

**2010 YUKON RIVER PANEL RESTORATION & ENHANCEMENT FUND
FINAL REPORT**

Project Number: URE-23N-10

Project Title: Stock composition of age-0 Chinook salmon rearing in nonnatal U.S. tributary streams of the Yukon River

Project Proponent: U.S. Fish and Wildlife Service (USFWS), Fairbanks FWFO

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Project Location

The study area includes clear-water Yukon River tributaries between Circle and the U.S.–Canada border (260 km) and between Tanana and Stevens Village (250 km).

Project Objectives

1. genotype collection of age-0 Chinook salmon from sampled streams; and
2. estimate stock composition of samples for regional genetic groups and country of origin by year and collection area.

Project Summary

Canadian-origin Chinook salmon juveniles have been recently documented rearing in downstream U.S. tributary streams of the Yukon River. A comprehensive three-year distribution study was funded by the Alaska Sustainable Salmon Fund (AKSSF) in 2008 to describe the extent of colonization in U.S. tributary streams of the Yukon River between the Tanana River confluence and U.S.–Canada border near Eagle. Genetic collections from captured fish were archived for future analysis if funding was made available. In 2010, the Yukon River Panel, through the R&E Fund, provided the necessary funding to analyze the three-year genetic collections (2008–2010). Genetic analytical techniques were used to determine stock and country of origin for the samples. Samples were grouped by collection year and sample area.

2010 YUKON RIVER PANEL RESTORATION & ENHANCEMENT FUND

**FINAL REPORT TO YUKON RIVER PANEL
URE-23N-10**

**STOCK COMPOSITION OF AGE-0 CHINOOK SALMON REARING IN NONNATAL
U.S. TRIBUTARY STREAMS OF THE YUKON RIVER**

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Stock composition of age-0 Chinook salmon rearing in nonnatal U.S. tributary streams of the Yukon River

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Final Report to the Yukon River Panel

URE-23N-10

Abstract

Yukon River Chinook salmon *Oncorhynchus tshawytscha* 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. Previous life history and distribution studies have shown that some age-0 Chinook salmon leave their natal streams and colonize downriver, nonnatal habitats for rearing and overwintering. A pilot study in 2006–2007 documented rearing of Canadian-origin Chinook salmon in downstream U.S. waters. A comprehensive three-year distribution study was funded by the Alaska Sustainable Salmon Fund in 2008 to describe the extent of Chinook salmon rearing in nonnatal U.S. tributary streams of the Yukon River between the U.S.–Canada border and Tanana, Alaska, a distance of over 850 km. Juvenile Chinook salmon were captured in 44 of the 56 streams sampled. Genetic material was collected from all 616 fish captured and the stock composition results from the samples are presented in this report. Using genetic mixed-stock and individual assignment analyses, sample mixtures and individuals were assigned to regional stock groups and country of origin. Canadian-origin Chinook salmon contributed between 88% and 100% of the yearly mixtures and between 91% and 100% of the yearly assigned samples, with Canadian percentages decreasing with increased distance from the U.S.–Canada border. The Carmacks regional group, 470 to 590 km upstream of the border, made up the majority of mixtures and individual assignments throughout the study area. Other Canadian groups were under-represented, including the large-river stocks from the Stewart, Pelly, and Teslin rivers. The furthest travel distance was estimated to be over 1,300 km. The Upper USA stock group was identified in some downstream creeks below the Dalton Highway Bridge, but always in low numbers. The mechanism that causes this disproportionate number of Carmacks area juveniles to leave their natal streams for downstream rearing areas and the cost, if any, of this dispersal strategy are unknown.

Introduction

Yukon River Chinook salmon *Oncorhynchus tshawytscha* are classified as “stream-type” (Gilbert 1922; Healey 1983). After emergence from river gravel, Yukon River Chinook salmon typically disperse downstream to suitable rearing habitat, feed and grow throughout the summer, overwinter in freshwater, and usually leave these rearing areas for marine waters during the second year (Beacham et al. 1989). Previous life history and distribution studies have shown that some age-0 Chinook salmon leave their natal streams and colonize downriver, nonnatal habitats for rearing and overwintering. Several hundred nonnatal 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). In sharp contrast, little information was available on the use of nonnatal streams by Chinook salmon juveniles in the upper U.S. portion of the drainage until a pilot study was conducted in 2006–2007 by U.S. Fish and Wildlife Service (USFWS). Eight streams below the U.S.–Canada border were found to contain rearing age-0 juveniles and genetic stock composition analysis indicated that 100% of the samples were of Canadian origin (Daum and Flannery 2011). Populations from the Carmacks region of Canada contributed 91% to the mixtures in 2006 and 82% in 2007. The Carmacks genetic regional group includes spawning populations from Tatchun Creek, and Little Salmon, Big Salmon, Nordenskiöld, and main-stem Yukon rivers. Canadian stocks nearest the border and from large river systems were underrepresented in the collections. Some age-0 Chinook salmon may have travelled over 1,200 km to reach downstream rearing areas.

Genetic mixed-stock (MSA) and individual assignment (IA) analyses are effective methods for estimating the source origin of unknown samples (Cadrin 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. Since development of the initial 19-population microsatellite genetic baseline for Yukon River Chinook salmon (Beacham et al. 2008), 15 new populations and additional collections have been added and 10 regional stock groups have been defined for apportioning mixtures from genetic samples (Daum and Flannery 2011; Table 1 and Figure 1). For the 13 standardized microsatellite loci established by the Genetic Analysis of Pacific Salmonids group (GAPS; Seeb et al. 2007), MSA and IA simulations were 98–100% accurate to the 10 regional Yukon River stock groups (Daum and Flannery 2011). Stock composition estimates for know-origin mixtures were within 10% of expected and IA of known-origin mixtures were 96% accurate to region and 100% accurate to country when the 95% probability criterion was used (Daum and Flannery 2011).

