

**Genetic analyses of Chinook Salmon  
caught in the Skeena River Sport Fishery  
2010.**

Ivan Winther

Fisheries & Oceans Canada  
Science Branch, Pacific Region  
417-2<sup>nd</sup> Avenue West  
Prince Rupert, British Columbia  
V8J-1G8

April, 2011

*A project funded by the Pacific Salmon Foundation.*

**CONTENTS**

Abstract.....	iii
List of Tables .....	iii
List of Figures.....	iii
List of Appendices .....	iii
Introduction.....	1
Methods.....	2
Results.....	3
Discussion.....	3
Acknowledgements.....	5
References.....	6
Tables.....	7
Figures.....	12
Appendices.....	14

## ABSTRACT

Samples were collected from 378 Chinook salmon (*Oncorhynchus tshawytscha*) caught by anglers fishing in the Skeena River downstream of Terrace, British Columbia. Genetic analyses indicate that the largest stock components in the sample were from the Morice River at 30.8%, the Kitsumkalum River at 20.3% and the Babine River at 7.4%. The largest age and sex specific components in the sample were age 4<sub>2</sub> males and age 5<sub>2</sub> females.

Genetics were used to determine Chinook salmon gender and to evaluate the use of visual cues to determine gender. Visual cues were not an effective method to accurately determine the gender of Chinook salmon encountered by this fishery.

Samples indicated a larger component of Kitsumkalum Chinook in the recreational catch than measured at the Tyee Test fishery in 2010. While this difference was not statistically significant it suggests that there was selection for Kitsumkalum Chinook salmon in the recreational fishery. Stock specific bias and the selection of Kitsumkalum Chinook salmon was discussed with respect to the effects on using genetic estimates from Tyee and escapement estimates from the Kitsumkalum River to produce estimates for the aggregate of Skeena River Chinook salmon returns.

## LIST OF TABLES

Table 1. Results of the genetic mixture model analysis of Chinook salmon caught by the 2010 recreational fishery on the Skeena River downstream of Terrace using the 32 stock baseline and 15 loci.....	7
Table 2. Monthly breakdown of the genetic results for Chinook salmon caught by the 2010 Skeena River recreational fishery using the 32 stock baseline and 15 loci. ....	8
Table 3. Results of the monthly genetic samples applied to the 2010 Skeena River recreational catch. ....	9
Table 4. Weekly stock composition estimates for the recreational Chinook catch. ....	10
Table 5. Chinook salmon age data from fish caught in the 2010 Skeena River recreational fishery downstream of Terrace. ....	11

## LIST OF FIGURES

Figure 1. The Skeena River watershed in northern British Columbia showing the largest tributaries and the location of Tyee. ....	12
Figure 2. Neighbor-joining tree (Saitou and Nei, 1987) for 32 Skeena Chinook salmon populations using Weir & Cockerham's (1984) $F_{ST}$ genetic distance measure. ....	13

## LIST OF APPENDICES

Appendix 1. 2010 Skeena Creel Survey Chinook scale sample instructions and sample form...	14
Appendix 2. Skeena Chinook baseline used in the 2010 genetic analyses.....	16



## INTRODUCTION

Funding for this project was provided by the Pacific Salmon Foundation (PSF) to examine the stock composition of Chinook salmon (*Oncorhynchus tshawytscha*) caught in the recreational fishery on the lower Skeena River in 2010. This report presents genetic analyses of samples collected from Chinook salmon angled from the Skeena River below Terrace. The intent of this document is to meet the reporting requirements for the *Terrace Recreational Fishery Sampling* portion of the collaborative agreement between the PSF and Fisheries and Oceans Canada, Science Branch, Pacific Region. Costs to the PSF consisted of the genetic analyses of the Chinook salmon samples. Other portions of the project were funded by the Pacific Salmon Commission and by Fisheries & Oceans Canada. Data presented in this report are preliminary.

The Terrace Recreational Fishery Sampling was a component of a creel survey conducted by LGL Limited and the Kitsumkalum First Nation on the Skeena River recreational fishery downstream of Terrace. The creel survey was one of several programs conducted on Skeena River Chinook salmon in 2010 which included catch monitoring programs in recreational and First Nations' fisheries, a program to estimate the aggregate abundance of Chinook using genetics, a radio telemetry program and genetic baseline collection programs. Results from these independent projects were in preparation at the time of writing so the genetic data from the Terrace recreational fishery sampling has not been fully incorporated or compared with other data. In addition, only a portion of the baseline improvements have been incorporated in the analyses presented here. Additional analyses and further incorporation of the results into other projects are expected. Data presented in this report are preliminary.

The primary objective was to identify the stock components that make up the Chinook caught by the recreational fishery in the Skeena River below Terrace. Stock specific catch estimates were produced using the combination of preliminary 2010 Skeena River creel survey catch data and the genetic stock identification data from this project.

Skeena River Chinook salmon are important to the Pacific Salmon Treaty (PST) for their contribution to Alaskan and Canadian fisheries. They are encountered in the PST Aggregate Abundance Based Management (AABM) fisheries in Southeast Alaska (SEAK, all gear types) and Northern British Columbia (NBC Troll and Haida Gwaii (QCI) Sport). They also contribute to the Individual Stock Based Management (ISBM) fisheries in Northern British Columbia including gillnet, tidal sport, non-tidal sport, tidal First Nations' (FN) and non-tidal FN fisheries. Skeena Chinook are north migrating so they do not contribute to the West Coast Vancouver Island (WCVI) AABM fisheries nor do they contribute appreciably to ISBM fisheries south of the Skeena River.

The Skeena River has the second largest aggregate of Chinook salmon in British Columbia. The escapement index for the Skeena River aggregate has averaged over 50,000 spawners since 1985. The index is comprised of the mark-recapture estimates for the Kitsumkalum, visual estimates for the Bear, Morice and other systems and fence counts for the Sustut, Kitwanga and part of the Babine populations. The Kitsumkalum indicator stock represents approximately 30% of the spawners in the escapement index. The Bear and Morice populations have comprised 20 and 26% of the escapement index respectively on average since 1985.

