Skeena River Chinook Baseline Sampling 2009-2010

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Executive Summary

A large sampling program was undertaken in 2009 and 2010 by the Skeena Fisheries Commission to improve the genetic baseline information on Skeena River Chinook. 3046 Chinook were sampled from 20 rivers throughout the Skeena Watershed and added to the DNA data set. Most of the sampled fish were fry in their natal rivers. The 2009 and 2010 sampling has increased the existing baseline from 12 populations in 2008 to 30 populations. The improved data is changing the understanding of wild Chinook populations in the Skeena. Evaluation of the genetic distinctiveness and the geographic distribution of Chinook populations led to the joining of various closely related populations into the 30 populations discussed here.The Skeena Test Fishery sampling has been reanalyzed by Ivan Winther with this improved baseline. Procedures for genetic separation of Skeena Chinook have been improved by Terry Beacham and a new dendrogram showing the relationship of Skeena populations has been prepared by John Candy of the DFO molecular genetics laboratory.

The cladogram presented here provides a useful objective tool to separate the Skeena Chinook into five clade groups which might well be the basis for Conservation Units under the Wild Salmon Policy.

Introduction

Salmon are the most conspicuous and most abundant large fishes of the Skeena watershed. They have long been the resource that supported the human population of the region. Even in recent decades as food produced in other regions has flooded in, the salmon remain an icon of the Skeena region. *Oncorhynchus tshawytscha,* the Chinook salmon, is the earliest appearing and largest species.

Skeena Chinook salmon are characteristic of large rivers and wander widely in the North Pacific ocean for one to six years before reentering their natal streams to spawn. Nearly all of the Skeena Chinook spend their first year in fresh water streams. At sea, Chinook from Northern British Columbia rear and feed northward of their home streams and return from the north. They are harvested for the most part in their last year of life on their return migrations to the north coast. On this return migration they are susceptible to interception in troll fisheries in Southeast Alaska and in troll and gill net fisheries of the north coast of BC.

The Pacific Salmon Treaty between Canada and the United States sets exploitation rates for the national fisheries on both sides of the border. The treaty specifies the aggregate national Chinook harvest in transboundary fisheries. Evaluating this aggregate in smaller units of individual rivers is monitored by the Chinook Technical Committee (CTC) designated by the treaty. The CTC is currently engaged in collecting data useful for recognizing and monitoring the escapement of Skeena Chinook with the intention of managing the Skeena for a single Chinook aggregate.

The larger rivers in British Columbia, such as the Fraser and the Nass contain many more-or less distinct populations (Holtby and Ciruna 2007). This complex population structure presumably contains much of the genetic diversity of the species. Canada's Wild Salmon Policy adopted in 2005 (Fisheries and Oceans Canada, 2005) is intended to conserve this diversity and hence promote the long-term survival of salmon.

The Skeena Fisheries Commission has been collecting baseline genetic samples for the past four years in order to better define the diversity of Skeena River Chinook. In the spring of 2009 the Skeena Watershed Initiative and the Northwest Institute with the support of the Moore Foundation funded a large scale effort toward the completion of a genetic baseline for Skeena Chinook. A smaller effort in 2010 was funded by the Skeena Watershed Initiative. The 2009 efforts obtained samples for most Skeena populations. The 2010 project was intended to complete the Skeena collections and focus more on the smaller populations. This report discusses the joint results of the 2009 and 2010 studies.

Chinook salmon are extraordinarily effective homing animals. In the Skeena, eggs are laid in suitable loosely-packed stream gravel in August and September, develop in the gravel through the winter, and fry emerge in April through June. The fry begin their downstream movement within a few weeks to a few months of emergence. Chinook fry occupy feeding stations in cobble-bed habitats, often sheltering behind cobbles or boulders and darting out to grab passing food items, often insects. For nearly all Skeena populations the first winter is spent in large rivers, for the most part the Skeena mainstem. Migration to sea occurs during the high turbid flows of the spring snow melt. The single known exception to this pattern are the Ecstall River Chinook at least some of which go to sea in their first year.

Nearly all of the adult Chinook are believed to return to their natal stream, in some cases to the same gravel bar where they were born (Quinn, 2005). This extreme fidelity accelerates specialization for the characteristics of each river and presumably results in numerous highly specialized sub-populations. The rate of and extent of evolution in the smaller of these subpopulations are increased by random effects of chance in small populations, called "genetic drift".

Increasing attention has been applied to biochemical characterization of the genetic differences between salmon populations since the 1990s, with a progression toward increasingly finer scale genetic characteristics. At first, separation was by analysis of protein differences, called allozymes. By the end of the 1990s attention had shifted to the details of the DNA of the major histocompatibility complex (MHC) and minisatellite components of the chromosomes. In the past decade analysis has been carried out with great success using microsatellite components which are non-coding sections of the chromosome, and in the past few years using single nucleotide polymorphisms (SNPs) of coding and non-coding parts of the chromosome.

