

PSC Northern Fund Final Report

Project Number: NF-2014-I-9 (COOP 14-002)

Project Title: Genetic Stock Identification of District 111 sockeye salmon, 2014

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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 2014 gillnet fishery in District 111 by screening 96 single nucleotide polymorphic genetic markers in 1,432 salmon. Advances in mixed stock analysis methodologies allowed the incorporation of hatchery-marked fish and age composition into genetic-based fishery estimates. The mixed stock analysis model indicated that the *Enhanced Snettisham* reporting group was the largest contributor in the District 111 fisheries in 2014, followed by the *Stikine/Taku Mainstem* reporting group. The *Taku Lakes* and *Stikine/Taku Mainstem* groups were more prevalent early in the season, while the *Enhanced Snettisham* group dominated the latter part of the season. The most common age groups were ages-1.2 and -1.3; the *Enhanced Snettisham* reporting group was dominated by age-1.2 fish, while the *Stikine/Taku Mainstem* reporting group was comprised of both age-1.3 and 0.x fish.

Introduction:

The Taku River in Southeast Alaska (SEAK) 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 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), 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 (GSI) 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 of sockeye salmon tissue samples collected from commercial gillnet fisheries in areas near the Taku River in 2014. The analysis focused on tissue samples collected in District 111, and replaces SPA for estimating stock composition of harvests near this transboundary river. Estimates are provided over the entire season for all age groups, for 9 time strata for all age groups, and over the entire season for 6 age groups. Estimates are reported as proportions of 8 reporting groups consisting of 4 groups of Taku-area wild fish (*Stikine/Taku Mainstem*, *Taku Lakes*, *Tatsamenie Wild*, and *Speel Wild*), 2 groups of Taku-area hatchery-origin fish (*Enhanced Tatsamenie* and *Enhanced Snettisham*), one group of Stikine hatchery-origin fish (*Enhanced Stikine*), and one group that includes all other fish in the baseline (*Other*).

Objectives:

The objective of this project was to estimate the stock composition of SEAK sockeye salmon fisheries near the Taku River in 2014 using GSI. Identified tasks were to:

- Determine the stock composition of sockeye salmon harvests from the District 111 drift gillnet fishery. For 2014, 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 current genetic baseline includes 171 populations and 96 markers (Table 1; Rogers Olive et al. *in prep*).

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 from 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 2014 fisheries, original analysis goals were to provide estimates for 1) Subdistrict 111-31, all ages, 200 samples per 3 weeks, 3 time strata, for a total of 600 samples; and 2) Subdistrict 111-32, all ages, 200 samples per 2 weeks, 4 time strata, for a total of 800 samples; grand total of 1,400 samples. 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.x, and other ages. A total of 11 separate estimates were made for the 2014 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 2014 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 8 reporting groups consisting of 4 groups of Taku-area wild fish (*Stikine/Taku Mainstem*, *Taku Lakes*, *Tatsamenie Wild*, and *Speel Wild*), 2 groups of Taku-area hatchery-origin fish (*Enhanced Tatsamenie* and *Enhanced Snettisham*), one group of Stikine hatchery-origin fish (*Enhanced Stikine*), and one group that includes all other fish in the baseline (*Other*).

Results/Findings:

Fishery sampling

A total of 4,955 sockeye salmon were sampled in the gillnet fisheries in District 111 during 2014 (Table 2). These fish were sampled from statistical weeks 25 through 32, and in statistical week 34.

Laboratory analyses

Of the samples collected in District 111, 1,432 samples were genotyped at 96 SNP genetic markers. During quality control procedures a total of 120 fish were reanalyzed at all 96 markers for a total of 11,520 comparisons. The average failure rate was 1.36%. Few inconsistencies were found (0.49% 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 1,432 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 1–4. 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 greatest contributor to the overall harvest in District 111 in 2014 was the *Enhanced Snettisham* reporting group (41%), followed by the *Stikine/Taku Mainstem* reporting group (29%; Figure 1). The *Other* reporting group was also an important contributor (16%), followed by the *Taku Lakes* reporting group (9%). The remaining reporting groups were present at low proportions (<5%).

Stock composition in District 111 varied by statistical week as the 2014 season progressed. Early in the season, the *Taku Lakes* reporting group dominated catches in statistical weeks 25 and 26 (49% and 47%, respectively; Figure 2). The *Stikine/Taku Mainstem* reporting group was a large contributor from statistical weeks 25–30 (range: 25–44%). Later in the season, the *Enhanced Snettisham* reporting group was the largest contributor from statistical weeks 30–32 and 34 (ranges: 40–89%). The *Other* reporting group was a larger contributor early in the season, from statistical weeks 25–28 (range: 14–32%).

The most common age groups throughout the 2014 season in District 111 were age-1.2 and -1.3 (42% and 41% of total, respectively; Figure 3). Age 1.2 was the largest component of the *Tatsamenie Wild*, *Speel Wild*, *Enhanced Tastamenie*, and *Enhanced Snettisham* reporting groups, while age 1.3 was the largest component of the remaining stocks (Figure 4). The *Stikine/Taku Mainstem* reporting group also had a large component of 0.x fish (39%). Ages 2.2, 2.3, and other were present at <5% overall.

