Pacific Salmon Commission
Northern Fund

Northern Boundary Area Sockeye Salmon Genetic Stock Identification For Year 2006 District 101 Gillnet and District 104 Purse Seine Fisheries

Final Report

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INTRODUCTION

Provisions outlined in Chapter 2 of the 1999 Pacific Salmon Treaty specify harvest sharing arrangements of Nass and Skeena River sockeye salmon returns 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 and of Nass and Skeena sockeye in the District 104 purse seine fishery prior to Statistical Week 31 (late July). There is also a District 101 purse seine fishery, 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 District 102, 103 seine and District 106 gillnet). Figure 1 illustrates the locations of the Alaska Department of Fish and Game (ADFG) 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 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 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 through inriver escapement enumeration projects. This study found that a significant percent of the fish caught in District 101 and 104 fisheries 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 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, scale pattern analysis (SPA) has been used by the Alaska Department of Fish and Game to determine stock proportions for sockeye salmon caught in the District 101 and 104 commercial sockeye fisheries.

While effective, scale pattern analysis 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, Sskeena and Fraser) whereas genetic analysis can separate 14 stocks adding the ability of managing area fisheries to target surplus stocks.

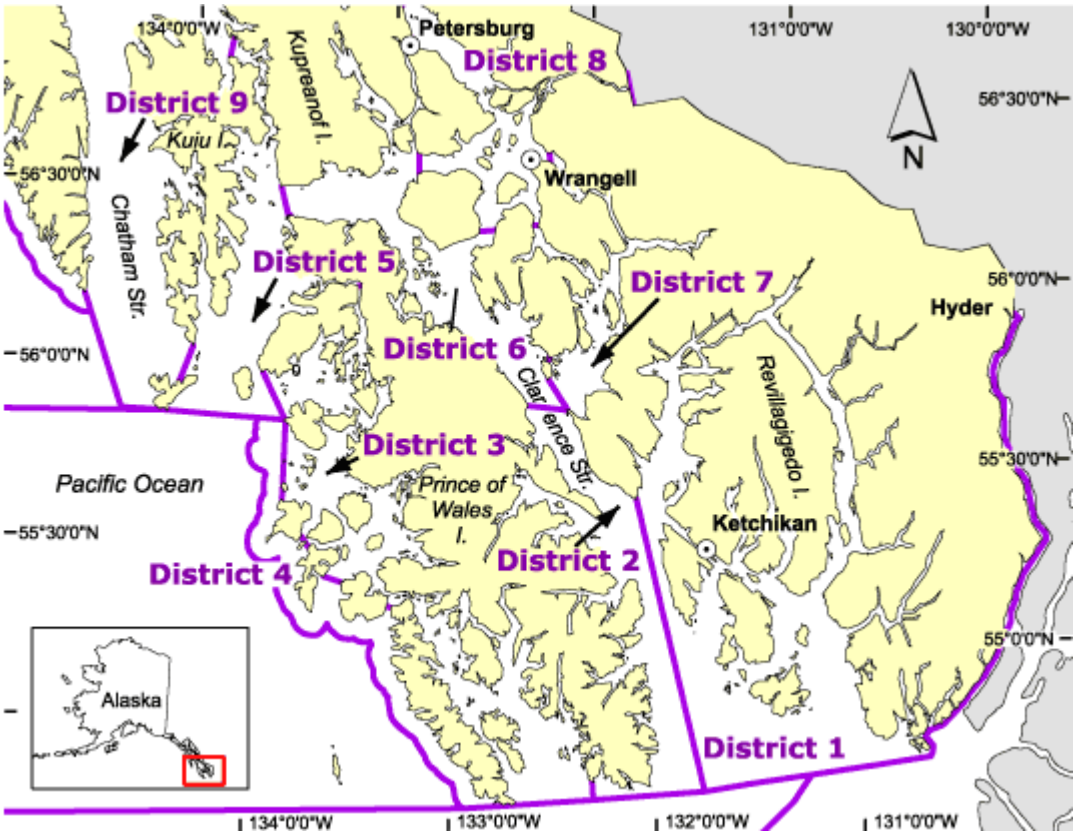

Figure 1. Geographic location of ADFG Commercial Fishing Districts 101 (labeled District 1) and 104 (labeled District 4). Map obtained from the ADF&G web page (http://www.cf.adfg.state.ak.us/region1/finfish/salmon/maps/ketchkan.php).

Allozymes are naturally occurring protein size 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 ADF&G 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 brain-tissue parasitism (*Myxobolus arcticus*). Freshwater age and pathogen exposure are traits that, in combination with other markers, can be used 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, predominantly from the Nass and Skeena River systems (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 experiments 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; Smith et al., 2005b). While the Canadians have opted to use microsatellite markers for many of their Northern Boundary studies, ADF&G has recently opted to use 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).

Over the last 5 years, the ADF&G has collaborated with numerous laboratories to develop a sockeye SNP baseline with 45 SNP markers. This baseline has been used by the ADF&G to produce the 2004 and 2005 genetic stock composition analyses for Districts 101 and 104. 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 14 Northern Boundary sockeye stock groups. Currently, 84 sockeye populations are part of the SNP baseline.

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 by the bilateral Northern Boundary Technical Committee of run reconstruction modeling. The Committee concluded that improved stock identification techniques are needed for run reconstruction models. The most current method being evaluated is the use of SNP markers to genetically separate 14 stock groups of sockeye salmon caught in the Northern Boundary region. This technique has the advantage of a relatively stable baseline (does not change yearly) and can be highly automated. The purpose of this study is to provide the third year of genetic data using SNP markers to compare with the scale pattern analysis. If congruence between the two techniques is evident, it is likely that genetic analysis will replace scale pattern analysis for estimating stock composition of sockeye salmon caught in Northern Boundary fisheries.

OBJECTIVE

The purpose of this study was to genetically analyze axillary process samples from 6,000 sockeye salmon harvested in the 2006 Districts 101 gillnet and 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 was developed by the ADFG. The 84 populations were grouped into 14 regions. Genetic samples from approximately 380 fish were collected each statistical week of the District 101 and 104 fisheries. With the exception of markers Prl2, U404, U502, U503, and the 3 groups of linked SNPs which are still being assayed, the same markers were evaluated in the

baseline and mixtures. Stock proportions were estimated using a Bayesian mixture analysis.

