

PSC Northern Fund Final Report

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Project Title: Genetic stock identification of District 111 sockeye salmon, 2012

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Abstract:

The Taku 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 District 111 by screening 96 single nucleotide polymorphism (SNP) genetic markers in 2,044 sockeye salmon. Recent advances in mixed stock analysis methodologies have allowed the incorporation of otolith marked fish and age composition into genetic-based fishery estimates. The mixed stock analysis model indicated that fish of hatchery origin comprised between 63% and 91% of the harvest in District 111, Subdistrict 31. Taku/Stikine Mainstem and Southeast Alaska were the largest wild stock contributors to harvest in this subdistrict. The mixed stock analysis model indicated that fish of hatchery origin comprised between 2% and 53% of the harvest in District 111, Subdistrict 32 and Taku/Stikine Mainstem, Taku, and Southeast Alaska were the largest wild stock contributors.

Introduction:

The Taku River in Southeast Alaska supports sockeye salmon runs important for various commercial, private, and aboriginal fisheries in both Alaska and Canada. Taku River sockeye salmon are harvested by commercial gillnet fisheries in U.S. District 111, by Alaska personal use fisheries in the river, by Canadian commercial gillnet fisheries, by Canadian recreational fisheries, and by Canadian aboriginal fisheries.

The Alaska District 111 gillnet fishery harvests wild stocks of sockeye salmon primarily bound for several systems in the Taku River or to nearby Crescent and Speel lakes in Alaska. Significant numbers of enhanced sockeye salmon bound for release sites in the Taku River or to Snettisham Hatchery are also caught in the fishery. Catches of Taku River sockeye salmon stocks in District 111 gillnet fishery are subject to a harvest sharing agreement outlined in Annex IV of the Pacific Salmon Treaty, in which the U.S. is allowed to harvest a variable proportion of the total allowable catch of Taku River sockeye salmon depending on the return of enhanced fish. 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) in addition to parasite presence or absence 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 Taku 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 commercial gillnet fisheries in areas in and near the Taku River in Southeast Alaska in 2012. The analysis focused on tissue samples collected in District 111, and replaces SPA for stock estimates in this transboundary river. Estimates are provided for 4 time strata in Subdistrict 111-31 and 9 time strata in Subdistrict 111-32. Estimates are reported as proportions of a single hatchery group and six wild-stock groups: Snettisham, Stikine/Taku Mainstem, Taku, Tahltan, Southeast Alaska, and Other.

Objectives:

The goal of this project was to estimate the stock composition of Southeast Alaska sockeye salmon fisheries near the Taku River in 2012 using GSI. The objective was to determine the stock composition of sockeye harvests from the District 111 drift gillnet fishery by providing estimates for:

- Subdistrict 111-31
 - Age 1.3, 4 time strata;
 - Age 1.2, total season;
- Subdistrict 111-32
 - Age 1.3, 6 time strata; and
 - Age 1.2, total season.

Approach:

Fishery Sampling

Landings from drift gillnet fisheries in Subdistricts 111-31 and 111-32 (District 111) were sampled by ADF&G at fish processing facilities in Juneau. 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 genetic baseline for Southeast Alaska (SEAK) and British Columbia (BC) including 45 SNP 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 additional collections have been analyzed at a total of 96 SNP markers 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 (Applied Biosystems). SNP assays were generally performed using the BioMark 96.96 Dynamic Array (Fluidigm). Re-analyses of failed assays were 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 and subdistrict from the District 111 gillnet fisheries were screened for genetic variation at 96 SNPs for a total of 2,044 samples. For 2012 fisheries, original analysis goals were to provide estimates for age-1.2 and -1.3 sockeye salmon from the harvest over 1 to 6 time strata for each subdistrict, for a grand total of 2,800 samples. However, in order to fully address management needs, which no longer required estimates of separate age groups, estimates were not broken into age-1.2 and -1.3 and instead effort was placed on providing estimates for additional time strata for all ages combined.

