Pacific Salmon Commission
Northern Fund

**Northern Boundary Area Sockeye Salmon Genetic Stock Identification
For Year 2011 District 101 Gillnet and District 104 Purse Seine Fisheries**

Final Report

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INTRODUCTION

Provisions outlined in Chapter 2 of the Pacific Salmon Treaty specify harvest sharing arrangements of Nass and Skeena River sockeye salmon (*Oncorhynchus nerka*) between the United States and Canada. This treaty allows the United States to harvest a fixed percentage, averaged over ten years, of the annual allowable harvest (AAH) of Nass sockeye in the Alaskan District 101 gillnet fishery (GNF) and of Nass and Skeena sockeye in the District 104 purse seine fishery (PSF) prior to Statistical Week 31 (late July). There is also a District 101 PSF, but the catch in this fishery is not limited by the annex; it is used however in calculating the total return of Alaska, Nass and Skeena River stocks (along with districts 102, 103 seine and 106 gillnet). Figure 1 illustrates the locations of the Alaska Department of Fish and Game (ADF&G) commercial fishing districts in the Northern Boundary area.

Accurate estimates of the stock composition of sockeye salmon caught in boundary area gillnet and purse seine fisheries (few are caught in troll fisheries) are required to estimate the total return (catch plus escapement) of stocks subject to harvest sharing agreements. The estimated total return is then used in calculating the percentage of the AAH caught in the District 101 gillnet and District 104 purse seine fisheries. The AAH is calculated over the ten-year annex period. This approach allows for traditional fishing patterns based on stock abundance, recognizing that for some years more fish would be caught which would be compensated by other years in which less would be harvested.

It has been recognized for some time that U.S. and Canadian fishermen intercept salmon originating from the other country. Initial studies investigating the stock origins of pink (*O. gorbuscha*) and sockeye salmon caught in the Northern Boundary region between Alaska and British Columbia used mark-recapture techniques (Pella et al., 1993). These techniques involved tagging fish caught in boundary fisheries and re-capturing them at various weirs and other in-river escapement enumeration projects. This study found that a significant percent of the fish caught in districts 101 and 104 originated from Canadian stocks (Pella et al., 1993). While informative, these tagging experiments were relatively expensive and labor intensive.

A study was undertaken in 1982 to evaluate scale pattern analysis (SPA) as a means to discriminate particular stocks of fish (Marshall, 1984). This important study showed that sockeye salmon in the Alaska-British Columbia Northern Boundary area could be accurately discriminated using scales. Since then, SPA has been used by ADF&G to determine stock proportions for sockeye salmon caught in the commercial sockeye fisheries in districts 101 and 104.

While effective, SPA requires yearly examination of source populations for each of the four major age classes (1.2, 1.3, 2.2 and 2.3) since the scale baseline patterns are strongly affected by varying environmental conditions. The requirement to reestablish or revalidate the scale pattern baseline can be expensive and burdensome. The use of more stable markers would eliminate this necessity. Like scale patterns, DNA patterns can also be used to discriminate stocks of salmon (Milner et al., 1985). Given that salmon return to their natal streams with high fidelity, they represent naturally occurring isolated populations in which genetic allele frequencies can change due to the isolation and adaptation of particular populations. These changes in allele frequencies can then be used to distinguish salmon stocks to a finer degree of resolution than SPA. For example,

scale analysis can efficiently separate 4 large stock groups (Alaska, Nass, Skeena and Fraser) whereas genetic analysis can separate 13 stock groups, adding to the knowledge available to manage area fisheries.
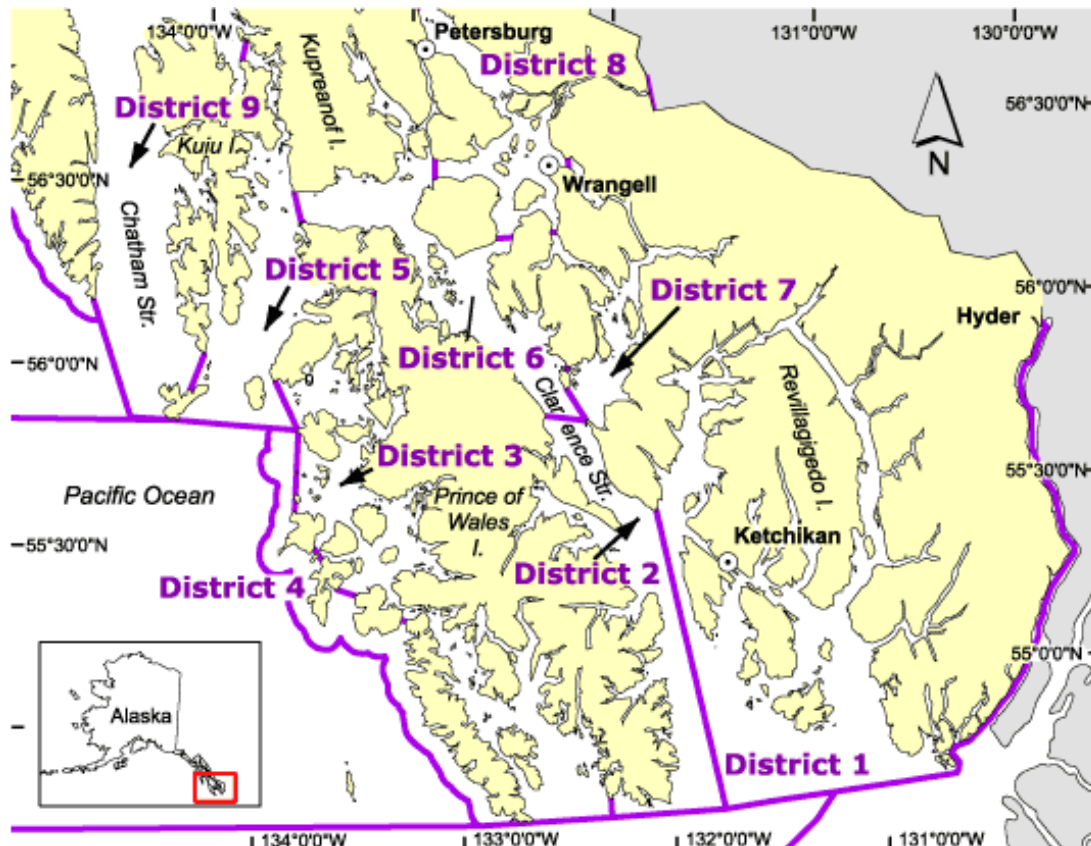
Figure 1. Geographic location of ADF&G commercial fishing districts 101 (labeled District 1) and 104 (labeled District 4). Map obtained from the ADF&G web page (http://www.cf.adfg.state.ak.us/region1/finfish/salmon/maps/ketchikan.php).