No.	SILLY	Description	Region	No.	SILLY	Description	Region
1	SEALS00	East Alsek	1	43	SHETT03	SO - Hetta Lake	5
2	SKLUK06	Alsek - Klukshu River Weir late	1	44	SKANA07	SO - Kanalku Lake	5
3	SUTATS03	Alsek - Upper Tatshenshini	1	45	SKLAK04	SO - Klakas Lake	5
4	SBERN03	NI - Berners Bay	2	46	SSARF05K00	SO - Sarkar	5
5	SCKAT07E	NI - Chilkat Lake early run	2	47	SSHIP03	SO - Shipley Lake	5
6	SMULE03	NI - Chilkat River - Mule Meadows	2	48	STHRE04	SO - Three Mile Creek - Klawock	6
7	SCHILB07	NI - Chilkoot Lake - beaches	2	49	SMCDO0103	SI - Hatchery Creek - McDonald Lake	7
8	SCHIK03	NI - Chilkoot River - Chilkoot River	2	50	SCOBB07	SI - Hugh Smith - Cobb Creek	8
9	SCRES03	NI - Crescent Lake	2	51	SHUGH04	SI - Hugh Smith Lake - Bushmann Creek	8
10	SFALL03	NI - Falls Lake	2	52	SBOWS01	Nass - Bowser Lake	9
11	SSITK03	NI - Sitkoh Lake	2	53	SDAMD01	Nass - Damdochax Creek	9
12	SSNET06PEE03	NI - Snettisham Hatchery/Speel Lake	2	54	SHANNA06	Nass - Hanna Creek	9
13	SSTEE03	NI - Steep Creek	2	55	SMEZI0106	Nass - Meziadin Lake	9
14	SWIND0307	NI - Windfall Lake	2	56	STINT06	Nass - Tintina Creek	9
15	SREDB93	NO - Redfish Lake Beaches	2	57	SALAS06	Skeena - Alastair Lake	10
16	SKUTH06	Taku - Kuthai Lake	3	58	SFMILE06	Skeena - Four Mile Creek	10
17	SLTAT9091	Taku - Little Tatsamenie	3	59	SFULT06	Skeena - Fulton River	10
18	SLTRA90	Taku - Little Trapper Lake	3	60	SKALUM06	Skeena - Kitsumkalum Lake	10
19	STAKU07	Taku - Taku River Mainstem	3	61	SLAKEL06	Skeena - Lakelse Lake (Williams)	10
20	STATS92	Taku - Tatsamenie	3	62	SLTAH8894	Skeena - Lower Tahlo River	10
21	STATS05	Taku - Tatsamenie Lake	3	63	SMCDON06	Skeena - McDonell Lake (Zymoetz River)	10
22	SISKU85860207	Stikine - Iskut River	4	64	SMORR07	Skeena - Morrison	10
23	SLTAH90	Stikine - Little Tahltan	4	65	SNANG06	Skeena - Nangeese River	10
24	SSCUD07	Stikine - Scud River	4	66	SNANI07	Skeena - Nanika River	10
25	STAHL06	Stikine - Tahltan Lake	4	67	SPIER06	Skeena - Pierre Creek	10
26	SKUTL03	NI - Kutlaku Lake	5	68	SPINK06	Skeena - Pinkut Creek	10
27	SHATSC0307	SI - Hatchery Creek - Sweetwater Lake	5	69	SSLAM06	Skeena - Slamgeesh River	10
28	SHECK0407	SI - Heckman Lake	5	70	SSUST06	Skeena - Sustut (Johanson Lake)	10
29	SHELM05	SI - Helm Lake	5	71	SSWANLK06	Skeena - Swan Lake	10
30	SKAHS03	SI - Kah Sheets Lake	5	72	SUBAB06	Skeena - Upper Babine River	10
31	SKART92MCGI03	SI - Karta	5	73	SNADE95	QCI - Naden River	11
32	SKEGA04	SI - Kegan Lake	5	74	SKITL06	Central - Kitlope Lake	12
33	SKUNK03	SI - Kunk Lake - Etolin Island system	5	75	SADAM07	Fraser - Adams River (Shuswap late)	13
34	SLUCK04	SI - Luck Lake - P.O.W. Island	5	76	SBIRK07	Fraser - Birkenhead	13
35	SMAHO03	SI - Mahoney Creek	5	77	SCHILK01	Fraser - Chilko Lake	13
36	SMILLC07E07L	SI - Mill Creek Weir - Virginia Lake	5	78	SHARR07	Fraser - Harrison River	13
37	SPETL04	SI - Petersburg Lake	5	79	SLHOR01UHOR01	Fraser - Horsefly River	13
38	SREDBL9204	SI - Red Bay Lake	5	80	SRAFT01	Fraser - Raft River	13
39	SSALM04	SI - Salmon Bay Lake	5	81	SSTEL07	Fraser - Stellako River	13
40	STHOM04	SI - Thoms Lake	5	82	SWEAV01	Fraser - Weaver Creek	13
41	SGENE07	SI - Unuk River - Gene's Lake	5	83	SBAKE96	Baker Lake	14
42	SBAR04	SO - Bar Creek - Essowah Lake	5	84	SCEDAR94	Cedar River	14

Table 1. Sockeye salmon baseline populations.

Table 2. Regional grouping designations. The 84 sockeye populations identified in Table 1 were grouped into 14 regions.

Region Number	Region Description
1	Alsek
2	NSE Alaska
3	Taku
4	Stikine
5	SSE Alaska
6	Klawock
7	McDonald
8	Hugh Smith
9	Nass
10	Skeena
11	Queen Charlotte Island
12	Central Coast BC
13	Fraser
14	Washington

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 NOAA's Auke Bay Laboratory and the Canadian Department of Fisheries and Oceans. The 84 populations were grouped into 14 regions (Table 2) based on geographical location and historical knowledge.

Sample Collection

Matched genetic and scale samples were collected by port samplers from ADF&G. Samples were collected from gillnetters in the District 101 fishery and from seiners in the District 104 fishery. Genetic samples were clipped axillary processes that were stored in denatured ethanol. The genetic samples were shipped to Auke Bay Laboratory for analysis and stored at room temperature. Approximately 380 samples were collected for each statistical week.

DNA Extraction

DNA was isolated using a DNeasy Blood and Tissue Kit 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 centrifuged to remove undigested tissue fragments. Samples (with buffer) were centrifuged through a 96- well DNeasy plate. The samples on the plate were washed twice, each time followed by a centrifugation step. Following the final wash, the Qiagen plates were heated to 55 ºC for up to one hour to remove the residual ethanol. 200 ul of elution buffer was added to the sample plate, centrifuged and the eluate containing the DNA was stored at -20 ºC.

