side channel
Sam Creek	4	188	0.6	Gravel	C4	Side channel
Coal Creek	4	222	0.9	Gravel	C4 (mined)	Main channel
Thanksgiving Creek	4	187	1.0	Large cobble	C3	Main channel
Minook Creek	4	495	0.7	Small cobble	C4	Main channel

Table 16. Water quality measurements for eight tributary streams of the Yukon River, 2006 and 2007. Measurements taken near mouth of each stream. Variables not measured represented by "NM".

Stream	Sample date	Water temperature (°C)	River stage	Water color	Conductivity (µS/cm)	pH
Mission Creek	Jul 26, 2006	10.5	Medium	Clear	NM	NM
	Jul 27, 2007	13.2	Medium	Tannic	347	8.14
Shade Creek	Aug 02, 2006	6.0	Medium	Clear	NM	NM
	Jul 26, 2007	8.0	Low	Clear	603	8.11
Seventymile River	Jul 30, 2006	9.0	Med/high	Muddy	NM	NM
	Jul 31, 2007	14 2	Med/high	Muddy	166	7.04
Trout Creek	Jul 28, 2006	10.5	Low	Clear	NM	NM
	Jul 29, 2007	9.3	Med/low	Clear	476	7.06
Sam Creek	Aug 16, 2006	9.0	Medium	Clear	NM	NM
	Aug 15, 2007	6.0	Flooding	Muddy	NM	NM
Coal Creek	Aug 15, 2006	7.5	Med/high	Muddy	NM	NM
	Aug 15, 2007	7.0	Flooding	Muddy	NM	NM
Thanksgiving Creek	Aug 16, 2006	8.0	Medium	Tannic	NM	NM
	Aug 17, 2007	7.0	Flooding	Muddy	NM	NM
Minook Creek	Jul 17, 2006	7.0	Med/high	Muddy	NM	NM
	Aug 29, 2006	6.0	Medium	Clear	NM	NM

Table 17. Stock composition estimates (brood year 2005 and 2006) for adult Chinook salmon returns into Canada (JTC 2006, 2007) and age-0 juvenile stock composition estimates from sampled U.S. streams in 2006 and 2007. Carmacks and main-stem stocks were split into two regional groups for the adult returns analyses but were combined in the juvenile analyses.

	2005 brood year		2006 brood year	
Regional group	Adult stock composition (SD)	Juvenile stock composition (SD)	Adult stock composition (SD)	Juvenile stock composition (SD)
Lower Canada	12.5 (1.6)	4.7 (1.4)	10.3 (1.7)	0.2 (0.4)
Stewart	9.1 (2.4)	1.2 (2.0)	13.4 (2.2)	5.2 (2.0)
White	0.5 (0.5)	0.0 (0.1)	1.7 (0.6)	1.2 (0.7)
Pelly	17.5 (2.4)	0.6 (0.9)	12.4 (1.9)	3.9 (1.5)
Carmacks	24.6 (3.2)	91.2 (3.0)	33.0 (2.9)	82 4 (3.6)
Main stem	11.1 (2.5)		10.2 (2.0)	
Upper Canada	5.6 (1.4)	1.3 (1.1)	6.0 (1.0)	3.2 (1.4)
Teslin	19.2 (2.3)	0.3 (0.7)	13.0 (1.9)	2.6 (2.5)

