Pacific Salmon Commission
Northern Fund

Northern Boundary Area Sockeye Salmon Genetic Stock Identification For Year 2016 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. SPA was used by ADF&G to determine stock proportions for sockeye salmon caught in the commercial sockeye fisheries in districts 101 and 104 until 2012.

While effective, SPA required 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 was expensive and burdensome. The use of more stable markers has eliminated 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 7 stock groups, adding to the knowledge available to manage area fisheries.

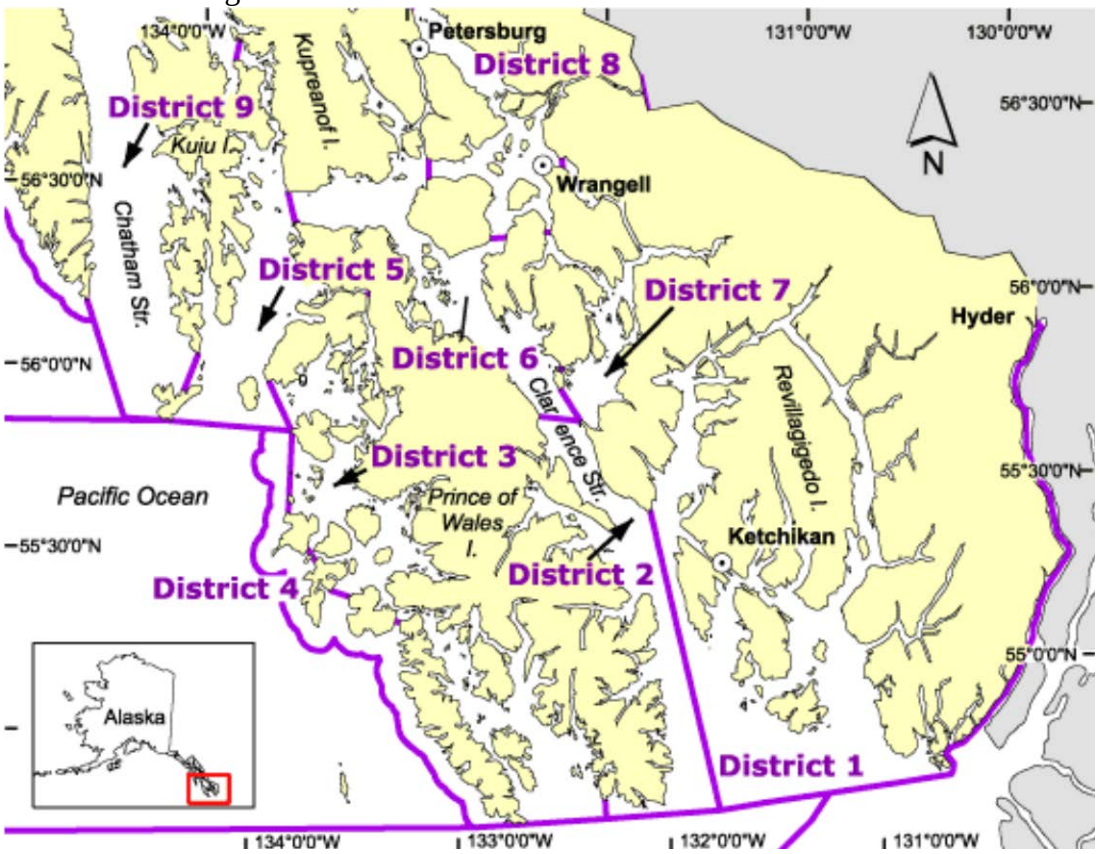

Figure 1. Geographic location of ADF&G commercial fishing districts 101 (labeled District 1) and 104 (labeled District 4). Map obtained from the ADF&G web page (http://www.cf.adfg.state.ak.us/region1/finfish/salmon/maps/ketchikan.php).

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

Table 1. Sockeye salmon baseline populations used in analysis.

