

PSC Northern Fund Final Report

Project Number: NF-2013-I-11 (COOP 14-002)

Project Title: Genetic Stock Identification of District 111 sockeye salmon, 2013

Project Manager: Sara Gilk-Baumer and Serena Rogers Olive, Alaska Dept. of Fish and Game - Gene Conservation Laboratory, (907) 267-2535, sara.gilk@alaska.gov

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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 use of mark- and age-enhanced genetic stock identification (GSI) of sockeye salmon harvested in the 2013 gillnet fishery in District 111 by screening 96 single nucleotide polymorphic genetic markers in 1,455 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 Taku Lakes origin fish were the largest contributors in the District 111 fisheries in 2013, followed by Stikine/Taku Mainstem fish. Enhanced Snettisham, Enhanced Tatsamenie, and Snettisham Wild were important contributors only later in the season. The most common age group was age-1.3; the Taku Lakes reporting group was dominated by age-1.3 fish, while the Stikine/Taku Mainstem reporting group was comprised of both age-1.3 and 0-check fish.

Introduction:

The Taku River in Southeast Alaska supports sockeye salmon runs important for various commercial 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 Crescent and Speel lakes in Port Snettisham, 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, in which the U.S. is allowed to harvest a variable proportion of the Total Allowable Catch of Taku River sockeye 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), 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 slightly 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 2013 commercial gillnet fisheries in areas near the Taku River in SEAK. The analysis focused on tissue samples collected in District 111, and replaces SPA for stock estimates in this transboundary river. Estimates are provided over the entire season for all age groups, for 7 time strata for all age groups, and over the entire season for 6 age groups. Estimates are reported as proportions of eight reporting groups consisting of three reporting groups of Taku area wild fish (Stikine/Taku Mainstem, Taku Lakes, and Snettisham Wild), three reporting groups of Taku area hatchery-origin fish (Enhanced Tatsamenie, Enhanced Tuya, and Enhanced Snettisham), one reporting group of Stikine hatchery-origin fish (Enhanced Stikine), and one reporting group that includes all other fish in the baseline (Other).

Objectives:

The goal of this project was to estimate the stock composition of Southeast Alaska sockeye fisheries near the Taku River in 2013 using genetic stock identification. Original objectives were to:

- Determine the stock composition of sockeye harvests from the District 111 drift gillnet fishery. For 2013, provide estimates for:
 - Subdistrict 111-31
 - All ages, 3 time strata;
 - Subdistrict 111-32
 - All ages, 4 time strata.

These analysis objectives were modified slightly post-season and additional goals were added to meet current needs of managers (see below).

Approach:

Fishery Sampling

Landings from drift gillnet fisheries in District 111 were sampled by ADF&G at fish processing facilities in Juneau and by observers on tenders. 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. Associated data 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 most recent version of the baseline includes 128 populations and 96 markers (populations: Figure 1, Table 1; markers: see Dann et al. 2012). A baseline update is currently in progress and will include an additional 50 populations; this baseline is expected to be completed in January 2015.

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 from DNA extraction forward 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

For 2013 fisheries, original analysis goals were to provide estimates for 1) Subdistrict 111-31, all ages, 3 time strata; and 2) Subdistrict 111-32, all ages, 4 time strata. Post-season conversations with fishery managers clarified management needs and project objectives were modified. First, managers indicated that it would not be useful to generate separate estimates for Subdistricts 111-31 and 111-32. Thus, although samples were analyzed to provide separate estimates, they were weighted by harvest and combined to give total District 111 estimates. Second, managers felt that additional estimates would be useful: 1) District 111, total season estimate weighted by harvest by subdistrict and statistical week, and 2) District 111, total season, by age groups including ages-1.2, -1.3, -2.2, -2.3, 0-checks, and other. A total of 9 separate estimates were made for the 2013 fisheries (7 were proposed).

In addition to changes in analysis goals, methods for mixture analysis have improved since the inception of this project. Mixture analyses can now 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- and 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 weighted by harvest per stratum; 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; thus only wild fish were genotyped for 2013 fisheries.

