Northern Boundary Area Sockeye Salmon Genetic Stock Identification For Year 2010 District 101 Gillnet and District 104 Purse Seine Fisheries Final Report to: Pacific Salmon Commiss...

Technical Report · August 2012

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**Northern Boundary Area Sockeye Salmon Genetic Stock Identification
For Year 2010 District 101 Gillnet and District 104 Purse Seine Fisheries**

Final Report

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Submitted August 13, 2012

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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.
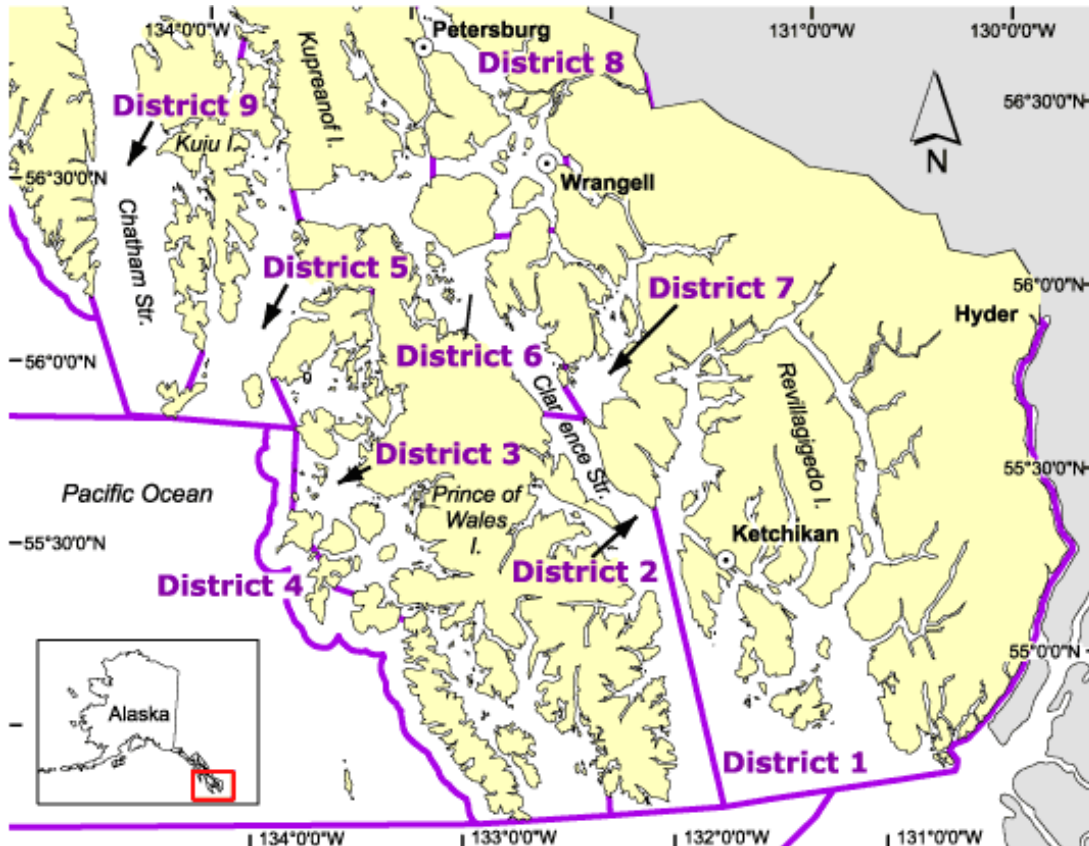
Figure 1. Geographic location of ADF&G fishing districts 101 (labeled District 1) and 104 (labeled District 4). Map obtained from the ADF&G web page (http://www.cf.adfg.state.ak.us/region1/finfish/salmon/maps/ketchikan.php).

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, 2007, 2008 and 2009 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). The number of stock groups differs from previous years when there were 14 groups: the Klawock stock group was merged with Southern Southeast Alaska group.

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 seventh year of genetic data using SNP markers to compare with the SPA. In a blind study completed in 2011 congruence was found between the two techniques, so genetic analysis will replace scale pattern analysis (SPA) for estimating stock composition of sockeye salmon caught in Northern Boundary fisheries starting in 2012.

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 3,574 sockeye salmon harvested in the 2010 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, British Columbia, and Washington was developed by ADF&G (Habicht et al, 2010). Stock proportions were estimated using a Bayesian mixture analysis.

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) fish per statistical week for each district, of which most were successfully analyzed (Table 4).