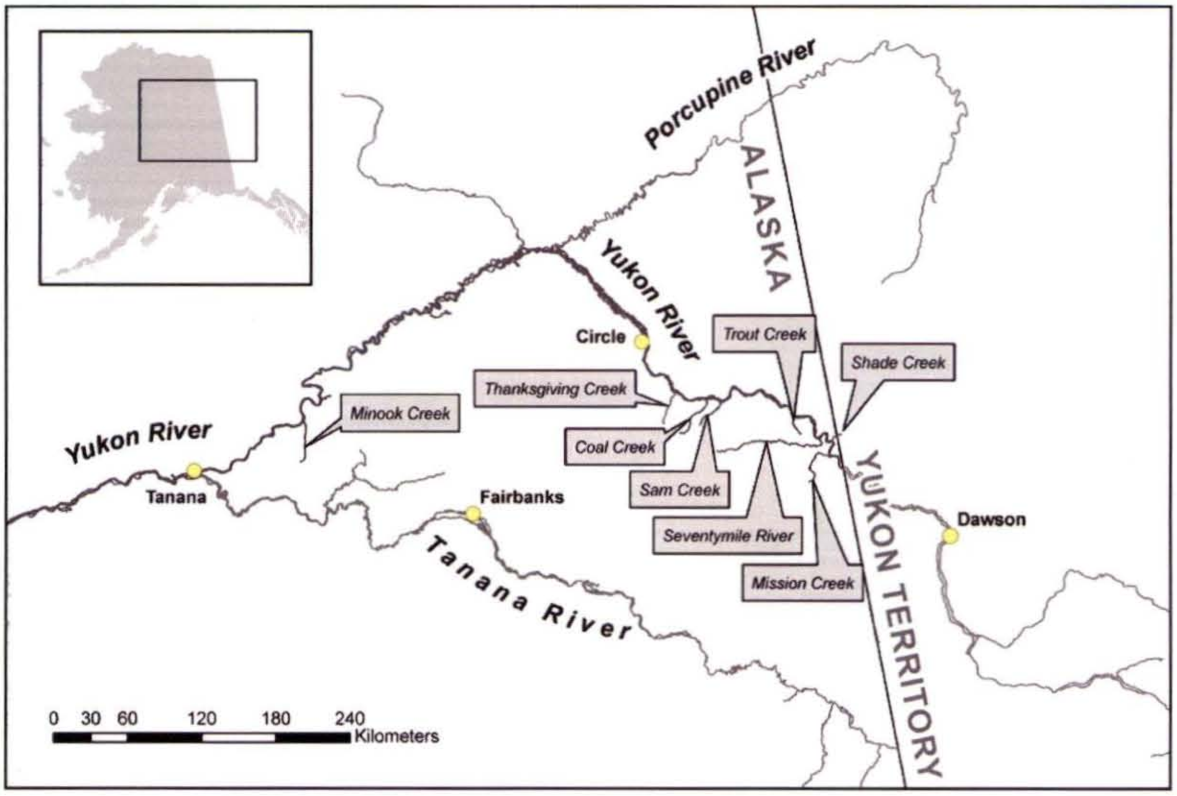

Figure 1. The eight tributary streams of the Yukon River sampled for juvenile Chinook salmon, 2006 and 2007.

Figure 2. The eight tributary streams of the Yukon River sampled for juvenile Chinook salmon, 2006 and 2007.