Pop. #	Description	Region	Pop. #	Description	Region
1	Bainbridge Lake	1	44	Mountain Stream	1
2	Coghill Lake	1	45	Situk Lake	1
3	Eshamy Creek	1	46	Chilkat Lake early_late	1
4	Main Bay	1	47	Chilkat Mainstem - Mosquito Lake	1
5	Miners Lake	1	48	Chilkat Mainstem - Bear Flats	1
6	Bering Lake	1	49	Chilkat River - Mule Meadows	1
7	Clear Creek at 40 Mile	1	50	Chilkoot Lake - beaches	1
8	Eyak Lake - Hatchery Creek	1	51	Chilkoot Lake - Bear Creek	1
9	Eyak Lake - Middle Arm	1	52	Chilkoot River - Chilkoot River	1
10	Eyak Lake - South beaches	1	53	Berners Bay	1
11	Fish Creek - East Fork Gulkana River	1	54	Lace River	1
12	Gulkana River - East Fork	1	55	Steep Creek	1
13	Klutina Lake - inlet	1	56	Windfall Lake	1
14	Klutina River - mainstem	1	57	Lake Creek (Auke Creek Weir)	1
15	Banana Lake - Klutina	1	58	Crescent Lake	1
16	Bear Hole - tributary Klutina	1	59	Snettisham Hatchery	1
17	Kushtaka Lake	1	60	Speel Lake	1
18	Long Lake weir	1	61	Vivid Lake	1
19	Mahlo River	1	62	Bartlett River - Creel survey	1
20	Martin Lake	1	63	North Berg Bay Inlet	1
21	Martin River Slough	1	64	Hoktaheen Lake	1
22	McKinley Lake1	1	65	Neva Lake	1
23	McKinley Lake	1	66	Sitkoh Lake	1
24	McKinley Lake - Salmon Creek	1	67	Lake Eva	1
25	Salmon Creek - Bremner	1	68	Kook Lake	1
26	Mendeltna Creek	1	69	Pavlof River	1
27	Mentasta Lake	1	70	Hasselborg Lake	1
28	Paxson Lake - outlet	1	71	Kanalku Lake	1
29	St. Anne Creek	1	72	Kutlaku Lake	1
30	Steamboat Lake - Bremner	1	73	Falls Lake	1
31	Swede Lake	1	74	Ford Arm Creek	1
32	Tanada Creek weir	1	75	Klag Bay Stream outlet	1
33	Tanada Lake - lower outlet	1	76	Redfish Lake Beaches	1
34	Tanada Lake - shore	1	77	Salmon Lake weir	1
35	Tebay River - Outlet	1	78	Redoubt Lake - outlet	1
36	Tokun Lake	1	79	Benzeman Lake	1
37	Tonsina Lake	1	80	Hugh Smith Lake	1
38	Ahrnklin River	1	81	Hatchery Creek - Sweetwater Lake	1
39	Akwe River	1	82	Kah Sheets Lake	1
40	Dangerous River	1	83	Kunk Lake	1
41	East Alsek River	1	84	Luck Lake	1
42	Lost/Tahwah Rivers	1	85	Big Lake	1
43	Old Situk River	1	86	Mill Creek Weir - Virginia Lake	1

Table 1. Continued.