Allozymes are naturally occurring protein variants which have been used as genetic markers. As part of a study to estimate stock composition of sockeye salmon harvested in the 1987 Northern Boundary sockeye fisheries in districts 104 and 106 (Pella et al., 1998), four markers were used which included two unlinked allozyme markers (*PGM-1** and *PGM-2**), freshwater age, and a brain-tissue parasite (*Myxobolus arcticus*). Freshwater age and pathogen exposure are traits that can be used in combination with other markers, to infer the stock composition of mixtures (Fournier et al., 1984; Pella and Milner, 1987). The 1987 study provided estimated proportions of 13 stock groups in the District 104 fisheries and confirmed that the majority of sockeye salmon caught were of Canadian origin (Pella et al., 1998). This analysis demonstrated that genetic markers could be effective in estimating the stock composition of sockeye salmon caught in Northern Boundary fisheries.

Although allozymes have been used in many genetic studies in salmon, it can be laborious to complete all the lab methods necessary to score them. Since then, additional genetic markers have been evaluated including microsatellite DNA repeats and single nucleotide polymorphisms (SNPs). Like allozymes, both microsatellite and SNP markers

can efficiently be used to separate stocks of salmon (Beacham et al., 2008; Habicht et al., 2004, 2010; Smith et al., 2005a). While Canadian scientists use microsatellite markers for many of their Northern Boundary studies, ADF&G uses SNPs. Numerous studies

Table 1. Sockeye salmon baseline populations used in mixed stock analysis.

Pop.#	Description	Region	Pop.#	Description	Region
1	East Alsek	1	43	Hetta Lake	5
2	Alsek - Klukshu River Weir late	1	44	Kanalku Lake	5
3	Alsek - Upper Tatshenshini	1	45	Klakas Lake	5
4	Berners Bay	2	46	Sarkar	5
5	Chilkat Lake early run	2	47	Shipley Lake	5
6	Chilkat River - Mule Meadows	2	48	Three Mile Creek - Klawock	5
7	Chilkoot Lake – beaches	2	49	Hatchery Creek – McDonald Lake	6
8	Chilkoot River	2	50	Hugh Smith - Cobb Creek	7
9	Crescent Lake	2	51	Hugh Smith Lake - Bushmann Creek	7
10	Falls Lake	2	52	Nass - Bowser Lake	8
11	Sitkoh Lake	2	53	Nass - Damdochax Creek	8
12	Snettisham Hatchery/Speel Lake	2	54	Nass - Hanna Creek	8
13	Steep Creek	2	55	Nass - Meziadin Lake	8
14	Windfall Lake	2	56	Nass - Tintina Creek	8
15	Redfish Lake Beaches	2	57	Skeena - Alastair Lake	9
16	Taku - Kuthai Lake	3	58	Skeena - Four Mile Creek	9
17	Taku - Little Tatsamenie	3	59	Skeena - Fulton River	9
18	Taku - Little Trapper Lake	3	60	Skeena - Kitsumkalum Lake	9
19	Taku - Taku River Mainstem	3	61	Skeena - Lakelse Lake (Williams)	9
20	Taku – Tatsamenie	3	62	Skeena - Lower Tahlo River	9
21	Taku - Tatsamenie Lake	3	63	Skeena - McDonell Lake (Zymoetz River)	9
22	Stikine - Iskut River	4	64	Skeena – Morrison	9
23	Stikine - Little Tahltan	4	65	Skeena - Nangeese River	9
24	Stikine - Scud River	4	66	Skeena - Nanika River	9
25	Stikine - Tahltan Lake	4	67	Skeena - Pierre Creek	9
26	Kutlaku Lake	5	68	Skeena - Pinkut Creek	9
27	Hatchery Creek - Sweetwater Lake	5	69	Skeena - Slamgeesh River	9
28	Heckman Lake	5	70	Skeena - Sustut (Johanson Lake)	9
29	Helm Lake	5	71	Skeena - Swan Lake	9
30	SI – Kah Sheets Lake	5	72	Skeena - Upper Babine River	9
31	Karta	5	73	QCI - Naden River	10
32	Kegan Lake	5	74	Central - Kitlope Lake	11
33	Kunk Lake - Etolin Island system	5	75	Fraser - Adams River (Shuswap late)	12
34	Luck Lake - P.O.W. Island	5	76	Fraser – Birkenhead	12
35	Mahoney Creek	5	77	Fraser - Chilko Lake	12
36	Mill Creek Weir - Virginia Lake	5	78	Fraser - Harrison River	12
37	Petersburg Lake	5	79	Fraser - Horsefly River	12
38	Red Bay Lake	5	80	Fraser - Raft River	12
39	Salmon Bay Lake	5	81	Fraser - Stellako River	12
40	Thoms Lake	5	82	Fraser - Weaver Creek	12
41	Unuk River - Gene's Lake	5	83	Baker Lake	13
42	Bar Creek - Essowah Lake	5	84	Cedar River	13

have been completed outlining the advantages and disadvantages of each, although both have the resolving power necessary to accurately perform stock composition studies (Smith et al., 2007).