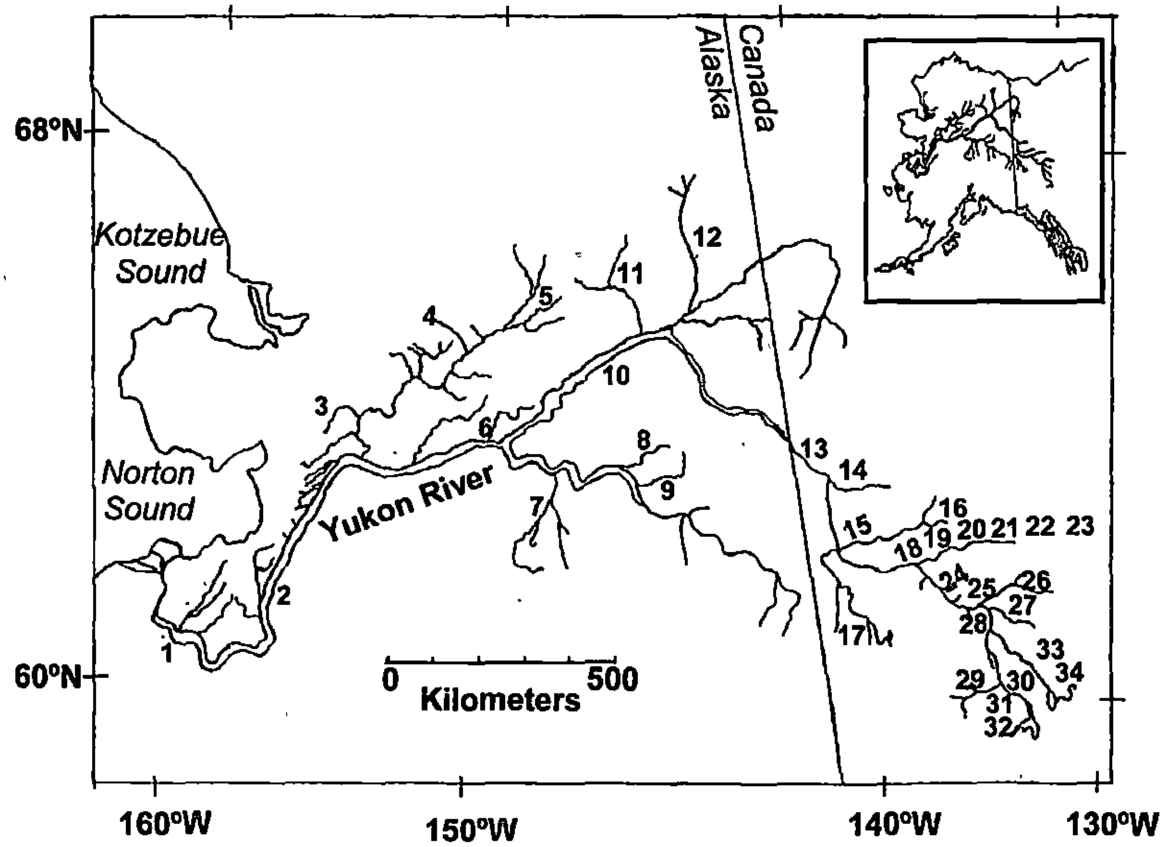

Figure 3. Locations of genetic baseline collections (described in Table 3) for 34 Yukon River Chinook salmon populations: 1=Andreafsky, 2=Anvik, 3=Gisasa, 4=Henshaw, 5=South Fork Koyukuk, 6=Tozitna, 7=Kantishna, 8=Chena, 9=Salcha, 10=Beaver, 11=Chandalar, 12=Sheenjek, 13=Chandindu, 14=Klondike, 15=Stewart, 16=Mayo, 17=Tincup, 18=Pelly, 19=Big Kalzas, 20=Little Kalzas, 21=Earn, 22=Glenlyon, 23=Blind, 24=Tatchun, 25=Yukon main stem, 26=Little Salmon, 27=Big Salmon, 28=Nordenskiold, 29=Takhini, 30=Whitehorse, 31=Wolf, 32=Michie, 33=Nisutlin, and 34=Morley.