Total escapements of Chinook salmon to the Skeena River are significantly larger than the indices. Projects funded by the Pacific Salmon Commission's Sentinel Stocks Program have been designed to estimate the total abundance of the Skeena Chinook salmon returns using genetic techniques. Skeena wide Chinook salmon escapement estimates and stock specific

estimates have been generated using the results from samples collected at the Tye Test Fishery. The component of the Tye sample identified as having originated from the Kitsumkalum River formed the basis for the expansions. These estimates have been generated for 2009 and 2010 and retrospective analyses are currently underway to examine historic samples.

The Kitsumkalum River Chinook salmon population is of sufficient magnitude and the mark-recapture program provides an escapement estimate with a reasonable level of accuracy such that the total return of Chinook to the Skeena River can be estimated from an unbiased sample of Skeena River Chinook. We assume the Tye Test fishery is an unbiased sampler of the Chinook salmon population entering the Skeena River.

The major recreational fishery for Skeena Chinook salmon occurs between Tye and the Kitsumkalum River. Stock specific bias in Chinook salmon removals by the recreational fishery could bias the estimates for the Skeena aggregate and its component stocks. In particular, Chinook salmon bound for the Kitsumkalum River were expected to be more vulnerable to the recreational fishery below Terrace. The recreational fishery sample collected in 2010 was compared to samples from the Tye Test Fishery to examine if stock specific bias was evident.

## METHODS

Chinook salmon caught in the recreational fishery were sampled for age (scales), nose-fork length, and visually examined to determine sex. Instructions and data forms appear as Appendix 1. Scale samples were collected onto scale books as described by MacLellan (1999). Scales were forwarded to the Fisheries & Oceans Canada, Sclerochronology Laboratory at the Pacific Biological Station for ageing. Scales were pressed for ageing then forwarded to the Molecular Genetics Laboratory (MGL) for genetic sampling.

Total genomic DNA was isolated from scale samples provided using Promega Wizard extractions in the MGL. Products amplified via PCR were size fractionated with the ABI 3730 automated DNA sequencer. Samples were analyzed using methods of DNA extraction, PCR reaction, electrophoresis, and allele scoring described by Candy et al. (2002) and Beacham et al. (2006). The MGL surveyed variation at 15 microsatellite loci for each individual Chinook salmon. Chinook salmon samples were compared against genetic baselines from 32 Skeena River populations (Appendix 2). The criteria for selecting spawning populations for the baseline were that they had to have genetic material from more than 30 individuals. A total of 368 Chinook salmon were surveyed for variation at the genetic markers. A Bayes-based estimation procedure for determining stock compositions was used in stock identification analysis (Pella and Masuda, 2001). The program CBAYES (Neaves et al 2005) can be downloaded from the Molecular Genetics Laboratory website. Estimated stock compositions were separated into specific populations. The model output included identification of gender and individual assignments to baseline populations where the posterior distribution provided probabilities for the five most likely populations for each sample.

Variance ( $v$ ) around the catch estimates of the Chinook salmon stock components identified in the recreational catch from the lower Skeena River ( $z$ ) was computed using calculations from TCChinook (99)-3 where:

$$v(z) = y^2v(x) + x^2v(y) - v(x)v(y)$$

Where  $y$  was the preliminary catch estimate from the creel survey and  $x$  was the estimated proportion of each stock component in the catch sample.

## RESULTS

Samples were collected during the Skeena River Creel survey from 16 June to 31 July 2010 from 378 Chinook salmon caught in the recreational fishery. Chinook salmon were sampled for size, gender, and scales.

Genetic results were produced for 368 fish of the 378 samples collected from the recreational fishery. The 10 fish not included in results of the genetic analyses were 3 fish without scale collections, 5 fish that exceeded the criteria for the number of missing loci and 2 fish that were mistakenly sampled in duplicate. When the genetic samples were compared against the 32 stock Skeena baseline the proportion of the sample assigned to the Kitsumkalum River was 20.3% with a standard deviation of 6.7% (Table 1). The Kitsumkalum component in the sample was second to the Morice component which made up 30.8% of the sample. The Babine component of the sample was third largest at 7.4%.

Contributions by the largest stock component in the sample, Morice River, were relatively stable in June and July, near 30% of the catch. The Kitsumkalum and Babine River stocks contributed higher proportions in July than in June (Table 2.). The catch of Morice, Babine, Bear and Kitsumkalum stocks increased from June to July while the catch of Kispiox, Kitwanga and Slamgeesh stocks decreased (Table 3.). The weekly catch proportions show Babine and Kitsumkalum stock proportions increasing through the sampling period 16 June to 31 July and the Morice proportions with a peak in the first week of July.

Within the 174 fish identified as females using genetics, 86 were correctly identified as females and 84 were incorrectly identified as males using visual identification. Within the 189 fish identified as males using genetics, 164 were correctly identified as males and 25 were incorrectly identified as females using visual identification. Overall, the visual sex identification error was 31%. Males were incorrectly identified as females 13% of the time and females were incorrectly identified as males 51% of the time.

Complete ages were derived for 294 fish and marine ages were derived for an additional 67 fish of the 378 Chinook salmon sampled from the 2010 Skeena River recreational fishery. The largest age and sex specific components in the sample were age 4<sub>2</sub> males and age 5<sub>2</sub> females. These stream type fish were from the 2006 and 2005 brood years respectively. Age 4<sub>2</sub> fish made up 60% of the males and age 5<sub>2</sub> fish made up 52% of the females sampled (Table 6.). Males made up 52% of the Chinook salmon catch for a male:female ratio of 1.08:1. Ocean type fish (ages 3<sub>1</sub>, 4<sub>1</sub> & 5<sub>1</sub>) made up 3.4% of the catch.

