

SC Northern Fund Final Report

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Project Title: Estimating the sockeye salmon stock composition of Southeast Alaska District 106 & 108 fisheries, 2012

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Abstract:

The Stikine River in Southeast Alaska supports sockeye salmon runs important for various commercial and aboriginal fisheries in both Alaska and Canada. This project continues the genetic stock identification (GSI) of sockeye salmon harvested in the 2012 gillnet fishery in Districts 106 and 108 by screening 96 single nucleotide polymorphic genetic markers in 5,127 salmon. Recent advances in mixed stock analysis methodologies have allowed the incorporation of hatchery-marked fish and age composition into genetic-based fishery estimates. The mixed stock analysis model indicated that Southeast Alaska, Other, Tahltan, McDonald, and Hatchery-origin fish were the largest contributors in the District 106 fisheries in 2012. In the District 108 fisheries, Stikine/Taku Mainstem, Southeast Alaska, Tahltan, and Hatchery-origin fish were the largest contributors.

Introduction:

The Stikine River in Southeast Alaska supports sockeye salmon runs important for various commercial and aboriginal fisheries in both the United States (U.S.) and Canada. Stikine River sockeye salmon are harvested in commercial gillnet fisheries in U.S. Districts 106 and 108, by U.S. subsistence fisheries in the lower river, by Canadian commercial gillnet in the lower and upper river, and by Canadian aboriginal fisheries in the upper river.

The gillnet fisheries in U.S. Districts 106 and 108 harvest wild stocks of sockeye salmon bound for Southeast Alaska (SEAK) island and mainland lakes, and for lakes and tributaries in the Stikine, Nass, and Skeena River drainages. Significant numbers of enhanced sockeye bound for release sites in the Stikine River are also caught in the fisheries. Catches of Stikine River sockeye salmon stocks in Districts 106 and 108 gillnet fisheries and the U.S. Stikine subsistence fishery are subject to a harvest sharing agreement, in which the U.S. is allowed 50% of the Total Allowable Catch of Stikine River sockeye. Stock contribution estimates are used to document compliance with the harvest sharing agreements, reconstruct runs of wild stocks, estimate the return of enhanced fish, forecast upcoming returns, and support sustainable management.

In the past, matched-samples collected from the fishery were analyzed using scale pattern analysis (SPA) and otolith marks to estimate the catch of wild and enhanced stocks. Collecting and analyzing these matched samples was logistically complex, labor intensive, and expensive. In particular, SPA became increasingly difficult to complete in a timely fashion due to continual turnover in highly trained technicians and the need to establish an annual 'escapement baseline'.

In addition, outdated and unsupported software and outdated hardware required expensive upgrades in order to remain feasible.

Genetic stock identification can improve stock composition estimates for sustainable management of sockeye salmon in the Stikine River. The Alaska Department of Fish and Game (ADF&G) and Department of Fisheries and Ocean Canada (DFO) compared SPA and GSI in limited sample sets from Alaska's District 101 gillnet fishery and found that although the two methods provide similar estimates, GSI analysis was more accurate and was able to discriminate stocks at a finer resolution than SPA (PSC NBTC 2005).

This project completed GSI analysis on sockeye salmon tissue samples collected from 2012 commercial gillnet fisheries in areas in and near the Stikine River in SEAK. The analysis focused on tissue samples collected in Districts 106 and 108, and replaces SPA for stock estimates in this transboundary river. For District 106, estimates are provided over the entire season for subdistrict 106-30, for 5 time strata for all age groups in subdistrict 106-41, and over the entire season in 106-41 for age-1.2 fish. For District 108, estimates are provided over the entire season in area 108A for all age groups and for 5 time strata for all age groups in area 108B, and for the entire season in each area for age-1.2 fish. Estimates are reported as proportions of a single hatchery group and six wild-stock groups: Taku, Stikine/Taku Mainstem, Tahltan, McDonald, Southeast Alaska, and Other.

Objectives:

The goal of this project was to estimate the stock composition of SEAK sockeye fishery harvests near the Stikine River in 2012 using GSI. The objectives were to:

- Determine the stock composition of sockeye harvests from the District 106 drift gillnet fishery. For 2012, provide estimates for:
 - Subdistrict 106-30
 - All age groups, total season;
 - Subdistrict 106-41
 - All age groups, 5 time strata;
 - Age-1.2 only, total season.
- Determine the stock composition of sockeye harvests from the District 108 drift gillnet fishery. For 2012, provide estimates for:
 - Section 108A
 - All age groups, total season;
 - Age-1.2 only, total season;
 - Section 108B
 - All age groups, 5 time strata;
 - Age-1.2 only, total season.

