

**Chinook Salmon Escapement Estimation
to the Skeena River Using Genetic
Techniques 2011.**

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ABSTRACT

The 2011 return of Chinook salmon (*Oncorhynchus tshawytscha*) to the Skeena River was estimated using genetic stock identification techniques. Genetic analyses of 903 Chinook salmon caught at the Tyee Test Fishery identified 25.1% of the sample as Kitsumkalum Chinook salmon (standard deviation = 1.8%). The preliminary escapement of large Chinook salmon to the Kitsumkalum River was estimated at 12,059 fish (standard deviation = 2,433 fish) from an independent mark-recapture estimate. The estimate of large Chinook salmon returning to the Skeena River as measured at Tyee was 48,125 fish with a standard deviation of 10,287 fish (coefficient of variation = 21.4%).

These results are preliminary as additions and modifications are scheduled for the genetic baseline used in the analyses of Skeena River Chinook salmon populations.

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INTRODUCTION

Funding for this project was provided by the Pacific Salmon Commission's Sentinel Stocks Program (SSP) to estimate Chinook salmon (*Oncorhynchus tshawytscha*) abundance in the Skeena River in 2011. This report presents the third year of genetic analyses of samples collected at the Tyee Test fishery and preliminary estimates of the Chinook salmon return to the Skeena River for 2011. Various programs on the Skeena River have contributed to aspects important to this project. Further baseline improvements are anticipated so this report represents one more step in an iterative process to improve the escapement estimates to the Skeena River. Costs to the SSP consisted of the genetic analyses and a small portion of the sampling costs at the Tyee Test fishery. Other parts of the project were funded by Fisheries & Oceans Canada in existing programs.

The primary objective of this study was to generate a watershed-wide estimate of Chinook salmon return to 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 escapement estimates of Chinook salmon to the Skeena River have been significantly larger than the indices.

Skeena Chinook salmon are encountered in the PST Aggregate Abundance Based Management (AABM) fisheries in Southeast Alaska (SEAK all gear) 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.

Genetic analyses completed for Chinook salmon samples collected at Tyee in 2000, 2001 and 2003 provided preliminary estimates for the Chinook return to the Skeena River with coefficients of variation between 15.2% and 17.2%. Improvements were expected after 2009 as the genetic baselines were improved, and four additional genetic markers used by Genetic Analysis of Pacific Salmonids (GAPS) consortium (Seeb et al. 2007) were added. Also sample sizes were expected to increase at Tyee. However, the expected improvements were not realized: Starting the Tyee Test Fishery on 25 May rather than 10 June resulted in modest increases to the Chinook sample size as the historic start date proved to be sampling more of the front tail of the summer run than initially thought. Broader variance around the mark-recapture estimates of Kitsumkalum River Chinook escapements resulted in larger CV's around the Skeena escapement estimates.

The Kitsumkalum River Chinook project produces Chinook salmon marked with coded wire tags (cwt's) for annual release as fry and yearlings. A mark-recapture program is conducted annually to estimate the escapement of the marked and unmarked fractions of the Chinook returning to the Kitsumkalum River. The data generated by the program contribute internationally as one of the stocks in the PSC Chinook model. Domestically the data contribute to Canada's Key Stream Program and provide the only exploitation rate indicator stock for Chinook salmon in the North Coast. These data are essential to the Chinook run reconstruction calculations.

The Kitsumkalum River hosts one of the largest spawning populations of Chinook salmon in the Skeena River watershed. The Kitsumkalum River indicator stock probably represents the ocean distribution of other spawning populations in the Skeena River however their age at maturity differs. Kitsumkalum River Chinook salmon have stream type life histories with the predominant portion of returns occurring at age 5₂ and 6₂ for males and at age 6₂ for females. Other Skeena Chinook salmon also have stream type life histories but age at return is usually composed of predominantly age 4₂ and 5₂ males and age 5₂ females. Other age components observed in Skeena Chinook salmon include males returning from 3 to 7 years from brood and females returning from 4 to 7 years from brood. Fish returning 7 years from brood are more common in the Kitsumkalum River. The spawning migration occurs in the summer with peak passage through river estuaries in early July. Spawning takes place in late August and early September. These life histories are consistent with those observed in most northern Chinook salmon populations other than the Kitsumkalum River returns tend to be a year older.

The Kitsumkalum River Chinook population is of sufficient magnitude and the mark-recapture program provides escapement estimates with a reasonable level of accuracy such that the total return of Chinook to the Skeena River may be estimated from an unbiased sample of the Skeena return. Expansion of the Kitsumkalum component to a Skeena wide population estimate requires that Chinook salmon from Kitsumkalum be equally vulnerable to the sample collection procedure as other components. Differences in timing and/or size of the returning sub-populations within the Skeena watershed could confound these analyses. We assume the Tyee Test fishery is an unbiased sampler of the Chinook salmon population entering the Skeena River.

Hatchery production of Chinook salmon in the Skeena watershed has been limited to small scale assessment projects and small scale production projects for community development. The hatchery production for the purposes of the exploitation rate indicator contributes an average of 2.6% to returns of Chinook salmon to the Kitsumkalum River (range from near zero to 1000 fish annually). Community production projects have been carried out and tag groups have been released from Chinook stocks in the Babine, Kispiox, Morice, Bulkley, Cedar, and Erlandsen tributaries of the Skeena River. Most releases were smaller than those to the Kitsumkalum River and success rates are unknown. The Bulkley River releases were of an early spring timed stock, not part of this proposal.