## DISCUSSION

Initial Chinook salmon sampling objectives for the 2010 Skeena River creel survey were to collect scales and biological data from 1000 fish; 100 fish per week over the 10 weeks of the fishery from 1 June to 7 August. Actual collections were far less (378) due to the late start of the sampling program and the relatively small number of angler interviews (585). The small sample sizes precluded meaningful comparisons of stock composition by week other than to examine trends for the largest components. Sample results were presented by month to match the temporal strata of the creel catch data.

The creel survey catch data were preliminary at the time of writing. Initial indications were that the 2010 creel survey encountered sampling problems with respect to accurately representing the full spectrum of angling activity. Angler interviews were conducted between 09:00 and 17:00 hours daily and we suspect that angling activity was underestimated for early morning and the evening periods. Corrections are proposed for the 2011 creel survey to properly

assess angler activity patterns for the full duration of daylight hours. Examination of full angler activity patterns in 2011 may allow for adjustment of the 2010 estimates.

Visual identification of gender is difficult for Chinook salmon that have recently entered the river and haven't fully developed the dimorphic sexual traits of spawning fish. Evidence of recent entry from the ocean was silver bright coloring and that 7 of the 378 fish sampled still had sea lice. Genetic analyses of gender allowed for an evaluation of the visual identification of sex with the result that males were identified correctly 87% of the time but females were identified correctly only 49% of the time. Future studies should rely on methods other than visual cues to determine gender, either through the use of genetics or by examination of the gonads.

The Skeena River baseline was revised prior to these genetic analyses to incorporate collections made in the watershed during 2009 and 2010 (Erhardt and Rabnett, 2009; Gottesfeld, 2009). The baseline included genetic material from 32 populations (Appendix 2). Baseline improvements have not been completed and additional material is scheduled for collection in 2011.

Selection for Kitsumkalum fish was expected in the recreational fishery due to their migration patterns and timing. Early indications are that Kitsumkalum fish appear to hold in the Skeena River prior to spawning and are probably more vulnerable to the recreational fishery below Terrace than passing stocks. The proportion of Kitsumkalum Chinook salmon estimated in the recreational fishery catch was 20.3% (SD 6.7%) and the proportion estimated in the Tyee Test fishery catch was 14.7% (SD 2.0%) (Winther and Candy, 2011). While the proportion in the recreational fishery was greater, the difference was not statistically significant (the proportion measured at Tyee was within one standard deviation of the proportion in the recreational fishery sample) in part due to the small sample size of the recreational catch. The difference in the point estimates of the proportions between the Tyee and recreational samples was 5.6% which represented approximately 131 fish from the recreational catch of 2351 fish.

A concern with using the ratio approach to estimate the aggregate Chinook escapement to the Skeena River was whether bias in recreational fishery removals influenced the results for the aggregate. The escapement of large Chinook salmon to the Kitsumkalum River was estimated at 13,712 fish with a standard deviation of 2,033 fish from an independent mark-recapture estimate. Using the proportion of Kitsumkalum Chinook encountered at Tyee, the estimate of the Skeena River return was 93,121 fish with a standard deviation of 18,688 fish (coefficient of variation = 20%). If the difference in the point estimates (the 131 fish removed by the recreational fishery) was added to the Kitsumkalum escapement estimate to account for the bias in recreational fishery removals the estimate for the Skeena aggregate was 94,007, less than 1% difference from the original estimate. Bias in recreational fishery removals had virtually no effect on the 2010 Skeena estimates for the aggregate or for component stocks.

At relatively low levels of catch, like the 2,351 Chinook salmon estimated in 2010, the selection bias by the recreational fishery would have to be extreme to have a significant impact on the estimate for the Skeena aggregate. In the most extreme example, if all 2,351 fish caught by the recreational fishery in 2010 were from Kitsumkalum River the estimate for the aggregate would change by 15%. Similarly, if the 2010 recreational catch was ~7000 (similar to levels estimated in 2003) the estimate for the Skeena aggregate would only increase by 3%. Stock specific bias in recreational catches appears to have modest influence on the aggregate abundance estimate under current conditions.

Caution should be used in interpretation of the stock specific results especially for small components and for stocks that are genetically similar to other stocks. Genetic similarity of the stocks in the baseline has been represented by the neighbor-joining tree (Saitou and Nei, 1987) for the 32 Skeena Chinook salmon stocks (Figure 2.). When Winther and Candy (2011) compared expansions of the stock components within the Skeena River from the Tyee samples



with independent estimates of escapement, estimates for the Babine River were higher than the independent estimates and genetic estimates to the Bear River were lower than the independent estimates. These two stocks appear very similar in the neighbor-joining tree of Skeena River stocks (Figure 2). The Tyee genetic samples overestimate the Kitwanga River component in the aggregate when compared to the fence counts in 2009 and 2010. The fence count of Kitwanga Chinook salmon was 824 fish in 2009 when the genetic ratio estimate was 3,526 fish and the fence count was 852 fish in 2010 when the genetic ratio estimate was 3,444 fish. The Kitwanga fish appear relatively similar to Kispiox and other stocks.

The project assumed that all the Chinook salmon caught in the recreational fishery below Terrace were from the Skeena River and had not strayed from other watersheds. This assumption was tested at the Tyee Test fishery in 2009 and 2010 (Winther and Candy, 2011). Virtually all of the Chinook salmon caught at Tyee were assigned to the Skeena region aggregate. Only 1.3% of the Tyee catch was assigned to the Nass River in 2009 and 0.1% was assigned to each of the Nass and Stikine River regions in 2010. Less than 0.1% was assigned to all other regions in both years. These results supported the assumption that all of the Chinook salmon caught were from the Skeena watershed and that any straying or nose-ins<sup>1</sup> were not a factor in the recreational fishery.