Approach:

Fishery Sampling

Landings from drift gillnet fisheries in Subdistricts 106-31 and 106-41 (District 106) and Sections 108-A and 108-B (District 108) were sampled by ADF&G at fish processing facilities in Wrangell and Petersburg. Sampling protocols ensured that the fish sampled were as representative of catches as possible. Axillary processes were excised and placed into individually labeled vials and preserved in ethanol. Metadata for each sample including fishery and capture date were recorded, and the tissue sample for each fish was paired with age, sex, and length (ASL) information and with otolith samples.

Laboratory Analysis

A single nucleotide polymorphism (SNP) baseline for SEAK and British Columbia (BC) including 45 markers was first completed in 2007. The baseline included all major sockeye salmon-producing systems in SEAK and in BC north of and including the Skeena River and from representative sockeye salmon-producing systems in BC south of the Skeena River. A cooperative project between ADF&G and DFO in 2007-2009 added several collections to the baseline for transboundary rivers (Northern Fund project no. NF-2008-I-15A). In addition, these and existing collections have been analyzed at a total of 96 SNP markers in order to further enhance the baseline for fishery applications. The current baseline includes 156 populations and 96 markers (Figure 1; Table 1).

Samples were analyzed for 96 SNP loci. Genomic DNA was extracted using a DNeasy® 96 Tissue Kit by QIAGEN®, (Valencia, CA). All SNPs were detected using a TaqMAN SNP Genotyping Assay (Life Technologies). SNP assays were generally performed using the BioMark 96.96 Dynamic Array (Fluidigm). Re-analyses of failed assays was performed on the Applied Biosystems Prism 7900HT Sequence Detection System. Genotype data are stored in an *Oracle* database (*LOKI*) on a network drive maintained by ADF&G computer services. Quality control measures included reanalysis of 8% of each collection for all markers to ensure that genotypes are reproducible and to identify laboratory errors and measure rates of inconsistencies during repeated analyses.

Mixture Analysis

Mixtures of fish representing catches by statistical week, age group, and subdistrict or section from the Districts 106 and 108 gillnet fisheries were screened for genetic variation at 96 SNPs for a total of 5,127 samples. For 2014 fisheries, analysis goals were to provide estimates for 1) Subdistrict 106-30, all age groups, 400 samples over entire season, for a total of 400 samples; 2) Subdistrict 106-41, all age groups, 200 samples per week, 5 time strata, for a total of 1,000 samples; 3) Subdistrict 106-41, age-1.2, 400 samples over entire season, for a total of 400 samples; 4) Section 108A, all age groups, 400 samples over entire season, for a total of 400 samples; 5) Section 108A, age-1.2, 400 samples over entire season, for a total of 400 samples; 6) Section 108B, all age groups, 200 samples per week, 5 time strata, for a total of 1,000 samples; and 7) Section 108B, age-1.2, 400 samples over entire season, for a total of 400 samples. Axillary processes were excised and placed into individually labeled vials and preserved in ethanol. Metadata for each sample including fishery and capture data was recorded.

Methods for mixture analysis have evolved from previous years' analyses to include additional available data to help inform the genetic estimates; specifically, ages from matched scales and hatchery marks on matched otoliths. In this method ("Mark-Age-Enhanced-GSI"), two sets of parameters are required: 1) a vector of stock compositions, summing to one, with a proportion for each of the wild and hatchery stocks; and 2) a matrix of age composition, with a row for each of the wild and hatchery stocks (summing to one), and a column for each age class. This information is "completed" iteratively by stochastically assigning each wild fish to a population, then estimating the stock proportions based on summaries of assignments from each iteration. In this process, all available information is used to assign individuals to stock of origin based on age, genotype, and/or otolith information. For this method, only genotypes from wild fish are necessary to complete stock composition estimates.

To initialize the algorithm, all wild fish are given a stock assignment stochastically. The initialized algorithm then proceeds in the following steps:

- 1) Summarize all age data by assigned and observed stocks for both wild and hatchery individuals;
- 2) Estimate the stock proportions and age composition from previous summaries (accounting for sampling error);
- 3) Stochastically assign each wild fish with genotypes to a wild stock of origin based on the product of its genotypic frequency, age frequency, and stock proportion for each population;
- 4) Stochastically assign each wild fish without genotypes to a stock of origin based on the product of its age frequency and stock proportion for each population; and
- 5) Repeat steps 1-4 while updating and recording the estimates of the stock proportions and age compositions with each iteration.

This algorithm was run for 10,000 repetitions, discarding the first 5,000 repetitions to eliminate the effect of the initial state. The point estimates and credibility intervals for the stock proportions and age composition are simple summary statistics of the output.

Results/Findings:

Fishery sampling

A total of 6,494 sockeye salmon were sampled in the gillnet fisheries in District 106 and 2,540 sockeye salmon were sampled in District 108 during 2012 (Table 2 and 3). In District 106, Subdistrict 30, 3,394 fish were sampled from statistical weeks 25 to 34 and in Subdistrict 41, 3,100 fish were sampled from statistical week 25 to 33 (Table 2). In District 108, sections A and B, 1,638 and 902 fish were sampled (respectively) from statistical weeks 25 through 33 (Table 3).