Pop. #	Description	Region	Pop. #	Description	Region
87	Petersburg Lake	1	130	Tweedsmuir River	5
88	Red Bay Lake	1	131	Vern Ritchie	5
89	Salmon Bay Lake	1	132	King Salmon Lake	5
90	Shipley Lake	1	133	Little Tatsamenie	5
91	Thoms Lake	1	134	Little Trapper Lake	5
92	Sarkar Lakes	1	135	Kuthai Lake	5
93	Heckman Lake - Naha River	1	136	Tatsamenie Lake	5
94	Helm Lake	1	137	Hackett River	5
95	Karta River	1	138	Nahlin River	5
96	Kegan Lake	1	139	Tulsequah River	5
97	Mahoney Creek	1	140	Yellow Bluff Slough	5
98	Unuk River - Gene's Lake	1	141	Shustahine Slough	5
99	Fillmore Lake - Hoffman Creek	1	142	Taku River	5
100	Klakas Lake	1	143	Takwahoni/Sinwa Creek	5
101	Bar Creek - Essowah Lake	1	144	Tuskwa/Chunk Slough	5
102	Eek Creek	1	145	Fish Creek	5
103	Hetta Creek - middle run	1	146	Yehring Creek	5
104	Hetta Creek - early run	1	147	Shakes Slough	5
105	Hetta Lake	1	148	Iskut River	5
106	Klawock-Half Mile Creek	1	149	Verrett River	5
107	Bowser Lake	2	150	Scud River	5
108	Damdochax Creek	2	151	Andy_Porcupine_Fowler	5
109	Meziadin Lake	2	152	Devil's Elbow	5
110	Tintina Creek	2	153	Chutine Lake	5
111	Alastair Lake	3	154	Chutine River	5
112	Four Mile_Pierre Creek	3	155	Christina Lake	5
113	Fulton River_Morrison Creek	3	156	Little Tahltan River	5
114	Kitsumkalum Lake	3	157	Tahltan Lake	5
115	Tahlo River	3	158	Adams River - Shuswap Lake late	6
116	McDonell Lake - Zymoetz River	3	159	Birkenhead River	6
117	Nangeese River	3	160	Chilko Lake	6
118	Nanika River	3	161	Gates Creek	6
119	Slamgeesh River	3	162	Harrison River	6
120	Sustut River - Johanson Lake	3	163	Horsefly River	6
121	Swan Lake	3	164	Raft River	6
122	Upper Babine River	3	165	Stellako River	6
123	McDonald Lake	4	166	Weaver Creek	6
124	Blanchard River	5	167	Naden River	7
125	Border Slough	5	168	Kitlope Lake	7
126	Klukshu River	5	169	Issaquah Creek	7
127	Kudwat Creek	5	170	Cedar River	7
128	Tatshenshini - Kwatini River	5	171	Baker Lake	7
129	Neskataheen Lake	5			

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 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 developed a sockeye new SNP baseline with 48 SNP markers (Habicht et al. 2007, 2010). This baseline replaces the 43 was used by ADF&G in 2004 and 2005; and by NOAA/NMFS/Alaska Fishery Science Center/Auke Bay Laboratories (ABL) in 2006-13 (Guthrie et al. 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017) for genetic stock composition analyses for districts 101 and 104. Previously, 84 sockeye populations were part of the SNP baseline, but in the new baseline that number has increased to 171 (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 7 Northern Boundary sockeye stock groups which are more relevant to the run reconstruction used by the Pacific Salmon Commission (PSC) than the 13 stock groups used last year (Table 2) (Oliver 2009).

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

Region	***Area***
1	Alaska
2	Nass River
3	Skeena River
4	McDonald Lake
5	Transboundry Rivers
6	Fraser River
7	South Migrating

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. Congruence was found between the two techniques, so genetic analysis replaced 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).

OBJECTIVE

The purpose of this study was to genetically analyze axillary process (AXP) samples from 4,419 sockeye salmon harvested in the 2016 District 101 gillnet and

District 104 purse seine sockeye fisheries to determine proportions of Canadian and U.S. fish. A SNP genetic baseline of 48 SNPs assayed in 171 sockeye populations from southeast Alaska and British Columbia, and Washington was developed by ADF&G (Habicht et al., 2010, Dann et al., 2012).

Table 3. 48 SNP assays used to discriminate Northern Boundary sockeye populations.

#	Name	#	Name
1	*One_agt-132*	25	*One_STR07*
2	*One_apoe-83*	26	*One_SUMO1-6*
3	*One_CFP1*	27	*One_sys1-230*
4	*One_cin-177*	28	*One_taf12-248*
5	*One_CO1 (mitochondrial)*	29	*One_Tf_ex3-182*
6	*One_E2*	30	*One_U1003-75*
7	*One_GHII-2461*	31	*One_U1004-183*
8	*One_ghsR-66*	32	*One_U1009-91*
9	*One_HGFA*	33	*One_U1010-81*
10	*One_HpaI-436*	34	*One_U1013-108*
11	*One_HpaI-99*	35	*One_U1016-115 (not resolved)*
12	*One_IL8r-362*	36	*One_U1101*
13	*One_metA-253*	37	*One_U1201-492*
14	*One_MHC2_190*	38	*One_U1203-175*
15	*One_Mkpro-129*	39	*One_U1205-57*
16	*One_Ots213-181*	40	*One_U1208-67*
17	*One_rab1a-76*	41	*One_U1212-106*
18	*One_RAG3-93*	42	*One_U1214-107*
19	*One_redd1-414*	43	*One_U1216-230*
20	*One_RF-112*	44	*One_U301-92*
21	*One_spf30-207*	45	*One_U503-170*
22	*One_srp09-127*	46	*One_U504-141*
23	*One_ssrd-135*	47	*One_vatf-214*
24	*One_STC-410*	48	*One_zP3b*