There is no evidence of Chinook salmon straying from other rivers to the Skeena River to date. No stray coded wire tags have been recovered at the Tyee Test Fishery. The Kitsumkalum River is sampled extensively and no Chinook tagged in other systems have been recovered since the beginning of the program in 1984. However, the recovery of cwt's is a relatively weak measure of straying as few populations in northern British Columbia are tagged. The nearest populations to the Skeena that have been marked with cwt's are in the Kincolith River to the north and the Kitimat River to the south. Genetic results from 2009 and 2010 samples supported the assumption that all of the Chinook salmon caught at the Tyee Test fishery were from the Skeena watershed and that any straying was extremely limited (<1%) if they occurred at all.

In addition to providing escapement estimates within the data standard, the Skeena DNA project may be linked to visual surveys to calibrate historic visual escapement estimates in large Skeena systems like the Bear and Morice Rivers.

METHODS

A Skeena wide Chinook salmon escapement estimate and stock specific estimates of escapement were produced using the genetic results from samples collected at Tyee. The component of the Tyee sample identified as originating in the Kitsumkalum River was the basis for the expansions.

Tyee is located on the tidal estuary of the Skeena River, on the north side, upstream of the confluence with the Ecstall River (Figure 1). The Tyee Test Fishery is a standardized fishery that has been conducted in the Skeena River estuary since 1955. Its' primary purpose has been to provide an in-season indication of sockeye salmon (*Oncorhynchus nerka*) abundance but is also used to monitor the relative abundance of other salmon species including Chinook (Cox-Rogers and Jantz, 1993). A gill net is deployed (set) in standard locations relative to tidal flow. Sets are made at high and low water slack tides during daylight hours. Usually three (3) sets are made per day except for some days late in the season when there are only two (2) tidal changes during daylight. An index consisting of standardized catch per effort is calculated daily. Typically more fish are caught during low water sets so the standardized catch consists of the mean of averaged high water and averaged low water catch measured per hour the net is fished.

The net used at the Tyee Test fishery is a multi-panel gill net 366 meters (200 fathoms) in length and 7.6 meters (25 feet) deep constructed of six strand monofilament nylon (Alaska twist). The net includes ten panels with web sizes ranging from 8.9 cm to 20.3 cm (3.5 inches to 8 inches) increasing in size by 1.3 cm (0.5 inch) increments. (Imperial units are included to match the web size designation by the manufacturer.) The different mesh sizes are arranged at random across the length of the net. The web is hung in a 2:1 ratio of webbing to fishing net length. A full description of the test fishery is provided by Jantz et. al. (1990).

Prior to 2009 the test fishery usually began around June 10 and continued until September. The Chinook run was underway by 10 June and peak migration past Tyee occurred at the end of June and early in July. The last Chinook are caught at Tyee around the middle of August (Figure 2.). The test fishery began 25 May, in 2009, 2010 and 2011 to capture more of the beginning of the Chinook salmon summer run.

Chinook salmon caught in the Tyee Test fishery were sampled for nose-fork length, eye orbit to hypural plate length, and were incised to determine sex. Scale samples were collected from each fish on to scale books as described by MacLellan (1999) and forwarded to the Fisheries & Oceans Canada, Sclerochronology Laboratory at the Pacific Biological Station for ageing. Tissue samples were collected for genetic analyses.

Chinook salmon collections were compared with baselines collected from 29 Skeena River populations (Appendix 1). The criteria for selecting a spawning population or site as baseline were that they had to have genetic material from over 30 individuals. Samples were analyzed for 15 microsatellite loci using methods of DNA extraction, PCR reaction, electrophoresis, and allele scoring described by Candy et al. (2002) and Beacham et al. (2006). The Molecular Genetics Laboratory at the Pacific Biological Station provided the sample analysis. A new version of the computer program as described by Pella and Masuda (2001) was used for the analyses. The program CBAYES (Neaves et al 2005) can be downloaded from the Molecular Genetics Laboratory website. The model output included individual assignments to baseline populations where the posterior distribution gives probabilities for the five most likely populations for each sample.

To examine changes in stock composition through time the 917 samples collected in 2011 were separated temporally by week and genetic results were compared for fish caught during different weeks.

A key stream program on the Kitsumkalum River estimates the escapement of large Chinook salmon to the system. In addition to the escapement estimate, biological samples are collected from live fish during the tagging event and from dead fish during the recovery event. The samples include data on size and gender and scale samples to determine age.

The mark re-capture estimate of Chinook salmon to the Kitsumkalum River consisted of simple Petersen estimates of the form:

$$N_{sr} = \frac{(M_{sr}+1)(C_{sr}+1)}{(R_{sr}+1)}$$

Where N is the estimate of large Chinook salmon, M is the number of large Chinook salmon marked, C is the total number of large Chinook salmon carcasses encountered in the dead pitch and R is the number of marked large Chinook salmon carcasses recovered in the dead pitch by sex (subscript s) and river reach (subscript r) (Ricker, 1975). Separate estimates were calculated for males and females. Variance was computed using:

$$v(N_{sr}) = N_{sr}^2(C_{sr}-R_{sr})/(C_{sr}+1)(R_{sr}+2)$$

Variance (v) for the estimate of the Chinook salmon return to the Skeena River (z) was computed using Calculations from TCChinook (99)-3 where:

$$v(z) \sim z^2((v(y)/y^2)+(v(x)/x^2))$$

or

$$v(z) \sim z^2(cv^2(y)+cv^2(x))$$

Where y was the estimate of the Kitsumkalum escapement and x was the estimate of the Kitsumkalum component measured at Tyee. The abbreviation cv refers to the coefficient of variation.

