

Stock Identification of Yukon River Chinook and Chum Salmon using Microsatellite DNA

Loci

Report to Yukon River Panel : Project CRE 79-08

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### **Abstract**

Stock identification of chum and Chinook salmon migrating past the DFO fish wheel program at Bio Island, as well as for Chinook salmon migrating past the Eagle sonar site near the Yukon-Alaska border, was conducted in 2008 through analysis of microsatellite variation. Variation at 14 microsatellite loci was surveyed for 735 chum salmon from the fish wheels and 758 Chinook salmon collected from the fish wheels and sonar site. The seasonal sample for chum salmon species was structured so that migrating salmon were sampled in proportion to run abundance on a weekly basis. For Chinook salmon, all fish sampled at the Eagle sonar site were analyzed, and fish sampled from three weekly intervals at the fish wheels were analyzed.

The analysis of chum salmon samples indicated that spawning populations from the White River drainage were estimated to comprise 50% of the fish migrating past the Bio Island fish wheels, while 48% were estimated to have been from mainstem Yukon River chum salmon spawning populations.

The analysis of Chinook salmon migrating past the Eagle sonar site indicated that the major regional stocks contributing to the run were the mainstem spawning stock (32%), Pelly River (21%), Carmacks area tributaries (Big Salmon River, Little Salmon River, Tatchun Creek) (15%), Teslin River (13%), Stewart River (8%), lower Yukon mainstem tributaries (Chandindu River, Klondike River) (9%), and upper Yukon tributaries (1%). Different stock compositions were observed for Chinook salmon sampled at the fish wheels, and the major regional stocks were estimated as Pelly River (24%), Carmacks area tributaries (20%), Teslin River (15%), lower Yukon mainstem tributaries (15%), Stewart (13%), and the mainstem spawning stock (12%).

## **Introduction**

Chum salmon (*Oncorhynchus keta*) and Chinook salmon (*O. tshawytscha*) are widely distributed throughout the Yukon River drainage, spawning in tributaries ranging from the extreme headwaters (e.g. Teslin River, British Columbia) to near the mouth of the river (e.g. Andreafsky River, Alaska). Management for conservation of biodiversity within the drainage requires knowledge of genetic variation among populations as well as population-specific information from fisheries. Effective management of fisheries in major drainages like the Yukon River generally requires information on the harvest and timing of specific populations, should managers wish to change exploitation rates on specific populations for conservation purposes. For example, the Canada/U.S. Yukon River Salmon Agreement has established escapement targets and harvest sharing provisions for Canadian-origin salmon stocks. It is therefore important to develop a management system that allows managers to accurately assess the status of these stocks in fisheries throughout the drainage during the season so that management decisions can ensure that Treaty obligations are achieved. Accurate post-season run reconstructions are essential in evaluating whether management actions were consistent with meeting overall objectives and Treaty obligations. Run reconstructions are also important in monitoring the productivity of stocks and assessing the adequacy of current escapement targets and both pre-season forecasting and in-season run assessment techniques. Without this knowledge, managing to achieve Treaty obligations is difficult and severely limits the assessment of factors influencing stock productivity, which appear to have fluctuated widely in recent years.

Stock identification of chum and Chinook salmon migrating through the mainstem Yukon River is a continuing management concern. Although allozyme-based methods of stock identification have proven useful in the estimation of chum salmon stock composition in mixed-

stock fisheries (Shaklee et al. 1999), and differentiation at allozyme loci occurs among Yukon River chum salmon (Beacham et al. 1988; Wilmot et al. 1992), the level of population discrimination available in the Yukon River is not yet sufficient for population-specific applications. Variation in microsatellite loci has been applied in other species requiring discrimination among salmonid populations within watersheds (Small et al. 1998; Beacham and Wood 1999; Beacham et al. 2001), and has been shown to be useful in stock discrimination in Chinook salmon (Banks et al. 2000). Variation at microsatellite loci has been particularly useful for population-specific estimates of stock composition of Fraser River Chinook salmon (Beacham et al. 2003).

In 2008, we surveyed variation at 14 microsatellite loci for chum salmon and 12 microsatellite loci for Chinook salmon. Samples were obtained from salmon live-captured at the Bio Island fish wheels in the lower portion of the Yukon River in Canada or at the Eagle sonar site in Alaska near the border. We used microsatellite variation to estimate stock composition in the samples collected.