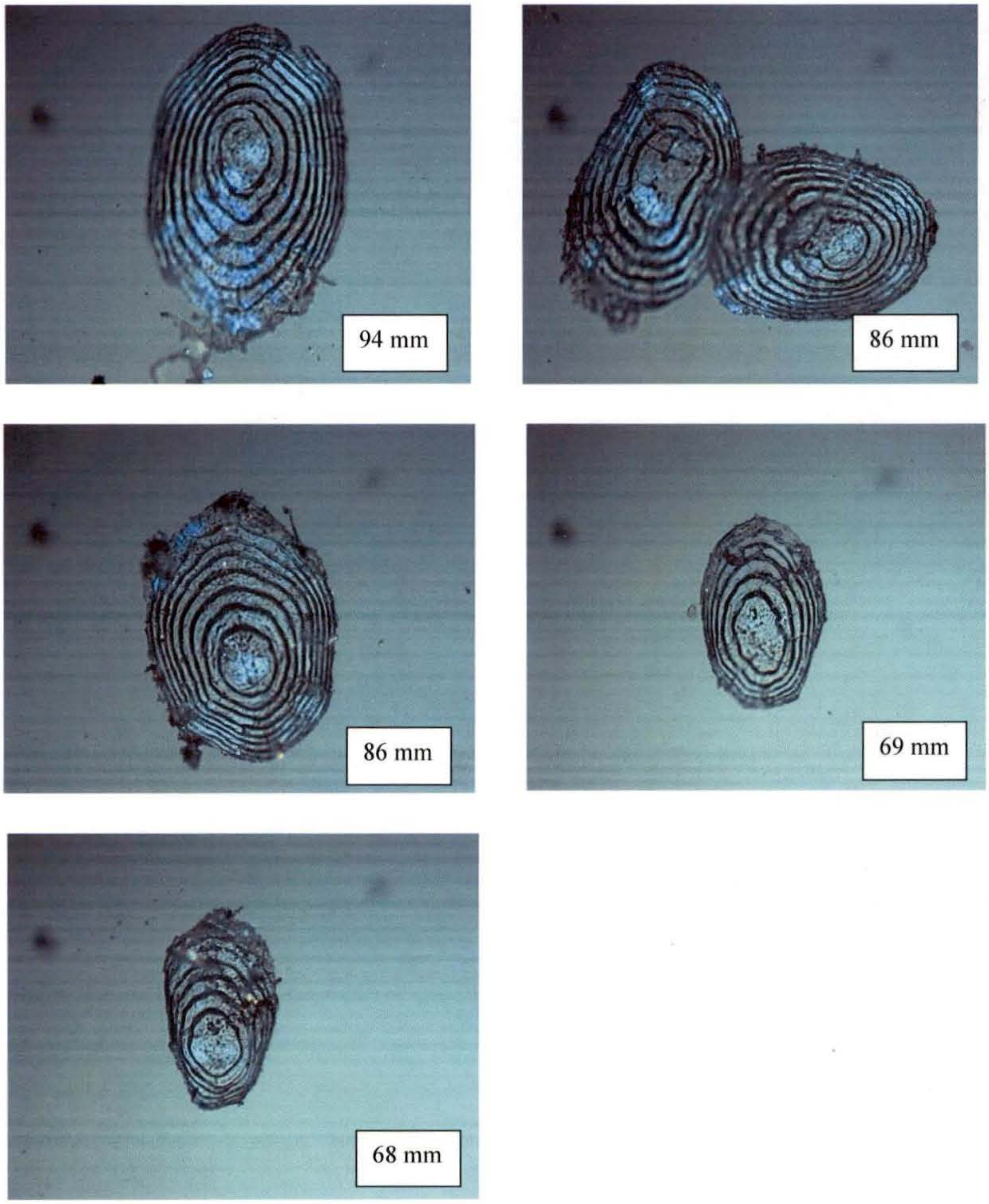

Figure 4. Scale samples from five age-0 Chinook salmon captured in Thanksgiving Creek, Aug 18, 2007. Age verified by Fish Ageing Unit, DFO.