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 purified DNA to wells of a 384 well plate. Four wells were reserved for non-template

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	

controls. Each Taqman reaction was conducted in a 5 μl volume containing the 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).

Allele Scoring

After amplification, the Taqman genotyping reactions were assayed on an ABI PRISM 7900HT Sequence Detection System and scored using ABI Sequence Detection Software 2.2. Individual genotypes were imported into our genetic database developed with Progeny software (Progeny, Inc.).

Table 4. Sockeye salmon harvested, genetic sample size, and genotyping success rate in each statistical week in the 2010 District 101 Gillnet fishery (http://dungie.adfg.state.ak.us:8080 /CatchByMultiYear.po).

		District 101 Gillnet			
Week	2010	2000-2009 Avg.	Extracted	Analyzed	%Analyzed
26	4,610	13,743	260	257	98.8
27	11,780	16,655	260	259	99.6
28	8,756	11,402	260	258	99.2
29	4,051	7,776	260	250	96.2
30	4,723	8,140	260	254	97.7
31	7,911	6,520	260	260	100.0
32	9,373	7,951	260	258	99.2
33	7,014	3,614	260	259	99.6
34	2,489	1,190	255	252	98.8
35	1280	1,086	260	255	98.1
36	463	541	0	0	0.0
37	196	250	0	0	0.0
38	30	122	0	0	0.0
39	4	17	0	0	0.0
Total Catch	62,680	79,005			
Sampled Catch	61,987	78,077	2,595	2,562	98.7

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

Table 5. Sockeye salmon harvested, genetic sample size, and genotyping success rate in each statistical week in the 2010 District 104 Purse Seine fishery. (http://dungie.adfg.state.ak.us:8080 /CatchByMultiYear.po).

		District 104 Purse Seine			
Week	2010	2000-2009 Avg.	Extracted	Analyzed	%Analyzed
28	326	13,086	0	0	0
29	2800	20,943	89	89	100.0
30	1491	29,329	130	130	100.0
31	3010	84,262	380	376	98.9
32	3175	66,932	130	129	99.2
33	3417	43,889	130	129	99.2
34	1435	47,310	80	80	100.0
35	1744	8,404	40	38	95.0
36	453	5	0	0	0.0
Total Catch	17,851	314,159			
Sampled Catch	17,072		979	971	99.2

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 except for District 101 week 32 which needed a chain length of 25,000 to converge.

RESULTS

In 2010, 62,680 sockeye salmon were harvested in District 101 GNF which is less than the 2000 to 2009 average of 79,005 (Table 4). In the District 104 PSF, 17,851 fish were harvested in 2010 which was less than 6% of the 2000-2009 average of 314,159 (Table 5). Sockeye salmon DNA was isolated (Table 4&5) and genotyped for 44 SNP markers from 3,533 fish in 2010. The data were 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 analyses, the Gelman and Rubin shrink factors were less than 1.2, indicating convergence of the chains to posterior distributions. 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% probability intervals for the 2010 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 2010 District 101 GNF predominantly harvested Nass fish; with a high of 73% in week 27, and a low of 18% in week 29. Skeena stocks peaked at 40% in week 35. Hugh Smith, SSE Alaska and McDonald stocks accounted for over 53% of the stock composition in weeks 29 through 31. During those weeks Hugh Smith had high of 33% in week 29; McDonald had highs of 26% and 31% in weeks 30 and 31 respectively.

The sockeye commercial fishery in the 2010 District 104 PSF predominantly harvested Southern Southeast (SSE) Alaska fish throughout the season; 57% in week 29, to a high of 88% in week 33. Skeena fish which normally predominate early in the season were most abundant at 33% in week 30 compared to 26 % for SSE Alaska, 15% for McDonald, and 13% for Stikine. Alaska stocks dominated the entire 104 PSF, which is a striking change from 2006-2009 where the average composition estimates were 22%, compared to 73% in 2010 (Guthrie 2009; 2010; 2011). SSE Alaska and Skeena fish accounted for at least 60% of the catch throughout the whole season.

The proportion estimates were used to estimate numbers of fish caught from each region for each fishery (Table 8). The one fish discrepancy between total numbers of fish in Tables 4 and 8 were due to rounding errors in estimating numbers of fish caught from estimated stock group proportions. Also there were no genetic samples obtained from District 104 PSF in week 28 (Table 5); therefore this week was 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 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 District 101 gillnet and District 104 purse seine fisheries for 2010. 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 originated from Canadian stocks in 2010. However, unlike the previous 4 years, the majority of sockeye salmon caught in the District 104 PSF were from Alaskan stocks, which might be due to the drastic decrease in the catch (Table 5).

