

# **Stock Identification of Yukon River Chinook and Chum Salmon using Microsatellites**

Report to Yukon River Panel : Project CRE 79-13

Terry D. Beacham and John Candy

Pacific Biological Station  
Department of Fisheries and Oceans  
3190 Hammond Bay Road  
Nanaimo, B. C.  
V9T 6N7

Phone: 250 756-7149

Fax: 756-7053

Email: [Terry.Beacham@dfo-mpo.gc.ca](mailto:Terry.Beacham@dfo-mpo.gc.ca)

## **Abstract**

Stock identification of chum and Chinook salmon migrating past the Eagle, Alaska sonar site near the Yukon-Alaska border was conducted in 2013 through analysis of microsatellite variation. Variation at 14 microsatellites was surveyed for 891 chum salmon and variation at 15 microsatellites was surveyed for 294 Chinook salmon collected from the sonar site. For chum and Chinook salmon, all fish sampled at the Eagle sonar site were analyzed.

The analysis of chum salmon samples indicated that spawning populations from the White River drainage were estimated to comprise 49% of the fish sampled that migrated past the sonar site, while approximately 51% were estimated to have been from mainstem Yukon River chum salmon spawning populations. The analysis of Chinook salmon migrating past the Eagle sonar site that were sampled indicated that the major regional stocks contributing to the run were the mainstem Yukon River (29%), Teslin River (26%), Carmacks area tributaries (18%), Pelly River (11%), upper Yukon tributaries (7%), Stewart River (5%), White River (3%), and lower Yukon tributaries (1%).

## **Acknowledgments**

Financial support for the project was provided by the Yukon River Restoration and Enhancement Fund as well as the Department of Fisheries and Oceans.

## TABLE OF CONTENTS

<b>ABSTRACT</b>	<b>II</b>
<b>ACKNOWLEDGMENTS</b>	<b>III</b>
<b>INTRODUCTION</b>	<b>1</b>
<b>MATERIALS AND METHODS</b>	<b>3</b>
<b>RESULTS AND DISCUSSION</b>	<b>6</b>
<b>1.0 CHUM SALMON</b>	<b>6</b>
<b>2.0 CHINOOK SALMON</b>	<b>6</b>
<b>LITERATURE CITED</b>	<b>7</b>

## LIST OF TABLES

Table 1. Baseline used to estimate stock compositions of chum and Chinook salmon from the Eagle sonar site 2013.	11
Table 2. Estimated percentage stock composition of chum salmon migrating past the Eagle sonar site, 2013. 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.	12
Table 3. Estimated percentage stock composition of Chinook salmon migrating past the Eagle sonar site in 2013. Stock compositions were estimated using 15 microsatellite loci and the baseline outlined in Table 1. Standard errors of the estimates are in parentheses.	14

## 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 assess accurately 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 was not 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) and Yukon River Chinook salmon (Beacham et al. 2008a). Microsatellites have also been useful for chum salmon stock identification on a Pacific-Rim basis (Beacham et al. 2009).

In 2013, we surveyed variation at 14 microsatellite loci for chum salmon and 15 microsatellite loci for Chinook salmon. Samples were obtained from salmon live-captured in the test fishery associated with the sonar program near Eagle, Alaska. 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 Eagle sonar site between August 1, 2013 and September 30, 2013. All chum salmon caught during this period were sampled. Axial processes were taken from sampled fish and DNA was extracted as described by Withler et al. (2000). Samples from all Chinook salmon sampled at the Eagle sonar site from July 15, 2013 to August 28, 2013 were analyzed.

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* (Beacham et al. 2008b), *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 15 microsatellite loci were surveyed for genetic variation: *Ots100*, *Ots101*, *Ots104*, *Ots107* (Nelson and Beacham 1999), *Ssa197* (O'Reilly et al. 1996), *Ogo2*, *Ogo4* (Olsen et al., 1998), *Oke4* (Buchholz et al., 2001), *Omy325* (O'Connell et al, 1997), *Oki100* (Beacham et al. 2008b), *Omm1080* (Rexroad et al. 2001), *Ots201b*, *Ots211* (Grieg 2003), 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),

0.4 $\mu$ M unlabeled forward primer, 0.4 $\mu$ M 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. Further information on laboratory equipment and techniques is available at the Molecular Genetics Laboratory website at <http://www.pac.dfo-mpo.gc.ca/science/facilities-installations/pbs-sbp/mgl-lgm>.