The fine scale analyses of chromosomal coding have become highly automated such that analysis for 15 loci in the microsatellite system or 96 SNPs can be carried out overnight at a cost of $10 to $30.

We have worked closely with the Salmon Genetics Laboratory at the Pacific Biological Station which has perfected the use of microsatellite DNA systems for Pacific salmon population separation. Outstanding Chinook studies include Beacham *et al.* 2003a, 2003b, 2006, and 2008. This genetic determination system is similar to that used for human forensic applications.

Sampling Techniques

Adult Chinook

Adult Chinook were collected on their spawning beds using 6 inch mesh tangle nets. Fish were kept in the water at all times. Two to five scales were taken from each fish for ageing. One of these scales and/or a tissue sample from the operculum were used for a DNA sample .DNA samples were submitted to the Department of Fisheries and Oceans Pacific Biological Station Molecular Genetics Laboratory for microsatellite DNA analysis.

Juvenile Chinook

Chinook juveniles were collected with beach seines 10 to 20 m long x 1.6 m deep made with ¼" woven nylon mesh. The nets were simple sheets manipulated with poles at the ends. The lengths could be adjusted by wrapping the net around the pole ends to shorten it. The nets can be manipulated when fishing to form a linear pocket for capturing fry. In boulder reaches of the Suskwa, Shegunia and Gitsegukla Rivers Chinook fry were taken with baited Gee traps baited and left overnight.

Collection sites were selected for being tens of kilometers below known major spawning areas and at least two kilometers above the confluence with the Skeena River. The concern about using juvenile Chinook for population characterization is that if collections are made near the spawning sites, siblings may be aggregated with siblings and other relatives and hence the population would appear to be less variable genetically than it is overall. We make the assumption that after fry have migrated many kilometers downstream they have likely stopped and fed more than once and are no longer closely associated with relatives. To test this assumption, one collection (Zymogotitz) was made from a site near the presumed spawning area.

We observed that juvenile Chinook migrate into small tributary streams to feed on their downstream travels. They may be found in the lowest reaches of streams that appear to be obviously unsuitable for spawning. We therefore took the precaution of collecting juveniles at least more than two or three kilometres above stream mouths. Rarely, these criteria could not be met, such as at Tantan Creek (the Kluatantan locality in Table 1) which is short (2 km) and joins the Kluatantan River which hosts the upstream Kluayaz juveniles. Juveniles were not collected at Tantan Creek.

Salmonid fry were measured and sorted by species in the lab. Identification of Chinook fry was made in the lab because of the difficulty in separating coho fry from Chinook. The separations were based on branchiostegal counts and to a minor degree on colour markings and pattern.

Results

Examination of spawning beds began in late July 2009. The first Chinook appeared in the first week of August. Only in mid-August did they arrive in substantial numbers. Contrary to our expectations, the timing of Chinook moving onto spawning beds was essentially simultaneous at all collected streams ranging from the Kasiks River at the head of tidal influence to the ultimate northern headwaters of the Skeena mainstem. Spawning had ended at nearly all the sites examined by early September.

The timing of the major lake outlet Chinook spawning populations is believed to extend a week or two longer in September (Hancock *et al.* 1983). Bear River Chinook spawning below Bear Lake were still spawning on 7 September 2010 when other stocks were apparently finished. Morice River Chinook spawn into mid September. But this does not seem to be the case for the third lake outlet populations where according to the Babine River Weir counts of 2009, Chinook had the same timing as non-lake associated populations. We did not collect samples or timing information for the early entry stocks of the Upper Bulkley and the Cedar River.

Adult collections were made in eight rivers (Table 1). Collections size ranged from 1 to 83 Chinook within a single spawning area. The largest collections were from Slamgeesh River (N=49) at a site called Gitangwalk two kilometres below the Damshilgwet confluence, at Squingula River about 3 kilometres below Motase Lake N=56), and at various sites along the Zymoetz River (N=83). There were hundreds to thousands of Chinook present in late August at these sites.

Juvenile collections were made from 16 rivers (Table 1) with collection sizes ranging from 20 to 336 specimens. Effective seine net fishing required fishing on cobble bed reaches with a shoreline patch of sandy sediment on which to land the net and prevent fish from escaping beneath the leading edge. There was great variation in catch per haul ranging from less than one fish with sites depleted in one or two passes to sites where catches ranged from 5 to 15 Chinook fry per pass, where fish would restore to the area that was fished within a few minutes. Fry density appeared to be proportional to the abundance of spawners on that river, which were similar in rank order to the percentage presence in the Skeena Test Fishery analysis. An adequate sample of Chinook fry was taken at Squingula River in two visits whereas collecting similar numbers of fry from Gitsegukla River was only possible after more than twelve crew-days.