Name	ADFG	ABL
One_ACBP-79	ACBP	ACBP
One_ALDOB-135	ALDOB135	ALDOB135
One_CO1	CO1	
One_ctgf-301	ctgf	ctgf
One_Cytb_17	Cytb17	
One_Cytb_26	Cytb26	
One_E2	E2	E2
One_GHII-2461	GHII2461	GHII2461
One_GPDH	GPDH	
One_GPDH2	GPDH2	
One_GPH-414	GPH	GPH
One_hcs71-220	hcs71	hcs71
One_HGFA	HGFA	HGFA
One_HpaI-436	Hpal436	Hpal436
One_HpaI-99	Hpal99	Hpal99
One_IL8r-362	IL8r362	IL8r362
One_KPNA-422	KPNA422	KPNA422
One_LEI-87	LEI	LEI
One_MARCKS-241	MARKS	MARKS
One_MHC2_190	MHC2190	
One_MHC2_251	MHC2251	
One_Ots213-181	Ots213	Ots213
One_p53-576	p53576	p53576
One_pIns	pIns	pIns
One_Prl2	Prl2	
One_RAG1-103	RAG1	RAG1
One_RAG3-93	RAG3	RAG3
One_RF-112	RF112	RF112
One_RF-295	RF295	RF295
One_RH2op-395	RH2op	RH2op
One_serpin	serpin	serpin
One_STC-410	STC	STC
One_STR07	STR07	STR07
One_Tf_ex10-750	TFex10	TFex10
One_Tf_ex3-182	TFex3182	TFex3182
One_U301-92	U301	U301
One_U401-224	U401	U401
One_U404-229	U404229	
One_U502-167	U502167	
One_U503-170	U503170	
One_U504-141	U504141	U504141
One_U508-533	U508533	U508533
One_VIM-569	VIM	VIM
One_ZNF-61	ZNF61	ZNF61
One_zP3b	zP3b	zP3b

Table 3. 34 SNP assays used to discriminate Northern Boundary sockeye populations. "Name" is the published name of the assay, "ADFG" is the list of all the SNPs in the Northern Boundary sockeye baseline, and "ABL" lists the assays used in this analysis.

Single Nucleotide Polymorphism (SNP) Analysis

SNP genotyping was performed using Taqman chemistries (Applied Biosciences, Inc.) for 34 previously identified sockeye SNP probes (Table 3). Of the 45 ADFG sockeye SNP markers (Table 3) (Elfstrom et al., 2006; Smith et al., 2005a), 34 were assayed in this analysis. The remaining assays include Prl2, U404229, U503170, U502167 and the following 3 linked sets: mitochondrial chromosome (CO1, Cytb17, Cytb26), glycerol-3-phosphate dehydrogenase gene (GPDH, GPDH2), and the major histocompatibility complex class II gene (MHC2190, MHC2251). These markers will be added next year to the 2006 samples as required in our 2007 proposal.

Taqman reactions were performed by transferring 1 ul of a 1:10 dilution of the eluted purifed DNA (estimated final DNA concentration of 10 nl/ul) to wells of a 384 well plate. Four wells were reserved for non-template controls. Each Taqman reaction was conducted in a 5 ul volume containing the template DNA, Taqman Universal PCR Mastermix, No AmpErase UNG (AB), 900 nm of each PCR primer, and 200 nm probe. Thermal cycling was performed on a Dual 384-Well GeneAmp PCR System 9700 (Applied Biosystems, Inc.) using the following protocol: an initial denaturation of 10 minutes at 95ºC and then 50 cycles of 92ºC for 1 second and 60ºC for 1 minute at a ramp speed of 1ºC per second.

Week	Dates	101 Gillnet	104 Seine	Total
25	6/18 - 6/24	8,280	0	8,280
26	6/25 - 7/1	7,230	0	7,230
27	7/2 - 7/8	14,002	1,000	15,002
28	7/9 - 7/15	7,273	3,898	11,171
29	7/16 - 7/22	8,098	18,564	26,662
30	7/23 - 7/29	4,382	66,153	70,535
31	7/30 - 8/5	4,415	82,770	87,185
32	8/6 - 8/12	3,690	43,878	47,568
33	8/13 - 8/19	1,675	13,028	14,703
34	8/20 - 8/26	747	12,743	13,490
35	8/27 - 9/2	1,536	0	1,536
36	9/3 - 9/9	890	0	890
37	9/10 - 9/16	482	0	482
38	9/17 - 9/23	45	0	45
39	9/24 - 9/30	25	0	25
40	10/1 - 10/7	0	0	0
Totals		62,770	242,034	304,804
Historic Average		101,335	352,558	453,893

Table 4. Numbers of sockeye salmon harvested in each statistical week in the District 101 Gillnet and District 104 purse seine fisheries in the year 2006 (ADFG web site http://dungie.adfg.state.ak.us:8080/CatchByMultiYear.po).

Allele Scoring

After amplification, the Taqman genotyping reactions were assayed on an ABI PRISM 7900HT Sequence Detection System and scored using Sequence Detection Software 2.2 (Applied Biosciences, Inc.). 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 every analysis, 14 Markov chain Monte Carlo chains started at disparate starting points were run for 50,000 samples each. 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.

RESULTS

In 2006, 62,770 sockeye salmon were harvested in District 101 and 242,034 were harvested in District 104 (Table 4). This was approximately 100,000 fish less than the historical average in each district. During that time period, ADF&G collected genetic and scale samples from approximately 520 fish per statistical week for each district, of which approximately 380 were analyzed (Table 5). DNA was isolated and genotyped for 34 SNP markers. In total, there were 5,791 sockeye salmon that were genotyped, and the data was imported into a Progeny database.

Table 5. Numbers of sockeye genetic and scale samples collected for each District and statistical week. Samples collected in District 101 were from the drift gillnet fishery and those from District 104 were from the seine fishery.

Week	District 101	District 104	Total
25	377	0	377
26	380	0	380
27	380	147	527
28	305	75	380
29	377	280	657
30	380	379	759
31	377	379	756
32	379	380	759
33	380	260	640
34	101	353	454
35	102	0	102
Totals	3,538	2,253	5,791

Status of current SNP baseline

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 the ADF&G for Southeast Alaska and British Columbia. ADF&G and NOAA's Auke Bay Laboratories 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.

Power of the 34 SNPs to resolve stock groups of sockeye salmon in Northern Boundary fisheries

The ADF&G SNP baseline is comprised of 84 populations of fish characterized for 41 markers (38 individual SNPs and 3 groups of linked SNPs). The 84 populations of sockeye salmon are grouped into 14 regions. The original proposal called for Auke Bay Laboratories to analyze 25 SNPs for the 2006 genetic samples, although the proposal for analysis of the 2007 samples increased that number to 39. We have completed 34 and are in the process of adding the remaining markers that will be included in the analysis of the 2007 samples.

To determine whether the 34 SNPs analyzed to date (Table 3) have the power to accurately discriminate the 14 regions, 100 percent simulation mixtures were performed. For this analysis, a sample of 400 individuals from a region were simulated and analyzed repeatedly with conditional maximum likelihood as implemented in software SPAM (Version 3.7) developed by the Alaska Department of Fish and Game (ADF&G, 2003; Debevec et al., 2000). For each region, estimates were derived from 1,000 simulations, plotted graphically (Figure 2) and described numerically with standard deviations (Table 6).