RESULTS

The Tyee Test fishery was operated from 25 May to 24 September 2011. Chinook salmon were caught from 25 May through 30 August (Figure 3.). A total of 1,043 Chinook salmon were encountered by the net; 959 large and 84 jacks. A total of 917 Chinook salmon were sampled for size, gender, scales and tissue. Depredation by seals accounted for most of the fish that could not be sampled. Often these fish were so badly mutilated that size and gender could not be determined.

The Skeena River baseline used for the analyses of the samples collected at Tyee included genetic material from 29 populations (Appendix 1) (Erhardt and Rabnett, 2009; Gottesfeld, 2009). When the 917 samples collected at Tyee in 2011 were compared against the baseline results were produced for 903 fish. The proportion of the sample assigned to the Kitsumkalum River was 25.1% with a standard deviation of 1.8% (Table 1). The Kitsumkalum component in the sample was second to the Morice component which made up 41.5% of the sample. The Bear River component of the sample was third largest at 6.1%. These rankings were near the expected values when compared with other estimates for 2011 Chinook escapements.

The 2011 escapement of Chinook salmon to the Kitsumkalum River was estimated at 12,059 large fish (jacks excluded) with a standard deviation of 2,433 fish. The total return to the Skeena River was estimated at 48,125 (standard deviation = 10,287) using the Kitsumkalum escapement estimate and the proportion of Kitsumkalum estimated at Tyee as the basis for expansion. The coefficient of variation for the estimated number of large Chinook returning to the Skeena River was 21.4%.

When we examined the stock components that make up the Chinook salmon catch at Tyee by statistical week (Table 2) catches of Morice River fish peaked during the week of July 2

to 9 (statistical week 072) with a catch of 88 fish. Catches of Kitsumkalum River Chinook salmon reached a maximum of 55 fish during the week of July 24 to 31 (statistical week 075). The timing of Babine and Bear stock components appear to be between the two larger components of Morice and Kitsumkalum (Figure 4). While the stock components may not share peak migrations or modes in migration timing, they share a common end with virtually all Chinook passing Tyee by 7 August. The timing of Babine and Bear stock components appear to be between the two larger components of Morice and Kitsumkalum (Figure 4).

DISCUSSION

The findings reported here represent preliminary estimates. Additional analyses are required to develop final estimates for the aggregate of Skeena River Chinook salmon as well as for the major component stocks. These analyses are proposed for 2012 and 2013 in combination with the Sentinel Stocks retrospective project that will examine the stock compositions of Chinook salmon samples collected at Tyee prior to 2009. Much of the remaining work depends upon revisions to the genetic baseline. Problems were identified with the baseline genetic material collected for the Morice and Babine populations in 2009. No fish were assigned to Babine even though it represented a significant portion of the stock mixes tested. New baseline samples were collected in 2010 and 2011 from Morice and Babine which resulted in assignments to the Babine population. Baseline samples collected in 2010 incorporated in the baseline for the data analyses presented here. Additional baseline changes are imminent as populations from the Morice, Babine and Zymoetz have been collected but not incorporated into the baseline yet. Further, the collection and addition of new baseline samples from the Bear River are required before the analyses may be finalized.

This project assumes that components of the Chinook salmon return to the Skeena River are equally vulnerable to the Tyee Test fishery. Starting the test fishery on 10 June appeared to truncate the front tail of the Chinook salmon migration pattern (Figure 2). Complete samples of the Chinook salmon migration were attempted by starting the test fishery on 25 May in 2009, 2010 and 2011 (Figure 3). The front tails of the migration pattern observed from 2009 to 2011 do not appear to be as substantial as might have been predicted when compared with the historic average. The proportion of the Chinook salmon runs sampled in the 25 May to 9 June period represented 6.6%, 9.5% and 3.2% of the 2009 to 2011 runs respectively.

Water levels may influence fish migration and may also affect how vulnerable they are to the test net. The 2009 to 2011 samples represented recent extremes in the range of water levels on the Skeena River. Extreme high water and flooding was experienced in 2009. This was followed by small winter snow packs and a warm, dry summer which resulted in very low water conditions in 2010. Very high water and prolonged freshet conditions were evident in 2011 as the result of heavy winter snow packs and a cool, wet spring and summer. The 2009 and 2010 migrations may have been delayed due to high water but it wasn't clear whether the fish were held up by the high water experienced in mid June or whether the high water levels made the fish passing Tyee less vulnerable to the fishery. However, the pattern of Chinook salmon catches at Tyee was not appreciably different between the three years (Figure 3).

The 2009 and 2010 Chinook salmon samples collected at Tyee were compared with the coast-wide stock baseline to test for closure in the system. The results supported the assumption that all of the Chinook salmon caught at the Tyee Test fishery were essentially from the Skeena watershed and that any straying or nose-ins¹ were extremely limited (<1%) if they occurred at all. The 2011 Tyee samples were not compared with the coast-wide stock mix since virtually all

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

of the Chinook salmon caught at Tyee were assigned to the Skeena region aggregate in 2009 and 2010.

This project does not account for removals of Chinook salmon by fisheries upstream of Tyee. Assessing whether removal rates differ among stocks encountered by in-river fisheries has yet to be measured. There were significant sport and First Nations' fisheries on the Skeena River in 2010 but final estimates were not available at the time of writing.

The genetic approach used in this study has benefitted from additional work to improve the baseline for Skeena River Chinook salmon populations. Further work to complete the improvements include sampling any remaining populations, running a simulation with the baseline to see where populations are miss-assigned; and re-sampling the Bear River Chinook salmon population for baseline genetic material.