Laboratory analyses

Of the 6,494 samples collected in District 106, 2,028 samples were genotyped at 96 SNP genetic markers. During quality control procedures a total of 218 fish were reanalyzed at all 96 markers for a total of 20,928 comparisons. The average failure rate for District 106 was 2.05%. Few inconsistencies were found (0.27% across all comparisons).

Of the 2,540 samples collected in District 108, 1,778 samples were genotyped at 96 SNP genetic markers. During quality control procedures a total of 214 fish were reanalyzed at all 96 markers for a total of 20,544 comparisons. The average failure rate for District 108 was 1.45%. Few inconsistencies were found (0.46% across all comparisons).

Mixture analysis

Of the samples extracted and genotyped, genotypes from 3,806 wild fish (no otolith mark present) were used for the genetic analyses in the Mark-Age-Enhanced-GSI method. Stock composition estimates can be found in Figures 2 - 6. Results are given for seven reporting groups consisting of six reporting groups of wild fish and one reporting group for all hatchery-origin fish. These results are given for fish of all age classes over every time stratum sampled, regardless of sample size, to meet current needs of fishery managers. Sample sizes in statistical weeks 26, 33, and 34 in Subdistrict 106-30, statistical week 33 in Subdistrict 106-41, statistical weeks 31 through 33 in Section 108-A, and statistical weeks 28 and 30-33 in Section 108-B were smaller than would usually be considered acceptable. However, metadata (otolith marks and ages on fish not genotyped) could be used in the model along with the genetic information to estimate stock composition. While the estimates from the small samples have greater precision than previous methods, the credibility intervals should be considered, especially when expanding estimates to total harvest by statistical week.

The largest component of the District 106-30 fishery sample in 2012 was Southeast Alaska-origin fish, between 24% and 97% (Figure 2). The McDonald stock was present in the fishery samples and generally increased in proportion over time from 2% to 25%. Hatchery-origin fish increased in proportion from 4% to 31% between statistical weeks 25 and 34. The Other stock contributed between 2% and 24% to the fishery sample and the Stikine/Taku Mainstem stock contributed a small amount to the fishery sample, between 0% and 6%. Taku and Tahltan stocks contributed less than 1% to fishery samples throughout the 2012 season. The largest component of the District 106-41 fishery sample in 2012 was Southeast Alaska-origin fish, generally increasing from 20% to 81% (Figure 3). The McDonald stock was present in small proportions of the fishery samples from 0% to 9%. Hatchery-origin fish generally decreased in proportion from 40% to 0% between statistical weeks 25 and 34. The Other stock contributed between 5% and 12% to the fishery sample and the Stikine/Taku Mainstem stock contributed between 0% and 13% to the fishery sample. The Taku stock contributed essentially nothing to the fishery sample and the Tahltan stock contributed 23% to fishery samples in statistical week 25 and decreased to 0% by statistical week 30.

The largest component of the District 108-A fishery sample in 2012 was the Stikine/Taku Mainstem-origin stock, which generally increased from 14% to 86% (Figure 4). Hatchery-origin fish contributed 3% to 50% between statistical weeks 25 and 33. The Tahltan stock contributed between 31% and 0%, decreasing to 0% by statistical week 30 and the Southeast Alaska stock contributed between 2% and 35% to the fishery sample. The Other stock contributed between 0% and 6% to the fishery sample, the Taku stock contributed less than 3% throughout the fishery samples, and the McDonald stock contributed essentially 0% to the fishery samples. The largest component of the District 108-B fishery sample in 2012 was the Hatchery-origin fish, which generally decreased from 59% to 10% (Figure 5). The Stikine/Taku Mainstem stocks contributed 14% to 44% between statistical weeks 25 and 33. The Southeast Alaska stock contributed between 2% and 53%, generally increasing between statistical week 25 and 33. The Other stock contributed between 3% and 30% to the fishery samples. The Tahltan stock contributed between 20% and 0% to the fishery samples, generally decreasing from statistical weeks 25 to 29 and essentially 0% from statistical weeks 30 to 33. The McDonald stock contributed between 0% and 11% to fishery samples and Taku stock contributed less than 3% throughout the fishery samples, and the McDonald stock contributed essentially 0% to the fishery samples.