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 40,000 repetitions, discarding the first 20,000 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 are given for eight reporting groups consisting of three reporting groups of Taku area wild fish (Stikine/Taku Mainstem, Taku Lakes, and Snettisham Wild), three reporting groups of Taku area hatchery-origin fish (Enhanced Tatsamenie, Enhanced Tuya, and Enhanced Snettisham), one reporting group of Stikine hatchery-origin fish (Enhanced Stikine), and one reporting group that includes all other fish in the baseline (Other).

Results/Findings:

Fishery sampling

A total of 3,287 sockeye salmon were sampled in the gillnet fisheries in District 111 during 2013 (Table 2). These fish were sampled from statistical weeks 25 through 31.

Laboratory analyses

Of the samples collected in District 111, 1,455 samples were genotyped at 96 SNP genetic markers. During quality control procedures a total of 122 fish were reanalyzed at all 96 markers for a total of 11,712 comparisons. The average failure rate was 1.98%. Few inconsistencies were found (0.32% across all comparisons).

Mixture analysis

Mixtures of fish representing catches by statistical week, age group, and subdistrict from the District 111 gillnet fishery were analyzed. Of the samples extracted and genotyped, genotypes from 1,455 wild fish (no otolith mark present) were used for the genetic analyses in the mark-and-age-enhanced GSI method. Stock composition estimates can be found in Figures 2–5. Total season estimates were made for each subdistrict or district by age class and over all ages, and were weighted by harvest in each stratum. In addition, 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. All of these estimates met the minimum criteria for precision and accuracy accepted

by the Pacific Salmon Commission (PSC) Transboundary Technical Committee (within 10% of the true mixture 90% of the time).

The majority of the overall harvest in District 111 in 2013 was of Taku-origin fish. The greatest contributor was the Taku Lakes reporting group (33%), followed by the Stikine/Taku Mainstem reporting group (29%; Figure 2). The Enhanced Snettisham reporting group was also an important contributor (15%), followed by the Enhanced Tatsamenie and Snettisham Wild reporting groups (each 9%). The remaining reporting groups were absent or present at low proportions (<5%).

Stock composition in District 111 varied by statistical week as the 2013 season progressed. Early in the season, the Taku Lakes reporting group dominated catches from statistical weeks 25–28 (range: 47–67%; Figure 3). Later in the season, the Enhanced Snettisham and Enhanced Tatsamenie reporting groups were important contributors from statistical weeks 29–31 (ranges: 22–27% and 9–20%, respectively). The Snettisham Wild reporting group was present in statistical weeks 27–31, peaking at 17% in week 30. The Stikine/Taku Mainstem reporting group was a consistent and important contributor throughout the season (range: 27–32%).

The most common age group throughout the 2013 season in District 111 was age-1.3 (69% of total; Figure 4). This age group was the largest component of all major contributing stocks. The catch also consisted of age-1.2 (11%), 0-checks (11%), and age-2.3 (7%). All other age groups were present at <5%.

There were some differences in age composition amongst reporting groups (Figure 5). The Taku Lakes reporting group consisted of primarily age-1.3 fish (79%), followed by age-2.3 (13%). The Sitkine/Taku Mainstem reporting group consisted of age-1.3 and 0-check fish (57% and 34%, respectively). Age-1.3 dominated the Enhanced Tatsamenie and Snettisham Wild stocks (97% and 81%, respectively), while both age-1.3 and age-1.2 were important age groups in the Enhanced Snettisham stock (55% and 45%, respectively). The Enhanced Trapper reporting group appeared to be dominated by age-2.3 fish (85%); however, this reporting group was not common in the harvest and thus sample sizes are small.

Evaluation:

We accomplished the following:

- A total of 3,287 sockeye salmon were sampled from District 111 gillnet fisheries during the 2013 season.
- A total of 1,455 samples from District 111 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 8 reporting groups including Taku-area wild and enhanced sockeye salmon to 7 temporal strata in District 111.
- Mixture analyses estimated the age compositions of harvests over the entire season in District 111 for 8 reporting groups.
- Mixture analyses estimate the seasonal stock composition over all ages for District 111 for 8 reporting groups.