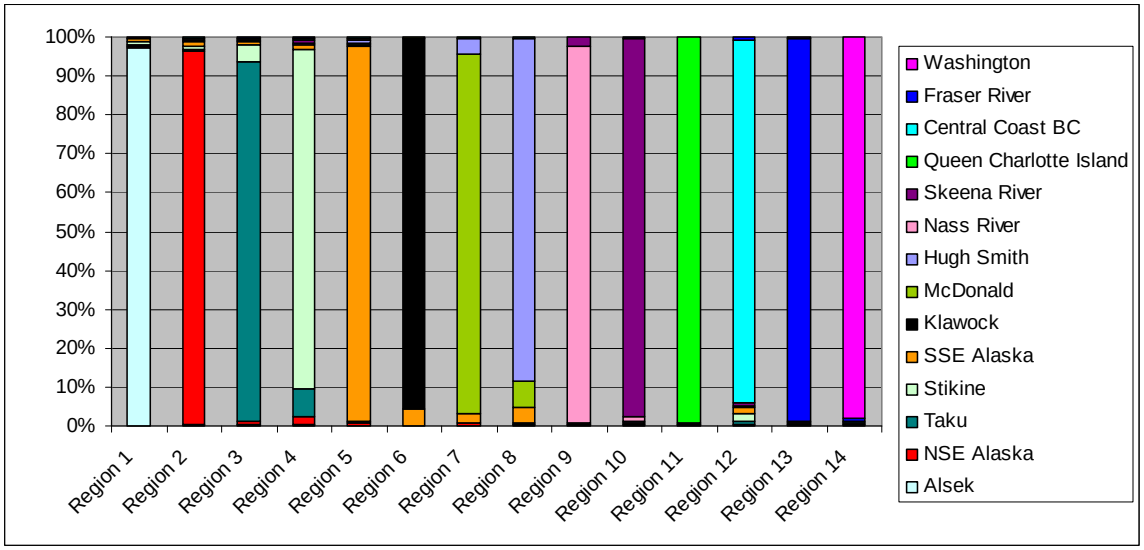

Figure 2. Estimated stock proportions from 100% mixture simulations. The regions identified below the bar graphs designate individual analyses for a simulated mixture of 400 fish from that region. The Y axis designates the percentages of individual stocks allocated from the SPAM software for the simulated mixtures.

The 100 percent simulation tests confirm that 34 SNPs in the baseline have the power to accurately identify the 14 stock groups. All estimates from this analysis were greater than 90% with the exception of the analysis for the Stikine Region (87.2%, region 4) in which 7.3% of was misallocated to the Taku region and the Hugh Smith Region (87.8%, Region 8) in which 6.6% was misallocated to the McDonald Lake Region. Regarding the Nass (Region 9) and Skeena (Region 10) Regions, there was very high

allocation in the simulated mixture analyses to the correct region. In addition, there was very little misallocation to these regions for any of the other simulated mixtures. These results suggest that the 34 SNP baseline has strong resolving power to correctly allocate the Nass and Skeena drainage sockeye from other sockeye populations in Southeast Alaska and British Columbia.

Region	Region 1	Region 2	Region 3	Region 4	Region 5	Region 6	Region 7
1	0.9705 +/- 0.0148	0.0029 +/- 0.0045	0.0023 +/- 0.0035	0.0054 +/- 0.0063	0.0015 +/- 0.0028	0.0001 +/- 0.0005	0.0012 +/- 0.0024
2	0.0075 +/- 0.0068	0.9627 +/- 0.0155	0.0092 +/- 0.0084	0.0173 +/- 0.0124	0.0075 +/- 0.0061	0.0015 +/- 0.0025	0.006 +/- 0.0061
3	0.0032 +/- 0.0054	0.0043 +/- 0.0064	0.926 +/- 0.0276	0.0728 +/- 0.0432	0.0018 +/- 0.0031	0.0001 +/- 0.0008	0.0007 +/- 0.0017
4	0.0055 +/- 0.0085	0.0061 +/- 0.0096	0.0428 +/- 0.0265	0.8724 +/- 0.0469	0.0016 +/- 0.0037	0 +/- 0.0003	0.0011 +/- 0.0031
5	0.0075 +/- 0.0062	0.014 +/- 0.0088	0.0074 +/- 0.0058	0.0109 +/- 0.0081	0.9629 +/- 0.0185	0.0418 +/- 0.0293	0.0225 +/- 0.0128
6	0.0001 +/- 0.0006	0.0007 +/- 0.0018	0.0003 +/- 0.001	0.0003 +/- 0.001	0.0036 +/- 0.0059	0.9539 +/- 0.0303	0.0009 +/- 0.0022
7	0.0004 +/- 0.0014	0.0007 +/- 0.0021	0.0002 +/- 0.0009	0.001 +/- 0.0025	0.0042 +/- 0.0077	0.0005 +/- 0.0018	0.9253 +/- 0.0354
8	0.0006 +/- 0.0018	0.0013 +/- 0.0028	0.0004 +/- 0.0013	0.0013 +/- 0.0029	0.0106 +/- 0.0121	0.0009 +/- 0.0025	0.0366 +/- 0.0316
9	0.0017 +/- 0.0026	0.0018 +/- 0.0027	0.0018 +/- 0.0028	0.003 +/- 0.0038	0.001 +/- 0.002	0.0002 +/- 0.0006	0.0008 +/- 0.0017
10	0.0015 +/- 0.0021	0.0026 +/- 0.003	0.0047 +/- 0.0043	0.0065 +/- 0.0056	0.0027 +/- 0.0032	0.0003 +/- 0.0009	0.0029 +/- 0.0039
11	0.0004 +/- 0.0011	0.0003 +/- 0.0009	0.0004 +/- 0.0011	0.0004 +/- 0.0011	0.0005 +/- 0.0013	0 +/- 0.0002	0.0005 +/- 0.0013
12	0.0004 +/- 0.0015	0.0007 +/- 0.0021	0.0021 +/- 0.004	0.0049 +/- 0.0076	0.0012 +/- 0.0029	0.0005 +/- 0.0017	0.0005 +/- 0.0015
13	0.0006 +/- 0.0012	0.0014 +/- 0.002	0.0019 +/- 0.0025	0.0027 +/- 0.0031	0.0007 +/- 0.0013	0 +/- 0.0003	0.0005 +/- 0.0012
14	0.0002 +/- 0.0008	0.0005 +/- 0.0012	0.0004 +/- 0.0013	0.0011 +/- 0.0023	0.0003 +/- 0.0009	0 +/- 0.0002	0.0005 +/- 0.0012