Beach seining juvenile Chinook is not quantitative because many Chinook escape past the ends and under the bottom of the net. Some of the best collecting sites were where there were natural obstacles at the end of the net and relatively smooth bottom topography. The Chinook fry appear to hold adjacent to cobbles on the stream bed. We could not collect boulder habitat effectively to determine approximate density of juvenile Chinook, but it is evident that juvenile Chinook use such habitat regularly. The Chinook fry catch at Suskwa, Shegunia and Gitsegukla using Gee traps in boulder reaches was about one per trap-night.

Based on beach seine catches in cobble-bed reaches, Chinook appeared to be distributed with densities ranging from $0.2/m^2$ to $2.0/m^2$. Mountain whitefish (*Prosopium williamsoni*) was the next most abundant species (see Figure 2). In order of decreasing abundance, juvenile bull trout, steelhead fry, and coho were also caught. The proportion of coho increased if seine passes were made on finer sediment substrate. There was a strong association of Chinook fry with loose cobbles surfaces. Few or no Chinook were present if the stream bed had more than a few percent sand, especially if fine sediments were abundant enough to embed the cobbles.

Approximately 85% of the salmon specimens brought into the lab for detailed examination were Chinook. The Chinook identifications were ultimately confirmed by DNA analysis. No doubt the high proportion of Chinook in the seine net collections was because of the selection of appropriate stream habitat for sampling. The proportion of coho was higher in the few cases where Gee traps were used to collect fry.

The state of Chinook knowledge in the Skeena

There are probably fewer than 50 stable Chinook populations in the Skeena. As of 2005 only 10 of these populations had baseline DNA samples of more than 100 individuals (Table 2). This is the minimum number necessary to characterize diversity, and larger samples are desirable. In 2007 Ivan Winther of the DFO Stock Assessment in Prince Rupert and the Skeena Fisheries Commission began to expand the DNA baseline. By the end of 2008 there were 12 populations with collections >100 represented in the DFO Salmon Genetics Laboratory baseline. Our concentrated effort of 2009 and 2010 increased the number of adequately sampled populations to 30.

The 2009 and 2010 Moore Foundation funded projects added about 2418 specimens from 17 populations. These included 2181 juveniles and 237 adults. At this point it appears that all of the large (>1000) and medium sized (200 to 1000) populations have been sampled, and all but a few of the known Chinook populations with more than 100 spawners have been sampled.

During the past five years, Skeena Fisheries Commission field studies sponsored in large part by the Pacific Salmon Commission and the Moore Foundation via various agencies (Tide Foundation, Northwest Institute for Bioregional Research, Skeena Watershed Initiative), have uncovered a suite of unknown or poorly known Chinook populations in the upper Skeena. The new populations include Nilkitkwa River, Kuldo Creek, Sicintine River, Slamgeesh River, Squingula River, Mosque River, Tantan Creek, Kluayetz Creek, Kluakaz Creek, and Otsi Creek. Of these, a few had been previously observed, while others were entirely unknown in the DFO catalogues. These sites account for 13% of the total 2010 Skeena escapement, and 20% of the 2009 Skeena escapement (Winther & Candy 2011). These sites along with the well-known Bear and Sustut Rivers these northern sites are now known to constitute about 20% of the total Skeena escapement.

The size of sampled Chinook populations is estimated in Table 2 based on a review of the existing Chinook escapement records, the analysis of the proportions of fish in the Skeena Test Fishery analysis and our observations while collecting the samples for this baseline set. The 30 represented populations consist of ten large populations identified either as having escapements of over 2000 or fluvial bedforms on the spawning grounds that suggest a population of this size (Gottesfeld et al. 2008), nine medium sized populations estimated as having annual escapements of 500 to 2000, and eleven small populations estimated with escapements of between 20 and 500. Of the small populations seven have complete samples. Another four have only small collections as yet. In addition there are two small populations, (Mosque River and Nilkitkwa River) which were discovered to have Chinook in 2010, that are as yet unsampled.

We have combined sub-populations which we originally treated as separate stocks into composite stock groups. We combined Otsi and Kluakaz Creek Chinook into one group since it is doubtful on genetic and geographic grounds that these populations are separate. The two localities are along the northernmost Skeena River 13 km apart with Chinook spawners distributed at several spots between these localities. On the eastern branch of the upper Skeena, Tantan Creek is a small short tributary of the Kluatantan River that differs greatly from most Chinook spawning sites. Northward 10 km, Kluayaz Creek hosts is a much larger population. A few mature Chinook were observed in 2010 and 2011 between these localities. The two Kluatantan localities are treated separately in Table 1 but it is likely that they will be combined in the future when a larger baseline sample is available for Tantan Creek.

Several of the Kispiox river tributary streams have spawning Chinook. In 2009 and 2010 we collected Chinook adults and juveniles in Sweetin River and the adjacent Nangeese River. The spawning zones of these streams are only a kilometer apart in a swampy area although the mouths of the streams are about 5 km apart. There are Chinook spawners in the Kispiox River near the mouths of both tributaries. It is likely that the three Kispiox River segregates will eventually be combined into a single unit. For this paper we have adopted an intermediate position and recognise two populations, Kispiox River and Nangeese River since they are represented by large baseline collections.