Evaluation:

We accomplished the following:

- A total of 6,494 sockeye salmon were sampled from District 106 gillnet fisheries during 2012 season. A total of 2,540 sockeye salmon were sampled from District 108 gillnet fisheries during 2012 season.
- A total of 2,028 samples from District 106 and 1,778 samples of sockeye salmon from District 108 were assayed for genotypes for the 96 SNP loci in the sockeye salmon baseline, and quality control procedures revealed a low rate of inconsistencies.
- Mixture analyses estimated the contributions of 7 reporting groups as well as otolith-marked sockeye salmon to 10 temporal strata in District 106 Subdistrict 30 and 9 temporal strata in Subdistrict 41.
- Mixture analyses estimated the contributions of 7 reporting groups as well as otolith-marked sockeye salmon to 9 temporal strata in District 108 Section A and 8 temporal strata in Section B.

Project Products:

Results from this project will be presented to ADF&G Commercial Fisheries management staff and will be presented to the PSC Transboundary Technical Committee. A report published in the ADF&G Fishery Data Series is expected in 2014.

Date Prepared: February, 2014

References:

Pacific Salmon Commission, Northern Boundary Technical Committee. 2005. Stock composition estimates and individual stock assignments based on genetic microsatellites and scale patterns for test mixtures of Alaskan and Canadian sockeye salmon. Report TCNB (05)-2, available online at www.psc.org/pubs/TCNB05-2.pdf.

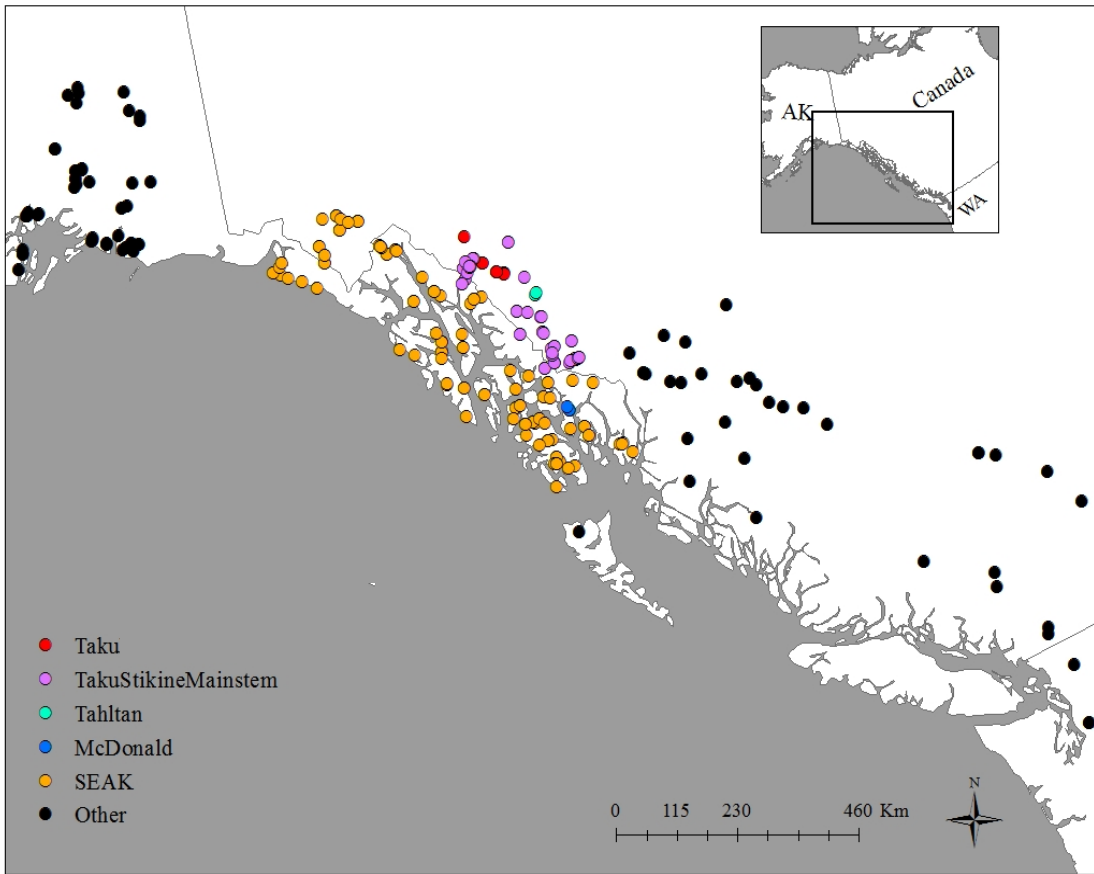


Figure 1. Map of Southeast Alaska sockeye baseline collections used for the 2012 genetic stock identification analysis of harvests in Districts 106 and 108.