Region	Region 8	Region 9	Region 10	Region 11	Region 12	Region 13	Region 14
1	0.001 +/- 0.0022	0.0009 +/- 0.0018	0.0004 +/- 0.0011	0.0002 +/- 0.0012	0.0018 +/- 0.003	0.0003 +/- 0.0008	0.0003 +/- 0.001
2	0.0045 +/- 0.0045	0.0022 +/- 0.0031	0.0019 +/- 0.0025	0.0003 +/- 0.0009	0.004 +/- 0.0041	0.0018 +/- 0.0025	0.0018 +/- 0.0027
3	0.0006 +/- 0.0019	0.0011 +/- 0.0023	0.0014 +/- 0.0027	0.0005 +/- 0.0027	0.0081 +/- 0.0143	0.001 +/- 0.0021	0.0007 +/- 0.0017
4	0.0009 +/- 0.0026	0.0008 +/- 0.0023	0.0013 +/- 0.0031	0.0005 +/- 0.0029	0.0192 +/- 0.0214	0.0007 +/- 0.0018	0.001 +/- 0.0024
5	0.0416 +/- 0.0219	0.002 +/- 0.0024	0.0044 +/- 0.0041	0.0033 +/- 0.008	0.0132 +/- 0.0099	0.0016 +/- 0.0021	0.0018 +/- 0.0024
6	0.0011 +/- 0.0026	0.0001 +/- 0.0005	0.0001 +/- 0.0007	0 +/- 0.0003	0.0007 +/- 0.0019	0 +/- 0.0003	0.0001 +/- 0.0004
7	0.0663 +/- 0.0399	0.0001 +/- 0.0006	0.0003 +/- 0.0011	0.0002 +/- 0.0016	0.0003 +/- 0.0013	0.0001 +/- 0.0004	0.0001 +/- 0.0007
8	0.8783 +/- 0.0454	0.0002 +/- 0.0007	0.0004 +/- 0.0013	0.0005 +/- 0.0019	0.0007 +/- 0.0019	0.0001 +/- 0.0006	0.0003 +/- 0.0011
9	0.0006 +/- 0.0014	0.968 +/- 0.0177	0.0138 +/- 0.0124	0.0001 +/- 0.0006	0.0024 +/- 0.0039	0.0007 +/- 0.0014	0.0014 +/- 0.0024
10	0.0025 +/- 0.0034	0.0231 +/- 0.0166	0.9726 +/- 0.0142	0.0004 +/- 0.0014	0.0075 +/- 0.0066	0.0044 +/- 0.0041	0.0019 +/- 0.0025
11	0.0007 +/- 0.0017	0.0001 +/- 0.0005	0.0001 +/- 0.0006	0.9937 +/- 0.0134	0.0002 +/- 0.0006	0.0001 +/- 0.0004	0.0002 +/- 0.0007
12	0.0007 +/- 0.0021	0.0004 +/- 0.0014	0.0007 +/- 0.0021	0.0001 +/- 0.0004	0.9343 +/- 0.0318	0.001 +/- 0.0024	0.0006 +/- 0.0017
13	0.0007 +/- 0.0014	0.0005 +/- 0.0012	0.002 +/- 0.0026	0.0001 +/- 0.0004	0.0065 +/- 0.0067	0.9847 +/- 0.0081	0.0092 +/- 0.0083
14	0.0007 +/- 0.0017	0.0004 +/- 0.0012	0.0005 +/- 0.0013	0.0001 +/- 0.0007	0.0012 +/- 0.0026	0.0035 +/- 0.005	0.9805 +/- 0.0116

Table 6. Estimated stock group proportions and standard deviations from 100% mixture simulations. The regions identified on the top of the estimates designate each individual analyses for a simulated mixture of 400 fish from that region. The regions on the left side of the table designate the regions to which the 100% simulated mixture was aportioned. The highlighted value is the region in which the 100% mixture was derived and this value should approach 100%.

Stock Mixture Proportions

Because of the limited numbers of samples, fish from District 101 weeks 34 (101 samples) and 35 (7 samples – the remaining samples remain to be genotyped) were combined into one mixture. Likewise, fish from District 104 weeks 27 (147 samples) and 28 (75 samples) were also combined. Weekly mixture samples were analyzed with Bayes software. In all analyses, the Gelman and Rubin shrink factors were less than 1.1, indicating convergence of the chains to posterior distributions.

Results from this analysis are presented in both graphical form (Figure 3) and Table form (Table 7 and 8). Figure 3 graphically illustrates the estimated proportions of sockeye salmon endemic to each of the 14 regions that were harvested in each District

and statistical week. Table 7 provides the same data for the 101 gillnet fisheries in numerical format showing the estimated stock group proportions, standard errors, and 95% probability intervals. Table 8 illustrates results for the 104 purse seine fisheries.

