

**Abstract**—Variation at 13 microsatellite loci was previously surveyed in approximately 7400 chinook salmon (*Oncorhynchus tshawytscha*) sampled from 50 localities in the Fraser River drainage in southern British Columbia. Evaluation of the utility of the microsatellite variation for population-specific stock identification applications indicated that the accuracy of the stock composition estimates generally improved with an increasing number of loci used in the estimation procedure, but an increase in accuracy was generally marginal after eight loci were used. With 10–14 populations in a simulated fishery sample, the mean error in population-specific estimated stock composition with a 50-population baseline was <1.4%. Identification of individuals to specific populations was highest for lower Fraser River and lower and North Thompson River populations; an average of 70% of the individual fish were correctly assigned to specific populations. The average error of the estimated percentage for the seven populations present in a coded-wire tag sample was 2% per population. Estimation of stock composition in the lower river commercial net fishery prior to June is of key local fishery management interest. Chinook salmon from the Chilcotin River and Nicola River drainages were important contributors to the early commercial fishery in the lower river because they comprised approximately 50% of the samples from the net fishery prior to mid April. Mid Fraser River populations were the dominant group of chinook salmon in the catch in April and comprised at least 30% of the catch until late May. Upper Fraser River populations did not occur in any significant proportions in the fishery until the last week of April. By late May, they were the dominant contributors to the lower river fishery, and by June generally comprised approximately 70% of the weekly catch. Microsatellite variation allows accurate estimation of population-specific contributions to lower river fisheries.

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## Evaluation and application of microsatellites for population identification of Fraser River chinook salmon (*Oncorhynchus tshawytscha*)

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Chinook salmon (*Oncorhynchus tshawytscha*) are widely distributed within the Fraser River drainage, spawning in tributaries ranging from the headwaters to near the mouth of the river. There is substantial variation in life history features among populations within the drainage; populations vary in size at maturity, timing of spawning, and juvenile freshwater residence. Juveniles (largely from the Harrison River population) can migrate directly to the marine environment after fry emerge in the spring or perhaps develop in nonnatal tributaries in the lower river (Murray and Rosenau, 1989). Juveniles from some populations migrate to the ocean during the first summer of rearing (“ocean-type”), whereas in other populations juveniles remain in fresh water for a year or longer (“stream-type”) before migrating to the ocean (Fraser et al., 1982). Management for conservation of genetic diversity within the drainage requires knowledge of genetic variation among populations, as well as population-specific information from fisheries.

Effective management of fisheries within major drainages like the Fraser River generally requires information on timing of return of specific populations, should managers wish to change exploitation rates on specific populations for conservation purposes. To acquire this information is a particularly daunting task within the Fraser River because chinook salmon spawn in approximately 65 tributaries of the Fraser River (Fraser et al., 1982). Maturing adults from these populations return annually to the Fraser River throughout the year—the majority of fish returning from February through November. For management purposes, Fraser River chinook salmon are currently divided into three groups based on their migration timing into the lower river: the spring run consists of all populations where at least 50% of the individuals are estimated to migrate through the lower river before 15 July; the summer run consists of populations that migrate through the lower river from 15 July to 31 August; and the fall run consists of populations that migrate through the lower river primarily in

September and October (DFO<sup>1,2</sup>). However, the adequacy of managing Fraser River chinook salmon based upon run timing is currently under review (Candy et al.<sup>3</sup>), and changes in management objectives are likely. During their migration through the lower river, chinook salmon are exploited by several distinct fisheries, among them commercial net fisheries, and the recreational fishery.

Conservation concerns for specific populations requires more information on timing of returns beyond the present designations of “spring,” “summer,” and “fall.” Timing of some specific populations through the lower river can be inferred from their arrival on the spawning grounds. For example, chinook from the Birkenhead River (about 300 km from the Fraser River mouth) have historically supported a local recreational fishery on that river in April and early May (Fraser et al., 1982), indicating a very early timing of passage through the lower Fraser River. Coded-wire tagging (CWT) has been conducted on some enhanced populations, but these populations have been limited in scope given the size of the drainage, and coded-wire tag returns within the Fraser River have provided limited information on the timing of population returns.

Stock or population identification of chinook salmon migrating through the lower river is a continuing issue of management concern, and until recently there has been no effective way to provide estimates of population composition in the detail required by fishery managers. Although allozyme-based methods of stock identification have proven useful in estimation of chinook salmon stock composition in mixed-stock fisheries (Shaklee et al., 1999), the level of population discrimination available in the Fraser River was not sufficient for population-specific applications. Chinook salmon returning to spawn in specific rivers were considered as populations in our analysis, whereas stocks were a collection of populations from a particular geographic area or management unit. Minisatellite variation has been very effective in discriminating among individual Fraser River populations (Beacham et al., 1996), but we considered this technology not practical because of the cost and the time required for laboratory analysis. Any new technology employed had to meet these criteria: rapidity of analysis, moderate cost, and ability to discriminate among populations. Because variation in microsatellite loci meets these criteria and has been applied to other species requiring discrimination among salmonid populations within watersheds (Small et al., 1998; Beacham and Wood, 1999; Beacham et al., 2000),

and has been shown to be useful in stock discrimination in chinook salmon (Banks et al., 2000), we chose to survey variation at microsatellite loci for Fraser River chinook salmon (Beacham et al., 2003) and evaluate and apply the variation to practical problems of stock identification.

In the current study, we surveyed variation at 13 microsatellite loci and evaluated the utility of using microsatellite variation for stock identification of Fraser River chinook salmon. These procedures were accomplished by analysis of simulated mixtures and application to a sample of chinook salmon that had previously been marked with coded-wire tags. We evaluate the accuracy of identifying individuals to population and region of origin. We also estimate stock compositions from fisheries in the lower river to determine the timing and relative abundance of specific populations through the fishery.

## Materials and methods

### Collection of baseline DNA samples and laboratory analysis

Genomic DNA was extracted from either liver, scales, operculum punches, or fin clips from chinook salmon sampled between 1987 and 1998 by using the phenol-chloroform protocol of Miller et al. (1996) (early extractions) or the chelex resin protocol of Small et al. (1998) (later extractions) (Table 1, Fig. 1). Samples were derived from adults in all areas except the McGregor River, where because of the difficulty of obtaining adults, juveniles were sampled. For the survey of baseline populations, PCR products at six microsatellite loci—*Ots100*, *Ots101*, *Ots102*, *Ots104*, *Ots107* (primers outlined by Nelson and Beacham, 1999) and *Ssa197* (O’Reilly et al., 1996)—were initially size-fractionated on nondenaturing polyacrylamide gels by staining with 0.5 mg/mL ethidium bromide in water and illuminating with ultraviolet light. Nelson et al. (1998) have provided a more complete description of gel electrophoretic conditions. Three 20-bp marker lanes were run on each gel, and the size of the amplified alleles was determined from the molecular size grid created with the 20-bp markers. Beacham and Wood (1999) have provided a more complete description of the methods used to identify alleles with this technology. With the acquisition of an automated sequencer (the ABI 377) in our laboratory, PCR products at seven additional loci—*Ogo2*, *Ogo4* (Olsen et al., 1998), *Oke4* (Buchholz et al., 1999), *Omy325* (O’Connell et al., 1997), *Oki100* (K. M. Miller, unpubl. data), and *Ots2*, *Ots9* (Banks et al., 1999)—were size-fractionated on denaturing polyacrylamide gels and allele sizes were determined with Genescan software (PE Biosystems, Foster City, CA). The six loci previously analyzed on nondenaturing polyacrylamide gels stained with ethidium bromide were subsequently analyzed on the automated sequencer when it became available.

### Collection of fishery samples

In 1995, samples were collected from a daily gillnet test fishery at Albion in the lower Fraser River in southern

<sup>1</sup> DFO (Department of Fisheries and Oceans). 1995. Fraser River chinook salmon. Fraser River Action Plan, Fishery Management Group, Vancouver, British Columbia, Canada, 24 p. [Available from Fisheries and Oceans, 555 West Hasting St., Suite 1220, Vancouver, British Columbia, Canada V6B 5G3.]

<sup>2</sup> DFO (Department of Fisheries and Oceans). 1999. Fraser River chinook salmon. DFO Science Stock Status Report D6-11, 7 p. [Available from Fisheries and Oceans, 555 West Hasting St., Suite 1220, Vancouver, British Columbia, Canada V6B 5G3.]

<sup>3</sup> Candy, J. R., J. R. Irvine, C. K. Parken, S. L. Lemke, R. E. Bailey, M. Wetklo, and K. Johsen. 2002. A discussion paper on possible new stock groupings (conservation units) for Fraser River chinook salmon. Can. Stock Assessment Secretariat. Res. Doc. 2002/85, 57 p. [Available from [http://www.dfo-mpo.gc.ca/Csas/English/Index\\_e.htm](http://www.dfo-mpo.gc.ca/Csas/English/Index_e.htm).]

**Table 1**

Regions and populations within regions included in the survey of variation at 13 microsatellite loci in Fraser River chinook salmon and used in estimation of stock composition in mixed-stock samples. Numbers of fish surveyed in each population are shown in parentheses.

Region	Number of populations	Populations
Lower Fraser	2	Harrison (333), <sup>2</sup> Chilliwack (172) <sup>1,2</sup>
Birkenhead	1	Birkenhead (121) <sup>2</sup>
Middle Fraser	16	Cottonwood (53), Quesnel (473), <sup>2</sup> Cariboo (12), Horsefly (29), Stuart (458), Nechako (388), Endako (57), Westroad (31), Chilko (122), Upper Chilcotin (43), Lower Chilcotin (74), Chilcotin (47), Taseko (64), Elkin (235), Portage (27), Bridge (384) <sup>2</sup>
Upper Fraser	13	McGregor (119), Salmon (226), Bowron (109), Fontoniko (57), Willow (69), Indianpoint (42), Slim (65), Swift (227), Holmes (97), Goat (24), Horsey (24), Dome (327), <sup>2</sup> Tete Jaune (248)
Lower Thompson	5	Nicola (251), <sup>2</sup> Coldwater (176), <sup>2</sup> Spius (58), <sup>2</sup> Bonaparte (306), Deadman (193)
North Thompson	5	Raft (129), Finn (101), Louis (139), Clearwater (169), Mahood (17)
South Thompson	8	Lower Adams (103), <sup>2</sup> Lower Shuswap (335), <sup>2</sup> Middle Shuswap (313), <sup>2</sup> Little (53), Eagle (36), <sup>2</sup> Salmon (128), Bessette (17), South Thompson (157)

<sup>1</sup> Fall-run population.