A comprehensive three-year distribution study was funded by the Alaska Sustainable Salmon Fund (AKSSF) in 2008 to describe the extent of Chinook salmon rearing in nonnatal U.S. tributary streams of the Yukon River above the Tanana River confluence. The study area included clear-water Yukon River tributaries between Circle and the U.S.–Canada border (260 km) and between Tanana and Stevens villages (250 km). Along with distributional, biological, and aquatic habitat information, fin-clips of sampled fish were collected and archived for future

genetic stock analysis. By the study's completion in 2010, 44 streams were found to contain age-0 Chinook salmon and over 600 individual genetic samples were collected. In 2010, the Yukon River Panel, through the R&E Fund, provided funding (project URE-23N-10) to genotype and estimate the stock composition of this three-year genetic collection. This paper describes the results from the genetic analysis. A future peer-reviewed journal article will present the combined biological, habitat, and genetic results into one citable publication.

Methods

Sample Collection and Laboratory Analysis

Genetic samples were collected from captured age-0 Chinook salmon as part of a broader juvenile distribution and rearing study (2008–2010) funded by AKSSF. Anal fin tissue was stored in 2-ml vials containing 100% ethanol. 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). When possible, stream collections were spread out over a large spatial area ($\gg 100$ m) to decrease the potential of sampling families (Hansen et al. 1997). Streams were sampled in a systematic order, beginning near the U.S.–Canada border and ending near Tanana village, a distance of approximately 850 km. The samples were genotyped from the 13 standardized microsatellite loci identified by the GAPS group (Seeb et al. 2007) using methods described in Daum and Flannery (2011). 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 genetic analysis.

Stock Composition and Individual Assignment Analyses of Genetic Samples

The genetic profiles for each age-0 Chinook salmon were compared to a genetic baseline representing 34 major spawning populations of Yukon River Chinook salmon (Table 1; Figure 1). The 34 genetically defined populations were further divided into 10 regional stock groupings based on neighbor-joining results, geography, and management goals (Daum and Flannery 2011). Distances from upper Yukon River baseline populations to the U.S.–Canada border and to the Yukon River mouth are presented in Table 2. Using genetic MSA and IA techniques, sample mixtures and individual samples were assigned to regional genetic stock groups and country of origin by cBAYES (Neaves et al. 2005). Individuals were assigned to region and country of origin if their posterior source probabilities were $\geq 95\%$; otherwise, they were classified as unknown. Samples were analyzed by collection year, with individual assignments also compiled by collection site or area. The lack of an exhaustive population-specific genetic baseline prevented stock composition estimation for individual populations. The probability of unrepresented extra-baseline stocks being present in the 2008–1010 samples was tested using HWLER (Pella and Masuda 2006). Prior to this study, simulation and known-origin mixture analyses were used to evaluate the accuracy and precision of MSA and IA estimates derived from the existing Yukon River Chinook salmon baseline. Results show these techniques to be highly accurate and precise in estimating regional and country of origin from sample mixtures and individual assignments. Detailed descriptions of the genetic techniques used and results from baseline testing are presented in Daum and Flannery (2011).

Results

Sample Collection and Laboratory Analysis

During the 2008–2010 study, 44 streams were found to contain age-0 Chinook salmon and a total of 616 genetic samples were collected (Table 3; Figures 2 – 6). Mission Creek near Eagle had been previously documented to contain nonnatal rearing juveniles Daum and Flannery (2011), but additional samples were collected opportunistically in 2008 and added to the collection. Drought conditions in the summer of 2009 precluded some selected streams from being sampled (streams dry) causing a lower than expected sample size, especially in areas upstream of Circle (Figure 4). Of the 616 genetic tissue samples collected, 611 (99%) were successfully genotyped at a minimum of 10 of the 13 loci (Table 3). All genotyped samples field identified as Chinook salmon were genetically confirmed. Distances from streams with juvenile genetic collection to the U.S.–Canada border and to the Yukon River mouth are presented in Table 4.

Stock Composition and Individual Assignment Analyses of Genetic Samples

No significant stocks were determined to be missing from the baseline in the analysis by HWLER. There was a 90%, 96%, and 94% probability that no extra baseline stocks were present in the collections from 2008, 2009, and 2010, respectively. Stock composition analysis of age-0 Chinook salmon in the 2008–2010 samples indicated that Canadian-origin Chinook salmon contributed between 88% and 100% to the yearly mixtures, with Canadian percentages decreasing with increased distance from the U.S.–Canada border (Table 5). Fish from the Carmacks region in Canada contributed 82% to the mixtures in 2008, 86% in 2009, and 71% in 2010. Individual assignment results were similar to the stock composition analysis with 100% of the assigned samples being of Canadian origin in 2008, 98% in 2009, and 91% in 2010 (Tables 6–8). The Carmacks regional group made up 96% of the IA individuals in 2008, 97% in 2009, and 85% in 2010. A few fish from the Pelly ($n = 5$) and Stewart ($n = 1$) rivers of Canada were present in upriver samples. Little Salt Creek (Figure 5, stream # 23), downstream of the Dalton Highway Bridge, was the first stream sampled containing a U.S.-origin stock (Table 7), 672 km downstream from the U.S.–Canada border (Table 4). The farthest downriver stream (Mission Creek near Tanana, 847 km downstream from the U.S.–Canada border) had a fish from the Carmacks regional group, an estimated travel distance of over 1,300 km (Table 3). Four 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. Overall, assigning individuals according to the $\geq 95\%$ probability criterion resulted in 54% of the individuals being assigned to specific regions and 96% to country.

Discussion

This study documents the presence of Canadian-origin, age-0 juvenile Chinook salmon in 44 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 nonnatal rearing habitats to the overall health and productivity of Canadian Chinook salmon.

Age-0 Chinook salmon from the Carmacks region made up the vast majority of captures in downstream tributary streams of the Yukon River. As in the 2006–2007 pilot study (Daum and Flannery 2011), this represents a disproportionately large number of Carmacks area fish in downstream juvenile captures. The largest Canadian river systems (Stewart, Pelly, and Teslin

ivers) were grossly underrepresented in the stream samples, <2% of the individually assigned samples. But unlike the pilot study, no Upper Canada, Teslin, White, or Lower Canada stock groups were found. The Upper U.S. stock group was identified in some downstream streams below the Dalton Highway Bridge, but always in low numbers.