- In total, 9 separate estimates are provided for Taku area fisheries in 2013 (7 were proposed).
- The improved methodology (mark- and age-enhanced GSI) has allowed us to combine several sources of data when estimating stock composition in District 111 for PST purposes. In the past, GSI was conducted on only wild fish, and stock composition estimates for enhanced fish were conducted in a separate analysis using otolith and other data. This approach allows us to combine these analyses to provide the most accurate and efficient estimates possible for Taku area fisheries. Work is currently underway to continue to improve this methodology to provide reliable estimates for statistical weeks where low sample sizes could be an issue.
- Results will be incorporated into harvest estimates for PST purposes by the Transboundary Technical Committee (TTC *in prep*).

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 multi-year (2011-2013) report published in the ADF&G Fishery Data Series is expected in 2015.

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References:

Dann, T. H., C. Habicht, J. R. Jasper, E. K. C. Fox, H. A. Hoyt, H. L. Liller, E. S. Lardizabal, P. A. Kuriscak, Z. D. Grauvogel, and W. D. Templin. 2012. Sockeye salmon baseline for the Western Alaska Salmon Stock Identification Project. Alaska Department of Fish and Game, Special Publication No. 12-12, Anchorage.

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.

TTC (Transboundary Technical Committee). *In prep*. Estimates of Transboundary River salmon production, harvest and escapement, and a review of joint enhancement activities in 2013. Pacific Salmon Commission Report TCTR, Vancouver.