<sup>2</sup> Hatchery population.

British Columbia (Dempson et al.<sup>4</sup>) (Fig. 1). The test fishery is conducted from April to October annually and operates daily (two sets of 30-min duration are made consecutively) except during commercial gillnet fishery openings. In 1995, a single mesh size of 20.3 cm (8.0 inch) was used to capture chinook salmon, and samples were collected from all chinook salmon caught in the fishery and surveyed for variation at five microsatellite loci. Further details of the test fishery have been outlined by Shubert et al. (1988). During 1997–99, operculum punches preserved in 90% ethanol were obtained from commercial fisheries in the lower Fraser River and mid Fraser. We were also able to obtain operculum punches from chinook salmon caught in marine fisheries in British Columbia that had previously been marked with coded-wire tags (CWTs) and for which the CWT had been recovered and decoded to determine marking location. We subsequently used this sample of 83 Fraser River fish to evaluate the accuracy of estimated stock compositions using a sample of known origin.

### Conversion of allele sizes between manual and automated sizing systems

In the 1998 and subsequent fishery samples, we surveyed variation at *Ots100*, *Ots101*, *Ots102*, *Ots104*, *Ots107*, and

*Ssa197* on the automated sequencer. However, estimated allele sizes at these loci differed between those derived from nondenaturing gels stained with ethidium bromide and those derived from the denaturing gels and fluorescent tags on the automated sequencer. In order to convert allele sizes between the two systems, we analyzed approximately 600 fish on both systems and determined the distributions of allele frequencies. By inspection of the allele frequencies, we were able to match specific allele sizes obtained from the sequencer to specific allele sizes from the manual gels, and then convert the sizing in the automated sequencer data set to match that obtained from the manual gels. Estimated allele sizes from both systems were very highly correlated ( $r^2 > 0.987$  for all loci). In general, sizes for the same allele from the sequencer were larger than those estimated from manual gels, with the differential increasing with allele size.

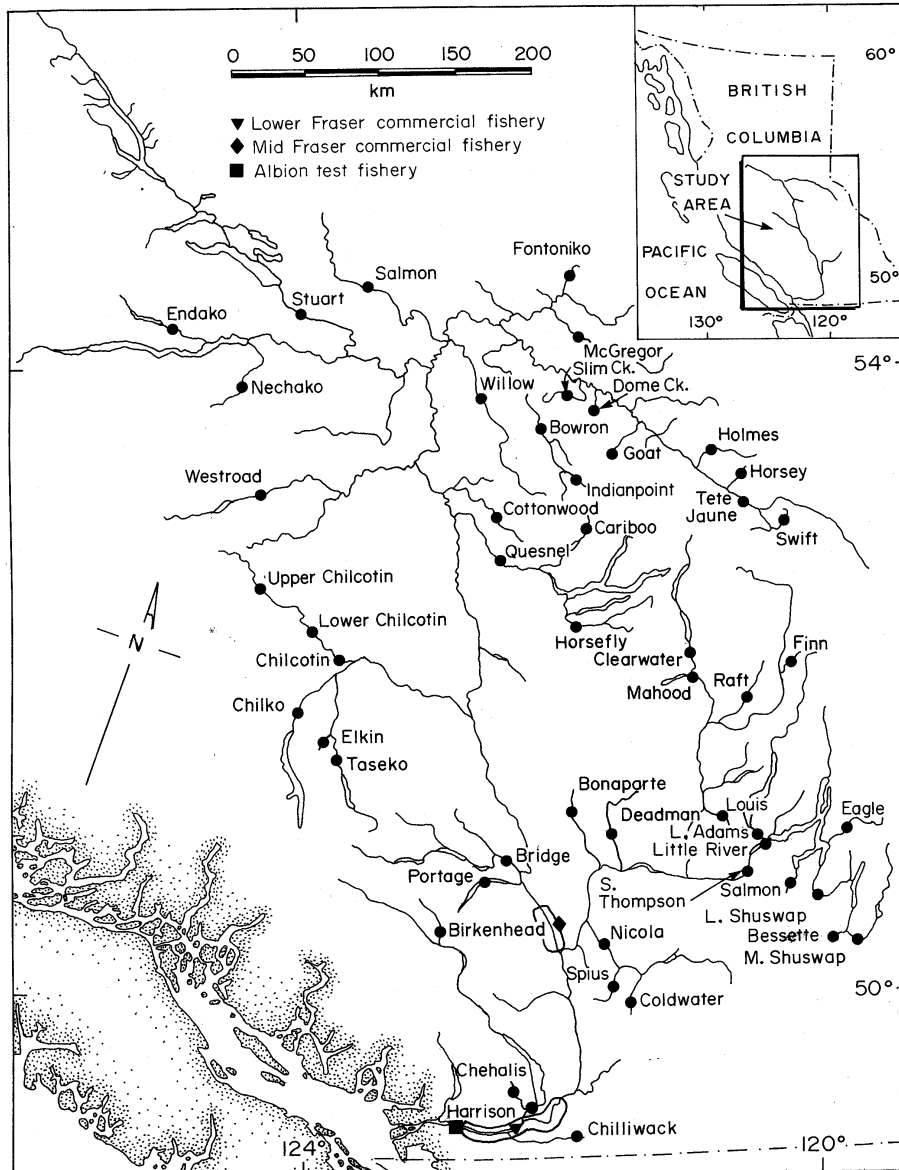
### Population structure

Regional structure was observed in the baseline populations; the Birkenhead River, the lower Fraser River, mid Fraser River, upper Fraser River, lower Thompson River, North Thompson River, and South Thompson River populations comprised seven geographically based groups or “stocks” (Beacham et al., 2003). The populations surveyed in each of these regions are summarized in Table 1.

### Identification of individuals

Identification of individuals to specific populations was done with the program GENECLASS 1.0 (Cornuet et al.,

<sup>4</sup> Dempson, J. B., J. R. Irvine, and R. E. Bailey. 1998. Relative abundance and migration timing of chinook salmon (*Oncorhynchus tshawytscha*) from the Fraser River, British Columbia, Albion test fishery, 1981–1995. Can. Man. Rep. Fish. Aquat. Sci. 2459, 25 p.



**Figure 1**

Locations in the Fraser River drainage where chinook salmon spawning aggregates were sampled at least once during 1988–98, as well as locations of the commercial and test fisheries in the lower river and commercial fishery in the mid Fraser.

1999). The probabilities of individuals belonging to all populations were calculated by using a Bayesian approach and each individual was assigned to the population in which it had the highest marginal probability.

### Estimation of stock composition

Genotypic frequencies were determined at each locus in each population and the statistical package for the analysis of mixtures software program (SPAM) (Debevec et al., 2000) was used to estimate stock composition of each mixture. More alleles were present at the microsatellite loci than was practical for stock identification applications. We combined

low frequency (frequency generally  $<0.02$  in all populations) adjacent alleles to reduce the number of genotypic frequencies to be estimated with the available samples with the pooling strategy for each locus outlined in Table 2. This was done to minimize and hopefully eliminate the occurrence of fish in the mixed sample from a specific population having an allele not observed in the baseline samples. Expected genotypic frequencies under Hardy-Weinberg equilibrium were determined from the observed allele frequencies and were used as model inputs. Genotypic frequencies at *Ots102* were not in Hardy-Weinberg equilibrium in approximately 50% of the populations surveyed (Beacham et al., 2003), but increased accuracy in estimated stock compositions was

**Table 2**

Method of pooling low-frequency alleles if they should occur in any population to reduce the number of genotypic frequencies to be estimated in baseline populations for mixed stock analysis. Not all allele bins considered for pooling may contain observed alleles for Fraser River chinook salmon.

Pooled alleles, renumbered	Microsatellite allele numbers pooled for each locus												
	<i>Ogo2</i>	<i>Ogo4</i>	<i>Oke4</i>	<i>Oki100</i>	<i>Ots100</i>	<i>Ots101</i>	<i>Ots102</i>	<i>Ots104</i>	<i>Ots107</i>	<i>Ots2</i>	<i>Ots9</i>	<i>Omy325</i>	<i>Ssa197</i>
1	1–8	1–3	19	1–11	1–4	1–9	1–8	1–5	1–3	1–9	1–7	1–4	1–7
2	9	4–5	10	12–14	5–8	10–11	9–10	6–7	4–5	10	8	5	8–11
3	10–11	6–7	11	15–16	9–12	12	11–12	8–11	6–7	11	9	6	12–13
4	12	8–9	12	17–18	13–15	13	13–16	12–13	8–9	12	10	7	14
5	13	10–11	13	19–19	16–18	14–15	17–18	14–15	10–11	13–15	11	8	15
6	14–15	12–13	14–19	20	19	16–18	19–20	16	12	16	12–15	9	16–17
7	16–17	14		21	20–22	19–20	21–22	17–18	13	17		10	18
8	18	15		22	23–24	21	23–25	19–20	14–15	18		11	19
9	19–21	16		23–24	25–26	22–23	26–28	21–22	16–18	19		12	20
10	22–30	17		25–26	27–28	24–25	29–30	23–24	19–20	20		13–14	21–22
11		18		27–28	29–30	26–27	31–33	25–26	21–22	21		15–16	23
12		19–21		29–30	31–32	28–29	34–35	27–28	23–24	22–24		17–18	24–25
13		22–24		31–32	33–34	30–31	36–37	29–30	25–26	25		19–24	26–27
14				33–36	35–36	32–50	38–40	31–34	27–28	26		25–32	28–29
15				37–40	37–41		41–44	35–36	29–31	27		33–44	30–31
16				41–54	42–45		45–52	37–45	32–36	28–32			32–33
17					46–54		53–60		37–47				34–36
18													37–40
19													41–45
Number of observed alleles	18	20	14	39	34	33	54	33	47	18	12	31	43

obtained by using expected genotypic frequencies for all loci. A comparison of estimated stock composition of a CWT sample with all loci in expected genotypic frequencies in the baseline populations compared with observed genotypic frequencies at *Ots102* resulted in more accurate estimates with expected genotypic frequencies at all loci. Similar results were observed by Beacham et al. (2001) in mixed-stock analysis of coho salmon. Stock compositions from the 1995 test fishery at Albion were estimated with five loci (*Ots100*, *Ots101*, *Ots102*, *Ots104*, and *Ssa197*), those from the 1997 net fisheries with six loci (previous five loci plus *Ots107*), and those from 1998 and 1999 fisheries with 13 loci. The change in the number of loci used in estimation of stock composition over time was reflected in the number of loci available in the baseline populations. The initial analysis of baseline populations started in 1994 and three loci were included the population survey (Nelson et al., 2001). By early 1996, at the time of analysis of the first test fishery samples, five loci were routinely scored in the baseline populations and mixed-stock fishery samples, and by 1997 six loci were routinely scored for both baseline and mixed-stock fishery samples. With the acquisition of an automated sequencer in our laboratory in 1998, an additional seven loci were added to the routine survey of baseline population and mixed-stock fishery samples.