METHODS

Genetic baseline and population grouping

Genetic samples from 171 baseline stocks (Table 1) were collected by ADF&G in collaboration with many other laboratories including ABL and the Canadian Department of Fisheries and Oceans. The 171 populations were grouped into 7 regions (Table 2) based on manager needs, the PSC 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 300 (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 the QIAGEN DNeasy Blood and Tissue Kits 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 at least 3 hours at 55ºC. Protease digestions were performed in 96 well plates. After digestion, the samples were purified with either QIAxtractor or 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 Life Technologies for 48 previously identified sockeye SNP probes. Of the 48 sockeye SNP markers (Table 3) (Elfstrom et al., 2006; Smith et al., 2005b; Habicht et al., 2007, 2010: Dann et al., 2012), 47 were assayed in this analysis. The remaining assay, *One_U1016-115* 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 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 an 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 a Life Technologies QuantStudio and scored using QuantStudio 12K Flex Software v1.2.2. 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, 7 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 0.00585 (calculated as 1/171) was used for all 171 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. Most Monte Carlo chain lengths were 10,000; one chain length was 100,000 to obtain convergence.

Table 4. Sockeye salmon harvested, genetic sample size, genotyping success rate, and percent catch analyzed in each statistical week in the 2016 District 101 Gillnet fishery.

District 101 Gillnet						
Week	***2016***	***2006-2015 Avg.***	***Extracted***	***Analyzed***	***% Analyzed***	***% Catch***
26	3,882	8,237	260	260	100.0	6.7
27	4,138	10,203	260	259	99.6	6.3
28	3,286	7,083	260	259	99.6	7.9
29	3,380	5,269	241	240	99.6	7.1
30	3,200	5,152	254	254	100.0	7.9
31	3,945	5,694	260	260	100.0	6.6
32	2,581	5,509	260	260	100.0	10.1
33	7,257	2,661	260	260	100.0	3.6
34	4,199	1,084	260	259	99.6	6.2
35	2,210	752	233	233	100.0	10.5
36	810	424	219	218	99.5	26.9
37	899	130	0	0	0.0	0.0
38	109	33	0	0	0.0	0.0
39	10	7	0	0	0.0	0.0
40	6	0	0	0	0.0	0.0
Total Catch	39,912	52,238				6.9
Sampled Catch	38,888	52,068	2,767	2,762	99.8	7.1

Table 5. Sockeye salmon harvested, genetic sample size, genotyping success rate, and percent catch analyzed in each statistical week in the 2016 District 104 Purse Seine fishery.

District 104 Purse Seine						
Week	***2016***	***2006-2015 Avg.***	***Extracted***	***Analyzed***	***% Analyzed***	***% Catch***
27	0	878	0	0	0.0	0.0
28	27,951	5,964	260	258	99.2	0.9
29	71,634	10,734	300	297	99.0	0.4
30	10,714	26,841	16	16	100.0	0.1
31	71,087	68,076	264	264	100.0	0.4
32	177,143	77,495	260	259	99.6	0.1
33	32,687	46,181	262	262	100.0	0.8
34	14,726	24,719	290	290	100.0	2.0
35	0	12,344	0	0	0.0	0.0
Total Catch	405,942	273.231				0.4
Sampled Catch	405,942	260,010	1,652	1,646	99.6	0.4

RESULTS

In 2016, 39,912 sockeye salmon were harvested in District 101 GNF which is less than the 2006 to 2015 average of 52,238 (Table 4). In the District 104 PSF 405,942 fish

were harvested in 2016 which is much larger than the 2006-2015 average of 273,231 (Table 5), and the second largest since 2007 (770,666). Sockeye salmon DNA was isolated (Table 4&5) and genotyped for 47 SNP markers from 4.408 fish in 2016. The data was imported into a Progeny database for analysis. Samples resolved for at least 42 of the 47 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 of the 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 7 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% credible intervals for the 2016 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 (Tables 6&7). For example, the sockeye commercial fishery in the 2016 District 101 GNF harvested a greater proportion of Nass Region fish; with a high of 58% in week 28, and a low of 19% in week 32. Skeena fish were also abundant, with a high of 57% in week 36, and a low of 10% in week 32. Alaska fish were sporadically abundant with a high of 49% in week 30 and a low of 9% in both weeks 27 and 36.