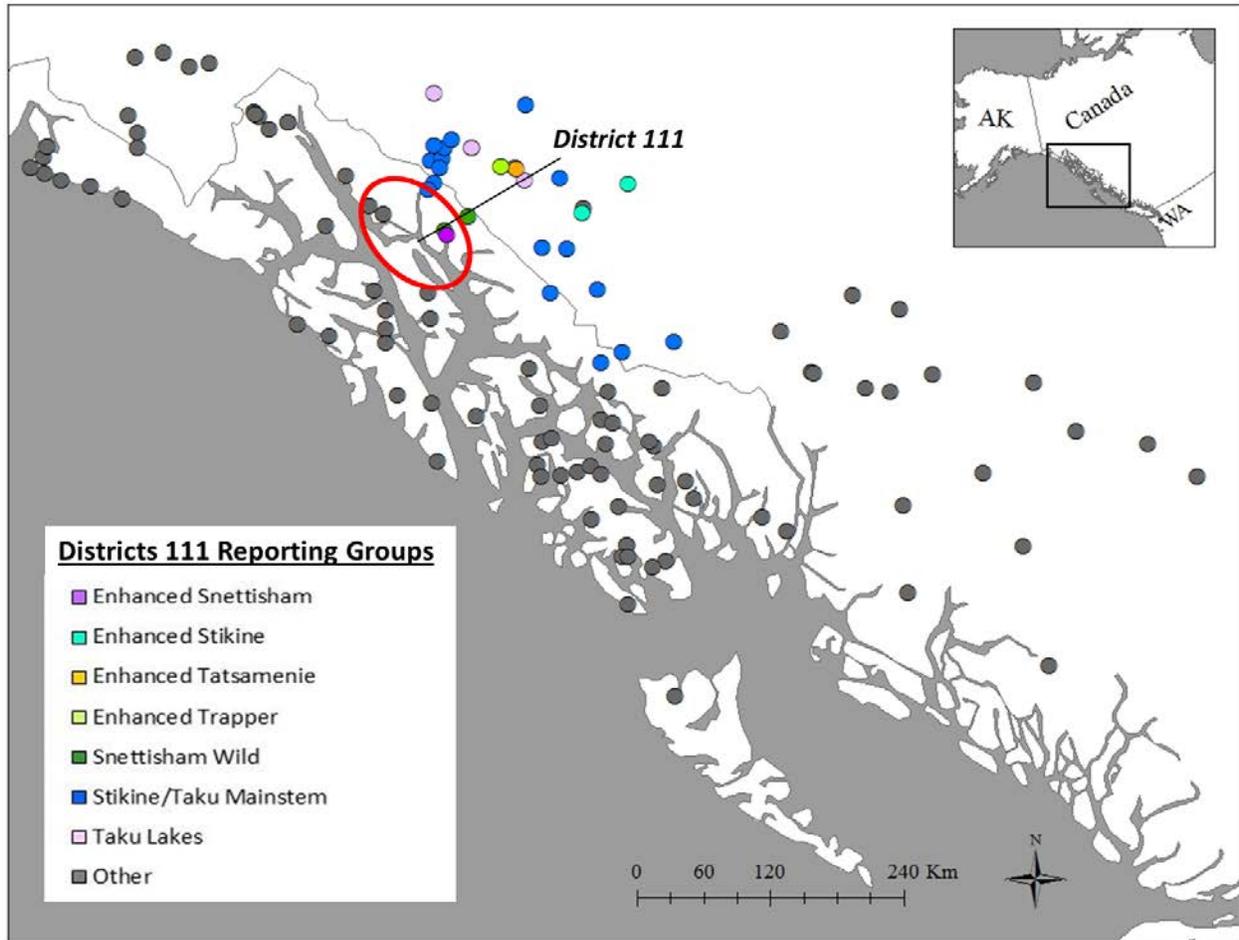


Figure 1. Map of Southeast Alaska sockeye baseline collections used for the 2013 genetic stock identification analysis of harvests in District 111, and fishery location.

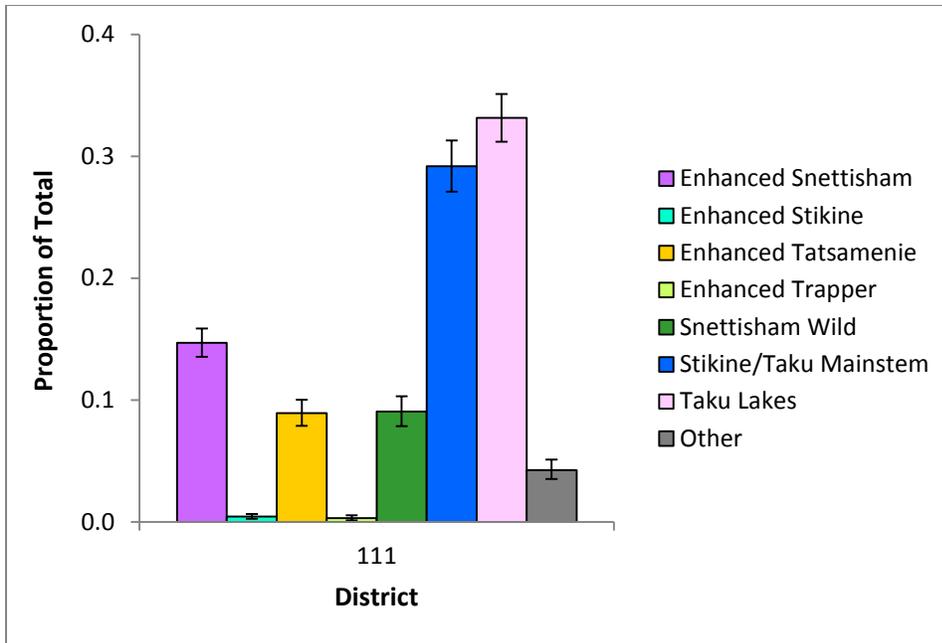


Figure 2. Total season stock composition estimates for Taku River area fisheries. Estimates were weighted by harvest per strata.