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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.
- Cox-Rogers, S., and L. Jantz. 1993. Recent trends in the catchability of sockeye salmon in the Skeena River gillnet test fishery, and impacts on escapement estimation. *Can. Manusc. Rep. Fish. Aquat. Sci.* 2219: 19 p.
- 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 1LO.
- 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.
- Jantz, L., R. Kadowaki and B. Spilsted. 1990. Skeena River Salmon Test fishery, 1987. *Can. Data. Rep of Fish. And Aquatic. Sci. No.* 804. 151 p.
- Koch, K. 2009. Unpublished data on the passage of Chinook salmon through the Kitwanga River fence. Gitanyow Fisheries Authority, P.O. Box 148, Kitwanga, B.C. V0J 2A0.
- 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
- Pacific Salmon Commission. 2000. Pacific Salmon Treaty, 1999 Revised Annexes, Memorandum of Understanding (1985), Exchanges of Notes.
- Parken, C.K. R.E. McNicol, J.R. Irvine. 2006. Habitat-based methods to estimate escapement goals for data limited Chinook salmon stocks in British Columbia, 2004. Canadian Stock Assessment Secretariat Research Document 2006/083. Ottawa, Ontario, Canada.
- Pella, J., and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. *Fishery Bulletin* 99: 151-167.

- Ricker, W.E. 1975. Computation and interpretation of biological statistics of fish populations. Department of Environment Fisheries and Marine Service. Ottawa.
- 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

TABLES

Table 1. Results of the genetic mixture model analysis of Chinook salmon caught at the Tyeec Test fishery in 2011 using the 29 stock Skeena baseline and 15 loci.

Data are presented as percent of the sample by stock. N= 903.

Code	Stock	2011 Estimate (% of sample)	2011 Standard Deviation
511	Babine	4.4	(1.4)
20	Bear	6.1	(1.3)
15	Bulkley_Early	2.0	(0.5)
86	Cedar_Early	0.0	(0.1)
21	Ecstall	1.7	(0.4)
54	Exchamsiks	0.0	(0.2)
496	Exstew_R	1.9	(0.6)
500	Fiddler_Cr	1.3	(0.7)
271	Gitnadoix	0.7	(0.5)
497	Kasiks_R	0.0	(0.1)
502	Khyex_R	0.6	(0.3)
55	Kispiox	2.7	(1.2)
494	Kitseguecla_R	0.0	(0.1)
24	Kitsumkalum	25.1	(1.8)
16	Kitwanga	3.7	(1.2)
418	Kluatantan	0.2	(0.4)
466	Kluayaz_Cr	1.3	(0.6)
480	Kuldo_C	0.1	(0.2)
510	Morice	41.5	(1.9)
501	Nangeese_R	0.0	(0.1)
492	Otsi_Cr	0.5	(0.6)
493	Shegunia_R	0.0	(0.1)
495	Sicintine_R	0.0	(0.0)
396	Slamgeesh	2.5	(0.9)
479	Squingula_R	0.0	(0.1)
399	Suskwa	2.1	(0.6)
51	Sustut	0.9	(0.3)
401	Sweetin	0.1	(0.2)
498	Zymogotitz_R	0.4	(0.3)

Table 2. Mixture model analyses of Chinook salmon caught at the 2011 Tye Test fishery using the 29 stock Skeena baseline by week.

Data are presented as percent of the sample by stock.