ADF&G has collaborated with numerous laboratories to develop a sockeye SNP baseline with 45 SNP markers (Habicht et al., 2007, 2010). This baseline was used by ADF&G in 2004 and 2005; and by NOAA/NMFS/Alaska Fishery Science Center/Auke Bay Laboratories (ABL) in 2006-10 for genetic stock composition analyses for districts 101 and 104. Currently, 84 sockeye populations are part of the SNP baseline (Table 1). As part of this process, the resolving power of the SNP baseline was evaluated using simulated mixture analyses, and this baseline was shown to be fully capable of distinguishing 13 Northern Boundary sockeye stock groups (Table 2) (Oliver 2009).

Problems in accurately estimating stock proportions of catches and total returns of sockeye salmon in the early years of the Pacific Salmon Treaty resulted in an extensive investigation of run reconstruction modeling by the bilateral Northern Boundary Technical Committee. The Committee concluded that improved stock identification techniques are needed for run reconstruction models. As opposed to SPA, genetic techniques have the advantage of a relatively stable baseline (does not change yearly) and the analysis can be highly automated. The purpose of this study is to provide the eighth year of genetic data using SNP markers to compare with the SPA. Congruence was found between the two techniques, so genetic analysis will replace SPA for estimating stock composition of sockeye salmon caught in Northern Boundary fisheries in 2012. A blind testing study performed determined genetic markers are the viable method to replace SPA (Oliver personal communication, 2011).

Table 2. Regional grouping of populations for stock composition analysis.

Region	Area
1	Alsek
2	Northern Southeast Alaska
3	Taku
4	Stikine
5	Southern Southeast Alaska
6	McDonald
7	Hugh Smith
8	Nass River
9	Skeena River
10	Queen Charlotte Island
11	Central Coast British Columbia
12	Fraser River
13	Washington

OBJECTIVE

The purpose of this study was to genetically analyze axillary process (AXP) samples from 3,302 sockeye salmon harvested in the 2011 District 101 gillnet and District 104 purse seine sockeye fisheries to determine proportions of Canadian and U.S. fish. A SNP genetic baseline of 45 SNPs (41 markers as 3 groups of SNPs are linked) assayed in 84 sockeye populations from southeast Alaska and British Columbia, and Washington was developed by ADF&G (Habicht et al, 2010).

METHODS

Genetic baseline and population grouping

Genetic samples from 84 baseline stocks (Table 1) were collated by ADF&G in collaboration with many other laboratories including ABL and the Canadian Department of Fisheries and Oceans. The 84 populations were grouped into 13 regions (Table 2)

based on manager needs, the SPA groupings, geographical location, and historical knowledge.

Sample Collection

Matched genetic and scale samples were collected by port samplers from ADF&G. Samples were collected from the District 101 GNF and from the District 104 PSF. Genetic samples were clipped AXP that were stored in ethanol. The genetic samples were shipped to ABL for analysis and stored at room temperature. ADF&G collected genetic and scale samples from a maximum of 260 (Table 4&5), fish per statistical week for each district, of which over 99% were successfully analyzed (Table 4&5).

DNA Extraction

DNA was extracted from the AXP into 96-well plates with either the QIAGEN DNeasy Blood and Tissue Kits or Corbett X-tractor Gene reagents as described by the manufacturer (QIAGEN, Inc.). In brief, small pieces of tissue (~20 mg) were excised from ethanol-stored axillary processes. The tissue pieces were digested in a proteinase solution for 3 hours and at 55ºC. Protease digestions were performed in 96 well plates. After digestion, the samples were purified with a Corbett X-tractor robot producing eluted DNA which was stored at -20 ºC.

Single Nucleotide Polymorphism (SNP) Analysis

SNP genotyping was performed using Taqman chemistries from Applied Biosciences, Inc (ABI) for 45 previously identified sockeye SNP probes. Of the 45 sockeye SNP markers (Table 3) (Elfstrom et al., 2006; Smith et al., 2005b; Habicht et al., 2007, 2010), 44 were assayed in this analysis. The remaining assay, *One_serpin* was excluded due to poor resolution. Taqman reactions were performed by transferring 1 μl of a 1:10 dilution of the eluted

Table 3. 45 SNP assays used to discriminate Northern Boundary sockeye populations.