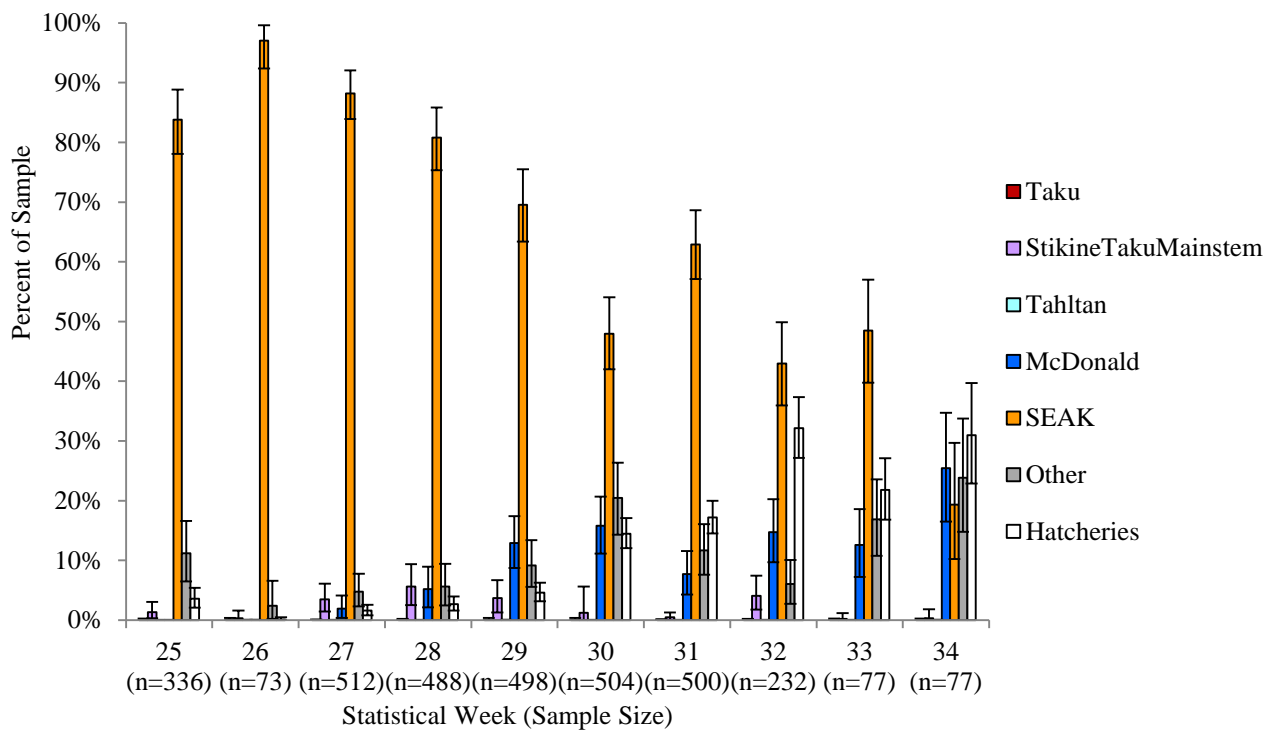


Figure 2. Stock composition estimates of sockeye salmon caught in the District 106-31 gillnet fishery in 2012. Sample size includes genotyped, aged, and otolith-marked fish.