Stat. week	054		061		062		063		064		071		072		073		074	
Time period	MAY 22 - 28		MAY 29 - JUN 04		JUN 05 - 11		JUN 12 - 18		JUN 19- 25		JUN 26 - 02		JUL 03 - 09		JUL 10 - 16		JUL 17 - 23	
Sample size	3(1)		2(0)		30(0)		30(1)		119(2)		106(2)		164(2)		127(3)		132(0)	
Stock	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD
Babine	0.9	(6.3)	1.2	(8.4)	1.5	(4.7)	11.4	(13.3)	1.1	(2.4)	0.2	(0.9)	0.8	(2.0)	4.1	(4.3)	4.0	(3.8)
Bear	3.5	(10.6)	47.7	(24.9)	0.1	(1.0)	0.1	(0.9)	3.2	(3.9)	5.0	(3.6)	0.8	(1.8)	7.1	(3.9)	14.6	(4.7)
Bulkley_Early	66.7	(22.6)	0.0	(5.1)	13.2	(6.0)	6.8	(4.5)	3.0	(1.7)	3.3	(1.8)	1.5	(1.0)	0.9	(0.8)	0.0	(0.2)
Cedar_Early	0.0	(4.9)	0.0	(5.4)	2.9	(3.2)	0.0	(0.5)	0.1	(0.5)	0.0	(0.2)	0.0	(0.1)	0.0	(0.2)	0.0	(0.2)
Ecstall	0.0	(3.6)	0.0	(6.9)	0.0	(0.7)	0.0	(0.5)	0.0	(0.2)	0.9	(0.9)	2.4	(1.2)	1.6	(1.1)	3.0	(1.5)
Exchamsiks	7.7	(14.2)	0.0	(5.1)	0.0	(0.6)	0.0	(0.4)	1.9	(2.4)	0.1	(0.7)	0.2	(0.7)	0.0	(0.3)	0.0	(0.1)
Exstew_R	0.8	(6.3)	0.0	(5.6)	2.4	(3.3)	2.0	(4.2)	3.1	(3.2)	4.2	(2.7)	2.4	(1.5)	0.2	(0.6)	0.0	(0.3)
Fiddler_Cr	0.0	(5.1)	0.0	(5.2)	0.1	(1.0)	0.4	(1.6)	6.6	(3.1)	0.7	(1.3)	0.1	(0.5)	0.0	(0.2)	0.0	(0.3)
Gitnadoix	0.2	(5.3)	0.0	(5.7)	0.3	(1.4)	0.0	(0.7)	1.4	(2.4)	0.2	(0.7)	1.4	(1.6)	0.0	(0.3)	0.0	(0.1)
Kasiks_R	0.0	(5.2)	0.0	(3.4)	0.4	(1.7)	0.1	(1.0)	0.1	(0.6)	0.2	(0.7)	0.2	(0.7)	0.0	(0.3)	0.0	(0.3)
Khyex_R	0.0	(3.8)	0.0	(5.9)	0.9	(2.9)	0.0	(1.0)	0.3	(0.7)	0.0	(0.2)	1.9	(1.2)	0.0	(0.1)	1.1	(1.0)
Kispiox	0.1	(3.8)	0.0	(5.2)	8.1	(11.0)	18.1	(9.1)	6.1	(5.6)	0.2	(0.8)	0.9	(1.8)	0.1	(0.3)	0.1	(0.6)
Kitseguecla_R	0.0	(3.2)	0.0	(5.3)	0.4	(1.7)	0.2	(0.9)	0.1	(0.6)	0.0	(0.2)	0.7	(1.1)	0.0	(0.3)	0.1	(0.5)
Kitsumkalum	14.3	(17.5)	0.4	(6.6)	12.9	(7.4)	0.0	(0.7)	10.3	(3.9)	0.5	(1.3)	19.7	(3.8)	29.5	(4.5)	36.8	(4.7)
Kitwanga	0.0	(3.5)	0.0	(5.5)	0.4	(2.2)	1.8	(5.5)	10.9	(4.9)	13.5	(4.1)	4.9	(4.1)	0.1	(0.4)	0.4	(1.2)
Kluatantan	0.0	(4.6)	0.0	(5.2)	0.0	(0.7)	0.5	(2.0)	0.6	(1.4)	1.9	(2.7)	0.2	(0.8)	0.0	(0.2)	0.0	(0.3)
Kluayaz_Cr	0.0	(4.4)	0.0	(5.7)	0.2	(1.3)	6.9	(7.5)	1.0	(1.3)	1.4	(2.1)	0.8	(1.4)	0.0	(0.2)	0.7	(1.2)
Kuldo_C	0.0	(4.4)	0.0	(6.3)	4.4	(6.1)	1.9	(3.8)	0.8	(1.8)	0.1	(0.5)	0.0	(0.2)	0.0	(0.4)	0.0	(0.3)
Morice	0.0	(2.8)	50.9	(25.1)	34.8	(11.2)	19.2	(8.2)	35.3	(4.9)	55.2	(5.5)	53.6	(4.8)	56.1	(5.0)	38.1	(4.5)
Nangeese_R	0.0	(4.0)	0.0	(4.8)	0.0	(0.9)	0.4	(2.1)	0.1	(0.5)	0.0	(0.2)	0.3	(1.1)	0.0	(0.2)	0.0	(0.2)
Otsi_Cr	0.0	(4.0)	0.0	(4.6)	0.2	(1.1)	0.4	(1.9)	0.1	(0.6)	2.1	(3.0)	1.5	(1.8)	0.0	(0.2)	0.4	(1.0)
Shegunia_R	0.0	(4.8)	0.0	(5.4)	1.9	(4.5)	0.4	(2.4)	0.4	(1.2)	0.0	(0.3)	0.0	(0.2)	0.0	(0.3)	0.1	(0.5)
Sicintine_R	0.0	(4.2)	0.0	(4.9)	0.0	(0.7)	0.0	(0.7)	0.0	(0.2)	0.0	(0.3)	0.0	(0.1)	0.0	(0.1)	0.0	(0.1)
Slamgeesh	3.7	(11.3)	0.0	(4.4)	2.1	(4.4)	10.4	(7.1)	3.0	(3.3)	3.7	(2.8)	2.0	(2.7)	0.0	(0.3)	0.0	(0.2)
Squingula_R	2.0	(7.1)	0.0	(4.4)	0.1	(0.8)	3.6	(5.1)	0.8	(1.6)	0.1	(0.7)	0.0	(0.2)	0.0	(0.4)	0.1	(0.3)
Suskwa	0.2	(4.5)	0.0	(5.0)	9.1	(6.3)	3.3	(5.3)	6.8	(2.9)	4.8	(2.5)	1.4	(1.1)	0.0	(0.2)	0.0	(0.2)
Sustut	0.0	(4.5)	0.0	(6.3)	3.4	(3.4)	3.3	(3.0)	2.6	(1.5)	0.0	(0.2)	1.2	(0.9)	0.0	(0.1)	0.0	(0.2)
Sweetin	0.1	(4.7)	0.0	(5.1)	0.1	(0.9)	0.5	(2.2)	0.2	(0.8)	0.0	(0.2)	0.9	(1.5)	0.0	(0.2)	0.3	(1.0)
Zymogotitz_R	0.0	(4.4)	0.0	(5.8)	0.1	(1.0)	8.2	(6.0)	0.1	(0.5)	1.5	(1.5)	0.1	(0.3)	0.0	(0.2)	0.0	(0.1)

SD = standard deviation

Stat. week = Statistical week

Table 2 continued.

Data are presented as percent of the sample by stock.