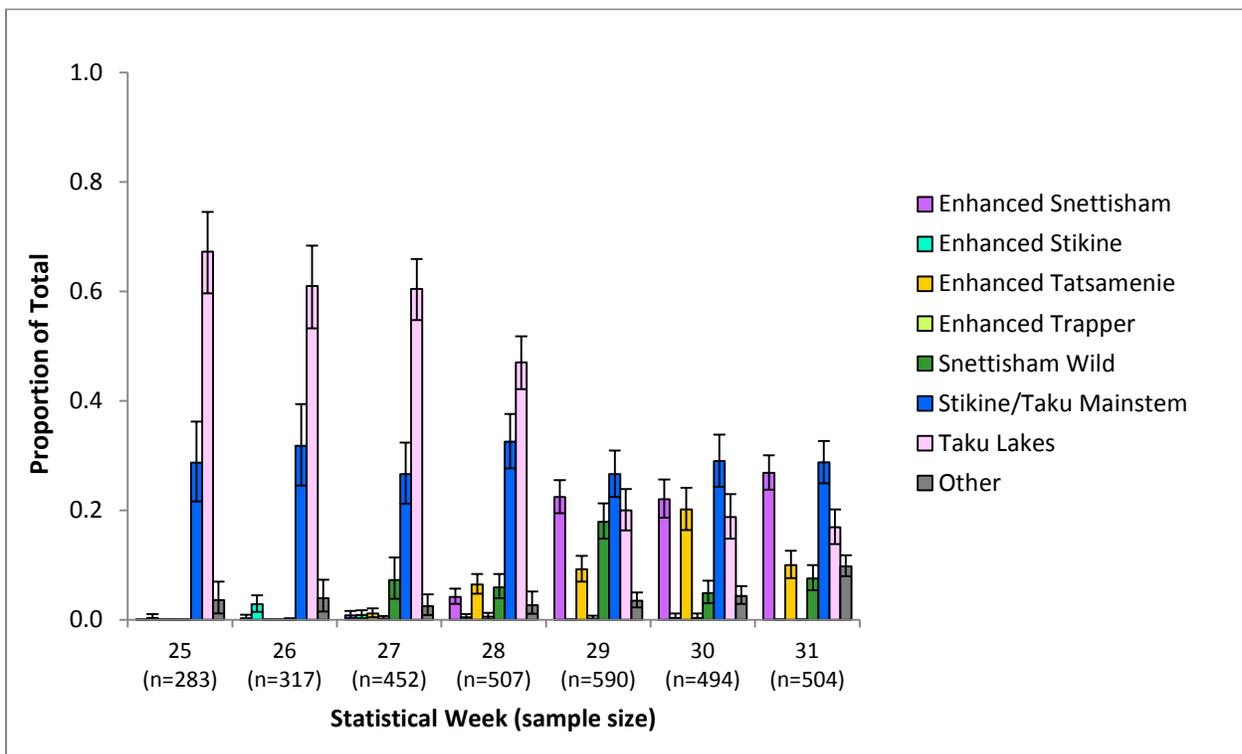


Figure 3. Stock composition estimates of sockeye salmon caught in the District 111 gillnet fishery in 2013. Sample size (n) includes genotyped, aged, and otolith-marked fish.

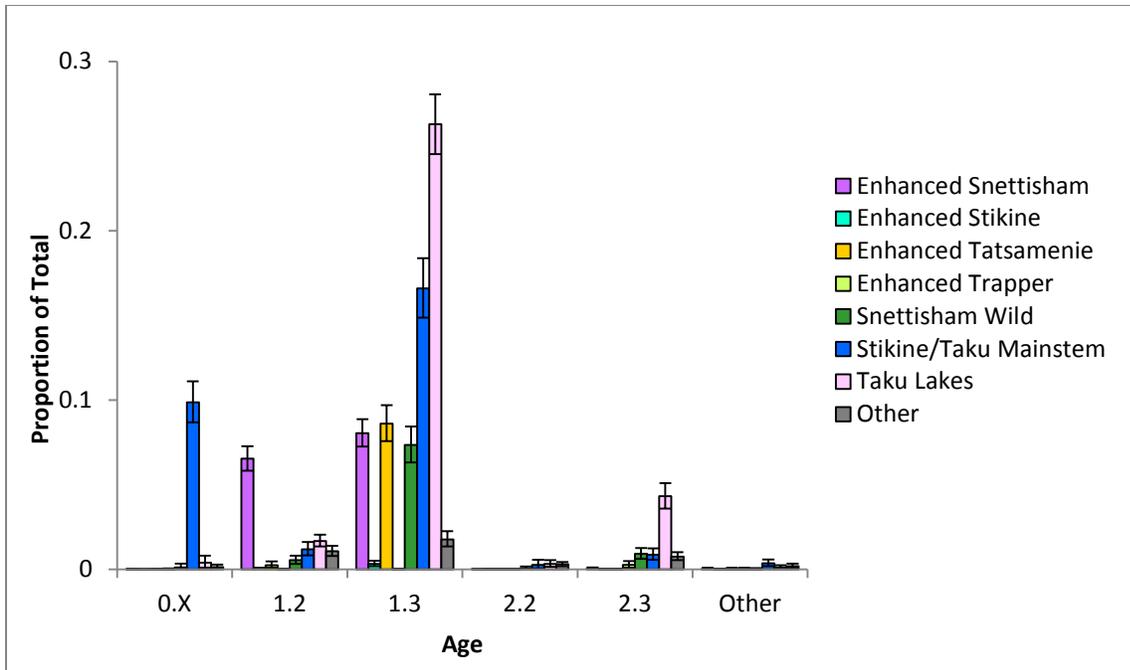


Figure 4. Age composition of sockeye salmon caught in the District 111 gillnet fishery in 2013 over the entire season.