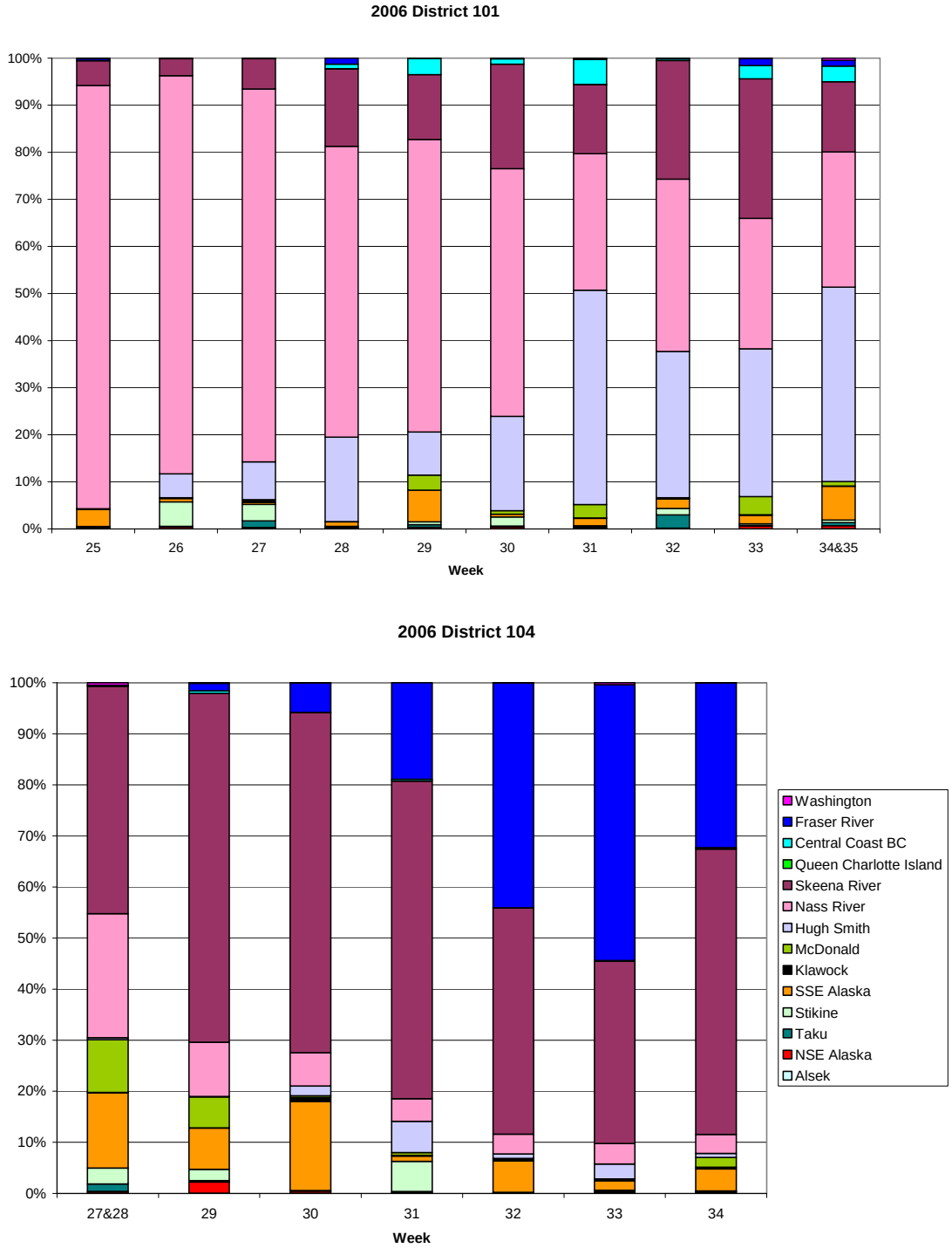

Figure 3. 2006 sockeye stock group proportions from the ADFG District 101 gillnet (top panel) and District 104 purse seine fisheries (lower panel). Stock group proportions (y-axis) are shown as a function of statistical week (x-axis).

	Week 25			Week 26			Week 27			Week 28		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.2	0.38	(0.0,1.3)	0.0	0.12	(0.0,0.3)	0.0	0.21	(0.0,0.5)	0.1	0.25	(0.0,0.7)
NSE Alaska	0.3	0.40	(0.0,1.4)	0.4	0.77	(0.0,2.8)	0.3	0.61	(0.0,2.2)	0.2	0.41	(0.0,1.4)
Taku	0.0	0.16	(0.0,0.4)	0.1	0.52	(0.0,1.6)	1.4	2.36	(0.0,7.7)	0.2	0.51	(0.0,1.6)
Stikine	0.1	0.23	(0.0,0.6)	5.2	2.09	(1.6,9.6)	3.5	2.85	(0.0,9.1)	0.2	0.64	(0.0,2.2)
SSE Alaska	3.6	1.44	(1.2,6.8)	0.7	0.94	(0.0,3.4)	0.4	0.59	(0.0,2.1)	0.9	1.32	(0.0,4.6)
Klawock	0.1	0.33	(0.0,1.2)	0.0	0.07	(0.0,0.1)	0.6	0.70	(0.0,2.3)	0.0	0.05	(0.0,0.0)
McDonald	0.0	0.14	(0.0,0.2)	0.2	0.73	(0.0,2.4)	0.0	0.15	(0.0,0.1)	0.1	0.35	(0.0,0.5)
Hugh Smith	0.1	0.25	(0.0,0.8)	5.1	1.69	(1.4,8.4)	8.0	1.69	(5.0,11.6)	17.9	2.61	(13.0,23.2)
Nass	89.9	1.88	(85.9,93.3)	84.5	2.41	(79.5,89.0)	79.2	4.29	(70.5,86.3)	61.8	5.15	(52.6,73.1)
Skeena	5.3	1.68	(2.3,8.9)	3.6	1.58	(1.1,7.2)	6.5	3.83	(1.3,14.6)	16.5	4.58	(6.8,25.0)
Queen Charlotte I.	0.0	0.09	(0.0,0.2)	0.0	0.03	(0.0,0.0)	0.0	0.03	(0.0,0.0)	0.1	0.25	(0.0,0.7)
Central Coast BC	0.0	0.08	(0.0,0.1)	0.0	0.13	(0.0,0.2)	0.1	0.32	(0.0,0.9)	1.0	1.87	(0.0,6.3)
Fraser	0.5	0.47	(0.0,1.7)	0.1	0.17	(0.0,0.5)	0.0	0.14	(0.0,0.4)	1.3	0.82	(0.0,3.2)
Washington	0.1	0.23	(0.0,0.8)	0.1	0.20	(0.0,0.6)	0.0	0.10	(0.0,0.2)	0.0	0.09	(0.0,0.2)

	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	0.0	0.17	(0.0,0.4)	0.0	0.14	(0.0,0.3)	0.1	0.38	(0.0,1.3)	0.0	0.08	(0.0,0.2)
NSE Alaska	0.3	0.64	(0.0,2.3)	0.4	0.51	(0.0,1.8)	0.1	0.33	(0.0,1.1)	0.2	0.36	(0.0,1.3)
Taku	0.5	1.01	(0.0,3.3)	0.2	0.40	(0.0,1.3)	0.2	0.71	(0.0,2.3)	2.8	2.57	(0.0,8.1)
Stikine	0.6	1.32	(0.0,5.1)	1.9	2.57	(0.0,8.2)	0.2	0.69	(0.0,2.4)	1.3	2.34	(0.0,7.7)
SSE Alaska	6.7	2.73	(1.9,12.7)	0.6	0.91	(0.0,3.2)	1.6	2.32	(0.0,8.9)	2.1	2.04	(0.0,7.2)
Klawock	0.0	0.05	(0.0,0.0)	0.0	0.09	(0.0,0.1)	0.1	0.39	(0.0,1.4)	0.0	0.22	(0.0,0.4)
McDonald	3.2	4.17	(0.0,13.2)	0.7	2.12	(0.0,8.1)	2.8	4.27	(0.0,13.7)	0.2	0.88	(0.0,2.5)
Hugh Smith	9.1	4.81	(0.0,16.9)	20.1	3.24	(12.6,25.9)	45.5	5.60	(32.6,54.1)	31.1	3.11	(24.8,37.0)
Nass	62.1	4.46	(53.7,70.7)	52.6	4.15	(42.9,59.7)	29.0	2.72	(23.8,34.5)	36.6	2.94	(30.8,42.4)
Skeena	13.8	4.05	(6.6,21.8)	22.2	3.87	(15.9,31.5)	14.7	2.24	(10.6,19.3)	25.2	2.91	(19.8,31.2)
Queen Charlotte I.	0.0	0.03	(0.0,0.0)	0.0	0.04	(0.0,0.0)	0.0	0.08	(0.0,0.1)	0.1	0.21	(0.0,0.7)
Central Coast BC	3.4	1.69	(0.0,7.0)	1.1	1.68	(0.0,5.4)	5.3	1.83	(2.2,9.3)	0.4	1.12	(0.0,4.3)
Fraser	0.0	0.14	(0.0,0.4)	0.2	0.34	(0.0,1.2)	0.2	0.42	(0.0,1.5)	0.1	0.31	(0.0,1.0)
Washington	0.0	0.06	(0.0,0.1)	0.0	0.08	(0.0,0.1)	0.1	0.30	(0.0,1.1)	0.0	0.06	(0.0,0.1)