Our results are in general agreement with the mark-recapture studies completed in the early 1980's (Pella et al., 1993), SPAs 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 for 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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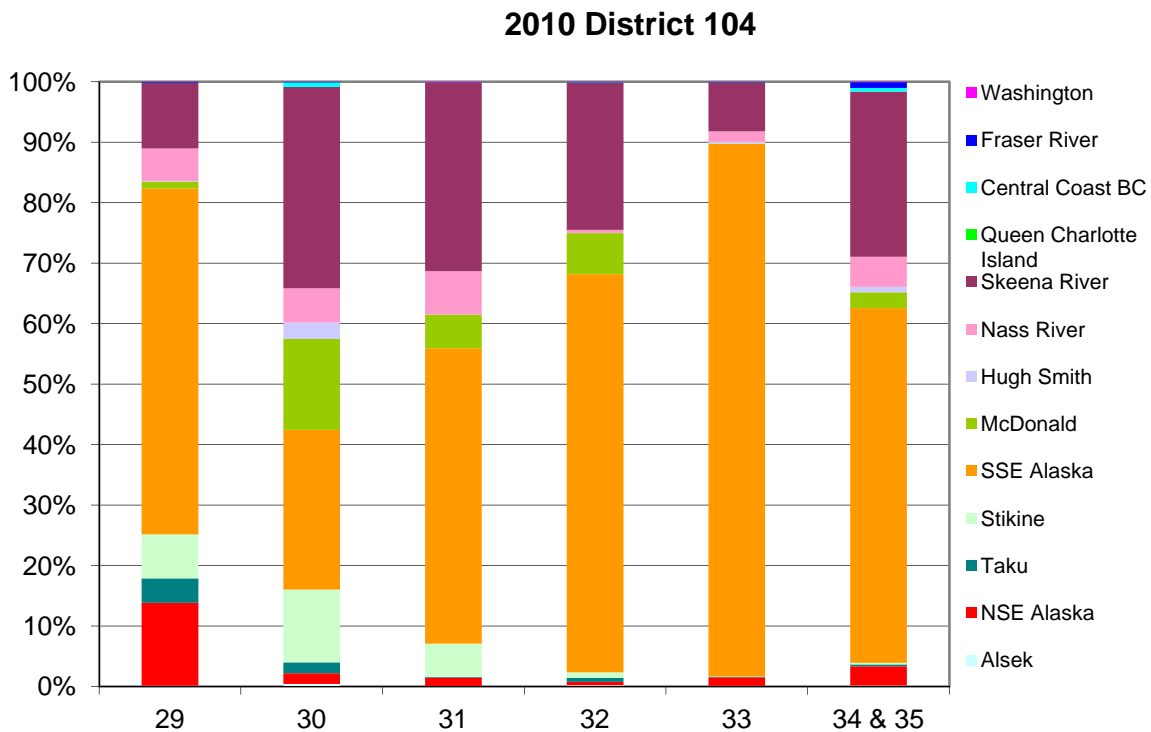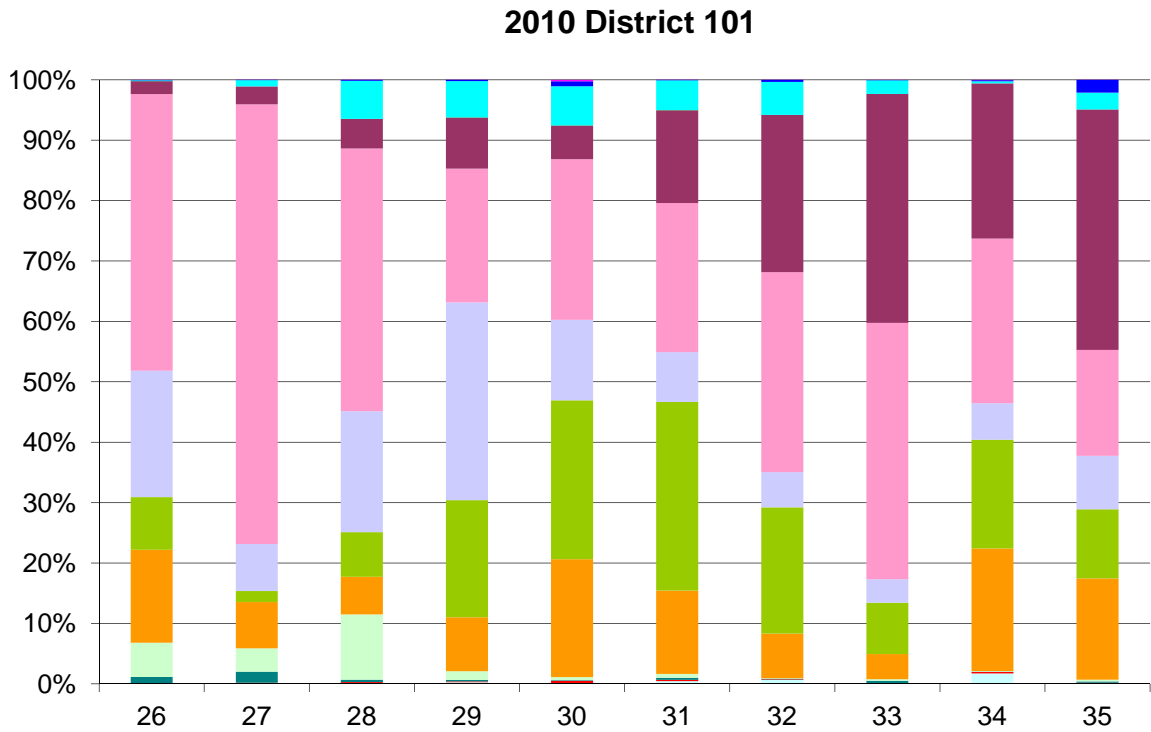## 2010 District 101