#	Name	Comments
1	One_ACBP-79	
2	One_ALDOB-135	
3	One_CO1 (mitochondrial)	linked with 5&6
4	One_ctgf-301	
5	One_Cytb_17 (mitochondrial)	linked with 3&6
6	One_Cytb_26 (mitochondrial)	linked with 3&5
7	One_E2-65	
8	One_GHII-2165	
9	One_GPDH-201	linked with 10
10	One_GPDH2-187	linked with 9
11	One_GPH-414	
12	One_hsc71-220	
13	One_HGFA-49	
14	One_HpaI-71	
15	One_HpaI-99	
16	One_IL8r-362	
17	One_KPNA-422	
18	One_LEI-87	
19	One_MARCKS-241	
20	One_MHC2_190	linked with 21
21	One_MHC2_251	linked with 20
22	One_Ots213-181	
23	One_p53-534	
24	One_ins-107	
25	One_Prl2	
26	One_RAG1-103	
27	One_RAG3-93	
28	One_RFC2-102	
29	One_RFC2-285	
30	One_RH2op-395	
31	One_serpin-75	not resolved
32	One_STC-410	
33	One_STR07	
34	One_Tf_ex11-750	
35	One_Tf_in3-182	
36	One_U301-92	
37	One_U401-224	
38	One_U404-229	
39	One_U502-167	
40	One_U503-170	
41	One_U504-141	
42	One_U508-533	
43	One_VIM-569	
44	One_ZNF-61	
45	One_Zp3b-49	

purified DNA to wells of a 384 well plate. Four wells were reserved for non-template
controls. Each Taqman reaction was conducted in a 5 μl volume containing the
 template DNA, Taqman Universal PCR Mastermix, No AmpErase UNG (ABI), 900 nm
of each PCR primer, and 200 nm probe. Thermal cycling was performed on a ABI Dual
384-Well GeneAmp PCR System 9700 using the protocol from Habicht et al. (2010).

Table 4. Sockeye salmon harvested, genetic sample size, and genotyping success rate in each statistical week in the 2011 District 101 Gillnet fishery.

		District 101 Gillnet			
Week	*2011*	*2001-2010 Avg.*	*Extracted*	*Analyzed*	*% Analyzed*
26	8,853	13,526	260	258	99.2
27	21,319	17,169	260	259	99.6
28	10,013	10,948	260	258	99.2
29	9,290	7,142	260	259	99.6
30	8,686	7,066	260	258	99.2
31	8,564	6,244	260	259	99.6
32	16,143	6,916	260	259	99.6
33	3,821	3,343	240	240	100.0
34	671	1,289	260	257	98.8
35	384	1,191	232	230	99.1
36	700	569	0	0	0.0
37	63	267	0	0	0.0
38	110	122	0	0	0.0
39	1	15	0	0	0.0
Total Catch	88,618	75,808			
Sampled Catch	87,744	74,835	2,552	2,537	99.4

Allele Scoring

After amplification, the Taqman genotyping reactions were assayed on an ABI
PRISM 7900HT Sequence Detection System and scored using ABI Sequence Detection

Table 5. Sockeye salmon harvested, genetic sample size, and genotyping success rate in each statistical week in the 2011 District 104 Pu
Seine fishery.

		District 104 Purse Seine			
Week	*2011*	*2001-2010 Avg.*	*Extracted*	*Analyzed*	*% Analyzed*
28	2,130	12,539	0	0	0
29	9,287	18,964	40	39	97.5
30	13,863	27,419	80	80	100.0
31	37,917	77,959	170	170	100.0
32	109,375	59,728	250	249	99.6
33	23,091	40,932	130	130	100.0
34	2,403	47,071	40	40	100.0
35	2,480	8,578	40	40	100.0
36	1,956	50	0	0	0.0
Total Catch	202,502	293,240			
Sampled Catch	198,416	280,651	750	748	99.7

Software 2.2. Individual genotypes were imported into our genetic database developed with Progeny software (Progeny, Inc.).

Mixture Analysis

   A mixture analysis using a Bayesian estimation method (Pella and Masuda, 2001) was implemented using BAYES software and was performed for each weekly mixture sample and each district. For each BAYES analysis, 13 Monte Carlo chains starting at disparate values of stock proportions were configured such that 95% of the stocks came from one designated region with weights equally distributed among the stocks of that region. The remaining 5% was equally distributed among remaining stocks from all other regions. For all estimates, a flat prior of 0.011905 (calculated as 1/84) was used for all 84 populations. Convergence of chains to posterior distributions of stock proportions was determined with Gelman and Rubin shrink factors (Gelman and Rubin 1992), and the first one-half of chains was discarded as burn-in before summarizing posterior distributions. Monte Carlo chain lengths were 10,000 with 4 exceptions; District 101 weeks 26, 27 and 29 needed a chain length of 50,000, 25,000, and 25,000 respectively to converge. Regional groups southern southeast Alaska and Hugh Smith Lake in Statistical Week 34 would not converge even with a chain length of 500,000, so the results were pooled, after which convergence was reached with a chain length of 10,000.

RESULTS

  In 2011, 88,618 sockeye salmon were harvested in District 101 GNF which is more than the 2001 to 2010 average of 75,808 (Table 4). In the District 104 PSF, 202,502 fish were harvested in 2011 which is 69% of the 2001-2010 average of 293,240 (Table 5). Sockeye salmon DNA was isolated (Table 4&5) and genotyped for 44 SNP markers from 3,533 fish in 2011. The data was imported into a Progeny database for analysis. Samples resolved for at least 38 of the 44 SNPs were included in the analyses (i.e. % analyzed in Tables 4&5).

Stock Mixture Proportions

   Weekly mixture samples were analyzed with BAYES software. In all but one of the analyses, the Gelman and Rubin shrink factors were less than 1.2, indicating convergence of the chains to posterior distributions. Regional groups southern southeast Alaska and Hugh Smith Lake in Statistical Week 34 would not converge so they were pooled resulting in convergence. Results from this analysis are presented in both graphical form (Figure 2) and Table form (Tables 6&7). Figure 2 graphically illustrates the estimated proportions of sockeye salmon endemic to each of the 13 regions that were harvested in each district and statistical week. Tables 6 and 7 provide the same data shown in Figure 2 in numerical format showing the estimated stock group proportions, standard errors, and 95% credibile intervals for the 2011 101 GNF and 104 PSF respectively.