## **Materials and Methods**

### **Collection of DNA Samples and Laboratory Analysis**

Tissue samples were collected from adult chum salmon migrating past the Bio Island fishwheels in the lower Yukon River between August 8 and October 8, 2008. Samples were weighted according to stratified abundance estimates as determined from the mark-recapture program, with a target sample size of 750 fish to be analyzed. Adipose punches were taken from sampled fish and DNA was extracted as described by Withler et al. (2000). Samples from all Chinook salmon (453) sampled at the Eagle sonar site between July 6 and August 16, 2008

were analyzed, as well as 305 fish sampled at the fish wheels between July 20 and August 9, 2008.

Once chum salmon genomic DNA was available, surveys of variation at the following 14 microsatellite loci were conducted: *Ots3* (Banks et al. 1999), *Oke3* (Buchholz et al. 2001), *Oki2* (Smith et al. 1998), *Oki100* (Miller et al. unpub), *Ots103* (Nelson and Beacham 1999), *Omm1070* (Rexroad et al. 2001), *Omy 1011* (Spies et al. 2005), *One101*, *One102*, *One104*, *One111*, and *One114* (Olsen et al. 2000), *Ssa419* (Cairney et al. 2000), and *OtsG68* (Williamson et al. 2002). Microsatellites were size fractionated in an Applied Biosystems (ABI) 3730 capillary DNA sequencer, and genotypes were scored by GeneMapper software 3.0 (Applied Biosystems, Foster City, CA) using an internal lane sizing standard.

For Chinook salmon, the following 12 microsatellite loci were surveyed for genetic variation: *Ots100*, *Ots101*, *Ots104*, *Ots107* (Nelson and Beacham 1999) and *Ssa197* (O'Reilly et al. 1996), *Ogo2*, *Ogo4* (Olsen et al., 1998), *Oke4* (Buchholz et al., 2001), *Omy325* (O'Connell et al, 1997), *Oki100* (K. M. Miller, unpublished data), and *Ots2*, *Ots9* (Banks et al. 1999). Microsatellites were size fractionated in an ABI 3730 capillary DNA sequencer, and genotypes were scored by GeneMapper software 3.0 (Applied Biosystems, Foster City, CA) using an internal lane sizing standard.

In general, polymerase chain (PCR) reactions were conducted in 10 µl volumes consisting of 0.06 units of Taq polymerase, 1µl of 30ng DNA, 1.5-2.5mM MgCl<sub>2</sub>, 1mM 10x buffer, 0.8mM dNTP's, 0.006-0.065µM of labeled forward primer (depending on the locus), 0.4µM unlabeled forward primer, 0.4µM unlabeled reverse primer, and deionized H<sub>2</sub>O. PCR was completed on an MJResearch™ DNA Engine™ PCT-200 or a DNA Engine Tetrad™ PCT-225. The amplification profile involved one cycle of 2 min @ 92°C, 30 cycles of 15 sec @ 92°C, 15 sec @ 52-60°C (depending on the locus) and 30 sec @ 72°C, and a final extension for 10 min @ 72°C. Specific PCR conditions for a particular locus could vary from this general outline.

### Baseline Populations

The baseline survey consisted of microsatellite analysis of chum salmon from 9 locations and microsatellite analysis of Chinook salmon from 21 locations within the Canadian portion of the drainage (Table 1). All annual samples available for a specific sample location were combined to estimate population allele frequencies, as was recommended by Waples (1990).

### Estimation of Stock Composition

Analysis of fishery samples was conducted with a Bayesian procedure (BAYES) as outlined by Pella and Masuda (2001). Each locus was assumed to be in Hardy-Weinberg equilibrium, and expected genotypic frequencies were determined from the observed allele frequencies and used as model inputs. For BAYES, the initial FORTRAN-based computer program as outlined by Pella and Masuda (2001) required large amounts of computer analytical time when applied to stock identification problems with a baseline as comprehensive as employed in the current study. Given this limitation, a new version of the program was developed by our laboratory as a C-based program which is available from the Molecular Genetics Laboratory website ([http://www-sci.pac.dfo-mpo.gc.ca/mgl/data\\_e.htm](http://www-sci.pac.dfo-mpo.gc.ca/mgl/data_e.htm)). In the analysis, ten 20,000-iteration Monte Carlo Markov chains of estimated stock compositions were produced, with initial starting values for each chain set at 0.90 for a particular population which was different for each chain. Estimated stock compositions were considered to have converged when the shrink factor was  $< 1.2$  for the 10 chains (Pella and Masuda 2001). The last 1,000 iterations from each of the 10 chains were then combined, and for each fish the probability of originating from each population in the baseline was determined. These individual probabilities were summed over all fish in the sample, and divided by the number of fish sampled to provide

the point estimate of stock composition. Standard deviations of estimated stock compositions were determined from the last 1,000 iterations from each of the 10 chains incorporated in the analysis.