The sockeye commercial fishery in the 2016 District 104 PSF harvested a greater proportion of Skeena River fish ranging from 44% to 67% in weeks 28 through 34. Nass fish were present early at 18% in week 28, while some Fraser fish appearing after week 29 with a high of 17% in week 33. Alaska fish were present throughout with a high of 31% in week 28, and a low of 9% in week 33. There were an inadequate number of samples to perform a stock composition analysis.

The proportion estimates were used to estimate numbers of fish caught from each region for each fishery (Table 8). The 1 fish discrepancy in Table 4 and the 3 fish discrepancy in the total numbers of fish when compared to Table 8 were due to rounding error in estimating numbers of fish caught from estimated stock group proportions. Since there were no genetic samples obtained from District 101 GNF weeks 37-40 (Table 4) and an inadequate number of samples for week 30 in the District 104 PSF (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 were being provided by ADF&G using scale pattern analysis (SPA). This technique was replaced by genetic analysis in 2012.

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 2016. It should be recognized that while a total of 48 SNPs are currently used in the Southeast Alaska-British Columbia baseline, not all SNPs are likely to be equally informative.

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 2016. 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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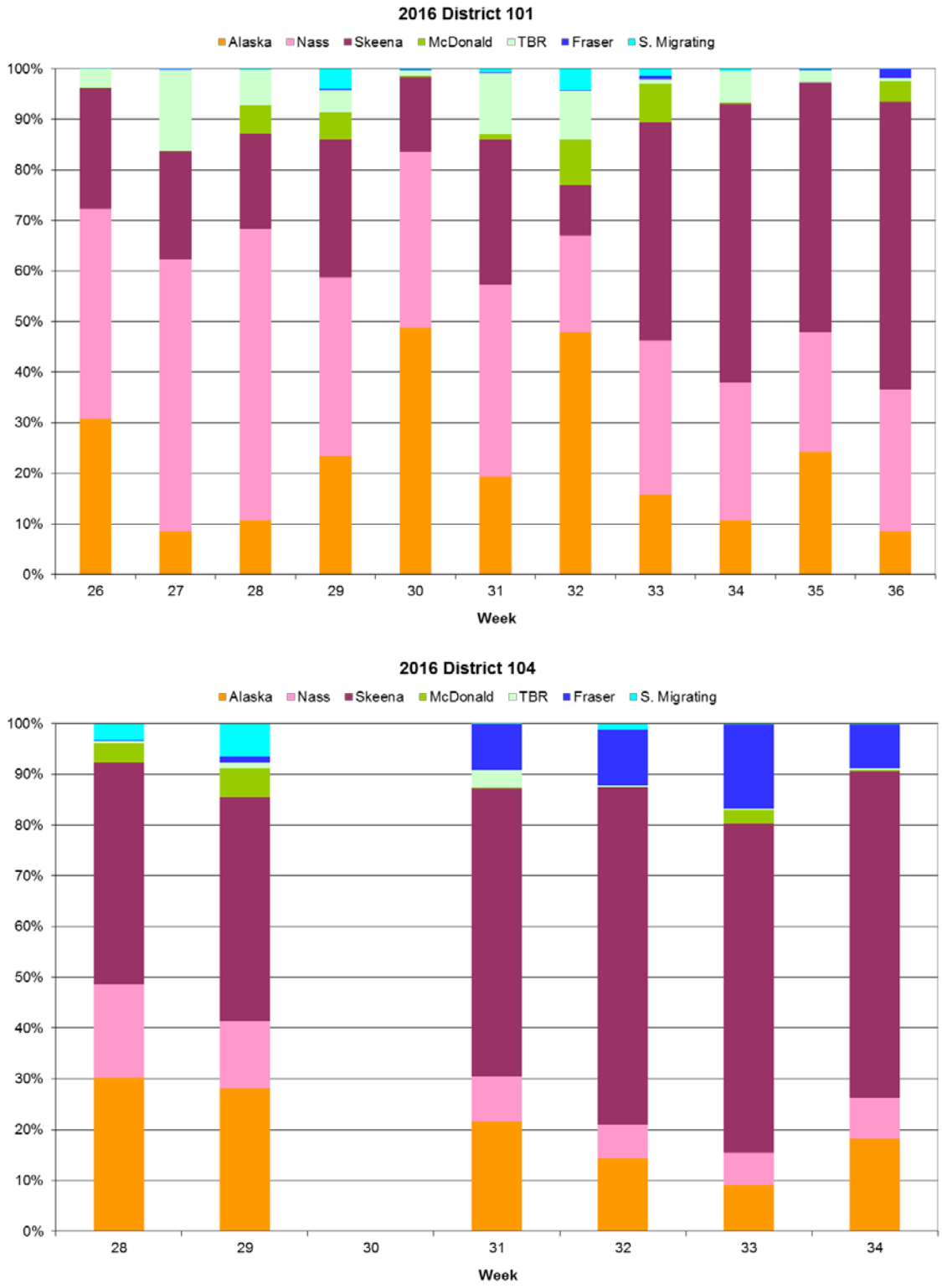