	Week 33			Weeks 34 & 35		
	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.0	0.10	(0.0,0.2)	0.1	0.36	(0.0,0.8)
NSE Alaska	0.6	0.71	(0.0,2.4)	0.6	1.34	(0.0,4.8)
Taku	0.1	0.36	(0.0,1.1)	0.7	1.67	(0.0,5.5)
Stikine	0.4	0.51	(0.0,1.7)	0.5	1.83	(0.0,6.5)
SSE Alaska	1.8	2.43	(0.0,8.8)	7.2	3.79	(1.0,15.8)
Klawock	0.1	0.46	(0.0,1.7)	0.0	0.31	(0.0,0.3)
McDonald	3.9	4.00	(0.0,12.5)	1.0	3.93	(0.0,15.5)
Hugh Smith	31.4	5.44	(20.0,40.6)	41.3	7.29	(24.1,54.0)
Nass	27.7	2.70	(22.5,33.1)	28.7	5.00	(19.5,39.0)
Skeena	29.6	2.81	(24.2,35.3)	14.9	4.81	(6.4,25.1)
Queen Charlotte I.	0.0	0.08	(0.0,0.2)	0.0	0.12	(0.0,0.1)
Central Coast BC	2.8	1.49	(0.3,6.1)	3.3	4.62	(0.0,14.7)
Fraser	1.5	0.94	(0.0,3.7)	1.2	1.45	(0.0,5.1)
Washington	0.0	0.24	(0.0,0.5)	0.5	1.20	(0.0,4.3)

Table 7. Parameters of the posterior densities for population region proportions composing weekly mixtures of the District 101 commercial gillnet sockeye fishery. Means (%), standard deviations (%), and 95% probability intervals (PI) were computed from 14 combined MCMC chains of length 25,000 (25,000 discarded as burn-in).

	Weeks 27 & 28			Week 29			Week 30			Week 31		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.1	0.35	(0.0,1.0)	0.0	0.18	(0.0,0.5)	0.1	0.20	(0.0,0.6)	0.0	0.09	(0.0,0.2)
NSE Alaska	0.3	0.69	(0.0,2.4)	2.2	2.08	(0.0,7.0)	0.4	0.61	(0.0,2.1)	0.2	0.44	(0.0,1.6)
Taku	1.5	2.49	(0.0,8.5)	0.3	0.71	(0.0,2.4)	0.1	0.22	(0.0,0.5)	0.2	0.78	(0.0,1.6)
Stikine	3.1	3.28	(0.0,10.5)	2.2	2.90	(0.0,10.2)	0.1	0.24	(0.0,0.6)	5.9	2.97	(0.0,11.5)
SSE Alaska	14.8	3.48	(8.4,22.1)	8.1	3.10	(2.1,14.5)	17.4	3.24	(11.2,23.6)	1.1	1.48	(0.0,5.3)
Klawock	0.0	0.24	(0.0,0.5)	0.0	0.20	(0.0,0.5)	0.8	0.77	(0.0,2.7)	0.1	0.42	(0.0,1.6)
McDonald	10.3	3.12	(4.6,16.8)	6.0	2.34	(1.7,11.0)	0.3	1.15	(0.0,4.4)	0.5	1.56	(0.0,6.0)
Hugh Smith	0.4	1.47	(0.0,5.2)	0.1	0.58	(0.0,1.0)	1.9	2.27	(0.0,7.1)	6.1	2.56	(0.0,10.5)
Nass	24.3	3.60	(17.7,31.8)	10.6	2.48	(6.0,15.7)	6.5	1.84	(3.3,10.4)	4.4	1.25	(2.4,7.2)
Skeena	44.5	3.89	(36.9,52.1)	68.3	3.66	(61.0,75.3)	66.6	2.81	(61.0,72.0)	62.2	3.01	(56.2,68.0)
Queen Charlotte I.	0.0	0.07	(0.0,0.1)	0.0	0.14	(0.0,0.3)	0.0	0.04	(0.0,0.0)	0.0	0.09	(0.0,0.2)
Central Coast BC	0.2	0.64	(0.0,2.2)	0.5	1.21	(0.0,4.3)	0.0	0.24	(0.0,0.6)	0.4	0.92	(0.0,3.3)
Fraser	0.1	0.25	(0.0,0.8)	1.5	1.24	(0.0,4.4)	5.8	1.46	(3.3,8.9)	18.9	2.57	(14.1,24.1)
Washington	0.5	0.58	(0.0,2.1)	0.1	0.32	(0.0,1.1)	0.0	0.15	(0.0,0.4)	0.0	0.09	(0.0,0.2)

	Week 32			Week 33			Week 34		
	Mean	SD	95% PI	Mean	SD	95% PI	Mean	SD	95% PI
Alsek	0.0	0.07	(0.0,0.2)	0.2	0.49	(0.0,1.8)	0.0	0.19	(0.0,0.5)
NSE Alaska	0.1	0.23	(0.0,0.8)	0.1	0.35	(0.0,1.2)	0.2	0.51	(0.0,1.8)
Taku	0.1	0.22	(0.0,0.7)	0.1	0.37	(0.0,1.2)	0.1	0.25	(0.0,0.7)
Stikine	0.1	0.22	(0.0,0.5)	0.2	0.70	(0.0,2.3)	0.1	0.44	(0.0,1.3)
SSE Alaska	6.2	1.90	(2.6,10.0)	1.9	1.50	(0.0,5.2)	4.3	1.91	(1.0,8.4)
Klawock	0.4	0.66	(0.0,2.2)	0.1	0.29	(0.0,1.0)	0.3	0.67	(0.0,2.3)
McDonald	0.0	0.20	(0.0,0.3)	0.3	0.91	(0.0,3.6)	1.9	1.67	(0.0,5.5)
Hugh Smith	0.9	1.35	(0.0,4.4)	3.0	1.59	(0.0,6.3)	0.8	1.50	(0.0,5.1)
Nass	3.9	1.52	(1.5,7.3)	4.0	1.35	(1.8,7.0)	3.7	1.23	(1.8,6.6)
Skeena	44.3	3.00	(38.5,50.2)	35.7	3.52	(29.0,42.7)	55.9	3.11	(49.7,61.9)
Queen Charlotte I.	0.0	0.06	(0.0,0.1)	0.0	0.17	(0.0,0.5)	0.0	0.04	(0.0,0.0)
Central Coast BC	0.0	0.12	(0.0,0.1)	0.0	0.24	(0.0,0.4)	0.3	0.78	(0.0,2.8)
Fraser	44.1	2.90	(38.4,49.8)	54.1	3.63	(46.9,61.1)	32.3	2.95	(26.6,38.2)
Washington	0.0	0.16	(0.0,0.3)	0.4	0.83	(0.0,3.0)	0.0	0.14	(0.0,0.2)

Table 8. Parameters of the posterior densities for population region proportions composing weekly mixtures of the District 104 commercial purse seine sockeye fishery. Means (%), standard deviations (%), and 95% probability intervals (PI) were computed from 14 combined MCMC chains of length 25,000 (25,000 discarded as burn-in).