## **Results and Discussion**

### **Chum Salmon**

On a seasonal basis, chum salmon spawning populations from the White River drainage accounted for 50% of the run, whereas, mainstem spawning Yukon River populations were estimated to comprise 48% of the chum salmon migrating past the Bio Island fish wheels (Table 2). Teslin River chum salmon contributed about 2% to the total run. Less than 1% of the chum salmon sampled were estimated to be from early-returning populations such as the Chandindu River. Mainstem spawning and White River populations were present throughout the sampling period. Teslin River chum salmon were most prevalent during September 16-28 in the migration past the fish wheel sampling site.

### **Chinook Salmon**

Based upon sampling at the Eagle sonar site, populations which tended to migrate earlier in the run included those from the Chandindu River, Pelly River, and Klondike River. Chinook salmon from the Pelly River drainage accounted for about 21% of total 2008 run past the sonar site, those from the Klondike River accounted for 6% of the run, and those from the Chandindu River about 3% of the run (Table 3). The main populations migrating past the sonar site in August were the mainstem spawning population and the Teslin River population, with each population accounting for 30% and 10% respectively of the total return.

Chinook salmon sampled at the fish wheels at Bio Island were analyzed for three weekly periods between July 20<sup>th</sup> and August 9<sup>th</sup>, with the objective of comparing stock compositions in each of the three weeks with those observed at the Eagle sonar site. As both sites are located



physically close to each other, and presumably within one day's migration for returning Chinook salmon, it is possible to compare stock compositions estimated for the same time interval between the two sites. During the first interval (July 20-26), Teslin River Chinook salmon were estimated at 35% of the run past the sonar site, but only 2% of the run past the fish wheels (Table 4). Pelly River Chinook salmon were estimated at 28% of the run past the sonar site, and 34% of the run past the fish wheels. Lower river tributaries were estimated at 4% of the run past the sonar site, but 24% of the run past the fish wheels. Different estimates of stock composition were again observed during the second week of comparison, and again during the third week of comparison. For, example, during the third week (August 3-9), mainstem spawning Chinook salmon were estimated to comprise 66% of the fish sampled at the sonar site, but only 30% of the fish sampled at the fish wheels (Table 4). Differences in stock composition between the sonar site and fish wheel site may reflect differences in gear (gillnet, fish wheel), and differences in population orientation with respect to river bank. The fish wheels sample individuals migrating close to the river bank, whereas the gillnet test fishery at the sonar site would sample individuals migrating further from shore.

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Pat Milligan of the Department of Fisheries and Oceans in Whitehorse provided suggestions for improvements to the report. Financial support for the project was provided by the Yukon River Restoration and Enhancement Fund as well as the Department of Fisheries and Oceans.

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Table 1. Baseline used to estimate stock compositions of chum and Chinook salmon from the fish wheel tagging program at Bio Island or Eagle sonar site 2008.

Region	Populations
Chum salmon	
Mainstem Yukon River	Mainstem Yukon at Pelly River, Tatchun Creek, Big Creek and Minto
White River	Kluane River, Kluane Lake, Donjek River
Teslin River	Teslin River
Yukon early	Chandindu River
Chinook salmon	
Upper Yukon tributaries	Wolf Creek/Michie Creek/Whitehorse hatchery, Takhini River
Teslin River	Morley River, Nisutlin River, Teslin River, Teslin Lake
Carmacks Area tributaries	Little Salmon, Big Salmon, Tatchun Creek
Mid-mainstem/Nordenskiold	Mainstem Yukon River, Nordenskiold River
Pelly River	Little Kalzas River, Blind Creek, Earn River, Glenlyon, Pelly River
Stewart River	Mayo River, Stewart River
North Yukon mainstem tributaries	Chandindu River, Klondike River
White River	Tincup Creek

Table 2. Estimated percentage stock composition of chum salmon migrating past the fish wheel tagging program at Bio Island, 2008. Stock compositions were estimated using 14 microsatellite loci and the baseline outlined in Table 1. Standard error of the estimated stock composition is in parentheses.