## ACKNOWLEDGEMENTS

This project was the result of a large number of people dedicated to assessments of Skeena River Chinook salmon. The Pacific Salmon Foundation funded the genetic analyses presented in this document. Russell T. Bolton from the Kitsumkalum First Nation collected the biological samples from Chinook salmon caught in the recreational fishery. LGL Limited and the Kitsumkalum First Nation conducted the creel survey of the lower Skeena River which was funded by the Pacific Salmon Commission's Northern Fund. The Molecular Genetics Laboratory at the Pacific Biological Station (PBS), Nanaimo, provided the genetic analyses. The Sclerochronology Laboratory at PBS provided the age analyses of the scale collections. Significant improvements to the genetic baseline were realized from collections made by Dr. Allen Gottesfeld and the staff at the Skeena Fisheries Commission; by Richard Erhardt and the staff at Taltan Fisheries; by Barry Finnegan and the staff at the Babine Fence; by Mike O'Neil and the staff at the Toboggan Creek hatchery; by Chris Culp and the staff at the Deep Creek hatchery; and by Ken Rabnett.

---

<sup>1</sup> Nose-ins refer to fish that enter a non-natal stream then leave.

## REFERENCES

- Beacham, T.D., J.R. Candy, K.L. Jonsen, J. Supernault, M. Wetklo, L. Deng, K.M. Miller, R.E. Withler, and N.V. Varnavskaya. 2006. Estimation of stock composition and individual identification of Chinook salmon across the Pacific Rim using microsatellite variation. *Transactions of the American Fisheries Society* 135:861-888.
- Candy, J.R., J.R. Irvine, C.K. Parken, S.L. Lemke, R.E. Bailey, M. Wetklo, and K. Jonsen. 2002. A discussion paper on possible new stock grouping (Conservation Units) for Fraser River Chinook salmon. *Canadian Science Advisory Secretariat Res. Doc.* 2002/085.
- Erhardt, R. and K.A. Rabnett. 2009. Unpublished data on the collection of Chinook baseline genetic samples from upper Skeena River tributaries. Tahltan Fisheries, Dease Lake, B.C., VOC ILO.
- Gottesfeld, A. S. 2009. Unpublished data on the collection of Chinook baseline genetic samples from Skeena River tributaries. Skeena Fisheries Commission, Box 18, Seymour Avenue, RR#1, South Hazelton, BC, V0J 2R0.
- MacLellan, S. E. 1999. Guide for sampling structures used in age determination of Pacific salmon. Fisheries & Oceans Canada, Stock Assessment Branch, Pacific Biological Station, Nanaimo, British Columbia.
- 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 v5.01. 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)
- Pacific Salmon Commission. 2000. Pacific Salmon Treaty, 1999 Revised Annexes, Memorandum of Understanding (1985), Exchanges of Notes.
- Pella, J., and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. *Fishery Bulletin* 99: 151-167.
- Saitou N., and M. Nei 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*, 4, 406–425.
- Seeb, L., A. Antonovich, M.A. Banks, T.D. Beacham, M.R. Bellinger, S.M. Blankenship, M.R. Campbell, N.A. Decovich, Garza, C.M. Guthrie, T.A. Lundrigan, P. Moran, S.R. Narum, J.J. Stephenson, K.J. Supernault, D.J. Teel, W.D. Templin, J.K. Wenburg, S.F. Young, and C. T. Smith. 2007. Development of a standardized DNA database for Chinook salmon. *Fisheries* 32:540-552.
- Weir B.S., C.C. Cockerham 1984. Estimation F-statistics from the analysis of population structure. *Evolution*, 38, 1358–1370
- Winther, I. and J.R. Candy. 2011. Chinook salmon escapement estimation to the Skeena River using genetic techniques 2010. Unpublished report for the Pacific Salmon Commission's Sentinel Stocks Program. File SSP-2010-1. 34 p.

## TABLES

Table 1. Results of the genetic mixture model analysis of Chinook salmon caught by the 2010 recreational fishery on the Skeena River downstream of Terrace using the 32 stock baseline and 15 loci.

Data are presented as percent of the sample by stock. N = 368.

Code	Stock	Estimate (% of sample)	Standard Deviation
52	Babine	7.4	(3.4)
20	Bear	4.3	(2.6)
15	Bulkley	0.2	(0.4)
86	Cedar	0.0	(0.2)
21	Ecstall	0.0	(0.3)
54	Exchamsiks	0.0	(0.4)
496	Exstew	0.1	(0.3)
500	Fiddler	0.0	(0.3)
271	Gitnadoix	0.3	(1.7)
494	Gitsegukla	1.0	(1.1)
497	Kasiks	0.2	(0.7)
502	Khyex	0.0	(0.5)
55	Kispiox	4.3	(3.8)
<b>24</b>	<b>Kitsumkalum</b>	<b>20.3</b>	<b>(6.7)</b>
16	Kitwanga	4.4	(4.9)
490	Kluakaz	0.3	(0.8)
418	Kluatantan	0.1	(0.9)
466	Kluayaz	1.6	(1.7)
480	Kuldo	0.1	(0.5)
19	Morice	30.8	(6.4)
501	Nangeese	3.3	(1.5)
492	Otsi	0.8	(1.3)
493	Shequnia	0.0	(0.4)
495	Sicintine	0.1	(0.4)
396	Slamgeesh	7.1	(4.8)
479	Squingula	1.1	(2.6)
399	Suskwa	2.1	(1.2)
51	Sustut	2.4	(1.0)
401	Sweetin	1.5	(2.2)
402	Thomas	4.4	(2.4)
60	Zymoetz	1.3	(2.1)
498	Zymogotitz	0.3	(0.4)

Table 2. Monthly breakdown of the genetic results for Chinook salmon caught by the 2010 Skeena River recreational fishery using the 32 stock baseline and 15 loci.

Data are presented as percent of the sample by stock. N= 110 in June and 258 in July.