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 3,720 sockeye salmon were sampled in the gillnet fisheries in District 111 during 2012 (Table 3). In Subdistrict 111-31, 1,334 samples were taken in statistical weeks 30 through 33. No samples were taken prior to statistical week 30 in this subdistrict due to low numbers of fishers participating in the fishery and pooling of harvest from multiple fishery districts before delivery to processing facilities. In Subdistrict 111-32, 2,386 samples were taken in statistical weeks 25 through 33.

Laboratory analyses

Of the 3,720 samples collected in District 111, 2,044 sockeye salmon were genotyped at 96 SNP genetic markers. Samples were selected relative to commercial fishery harvest. During quality control procedures a total of 606 fish were reanalyzed for all 96 markers for a total of 58,176 comparisons. The average failure rate across collections was 1.8%. The few inconsistencies found (0.4% across all comparisons) were due primarily to scoring errors.

Mixture analysis

Of the samples extracted and genotyped, genotypes from 969 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 and 3. Results are given for six reporting groups consisting of five 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 from the harvest in statistical weeks 25 and 26 in Subdistrict 111-32 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 111-31 fishery sample in 2012 was hatchery-origin fish, between 63% and 92% (Figure 2). Southeast Alaska stocks were present in the fishery samples from District 111-31 between 3% and 14% in statistical weeks 30 through 33. Snettisham contributed 6% or less throughout the sampling season and Stikine/Taku Mainstem contributed 15% or less. The Other, Taku, and Tahltan groups each contributed less than 3% to any fishery sample. In District 111-32, hatchery-origin fish generally increased in their contribution to the fishery samples from 2% in statistical week 25 to 45% in statistical week 33 (Figure 3). Southeast Alaska stocks were present in the fishery sample between 0% and 23%. Snettisham contributed 5% or less throughout the sampling season and Stikine/Taku Mainstem contributed between 19% and 46%. The Other group contributed less than 1% throughout the entire season. The Taku contribution to the fishery sample generally decreased from 44% to 12% throughout the season but peaked in contribution at 71% to the fishery sample in statistical week 27. Tahltan contributed 7% or less to the fishery samples throughout the season.

Evaluation:

We accomplished the following:

- A total of 3,720 sockeye salmon were sampled from District 111 gillnet fisheries during 2012 season.

- A total of 2,044 samples of sockeye salmon 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 6 reporting groups as well as otolith marked sockeye salmon to 4 temporal strata in Subdistrict 31 and 9 temporal strata in Subdistrict 32.

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: January 20, 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.