Harold Price Creek is the largest tributary of the Suskwa River. Chinook spawn in both streams near their confluence. Unsurprisingly, the populations are not clearly separable based on genetics. We have therefore combined these two units.

In the Zymoetz River watershed, the Upper Zymoetz and Clore River (Thomas Creek) localities were collected separately since they are about 70 km apart and might prove different; but it seems doubtful that this separation is appropriate. The distribution of radio tags observed in 2010 (Gottesfeld *et al.* 2011) shows Chinook spawners are distributed throughout the Zymoetz watershed.

Mature Chinook have been observed in the Skeena River near the mouth of the Kalum River. The locality "Skeena at Terrace" is a collection from about 1km above the Kalum River, just off the Kitsumkalum alluvial fan. This stock is very similar genetically to the lower Kalum stock and might well be combined with it.

These reduction in stocks leaves the baseline in Table 1 with 30 populations. The net effect of these conglomerations is to make Chinook stocks population units coincident with major subwatersheds. There are few examples remaining of large subwatersheds with more than one population assigned. The Sustut River has an upstream dispersed population and a lake outlet population below Bear Lake which is quite distinct genetically and has somewhat later spawning timing. The Kalum River has a large spawning population below Kalum Lake and an early run population above Kalum Lake at Cedar River. The Bulkley River watershed has a large population in the Morice River most abundant below Morice Lake and an early run population in the eastern headwaters of the Upper Bulkley. All other units are exclusive to one major stream system.

Table 1. Baseline DNA samples of Skeena Chinook Spawning Populations in the DFO molecular Genetics Laboratory.

Chinook DNA specimens 2011 (preliminary data)

	Estm Population Size	Juv 09-10	Adult 09-10	Total Added 2009-10	Total 2007	Total 2008	Total 2009	Total 2010
Ecstall	M				293	293	293	293
Khyex	S	38	0	38	0	0	38	38
Kasiks	S	61	0	61	0	0	61	61
Exchamsiks	S	107	0	107	9	9	116	116
Gitnadoix	M	179	0	179	66	66	245	245
Exstew	M	140	0	140	0	0	140	140
Zymogotitz	S	119	0	119	0	0	119	119
Lakelse	S	22		22	0	0	0	22
Kalum (lower)	L			200	523	523	523	753
Cedar	M				116	116	116	116
Zymoetz	M	20	83	103	2	26	61	129
Fiddler	S	118		118	0	0	0	118
Kitwanga	L				288	288	288	288
Gitsegukla	S	260		260	0	0	260	260
Suskwa & Harold Price	S	91	6	97	22	22	119	119
Bulkley/Morice	L			82	228	228	228	310
Upper Bulkley	M				588	588	588	588
Shegunia	S	130	14	144	0	0	79	144
Kispiox	L				197	197	197	197
Sweetin	S	176	13	189	44	54	243	432
Babine	L			141	266	266	266	407
Kuldo	M	170	1	170			170	170
Sicintine	M	336		336	0	0	112	112
Slamgeesh	L		49	49	?	81	130	130
Squingula	L	214	56	270		0	270	270
Bear	L				182	182	182	182
Sustut	L				519	519	519	519
Kluatantan	S		15	15	7	18	33	41
Kluayaz	L			30	86	120	150	150
Otsi & Kluakaz	M			176	30	102	209	278
Totals		2**18**1	237	3046				

Sample size sources J. Candy Mar 2009 Gottesfeld collection notes 2007-2010.
Samples shown with no fill in the right hand column are complete (>100), samples with yellow fill are incomplete (<100), samples shown with orange fill need future collecting. Two small populations (Mosque river and Nilkitkwa River) found to host spawning Chinook in 2010 are omitted from this table.