Code	Stock	June Estimate (% of sample)	June Standard Deviation	July Estimate (% of sample)	July Standard Deviation
52	Babine	0.2	(0.9)	11.1	(5.0)
20	Bear	1.1	(2.1)	5.9	(3.8)
15	Bulkley	0.7	(0.9)	0.0	(0.3)
86	Cedar	0.0	(0.2)	0.0	(0.3)
21	Ecstall	0.0	(0.2)	0.0	(0.4)
54	Exchamsiks	0.0	(0.3)	0.1	(0.6)
496	Exstew	0.1	(0.4)	0.1	(0.5)
500	Fiddler	0.0	(0.2)	0.0	(0.5)
271	Gitnadoix	0.0	(0.3)	0.4	(2.5)
494	Gitsegukla	2.6	(2.0)	0.1	(1.3)
497	Kasiks	0.0	(0.2)	0.2	(1.0)
502	Khyex	0.0	(0.2)	0.0	(0.7)
55	Kispiox	9.3	(7.8)	1.8	(4.1)
<b>24</b>	<b>Kitsumkalum</b>	<b>1.0</b>	<b>(2.0)</b>	<b>31.2</b>	<b>(6.5)</b>
16	Kitwanga	9.6	(6.5)	1.8	(6.5)
490	Kluakaz	0.7	(1.5)	0.1	(0.9)
418	Kluatantan	0.1	(0.4)	0.2	(1.4)
466	Kluayaz	3.2	(3.0)	0.8	(2.1)
480	Kuldo	0.1	(0.5)	0.1	(0.6)
19	Morice	28.3	(4.7)	32.1	(8.7)
501	Nangeese	9.6	(3.8)	0.1	(1.0)
492	Otsi	1.0	(1.7)	0.7	(1.8)
493	Shegunia	0.1	(0.6)	0.0	(0.5)
495	Sicintine	0.2	(0.9)	0.0	(0.3)
396	Slamgeesh	14.0	(5.6)	3.7	(6.6)
479	Squingula	1.9	(3.1)	0.7	(3.6)
399	Suskwa	4.0	(2.3)	1.1	(1.4)
51	Sustut	4.8	(2.2)	1.2	(1.1)
401	Sweetin	0.7	(1.9)	1.9	(3.1)
402	Thomas	3.7	(2.5)	4.7	(3.3)
60	Zymoetz	2.0	(2.4)	0.9	(2.9)
498	Zymogotitz	0.9	(1.0)	0.0	(0.4)

Table 3. Results of the monthly genetic samples applied to the 2010 Skeena River recreational catch.

Data are presented as number of fish in the catch of the sample by stock. N= 110 in June and 258 in July. Catches are preliminary from LGL Limited.

Code	Stock	June Estimate (# of fish)	June Standard Deviation	July & August Estimate (# of fish)	July & August Standard Deviation
	Total Catch	792	(78.7)	1559	(157.3)
52	Babine	2	(7.0)	173	(79.5)
20	Bear	8	(16.6)	92	(59.3)
15	Bulkley	5	(7.3)	0	(5.2)
86	Cedar	0	(1.2)	0	(5.3)
21	Ecstall	0	(1.4)	0	(6.5)
54	Exchamsiks	0	(2.0)	1	(8.9)
496	Exstew	1	(3.1)	1	(7.5)
500	Fiddler	0	(1.5)	1	(7.7)
271	Gitnadoix	0	(2.7)	7	(39.4)
494	Gitsegukla	21	(16.2)	2	(20.6)
497	Kasiks	0	(1.5)	4	(15.3)
502	Khyex	0	(1.6)	1	(11.6)
55	Kispiox	74	(61.7)	28	(63.7)
<b>24</b>	<b>Kitsumkalum</b>	8	(16.0)	468	(156.2)
16	Kitwanga	76	(52.1)	28	(101.5)
490	Kluakaz	6	(11.8)	2	(13.6)
418	Kluatantan	0	(3.5)	2	(22.0)
466	Kluayaz	25	(24.1)	13	(33.0)
480	Kuldo	1	(3.9)	1	(10.0)
19	Morice	224	(43.5)	501	(144.1)
501	Nangeese	76	(31.1)	1	(15.4)
492	Otsi	8	(13.6)	11	(27.7)
493	Shegunia	1	(4.4)	0	(7.9)
495	Sicintine	2	(6.8)	0	(5.0)
396	Slamgeesh	111	(45.2)	57	(102.9)
479	Squingula	15	(24.7)	11	(55.7)
399	Suskwa	32	(18.7)	18	(21.6)
51	Sustut	38	(17.4)	18	(16.9)
401	Sweetin	5	(15.3)	29	(48.3)
402	Thomas	29	(20.0)	73	(51.5)
60	Zymoetz	16	(19.1)	15	(45.0)
498	Zymogotitz	7	(7.7)	0	(5.7)

Table 4. Weekly stock composition estimates for the recreational Chinook catch.

Data presented as percent (%) of the sample size N.