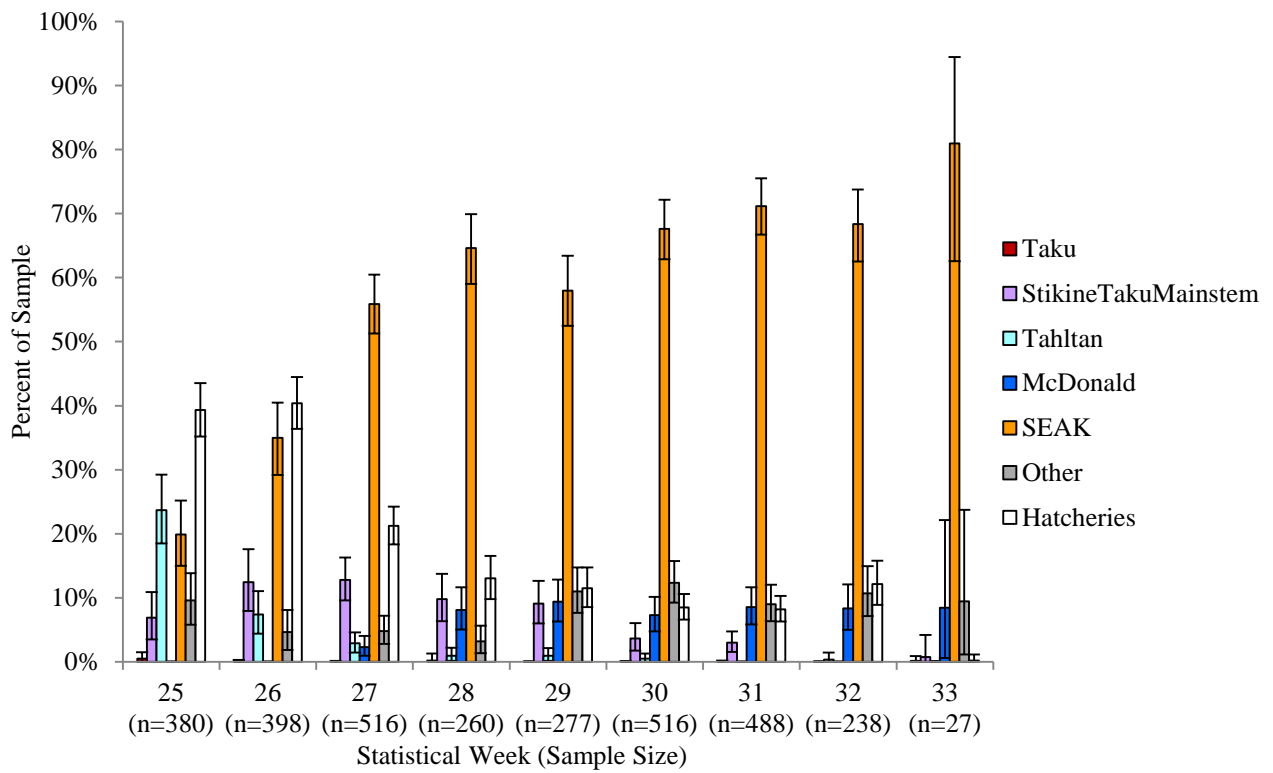


Figure 3. Stock composition estimates of sockeye salmon caught in the District 106-41 gillnet fishery in 2012. Sample size includes genotyped, aged, and otolith-marked fish.

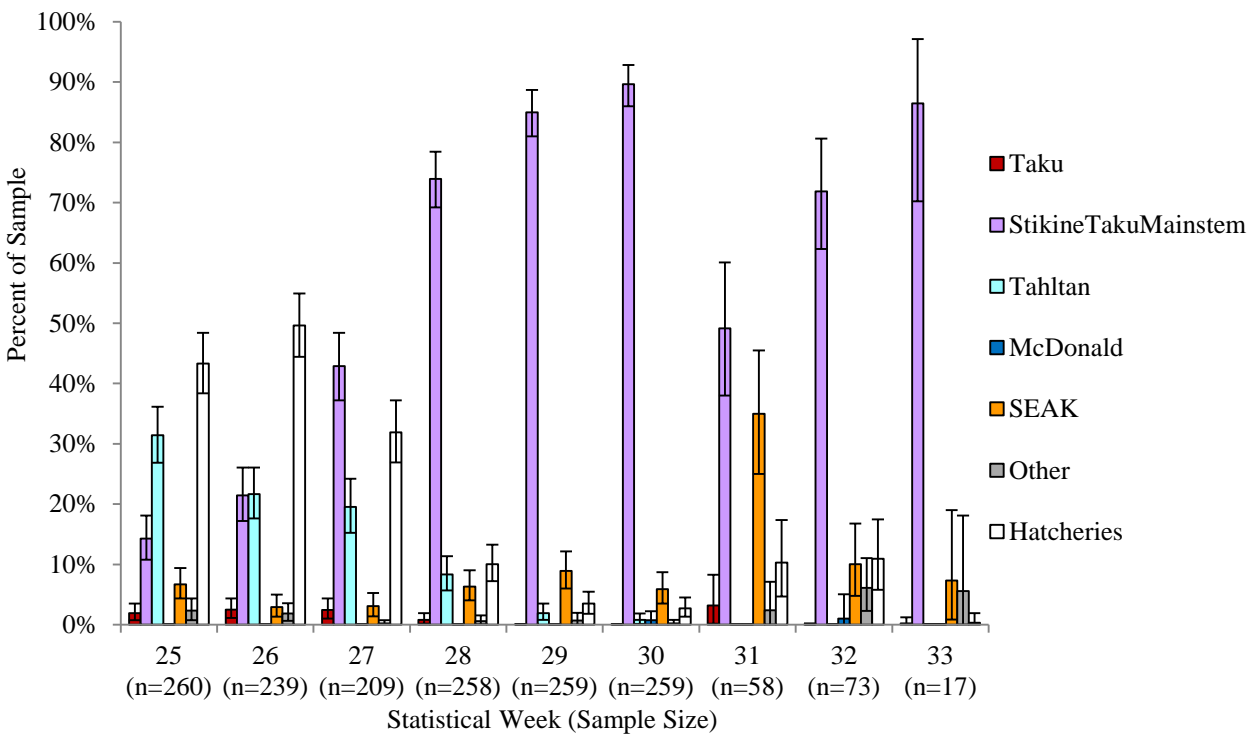


Figure 4. Stock composition estimates of sockeye salmon caught in the District 108 Section A gillnet fishery in 2012. Sample size includes genotyped, aged, and otolith-marked fish.