Stat. week	075		081		082		083		084		091	
Time period	JUL 24 - 30		JUL 31 - AUG 6		AUG 7 - 13		AUG 14 - 20		AUG 21 - 27		AUG 28 - SEP 03	
Sample size	106(1)		62(0)		15(0)		2(1)		4(0)		1(0)	
Stock	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD	Estimate	SD
Babine	6.1	(5.0)	4.5	(6.6)	33.0	(15.2)	3.9	(12.9)	5.6	(16.2)	18.8	(23.2)
Bear	10.0	(3.7)	12.9	(6.1)	1.8	(6.0)	0.1	(5.5)	22.5	(27.7)	22.2	(25.9)
Bulkley_Early	0.0	(0.1)	0.0	(0.3)	0.0	(1.4)	0.0	(5.7)	0.0	(3.5)	0.0	(5.8)
Cedar_Early	0.0	(0.2)	0.0	(0.3)	0.0	(1.2)	0.1	(4.5)	0.6	(4.9)	0.0	(8.5)
Ecstall	2.8	(1.6)	1.6	(1.6)	0.0	(1.0)	0.0	(4.6)	0.0	(3.4)	0.0	(8.5)
Exchamsiks	0.0	(0.4)	0.0	(0.5)	0.1	(1.6)	0.0	(4.2)	0.0	(3.1)	0.1	(8.7)
Extew_R	0.0	(0.3)	0.0	(0.4)	0.0	(1.1)	0.0	(6.2)	0.2	(4.0)	17.1	(22.9)
Fiddler_Cr	0.0	(0.2)	0.2	(0.7)	0.1	(1.8)	0.0	(4.3)	0.0	(2.1)	0.0	(7.6)
Gitnadoix	2.0	(1.5)	0.1	(0.6)	0.0	(0.9)	0.0	(5.7)	0.0	(3.0)	14.4	(22.6)
Kasiks_R	0.0	(0.3)	0.0	(0.3)	0.7	(2.6)	0.0	(4.7)	0.0	(3.5)	11.7	(20.3)
Khyex_R	0.1	(0.4)	0.0	(0.3)	0.1	(1.4)	0.0	(5.6)	0.0	(3.8)	0.0	(6.8)
Kispiox	0.0	(0.3)	1.0	(2.4)	1.7	(5.3)	9.7	(19.8)	0.4	(4.0)	0.8	(9.3)
Kitseguecla_R	0.0	(0.2)	0.0	(0.3)	0.0	(1.0)	0.0	(5.9)	0.0	(4.2)	0.1	(8.2)
Kitsumkalum	52.4	(5.6)	42.9	(7.0)	22.5	(12.3)	43.0	(29.2)	27.6	(22.5)	0.0	(8.1)
Kitwanga	0.1	(0.6)	0.2	(1.1)	1.6	(4.4)	5.9	(14.8)	0.5	(3.6)	0.1	(7.6)
Kluatantan	0.0	(0.3)	0.1	(0.6)	0.9	(3.3)	0.1	(4.7)	0.4	(4.1)	0.6	(8.3)
Kluayaz_Cr	0.0	(0.2)	3.4	(3.7)	0.7	(3.2)	0.0	(5.8)	0.0	(2.8)	11.3	(17.0)
Kuldo_C	0.0	(0.2)	0.1	(0.6)	0.1	(1.4)	0.0	(5.3)	0.1	(4.1)	0.1	(8.9)
Morice	25.5	(5.0)	31.1	(6.7)	24.0	(11.9)	33.9	(25.1)	40.1	(31.2)	0.2	(7.9)
Nangeese_R	0.0	(0.2)	0.0	(0.4)	0.3	(2.6)	0.0	(4.7)	0.0	(2.8)	0.0	(7.6)
Otsi_Cr	0.0	(0.4)	0.0	(0.5)	9.0	(10.2)	0.4	(4.7)	0.1	(4.0)	0.1	(8.3)
Shegunia_R	0.0	(0.2)	0.0	(0.4)	0.2	(1.7)	0.0	(4.5)	0.0	(2.4)	0.0	(7.2)
Sicintine_R	0.1	(0.5)	0.0	(0.4)	0.1	(1.1)	0.0	(5.3)	0.0	(3.8)	0.0	(8.8)
Slamgeesh	0.4	(1.3)	1.9	(3.1)	0.0	(1.3)	0.0	(5.2)	1.1	(6.6)	1.9	(10.3)
Squingula_R	0.0	(0.2)	0.0	(0.3)	0.3	(2.4)	0.1	(4.5)	0.0	(3.3)	0.0	(8.1)
Suskwa	0.0	(0.3)	0.0	(0.3)	0.0	(1.1)	0.1	(5.4)	0.0	(3.2)	0.0	(7.4)
Sustut	0.0	(0.3)	0.0	(0.3)	1.9	(4.5)	0.0	(3.8)	0.0	(3.6)	0.0	(8.6)
Sweetin	0.1	(0.5)	0.0	(0.4)	0.8	(3.5)	3.0	(12.3)	1.1	(6.2)	0.0	(5.5)
Zymogotitz_R	0.0	(0.2)	0.0	(0.3)	0.0	(1.0)	0.0	(5.7)	0.0	(3.5)	0.5	(7.7)