The mechanism that causes this disproportionate number of Carmacks area, age-0 Chinook salmon to leave their natal streams is 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 near Dawson (Bradford et al. 2008) and the mixture of different stock groups in these main-stem catches (Bradford et al. 2009) suggest 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.

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 an exhaustive, 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 nonnatal streams during the first summer’s rearing period. The longest migratory distance was from the Carmacks regional group found in Mission Creek near Tanana, a distance of between 1,316 and 1,435 km downstream from natal stream origins (Tables 2 and 4). Previously, Daum and Flannery (2011) described a Minook Creek sample near Rampart as containing the Carmacks stock group, but the present Mission Creek sample may extend this distance by over 100 km. Future sampling of Yukon River tributary streams below Tanana village should yield even further downstream dispersal distances. These results beg the question as to why Carmacks area fish have a greater propensity to disperse to distant rearing streams than other stock groups in the upper Yukon River drainage and what, if any, cost is associated with this long-distance dispersal strategy.

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Table 1. 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 1 for stream locations.

Population	Region	Sample year	<i>n</i>
Andreafsky	Lower USA	2003	208
Anvik	Lower USA	2002	94
Gisasa	Lower USA	2001	188
Henshaw	Upper USA	2001	147
South Fork Koyukuk	Upper USA	2003	56
Tozitna	Lower USA	2003	190
Kantishna	Tanana	2005	187
Chena	Tanana	2001	189
Salcha	Tanana	2003, 2004	133
Beaver	Upper USA	1997	100
Chandalar	Upper USA	2002, 2003	113
Sheenjok	Upper USA	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 2. Distances (km) from the confluence of each tributary to Yukon River mouth and U.S.–Canada border for genetic baseline populations in the upper Yukon River drainage.

Regional groups/populations	Km from mouth	Km from U.S.–Canada border
Upper USA		
Beaver Creek	1,436	534
Chandalar River	1,580	390
Sheenjok River	1,696	441
<i>U.S.–Canada Border</i>	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 Kalzas River	2,481	511
Little Kalzas River	2,486	516
Earn River	2,526	556
Glenlyon River	2,581	611
Blind Creek	2,641	671
Carmacks		
Tatchun Creek	2,439	469
Yukon main stem (above Tatchun Creek)	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

Table 3. Streams with genetic collections of age-0 Chinook salmon by location and collection date, 2008–2010. Coordinates (datum NAD 83) are from the uppermost capture site for each stream. Map reference refers to numbering of stream locations on Figures 3–6. Data arranged by stream location, upstream to downstream.

Stream	Map reference	Coordinates		Collection date	Field collected (<i>n</i>)	Genotyped (<i>n</i>)
		Lat (N)	Long (W)			
2008						
Boundary Creek	1	64.68027	141.00546	7/17/2008	30	30
Eagle Creek	2	64.77488	141.03609	7/17/2008	29	27
Mission Creek*	3	64.79539	141.20703	9/9/2008	23	23
American Creek (trib to Mission Creek)	4	64.79128	141.23784	7/17/2008 9/9/2008	30 17	30 17
Unnamed Creek # 6	5	65.14222	141.66050	7/25/2008	12	11
Michigan Creek	6	65.19445	141.80950	8/9/2008	21	21
Fourth of July Creek	7	65.19514	141.82910	8/9/2008	4	4
Schley Creek	8	65.21528	141.88545	7/23/2008	5	5
Unnamed Creek # 13	9	65.24973	141.88942	8/7/2008	30	29
Butte Creek	10	65.25477	141.95822	7/23/2008	14	14
Rock Creek	11	65.27908	141.93770	8/11/2008	6	6
Logan Creek	12	65.27045	141.99664	7/23/2008	11	11
Glenn Creek	13	65.29718	142.09320	8/11/2008	16	16
Washington Creek	14	65.31777	142.31344	8/13/2008	1	1
Unnamed Creek # 19	15	65.33649	142.39714	8/13/2008	3	3
Weshrinarin Creek	16	65.33152	142.46496	8/12/2008	4	4
Unnamed Creek # 21	17	65.40006	142.64161	8/14/2008	6	6
				Total	262	258
2009						
Woodchopper Creek	18	65.35153	143.32633	7/31/2009	2	2
Unnamed Creek # 25	19	65.35512	143.39650	7/30/2009	3	3
Webber Creek	20	65.40512	143.54997	7/31/2009	11	11
Eureka Creek	21	65.44012	143.57140	8/1/2009	15	15
Big Salt River	22	65.85433	149.90849	8/22/2009	30	30
Little Salt Creek	23	65.80754	150.07631	8/22/2009	30	30
Unnamed Creek # 53	24	65.79322	150.11218	8/23/2009	8	8
Isom Creek	25	65.75027	149.78691	8/25/2009	3	3
Twentymile Creek	26	65.64054	149.92165	8/26/2009	30	30
Sarah Creek	27	65.60250	150.18545	8/28/2009	4	4
Susie Creek	28	65.58228	150.17119	8/29/2009	1	1
				Total	137	137

Table 3. continued.

Stream	Map reference	Coordinates		Collection date	Field collected (n)	Genotyped (n)
		Lat (N)	Long (W)			
2010						
Russian Creek	29	65.47957	150.27302	8/4/2010	18	18
Sixmile Creek	30	65.48582	150.37627	8/4/2010	1	1
Roadhouse Creek	31	65.50059	150.55666	8/5/2010	2	2
Moose Creek	32	65.46625	150.68737	8/6/2010	2	2
Unnamed Creek # 83	33	65.43464	150.75744	8/7/2010	2	2
Unnamed Creek # 97	34	65.41210	150.89910	8/9/2010	2	2
Bear Creek	35	65.36561	151.00031	8/10/2010	28	28
Texas Creek	36	65.34478	150.99454	8/11/2010	25	25
Jordan Creek	37	65.29466	151.12137	8/19/2010	1	1
Cheyenne Creek	38	65.24680	151.23330	8/19/2010	2	2
Quartz Creek	39	65.26223	151.36369	8/20/2010	28	28
Schieffelin Creek	40	65.22890	151.44560	8/21/2010	30	30
Unnamed Creek # 99	41	65.18211	151.46074	8/22/2010	24	24
Spicer Creek	42	65.20162	151.71960	8/24/2010	30	29
Coal Creek	43	65.20742	151.77553	8/24/2010	12	12
Jackson Creek	44	65.20872	151.82990	8/25/2010	6	6
Mission Creek	45	65.19512	151.96862	8/26/2010	4	4
Total					217	216
Total (all years)					616	611

* Genetic samples from Mission Creek (near Eagle) were added to the 44 stream collections from the stream inventory study.