Week	June 16-19	June 20-26	June 27- July 3	July 3-10	July 11-17	July 18-24	July 19-31
N	<b>13</b>	<b>74</b>	<b>81</b>	<b>79</b>	<b>46</b>	<b>51</b>	<b>24</b>
Babine	0.0	0.1	7.8	7.7	11.6	11.7	19.7
Bear	0.0	0.4	6.4	4.5	2.8	5.8	11.9
Bulkley	0.0	1.0	0.0	0.0	0.0	0.0	0.0
Ecstall	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Exchamsiks	0.0	0.0	0.1	0.0	0.0	0.0	0.0
Exstew	0.5	0.0	0.0	0.0	0.0	0.0	0.0
Fiddler	0.0	0.0	0.1	0.0	0.0	0.0	0.0
Gitnadoix	0.3	0.0	0.2	0.9	0.2	0.1	0.0
Gitsegukla	8.1	2.1	0.3	0.2	0.0	0.0	0.0
Kasiks	0.0	0.0	0.2	0.3	0.0	0.1	0.0
Khyex	0.0	0.0	0.0	0.0	0.1	0.0	0.0
Kispiox	6.2	9.9	5.4	0.9	0.7	0.6	1.1
Kitsumkalum	0.7	0.3	13.8	20.0	38.9	46.9	47.8
Kitwanga	5.9	10.5	3.1	3.5	1.3	0.4	0.1
Kluakaz	0.2	0.7	0.0	0.0	0.0	0.1	0.2
Kluatantan	0.0	0.0	0.1	0.0	0.0	0.0	0.0
Kluayaz	0.0	2.8	2.2	0.4	0.2	0.9	1.8
Kuldo	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Morice	25.4	31.9	32.3	41.4	36.7	24.0	14.1
Nangeese	24.7	7.5	2.6	0.1	0.0	0.0	0.0
Otsi	0.0	1.2	0.3	0.1	0.6	1.1	1.3
Shequnia	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Sicintine	0.4	0.1	0.2	0.0	0.0	0.0	0.0
Slangeesh	8.3	14.9	5.0	9.7	2.2	0.3	0.3
Squingula	1.6	2.0	0.4	1.1	0.5	0.3	0.4
Suskwa	0.0	3.7	2.5	1.3	0.4	2.6	0.0
Sustut	8.0	5.9	2.9	0.5	0.6	0.2	0.0
Sweetin	0.1	0.6	3.8	0.6	0.5	1.0	0.4
Thomas_Cr	0.0	2.3	9.1	5.4	2.2	4.0	0.5
Zymoetz	2.2	2.0	1.2	1.3	0.5	0.0	0.2
Zymogotitz	7.3	0.1	0.0	0.0	0.0	0.0	0.0

Table 5. Chinook salmon age data from fish caught in the 2010 Skeena River recreational fishery downstream of Terrace.

Age	Males	Females	Total
3 <sub>1</sub>	3	1	4
4 <sub>1</sub>	1		1
5 <sub>1</sub>	2	3	5
3 <sub>2</sub>	9		9
4 <sub>2</sub>	89	2	91
5 <sub>2</sub>	27	76	103
6 <sub>2</sub>	18	62	80
7 <sub>2</sub>		1	1
1 marine year	1		1
2 marine years	21		21
3 marine years	7	14	21
4 marine years	9	15	24
Total	187	174	361
Complete ages	149	145	294
Ocean type	4.0%	2.8%	3.4%
Proportion 4 <sub>2</sub>	59.7%	1.4%	31.0%
Proportion 5 <sub>2</sub>	18.1%	52.4%	35.0%
Proportion 6 <sub>2</sub>	12.1%	42.8%	27.2%

## FIGURES

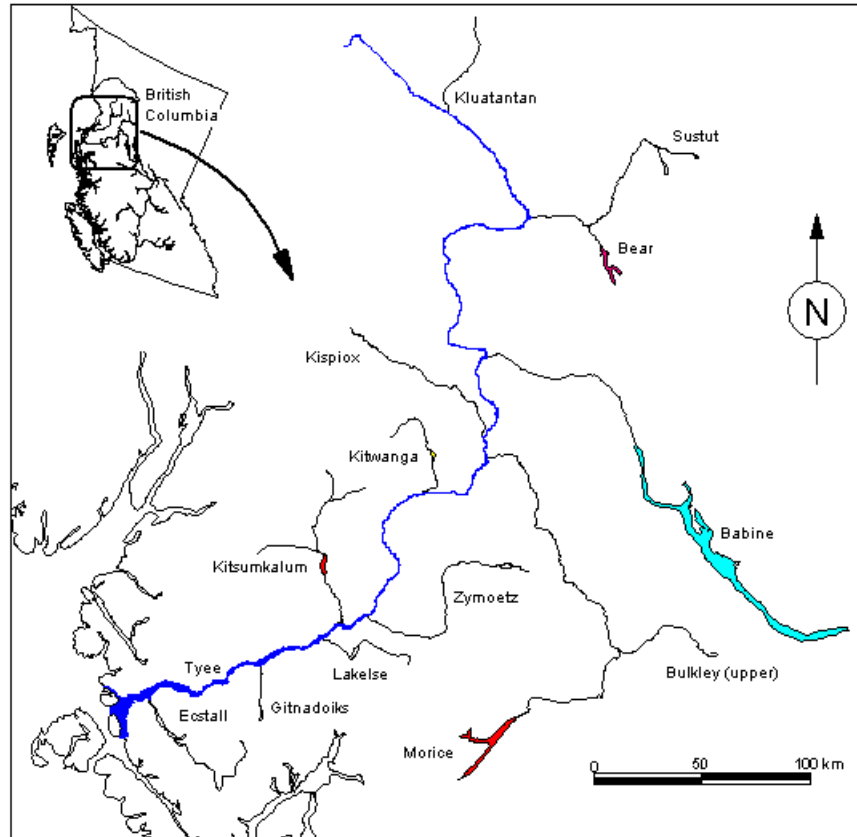


Figure 1. The Skeena River watershed in northern British Columbia showing the largest tributaries and the location of Tye.

Terrace is located at the confluence of the Kitsumkalum and Skeena Rivers.