Figure 2. 2015 sockeye stock group proportions for each statistical week from the ADF&G District 101 gillnet (top panel) and 104 purse seine fisheries (lower panel).

Table 6. Stock composition of weekly mixtures of sockeye salmon the 2016 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
Alaska	30.8	3.96	(23.9,37.6)	8.5	2.20	(4.6,13.2)	10.7	2.78	(5.8,16.6)	23.4	4.68	(14.7,32.8)
Nass River	41.6	3.17	(35.4,47.8)	53.8	3.32	(47.2,60.2)	57.6	3.42	(50.9,64.3)	35.4	4.20	(27.4,43.9)
Skeena River	23.9	2.82	(18.6,29.7)	21.4	3.07	(15.7,27.7)	18.8	2.78	(13.6,24.5)	27.3	4.23	(19.0,35.6)
McDonald Lake	0.0	0.23	(0.0,0.1)	0.2	0.79	(0.0,3.0)	5.6	2.29	(1.5,10.4)	5.4	3.65	(0.0,12.7)
Transboundry Rivers	3.7	2.93	(0.7,8.6)	16.0	2.78	(10.8,21.7)	7.1	2.46	(2.6,12.2)	4.3	3.04	(0.2,11.0)
Fraser River	0.0	0.10	(0.0,0.3)	0.0	0.12	(0.0,0.4)	0.0	0.13	(0.0,0.3)	0.2	0.44	(0.0,1.5)
South Migrating	0.0	0.19	(0.0,0.4)	0.1	0.32	(0.0,0.8)	0.1	0.41	(0.0,1.4)	4.0	1.52	(1.5,7.4)

	Week 30			Week 31			Week 32			Week 33		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alaska	48.8	3.56	(41.6,55.6)	19.3	3.48	(12.5,26.2)	47.9	5.09	(38.3,58.1)	15.8	3.25	(9.6,22.4)
Nass River	34.8	3.32	(28.5,41.4)	38.1	4.15	(29.5,45.8)	19.0	2.66	(14.1,24.5)	30.4	3.21	(24.2,36.9)
Skeena River	14.8	2.55	(10.1,20.1)	28.6	4.10	(21.4,37.4)	10.1	2.02	(6.4,14.4)	43.2	3.48	(36.5,50.1)
McDonald Lake	0.2	1.05	(0.0,3.9)	1.1	1.98	(0.0,6.6)	9.0	3.43	(1.6,15.9)	7.6	2.52	(3.1,12.9)
Transboundry Rivers	1.1	1.57	(0.0,5.5)	12.1	3.14	(6.2,18.5)	9.7	4.04	(2.0,17.6)	1.0	1.54	(0.0,5.3)
Fraser River	0.1	0.19	(0.0,0.6)	0.1	0.31	(0.0,1.1)	0.0	0.16	(0.0,0.4)	0.7	0.57	(0.0,2.1)
South Migrating	0.2	0.57	(0.0,2.1)	0.7	1.25	(0.0,4.1)	4.3	1.58	(1.7,7.9)	1.4	0.98	(0.0,3.7)