   Analysis of the stock proportions of sockeye caught in districts 101 GNF and 104 PSF over varying weeks shows interesting trends (Table 6). For example, the sockeye commercial fishery in the 2011 District 101 GNF predominantly harvested Nass Region fish; with a high of 85% in week 27, and a low of 21% in week 34. Skeena stocks peaked

at 45% in week 32. Hugh Smith, SSE Alaska and McDonald stocks accounted for over 58% of the stock composition in week 34.

The sockeye commercial fishery in the 2011 District 104 PSF predominantly harvested Skeena River fish throughout the season; a high of 63% in week 33,to a low of 30% in week 34&35. Fraser fish were most abundant at 37% in week 34&35 as were SSE Alaska (31 %). Nass was the second most abundant in weeks 29, 30 and 31 and was replaced SSE Alaska in weeks 32 and 33. Caution should be used when using the estimates from PSF, since the samples sizes in comparison to the catch were small.

The proportion estimates were used to estimate numbers of fish caught from each region for each fishery (Table 8). The one fish discrepancy in Table 4, and the 4 fish discrepancy in Table 5 in the total numbers of fish when compared to Table 8 were due to rounding errors in estimating numbers of fish caught from estimated stock group proportions. Since there were no genetic samples obtained from District 104 PSF in week 28 and 36; and District 101 GNF weeks 36-39 (Table 5); those weeks were not represented in the regional estimates in Table 8. Table 8 also shows the estimated number of fish caught per region prior to Statistical Week 31. The Pacific Salmon Treaty allows for the harvest of a fixed percentage of Nass (for District 101) and Nass/Skeena (for District 104) sockeye prior to week 31.

DISCUSSION

Chapter 2 of the 1999 Pacific Salmon Treaty specifies U.S. and Canada harvest sharing arrangements of Nass and Skeena River sockeye salmon in Northern Boundary fisheries. In Alaska's District 101 and District 104 sockeye fisheries, the United States is allowed to harvest a fixed percentage of the annual allowable harvest (AAH) of Nass and Skeena River sockeye salmon. Estimates of the stock-specific catch in these commercial fisheries are currently being provided by ADF&G using scale pattern analysis (SPA). This technique has been shown to be accurate, but requires the collection of yearly scale patterns to determine the year specific baseline for individual rivers. This is because annual fluctuations in environmental conditions can dramatically affect scale patterns.

In comparison to SPA, genetic analysis has the potential for greatly increasing the precision and accuracy of stock composition estimates in the District 101 and 104 fisheries. An additional advantage of using DNA markers is that in-season results can theoretically be provided to fishery managers because, unlike SPA, it does not require annual baseline sampling. Importantly, a SNP baseline with good coverage has already been developed by ADF&G for Southeast Alaska and British Columbia. ADF&G and ABL are continuously updating the baseline by adding new populations and developing new markers. ADF&G made the most current sockeye baseline available to the ABL/TSMRI Genetics group for use in this analysis.

Genetic markers are more stable than scale patterns and are not normally influenced by small environmental changes in short periods of time. Allelic frequency differences of genetic markers can be used to distinguish individual stocks of fish. These allele frequency differences can be reflective of adaptive measures taken by unique stocks of fish to thrive in different environmental conditions, although these changes can often take many generations. Genetic stock identification is a powerful technique that takes advantage of these genetic differences to discriminate stocks of fish caught in a mixed stock fishery.

Auke Bay Laboratories has completed its genetic analysis of sockeye salmon caught in Districts 101 gillnet and District 104 purse seine fisheries for 2011. It should be recognized that while a total of 45 SNPs (41 markers) are currently used in the Southeast Alaska-British Columbia baseline, not all SNPs are likely to be equally informative. A thorough analysis of the effectiveness of combinations of SNPs to resolve sockeye in southeast Alaska and British Columbia could help reduce the numbers of SNPs that need to be assayed to obtain the same resolution.

CONCLUSION

Our results indicate that a majority of sockeye salmon caught in the ADF&G District 101 GNF and District 104 PSF originated from Canadian stocks in 2011. Our results are in general agreement with the mark-recapture studies completed in the early 1980's (Pella et al., 1993), SPA completed since 1982 (Marshall, 1984), allozyme/freshwater age/parasitism analyses completed in the late 1980's (Pella et al., 1998), and SNP based genetic stock composition analyses completed since 2004. These correlations strongly suggest that all stock assessment methods have produced accurate and meaningful results in the management of these Northern Boundary fisheries. Compared with other methods, SNP genotyping is the most efficient method for stock assessment since it can be partially automated and the baseline does not require annual resampling. These advantages make it possible to use SNP markers to determine stock composition in a quicker time interval, allowing for improved management of the Northern Boundary fisheries. The similarity between stock composition estimates produced using scale pattern analysis and genetic analysis helps validate both approaches for determining stock assessments (Oliver 2009, Guthrie et al. 2009).