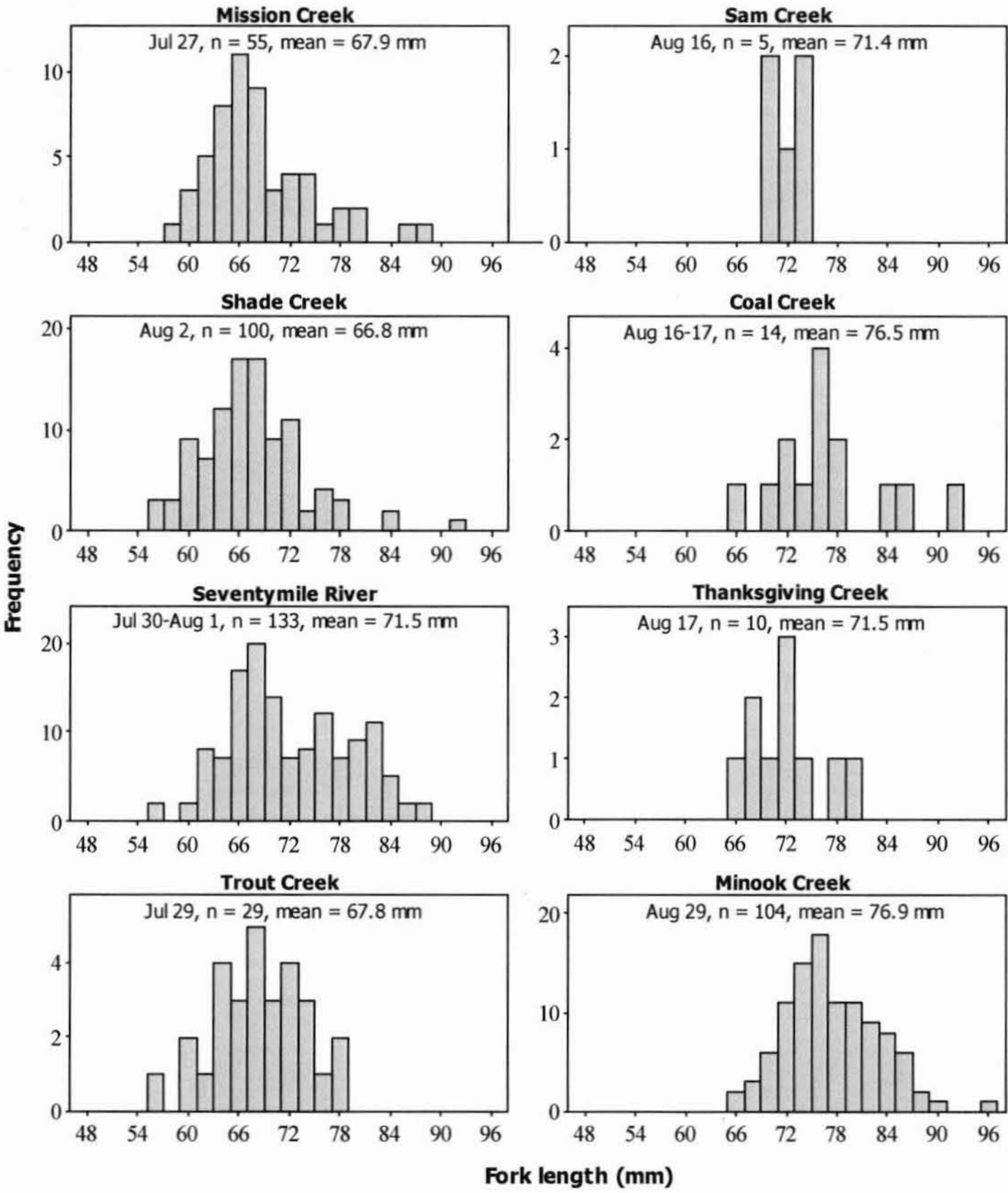

Figure 5. Length frequency of age-0 Chinook salmon captured from eight tributary streams of the Yukon River, 2006.