### Baseline Populations

The baseline survey consisted of microsatellite analysis of chum salmon from 9 locations and microsatellite analysis of Chinook salmon from 25 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 (Neaves et al. 2005). 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

### 1.0 Chum Salmon

On a seasonal basis, chum salmon spawning populations from the White River drainage accounted for 49% of the run, whereas mainstem spawning Yukon River populations were estimated to comprise about 51% of the chum salmon migrating past the Eagle sonar site (Table 2). Mainstem spawning and White River populations were present throughout the sampling period, but the proportion of White River chum salmon declined as the season progressed. Teslin River chum salmon were most prevalent during the September 14<sup>th</sup> to 19<sup>th</sup> sample, but were also observed in the September 20<sup>th</sup> to 25<sup>th</sup> sample.

### 2.0 Chinook Salmon

Based upon sampling at the Eagle sonar site, populations which tended to migrate earlier in the run included those from the White River and lower Yukon tributaries (Chandindu River, Klondike River). The mainstem spawning stock returned noticeably later than the other stocks (Table 3). The Teslin Lake population migrated earlier than did the Teslin River population. The analysis of Chinook salmon migrating past the Eagle sonar site that were sampled indicated that the major regional stocks contributing to the run were the mainstem Yukon River (29%), Teslin River drainage (26%), Carmacks area tributaries (18%), Pelly River (11%), upper Yukon tributaries (7%), Stewart River (5%), White River (3%), and lower Yukon tributaries (1%). The application of the estimated stock compositions to estimate stock-specific abundance as determined at the sonar site was outlined in the report of the Joint Technical Committee of the Yukon River Panel for 2013.

## Literature Cited

- Banks, M. A., Blouin, M. S., Baldwin, B. A., Rashbrook, V. K., Fitzgerald, H. A., Blankenship, S. M and Hedgecock, D. 1999. Isolation and inheritance of novel microsatellites in chinook salmon (*Oncorhynchus tshawytscha*). J. Hered. 90: 281-288.
- Banks, M. A., V. K. Rashbrook, M. J. Calavetta, C. A. Dean, and D. Hedgecock. 2000. Analysis of microsatellite DNA resolves genetic structure and diversity of chinook salmon (*Oncorhynchus tshawytscha*) in California's Central Valley. Can. J. Fish. Aquat. Sci. 57: 915-927.
- Beacham, T.D., C.B. Murray, and R.E. Withler. 1988. Age, morphology, developmental biology, and biochemical genetic variation of Yukon River fall chum salmon (*Oncorhynchus keta*), and comparisons with British Columbia populations. U.S. Fish. Wild. Serv. Fish. Bull. 86: 663-674.
- Beacham, T.D., and Wood, C.C. 1999. Application of microsatellite DNA variation to estimation of stock composition and escapement of Nass River sockeye salmon (*Oncorhynchus nerka*). Can. J. Fish. Aquat. Sci. 56: 1-14.
- Beacham, T.D., J.R. Candy, K.J. Supernault, T. Ming, B. Deagle, A. Schultz, D. Tuck, K. Kaukinen, J.R. Irvine, K.M. Miller, and R. E. Withler. 2001. Evaluation and application of microsatellite and major histocompatibility complex variation for stock identification of coho salmon in British Columbia. Trans. Am. Fish. Soc. 130: 1116-1155.
- Beacham, T.D., J. R. Candy, K. J. Supernault, M. Wetklo, B. Deagle, K. Labaree, J. R. Irvine, K. M. Miller, R. J. Nelson, and R. E. Withler. 2003. Evaluation and application of microsatellites for population identification of Fraser River Chinook salmon (*Oncorhynchus tshawytscha*). Fishery Bulletin 101: 243-259.
- Beacham, T. D., M. Wetklo, C. Wallace, J. B. Olsen, B. G. Flannery, J. K. Wenburg, W. D. Templin, A. Antonovich, and L.. W. Seeb. 2008a. The application of