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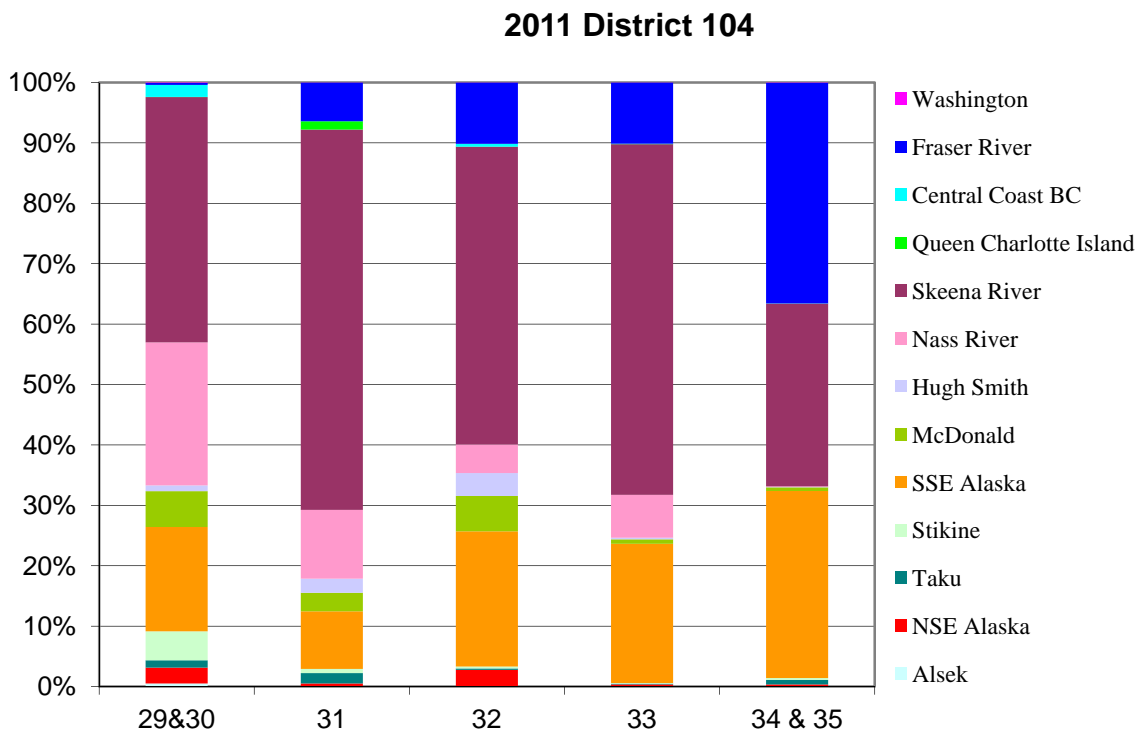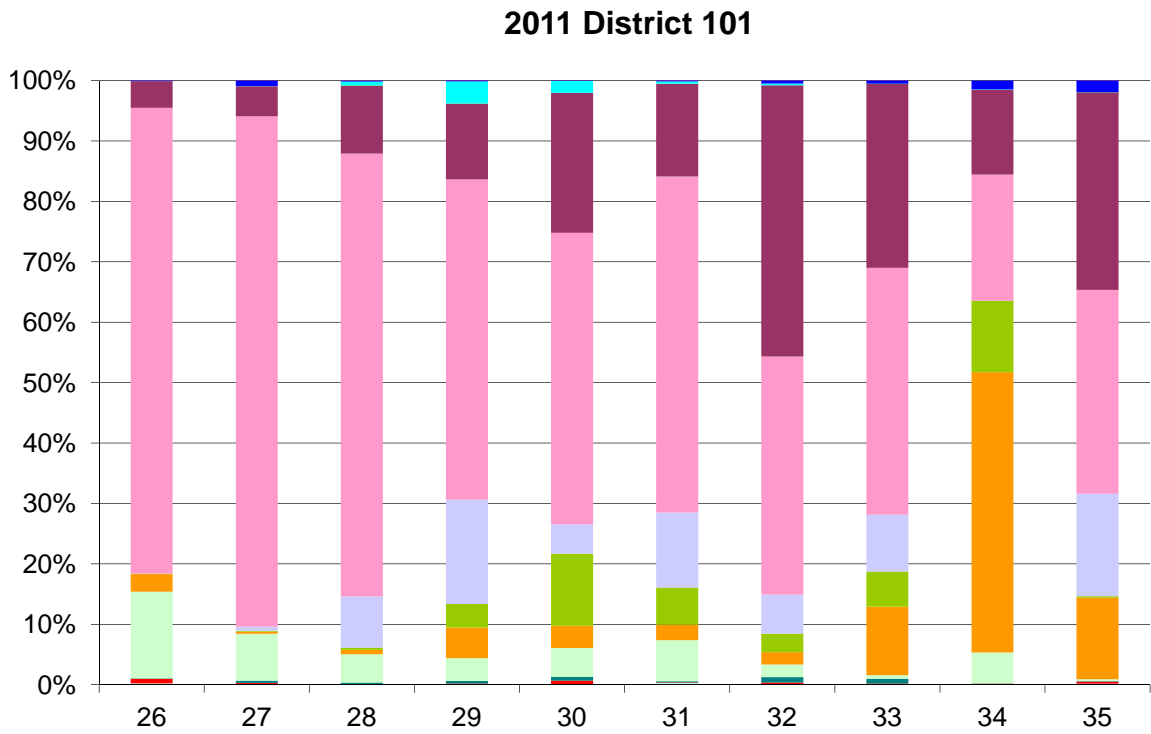
Figure 2. 2011 sockeye stock group proportions for each statistical week from the ADF&G District 101 gillnet (top panel) and 104 purse seine fisheries (lower panel).

Table 6. Stock composition estimates of weekly mixtures of the 2011 District 101 commercial gillnet fishery.