SD = standard deviation

Stat. week = Statistical week

FIGURES

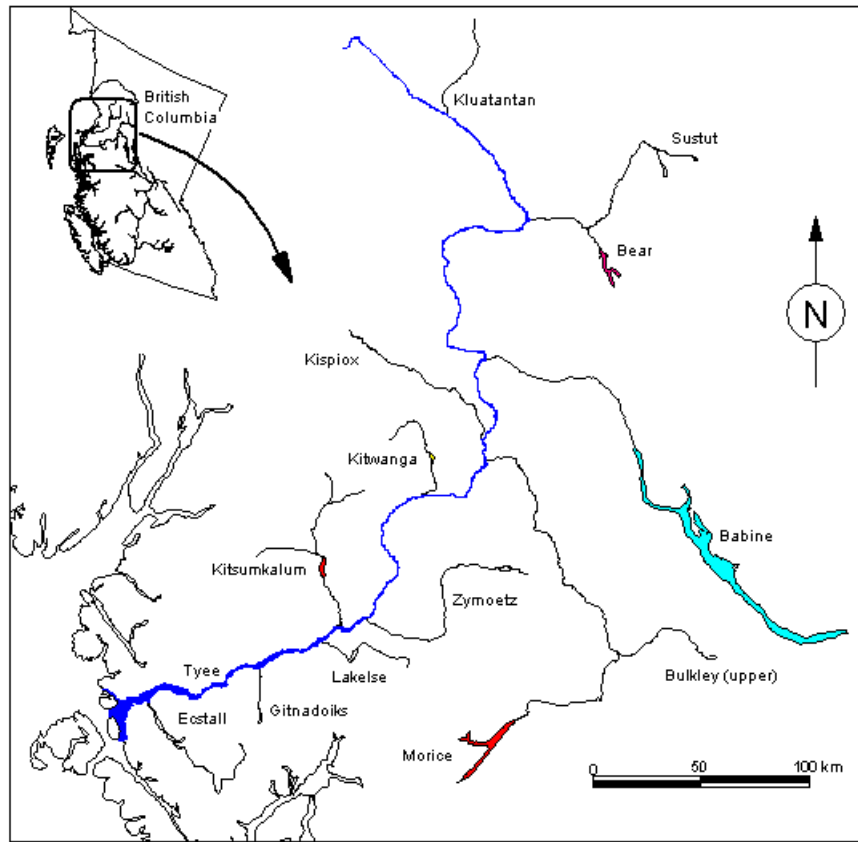


Figure 1. The Skeena River watershed in northern British Columbia showing the largest tributaries and the location of Tyee.

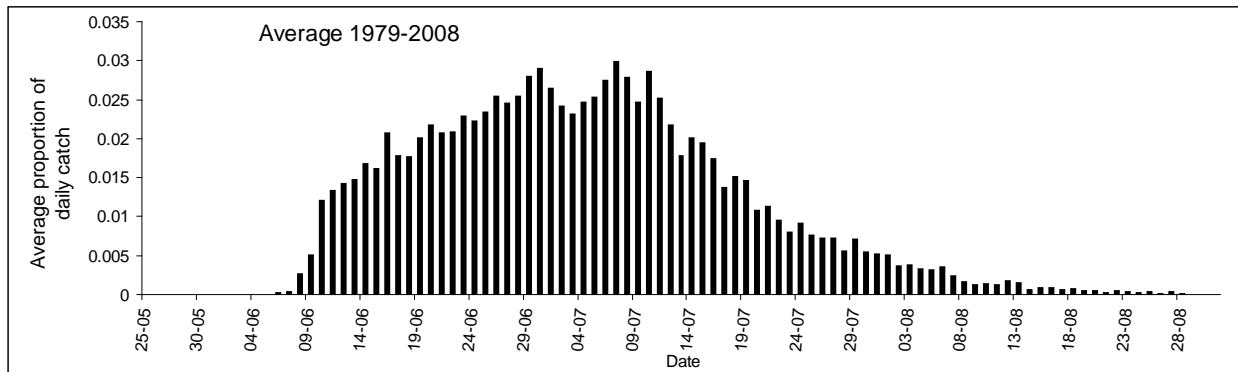


Figure 2. Skeena River Chinook salmon run timing past Tyee as measured by the average proportion of daily catch at the Tyee Test Fishery from 1979 to 2008.