Table 4. Distances (km) from the confluence of each tributary to Yukon River mouth and U.S.–Canada border for streams with juvenile Chinook salmon genetic samples, 2008–2010.

Sampled stream	Km from mouth	Km from U.S.–Canada border
<i>U.S.–Canada Border</i>	1,970	0
Boundary Creek	1,969	1
Eagle Creek	1,959	11
<i>Eagle</i>	1,952	18
Mission Creek	1,951	19
American Creek (trib to Mission Creek)	1,953	20
Unnamed Creek #6	1,881	89
Michigan Creek	1,870	100
Fourth of July Creek	1,869	101
Schley Creek	1,867	103
Unnamed Creek #13	1,863	107
Butte Creek	1,860	110
Rock Creek	1,859	111
Logan Creek	1,858	112
Glenn Creek	1,853	117
Washington Creek	1,838	132
Unnamed Creek #19	1,834	136
Weshrinarin Creek	1,830	140
Unnamed Creek #21	1,819	151
Woodchopper Creek	1,786	184
Unknown Stream #25	1,783	187
Webber Creek	1,774	196
Eureka Creek	1,771	199
<i>Circle</i>	1,708	262
<i>Yukon River Bridge (Haul Road)</i>	1,320	650
Big Salt River	1,308	662
Little Salt Creek	1,298	672
Unnamed Creek #53	1,296	674
Isom Creek	1,279	691
Twentymile Creek	1,261	709
Sarah Creek	1,242	728
Susie Creek	1,239	731
<i>Rampart</i>	1,228	742
Russian Creek	1,222	748
Sixmile Creek	1,217	753
Roadhouse Creek	1,208	762
Moose Creek	1,200	770
Unnamed Creek #83	1,194	776
Unnamed Creek #97	1,187	783
Bear Creek	1,179	791
Texas Creek	1,177	793
Jordan Creek	1,170	800
Cheyenne Creek	1,162	808
Quartz Creek	1,157	813
Schieffelin Creek	1,152	818
Unnamed Creek # 99	1,147	823
Spicer Creek	1,134	836
Coal Creek	1,132	838
Jackson Creek	1,130	840
Mission Creek	1,123	847
<i>Tanana</i>	1,118	852

Table 5. Age-0 Chinook salmon stock composition estimates from genetic collections (2008, $n = 258$; 2009, $n = 137$; 2010, $n = 216$) with associated standard deviations (SD) and 95% confidence intervals (CI). Mean stock compositions, standard deviations, and 95% confidence intervals were estimated using cBAYES (Neaves et al. 2005).

Regional and country groups	Stock composition			
	Estimate	SD	95% CI	
2008				
Lower USA	0.001	0.002	0.000	0.007
Tanana	0.001	0.001	0.000	0.004
Upper USA	0.002	0.004	0.000	0.016
Lower Canada	0.007	0.007	0.000	0.024
Stewart	0.103	0.033	0.044	0.174
White	0.000	0.002	0.000	0.005
Pelly	0.058	0.019	0.025	0.101
Carmacks	0.815	0.039	0.735	0.885
Upper Canada	0.012	0.013	0.000	0.045
Teslin	0.001	0.002	0.000	0.007
USA	0.004	0.005	0.000	0.018
Canada	0.996	0.005	0.982	1.000
2009				
Lower USA	0.004	0.009	0.000	0.031
Tanana	0.001	0.002	0.000	0.007
Upper USA	0.031	0.018	0.006	0.072
Lower Canada	0.001	0.002	0.000	0.006
Stewart	0.009	0.021	0.000	0.076
White	0.000	0.001	0.000	0.002
Pelly	0.032	0.022	0.002	0.085
Carmacks	0.855	0.046	0.752	0.932
Upper Canada	0.066	0.032	0.010	0.137
Teslin	0.002	0.007	0.000	0.020
USA	0.036	0.020	0.007	0.082
Canada	0.964	0.020	0.918	0.993
2010				
Lower USA	0.001	0.003	0.000	0.011
Tanana	0.006	0.008	0.000	0.028
Upper USA	0.113	0.024	0.069	0.165
Lower Canada	0.012	0.011	0.000	0.037
Stewart	0.111	0.040	0.040	0.198
White	0.000	0.001	0.000	0.002
Pelly	0.037	0.026	0.000	0.097
Carmacks	0.709	0.048	0.612	0.798
Upper Canada	0.008	0.010	0.000	0.035
Teslin	0.001	0.005	0.000	0.017
USA	0.120	0.024	0.076	0.172
Canada	0.880	0.024	0.828	0.924

Table 6. Individual assignments of age-0 Chinook salmon stream samples from 2008 to region and country using cBAYES (Neaves et al. 2005). Individuals were assigned if their source probabilities were at least 95%. Differences in total individuals assigned between region and country result 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 upstream.