	August 8-17		August 18-24		August 25-31		September 1-7		September 8-15		September 16-21	
Sample size	1		8		8		55		201		125	
Populations	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE
Tatchun	0.0	(13.3)	2.4	(8.2)	14.7	(17.3)	15.1	(7.8)	9.0	(3.9)	10.7	(5.0)
Pelly	0.1	(13.2)	0.3	(4.2)	1.2	(6.2)	0.4	(1.4)	0.3	(0.9)	0.5	(1.5)
Big Creek	0.3	(13.6)	18.1	(15.9)	13.2	(17.0)	10.1	(7.5)	20.9	(4.4)	34.8	(6.6)
Minto	0.3	(13.5)	0.3	(4.1)	4.4	(9.7)	4.4	(4.3)	7.4	(3.3)	1.1	(2.6)
Kluane	0.0	(13.2)	3.1	(8.3)	2.0	(7.9)	5.7	(5.8)	6.1	(3.7)	1.2	(2.2)
Kluane Lake	0.0	(13.2)	56.4	(25.5)	19.1	(17.5)	38.3	(9.8)	31.5	(6.5)	35.9	(6.5)
Donjek	0.0	(13.3)	14.4	(23.1)	31.6	(17.6)	25.8	(8.6)	22.6	(6.0)	11.4	(5.5)
Teslin	0.0	(13.3)	4.2	(9.8)	0.0	(3.5)	0.1	(0.8)	2.0	(1.2)	4.3	(2.9)
Chandindu	99.3	(28.6)	0.7	(4.9)	13.8	(15.7)	0.0	(0.6)	0.2	(0.6)	0.1	(0.4)
Regions												
Mainstem	0.7	(24.2)	21.2	(16.3)	33.5	(20.7)	30.1	(6.6)	37.7	(3.7)	47.2	(5.2)
White	0.0	(21.5)	73.9	(15.6)	52.7	(17.6)	69.9	(6.6)	60.1	(3.7)	48.4	(4.7)
Teslin	0.0	(13.3)	4.2	(9.8)	0.0	(3.5)	0.1	(0.8)	2.0	(1.2)	4.3	(2.9)
Yukon summer	99.3	(28.6)	0.7	(4.9)	13.8	(15.7)	0.0	(0.6)	0.2	(0.6)	0.1	(0.4)

  

	September 22-28		Sept. 29-October 8		Seasonal	
Sample size	163		184		745	
Stock	Estimate	SE	Estimate	SE	Estimate	SE
Tatchun	11.0	(5.4)	3.3	(3.8)	6.8	(2.6)
Pelly	1.4	(2.1)	5.7	(3.0)	1.1	(1.5)
Big Creek	25.9	(6.9)	37.3	(5.5)	39.4	(3.9)
Minto	14.6	(5.0)	10.6	(4.8)	0.6	(1.7)
Kluane	12.6	(5.6)	4.9	(5.0)	0.2	(0.4)
Kluane Lake	29.6	(6.6)	23.9	(7.3)	43.6	(4.2)

Donjek	2.5	(3.7)	12.7	(5.1)	6.1	(4.0)
Teslin	2.4	(2.0)	1.4	(1.6)	2.1	(0.8)
Chandindu	0.1	(0.4)	0.0	(0.3)	0.1	(0.2)
Regions						
Mainstem	52.8	(4.5)	57.1	(4.2)	48.0	(2.0)
White	44.7	(4.1)	41.5	(3.9)	49.9	(1.9)
Teslin	2.4	(2.0)	1.4	(1.6)	2.1	(0.8)
Yukon summer	0.1	(0.4)	0.0	(0.3)	0.1	(0.2)

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Table 3. Estimated percentage stock composition of Chinook salmon migrating past the Eagle sonar site in 2008. Stock compositions were estimated using 12 microsatellite loci and the baseline outlined in Table 1. Standard error of the estimates is in parentheses.