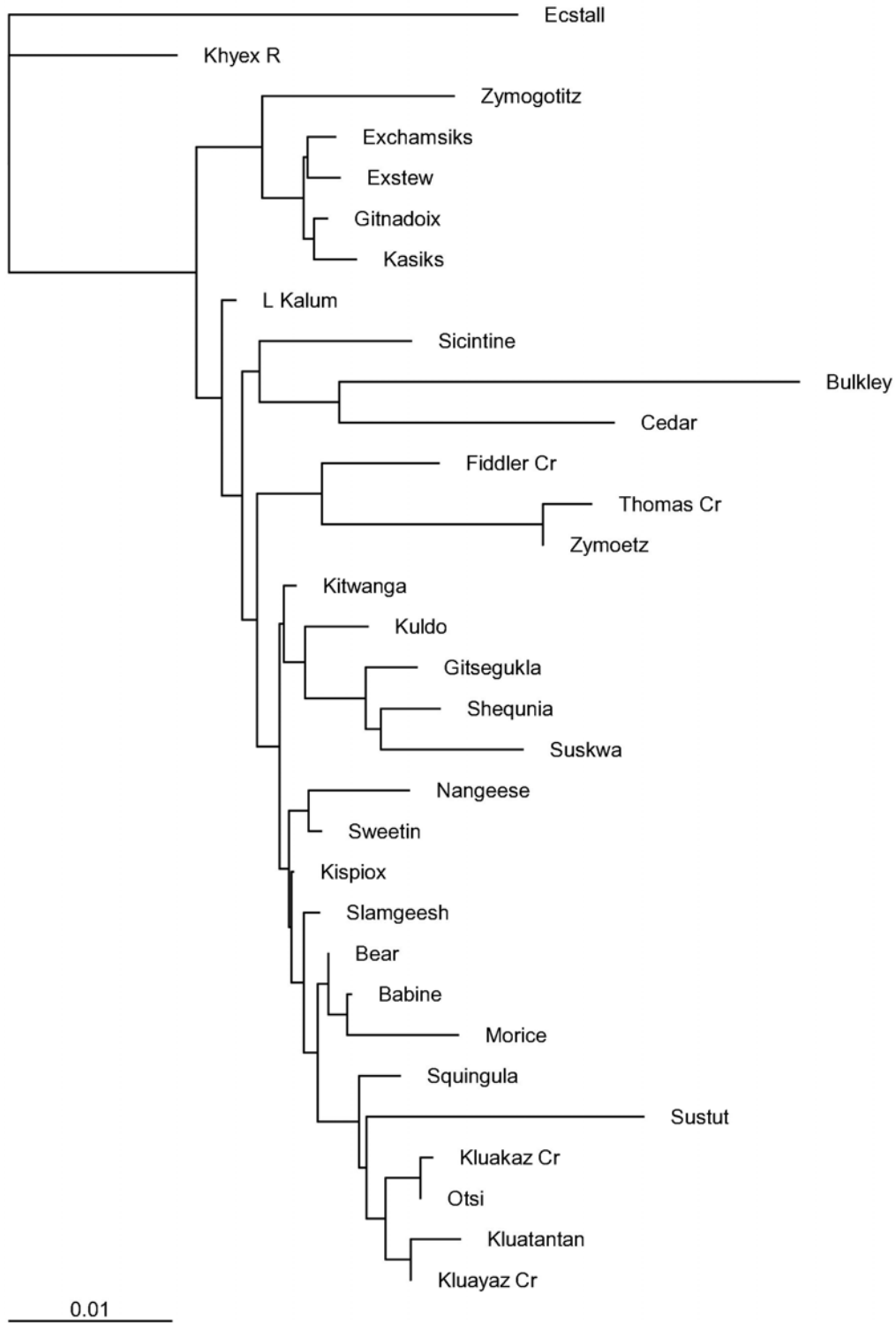


Figure 2. Neighbor-joining tree (Saitou and Nei, 1987) for 32 Skeena Chinook salmon populations using Weir & Cockerham's (1984)  $F_{ST}$  genetic distance measure.

## APPENDICES

### Appendix 1. 2010 Skeena Creel Survey Chinook scale sample instructions and sample form.

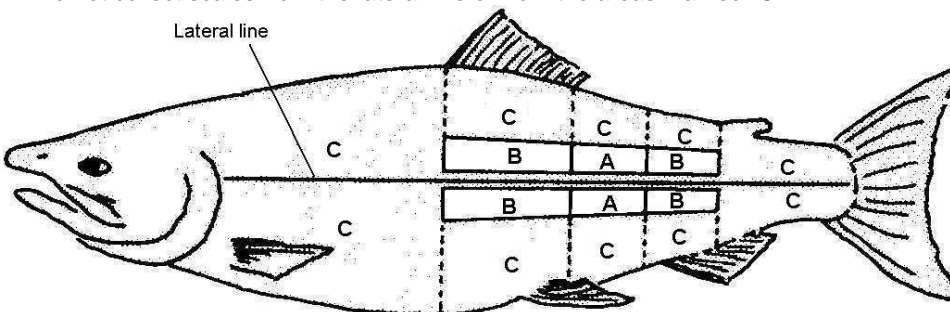
Chinook salmon caught in sport fisheries on the Skeena River will be scale sampled. These samples are in addition to the normal Creel survey sampling protocols.

The objectives will be to sample 1000 Chinook salmon over the course of the season. Sample each fish in sequence regardless of whether they have a tag, a fin clip or not. Examine and sample each fish for scales, length and sex according to the following protocol:

- Record the samplers' names at the top of each page.
- Record the scale book number in the space provided above every 10<sup>th</sup> fish.
- Record the date for each fish (you can use dittos or arrows for fish sampled on the same day).
- Record the location for each fish (" " ").
- Measure the fish from the tip of the nose to the fork of the tail and record the length in cm on the data sheet.
- Check for an adipose fin clip. In the "Fin clipped" column circle Y if the fin is missing or N if the fin is intact.
- For fin clipped fish, try to recover the head record the head label number.
- Check if the fish has an operculum tag and/or a radio tag. Radio tags are evident from the antenna which appears as a long wire protruding from the mouth.
- Record the operculum tag number and try to recover the radio tags.
- Collect 5 scales from each fish as noted below.
- Note the sex of the fish and indicate the sex by circling M for male or F for female on the data sheet.

#### Scale Samples:

- Record the scale book number on the data sheet.
- Each book will contain scales from 10 fish.
- Scale samples must come from preferred locations on the fish as indicated by an "A" in the diagram below.
- Avoid collecting scales near scars, wounds or net marks. To avoid scars you may have to collect scales from the locations marked "B" in the diagram below.
- Do not collect scales from the lateral line or from the areas marked "C".