Regional and country groups	Absolute no.	Relative no.	Regional and country groups	Absolute no.	Relative no.
Boundary Creek			Butte Creek		
Pelly	1	0.059	Carmacks	7	1.000
Carmacks	16	0.941	Canada	13	1.000
Canada	29	1.000	Rock Creek		
Eagle Creek			Carmacks	3	1.000
Pelly	1	0.091	Canada	6	1.000
Carmacks	10	0.909	Logan Creek		
Canada	27	1.000	Carmacks	8	1.000
Mission Creek			Canada	11	1.000
Carmacks	11	1.000	Glenn Creek		
Canada	23	1.000	Stewart	1	0.077
American Creek			Carmacks	12	0.923
Pelly	2	0.077	Canada	16	1.000
Carmacks	24	0.923	Washington Creek		
Canada	47	1.000	Carmacks	1	1.000
Unnamed Creek # 6			Canada	1	1.000
Carmacks	7	1.000	Unnamed Creek # 19		
Canada	11	1.000	Carmacks	1	1.000
Michigan Creek			Canada	3	1.000
Carmacks	10	1.000	Weshrinarin Creek		
Canada	21	1.000	Carmacks	1	1.000
Fourth of July Creek			Canada	4	1.000
Carmacks	1	1.000	Unnamed Creek # 21		
Canada	4	1.000	Carmacks	4	1.000
Schley Creek			Canada	6	1.000
Carmacks	3	1.000			
Canada	5	1.000			
Unnamed Creek # 13					
Carmacks	15	1.000			
Canada	29	1.000			

Table 7. Individual assignments of age-0 Chinook salmon stream samples from 2009 to region and country using cBAYES (Neaves et al. 2005). Individuals were assigned if their source probabilities were at least 95%. Differences in total individuals assigned between region and country result 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 upstream.

Regional and country groups	Absolute no.	Relative no.	Regional and country groups	Absolute no.	Relative no.
Woodchopper Creek			Unnamed Creek # 53		
Canada	2	1.000	Pelly	1	0.167
Unnamed Creek # 25			Carmacks	5	0.833
Carmacks	2	1.000	Canada	8	1.000
Canada	3	1.000	Isom Creek		
Webber Creek			Carmacks	2	1.000
Carmacks	7	1.000	Canada	3	1.000
Canada	11	1.000	Twentymile Creek		
Eureka Creek			Upper USA	1	0.056
Carmacks	12	1.000	Carmacks	17	0.944
Canada	14	1.000	USA	1	0.033
Big Salt River			Canada	29	0.967
Carmacks	23	1.000	Sarah Creek		
Canada	28	1.000	Carmacks	2	1.000
Little Salt Creek			Canada	3	1.000
Upper USA	1	0.050	Susie Creek		
Carmacks	19	0.950	Carmacks	1	1.000
USA	1	0.037	Canada	1	1.000
Canada	26	0.963			

Table 8. Individual assignments of age-0 Chinook salmon stream samples from 2010 to region and country using cBAYES (Neaves et al. 2005). Individuals were assigned if their source probabilities were at least 95%. Differences in total individuals assigned between region and country result 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 upstream.

Regional and country groups	Absolute no.	Relative no.	Regional and country groups	Absolute no.	Relative no.
Russian Creek			Schieffelin Creek		
Carmacks	10	1.000	Upper USA	5	0.357
Canada	16	1.000	Carmacks	9	0.643
Sixmile Creek			USA	5	0.192
Upper USA	1	1.000	Canada	21	0.808
USA	1	1.000	Unnamed Creek # 99		
Roadhouse Creek			Upper USA	1	0.077
Canada	1	1.000	Carmacks	12	0.923
Moose Creek			USA	1	0.042
Upper USA	1	1.000	Canada	23	0.958
USA	1	0.500	Spicer Creek		
Canada	1	0.500	Upper USA	3	0.214
Unnamed Creek # 83			Carmacks	11	0.786
Canada	2	1.000	USA	3	0.111
Unnamed Creek # 97			Canada	24	0.889
Carmacks	1	1.000	Coal Creek		
Canada	2	1.000	Carmacks	5	1.000
Bear Creek			USA	1	0.091
Upper USA	2	0.200	Canada	10	0.909
Carmacks	8	0.800	Jackson Creek		
USA	2	0.080	Upper USA	1	0.500
Canada	23	0.920	Carmacks	1	0.500
Texas Creek			USA	1	0.200
Carmacks	13	1.000	Canada	4	0.800
Canada	24	1.000	Mission Creek		
Jordan Creek			Upper USA	1	0.500
Canada	1	1.000	Carmacks	1	0.500
Cheyenne Creek			USA	2	0.500
Canada	2	1.000	Canada	2	0.500
Quartz Creek					
Carmacks	13	1.000			
Canada	25	1.000			