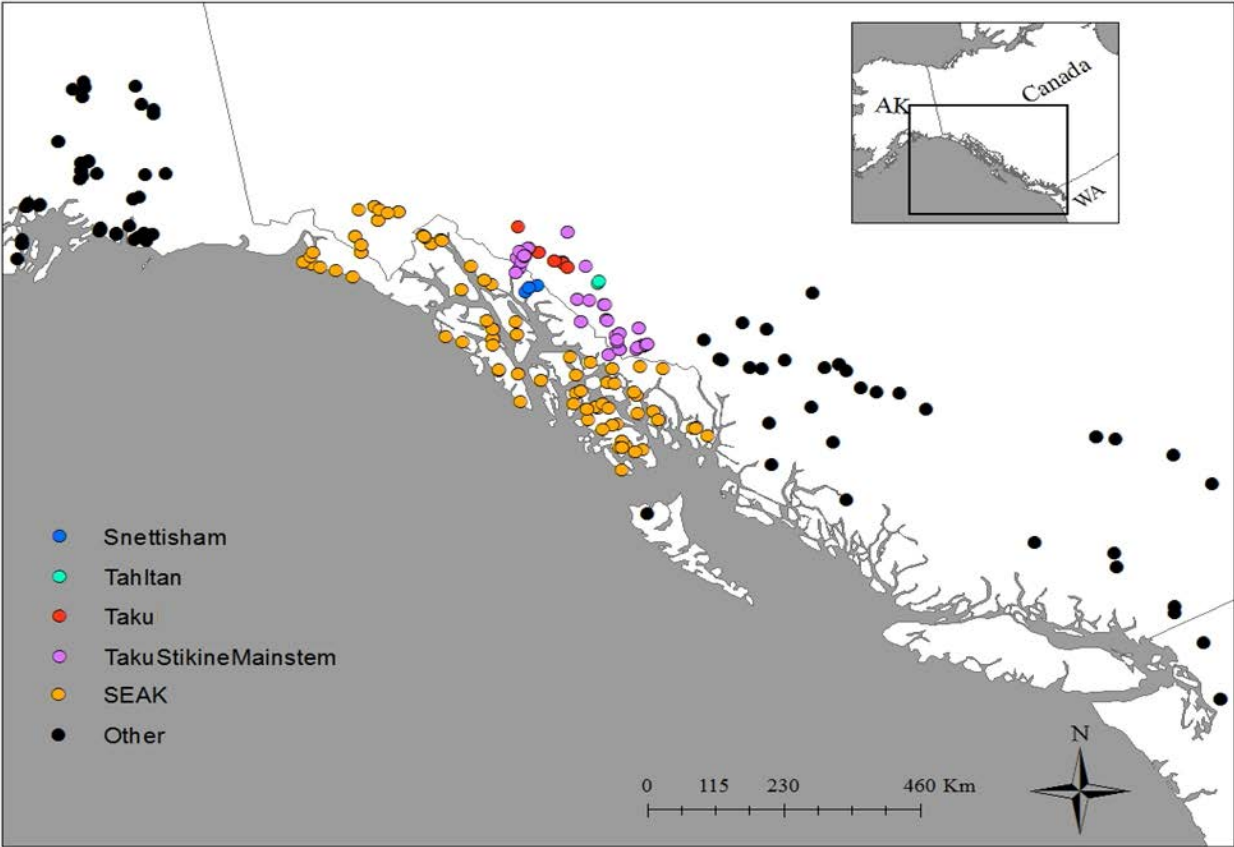


Figure 1. Map of Southeast Alaska sockeye baseline collections used for the 2012 genetic stock identification analysis of harvests in District 111.

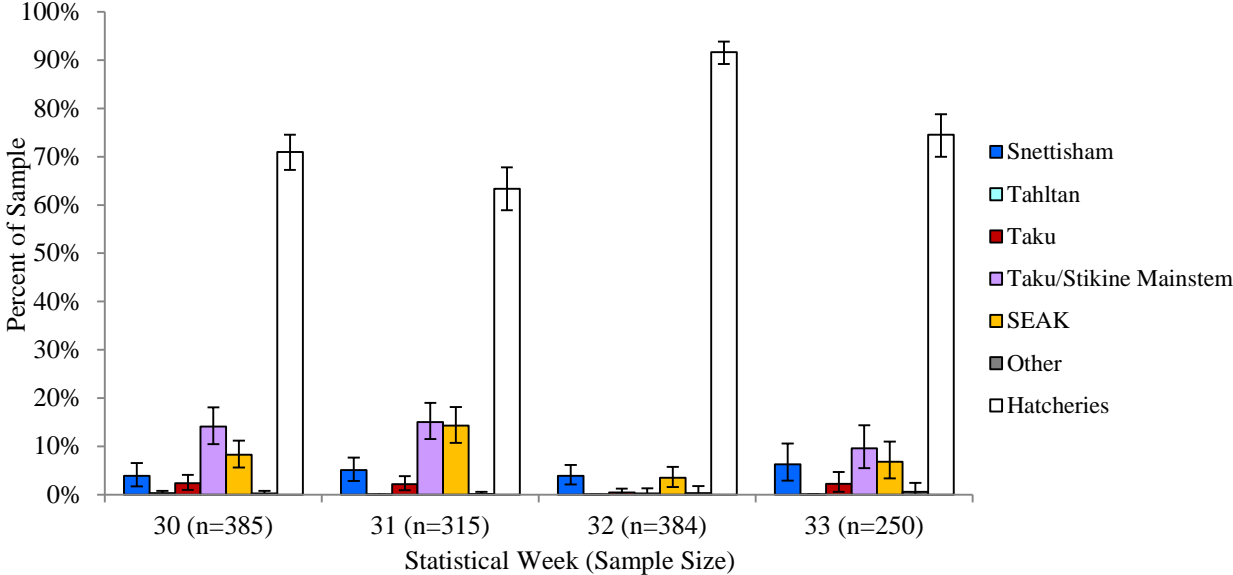


Figure 2. Stock composition estimates of sockeye salmon caught in the District 111-31 gillnet fishery in 2012. Sample size includes genotyped, aged, and otolith-marked fish.