Sample size Populations	July 6-12 14		July 13-19 103		July 20-26 81		July 27-Aug2 137		Aug3-9 93		Aug 10-16 25		Seasonal 453	
	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE
Takhini_	0.0	(1.6)	0.0	(0.2)	0.0	(0.4)	2.9	(2.2)	3.3	(3.7)	0.3	(2.0)	1.0	(0.9)
WhiteWolfMichie	0.0	(1.7)	0.0	(0.2)	0.0	(0.4)	0.1	(0.5)	0.1	(0.5)	0.0	(0.9)	0.0	(0.2)
Morley	0.0	(1.6)	0.1	(0.7)	0.7	(1.9)	0.1	(0.6)	0.1	(0.5)	0.7	(2.8)	0.0	(0.2)
Nisutlin	0.1	(1.9)	0.1	(0.5)	0.1	(0.6)	2.1	(3.0)	0.3	(1.1)	0.2	(1.6)	0.2	(0.6)
Teslin_Lake	0.0	(1.0)	1.5	(2.1)	3.7	(3.6)	2.6	(2.5)	0.1	(0.5)	1.7	(4.8)	2.9	(1.2)
Teslin	0.3	(2.5)	1.6	(2.3)	30.0	(6.7)	14.5	(5.5)	17.0	(7.0)	34.0	(16.1)	10.2	(2.5)
Big_Salmon	1.8	(6.4)	0.7	(2.0)	12.8	(6.4)	2.3	(4.3)	0.2	(1.0)	11.4	(13.4)	1.1	(1.9)
L._Salmon	30.6	(15.0)	10.8	(6.6)	2.3	(4.4)	22.4	(10.0)	1.0	(2.7)	0.4	(2.2)	11.3	(3.9)
Tatchun_	0.9	(4.0)	0.7	(1.5)	0.0	(0.4)	7.1	(4.1)	1.7	(3.6)	1.1	(3.5)	2.7	(2.0)
Nordenskiold	0.0	(1.1)	1.3	(1.6)	5.9	(2.9)	0.2	(0.7)	0.0	(0.4)	0.0	(0.8)	1.9	(0.9)
Yukon_main	0.3	(1.9)	3.2	(3.6)	1.7	(3.6)	22.9	(9.4)	66.3	(9.3)	35.4	(20.5)	30.4	(4.1)
Blind_Cr_	3.5	(6.3)	4.8	(3.9)	0.5	(1.5)	0.2	(0.8)	0.4	(1.2)	5.0	(5.5)	1.0	(1.2)
Earn_River	0.2	(2.5)	0.7	(2.8)	0.5	(1.7)	2.1	(3.2)	0.1	(0.6)	0.9	(3.3)	0.2	(0.7)
Glenlyon	0.1	(1.3)	0.4	(1.2)	2.3	(4.0)	0.6	(1.4)	0.0	(0.3)	2.3	(4.6)	2.3	(1.5)
Little_Kalzas	0.4	(2.7)	6.8	(7.0)	0.2	(0.9)	0.1	(0.6)	0.1	(0.9)	0.6	(2.2)	0.1	(0.4)
Pelly	3.6	(8.0)	23.5	(8.4)	24.2	(7.6)	14.8	(5.2)	0.3	(1.2)	0.8	(3.0)	17.1	(3.0)
Mayo	2.5	(6.5)	5.0	(7.1)	1.3	(3.1)	0.3	(1.1)	0.5	(1.8)	1.0	(3.8)	0.5	(1.1)
Stewart	5.8	(8.5)	10.5	(7.4)	9.6	(6.4)	1.4	(2.7)	7.7	(4.9)	0.2	(1.7)	7.3	(2.3)
Chandindu	47.6	(15.0)	9.4	(6.5)	0.6	(1.4)	0.7	(1.2)	0.4	(0.9)	0.7	(2.4)	3.3	(1.9)
Klondike	1.9	(8.5)	18.3	(7.3)	3.1	(2.6)	1.6	(1.6)	0.2	(0.7)	3.3	(4.0)	5.7	(2.2)
Tincup	0.5	(2.8)	0.5	(1.5)	0.5	(1.6)	0.7	(1.6)	0.2	(0.8)	0.0	(0.9)	0.5	(0.9)
Regions														
Yukon upper	0.0	(2.4)	0.0	(0.3)	0.1	(0.5)	3.0	(2.2)	3.4	(3.7)	0.4	(2.2)	1.1	(0.9)
Yukon Teslin	0.4	(3.7)	3.3	(3.1)	34.6	(7.4)	19.4	(6.2)	17.4	(7.1)	36.7	(16.1)	13.4	(2.7)
Yukon Carmacks	33.3	(13.7)	12.2	(6.6)	15.1	(7.0)	31.9	(8.9)	2.9	(4.5)	12.8	(13.7)	15.1	(3.7)