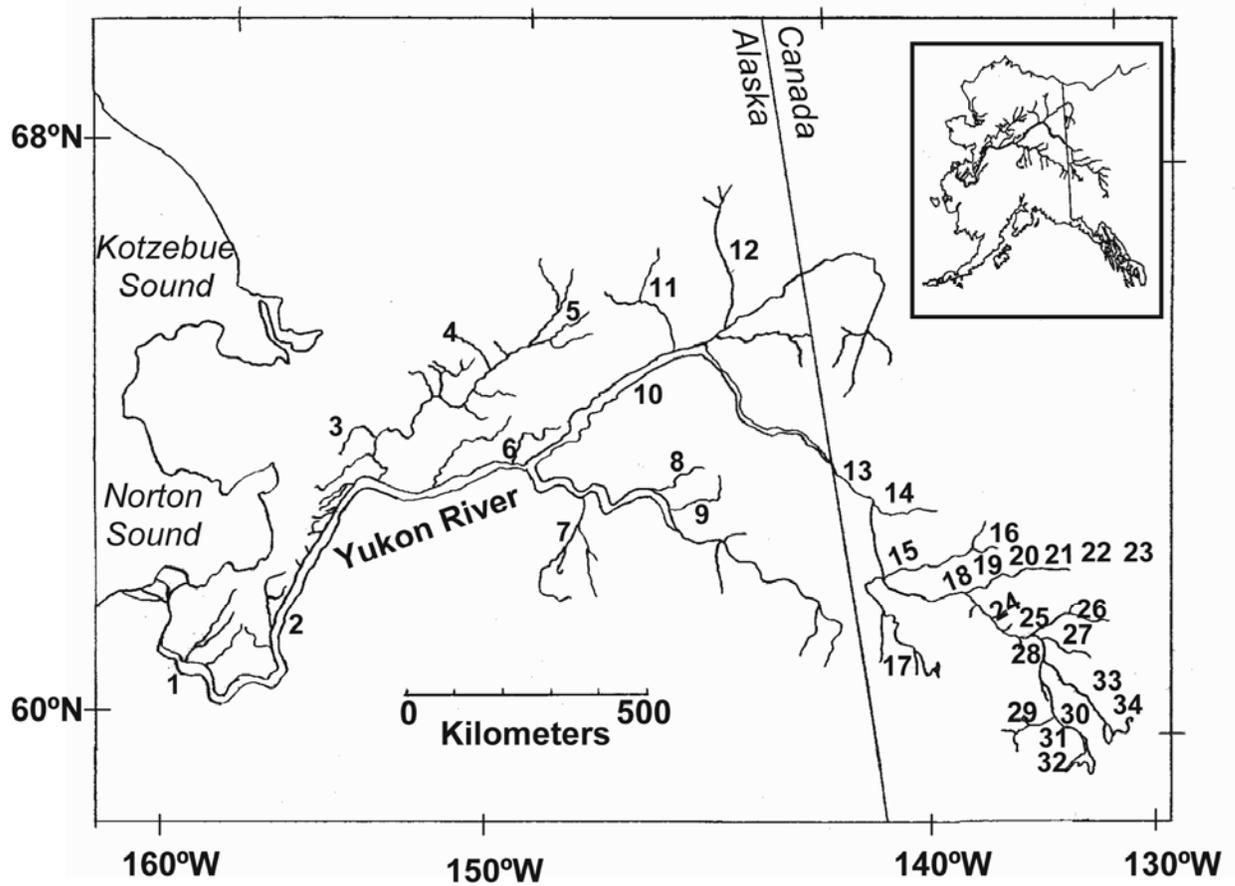


Figure 1. Locations of genetic baseline collections (described in Table 1) for 34 Yukon River Chinook salmon populations: 1=Andreafsky, 2=Anvik, 3=Gisasa, 4=Henshaw, 5=South Fork Koyukuk, 6=Tozitna, 7=Kantishna, 8=Chena, 9=Salcha, 10=Beaver, 11=Chandalar, 12=Sheenjek, 13=Chandindu, 14=Klondike, 15=Stewart, 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.

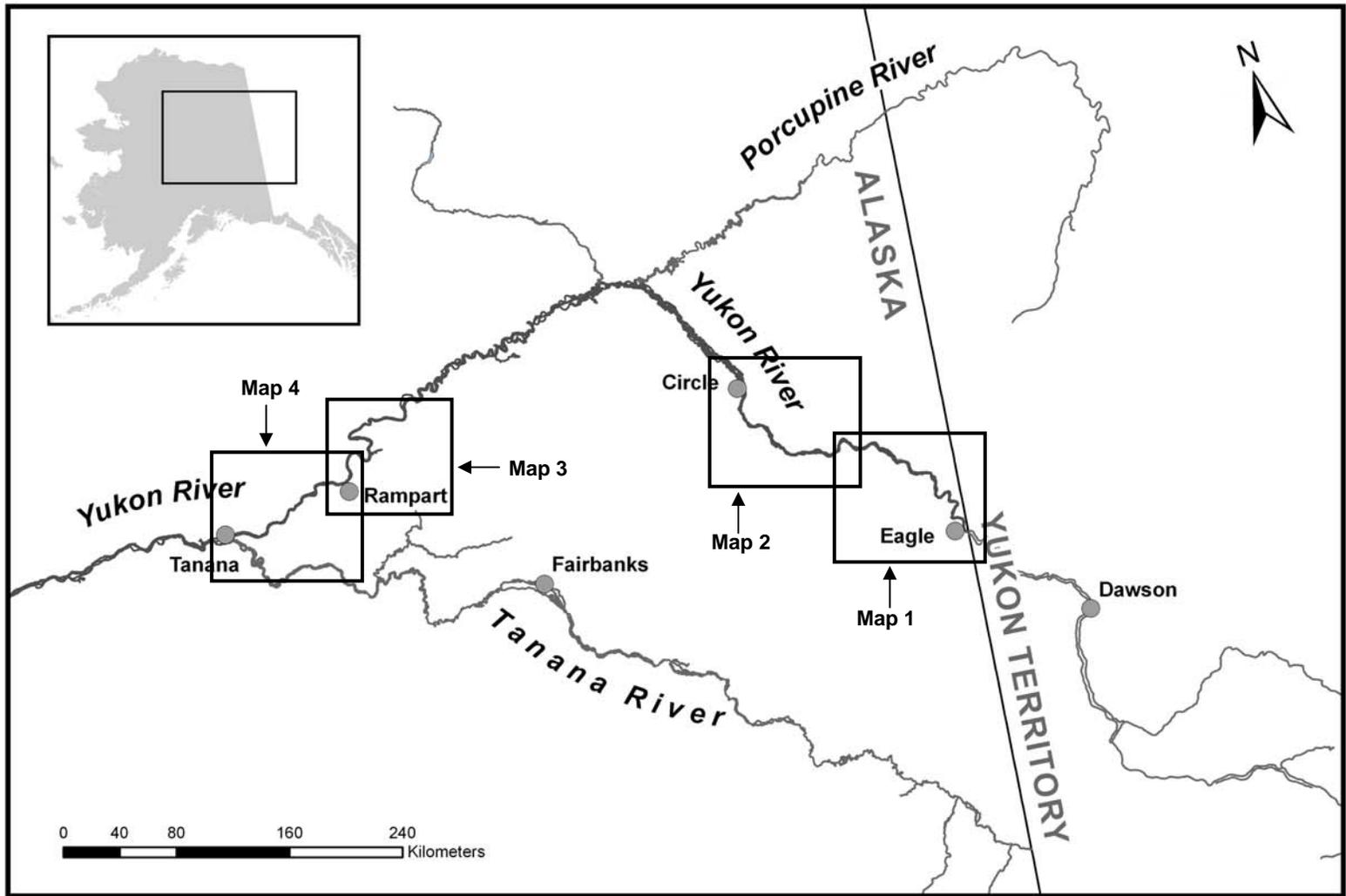


Figure 2. Generalized map of region with study areas represented by enclosed rectangles (Maps 1–4 presented in Figures 3-6).