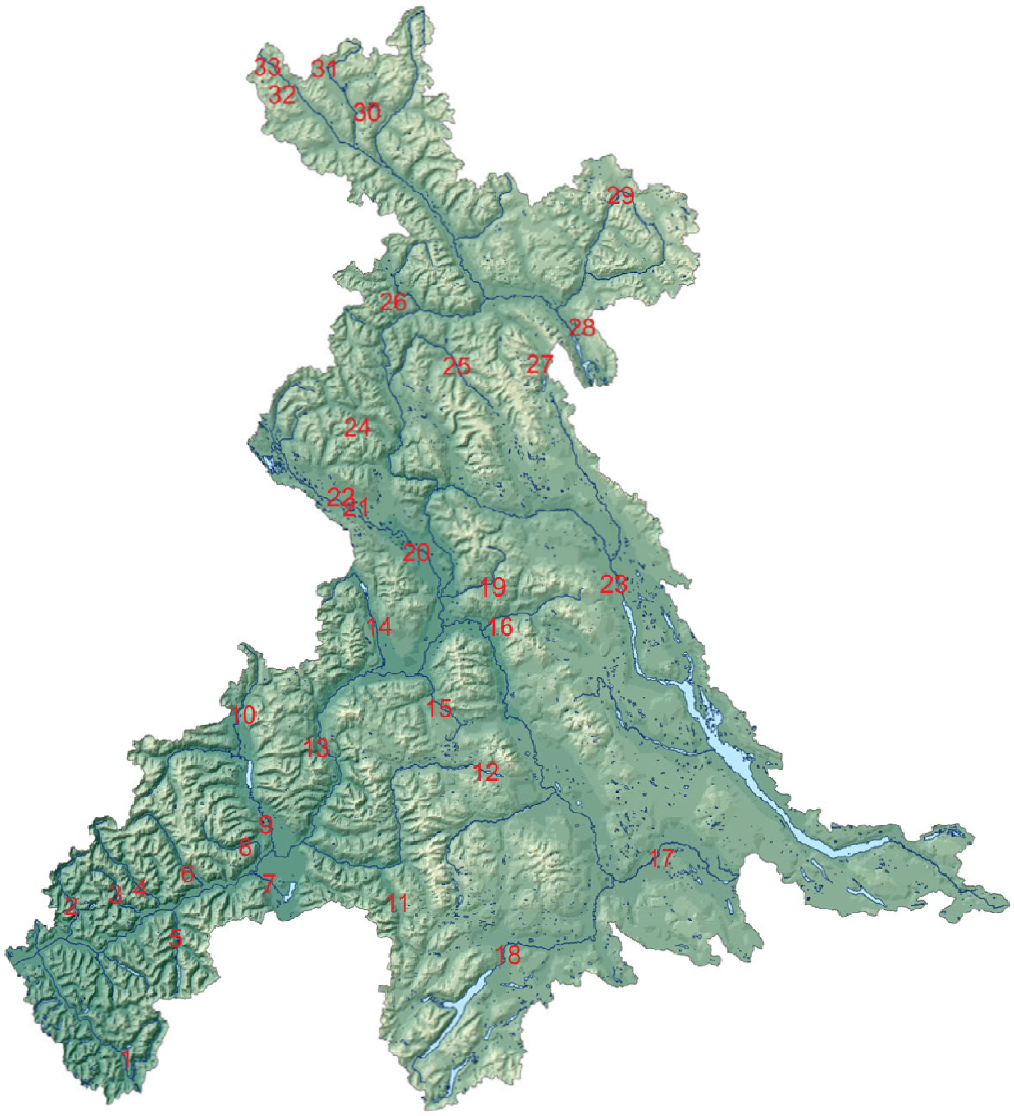

Figure 1. Chinook Baseline collections localities as of December 2010.
1 Ecstall River, 2 Khyex River, 3 Kasiks River, 4 Exchamsiks River, 5 Gitnadoix River, 6 Exstew River, 7 Lakelse River, 8 Zymogotitz River, 9 Kalum River, 10 Cedar River, 11 Thomas Creek, 12 Zymoetz River, 13 Fiddler Creek, 14 Kitwanga River, 15 Gitsegukla River, 16 Suskwa River, 17 Upper Bulkley River, 18 Morice River, 19 Shegunia River, 20 Kispiox River, 21 Sweetin River, 22 Nangeese River, 23 Babine River, 24 Kuldo Creek, 25 Sicintine River, 26 Slamgeesh River, 27 Squingula River, 28 Bear River, 29 Sustut River, 30 Tantan Creek (Kluatantan), 31 Kluayaz Creek,. 32 Otsi Creeks, 33 Kluakaz Creek

Applications of this research

The improvement of the Skeena DNA baseline has changed the understanding of Skeena Chinook populations. The new data has encouraged the improvement of the techniques for separating Skeena Chinook populations. An ongoing reanalysis of the population genetics of Skeena Chinook is expected to be used to evaluate the effectiveness of sampling juvenile salmon and has been applied to interpretation of the Skeena Test Fishery.

Change in technique for sampling Chinook populations

It became clear early in the 2009 field season that insufficient adult Chinook could be collected to complete the baseline in less than five years. We therefore switched to collecting juveniles where it seemed justifiable. We took care to sample well downstream of the spawning areas, frequently in the most downstream area of suitable habitat while taking care to be at least three kilometres above the mouth of the river.

Sibling analysis of juvenile samples

Ruth Withler of the Pacific Biological Station has analyzed some of the juvenile samples to check on the abundance of siblings in the collections. Siblings are recognizable in any single generations' collection in that they share 50% of their genes. The samples submitted included collections from Gitnadoix River, Gitsegukla River, Zymogotitz River, Shegunia River and Squingula River. The analyses did not show exceptional levels of relatedness in any of the collections, even the Zymogotitz collection which was made within several hundred meters of the presumed spawning site. It appears that the juvenile collections of Chinook are well-mixed. In the future collections of Chinook can be made efficiently at much reduced cost compared to sampling adults.

The abundance of siblings is also an indication of the effective population size (P_e) and holds promise for future work on population size estimation. We might expect that the amount of relatedness of any two individuals is in part related to the size of the spawning population, assmall populations are more likely to have close relatives.