	Week 34			Week 35			Week 36		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alaska	10.7	2.38	(6.4,15.7)	24.3	3.17	(18.2,30.6)	8.5	2.90	(3.3,14.7)
Nass River	27.3	3.18	(21.0,33.5)	23.6	3.23	(17.5,30.2)	28.0	3.24	(21.9,34.5)
Skeena River	55.0	3.56	(48.0,62.1)	49.3	3.72	(42.1,56.6)	56.9	3.66	(49.6,64.0)
McDonald Lake	0.3	1.01	(0.0,3.9)	0.0	0.27	(0.0,0.1)	4.1	2.60	(0.0,9.5)
Transboundry Rivers	6.3	2.26	(1.8,10.9)	2.5	1.95	(0.0,7.1)	0.8	1.11	(0.0,3.8)
Fraser River	0.0	0.10	(0.0,0.3)	0.1	0.33	(0.0,1.2)	1.7	0.94	(0.4,4.0)
South Migrating	0.5	0.70	(0.0,2.4)	0.1	0.30	(0.0,1.1)	0.0	0.21	(0.0,0.6)

Table 7. Stock composition of weekly mixtures of sockeye salmon in the 2016 District 104 commercial purse seine fishery.

	Week 28			Week 29			Week 31		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alaska	30.3	4.02	(22.8,38.3)	28.2	3.17	(22.1,34.6)	21.6	2.72	(16.5,27.1)
Nass River	18.4	2.71	(13.3,23.9)	13.1	2.26	(9.0,17.9)	8.9	1.83	(5.6,12.7)
Skeena River	43.6	3.47	(37.0,50.6)	44.2	3.15	(38.0,50.3)	56.8	3.17	(50.6,63.0)
McDonald Lake	3.9	3.04	(0.0,9.7)	5.7	2.03	(2.3,10.2)	0.1	0.49	(0.0,0.7)
Transboundry Rivers	0.4	0.79	(0.0,2.8)	1.1	1.16	(0.1,4.5)	3.6	1.61	(0.9,7.1)
Fraser River	0.2	0.31	(0.0,1.1)	1.2	0.69	(0.2,2.8)	9.1	1.80	(5.9,12.9)
South Migrating	3.2	1.32	(1.1,6.2)	6.5	1.73	(3.5,10.2)	0.0	0.20	(0.0,0.5)

	Week 32			Week 33			Week 34		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alaska	14.4	2.27	(10.2,19.1)	9.0	2.34	(5.0,14.1)	18.4	2.46	(13.6,23.2)
Nass River	6.6	1.97	(3.5,11.2)	6.5	1.54	(3.8,9.8)	7.9	1.76	(4.9,11.8)
Skeena River	66.6	3.14	(60.2,72.4)	64.8	3.00	(58.8,70.6)	64.4	2.94	(58.5,70.0)
McDonald Lake	0.0	0.15	(0.0,0.1)	2.8	1.81	(0.0,6.4)	0.3	0.84	(0.0,3.2)
Transboundry Rivers	0.2	0.47	(0.0,1.6)	0.3	0.50	(0.0,1.7)	0.2	0.48	(0.0,1.7)
Fraser River	11.1	1.97	(7.6,15.2)	16.6	2.31	(12.3,21.3)	8.7	1.68	(5.7,12.3)
South Migrating	1.2	0.68	(0.3,2.8)	0.1	0.36	(0.0,1.3)	0.2	0.45	(0.0,1.6)

Table 8. Estimated numbers of sockeye salmon caught in the 2016 District 101 gillnet and 104 seine fisheries prior to statistcal week 31 and throughout all statistical weeks analyzed (see Tables 4&5). The estimate for district 104 does not include statistcial week 30 due to small sample size.

		District 101 Gillnet		***District 104 Seine***	
Region	***Area***	***Prior to 31***	***Total***	***Prior to 31***	***Total***
1	Alaska	4,248	8,449	28,681	75,175
2	Nass River	8,042	14,136	14,531	35,702
3	Skeena River	3,828	12,209	43,836	232,797
4	McDonald Lake	386	1,254	5,179	6,212
5	Transboundry Rivers	1,221	2,346	926	3,957
6	Fraser River	13	83	880	33,646
7	South Migrating	148	410	5,556	7,736
	Totals	17,886	38,887	99,589	395,225