2010 District 104

Figure 2. 2010 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 2010 District 101 commercial gillnet sockeye 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	0.0	0.16	(0.0,0.3)	0.1	0.44	(0.0,1.4)	0.0	0.15	(0.0,0.3)	0.3	0.60	(0.0,2.1)
NSE Alaska	0.1	0.28	(0.0,0.9)	0.1	0.21	(0.0,0.7)	0.3	0.52	(0.0,1.8)	0.1	0.35	(0.0,1.2)
Taku	1.0	1.86	(0.0,6.2)	1.8	2.66	(0.0,8.2)	0.4	0.97	(0.0,3.1)	0.2	0.51	(0.0,1.6)
Stikine	5.7	2.67	(1.5,11.1)	3.9	2.80	(0.4,9.8)	10.8	2.91	(5.1,16.7)	1.5	1.30	(0.0,5.2)
SSE Alaska	15.4	2.94	(10.3,21.7)	7.7	2.23	(3.8,12.5)	6.2	2.82	(1.5,12.5)	8.9	2.91	(4.1,15.4)
McDonald	8.7	2.77	(3.8,14.6)	1.8	2.43	(0.0,7.9)	7.4	3.27	(1.5,14.3)	19.4	4.70	(10.6,28.9)
Hugh Smith	20.9	3.43	(14.4,27.8)	7.8	2.67	(2.5,13.0)	20.0	3.81	(12.9,27.8)	32.7	5.45	(22.3,43.5)
Nass River	45.8	3.23	(39.5,52.2)	72.8	2.94	(66.9,78.3)	43.5	3.38	(36.9,50.2)	22.2	2.95	(16.6,28.2)
Skeena River	2.1	1.16	(0.4,4.9)	3.0	1.31	(0.9,6.0)	4.9	1.90	(1.9,9.2)	8.5	2.31	(4.4,13.4)
Queen Charlotte I.	0.0	0.06	(0.0,0.0)	0.0	0.04	(0.0,0.0)	0.0	0.05	(0.0,0.0)	0.0	0.10	(0.0,0.1)
Central Coast BC	0.1	0.49	(0.0,1.6)	1.0	1.14	(0.0,3.9)	6.3	1.87	(3.1,10.4)	6.0	1.94	(2.7,10.2)
Fraser River	0.1	0.17	(0.0,0.6)	0.1	0.19	(0.0,0.6)	0.2	0.35	(0.0,1.2)	0.2	0.42	(0.0,1.5)
Washington	0.0	0.19	(0.0,0.5)	0.0	0.06	(0.0,0.1)	0.0	0.12	(0.0,0.2)	0.0	0.07	(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	0.1	0.55	(0.0,1.8)	0.5	0.69	(0.0,2.3)	0.7	0.91	(0.0,3.1)	0.0	0.12	(0.0,0.3)
NSE Alaska	0.4	0.68	(0.0,2.4)	0.2	0.50	(0.0,1.8)	0.1	0.23	(0.0,0.7)	0.1	0.28	(0.0,0.9)
Taku	0.1	0.32	(0.0,1.1)	0.3	0.97	(0.0,3.6)	0.1	0.28	(0.0,1.0)	0.4	1.01	(0.0,3.8)
Stikine	0.5	0.53	(0.0,1.9)	0.6	1.45	(0.0,5.2)	0.1	0.35	(0.0,1.1)	0.3	0.84	(0.0,3.2)
SSE Alaska	19.5	3.71	(12.5,27.0)	13.8	3.13	(8.1,20.4)	7.4	2.24	(3.5,12.2)	4.2	1.67	(1.3,7.8)
McDonald	26.3	4.44	(18.0,35.3)	31.2	4.69	(22.3,40.8)	20.9	3.80	(13.8,28.7)	8.5	2.27	(4.5,13.3)
Hugh Smith	13.3	3.99	(6.1,21.6)	8.2	3.81	(0.0,16.2)	5.8	3.35	(0.0,12.4)	3.9	1.88	(0.7,8.0)
Nass River	26.6	2.90	(21.1,32.5)	24.7	2.87	(19.3,30.5)	33.1	3.04	(27.3,39.2)	42.4	3.28	(36.1,49.0)
Skeena River	5.6	1.59	(2.9,9.1)	15.4	2.44	(10.9,20.5)	26.0	2.81	(20.7,31.7)	37.9	3.32	(31.5,44.5)
Queen Charlotte I.	0.0	0.05	(0.0,0.0)	0.0	0.05	(0.0,0.0)	0.0	0.05	(0.0,0.0)	0.0	0.07	(0.0,0.1)
Central Coast BC	6.5	1.76	(3.4,10.3)	4.9	2.03	(1.0,9.2)	5.5	1.72	(2.5,9.2)	2.3	1.40	(0.0,5.3)
Fraser River	0.8	0.63	(0.0,2.4)	0.1	0.25	(0.0,0.9)	0.3	0.40	(0.0,1.4)	0.0	0.14	(0.0,0.4)
Washington	0.2	0.41	(0.0,1.4)	0.0	0.08	(0.0,0.1)	0.0	0.06	(0.0,0.1)	0.0	0.16	(0.0,0.5)