Reported stock compositions for the CWT and actual fishery samples are the point estimate of each mixture analyzed, with variance estimates derived from 100 bootstrap simulations. Each baseline population and fishery sample was sampled with replacement in order to simulate random variation involved in the collection of the baseline and fishery samples. Reported stock composition for simulated mixtures was the bootstrap mean, along with the standard deviation of the mean.

## Results

### Comparison of individual loci

Determination of the relative power of individual loci for either population or regional discrimination is of prime significance for practical stock identification applications. In simulations comparing the relative power of the microsatellite loci to estimate stock compositions of representative single-population samples, there were only minor differences in the relative power of the best nine loci, with “best” defined as those loci resulting in the minimum bias in the estimated stock compositions. The mean error of the estimates ranged between 20% and 31% (Table 3). The power of

**Table 3**

Mean bias (%) in estimated stock compositions for nine representative populations of chinook salmon calculated with individual loci and with combinations of four loci (*Omy325*, *Oki100*, *Ogo4*, *Ots107*), eight (previous four plus *Ots102*, *Ots104*, *Ots107*), and all 13 microsatellite loci. Simulations were conducted using a 50-population baseline, 200 fish in the mixture sample, and 500 resamplings in the mixture sample, and 500 resamplings in the mixture sample, with each mixture sample composed solely of chinook salmon from one population. Standard deviations are shown in parentheses.

Locus	Birkenhead	Harrison	Elkin	Quesnel	Stuart-Nechako	Tete Jaune	Nicola drainage	Lower Shuswap	Clearwater	Mean
<i>Omy325</i>	1.9 (1.9)	26.7 (20.8)	12.7 (7.3)	31.9 (15.6)	29.5 (15.3)	26.2 (15.4)	13.0 (9.6)	24.3 (16.6)	12.7 (7.3)	20.7
<i>Oki100</i>	3.3 (3.3)	34.1 (11.9)	21.8 (9.5)	35.5 (13.2)	55.7 (18.4)	19.0 (9.3)	11.0 (6.6)	15.0 (8.0)	21.8 (9.5)	23.4
<i>Ogo4</i>	0.7 (1.0)	23.9 (12.3)	21.3 (13.4)	40.3 (15.1)	33.2 (14.7)	29.1 (18.1)	28.6 (15.9)	25.4 (15.0)	21.3 (13.4)	26.0
<i>Ots107</i>	2.6 (2.7)	32.5 (17.9)	32.5 (17.9)	28.0 (14.8)	66.5 (20.0)	4.6 (2.5)	24.3 (14.3)	35.3 (16.2)	32.5 (17.9)	26.8
<i>Ots102</i>	18.8 (99.8)	18.3 (11.9)	34.0 (15.2)	67.2 (23.8)	34.0 (14.7)	8.2 (6.9)	24.8 (14.3)	15.6 (9.7)	34.0 (15.2)	28.2
<i>Ots104</i>	6.8 (5.9)	27.6 (13.1)	9.7 (6.4)	34.3 (16.3)	73.8 (20.8)	43.7 (21.9)	21.3 (14.3)	21.3 (14.3)	9.7 (6.4)	29.8
<i>Ots100</i>	9.7 (6.5)	26.8 (15.5)	20.0 (11.0)	32.5 (14.5)	46.0 (19.9)	47.5 (21.4)	25.7 (16.4)	25.2 (19.6)	20.0 (11.0)	30.2
<i>Ots101</i>	8.3 (7.1)	37.1 (17.6)	22.4 (11.7)	35.4 (13.8)	50.4 (18.7)	32.1 (14.1)	36.7 (16.5)	22.9 (12.4)	22.4 (11.7)	31.6
<i>Ogo2</i>	7.0 (5.6)	25.4 (14.9)	19.2 (13.4)	32.8 (23.5)	78.3 (21.2)	51.7 (29.1)	27.0 (16.7)	14.9 (12.6)	19.2 (13.4)	31.6
<i>Ots2</i>	6.2 (7.1)	39.2 (24.6)	28.4 (17.3)	45.6 (27.1)	43.4 (23.6)	27.0 (17.4)	29.4 (18.2)	45.7 (22.3)	28.4 (17.3)	36.3
<i>Ssa197</i>	10.1 (6.7)	34.7 (17.5)	35.0 (16.4)	55.9 (22.7)	60.6 (22.2)	61.2 (24.8)	41.1 (20.4)	23.5 (13.1)	35.0 (16.4)	38.4
<i>Oke4</i>	12.5 (9.0)	20.9 (19.4)	79.8 (22.2)	86.9 (19.1)	78.5 (21.9)	16.3 (11.3)	32.6 (19.2)	69.8 (27.9)	79.8 (22.2)	52.7
<i>Ots9</i>	15.5 (15.4)	64.6 (27.9)	32.2 (27.2)	96.5 (9.4)	92.0 (14.9)	82.1 (23.9)	14.7 (13.3)	69.4 (27.0)	32.2 (27.2)	60.8
Best four	2.4 (1.9)	9.2 (5.9)	7.1 (3.8)	14.3 (5.9)	12.2 (6.3)	9.4 (4.5)	6.9 (4.5)	9.2 (5.0)	7.1 (3.8)	8.5
Best eight	5.0 (2.5)	6.6 (4.4)	5.3 (3.0)	7.2 (4.1)	12.2 (3.5)	5.3 (2.9)	6.6 (3.6)	6.2 (3.9)	5.3 (3.0)	6.7
All thirteen	5.6 (3.4)	5.4 (3.2)	5.0 (2.9)	4.5 (2.9)	12.2 (3.0)	4.6 (2.5)	6.7 (3.7)	6.1 (3.4)	5.0 (2.9)	6.3

a single locus to provide accurate estimates of stock composition varied considerably among loci and among populations. For example, the mean error in estimation of stock composition of a sample of pure Birkenhead River chinook salmon was less than 1% when only *Ogo4* was used to estimate stock compositions but ranged as high as 40% when a sample of pure Quesnel River chinook salmon was evaluated. Clearly, not all loci were equally effective in stock identification, and the usefulness of the loci varied among populations. The accuracy of the estimates generally improved with an increasing number of loci used in the estimation procedure, but the increase in accuracy was generally marginal after eight loci were used to estimate stock compositions. In the case of the Birkenhead River, additional loci did not increase the accuracy over that observed with only *Ogo4*. The precision of the estimates generally increased with an increasing number of loci used, but the increase in precision was marginal when the least effective five loci were added to the estimation procedure.

On average, the number of alleles present at a locus was related to the power of the locus to provide accurate estimation of stock composition. For example, the mean bias of estimated stock composition for loci with fewer than 20 observed alleles (*Ogo2*, *Oke4*, *Ots2*, *Ots9*) was 45% per locus, whereas the mean bias for loci with 20 or more alleles was 26% per locus (Table 3). Loci with fewer than 20 observed alleles were generally less valuable for stock identification applications than loci with greater numbers of alleles.

### Population estimation of stock composition

We evaluated whether the degree of genetic differentiation observed among Fraser River populations included in the baseline was sufficient for mixed-stock analysis in which the objective was estimation of specific population contributions to fishery samples. Three simulated fishery mixture samples were developed, representing an early, middle, and late-timing return to the lower Fraser River. With 14 populations present in a simulated spring fishery sample, the mean error in population specific estimated stock composition with a 50-population baseline was 1.4% (Table 4). Similar mean population-specific error rates were observed in the simulated summer fishery sample containing fish from 10 populations (1.2%), and in the simulated fall sample containing fish from seven populations (1.1%). Regional estimates of stock contributions were all within 2% of the actual value. We concluded that accurate

**Table 4**

Estimated percentage composition of three simulated mixtures of Fraser River chinook salmon incorporating variation at 13 microsatellite loci and estimated with a 50-population baseline. Each mixture of 150 fish was generated 500 times with replacement, and stock compositions of the mixtures were estimated by resampling each baseline population with replacement to obtain a new distribution of allele frequencies. "Regional sum" is the regional sum of all populations in the region. The appearance of each population in each of the simulated mixtures is indicated in parentheses after the population name. Standard deviations are given in parentheses.