Yukon mainstem	0.3	(2.2)	4.5	(3.9)	7.6	(4.6)	23.1	(9.4)	66.4	(9.3)	35.4	(20.5)	32.3	(4.2)
Yukon Pelly	7.7	(10.3)	36.2	(7.1)	27.6	(7.2)	17.9	(4.9)	0.9	(2.0)	9.5	(7.2)	20.7	(3.0)
Yukon Stewart	8.2	(9.5)	15.5	(6.8)	10.9	(6.1)	1.7	(2.9)	8.1	(4.7)	1.2	(4.1)	7.8	(2.3)
Yukon Lower	49.6	(13.5)	27.7	(4.9)	3.7	(2.5)	2.2	(1.5)	0.7	(1.0)	4.0	(4.2)	9.1	(1.5)
Yukon White	0.5	(2.8)	0.5	(1.5)	0.5	(1.6)	0.7	(1.6)	0.2	(0.8)	0.0	(0.9)	0.5	(0.9)

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Table 4. Estimated percentage stock composition of Chinook salmon migrating past the Bio Island fish wheel site in 2008. Stock compositions were estimated using 12 microsatellite loci and the baseline outlined in Table 1. Standard deviations of the estimates are in parentheses.

Sample size Populations	July 20-26 99		July 27-Aug2 138		Aug 3- 9 68		Seasonal 305	
	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD
Takhini_	0.0	(0.2)	0.0	(0.2)	0.0	(0.4)	0.0	(0.1)
WhiteWolfMichie	0.0	(0.3)	0.0	(0.2)	0.0	(0.3)	0.0	(0.1)
Morley	0.1	(0.6)	0.1	(0.4)	0.3	(1.3)	0.0	(0.2)
Nisutlin	0.4	(1.3)	8.6	(3.2)	1.0	(2.4)	4.1	(2.5)
Teslin_Lake	0.7	(1.8)	0.5	(1.3)	9.4	(6.3)	2.5	(2.6)
Teslin	0.9	(2.6)	0.3	(1.1)	20.2	(7.9)	8.1	(3.4)
Big_Salmon	24.4	(6.8)	5.4	(5.3)	5.9	(7.6)	9.3	(6.0)
L_Salmon	0.1	(0.7)	30.7	(6.6)	1.0	(3.2)	11.0	(14.3)
Tatchun_	0.1	(0.5)	0.1	(0.6)	1.0	(2.6)	0.1	(0.4)
Nordenskiold	0.1	(0.4)	2.6	(1.9)	0.1	(0.6)	0.9	(0.9)
Yukon_main	0.1	(0.6)	4.5	(4.6)	29.8	(8.4)	10.6	(8.0)
Blind_Cr_	0.2	(0.8)	4.6	(2.7)	0.2	(1.0)	1.5	(1.3)
Earn_River	2.5	(5.4)	3.0	(2.6)	0.9	(2.4)	3.4	(3.1)
Glenlyon	0.1	(0.5)	0.0	(0.3)	0.1	(0.6)	0.0	(0.1)
Little_Kalzas	0.4	(1.2)	0.1	(0.5)	0.0	(0.5)	0.2	(0.7)
Pelly	30.3	(8.1)	13.1	(5.8)	3.4	(4.9)	18.8	(4.5)
Mayo	3.2	(4.4)	9.1	(5.2)	11.9	(10.4)	8.0	(3.4)
Stewart	12.9	(7.1)	0.5	(1.7)	12.2	(10.8)	5.2	(3.7)
Chandindu	17.2	(6.9)	11.7	(3.8)	0.1	(0.7)	8.4	(2.8)
Klondike	6.3	(6.5)	1.7	(3.0)	1.5	(2.2)	6.2	(3.0)
Tincup	0.1	(0.6)	3.4	(2.8)	1.0	(1.9)	1.7	(1.6)
Regions								
Yukon upper	0.0	(0.4)	0.0	(0.3)	0.0	(0.5)	0.0	(0.2)
Yukon Teslin	2.0	(3.3)	9.5	(3.2)	30.9	(8.9)	14.7	(3.8)
Yukon Carmacks	24.6	(6.8)	36.1	(6.8)	7.9	(8.3)	20.4	(10.4)
Yukon mainstem	0.1	(0.7)	7.1	(5.0)	29.9	(8.4)	11.6	(8.1)
Yukon Pelly	33.5	(6.6)	20.8	(5.7)	4.6	(5.2)	23.9	(4.4)

Yukon Stewart	16.1	(6.3)	9.6	(5.2)	24.1	(9.3)	13.1	(3.7)
Yukon Lower	23.5	(4.6)	13.4	(3.1)	1.6	(2.2)	14.6	(2.3)
Yukon White	0.1	(0.6)	3.4	(2.8)	1.0	(1.9)	1.7	(1.6)

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