Evaluation:

We accomplished the following:

- A total of 4,955 sockeye salmon were sampled from District 111 gillnet fisheries during the 2014 season.
- A total of 1,432 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 9 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, 11 separate estimates are provided for Taku-area fisheries in 2014 (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 Pacific Salmon Treaty (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 have been presented both to ADF&G Commercial Fisheries management staff and to the bilateral PSC Transboundary Technical Committee. A report published in the ADF&G Fishery Data Series is expected in 2015.

Date Prepared: July 1, 2015

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.

Rogers Olive, S. D., S. E. Gilk-Baumer, E. K. C. Fox, and W. D. Templin. *In prep*. Genetic baseline of Southeast Alaska sockeye salmon for mixed stock analyses, 2014. Alaska Department of Fish and Game, Fishery Data Series No. YY-XX, Anchorage.

TTC (Transboundary Technical Committee). *In prep*. Estimates of Transboundary River salmon production, harvest and escapement, and a review of joint enhancement activities in 2014. Pacific Salmon Commission Report TCTR, Vancouver.

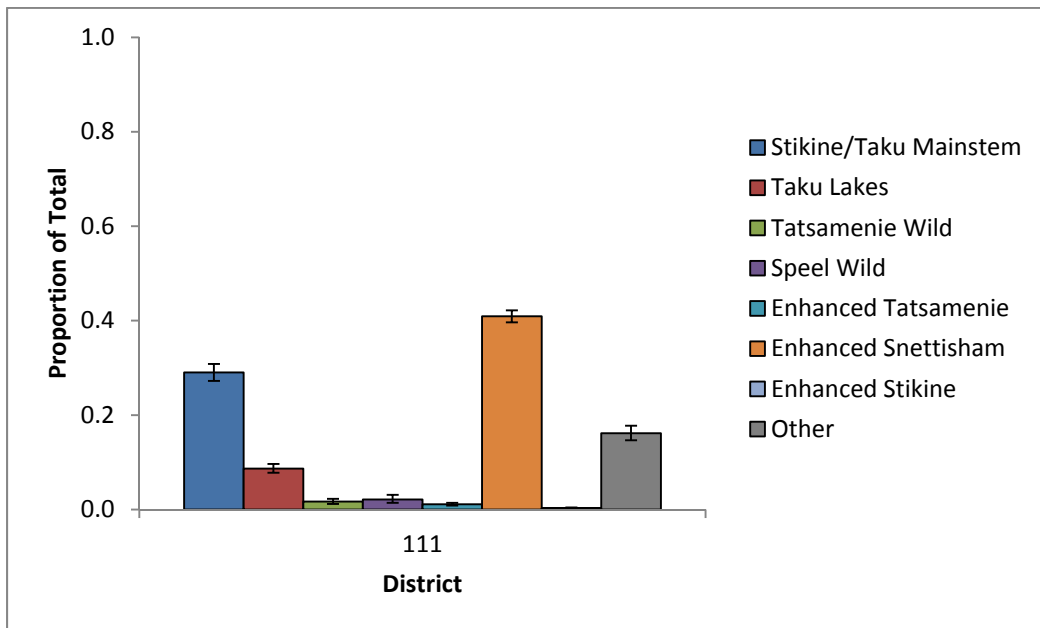


Figure 1. Total season stock composition estimates for Taku River area gillnet fisheries in 2014. Estimates were weighted by harvest per stratum.