Analysis of the stock proportions of sockeye caught in Districts 101 and 104 over varying weeks shows interesting trends. For example, the sockeye commercial fishery in District 101 predominantly harvests Nass Region fish early in the season (90%), but over 10 weeks, this stock decreased to 29% of the catch. These fish were replaced with Skeena and Hugh Smith fish. Skeena stocks increased from 5% in week 25 to 15% in weeks 34/35. Hugh Smith stocks increased from 0% in week 25 to 42% in weeks 34/35.

In the District 104 fishery, Skeena region stocks predominated throughout the entire fishery (44% in weeks 27/28 and 56% in week 34). In contrast, the proportion of Nass Region fish decreased during that same time period (24% starting and 4% ending) whereas the proportion of Fraser River fish increased (0% starting and 32% ending).

When the proportion estimates were converted to numbers of fish caught (Table 9), the majority of fish caught in the District 101 fishery (58,315 of 103,746) were from the Nass Region although large numbers of Hugh Smith (21,050) and Skeena River (15,532) fish were also caught. In the 104 fishery, the majority of fish were from the Skeena Region (141,705 of 242,032) although large numbers of fish were also caught from the Fraser (50,178), SSE Alaska (17,904), and Nass River (13,817) Regions. Together, almost 350,000 fish were caught in the District 101 and 104 sockeye fisheries. Of those fish, 279,918 of the total 345,778 fish caught (81%) were from either the Skeena River (45%), Nass River (21%), or Fraser River (15%) Regions. The small discrepancies between total numbers of fish in Tables 9 and 4 were due to rounding errors in calculating numbers of fish from estimated stock group proportions. Table 10 shows the 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/Skeens (for District 104) sockeye prior to week 31.

Table 9. Estimated numbers of sockeye salmon caught in the District 101 gillnet and 104 seine fisheries throughout all statistical weeks. Estimates are based on total catches and estimated stock group proportions.

Region	Area	101 Gillnet	104 Seine	Totals
1	Alsek	60	95	155
2	NSE Alaska	301	981	1282
3	Taku	707	353	1060
4	Stikine	1534	5407	6941
5	SSE Alaska	2486	17904	20390
6	Klawock	140	879	1020
7	McDonald	1343	2364	3707
8	Hugh Smith	21050	7668	28717
9	Nass River	58315	13817	72132
10	Skeena River	15532	141705	157237
11	Queen Charlotte Island	15	22	38
12	Central Coast BC	1832	522	2354
13	Fraser River	370	50178	50549
14	Washington	60	137	196
	Totals	103746	242032	345778

Table 10. Estimated numbers of sockeye salmon caught in District 101 gillnet and 104 seine fisheries prior to statistical week 31. Estimates are based on total catches and estimated stock group proportions.

Region	Area	101 Gillnet	104 Seine	Totals
1	Alsek	39	44	83
2	NSE Alaska	203	730	933
3	Taku	318	162	480
4	Stikine	1266	590	1856
5	SSE Alaska	1518	13663	15181
6	Klawock	114	519	633
7	McDonald	662	1905	2567
8	Hugh Smith	7125	1332	8457
9	Nass River	46836	7406	54242
10	Skeena River	8243	58967	67210
11	Queen Charlotte Island	7	4	11
12	Central Coast BC	722	128	850
13	Fraser River	204	4103	4307
14	Washington	16	61	77
	Totals	67273	89614	156887

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. Estimates of the stock-specific catch in these commercial fisheries are currently being provided by the Alaska Department of Fish and Game using scale pattern analysis (SPA). This technique has been shown to be accurate, but requires the collection of post-season scale patterns to determine the year specific baseline for individual rivers. This is because yearly fluctuations in environmental conditions can dramatically affect scale patterns.

Genetic markers are more stable than scale patterns and are not normally influenced by small environmental changes in short periods of time. Differences in allele frequencies in groups of genetic markers can be used to distinguish individual stocks of fish. These allele frequency differences can be reflective of evolutionary selective pressures that reflect the 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 104 purse seine fisheries. Our findings indicate that 34 SNP markers can be used to separate regions of sockeye salmon caught in Districts 101 and 104 fisheries. The 100 percent simulation tests show that the baseline can resolve 14 regional stock groups. Over the next year, the 2006 samples will be reanalyzed with an additional 7 markers to match those in the complete 45 SNP baseline. After the full complement of SNPs has been realized, stock proportion assessments and 100 percent simulation studies will be completed to compare the utility of the varying SNP markers. 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 will be informative. For example, this same group of SNPs has been used by the Alaska Department of Fish and Game to separate stocks of fish is many regions of Alaska (Habicht et al., 2004; Habicht et al., 2007). SNPs that are effective at separating populations in one geographical location may not be effective at another location. A thorough analysis of the effectiveness of combinations of SNPs to resolve sockeye in southeast Alaska and British Columbia could help limit the numbers of SNPs that need to be assayed to obtain the same stock assessment confidence intervals.

CONCLUSION

Our results indicate that a majority of sockeye salmon caught in the ADF&G District 101 gillnet and 104 purse seine fisheries originate from Canadian stocks. Our results are in general agreement with the mark-recapture studies completed in the early 1980's (Pella et al., 1993), scale pattern analyses completed since 1982 (Marshall, 1984),

and allozyme/freshwater age/parasitism analyses completed in the late 1980's (Pella et al., 1998). 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 estimates produced using scale pattern analysis and genetic analysis helps validate both approaches for determining stock assessments. The similarity between the 2006 stock estimates for Districts 101 and 104 and the 2004 and 2005 estimates for those same Districts (ADFG, preliminary data) suggest that the stock compositions are stable over a short interval. The finding that stock estimates have not changed by large measure since 1982 suggests a strong temporal stability in stock structure over long periods of time. Given that the large majority of fish (>75%) caught in the District 101 and 104 fisheries originate in 5 Canadian regions (mostly Nass, Skeena, and Fraser), it is likely that large changes in the escapements for those systems could have dramatic effects on the stock composition for the 101 and 104 fisheries.

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