Population and sum for region	Spring		Summer		Fall	
	Actual	Estimated	Actual	Estimated	Actual	Estimated
Birkenhead (spring)	2.4	2.2 (1.7)	0.0	0.0 (0.1)	0.0	0.0 (0.0)
Harrison (fall)	0.0	0.1 (0.3)	0.0	0.2 (0.5)	60.0	59.8 (6.7)
Chilliwack (fall) <sup>1</sup>	0.0	0.0 (0.2)	0.0	0.0 (0.1)	20.0	18.4 (5.6)
Sum for Lower Fraser region	0.0	0.2 (0.4)	0.0	0.2 (0.5)	80.0	78.9 (4.3)
Westroad (spring)	11.8	5.8 (2.4)	0.0	0.1 (0.3)	0.0	0.0 (0.1)
Bridge (summer)	0.0	1.6 (1.9)	10.0	8.8 (3.8)	0.0	0.2 (0.4)
Cottonwood (spring)	5.9	4.2 (2.1)	0.0	0.1 (0.3)	0.0	0.0 (0.1)
Elkin (spring)	11.8	11.0 (3.4)	0.0	0.2 (0.4)	0.0	0.1 (0.2)
L.Chilcotin (spring)	11.8	8.5 (3.1)	0.0	0.2 (0.4)	0.0	0.1 (0.4)
Quesnel (summer, fall)	0.0	1.4 (1.8)	10.0	10.2 (3.9)	5.0	4.7 (2.8)
Stuart–Nechako (summer, fall)	0.0	4.0 (3.2)	10.0	10.7 (4.4)	5.0	6.0 (2.8)
Sum for Mid Fraser region	41.2	39.2 (5.6)	30.0	30.5 (4.9)	10.0	11.5 (3.4)
Slim (spring)	11.8	7.8 (3.0)	0.0	0.1 (0.3)	0.0	0.0 (0.2)
Swift (summer)	0.0	0.2 (0.4)	2.0	1.8 (1.3)	0.0	0.0 (0.2)
Bowron (spring)	11.8	11.7 (4.2)	0.0	0.1 (0.4)	0.0	0.2 (0.6)
Willow (spring)	5.9	5.0 (2.6)	0.0	0.1 (0.3)	0.0	0.1 (0.2)
Holmes (spring, summer)	11.8	11.1 (3.9)	3.0	2.2 (2.1)	0.0	0.0 (0.2)
MacGregor (spring)	3.5	4.2 (3.5)	0.0	0.2 (0.5)	0.0	0.1 (0.3)
Sum for Upper Fraser region	44.7	46.0 (5.7)	5.0	5.4 (2.6)	0.0	0.6 (0.9)
Clearwater (summer)	0.0	0.1 (0.4)	10.0	9.4 (3.0)	0.0	1.0 (1.1)
Finn (summer)	2.4	2.1 (1.8)	5.0	4.5 (2.4)	0.0	0.0 (0.2)
Louis	0.0	0.0 (0.1)	0.0	0.0 (0.0)	0.0	0.0 (0.1)
Mahood (fall)	0.0	0.0 (0.1)	0.0	0.0 (0.1)	5.0	1.4 (1.5)
Raft (spring, summer)	3.5	3.5 (2.3)	5.0	5.1 (2.7)	0.0	1.4 (1.3)
Sum for North Thompson region	5.9	5.8 (2.9)	20.0	19.1 (4.3)	5.0	3.8 (1.9)
Eagle (summer, fall)	0.0	0.1 (0.2)	10.0	5.9 (2.6)	2.0	1.1 (1.2)
L Shuswap (spring, summer)	2.4	2.2 (1.6)	20.0	21.7 (5.0)	0.0	0.4 (0.7)
M Shuswap (spring, summer)	3.5	3.7 (2.0)	5.0	5.9 (3.0)	0.0	0.1 (0.5)
South Thompson (summer, fall)	0.0	0.3 (0.6)	10.0	9.9 (3.5)	3.0	2.8 (2.0)
Sum for South Thompson region	5.9	6.4 (2.5)	45.0	44.7 (4.9)	5.0	5.0 (2.4)
Sum for Lower Thompson region	0.0	0.2 (0.4)	0.0	0.2 (0.4)	0.0	0.1 (0.3)

<sup>1</sup> White-fleshed population.

estimation of regional stock compositions should be available when the genetic data outlined in our study is applied to actual mixed-fishery samples.

### Identification of individuals

Individuals were classified with respect to origin for 50 populations in the Fraser River drainage. Success rate of classification of individuals varied considerably among populations and to some extent was reflective of sample size of individual populations. For example, success rate of identification of individual Goat Creek and Horsey River chinook salmon was about 5%, but approximately only 20 fish

from each population were included in the analysis used to characterize the populations (Table 5). Success rate of classification of other upper Fraser River populations was higher, but more fish were available to quantify the variation in the populations. Success rate was partially attributable to sample size but was also markedly influenced by genetic differentiation in the population. For example, all individual Birkenhead River fish were correctly assigned to the population of origin in a 50-population baseline—indicative of the genetic distinctiveness of this population. Overall, highest rates of classification to individual populations were observed for lower Fraser River and lower and North Thompson River populations, with an average

**Table 5**

Percent correct classification of individual chinook salmon to population and region of origin for 50 populations in the Fraser River drainage. Individuals must have been scored for at least 10 loci in order to be included in the analysis.  $n$  = number of fish in sample.

Population	$n$	Population	Region	Population	$n$	Population	Region
Sum for Birkenhead region	117	100.0	100.0	Indianpoint	41	4.9	80.5
Harrison	317	74.4	97.5	Willow	68	25.0	80.9
Chilliwack	170	60.6	95.3	Fontoniko	57	42.1 <sup>4</sup>	93.0
Sum for Lower Fraser region	487	69.7	96.8	McGregor	118	27.1 <sup>5</sup>	85.6
Cottonwood	49	57.1	73.5	Salmon River	226	58.4	80.1
Quesnel	423	52.2	84.2	Bowron	79	30.3	81.0
Cariboo	2	0.0	50.0	Sum for Upper Fraser region	1594	50.9	80.5
Horsefly	15	13.3	46.2	Nicola <sup>6</sup>	251	84.4	93.6
Stuart	430	47.7 <sup>1</sup>	89.3	Coldwater <sup>6</sup>	162	86.4	96.3
Nechako	309	30.1 <sup>2</sup>	77.7	Spilus <sup>6</sup>	57	66.6	86.0
Endako	59	54.2	81.3	Deadman	193	49.7	91.7
Westroad	27	29.6	77.8	Bonaparte	306	69.3	95.6
Upper Chilcotin <sup>3</sup>	42	61.9	88.1	Sum for Lower Thompson region	969	72.0	93.6
Lower Chilcotin <sup>3</sup>	69	47.8	73.9	Mahood	17	11.8	64.7
Chilcotin <sup>3</sup>	47	51.1	83.0	Raft	122	44.3	59.8
Chilko	122	61.5	91.0	Finn	101	81.2	92.1
Elkin	211	68.2	84.8	Louis	139	92.8	97.8
Taseko	51	60.8	88.2	Clearwater	165	82.4	92.1
Bridge	384	53.9	75.8	Sum for North Thompson region	544	74.1	85.5
Portage	23	78.3	87.0	Little River	42	28.6	88.1
Sum for Mid Fraser region	2263	50.7	80.5	Lower Shuswap	335	68.1 <sup>7</sup>	96.1
Tete Jaune	248	68.5	89.9	Middle Shuswap	313	73.2 <sup>8</sup>	95.8
Dome Creek	327	62.7	93.9	Salmon	128	76.6	91.4
Horsey	22	27.3	90.1	Eagle	36	58.3	86.1
Goat	19	5.2	73.7	Lower Adams	96	46.9	89.6
Holmes	97	18.6	82.5	South Thompson	144	48.6	91.7
Swift	227	78.4	94.3	Besette	16	31.3	100.0
Slim Creek	65	43.0	92.3	Sum for South Thompson region	1110	63.8	93.8

<sup>1</sup> 64.4% correct to Stuart–Nechako complex.

<sup>2</sup> 46.9% correct to Stuart–Nechako complex.

<sup>3</sup> Upper Chilcotin, Lower Chilcotin, and Chilcotin considered as a single population in the analysis. The Chilcotin sample was a mixed-population sample collected in the Chilcotin River.

<sup>4</sup> 68.4% correct to McGregor River watershed.

<sup>5</sup> 38.1% correct to McGregor River watershed.

<sup>6</sup> Coldwater, Spilus, and Nicola considered as single population in the analysis.

<sup>7</sup> 81.2% correct to Shuswap River watershed.

<sup>8</sup> 86.6% correct to Shuswap River watershed.

of 70% of the individual fish correctly assigned to specific populations. Correct assignment to region of origin was achieved for at least 80% of the chinook salmon from all regions; the highest rates were for the Birkenhead River and three Thompson River regions, and the lowest rates for the middle and upper Fraser regions.

### Application to a coded-wire tag (CWT) sample

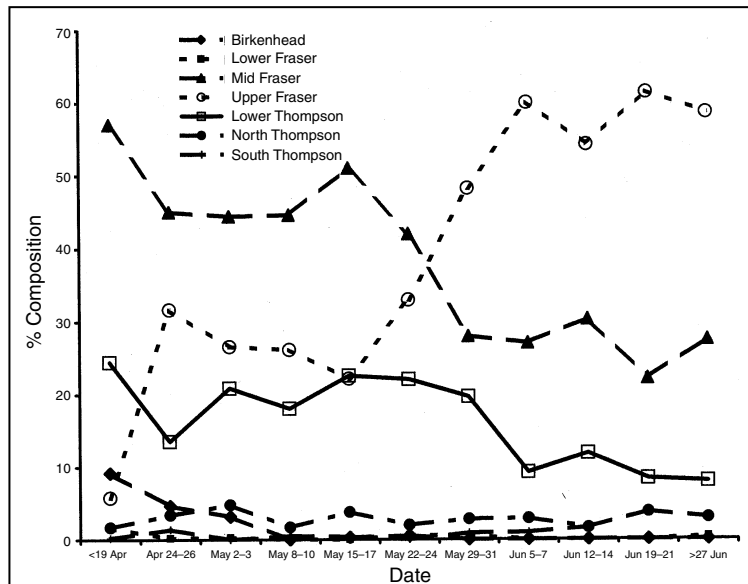
CWTs were available from seven Fraser River populations caught in marine fisheries. The average error of the estimated percentage for the seven populations present was 2% per population for the 83-fish sample estimated with a 50-population baseline (Table 6). Tags recovered from the upper Adams River population were combined with the

lower Shuswap River because the Upper Adams fish were recent transplants from the Lower Shuswap River population. Similarly, tags recovered from the Stave River population were combined with the Harrison River population because the Stave River fish were recent transplants from the Harrison River. The average error of the estimated percentage for the five regions present was 1.4%. The accuracy of estimated stock compositions obtained from analysis of the CWT sample were within the range expected based upon the analysis of the simulated mixtures.