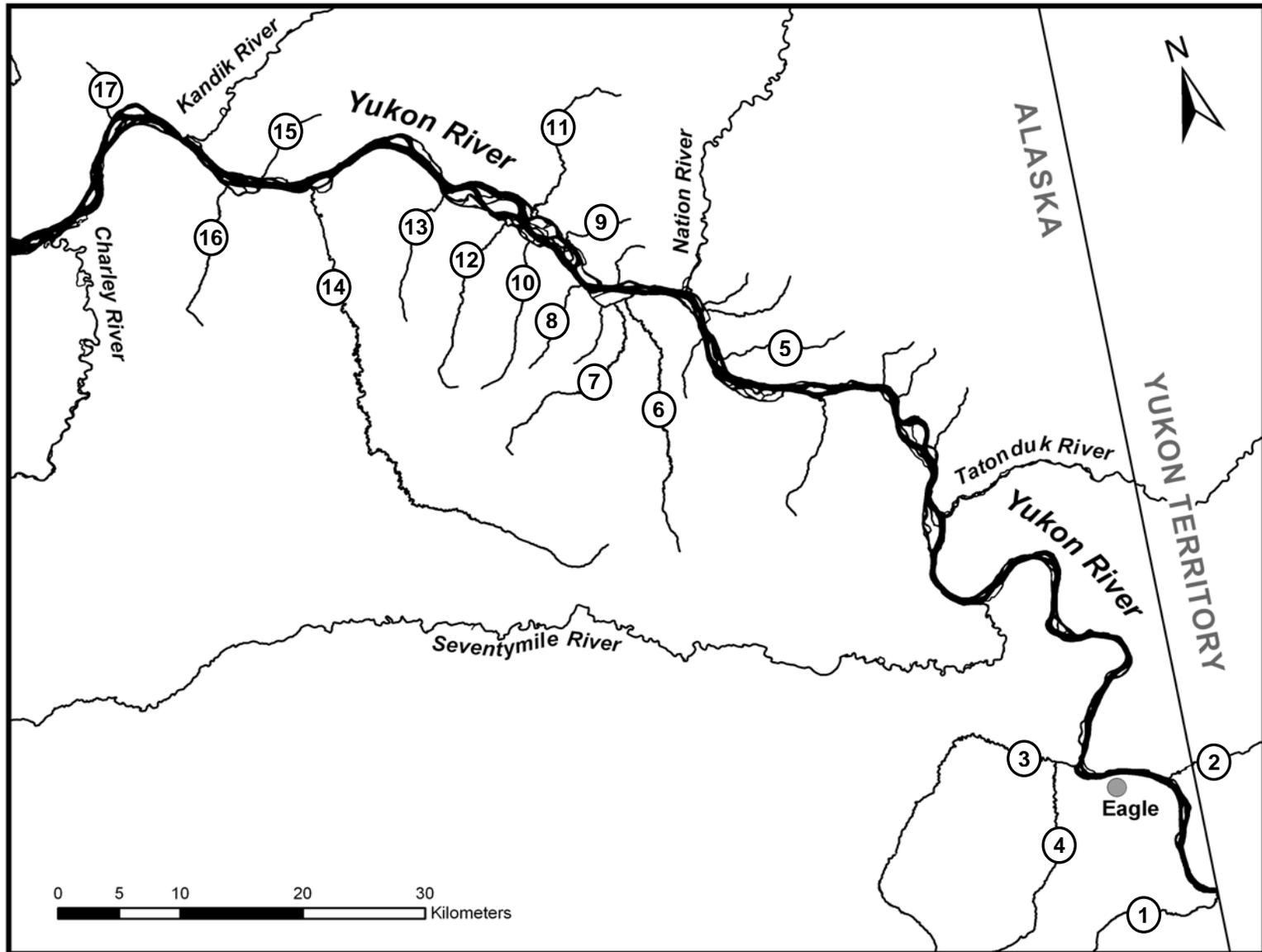


Figure 3. Map 1 (see Figure 2) representing streams with genetic collections in 2008. Table 3 cross-references stream name with map numbering.