	Week 34			Week 35		
	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	1.7	1.71	(0.0,5.8)	0.0	0.18	(0.0,0.5)
NSE Alaska	0.2	0.44	(0.0,1.5)	0.1	0.35	(0.0,1.2)
Taku	0.1	0.23	(0.0,0.6)	0.2	0.65	(0.0,2.2)
Stikine	0.1	0.38	(0.0,1.1)	0.3	0.83	(0.0,3.0)
SSE Alaska	20.3	4.11	(12.5,28.5)	16.8	3.19	(10.9,23.3)
McDonald	18.0	4.28	(10.3,26.7)	11.4	3.07	(6.0,17.9)
Hugh Smith	6.0	5.13	(0.0,16.0)	8.9	2.65	(4.2,14.5)
Nass River	27.3	2.86	(21.8,33.0)	17.5	2.52	(12.8,22.7)
Skeena River	25.7	2.93	(20.1,31.6)	39.8	3.30	(33.5,46.4)
Queen Charlotte I.	0.0	0.04	(0.0,0.0)	0.0	0.05	(0.0,0.0)
Central Coast BC	0.3	0.74	(0.0,2.6)	2.8	1.37	(0.2,5.8)
Fraser River	0.2	0.43	(0.0,1.5)	2.1	1.01	(0.6,4.5)
Washington	0.1	0.26	(0.0,0.9)	0.0	0.08	(0.0,0.1)

Table 7. Stock composition estimates of weekly mixtures of the 2010 District 104 commercial purse seine sockeye fishery.