Improvements to Skeena Chinook genetic technology

The existence of a larger set of Skeena populations encouraged Terry Beacham of the salmon genetics laboratory to add three additional microsatellite alleles to the existing set of 12 alleles to improve the interpretation of Skeena populations. This new data has been used in the creation of a new dendrogram of Chinook populations and the PORGS analysis of the relatedness of these populations by John Candy similar to the existing analysis of the west coast of Vancouver Island populations (Candy *et al.* 2009).

Reinterpretation of the Skeena Test Fishery by Ivan Winther

The Skeena Test Fishery season was extended to begin earlier in 2009 and 2010 than in previous years to better sample the Chinook runs. If the baseline is of high enough quality and enough specimens are collected and analyzed, the test fishery results can be used to estimate the escapement of the larger Skeena stocks. This was attempted by Winther (2010) for 2009 data and Winther and Candy (2011) using the improved baseline for both year's data. The estimated escapements were compared to the available data on escapements based on the mark and recapture estimate for the Kalum River, the fence count for the Kitwanga River, the partial fence counts for the Babine River and the Sustut River and visual estimates for the Morice River and several other streams. The Kalum River mark and recapture estimate was assumed to be accurate and used to calculate the total Skeena Chinook escapement. Other Chinook populations were estimated by using their relative proportion of the total.

In general the most recent recalculation of Winther and Candy 2011 (Table 2) provides results quite similar to those of the other estimates. The new baseline gives better results than previous iterations (Winther 2009, Winther 2007). The results of the Skeena Test Fishery analysis are sufficiently close to the other escapement data and radiotelemetry results (Gottesfeld *et al.* 2011) to support the continued use of Skeena Test Fishery analyses, when factors such as in-river fishing pressure on the largest stocks, and the weak ability to separate closely related stocks are taken into account.

Interpretation of dendrogram of November 2010

The new dendrogram of Skeena Chinook populations produced by John Candy (Figure 6) clarifies the relationship of the Skeena Chinook populations. The overall degree of genetic differentiation of the breeding populations is expressed by the horizontal distance units in this dendrogram,. They are F_{st} values presented as the proportion of intrapopulation genetic variation compared to the combined population genetic variation.

There is a strong geographic component to this dendrogram with its Lower, Middle, and Upper Skeena clades.In addition there is a clade of early migrants (springs) and a natural grouping of three large lake outlet spawning populations. The five clade groups shown in Figure 6 constitute objective natural groupings. They could serve as the basis for the creation of Conservation Units under the Wild Salmon Policy of the DFO.

The population grouping supported by this diagram are as follows:

Lower Skeena

The rivers tributary to the Skeena from the Zymoetz River downstream to the Kasiks River form a compact grouping. The Kalum River population is near the base of the classification for the lower Skeena rivers. The rivers downstream of the Kalum are especially tightly clustered. . As far as is known these Chinook have similar life history patterns: they are all river type Chinook that spend their first year in the river environment, and they return to the Skeena from late June to early August. These Chinook move into their spawning rivers in August and spawn from late August to early September. The Kalum stock differ from the other lower Skeena stocks in that it is dominated by six-year old returning fish whereas the other Skeena stocks are dominated by five-year old fish. The Skeena Terrace collection is just above the Kalum River alluvial fan. It probably should be combined with the Lower Kalum stock.

The Ecstall River enters the Skeena Estuary south of Prince Rupert. It is the most divergent genetically of the Skeena Chinook populations. The Ecstall appears to be the only Skeena population that has a significant ocean-rearing component; that is, the fry leave in their first summer after emergence to rear on the coast. The fry may not migrate north to the Gulf of Alaska as the river type Chinook do, but remain in the coastal environment. In 2007 we collected a single immature Ecstall River Chinook in Prince Rupert Harbour in mid winter. All other Chinook in the small collection of winter resident Chinook were from rivers in southern British Columbia and Puget Sound where the ocean-type life historyis dominant.

The Khyex River is the next river upstream in the Skeena Estuary. It is represented by a small baseline sample (N=38), but appears to group with the Ecstall River.

The two Zymoetz localities are very similar genetically although they are 70 km apart and have been combined. They group with Fiddler Creek, the next Chinook bearing stream upriver.

Middle Skeena

The Middle Skeena Chinook stocks form a compact group with roots in the Kispiox and/or Kitwanga stocks. As far as is known these Chinook have similar life history patterns, they are all river type Chinook that spend their first year in the river environment and they return to the Skeena from late June to early August. These Chinook move into their spawning rivers in August and spawn in mid to late August. Chinook from the Kispiox River and its tributaries Sweetin River and Nangeese River are very similar genetically. The Nangeese's distinct position is likely due to sampling effects in this small population. We have combined the two adjacent tributaries for discussion in this report. It is possible that both of these tributaries will be joined to the Kispiox River population in the future as all have breeding individuals within a few kilometers of each other. The Suskwa River sample has been amalgamated with that of its tributary Harold Price Creek for similar reasons.