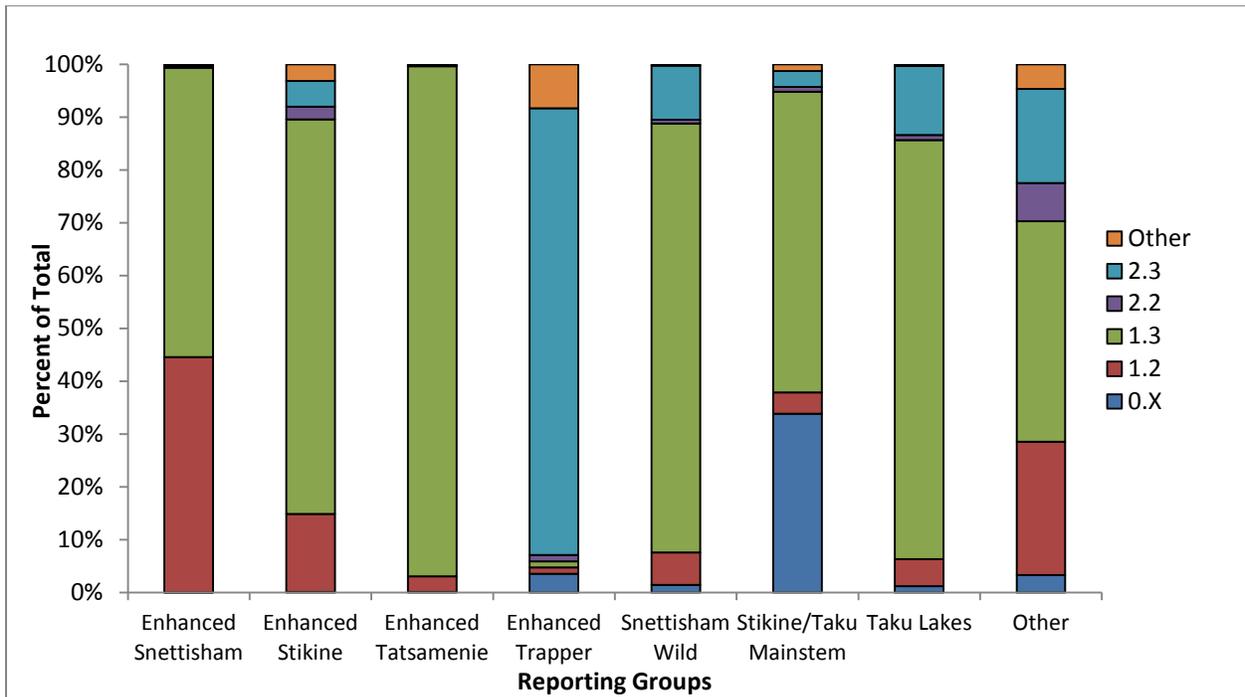


Figure 5. Age composition by reporting group of sockeye caught in the District 111 gillnet fishery in 2013.

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 2013. Wild collections are ordered north to south and followed by enhanced collections ordered alphabetically.