- microsatellites for stock identification of Yukon River Chinook salmon. North American Journal of Fisheries Management 28: 283-295.
- Beacham, T. D., S. Urawa, K. D. Le, and M. Wetklo. 2008b. Population structure and stock identification of chum salmon from Japan determined with microsatellite DNA variation. Fisheries Science 74: 983-994.
- Beacham, T. D., J. R. Candy, C. Wallace, S. Urawa, S. Sato, N. V. Varnavskaya, K. D. Le, and M. Wetklo. 2009. Microsatellite stock identification of chum salmon on a Pacific Rim basis. North American Journal of Fisheries Management 29: 1757-1776.
- Buchholz W.G, S. J. Miller, and W. J. Spearman . 2001. Isolation and characterization of chum salmon microsatellite loci and use across species. Animal Genetics 32: 160-167.
- Cairney, M., Taggart, J. B., and Hoyheim, B. 2000. Characterization of microsatellite and minisatellite loci in Atlantic salmon (*Salmo salar* L.) and cross-species amplification in other salmonids. Mol. Ecol. 9: 2175-2178.
- Grieg, C., D. P. Jacobson, and M. A. Banks. 2003. New tetranucleotide microsatellites for fine-scale discrimination among endangered Chinook salmon (*Oncorhynchus tshawytscha*). Molecular Ecology Notes 3: 376-379.
- Neaves, P. I., C. G. Wallace, J. R. Candy, and T. D. Beacham. 2005. CBayes: Computer program for mixed stock analysis of allelic data. Version v4.02. Free program distributed by the authors over the internet from [http://www.pac.dfo-mpo.gc.ca/sci/mgl/Cbayes\\_e.htm](http://www.pac.dfo-mpo.gc.ca/sci/mgl/Cbayes_e.htm)
- Nelson, R. J., and T. D. Beacham. 1999. Isolation and cross species amplification of microsatellite loci useful for study of Pacific salmon. Animal Genetics. 30: 228-229.
- O'Connell, M., R. G. Danzmann, J. M. Cornuet, J.M. Wright, and M. M. Ferguson. 1997. Differentiation of rainbow trout populations in Lake Ontario and the evaluation of the

- stepwise mutation and infinite allele mutation models using microsatellite variability. Canadian Journal of Fisheries and Aquatic Sciences 54: 1391-1399.
- Olsen, J. B., P. Bentzen, and J. E. Seeb. 1998. Characterization of seven microsatellite loci derived from pink salmon. Molecular Ecology 7: 1083-1090.
- Olsen, J. B., S. L. Wilson, E. J. Kretschmer, K. C. Jones, and J. E. Seeb. 2000. Characterization of 14 tetranucleotide microsatellite loci derived from sockeye salmon. Molecular Ecology 9: 2185-2187.
- O'Reilly, P. T., L. C. Hamilton, S. K. McConnell, and J. M. Wright. 1996. Rapid analysis of genetic variation in Atlantic salmon (*Salmo salar*) by PCR multiplexing of dinucleotide and tetranucleotide microsatellites. Canadian Journal of Fisheries and Aquatic Sciences 53: 2292-2298.
- Pella, J. and Masuda, M. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. Fish. Bull. 99: 151-167.
- Rexroad, C. E., Coleman, R. L., Martin, A. M., Hershberger, W. K., and Killefer, J. 2001. Thirty-five polymorphic microsatellite markers for rainbow trout (*Oncorhynchus mykiss*). Animal Genetics 32: 283-319
- Shaklee, J. B., T. D. Beacham, L. Seeb, and B. A. White. 1999. Managing fisheries using genetic data: Case studies from four species of Pacific salmon. Fisheries Research 43: 45-78.
- Small, M. P., Beacham, T. D., Withler, R. E., and Nelson, R. J. 1998. Discriminating Coho salmon (*Oncorhynchus kisutch*) populations within the Fraser River, British Columbia using microsatellite DNA markers. Molecular Ecology 7: 141-155.
- Smith, C. T., Koop, B. F., and Nelson, R. J. 1998. Isolation and characterization of Coho salmon (*Oncorhynchus kisutch*) microsatellites and their use in other salmonids. Mol. Ecol. 7: 1613-1621.

- Spies, I. B., D. J. Brasier, P. T. L. O'Reilly, T. R. Seamons, and P. Bentzen. 2005. Development and characterization of novel tetra-, tri-, and dinucleotide microsatellite markers in rainbow trout (*Oncorhynchus mykiss*). *Molecular Ecology Notes* 5: 278-281.
- Waples, R. S. 1990. Temporal changes of allele frequency in Pacific salmon populations: implications for mixed-stock fishery analysis. *Can. J. Fish. Aquat. Sci.* 47: 968-976.
- Williamson, K. S., J. F. Cordes, and B. P. May. 2002. Characterization of microsatellite loci in Chinook salmon (*Oncorhynchus tshawytscha*) and cross-species amplification in other salmonids. *Molecular Ecology Notes* 2: 17-19.
- Wilmot, R. L., Everett, R. E., Spearman, W. J., and Baccus, R. 1992. Genetic stock identification of Yukon River chum and Chinook salmon 1987 to 1990. *Prog. Rep. U.S. Fish and Wild. Serv., Anchorage.* 132p.
- Withler, R. E., Le, K. D., Nelson, R. J., Miller, K. M., and Beacham, T. D. 2000. Intact genetic structure and high levels of genetic diversity in bottlenecked sockeye salmon, *Oncorhynchus nerka*, populations of the Fraser River, British Columbia, Canada. *Can. J. Fish. Aquat. Sci.* 57: 1985-1998.