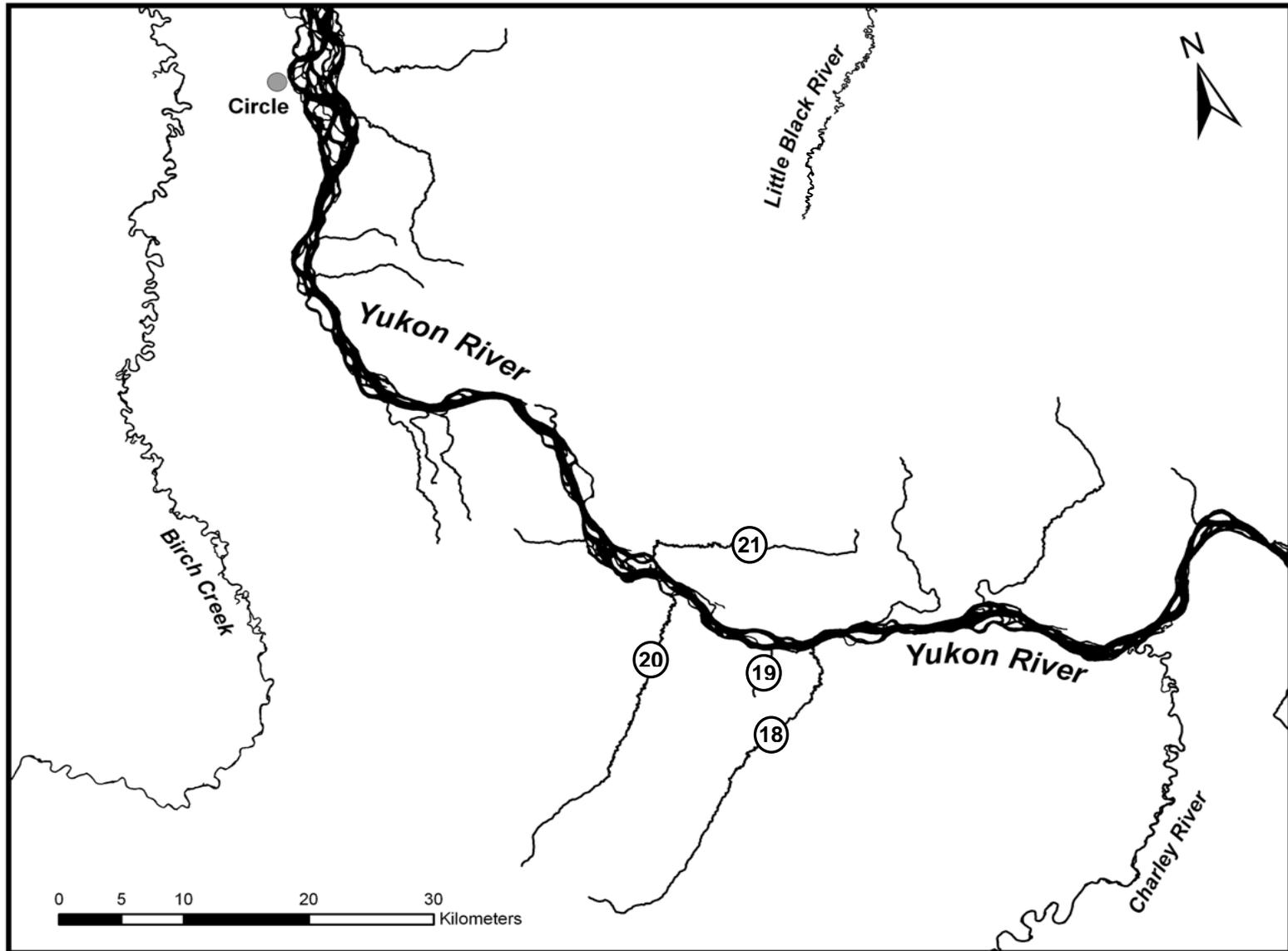


Figure 4. Map 2 (see Figure 2) representing streams with genetic collections in early period, 2009. Table 3 cross-references stream name with map numbering.

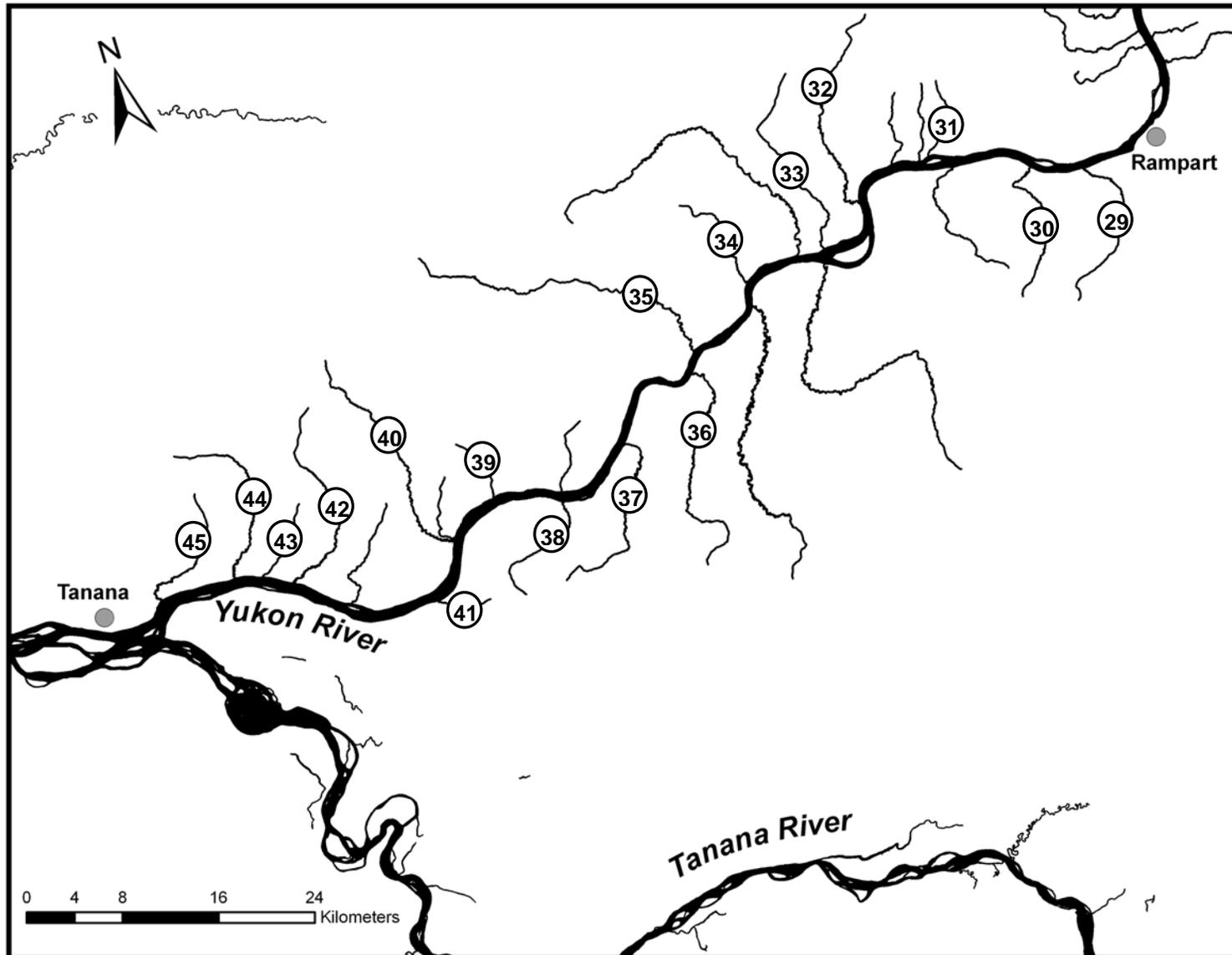


Figure 6. Map 4 (see Figure 2) representing streams with genetic collections in 2010. Table 3 cross-references stream name with map numbering.