Reporting Group	Collection Location	Reporting Group	Collection Location
<i>Non-Stikine</i>	Ahrnklin River	<i>Stikine/Taku Mainstem</i> (cont.)	Scud River
	Akwe River		Chutine Lake
	Dangerous River	Chutine River	
	East Alsek River	Christina Lake	
	Lost/Tahwah Rivers	<i>Tahltan Wild</i> <i>Non-Stikine</i>	Tahltan Lake, Little Tahltan
	Old Situk		Hugh Smith Lake
	Situk Lake		McDonald - Hatchery Ck
	Blanchard River		Hatchery Ck - Sweetwater
	Border Slough		Heckman Lake
	Klukshu River		Helm Lake
	Kudwat Creek		Kanalku Lake
	Tatshenshi/Kwatini		Kutlaku Lake
	Neskataheen Lake		Kah Sheets Lake
	Tweedsmuir		Karta R, McGilvery Ck
	Vern Ritchie	Kegan Lake	
	Chilkat Lake - early and late run	Kunk Lake - Etolin Island	
	Chilkat Mainstem - Mosquito Lk	P.O.W. Island - Luck Lake	
	Chilkat Mainstem - Bear Flats	P.O.W. Island - Big Lake	
	Chilkat Mainstem - Mule Mead.	Mahoney Creek	
	Chilkoot Lake - beaches	Mill Ck early - Virginia Lk	
	Chilkoot Lake - Bear Creek	Petersburg Lake	
	Berners Bay	Red Bay Lake	
	Falls Lake - East Baranof Island	Salmon Bay Lake	
	Neva Lake weir	Unuk River - Gene's Lake	
	Sitkoh Lake	Bar Creek - Essowah Lake	
	Lake Eva	Fillmore Lk - Hoffman Ck	
	Steep Creek	Hetta Creek - late run	
	Windfall Lake	Hetta Creek - middle run	
	Ford Arm Lake weir	Hetta Creek - early run	
	Klag Bay Stream outlet	Klakas Lake	
	Kook Lake	Klawock - Half Mile Creek	
	Pavlof Lake	Sarkar - Five Finger Creek	
	Hasselborg Lake	Shiple Lake	
	Redfish Lake beaches	Salmon Bay Lake	
	Salmon Lake weir	Unuk River - Gene's Lake	
	Crescent Lake	Bar Creek - Essowah Lake	
	Snettisham	Fillmore Lk - Hoffman Ck	
	King Salmon Lake weir	Hetta Creek - late run	
	Little Tatsamenie	Hetta Creek - middle run	
	Tatsamenie Lake	Hetta Creek - early run	
	Little Trapper	Klakas Lake	
	Kuthai Lake	Klawock - Half Mile Creek	
	<i>Stikine/Taku Mainstem</i>	Fish Creek	Sarkar - Five Finger Creek
		Yehring Creek	Shiple Lake
		Tulsequah	Eek Creek
		Yellow Bluff	Thoms Lake
		Shustahine	Bowser Lake
Taku River		Damdochax Creek	
Takwahoni/Sinwa		Meziadin Beach	
Betw Tuskwa and Chunk		Tintina Creek	
Hackett River		Alastair Lake	
Nahlin River		Four Mile Creek	
Shakes Slough Creek	Fulton River		
Iskut River	Kitsumkalum Lake		
Verrett River	Lower Tahlo River		
Scud River	McDonnell - Zymoetz River		

-continued-

Table 1 (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 2013. Wild collections are ordered north to south and followed by enhanced collections ordered alphabetically.

Reporting Group	Collection Location
<i>Non-Stikine (cont.)</i>	Nangeese River
	Nanika River
	Slangeesh River
	Sustut - Johanson Lake
	Swan Lake
	Upper Babine River
	QCI - Naden River
	Central - Kitlope Lake
	Adams River - Shuswap late
	Birkenhead
	Chilko Lake
	Gates Creek
	Harrison River
	Horsefly River
	Raft River
	Stellako River
	Weaver Creek
	Baker Lake
	Issaquah Creek - Puget Sound
	Enhanced - Burnett Inlet
Enhanced - Main Bay	
Enhanced - McDonald	
Enhanced - Sweetheart	
Enhanced - Speel Arm	
Enhanced - Tatsamenie	
Enhanced - Trapper	
<i>Enhanced Tahltan</i>	Enhanced - Tahltan
<i>Enhanced Tuya</i>	Enhanced - Tuya

Table 2. Number of sockeye salmon sampled from District 111 sockeye gillnet harvests during each statistical week in 2013, samples genotyped, and otolith-marked or aged samples not genotyped for each statistical week. Samples were weighted by harvest for total season estimates.

District	Statistical Week	Total Samples Collected	Genotypes Used in Analysis	Not Genotyped (otolith-marked or aged or both)
111	25	285	99	186
	26	349	100	217
	27	480	231	221
	28	520	281	226
	29	620	295	299
	30	500	170	327
	31	533	279	227
Totals		3,287	1,455	1,703