**Table 1.** Baseline used to estimate stock compositions of chum and Chinook salmon from the Eagle sonar site 2013.

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	Whitehorse hatchery, Takhini River
Teslin River	Jennings River, Morley River, Nisutlin River, Teslin River, Teslin Lake
Carmacks Area tributaries	Little Salmon, Big Salmon, North Big Salmon, Tatchun Creek
Mid-mainstem/Nordenskiold	Mainstem Yukon River, Nordenskiold River
Pelly River	Little Kalzas River, Blind Creek, Earn River, Glenlyon, Hoole River, Pelly River
Stewart River	Mayo River, Stewart River
North Yukon mainstem tributaries	Chandindu River, Klondike River
White River	Tincup Creek, Nisling River

**Table 2.** Estimated percentage stock composition of chum salmon migrating past the Eagle sonar site, 2013. 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.

Sample size Populations	August 1- September 13 247		September 14-19 246		September 20-25 207		September 26-30 191	
	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE
Big Creek	35.6	(10.5)	24.6	(10.0)	34.7	(12.2)	67.9	(3.8)
Minto	0.1	(0.5)	0.0	(0.2)	0.2	(0.6)	0.1	(0.3)
Pelly	5.8	(15.2)	20.8	(22.1)	12.2	(16.8)	0.7	(1.3)
Tatchun	0.1	(0.3)	0.2	(0.5)	0.1	(0.6)	0.0	(0.3)
Donjek	31.7	(28.4)	45.3	(24.3)	23.5	(26.2)	20.5	(14.7)
Kluane	4.5	(12.6)	0.1	(0.3)	3.9	(11.0)	0.0	(0.2)
Kluane Lake	19.2	(27.0)	6.7	(18.8)	23.9	(26.7)	10.6	(15.0)
Teslin	0.1	(0.3)	2.3	(1.2)	1.5	(1.2)	0.1	(0.3)
Chandindu	3.0	(1.5)	0.1	(0.3)	0.0	(0.2)	0.2	(0.5)
Regions								
Mainstem	41.6	(6.6)	45.6	(18.4)	47.2	(6.9)	68.7	(3.7)
White	55.4	(6.4)	52.0	(18.5)	51.2	(7.0)	31.1	(3.6)
Teslin	0.1	(0.3)	2.3	(1.2)	1.5	(1.2)	0.1	(0.3)
Yukon summer	3.0	(1.5)	0.1	(0.3)	0.0	(0.2)	0.2	(0.5)



**Table 2.** Continued

Sample size Populations	Seasonal 891	
	Estimate	SE
Big Creek	50.5	(2.1)
Minto	0.0	(0.1)
Pelly	0.0	(0.1)
Tatchun	0.0	(0.1)
Donjek	38.3	(20.5)
Kluane	5.1	(14.5)
Kluane Lake	5.5	(15.5)
Teslin	0.4	(0.4)
Chandindu	0.2	(0.2)
Regions		
Mainstem	50.5	(2.1)
White	48.9	(2.1)
Teslin	0.4	(0.4)
Yukon summer	0.2	(0.2)

**Table 3.** Estimated percentage stock composition of Chinook salmon migrating past the Eagle sonar site in 2013. Stock compositions were estimated using 15 microsatellite loci and the baseline outlined in Table 1. Standard errors of the estimates are in parentheses.