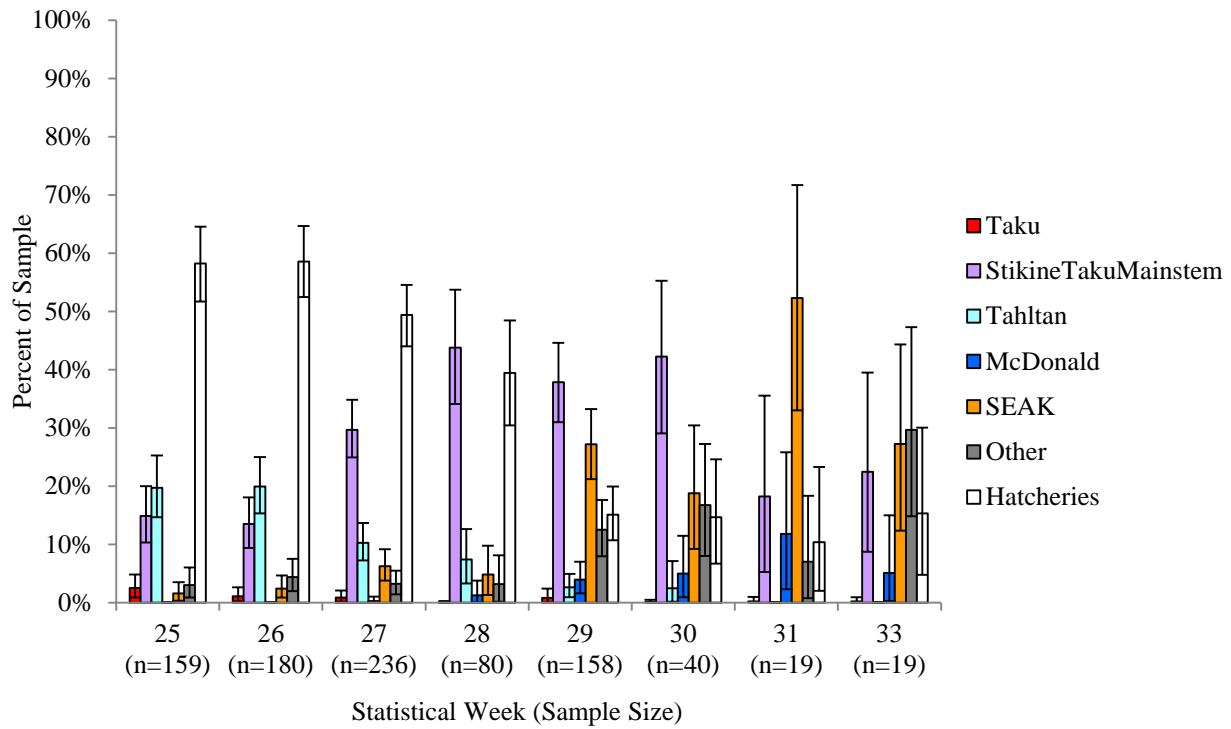


Figure 5. Stock composition estimates of sockeye salmon caught in the District 108 Section B gillnet fishery in 2012. Sample size includes genotyped, aged, and otolith marked fish.

Table 1. Reporting groups and collection locations defined for use in genetic stock identification of sockeye salmon caught in gillnet fisheries in Districts 106 and 108 in 2012.

Reporting Group	Collection Location	Reporting Group	Collection Location
Other	Bainbridge Lake	Southeast Alaska (con't)	Dangerous River
	Coghill Lake		East Alsek River
	Coghill Lake - east stream		Lost/Tahwah Rivers
	Eshamy Creek		Old Situk
	Main Bay		Situk Lake
	Miners Lake		Blanchard River
	Bering Lake		Border Slough
	Clear Creek at 40 Mile		Klukshu River
	Eyak Lake - Hatchery Creek		Kudwat Creek
	Eyak Lake - Middle Arm		Tatshenshi/Kwatini
	Eyak Lake - South beaches		Neskataheen Lake
	Gulkana River - Fish Creek		Tweedsmuir
	Gulkana River - East Fork		Vern Ritchie
	Klutina Lake - inlet		Chilkat Lake - early and late run
	Klutina River - mainstem		Chilkat Mainstem - Mosquito Lk
	Klutina - Banana Lake		Chilkat Mainstem - Bear Flats
			Chilkat Mainstem - Mule Meadows
	Klutina - Bear Hole		Chilkoot Lake - beaches
	Kushtaka Lake		Chilkoot Lake - Bear Creek
	Long Lake weir		Berners Bay
	Mahlo River		Falls Lake - East Baranof Island
	Martin Lake		Neva Lake weir
	Martin River Slough		Sitkoh Lake
	McKinley Lake		Lake Eva
	Bremner - Salmon Creek		Steep Creek
	Bremner - Steamboat Lake		Windfall Lake
	Mendeltna Creek		Ford Arm Lake weir
	Mentasta Lake		Klag Bay Stream outlet
	Paxson Lake - outlet		Kook Lake
	St. Anne Creek		Pavlof Lake
	Swede Lake		Hasselborg Lake
	Tanada Creek weir		Redfish Lake beaches
	Tanada Lake - shore		Salmon Lake weir
Tebay - outlet (Chitina River)	Crescent Lake		
Tokun Lake	Snettisham		
Tonsina Lake	King Salmon Lake weir		
	Little Tatsamenie		
Southeast Alaska	Ahrnklin River	Taku	
	Akwe River		

Table 1 (con't). Reporting groups and collection locations defined for use in genetic stock identification of sockeye salmon caught in gillnet fisheries in Districts 106 and 108 in 2012.