### Lower Fraser commercial net fishery

Estimation of stock composition in the lower river commercial net fishery is of key local fishery management interest,





**Figure 2**  
Average percentage of Birkenhead, Lower Fraser, Mid Fraser, Upper Fraser, Lower Thompson, North Thompson, and South Thompson stocks at specific time intervals in samples from the lower Fraser River commercial gillnet fishery, 1997–99.

particularly prior to June. For the fishery samples from 1997 to 1999 collected in April of each year, chinook salmon from the Chilcotin River and Nicola River drainage were important contributors to the fishery, as they, combined, comprised approximately 50% of the samples from the net fishery prior to 19 April (Appendix Table 1). By late April, the Chilcotin River population constituted on average approximately 20% of the fishery samples, and the Nicola drainage populations about 10%. The Birkenhead River population was also identified as contributing 5% to 10% of the catch in the early lower river fishery but was virtually absent from the fishery after 3 May. The Stuart and Nechako river drainage populations were identified as contributing significantly to the early catches, with estimates as high as 20% in some weeks in some years. Upper Fraser River populations contributed more to the fishery in May, and the significant populations were from the Holmes River, the Fraser River mainstem at Tete Jaune, the Salmon River, and the McGregor River (Appendix Table 1).

On a regional basis, mid Fraser River populations were the dominant group of chinook salmon in the catch in April, and comprised at least 30% of the catch until late May (Fig. 2). Upper Fraser River populations did not occur in any significant proportions in the fishery until the last week of April. By late May, they were the dominant contributors to the lower river fishery and by June could comprise approximately 70% of the weekly catch. South Thompson River and North Thompson River populations comprised only trace proportions of the fishery samples from April through to the end of June. In fact, the contributions of populations in the entire Thompson River drainage were dominated by the tributary Nicola River

**Table 6**

Percentage composition of a sample of 83 coded-wire tagged (CWT) Fraser River chinook salmon obtained from fisheries in British Columbia in 1997 and estimated using 13 microsatellite loci with a 50-population Fraser River baseline. Because all fish in the sample were marked with CWTs, the actual composition of the sample is known. Standard deviations are shown in parentheses.

Population and sum for region	Actual %	Estimated %
Dome Creek	1.2	1.2 (1.0)
Sum for Upper Fraser region	1.2	1.2 (1.0)
Nechako–Stuart	4.9	4.1 (3.3)
Quesnel	17.1	12.7 (4.0)
Sum for Mid Fraser region	22.0	22.5 (4.4)
Chilliwack	25.6	25.5 (6.5)
Harrison–Stave	19.5	20.6 (6.5)
Sum for Lower Fraser region	45.1	46.1 (4.5)
Sum for Birkenhead region	0.0	0.0 (0.0)
Sum for North Thompson region	0.0	0.0 (0.9)
Lower Shuswap–Upper Adams	13.4	13.0 (5.9)
Middle Shuswap	15.9	12.7 (4.0)
Sum for South Thompson region	29.3	28.9 (5.2)
Sum for Lower Thompson region	2.4	1.4 (1.4)

drainage populations, and these populations were present from the beginning of sampling in early April to the end of sampling in late June. Lower Fraser River popula-

tions virtually did not contribute to the fishery from April through June.

### Mid Fraser commercial net fishery

Samples from the net fishery in the mainstem Fraser River were obtained from areas largely upstream of the confluence of the Thompson and Fraser rivers. Thus, the estimated percentage of Thompson River chinook salmon was <2% in this fishery (Appendix Table 2). Mid-Fraser populations were estimated to comprise 63% of the samples from late June and early July in 1998 in this fishery, and the Chilcotin River population was the dominant population. By mid July, the majority of the fish sampled originated from upper Fraser populations, and chinook salmon from Salmon River, Bowron River, McGregor River, and the mainstem Fraser River at Tete Jaune were the dominant contributors to the catch (Appendix Table 2).

### Lower Fraser test fishery

As was observed in the commercial gillnet fishery in the lower Fraser River, chinook salmon from mid-Fraser populations dominated the catch in April and May, comprising over 50% of the fish sampled (Appendix Table 3). The Chilcotin River and Stuart/Nechako rivers populations were the main populations from the mid-Fraser region. However, unlike the commercial gillnet fishery, salmon from the lower Thompson River comprised 5% or less of the catch in April and May. North and South Thompson River populations comprised <5% of the catch as well, as was observed in the commercial gillnet fishery. Upper Fraser River populations had largely passed through the test fishery by the end of July. Chinook salmon from the North and South Thompson rivers dominated the samples in August, and the mainstem-spawning South Thompson population was the dominant population in the fishery. By September chinook salmon from the lower Fraser River were the main group of fish sampled in the test fishery, and they comprised 45% of the catch. By October, they dominated the test fishery, comprising more than 80% of the chinook salmon sampled.

## Discussion

### Evaluation of microsatellites

The survey of microsatellite variation of Fraser River chinook salmon was initiated to determine genetic structure of chinook salmon populations within the Fraser River drainage and to provide population-specific estimates of stock composition in mixed-stock fisheries in the drainage for management purposes. Analysis of simulated mixtures has generally indicated that the estimates of stock composition are sufficiently accurate such that reliable estimates of population-specific composition should be obtained when applied to mixed-stock fisheries. Application to a CWT sample indicated that the average error of the estimated percentage for the seven populations present was 2% per population and for

the five regions present was 1.4%. These levels of accuracy were judged to be sufficient for management applications. Indeed, there is no other technique currently available that can provide current levels of accuracy in estimation of stock composition for Fraser River chinook salmon.

The 13 microsatellite loci evaluated in our survey clearly differed in their ability to provide accurate estimates of stock composition. Generally, loci with fewer numbers of alleles (<20) were less effective for population identification than were loci with greater numbers of alleles. Theoretical studies of locus characteristics to guide selection for individual identification suggested that a modest number of independent loci was best, where each locus would have a modest number of alleles and where each allele had a modest frequency (Smouse and Chevillon, 1998). For chinook salmon, loci with greater than 20 observed alleles would likely be more effective for stock or individual identification than loci with fewer alleles. With respect to number of loci to include in stock identification applications, analysis of the simulated samples indicated that bias was minimized when all 13 loci surveyed were included in the analysis, but the least effective loci provided only a modest increase in accuracy of estimated stock compositions. Increasing the number of loci included in the stock identification applications would be the preferred option, provided that the number of loci included in the analysis provided a cost-effective method for fishery management applications.

Estimation of stock composition and classification of individuals to specific populations are two goals for stock identification, but estimation of stock composition is the more practical goal for fisheries management. In stock composition analysis, the characteristics of the whole sample are used to provide the most likely estimate. For classification of individuals, only the characteristics of the individual to be identified are used. Because more information is available from a stock mixture rather than from a single individual, and misallocations between individual populations will cancel, estimates of stock composition will generally be more accurate than classifications of individual fish. For example, individual Chilliwack River fish were correctly identified to river of origin approximately 61% of the time, but in the 83-fish CWT sample, the estimate of the Chilliwack River component was within 4% of the true estimate, equivalent to estimating about 25 Chilliwack River fish present instead of 21 fish. Although more difficult, identification of individual fish to specific river of origin does have some management applications for Fraser River chinook salmon. Because the Birkenhead River population is very distinct genetically, it is possible to identify specific individuals as originating from the Birkenhead River with a high degree of accuracy in fisheries both within and outside of the Fraser River drainage. Given current conservation concerns for the Birkenhead River population and with the appropriate level of sampling, it is possible to identify all areas and periods in which chinook salmon from this population are present.

Given the large number of chinook salmon populations spawning in the Fraser River drainage, the area of the drainage, and the cost of both obtaining representative samples from spawning populations and their analysis,

it is necessary that the annual variation in population-discriminating characters within populations be substantially less than the differences among populations. If the annual variation in population-discriminating characters within populations is less, then annual baseline sampling of populations would not be necessary, and samples from individual populations could be pooled over time to increase the reliability of observed allele frequencies. This procedure is required in order that a stock identification method be feasible from both technical and financial perspectives. For Fraser River chinook salmon, the genetic variation attributable to population differentiation was about eight times the variation attributable to annual variation within populations (Beacham et al., 2003), rendering annual variation in allele frequencies of little practical significance in estimation of stock composition for fisheries in the drainage. In particular, annual estimation of microsatellite allele frequencies in baseline populations would not be required for practical applications, although some level of monitoring of allele frequencies over time would clearly be desirable. The annual stability of microsatellite allele frequencies for Fraser River chinook salmon in relation to population differentiation is very similar to that reported for other salmonids (Beacham et al., 1999; Tessier and Bernatchez, 1999).

The two major fall-return populations in the lower Fraser River are from the Harrison River and Chilliwack River. Analysis of simulated mixtures and the CWT sample suggested that discrimination between the Harrison River and Chilliwack River populations was possible. Transplants have occurred between these two populations (Candy and Beacham, 2000), but the level of transplantation has not been sufficient to homogenize genetic differentiation between the populations.

### Application to commercial and test fisheries

Analysis of estimated stock compositions of the 1997–99 lower river commercial gillnet fishery and the 1995 lower river test gillnet fishery indicated a discrepancy between the relative abundance of lower Thompson River populations, particularly the Nicola River drainage populations. In the commercial gillnet fishery, Nicola River drainage populations comprised 10–30% of the samples in April and May, but only 0–5% of the test fishery samples. Absolute population abundance may have differed between the two time periods, but a more likely explanation was the fact that the 1995 test fishery was conducted with a single mesh gillnet of 20.3 cm, a mesh size selective for larger-bodied chinook salmon. Lower Thompson River chinook salmon populations are substantially smaller in body size than other chinook salmon populations in the Fraser River drainage (Beacham and Murray, 1993), and thus were not likely to have been sampled in proportion to their abundance by the gear used in the test fishery. Multipanel, multimesh gillnets have been used in the test fishery since 1997 in order to obtain more representative sampling of migrating chinook salmon.