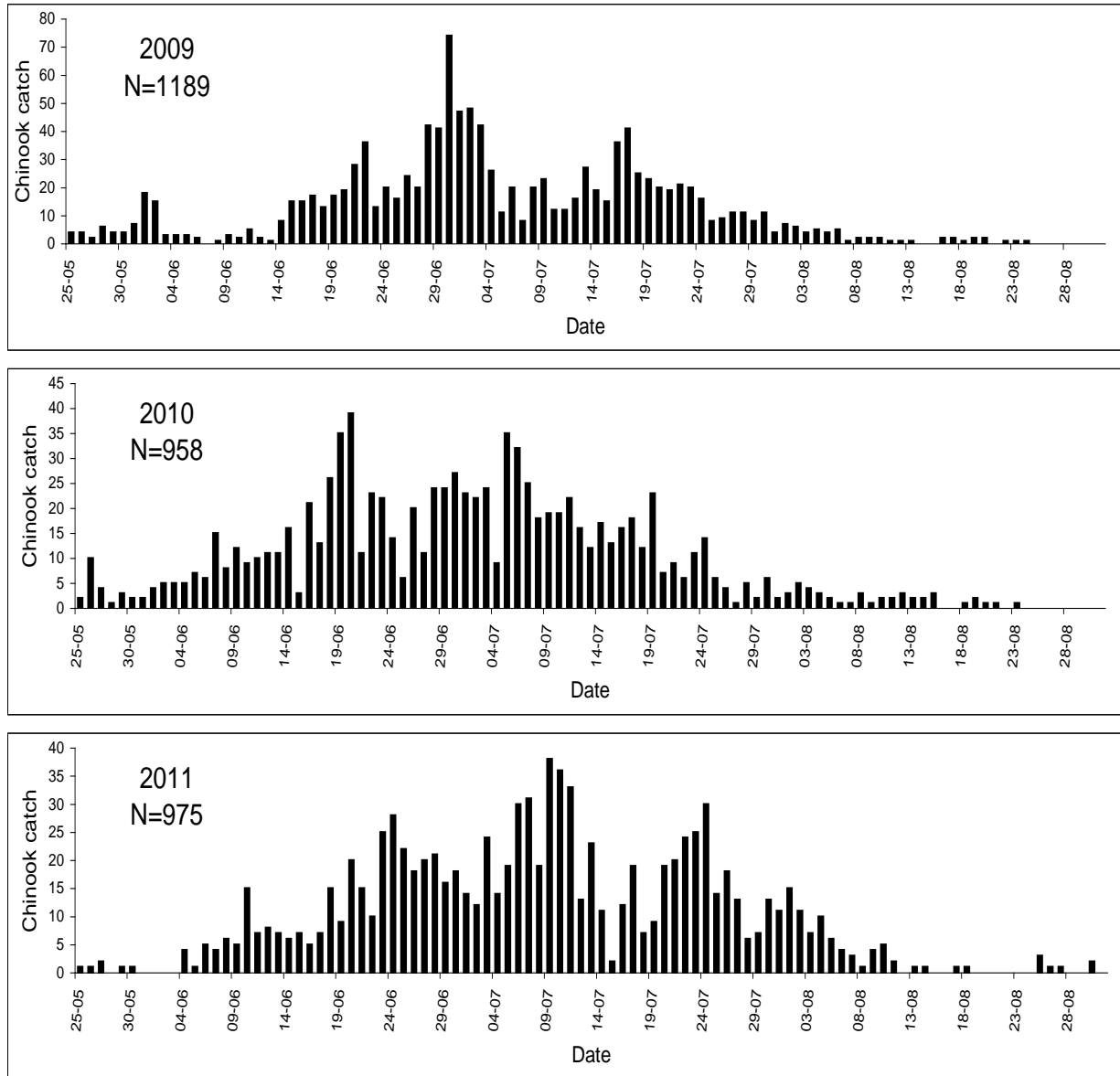


Figure 3. Skeena River Chinook salmon daily catch at the Tye Test fishery from 2009 to 2011.

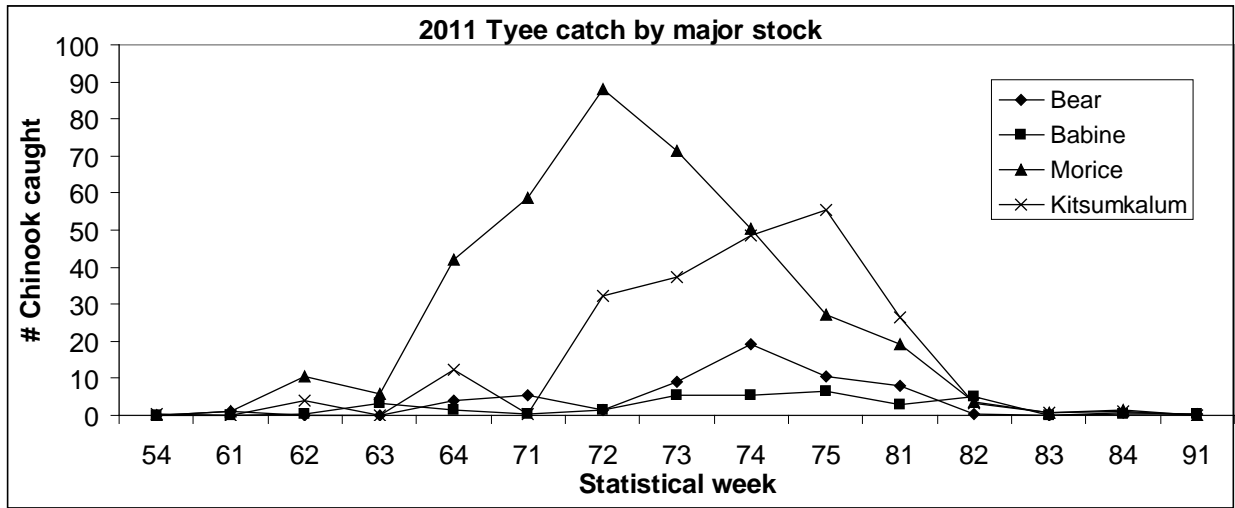


Figure 4. Catch of Chinook salmon from large component stocks at the 2011 Tye Test Fishery by week.

APPENDICES

Appendix 1. 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	Kitsegukla	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
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	160	157	158	162	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
498	Zymogotitz	119	119	118	117	117	120	117	117	120	118	116	116	116	117	120	120

Appendix 2. Comparison of 2011 project results with the objectives identified in the proposal to the Pacific Salmon Commission's Sentinel Stocks Program.

1. Estimate the 2011 Chinook salmon escapement to the Skeena River with an estimated coefficient of variation (CV) of 15% or less.

The 2011 escapement of Chinook salmon to the Skeena River was estimated but the program failed to meet the data standard of a CV of 15%. The CV for the 2011 estimate was 21%. Failure of the program to meet the data standard was largely a result of weather events that influenced the outcome of the Kitsumkalum mark-recapture estimate. Heavy rains in late August reduced tag application opportunities and severe rains with flood conditions during second week of September reduced recoveries.

2. Sample all Chinook salmon captured at the Tye Test Fishery for the biological attributes of length, sex and age and determine the age and sex composition for large components of the Chinook return to the Skeena River.

All of the Chinook salmon captured at the Tye Test Fishery were sampled. Component populations will be identified when baselines are finalized.

3. Meet the objectives above in subsequent years 2012 and 2013.

This project has been proposed to the SSC for 2012 and further improvements to the genetic baseline for Skeena River Chinook have been recommended.