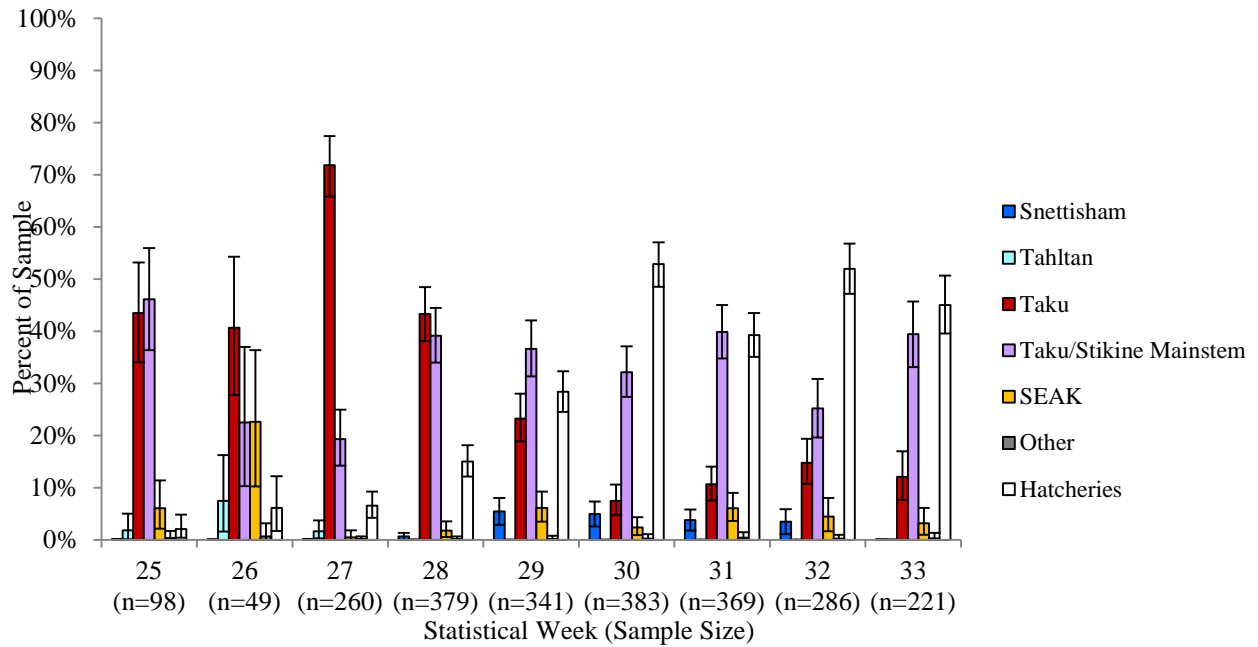


Figure 3. Stock composition estimates of sockeye salmon caught in the District 111-32 gillnet fishery in 2012. Sample size includes genotyped, aged, and otolith-marked fish.

Table 1. Reporting groups and collection locations defined for use in genetic stock identification of sockeye salmon caught in gillnet fisheries in District 111 in 2012.