Timing of return of specific populations through the lower Fraser River has been outlined by DFO.<sup>1</sup> The designation

of populations as “spring run,” “summer run,” or “fall run” is based upon a number of factors, of which peaks of occurrence of CWTs in the test fishery in the lower river and peak of arrival on the spawning grounds are key factors. Recoveries of CWTs are largely restricted to tagged, enhanced populations because little CWT marking has been conducted for wild populations. There was, in general, good correspondence between run timing determined by CWTs or other factors and those observed in our analyses of the lower river commercial fishery. For example, the Birkenhead River population is known to return very early through the lower Fraser River (Fraser et al., 1982). Highest proportions of Birkenhead River chinook salmon were consistently observed in the lower Fraser River commercial fishery prior to 19 April, indicative of an early passage through the lower Fraser River. The Coldwater River, Spius Creek, and Nicola River populations are all found in the Nicola River drainage, and all are classified as spring-run populations (DFO<sup>1</sup>). The Nicola River drainage aggregate was a major contributor to catch in the commercial fishery from April to early June. The other lower Thompson River populations, the Deadman River and Bonaparte River, were classified as spring-run populations, and they were detected in the lower river commercial fishery. The Chilcotin River stock aggregate (upper and lower Chilcotin populations) was classified as spring run (DFO<sup>1</sup>), and again this stock was a dominant contributor to the lower river commercial fishery in April and May. In the upper Fraser River, the mainstem spawning population at Tete Jaune and the Bowron River population are thought to be spring run, and this timing was observed in both the commercial fishery and the test fishery.

The summer-run populations migrate through the lower Fraser River mainly after 15 July and originate primarily from the North and South Thompson River watersheds (a few major populations come from the middle Fraser River (DFO<sup>1</sup>). Analysis of the lower Fraser River test fishery supports this conclusion, with 60–75% of the fish sampled in the test fishery in August of North and South Thompson River origin. Populations contributing significantly to the test fishery included the Clearwater River, Adams River, and Shuswap River, and these have been defined as summer-run populations. Fall-run populations occur after 1 September and are thought to be largely restricted to the lower Fraser River (DFO<sup>1</sup>). Lower Fraser River populations certainly dominated the test fishery catch in October, but lower Fraser populations were estimated to have comprised only 45% of the catch in September. Summer-run populations were clearly present in the lower river in September, and in fact comprised the majority of the catch.

There was one significant discrepancy between the previous designation of timing of return (DFO<sup>1</sup>) and that observed in the fishery sampling in our study. The populations in the Nechako River and Stuart River in the mid Fraser region have been defined as summer run, based largely on the timing of recoveries of CWTs from Stuart River chinook salmon in the lower river test fishery. However, in the analysis of the lower river commercial and test fisheries, the Stuart-Nechako population was estimated to have comprised up to 20% of the catch in a period prior to 15 July. The Stuart-Nechako drainage is large, and there

are some spawning populations that we have not yet analyzed. These populations include those in the Driftwood River and Middle River in the Stuart River drainage, and the Chilako River and Nadina River in the Nechako River drainage. These populations are likely most similar to the Stuart River and Nechako River populations with respect to microsatellite variation, and the Stuart-Nechako stock in the baseline may be a proxy for the occurrence of one or more of these populations in the fishery samples.

The application of microsatellite variation to estimation of stock composition of chinook salmon in Fraser River mixed-stock fisheries was conducted as a result of conservation concerns, particularly for early-migrating populations. The mixed-stock analysis enabled accurate estimates of stock composition in mixed-stock fishery samples and can even be applied to nonretention fisheries because the fish can be released alive after sampling. The applications developed for Fraser River chinook salmon is an example of the power of microsatellite variation that will likely be applied to an increasing number of species and fisheries for which the management concerns of identifying population structure and detecting specific populations in mixed-stock fisheries arise.

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**Appendix Table 1**

Estimated percentage stock compositions of chinook salmon from lower Fraser River commercial fisheries in 1997–99. Stock compositions were estimated with a 50-population Fraser baseline by using six loci for the 1997 samples and 13 loci for the 1998 and 1999 samples. Main populations identified within regions are listed, and populations within regions having minor allocations grouped as “Other Mid Fraser,” etc. *n* is the number of fish sampled in each period. Standard deviations are shown in parentheses and were estimated from 100 resamplings of both the baseline and mixtures.

Population	Prior to 19 April			24–26 April			
	1997	1998	1999	1997	1998	1999	
<i>n</i>	115	114	142	29	30	191	
Birkenhead	Birkenhead	7.2 (2.9)	8.4 (2.5)	12.1 (2.7)	4.0 (4.2)	8.6 (5.7)	1.6 (0.8)
Lower Fraser	All populations	4.8 (2.2)	0.0 (0.4)	0.0 (0.4)	0.0 (3.0)	0.0 (0.0)	0.7 (0.7)
Mid Fraser	Nechako–Stuart	20.1 (6.5)	16.0 (5.8)	8.6 (4.4)	0.0 (5.6)	0.0 (6.7)	12.7 (4.1)
	Endako	1.5 (2.1)	2.7 (2.4)	0.0 (0.0)	0.0 (3.3)	0.0 (5.7)	3.8 (1.5)
	Up.–Lower Chilcotin	32.3 (6.2)	30.3 (6.2)	34.8 (6.0)	18.5 (10.3)	26.2 (11.3)	13.4 (2.8)
	Bridge	0.0 (4.2)	4.0 (6.5)	2.5 (2.5)	9.6 (7.3)	0.1 (8.5)	7.4 (4.2)
	Cottonwood	4.4 (2.3)	3.2 (2.1)	0.0 (1.4)	20.8 (10.0)	8.2 (6.5)	9.4 (2.2)
	Chilko	0.0 (0.3)	0.0 (0.2)	1.3 (1.2)	0.0 (2.1)	0.0 (1.1)	0.7 (0.8)
	Elkin	0.0 (0.0)	0.0 (0.2)	0.0 (0.2)	0.0 (2.2)	0.0 (0.0)	0.0 (0.0)
	Westroad	0.0 (1.3)	3.8 (3.4)	0.0 (2.9)	0.0 (0.9)	0.0 (1.8)	4.1 (1.5)
	Other Mid Fraser	0.0 (1.3)	0.0 (0.7)	5.6 (3.0)	0.0 (2.2)	0.0 (1.1)	0.0 (0.9)
	Upper Fraser	Tete Jaune	0.0 (0.0)	0.0 (0.2)	0.0 (0.0)	0.0 (2.0)	0.0 (2.4)
Willow		0.0 (1.0)	0.0 (1.1)	0.0 (2.1)	0.0 (5.7)	0.0 (4.6)	5.1 (2.2)
Holmes		0.0 (0.5)	0.4 (1.2)	0.0 (1.0)	0.0 (6.2)	11.6 (7.1)	5.8 (3.5)
Salmon		3.2 (2.9)	1.7 (3.4)	1.3 (3.1)	0.0 (4.6)	10.6 (10.4)	6.8 (2.9)
Bowron		0.0 (2.9)	0.0 (0.3)	0.0 (3.5)	1.4 (11.0)	6.2 (9.8)	1.5 (2.4)
McGregor		0.0 (0.4)	0.0 (0.0)	0.0 (0.0)	0.5 (7.2)	10.3 (8.7)	0.0 (0.7)
Dome		2.4 (1.7)	0.0 (0.8)	0.0 (1.4)	0.0 (3.8)	0.0 (2.2)	2.0 (1.7)
Goat		2.5 (1.4)	0.0 (0.9)	0.0 (1.1)	9.6 (6.9)	0.3 (4.9)	3.4 (1.5)
Other Upper Fraser		0.0 (1.6)	0.5 (1.0)	5.3 (3.0)	18.3 (9.0)	0.0 (2.1)	1.6 (1.2)
Lower Thompson	Cold–Spius–Nicola	11.1 (5.6)	24.6 (5.3)	26.0 (5.2)	9.4 (5.9)	13.5 (7.6)	13.8 (2.6)
	Deadman	8.5 (4.9)	2.5 (3.4)	0.0 (1.4)	0.0 (2.5)	0.0 (2.8)	0.0 (0.9)
	Bonaparte	0.1 (3.1)	0.8 (3.3)	0.0 (0.9)	0.0 (4.0)	0.0 (0.1)	4.2 (1.8)
North Thompson	All populations	1.7 (1.9)	1.2 (1.1)	2.3 (1.6)	3.6 (4.5)	4.4 (4.1)	2.3 (1.2)
South Thompson	All populations	0.2 (1.2)	0.1 (0.9)	0.2 (1.0)	4.3 (3.7)	0.0 (1.1)	0.0 (0.1)

Continued

Appendix Table 1 (continued)