Upper Skeena

The Upper Skeena Chinook stocks form a compact group with roots in the Slamgeesh stock. As far as is known these Chinook have similar life history patterns, they are all river type Chinook that spend their first year in the river environment and they return to the Skeena from late June to early August. These Chinook move into their spawning rivers in August and spawn in mid to late August. According to this dendrogram the Kluakaz Creek and Otsi Creek samples are not significantly different. The two localities are both in the northern headwaters reach of the Skeena at alluvial fans about 15 km apart. They have now been combined in the Skeena baseline. It is likely that once a larger sample of Kluatantan Chinook is collected, it will be combined with the nearby larger Kluayaz Creek population.

Early Run Stocks

The early Bulkley River Chinook spawn above Houston in the upper Bulkley River. They are an early returning stock that passes through Tyee in May and June and is complete by the time the bulk of Skeena Chinook arrive. Upstream passage of these Chinook in the upper Bulkley River is restricted to high flow conditions at Bulkley Falls. The Cedar River Chinook spawn in northern tributaries of Kalum Lake. They also have early timing entering the Skeena in May and peak in early June. The third stock that sorts out with the early Chinook is Sicintine River. This stock was not formerly represented in the Skeena baseline. There are relatively few Sicintine River Chinook in the 2009and 2010 Skeena Test Fishery and radio-tagging sampling but all of the fish (N=16) that were observed were in June, mostly in early June.

Large Lake Outlet

The three large upriver Chinook stocks are very similar and may be a distinct genetic unit. They occupy spawning habitats below major lakes and may spawn later (into September) than other Skeena stocks. The lake outlet spawning habitat may provide a more moderate (warmer) winter environment for egg development and permit later spawning. The large lake outlet populations are so similar that there has apparently been misassignment of Chinook between Morice, Babine and Bear Rivers in past iterations of this genetic assignment scheme.

The stock groupings presented above can be proposed as five "natural" conservation units based on genetics. These proposed conservation units are similar to those proposed by Holtby in 2008 and distributed at least within the DFO and apparently used for the 2009 Science Advisory report "Framework for Implementation of the Wild Salmon Policy" (CSAS 2009). The Lower Skeena, Middle Skeena, and Upper Skeena units of Holtby 2008 are retained but the included populations have changed somewhat. The characterization of the middle Skeena CU has changed somewhat. A separate CU for Gitnadoix, suggested by Holtby, is rejected as with better data the Gitnadoix population is placed firmly within the Lower Skeena unit. Separate conservation units for the upper Bulkley and the Cedar river are combined into a Skeena Early Run unit. A conservation unit for large lake outlet populations might be established and restricted to the three large lake populations below the Morice Lake, Babine Lake and Bear Lake. Overall this genetics based proposal represents a minor reduction of CUs from nine in CSAS 2009 to five or six.

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Figure 2. Beach seine for juvenile Chinook. Typical habitat is in the higher energy reach of the distant channel.

Figure 3. Chinook, larger robust specimens and mountain whitefish, smaller more gracile forms.

Figure 4. Scale sampling of Chinook at Tantan Creek (Kluatantan).

Figure 5. Tangle net fished at Gitangwalk on the Slamgeesh River.