Reporting Group	Collection Location	Reporting Group	Collection Location
Other	Bainbridge Lake	Southeast Alaska (cont.)	Tatshenshini
	Coghill Lake		Neskataheen Lake
	Coghill Lake - east side stream		Tweedsmuir
	Eshamy Creek		Vern Ritchie
	Main Bay		Chilkat Lake - early and late run
	Miners Lake		Chilkat Mainstem - Mosquito Lake
	Bering Lake		Chilkat Mainstem - Bear Flats
	Clear Creek at 40 Mile		Chilkat Mainstem - Mule Meadows
	Eyak Lake - Hatchery Creek		Chilkoot Lake - beaches
	Eyak Lake - Middle Arm		Chilkoot Lake - Bear Creek
	Eyak Lake - South beaches		Berners Bay
	Gulkana River - Fish Creek		Falls Lake - East Baranof Island
	Gulkana River - East Fork		Neva Lake weir
	Klutina Lake - inlet		Sitkoh Lake
	Klutina River - mainstem		Lake Eva
	Klutina - Banana Lake		Steep Creek
	Klutina - Bear Hole		Windfall Lake
	Kushtaka Lake		Ford Arm Lake weir
	Long Lake weir		Klag Bay Stream outlet
	Mahlo River		Kook Lake
	Martin Lake		Pavlof Lake
	Martin River Slough		Hasselborg Lake
	McKinley Lake		Redfish Lake beaches
	Bremner - Salmon Creek		Salmon Lake weir
	Bremner - Steamboat Lake		Port Snettisham
	Mentasta Lake		Crescent Lake
	Paxson Lake - outlet		Taku
	St. Anne Creek		King Salmon Lake weir
	Mendeltna Creek		Little Tatsamenie
	Swede Lake		Tatsamenie Lake
	Tanada Creek - weir		Little Trapper
	Tanada Lake - shore		Kuthai Lake
	Tebay - Outlet/Mouth (Chitina)		Taku/Stikine Mainstem
	Tokun Lake		Fish Creek
	Tonsina Lake		Yehring Creek
	Southeast Alaska	Ahrnklin River	Tulsequah
Akwe River		Yellow Bluff	
Dangerous River		Shustahine	
East Alsek River		Taku River	
Lost/Tahwah Rivers		Takwahoni/Sinwa	
Old Situk		Between Tuskwa and Chunk	
Situk Lake		Hackett River	
Blanchard River		Nahlin River	
Border Slough		Shakes Slough Creek	
Klukshu River		Iskut River	
Kudwat Creek		Verrett River	
		Scud River	
	Chutine Lake		

(continued)

Table 2 (con't). Reporting groups and collection locations defined for use in genetic stock identification of sockeye salmon caught in gillnet fisheries in District 111 in 2012.

Reporting Group	Collection Location	Reporting Group	Collection Location
Taku/Stikine Mainstem (cont.)	Chutine River	Other (cont.)	Alastair Lake
Tahltan	Christina Lake		Four Mile Creek
Southeast Alaska	Tahltan Lake/ Little Tahltan		Fulton River
	Hugh Smith Lake		Kitsumkalum Lake
	Hatchery Creek - McDonald		Lower Tahlo River
	Hatchery Creek - Sweetwater		McDonnell - Zymoetz River
	Heckman Lake		Nangeese River
	Helm Lake		Nanika River
	Kanalku Lake		Slamgeesh River
	Kutlaku Lake		Johanson Lake - Sustut
	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 - Virginia Lake		Gates Creek
	Petersburg Lake		Harrison River
	Red Bay Lake		Horsefly River
	Salmon Bay Lake		Raft River
	Unuk River - Gene's Lake		Stellako River
	Bar Creek - Essowah Lake		Weaver Creek
	Fillmore Lake - Hoffman Creek		Baker Lake
	Hetta Creek - late run		Issaquah Creek - Puget Sound
	Hetta Creek - middle run		
	Hetta Creek - early run		
	Klakas Lake		
	Klawock - Half Mile Creek		
	Sarkar - Five Finger Creek		
	Shipley Lake		
	Eek Creek		
	Thoms Lake		
Other	Bowser Lake		
	Damdochax Creek		
	Meziadin Beach		
	Tintina Creek		

Table 3. Number of sockeye salmon sampled from gillnet harvests in the sockeye salmon fisheries in Districts 111 during 2012 divided by Subdistrict, Statistical Week, samples genotyped, and otolith-marked samples not genotyped. Some samples collected were not genotyped and also did not have an otolith mark.

District	Subdistrict	Statistical Week	Total Samples Collected	Genotyped	Otolith Marked (Not Genotyped)
111	31	30	385	65	274
		31	315	77	200
		32	384	12	353
		33	250	24	187
	32	25	98	54	2
		26	49	25	3
		27	260	112	17
		28	379	152	57
		29	341	140	97
		30	383	90	203
		31	369	112	145
		32	286	57	149
		33	221	49	100
		Totals			3,720