	Week 26			Week 27			Week 28			Week 29		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.2	0.58	(0.0,2.1)	0.0	0.09	(0.0,0.2)	0.0	0.10	(0.0,0.2)	0.1	0.33	(0.0,0.9)
NSE Alaska	0.7	0.58	(0.0,2.2)	0.3	0.39	(0.0,1.4)	0.1	0.27	(0.0,0.8)	0.1	0.33	(0.0,1.1)
Taku	0.1	0.32	(0.0,0.9)	0.4	1.26	(0.0,5.2)	0.2	0.52	(0.0,1.5)	0.4	0.95	(0.0,3.2)
Stikine	14.4	2.64	(9.5,19.9)	7.8	2.70	(0.8,12.8)	4.7	2.01	(0.9,8.9)	3.8	2.75	(0.3,9.8)
SSE Alaska	2.9	1.70	(0.0,6.5)	0.3	0.59	(0.0,2.1)	0.7	1.04	(0.0,3.7)	5.1	2.85	(0.3,11.3)
McDonald	0.1	0.28	(0.0,0.8)	0.2	0.52	(0.0,1.9)	0.4	1.05	(0.0,3.9)	3.9	3.11	(0.0,10.4)
Hugh Smith	0.1	0.21	(0.0,0.6)	0.7	0.75	(0.0,2.6)	8.5	2.04	(4.8,12.7)	17.3	3.44	(10.7,24.2)
Nass River	77.1	2.78	(71.4,82.3)	84.5	2.95	(78.2,89.7)	73.3	3.01	(67.2,79.0)	53.0	3.47	(46.1,59.7)
Skeena River	4.4	1.44	(2.0,7.6)	5.0	2.18	(1.8,10.1)	11.3	2.26	(7.2,16.1)	12.5	2.44	(8.2,17.8)
Queen Charlotte I.	0.0	0.04	(0.0,0.0)	0.0	0.04	(0.0,0.0)	0.0	0.07	(0.0,0.1)	0.0	0.05	(0.0,0.0)
Central Coast BC	0.0	0.06	(0.0,0.1)	0.0	0.19	(0.0,0.5)	0.6	1.17	(0.0,4.0)	3.7	1.73	(0.4,7.4)
Fraser River	0.1	0.21	(0.0,0.7)	0.9	0.61	(0.1,2.4)	0.1	0.32	(0.0,1.1)	0.1	0.33	(0.0,1.2)
Washington	0.0	0.06	(0.0,0.1)	0.0	0.07	(0.0,0.1)	0.0	0.16	(0.0,0.4)	0.0	0.06	(0.0,0.1)

	Week 30			Week 31			Week 32			Week 33		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.0	0.10	(0.0,0.2)	0.3	0.75	(0.0,2.7)	0.1	0.42	(0.0,1.5)	0.1	0.30	(0.0,0.8)
NSE Alaska	0.7	1.16	(0.0,4.2)	0.1	0.23	(0.0,0.8)	0.3	0.55	(0.0,1.9)	0.1	0.38	(0.0,1.3)
Taku	0.6	1.59	(0.0,5.9)	0.2	0.77	(0.0,2.2)	0.9	1.62	(0.0,5.6)	0.8	1.26	(0.0,4.3)
Stikine	4.8	2.93	(0.0,10.4)	6.8	2.40	(2.1,11.7)	2.1	2.02	(0.0,6.5)	0.6	1.19	(0.0,4.2)
SSE Alaska	3.7	2.75	(0.0,9.5)	2.6	1.84	(0.0,6.8)	2.1	1.51	(0.0,5.6)	11.3	3.17	(5.4,17.8)
McDonald	11.9	3.37	(5.7,18.8)	6.1	2.57	(1.4,11.6)	3.1	2.09	(0.0,7.4)	5.8	3.46	(0.0,12.8)
Hugh Smith	4.9	4.09	(0.0,13.1)	12.4	2.83	(7.3,18.4)	6.5	2.46	(2.2,11.8)	9.4	4.15	(2.7,18.6)
Nass River	48.3	3.80	(40.6,55.6)	55.6	3.52	(48.6,62.4)	39.4	3.37	(32.9,46.1)	40.9	3.32	(34.5,47.5)
Skeena River	23.2	3.34	(17.1,30.2)	15.4	2.61	(10.7,20.8)	44.9	3.46	(38.2,51.8)	30.4	3.22	(24.3,36.9)
Queen Charlotte I.	0.0	0.07	(0.0,0.1)	0.0	0.09	(0.0,0.1)	0.0	0.04	(0.0,0.0)	0.0	0.09	(0.0,0.1)
Central Coast BC	2.0	1.56	(0.0,5.3)	0.4	0.96	(0.0,3.4)	0.3	0.77	(0.0,2.8)	0.0	0.21	(0.0,0.4)
Fraser River	0.1	0.16	(0.0,0.5)	0.1	0.30	(0.0,1.0)	0.5	0.60	(0.0,2.1)	0.5	0.51	(0.0,1.8)
Washington	0.0	0.12	(0.0,0.2)	0.0	0.10	(0.0,0.2)	0.0	0.11	(0.0,0.2)	0.0	0.08	(0.0,0.1)