Reporting Group	Collection Location	Reporting Group	Collection Location
Taku (con't)	Tatsamenie Lake	Southeast Alaska	Red Bay Lake
	Little Trapper	(con't)	Salmon Bay Lake
	Kuthai Lake		Unuk River - Gene's Lake
Stikine/Taku	Fish Creek		Bar Creek - Essowah Lake
Mainstem	Yehring Creek		Fillmore Lake - Hoffman Creek
	Tulsequah		Hetta Creek - late run
	Yellow Bluff		Hetta Creek - middle run
	Shustahine		Hetta Creek - early run
	Taku River		Klakas Lake
	Takwahoni/Sinwa		Klawock - Half Mile Creek
	Between Tuskwa and Chunk		Sarkar - Five Finger Creek
	Hackett River		Shipley Lake
	Nahlin River		Eek Creek
	Shakes Slough Creek		Thoms Lake
	Iskut River	Other	Bowser Lake
	Verrett River		Damdochax Creek
	Scud River		Meziadin Beach
	Chutine Lake		Tintina Creek
	Chutine River		Alastair Lake
	Christina Lake		Four Mile Creek
Tahltan	Tahltan Lake, Little Tahltan		Fulton River
McDonald	McDonald Lk - Hatchery Ck		Kitsumkalum Lake
Southeast Alaska	Hugh Smith Lake		Lower Tahlo River
	Hatchery Creek - Sweetwater		McDonell - Zymoetz River
	Heckman Lake		Nangeese River
	Helm Lake		Nanika River
	Kanalku Lake		Slamgeesh River
	Kutlaku Lake		Sustut - Johanson Lake
	Kah Sheets Lake		Swan Lake
	Karta River, McGilvery Creek		Upper Babine River
	Kegan Lake		QCI - Naden River
	Kunk Lake - Etolin Island		Central - Kitlope Lake
	P.O.W. Island - Luck Lake		Adams River - Shuswap late
	P.O.W. Island - Big Lake		Birkenhead
	Mahoney Creek		Chilko Lake
	Mill Creek early - Virginia Lk		Gates Creek
	Petersburg Lake		Harrison River

Table 1 (con't). Reporting groups and collection locations defined for use in genetic stock identification of sockeye salmon caught in gillnet fisheries in Districts 106 and 108 in 2012.

Reporting Group	Collection Location
Other (con't)	Horsefly River
	Raft River
	Stellako River
	Weaver Creek
	Baker Lake
	Issaquah Creek - Puget Sound

Table 2. Number of sockeye salmon sampled from gillnet harvests in the sockeye salmon fisheries in District 106 during 2012 divided by subdistrict, statistical week, samples genotyped, and otolith-marked samples not genotyped.

District	Subdistrict	Statistical Week	Total Samples Collected	Genotypes Used in Analysis	Otolith Marked (Not Genotyped)		
106	30	25	336	75	12		
		26	73	20	0		
		27	512	122	8		
		28	488	112	13		
		29	498	108	23		
		30	504	101	73		
		31	500	109	86		
		32	232	72	75		
		33	174	68	38		
		34	77	21	24		
		41	25	380	61	150	
			26	398	65	161	
			27	516	164	110	
			28	260	174	34	
	29		277	178	32		
	30		516	207	44		
	31		488	201	40		
	32		238	151	29		
	33		27	19	0		
	Totals			6,494	2,028	952	

Table 3. Number of sockeye salmon sampled from gillnet harvests in the sockeye salmon fisheries in District 108 during 2012 divided by subdistrict, statistical week, samples genotyped, and otolith-marked samples not genotyped.

District	Subdistrict	Statistical Week	Total Samples Collected	Genotypes Used in Analysis	Otolith Marked (Not Genotyped)
108	A	25	260	147	113
		26	240	120	119
		27	210	142	67
		28	260	232	26
		29	260	250	9
		30	260	250	7
		31	58	52	6
		32	73	65	8
		33	17	17	0
	B	25	160	65	93
		26	184	74	106
		27	240	117	117
		28	80	48	32
		29	160	132	24
		30	40	34	6
		31	19	17	2
		32	19	16	3
		Totals		2,540	1,778