	Week 29			Week 30			Week 31			Week 32		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.1	0.65	(0.0,1.6)	0.4	1.25	(0.0,4.6)	0.1	0.22	(0.0,0.6)	0.2	0.66	(0.0,2.4)
NSE Alaska	13.7	6.43	(1.6,26.8)	1.8	2.58	(0.0,9.0)	1.4	0.84	(0.4,3.6)	0.6	1.09	(0.0,3.9)
Taku	4.1	2.79	(0.0,10.8)	1.8	3.41	(0.0,11.8)	0.1	0.51	(0.0,1.1)	0.7	1.64	(0.0,6.0)
Stikine	7.3	6.65	(0.0,22.8)	12.1	5.92	(0.0,22.4)	5.5	1.79	(2.2,9.2)	0.9	1.97	(0.0,7.0)
SSE Alaska	57.2	6.82	(43.8,70.4)	26.4	4.94	(17.4,36.7)	48.9	2.99	(43.0,54.7)	65.8	4.95	(55.8,75.2)
McDonald	1.1	2.49	(0.0,8.8)	15.0	4.09	(7.6,23.6)	5.5	1.74	(2.4,9.2)	6.8	3.31	(0.9,14.0)
Hugh Smith	0.1	0.62	(0.0,1.5)	2.7	2.90	(0.0,9.7)	0.0	0.23	(0.0,0.5)	0.1	0.29	(0.0,0.5)
Nass River	5.4	2.81	(1.0,11.8)	5.7	2.33	(2.1,11.1)	7.2	1.61	(4.3,10.6)	0.5	0.91	(0.0,3.2)
Skeena River	10.8	3.74	(4.6,19.1)	33.3	4.53	(24.6,42.3)	31.2	2.57	(26.3,36.3)	24.3	3.89	(17.1,32.3)
Queen Charlotte I.	0.0	0.13	(0.0,0.1)	0.0	0.08	(0.0,0.1)	0.0	0.05	(0.0,0.0)	0.0	0.17	(0.0,0.2)
Central Coast BC	0.1	0.50	(0.0,0.4)	0.8	1.66	(0.0,5.9)	0.0	0.07	(0.0,0.0)	0.1	0.43	(0.0,1.1)
Fraser River	0.1	0.34	(0.0,1.1)	0.1	0.29	(0.0,0.9)	0.0	0.14	(0.0,0.4)	0.1	0.25	(0.0,0.8)
Washington	0.0	0.20	(0.0,0.3)	0.0	0.13	(0.0,0.2)	0.1	0.21	(0.0,0.7)	0.0	0.12	(0.0,0.2)

	Week 33			Week 34 & 35		
	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.1	0.52	(0.0,1.5)	0.2	0.65	(0.0,2.1)
NSE Alaska	1.4	1.32	(0.1,4.9)	3.2	2.12	(0.4,8.3)
Taku	0.1	0.32	(0.0,0.9)	0.3	1.03	(0.0,3.5)
Stikine	0.1	0.32	(0.0,0.7)	0.3	0.94	(0.0,3.2)
SSE Alaska	88.0	3.17	(81.0,93.4)	58.6	6.32	(45.9,70.6)
McDonald	0.1	0.39	(0.0,0.8)	2.6	3.73	(0.0,12.1)
Hugh Smith	0.3	0.95	(0.0,3.5)	0.9	2.34	(0.0,8.6)
Nass River	1.7	1.23	(0.2,4.9)	5.0	2.42	(1.4,10.7)
Skeena River	8.1	2.49	(3.9,13.6)	27.3	5.07	(18.0,37.8)
Queen Charlotte I.	0.0	0.08	(0.0,0.1)	0.0	0.19	(0.0,0.2)
Central Coast BC	0.0	0.14	(0.0,0.1)	0.6	1.42	(0.0,5.1)
Fraser River	0.1	0.25	(0.0,0.8)	1.0	1.42	(0.0,4.9)
Washington	0.0	0.16	(0.0,0.3)	0.1	0.35	(0.0,0.8)

Table 8. Estimated numbers of sockeye salmon caught in the 2010 District 101 gillnet and District 104 purse seine fisheries prior to statistical week 31 and throughout all statistical weeks analyzed (see Tables 4&5).

		District 101 Gillnet		District 104 Seine	
Region	Area	Prior to 31	Total	Prior to 31	Total
1	Alsek	34	176	10	23
2	NSE Alaska	62	104	410	578
3	Taku	310	378	140	178
4	Stikine	1,744	1,827	383	598
5	SSE Alaska	3,443	6,237	1,995	10,489
6	McDonald	3,292	8,914	256	746
7	Hugh Smith	5,587	7,320	44	92
8	Nass River	16,651	25,584	234	712
9	Skeena River	1,481	8,945	799	3,584
10	Queen Charlotte I.	1	4	0	2
11	Central Coast BC	1,227	2,331	13	25
12	Fraser River	72	144	4	39
13	Washington	17	23	1	8
	Totals	33,921	61,987	4,291	17,071