Sample size Populations	July 15-21 92		July 22-28 69		July 30-Aug. 4 78		August 5-28 54	
	Estimate	SE	Estimate	SE	Estimate	SE	Estimate	SE
Takhini	0.0	(0.3)	4.1	(2.7)	5.8	(2.8)	4.6	(2.9)
Whitehorse	2.4	(1.6)	1.4	(1.5)	4.0	(2.2)	4.6	(3.2)
Jennings	0.1	(0.4)	0.4	(1.4)	0.1	(0.5)	0.7	(1.6)
Morley	0.6	(1.8)	0.2	(1.1)	1.1	(1.6)	0.0	(0.4)
Nisutlin	0.4	(1.2)	0.5	(1.8)	0.2	(0.9)	0.0	(0.4)
Teslin River	4.5	(4.9)	14.6	(9.3)	0.6	(2.4)	58.7	(10.2)
Teslin Lake	21.6	(5.4)	9.4	(4.3)	0.5	(1.5)	0.0	(0.5)
Big Salmon	10.2	(8.5)	9.7	(7.5)	0.2	(0.9)	0.2	(0.9)
Little Salmon	10.0	(8.1)	9.5	(9.0)	13.6	(7.6)	0.4	(1.8)
N Big_Salmon	0.1	(0.6)	0.0	(0.3)	0.0	(0.4)	0.1	(0.9)
Tatchun	0.1	(0.5)	0.8	(2.4)	3.2	(4.1)	1.2	(2.4)
Nordenskiold	0.0	(0.2)	0.0	(0.3)	0.0	(0.2)	0.0	(0.3)
Yukon main	3.9	(5.6)	24.1	(9.0)	64.1	(9.2)	27.3	(9.7)
Blind Creek	12.4	(4.0)	0.4	(1.5)	3.7	(2.6)	0.3	(1.0)
Earn	2.7	(3.3)	0.8	(2.0)	0.1	(0.7)	0.0	(0.6)
Glenlyon	0.3	(1.0)	3.6	(3.0)	0.5	(1.4)	0.1	(0.6)
Kalzas	0.3	(1.0)	2.7	(2.8)	0.0	(0.3)	0.0	(0.3)
Pelly	8.6	(5.2)	5.6	(5.0)	0.4	(1.4)	0.1	(0.8)
Mayo	0.4	(1.4)	3.4	(5.2)	0.5	(1.6)	0.1	(0.6)
Stewart	12.9	(4.9)	5.3	(5.8)	0.1	(0.6)	0.1	(0.7)
Chandindu	2.5	(2.2)	0.0	(0.4)	0.0	(0.3)	0.0	(0.4)
Klondike	0.6	(1.4)	0.0	(0.3)	0.0	(0.2)	0.0	(0.3)
Nisling	0.6	(1.5)	0.0	(0.5)	0.0	(0.4)	0.2	(1.2)
Tincup	4.9	(2.5)	2.5	(2.0)	1.2	(1.3)	1.3	(1.6)
McQuesten	0.0	(0.3)	1.0	(2.1)	0.1	(0.5)	0.0	(0.2)
Region								
Yukon upper	2.4	(1.7)	5.5	(3.0)	9.8	(3.5)	9.2	(4.2)
Yukon Teslin	27.2	(6.8)	25.1	(9.8)	2.5	(3.1)	59.4	(10.2)
Yukon Carmacks	20.3	(6.2)	20.0	(8.2)	16.9	(8.5)	1.9	(3.2)
Yukon mainstem	3.9	(5.6)	24.1	(9.0)	64.1	(9.2)	27.3	(9.7)
Yukon Pelly	24.2	(5.7)	13.1	(5.1)	4.7	(2.7)	0.5	(1.5)
Yukon Stewart	13.3	(4.9)	9.7	(5.7)	0.7	(1.7)	0.2	(0.9)
Yukon Lower	3.1	(2.1)	0.0	(0.5)	0.0	(0.3)	0.0	(0.5)
Yukon White	5.5	(2.9)	2.6	(2.1)	1.3	(1.3)	1.5	(1.9)

**Table 3. Continued**

Sample size Populations	Seasonal (July 15- Aug 28) 293	
	Estimate	SE
Takhini	3.6	(1.2)
Whitehorse	3.1	(1.1)
Jennings	0.0	(0.2)
Morley	0.5	(1.0)
Nisutlin	0.4	(0.8)
Teslin	16.2	(5.1)
Teslin Lake	8.5	(2.2)
Big Salmon	6.6	(2.7)
Little Salmon	8.9	(3.7)
N Big_Salmon	0.0	(0.1)
Tatchun	2.9	(1.9)
Nordenskiold	0.0	(0.1)
Yukon main	28.6	(5.4)
Blind Creek	5.5	(1.8)
Earn	1.4	(1.6)
Glenlyon	1.5	(1.3)
Kalzas	0.4	(0.7)
Pelly	2.8	(2.6)
Mayo	3.1	(2.5)
Stewart	2.1	(2.4)
Chandindu	0.5	(0.6)
Klondike	0.2	(0.4)
Nisling	0.4	(0.8)
Tincup	2.8	(1.0)
McQuesten	0.1	(0.3)
Region		
Yukon upper	6.7	(1.6)
Yukon Teslin	25.6	(5.2)
Yukon Carmacks	18.5	(3.9)
Yukon mainstem	28.6	(5.4)
Yukon Pelly	11.5	(2.4)
Yukon Stewart	5.3	(2.0)
Yukon Lower	0.7	(0.6)
Yukon White	3.2	(1.3)