	Week 34			Week 35		
	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.1	0.42	(0.0,1.0)	0.2	0.54	(0.0,1.9)
NSE Alaska	0.1	0.22	(0.0,0.7)	0.4	0.62	(0.0,2.2)
Taku	0.1	0.33	(0.0,0.6)	0.1	0.28	(0.0,0.8)
Stikine	5.1	3.08	(0.0,11.3)	0.3	0.94	(0.0,3.5)
SSE Alaska	46.4	4.62	(37.7,55.7)	13.5	3.09	(7.7,19.8)
McDonald	11.8	3.42	(5.5,18.9)	0.2	0.95	(0.0,3.5)
Hugh Smith	**pooled with SSE Alaska**			17.0	3.31	(10.8,23.8)
Nass River	20.9	2.67	(15.9,26.3)	33.7	3.35	(27.3,40.4)
Skeena River	14.0	2.45	(9.5,19.1)	32.7	3.38	(26.3,39.6)
Queen Charlotte I.	0.0	0.05	(0.0,0.0)	0.0	0.05	(0.0,0.0)
Central Coast BC	0.1	0.43	(0.0,0.7)	0.0	0.11	(0.0,0.1)
Fraser River	1.5	0.91	(0.0,3.6)	1.9	1.09	(0.3,4.5)
Washington	0.0	0.00	(0.0,0.0)	0.0	0.12	(0.0,0.2)

Table 7. Stock composition estimates of weekly mixtures of the 2011 District 104 commercial purse seine fishery.

	Week 29 &30			Week 31			Week 32			Week 33		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.5	1.27	(0.0,4.5)	0.1	0.26	(0.0,0.7)	0.1	0.24	(0.0,0.8)	0.1	0.37	(0.0,1.0)
NSE Alaska	2.6	2.79	(0.0,9.5)	0.4	0.78	(0.0,2.7)	2.7	1.94	(0.0,6.8)	0.3	0.60	(0.0,2.1)
Taku	1.2	3.02	(0.0,11.1)	1.7	2.17	(0.0,7.0)	0.2	0.66	(0.0,2.4)	0.1	0.47	(0.0,1.5)
Stikine	4.8	5.37	(0.0,16.6)	0.7	1.28	(0.0,4.4)	0.3	0.95	(0.0,3.5)	0.1	0.47	(0.0,1.2)
SSE Alaska	17.3	4.39	(9.6,26.7)	9.5	2.62	(4.9,15.2)	22.4	3.72	(14.7,29.5)	23.1	4.11	(15.2,31.4)
McDonald	5.9	4.51	(0.0,15.4)	3.1	2.11	(0.0,7.8)	5.9	4.05	(0.0,12.9)	0.7	1.76	(0.0,6.3)
Hugh Smith	1.0	2.14	(0.0,7.7)	2.3	2.02	(0.0,6.9)	3.8	4.99	(0.0,15.3)	0.3	0.99	(0.0,3.6)
Nass River	23.7	4.19	(15.9,32.3)	11.4	2.48	(7.0,16.7)	4.8	1.51	(2.2,8.2)	7.1	2.79	(2.7,13.4)
Skeena River	40.6	4.81	(31.4,50.2)	62.9	3.81	(55.4,70.2)	49.3	3.35	(42.7,55.9)	58.1	4.62	(48.8,67.0)
Queen Charlotte I.	0.0	0.10	(0.0,0.1)	1.4	0.99	(0.1,3.8)	0.0	0.05	(0.0,0.0)	0.0	0.08	(0.0,0.1)
Central Coast BC	2.0	2.68	(0.0,9.0)	0.0	0.14	(0.0,0.1)	0.5	0.93	(0.0,3.2)	0.1	0.43	(0.0,1.1)
Fraser River	0.3	0.77	(0.0,2.7)	6.4	2.04	(2.9,10.8)	10.1	2.05	(6.4,14.5)	10.1	2.74	(5.3,16.1)
Washington	0.1	0.44	(0.0,1.2)	0.0	0.20	(0.0,0.3)	0.0	0.22	(0.0,0.5)	0.0	0.24	(0.0,0.5)

	Week 34 & 35		
	Mean	SD	95% PI
Alsek	0.1	0.34	(0.0,0.7)
NSE Alaska	0.3	0.79	(0.0,2.6)
Taku	0.7	1.94	(0.0,7.2)
Stikine	0.3	1.17	(0.0,3.8)
SSE Alaska	31.0	5.61	(20.3,42.3)
McDonald	0.6	1.39	(0.0,4.9)
Hugh Smith	0.1	0.31	(0.0,0.6)
Nass River	0.1	0.38	(0.0,1.0)
Skeena River	30.2	5.19	(20.6,40.8)
Queen Charlotte I.	0.0	0.15	(0.0,0.1)
Central Coast BC	0.0	0.30	(0.0,0.3)
Fraser River	36.5	5.56	(26.0,47.7)
Washington	0.1	0.38	(0.0,0.9)

Table 8. Estimated numbers of sockeye salmon caught in the 2011 District 101 gillnet and 104 seine fisheries prior to statistcal week 31 and throughout all statistical weeks analyzed (see Tables 4&5).

Region	Area	District 101 Gillnet		District 104 Seine	
		Prior to 31	Total	Prior to 31	Total
1	Alsek	34	79	118	228
2	NSE Alaska	202	258	607	3,790
3	Taku	203	393	285	1,271
4	Stikine	4,157	5,135	1,107	1,761
5	SSE Alaska	1,192	2,540	3,996	38,922
6	McDonald	1,472	2,792	1,375	9,139
7	Hugh Smith	3,027	5,561	225	5,317
8	Nass River	41,292	54,251	5,480	16,637
9	Skeena River	5,760	15,704	9,401	102,049
10	Queen Charlotte I.	3	4	2	536
11	Central Coast BC	584	666	463	1,027
12	Fraser River	227	348	72	17,648
13	Washington	9	14	21	89
	Totals	58,162	87,745	23,150	198,412