Region	Population	2–3 May			8–10 May		15–17 May	
		1997	1998	1999	1998	1999	1998	1999
<i>n</i>		51	50	62	119	137	164	126
Birkenhead	Birkenhead	5.3 (3.1)	4.4 (2.7)	0.0 (0.0)	0.0 (0.0)	0.0 (0.0)	0.6 (1.1)	0.0 (0.0)
Lower Fraser	All populations	0.8 (4.6)	0.0 (0.6)	0.0 (0.2)	0.0 (0.0)	0.0 (0.3)	0.0 (0.5)	0.0 (0.1)
Mid Fraser	Nechako–Stuart	6.9 (6.4)	5.4 (7.9)	21.1 (7.6)	9.0 (4.8)	13.6 (5.0)	5.8 (6.7)	9.0 (4.4)
	Endako	0.9 (4.2)	3.7 (3.9)	0.0 (1.6)	2.7 (3.0)	0.0 (1.1)	1.5 (3.2)	0.0 (0.8)
	Up.–Lower Chilcotin	13.9 (7.7)	9.7 (5.7)	18.1 (6.2)	10.7 (4.0)	23.3 (4.6)	19.6 (4.5)	18.6 (4.4)
	Bridge	5.9 (7.2)	0.0 (8.8)	2.6 (4.4)	1.7 (5.6)	6.8 (5.5)	6.3 (5.3)	1.6 (5.0)
	Cottonwood	8.9 (5.4)	20.2 (8.4)	1.4 (2.7)	10.5 (5.1)	1.9 (1.4)	17.5 (4.5)	14.9 (4.0)
	Chilko	9.0 (5.6)	0.0 (2.6)	0.0 (0.4)	2.6 (3.3)	0.0 (1.3)	0.0 (0.2)	0.0 (0.8)
	Elkin	0.0 (3.1)	0.0 (0.0)	0.0 (0.3)	0.0 (0.2)	0.0 (0.3)	0.0 (0.0)	0.0 (0.1)
	Westroad	0.0 (1.7)	0.0 (3.4)	5.5 (2.6)	0.0 (0.6)	4.3 (1.9)	1.7 (1.9)	3.4 (1.5)
	Other Mid Fraser	0.0 (1.0)	0.0 (1.2)	0.0 (1.1)	0.1 (1.2)	2.0 (0.9)	1.3 (1.3)	0.8 (0.8)
Region	Population	2–3 May			8–10 May		15–17 May	
		1997	1998	1999	1998	1999	1998	1999
Upper Fraser	Tete Jaune	0.0 (1.3)	2.5 (3.3)	0.0 (2.1)	0.0 (1.3)	0.0 (0.3)	8.7 (4.1)	0.0 (0.9)
	Willow	2.5 (4.7)	8.8 (5.5)	0.0 (2.1)	9.2 (4.4)	2.5 (2.3)	1.6 (2.3)	2.7 (1.9)
	Holmes	0.0 (0.8)	0.0 (2.4)	10.3 (4.6)	11.3 (7.2)	4.6 (2.9)	3.0 (5.1)	5.5 (3.5)
	Salmon	12.8 (7.9)	7.5 (9.3)	0.1 (4.4)	14.2 (7.5)	4.9 (3.5)	8.9 (4.9)	4.7 (3.4)
	Bowron	0.3 (6.6)	3.0 (6.0)	0.3 (2.3)	0.0 (3.4)	0.0 (1.8)	0.0 (3.6)	0.0 (1.8)
	McGregor	0.0 (2.5)	0.0 (2.8)	0.0 (1.4)	0.0 (0.9)	0.0 (0.6)	1.9 (2.2)	1.0 (2.1)
	Dome	6.9 (6.6)	0.0 (3.6)	0.0 (0.0)	1.3 (5.9)	1.1 (1.7)	0.0 (2.9)	0.0 (0.8)
	Goat	0.0 (3.4)	3.3 (3.8)	1.8 (1.1)	0.1 (2.4)	0.0 (0.5)	0.3 (2.2)	1.1 (1.0)
Other Upper Fraser	9.2 (5.9)	6.3 (5.3)	4.2 (3.0)	3.2 (2.5)	0.0 (1.0)	3.2 (2.9)	1.8 (1.6)	
Lower Thompson	Cold-Spius-Nicola	7.3 (5.4)	6.0 (7.0)	15.6 (6.1)	15.0 (5.8)	28.4 (4.8)	13.5 (4.0)	25.1 (4.7)
	Deadman	9.5 (5.1)	0.2 (2.2)	5.5 (4.5)	7.7 (4.3)	3.3 (2.8)	0.0 (1.4)	3.0 (3.0)
	Bonaparte	.0 (2.9)	0.0 (0.0)	8.7 (5.5)	0.0 (3.4)	0.0 (2.5)	0.0 (1.6)	3.5 (2.5)
North Thompson	All populations	0.0 (1.1)	9.1 (6.4)	5.2 (4.5)	0.0 (0.8)	3.4 (2.4)	4.7 (3.2)	2.8 (2.5)
South Thompson	All populations	0.0 (0.1)	0.0 (0.2)	0.0 (0.0)	1.0 (1.0)	0.0 (0.3)	0.0 (0.3)	0.7 (0.8)

*Continued*

Appendix Table 1 (continued)

Region	Population	May 22–24		May 29–31		June 5–7	
		1998	1999	1998	1999	1998	1999
	<i>n</i>	234	99	201	37	245	85
Birkenhead	Birkenhead	0.0 (0.8)	1.0 (1.5)	0.0 (0.0)	0.0 (0.0)	0.0 (0.0)	0.0 (0.0)
Lower Fraser	All populations	1.2 (1.1)	0.0 (0.2)	1.0 (1.0)	0.0 (0.0)	0.0 (0.2)	0.0 (0.0)
Mid Fraser	Nechako–Stuart	9.7 (4.7)	15.4 (5.5)	3.6 (3.7)	2.8 (5.6)	4.8 (3.3)	9.3 (5.6)
	Endako	8.1 (3.6)	2.3 (2.0)	7.5 (3.0)	0.0 (0.0)	4.9 (2.6)	0.0 (0.8)
	Up.–Lower Chilcot	12.2 (3.7)	13.3 (4.3)	4.8 (2.5)	4.7 (5.5)	3.2 (1.9)	2.5 (1.8)
	Bridge	0.3 (3.7)	0.6 (2.6)	4.0 (5.0)	4.1 (4.8)	3.0 (3.5)	10.2 (5.2)
	Cottonwood	7.0 (3.5)	8.0 (2.9)	6.6 (2.8)	5.0 (3.3)	5.5 (2.5)	6.8 (3.4)
	Chilko	0.0 (1.4)	0.0 (0.0)	0.0 (1.0)	3.6 (2.9)	0.0 (0.4)	0.0 (0.4)
	Elkin	0.0 (0.1)	0.0 (0.0)	0.0 (0.5)	0.0 (0.0)	0.0 (0.2)	0.0 (0.4)
	Westroad	3.9 (1.5)	0.0 (1.2)	1.6 (1.4)	0.0 (1.4)	0.0 (0.4)	0.0 (0.5)
	Other mid Fraser	0.4 (1.2)	2.8 (2.0)	0.0 (0.9)	7.6 (5.3)	1.4 (1.5)	2.6 (4.1)
	Upper Fraser	Tete Jaune	1.7 (1.8)	0.0 (2.7)	6.9 (4.2)	0.0 (1.0)	1.7 (2.7)
Willow		1.2 (2.3)	4.6 (2.7)	8.1 (4.1)	0.3 (5.3)	7.0 (3.5)	1.6 (2.3)
Holmes		14.0 (5.4)	9.9 (4.9)	8.3 (6.1)	9.5 (5.8)	10.5 (6.1)	19.9 (6.4)
Salmon		11.1 (4.7)	1.7 (3.0)	5.2 (4.0)	17.7 (11.6)	12.2 (4.8)	3.8 (3.7)
Bowron		5.9 (3.9)	3.0 (3.1)	0.0 (2.7)	10.0 (9.2)	1.1 (3.3)	0.0 (2.6)
MacGregor		1.7 (1.8)	0.0 (2.4)	2.9 (3.5)	0.0 (3.8)	13.5 (4.4)	0.0 (2.0)
Dome		5.9 (4.5)	0.0 (2.4)	8.6 (5.6)	0.0 (2.4)	7.2 (4.4)	9.1 (4.7)
Goat		1.3 (2.1)	0.0 (0.7)	7.8 (3.0)	0.0 (0.6)	11.9 (3.8)	0.0 (0.7)
Other Upper Fraser	0.6 (1.7)	3.4 (2.2)	4.1 (3.5)	7.1 (5.2)	1.6 (1.7)	8.7 (4.2)	
Lower Thompson	Cold–Spius–Nicola	9.7 (2.8)	30.7 (4.9)	9.8 (3.6)	27.6 (9.4)	4.2 (2.6)	13.2 (3.5)
	Deadman	0.0 (0.6)	0.0 (2.9)	0.0 (0.7)	0.0 (2.3)	1.1 (1.2)	0.0 (1.0)
	Bonaparte	1.2 (1.7)	2.5 (2.2)	1.9 (2.5)	0.0 (2.0)	0.0 (0.6)	0.0 (0.5)
North Thompson	All populations	3.0 (2.1)	0.9 (0.8)	5.5 (3.7)	0.0 (1.1)	3.5 (2.6)	2.3 (2.7)
South Thompson	All populations	0.0 (0.3)	0.0 (0.0)	1.8 (1.2)	0.0 (0.3)	1.9 (1.0)	0.0 (0.3)

Continued

Appendix Table 1 (continued)

Region	Population	12–15 June		19–June		After 27 June	
		1998	1999	1998	1999	1998	1999
<i>n</i>		258	172	322	203	63	113
Birkenhead	Birkenhead	0.0 (0.0)	0.0 (0.0)	0.0 (0.0)	0.0 (0.0)	0.0 (0.7)	0.0 (0.0)
Lower Fraser	All populations	0.0 (0.0)	0.0 (0.0)	0.0 (0.0)	0.0 (0.0)	0.8 (1.9)	0.0 (0.0)
Mid Fraser	Nechako–Stuart	0.0 (0.0)	14.2 (3.9)	0.0 (2.6)	4.6 (3.4)	6.0 (5.1)	7.2 (4.9)
	Endako	2.1 (1.6)	3.1 (1.7)	0.6 (1.6)	0.0 (0.9)	6.6 (4.6)	2.0 (1.6)
	Up.–Lower Chilcotin	0.8 (1.8)	8.4 (2.2)	3.2 (2.6)	10.4 (3.0)	6.5 (4.6)	12.1 (4.2)
	Bridge	16.3 (4.3)	2.6 (3.5)	8.5 (4.1)	4.2 (3.3)	0.0 (2.4)	0.0 (0.0)
	Cottonwood	2.7 (1.8)	2.5 (1.5)	0.0 (1.0)	6.0 (1.9)	0.0 (1.1)	3.9 (2.4)
	Chilko	0.0 (1.1)	0.0 (1.0)	3.4 (2.0)	0.5 (0.8)	0.0 (0.8)	1.9 (1.3)
	Elkin	0.2 (1.2)	0.0 (1.0)	0.0 (0.4)	0.0 (0.0)	0.0 (0.4)	1.6 (1.3)
	Westroad	0.3 (1.2)	1.6 (1.1)	0.0 (0.2)	0.3 (0.6)	3.4 (2.8)	0.9 (1.0)
	Other Mid Fraser	1.0 (1.1)	4.8 (3.2)	0.9 (1.5)	1.7 (1.9)	0.2 (6.3)	2.6 (5.1)
	Upper Fraser	Tete Jaune	3.4 (4.1)	0.0 (0.9)	12.0 (3.8)	3.4 (2.5)	6.6 (8.9)
Willow		3.4 (2.9)	6.9 (3.0)	0.1 (2.1)	0.9 (1.6)	0.0 (2.5)	1.1 (1.9)
Holmes		16.2 (5.6)	12.5 (4.3)	18.0 (5.0)	17.8 (4.4)	16.6 (10.0)	8.7 (3.6)
Salmon		4.2 (3.3)	2.8 (2.8)	4.7 (3.1)	12.9 (4.0)	0.0 (3.9)	15.0 (4.9)
Bowron		1.8 (4.2)	0.9 (2.6)	1.1 (3.1)	0.5 (1.8)	9.1 (6.5)	6.5 (4.1)
McGregor		15.1 (6.2)	8.8 (3.4)	8.1 (3.8)	6.3 (3.5)	0.0 (3.9)	5.3 (4.3)
Dome		0.0 (3.2)	10.1 (4.0)	10.1 (3.7)	10.4 (3.9)	11.0 (7.0)	6.7 (4.1)
Goat		13.7 (3.3)	0.7 (0.5)	6.2 (2.6)	0.0 (1.0)	16.5 (6.6)	1.9 (0.8)
Other Upper Fraser		5.6 (3.8)	2.3 (1.9)	7.8 (4.6)	2.5 (2.5)	5.0 (5.2)	5.4 (2.9)
Lower Thompson		Cold–Spius–Nicola	8.2 (2.5)	12.4 (3.2)	3.0 (1.5)	8.2 (2.3)	6.0 (5.1)
	Deadman	0.0 (0.7)	0.9 (1.7)	0.0 (0.8)	2.7 (1.8)	0.0 (0.0)	0.0 (0.6)
	Bonaparte	0.4 (1.1)	2.7 (2.1)	0.3 (0.8)	2.6 (1.6)	0.0 (0.0)	3.5 (2.3)
North Thompson	All populations	2.2 (1.3)	1.0 (1.6)	5.2 (2.9)	3.5 (3.4)	2.9 (2.8)	2.3 (1.8)
South Thompson	All populations	2.4 (2.3)	0.8 (0.7)	7.0 (3.1)	0.6 (0.7)	2.8 (2.2)	3.2 (2.4)