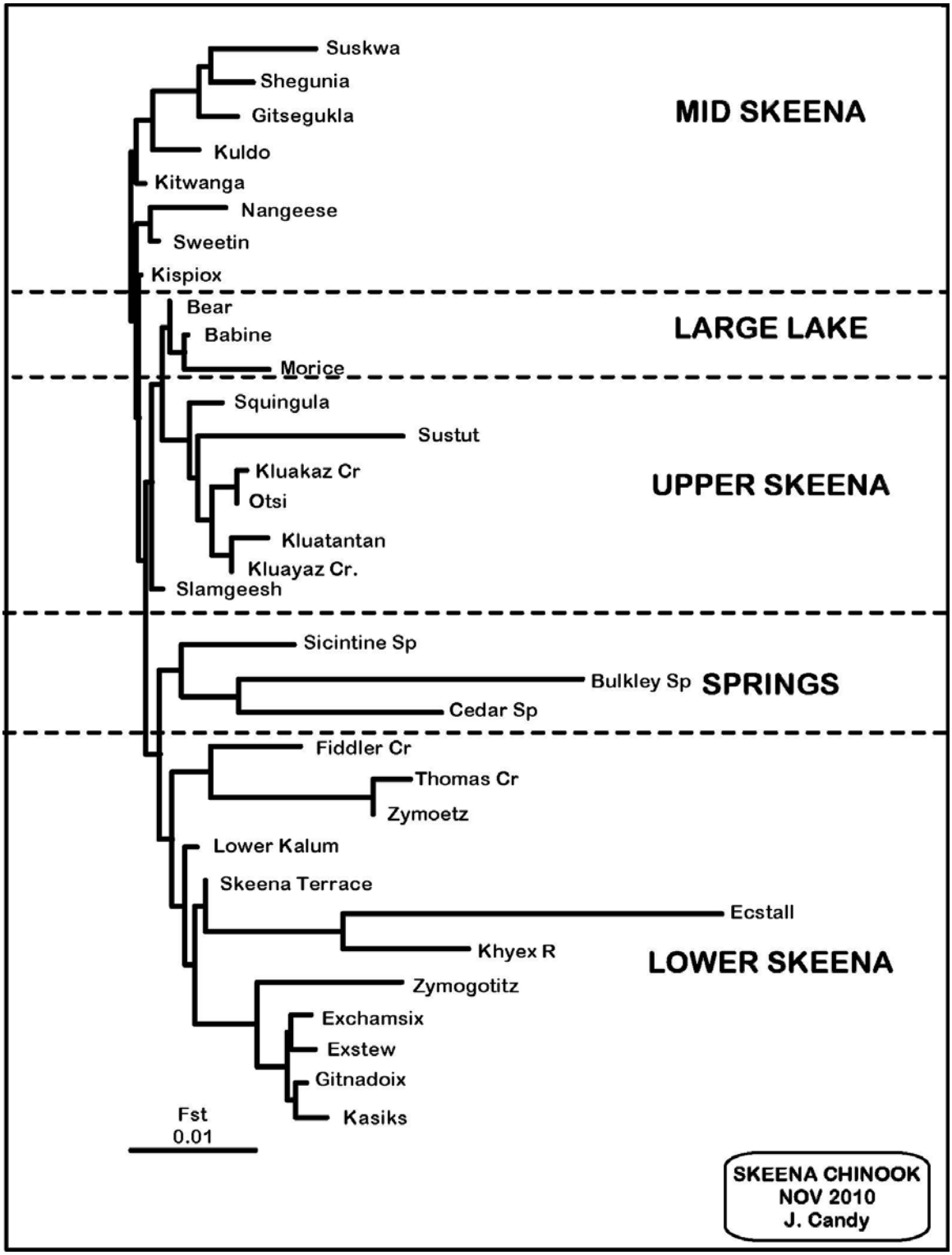

Figure 6. Dendrogram of Skeena Chinook populations as of November, 2010. The horizontal distances are proportional to interpopulation F_{ST} values. Prepared by J. Candy DFO Salmon Genetics Laboratory

Table 1. of Winther & Candy 2011. Results of the genetic mixture model analysis of Chinook salmon caught at the Tyee Test fishery in 2009 and 2010 using the 32 stock Skeena baseline and 15 loci.
Data are presented as percent of the sample by stock. N= 1,155 in 2009 and 839 in 2010.

Stock	2009 Estimate (% of sample)	2009 Standard Deviation	2010 Estimate (% of sample)	2010 Standard Deviation
Babine	8.1	(1.8)	8.8	(1.6)
Bear	6.3	(1.4)	5.9	(1.5)
Bulkley_sp	0.9	(0.3)	0.9	(0.3)
Cedar_sp	0.3	(0.2)	0.1	(0.1)
Ecstall	2.9	(0.5)	2.0	(0.5)
Exchamsiks	1.3	(0.4)	0.9	(0.6)
Exstew	0.8	(0.4)	1.4	(0.6)
Fiddler_Cr	0.0	(0.0)	0.0	(0.1)
Gitnadoix	1.7	(0.5)	0.6	(0.6)
Gitsegukla	0.5	(0.3)	1.0	(0.5)
Kasiks	0.1	(0.2)	0.1	(0.3)
Khyex_R	0.0	(0.1)	0.8	(0.4)
Kispiox	6.1	(1.6)	2.1	(1.2)
Kitsumkalum	13.2	(1.4)	14.7	(2.0)
Kitwanga	4.4	(1.1)	3.7	(1.3)
Kluakaz_Cr	0.7	(0.5)	0.0	(0.2)
Kluatantan	0.0	(0.1)	0.1	(0.2)
Kluayaz_Cr	0.8	(0.8)	1.9	(0.7)
Kuldo	0.9	(0.6)	0.1	(0.3)
Morice	31.1	(1.6)	30.6	(1.8)
Nangeese_R	0.2	(0.3)	0.3	(0.5)
Otsi	1.5	(0.8)	2.6	(0.9)
Shequnia	0.0	(0.1)	0.5	(0.6)
Sicintine	1.1	(0.4)	0.1	(0.2)
Slamgeesh	3.9	(1.2)	5.3	(1.3)
Squingula	4.5	(0.9)	2.5	(0.9)
Suskwa	0.0	(0.1)	1.3	(0.5)
Sustut	1.9	(0.4)	1.0	(0.4)
Sweetin	3.2	(0.9)	4.8	(1.2)
Thomas_Cr	2.6	(0.8)	2.6	(0.7)
Zymoetz	0.8	(0.8)	2.7	(0.8)
Zymogotitz	0.0	(0.1)	0.6	(0.3)

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