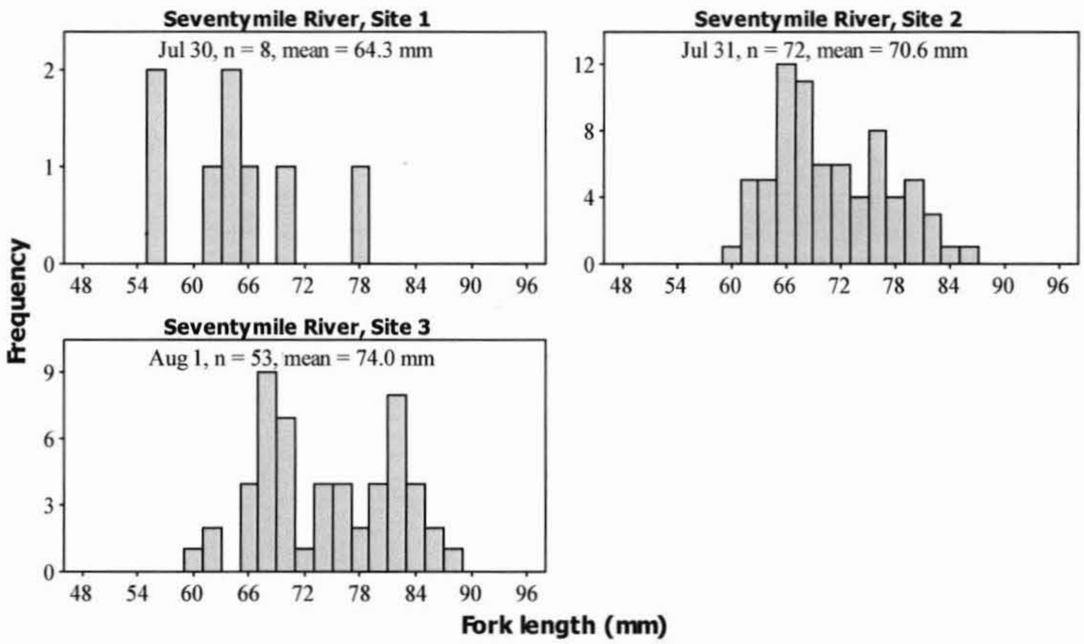

Figure 6. Length frequency of age-0 Chinook salmon captured from three sites in the Seventymile River, 2006.

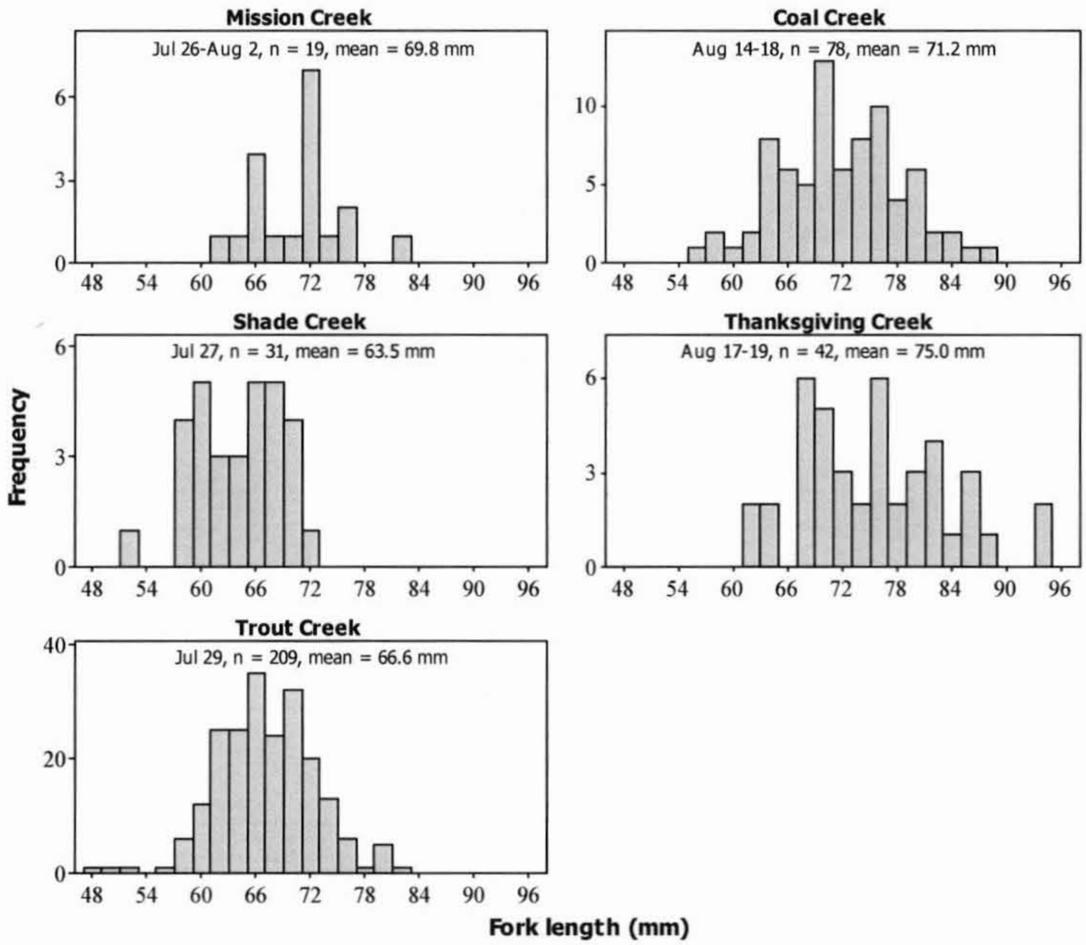

Figure 7. Length frequency of age-0 Chinook salmon captured from five tributary streams of the Yukon River, 2007.