Appendix Table 2

Estimated percentage stock compositions of chinook salmon from a mid-Fraser River commercial fishery in 1998. Main populations identified within regions are listed, and populations within regions having minor allocations are grouped as “Other Mid Fraser,” etc. *n* is the number of fish sampled in each period. Standard deviations are shown in parentheses and were estimated from 100 bootstrap resamplings of both the baseline and mixtures.

Region	Population	21 Jun–4 July	5–13 July
<i>n</i>		59	101
Mid Fraser	Upper-Lower Chilcotin	35.6 (8.6)	4.9 (2.6)
	Stuart-Nechako	13.1 (8.3)	7.9 (6.1)
	Cottonwood	5.3 (3.9)	5.4 (3.6)
	Horsefly	8.7 (3.5)	3.2 (3.2)
	Other Mid Fraser	0.0 (2.0)	9.9 (4.6)
	All Mid Fraser	62.7 (11.3)	31.3 (8.3)
Upper Fraser	Salmon	30.3 (10.4)	5.6 (5.1)
	Bowron	0.0 (6.0)	14.1 (8.1)
	McGregor	0.0 (1.1)	13.5 (7.9)
	Tete Jeune	0.0 (1.4)	13.3 (6.2)
	Goat	2.9 (2.7)	13.6 (5.6)
	Other Upper Fraser	2.1 (3.3)	7.5 (4.9)
	All Upper Fraser	35.3 (11.7)	67.6 (9.0)
Lower Thompson	All populations	2.0 (2.2)	0.0 (0.3)
South Thompson	All populations	0.0 (0.5)	1.1 (1.4)



**Appendix Table 3**

Estimated percentage stock compositions of chinook salmon from a lower Fraser River test fishery at Albion in 1995. Stock compositions were estimated with a 50-population Fraser baseline and five microsatellite loci. Main populations identified within regions are listed. *n* is the number of fish sampled in each period. Standard deviations are shown in parentheses and were estimated from 100 bootstrap resamplings of both the baseline and mixtures.

Region	Population	14–30 Apr	1–31 May	1–15 Jun	16–30 Jun	1–15 Jul
<i>n</i>		44	94	128	415	251
Birkenhead	Birkenhead	2.3 (2.0)	0.0 (0.0)	1.1 (1.2)	0.0 (0.2)	0.0 (0.2)
Lower Fraser	All populations	1.8 (2.4)	0.0 (0.0)	0.0 (0.6)	0.0 (0.8)	0.0 (1.1)
Mid Fraser	Chilcotin	38.0 (8.8)	10.9 (3.0)	9.9 (3.7)	4.4 (1.9)	2.2 (2.2)
	Stuart–Nechako	10.6 (8.2)	22.2 (6.6)	1.9 (2.4)	4.1 (3.4)	4.6 (3.8)
	Quesnel	3.1 (5.5)	0.8 (4.4)	0.0 (3.4)	2.8 (2.4)	4.0 (3.6)
	Chilko	0.0 (2.2)	0.0 (1.4)	5.9 (4.3)	9.6 (3.2)	11.0 (3.5)
	All populations	64.6 (9.6)	51.2 (6.2)	40.1 (7.8)	31.1 (4.4)	34.3 (5.5)
Upper Fraser	Tete Jaune	2.4 (3.9)	2.9 (2.5)	0.0 (2.4)	2.9 (2.3)	10.8 (3.8)
	McGregor	0.0 (1.1)	14.3 (5.0)	11.8 (5.3)	11.1 (3.3)	0.0 (2.7)
	Salmon	10.3 (6.0)	3.8 (3.8)	7.3 (5.3)	0.0 (1.5)	2.3 (2.8)
	Goat	0.0 (0.5)	0.3 (1.0)	7.0 (3.8)	1.8 (1.6)	6.0 (2.9)
	Holmes	9.8 (5.2)	2.8 (3.7)	0.0 (2.2)	3.6 (3.1)	0.0 (2.3)
	All populations	22.5 (8.3)	43.3 (6.4)	44.4 (7.4)	51.6 (4.0)	38.6 (4.9)
Lower Thompson	Cold–Spius–Nicola	5.2 (3.5)	0.0 (1.3)	5.5 (3.7)	2.5 (1.67)	4.5 (2.1)
	All populations	5.2 (3.5)	2.5 (1.7)	5.6 (3.5)	5.1 (1.7)	5.0 (2.3)
North Thompson	Clearwater	0.0 (0.9)	0.0 (0.2)	3.0 (2.4)	0.0 (0.8)	4.7 (2.4)
	Raft	3.6 (4.3)	0.0 (0.0)	0.0 (1.6)	1.8 (1.8)	0.0 (0.9)
	All populations	3.6 (4.4)	2.0 (0.9)	3.0 (2.9)	2.1 (2.0)	6.2 (3.3)
South Thompson	South Thompson	0.0 (0.0)	0.0 (0.0)	0.0 (0.4)	1.6 (1.4)	1.0 (1.4)
	Lower Adams	0.0 (0.6)	0.0 (0.0)	1.5 (1.6)	0.0 (0.5)	2.5 (1.7)
	Lower Shuswap	0.0 (0.0)	1.1 (0.9)	2.2 (1.8)	3.3 (1.8)	5.1 (2.5)
	All populations	0.0 (0.8)	1.1 (0.9)	5.9 (2.7)	10.0 (2.2)	16.0 (2.8)
Region	Population	16–31 Jul	1–15 Aug	16–31 Aug	1–30 Sep	1–25 Oct
<i>n</i>		292	302	180	83	61
Birkenhead	Birkenhead	0.0 (0.1)	0.0 (0.0)	0.0 (0.2)	0.0 (1.2)	3.8 (2.7)
Lower Fraser	All populations	1.6 (1.5)	0.4 (1.0)	3.1 (2.3)	44.8 (7.5)	80.7 (6.2)
Mid Fraser	Chilcotin	1.9 (1.4)	0.8 (1.4)	3.6 (2.4)	6.1 (5.1)	2.2 (2.1)
	Stuart–Nechako	10.9 (4.2)	6.8 (3.0)	2.8 (2.7)	1.8 (3.7)	2.5 (3.4)
	Quesnel	5.0 (3.5)	10.8 (3.7)	12.1 (4.4)	3.0 (4.5)	0.0 (0.8)
	Chilko	8.1 (3.0)	5.9 (2.8)	0.2 (1.5)	2.4 (3.1)	2.4 (2.9)
	All populations	31.5 (4.6)	29.2 (4.2)	22.0 (4.2)	23.6 (7.4)	7.1 (4.9)
Upper Fraser	Tete Jaune	3.7 (2.1)	1.9 (1.5)	0.0 (0.0)	0.6 (2.6)	0.0 (0.4)
	McGregor	1.7 (2.0)	0.0 (0.5)	0.0 (0.0)	0.0 (0.3)	0.0 (0.0)
	Salmon	1.6 (1.8)	1.1 (1.2)	0.0 (0.0)	0.0 (0.4)	0.4 (1.4)
	Goat	0.8 (1.1)	0.0 (1.1)	0.1 (0.7)	0.0 (1.3)	0.0 (0.0)
	Holmes	1.1 (2.9)	0.0 (0.9)	0.0 (0.0)	0.0 (2.3)	0.0 (0.4)
	All populations	20.7 (4.6)	7.2 (2.7)	0.8 (1.6)	7.3 (5.1)	0.4 (1.9)
Lower Thompson	Cold–Spius–Nicola	2.5 (1.2)	0.0 (0.4)	0.0 (0.8)	0.0 (0.9)	0.0 (1.3)
	All populations	2.5 (1.5)	0.0 (0.5)	0.0 (1.4)	0.0 (1.8)	0.0 (1.4)
North Thompson	Clearwater	18.5 (3.7)	7.9 (2.9)	14.0 (3.9)	4.9 (3.5)	0.0 (1.6)
	Raft	4.2 (3.4)	7.5 (3.3)	0.0 (1.7)	0.0 (2.5)	3.5 (5.0)
	All populations	26.2 (4.6)	18.7 (3.4)	16.3 (4.3)	4.9 (4.2)	5.8 (5.7)
South Thompson	South Thompson	6.0 (3.4)	24.7 (5.9)	24.6 (6.4)	14.7 (7.1)	2.2 (1.8)
	Lower Adams	5.7 (2.6)	2.3 (3.5)	10.1 (5.2)	0.0 (3.6)	0.0 (0.0)
	Lower Shuswap	2.6 (1.8)	14.4 (3.9)	7.6 (5.2)	0.0 (2.7)	0.0 (0.0)
	All populations	17.6 (3.7)	44.4 (4.2)	57.7 (4.8)	19.4 (6.3)	2.2 (2.4)