- Wipe the slime and blood off of the preferred location on the fish.
- Using forceps, collect a scale from the preferred location.
- Check the scale to ensure the rings extend all the way to the center of the scale. If not, discard the scale and select another. Regenerated scales have a clear spot in the center of the scale that is missing the rings necessary to determine the age of the fish.
- Wipe off the scale and add it to the scale book on the appropriate numbered square.
- Do not turn the scale over; stick the scale to the book with the same side up as it was on the fish.
- Select 5 scales from the fish, 3 from one side and 2 from the other.
- The 5 scales are applied to the numbered squares in the book from top to bottom starting at the column with numbers 1, 11, 21, 31 & 41. Scales from the second fish are applied to squares 2, 12, 22, 32 & 42. etc.
- Keep the scale books dry.
- Once the book is full, fill out all of the information on the back of the page bearing the scales.
- THE LOCATION OF THE SCALES IN THE BOOKS MUST MATCH THE NUMBERS ON THE DATA SHEETS.

**SKEENA CHINOOK SAMPLES 2010**

USE PENCIL

Scale Book # \_\_\_\_\_

Sampler: \_\_\_\_\_

Fish #	SCALE #	DATE	Location	Fork Length (cm)	SEX (M / F)	Fin clipped (Y / N)	Head label number for fin clipped fish or tag #
1	1 to 41				M / F	Y / N	
2	2 to 42				M / F	Y / N	
3	3 to 43				M / F	Y / N	
4	4 to 44				M / F	Y / N	
5	5 to 45				M / F	Y / N	
6	6 to 46				M / F	Y / N	
7	7 to 47				M / F	Y / N	
8	8 to 48				M / F	Y / N	
9	9 to 49				M / F	Y / N	
10	10 to 50				M / F	Y / N	

Scale Book # \_\_\_\_\_

11	1 to 41				M / F	Y / N	
12	2 to 42				M / F	Y / N	
13	3 to 43				M / F	Y / N	
14	4 to 44				M / F	Y / N	
15	5 to 45				M / F	Y / N	
16	6 to 46				M / F	Y / N	
17	7 to 47				M / F	Y / N	
18	8 to 48				M / F	Y / N	
19	9 to 49				M / F	Y / N	
20	10 to 50				M / F	Y / N	

Scale Book # \_\_\_\_\_

21	1 to 41				M / F	Y / N	
22	2 to 42				M / F	Y / N	
23	3 to 43				M / F	Y / N	
24	4 to 44				M / F	Y / N	
25	5 to 45				M / F	Y / N	
26	6 to 46				M / F	Y / N	
27	7 to 47				M / F	Y / N	
28	8 to 48				M / F	Y / N	
29	9 to 49				M / F	Y / N	
30	10 to 50				M / F	Y / N	

## Appendix 2. Skeena Chinook baseline used in the 2010 genetic analyses.

Stock #	Stock name	Locus specific N															Maximum
		1b	i1	3g	a1	go2	go4	oke	oki	omy	ots2	ots 201b	ots 211	ots 213	ots9	sa	
52	Babine	361	385	407	388	371	382	348	365	378	393	309	296	290	400	417	407
20	Bear	155	176	174	173	156	163	148	157	161	165	99	102	92	171	175	176
15	Bulkley_sp	424	475	470	472	435	446	417	433	509	475	368	362	349	525	447	525
86	Cedar_sp	106	114	116	116	114	111	110	109	112	114	108	115	111	115	116	116
21	Ecstall	270	268	262	268	276	280	273	266	276	274	182	175	177	279	271	280
54	Exchamsiks	111	111	112	114	109	103	111	112	103	105	110	110	108	108	115	114
496	Exstew	136	138	135	137	138	138	138	134	138	136	138	138	139	136	138	139
500	Fiddler_Cr	109	109	108	106	109	109	109	109	109	109	111	110	113	109	109	113
271	Gitnadoix	204	206	207	215	222	211	224	226	212	226	174	174	183	235	213	235
494	Gitsegukla	257	258	254	246	258	255	258	253	256	260	259	255	258	259	258	260
497	Kasiks	61	59	62	61	62	61	62	61	59	61	62	62	62	63	62	63
502	Khyex_R	37	37	37	37	35	37	35	37	37	37	36	36	37	36	37	37
55	Kispiox	152	174	174	162	159	155	126	153	148	176	106	105	106	172	174	176
24	Kitsumkalum	690	722	729	709	801	797	695	788	777	787	587	566	586	706	739	801
16	Kitwanga	226	260	270	245	258	244	240	245	244	229	186	186	179	248	263	270
490	Kluakaz_Cr	119	117	120	89	115	122	117	120	124	118	122	119	120	122	118	124
418	Kluatantan	33	38	38	38	37	38	35	38	37	38	31	35	29	38	37	38
466	Kluayaz_Cr	158	159	157	162	158	158	157	161	160	158	158	158	160	157	158	162
480	Kuldo	170	169	170	170	168	164	167	168	166	169	170	160	170	168	170	170
19	Morice	241	256	287	285	244	259	228	233	253	261	208	218	195	263	306	287
501	Nangeese_R	29	32	32	32	29	31	30	32	32	30	28	30	29	30	31	32
492	Otsi	139	139	138	138	139	139	139	138	139	138	139	138	139	138	136	139
493	Shequnia	130	128	131	132	130	131	130	131	132	131	128	129	129	131	127	132
495	Sicintine	309	311	312	309	312	312	315	313	313	317	315	311	312	316	316	317
396	Slamgeesh	128	127	129	124	129	127	129	129	129	129	126	127	128	129	129	129
479	Squingula	268	266	271	266	269	267	270	265	266	262	264	258	266	264	263	271
399	Suskwa	98	98	103	102	105	104	102	108	100	102	91	100	95	99	102	108
51	Sustut	473	476	460	451	456	435	440	465	440	451	337	321	329	467	489	476
401	Sweetin	242	241	242	238	243	243	242	242	242	243	242	243	242	243	243	243
402	Thomas_Cr	62	60	62	61	62	62	61	62	62	62	60	61	61	61	61	62
60	Zymoetz	56	56	59	59	58	53	58	57	55	59	58	55	57	58	60	59
498	Zymogotitz	119	119	118	117	117	120	117	117	120	118	116	116	116	117	120	120