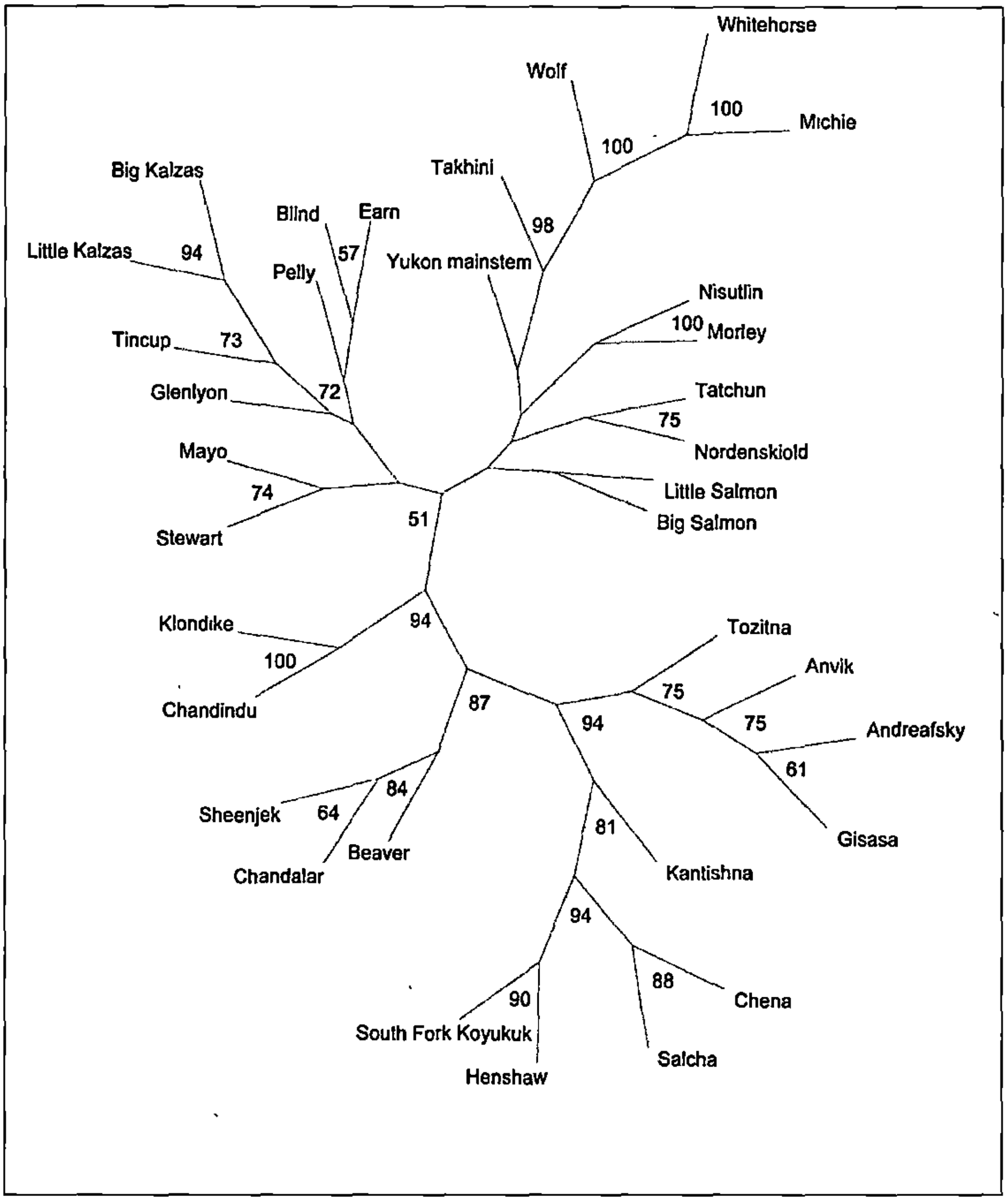

Figure 8. Consensus neighbor-joining dendrogram of Cavalli-Sforza and Edwards (1967) chord distances (CSE) calculated from allele frequencies at 13 loci. Bootstrap values are shown for nodes that clustered together at least 50% of the time.