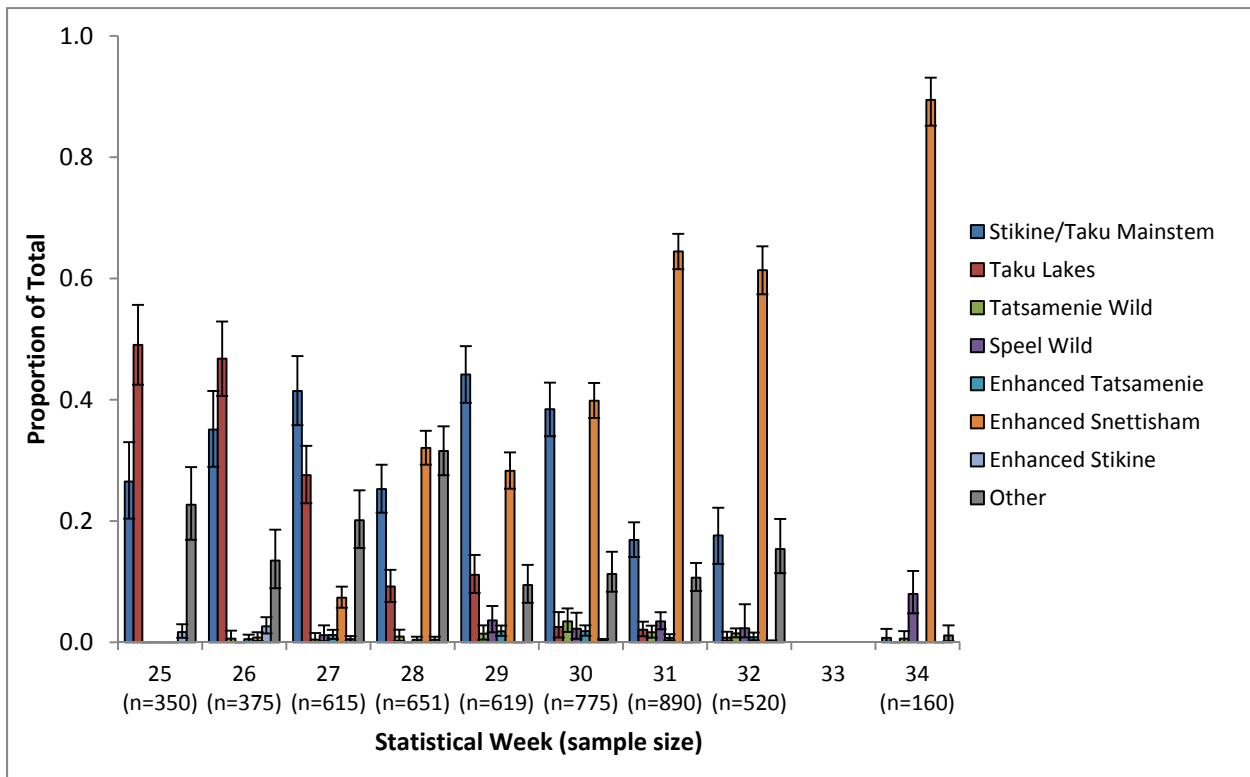


Figure 2. Stock composition estimates of sockeye salmon caught in the District 111 gillnet fishery in 2014. Sample size (n) includes genotyped, aged, and otolith-marked fish. Samples were not available for statistical week 33.

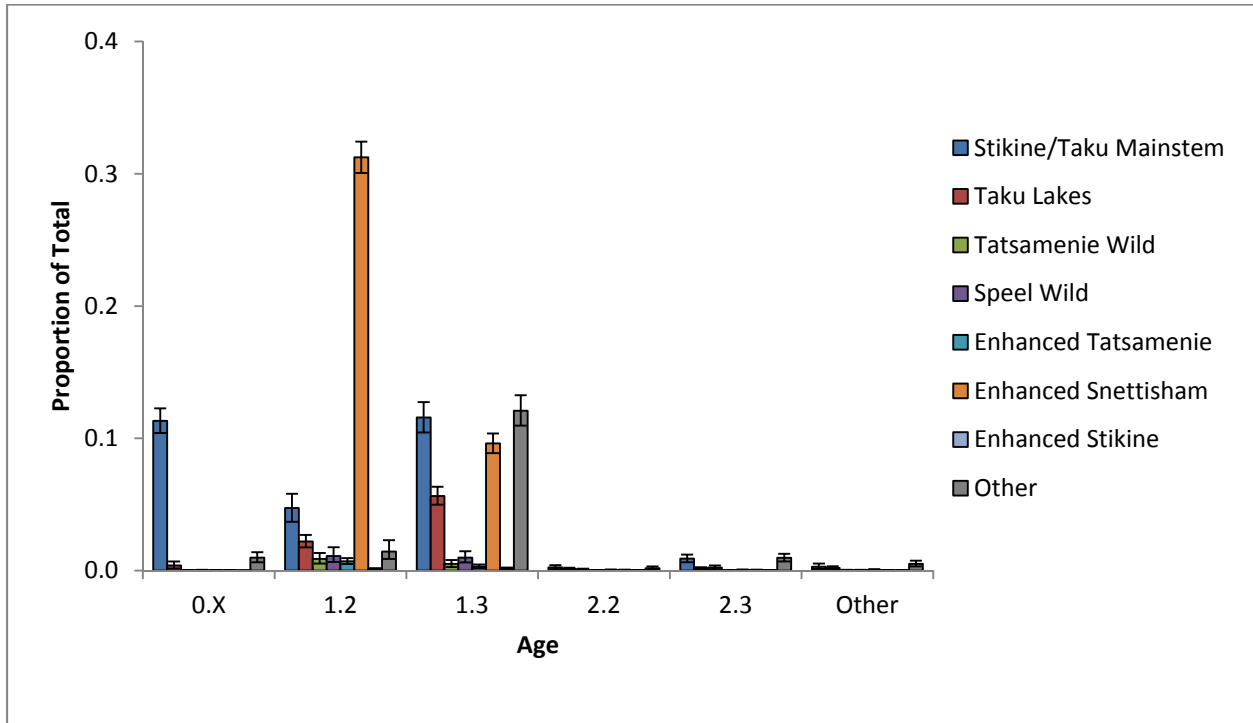


Figure 3. Age composition of sockeye salmon caught in the District 111 gillnet fishery in 2014 over the entire season.

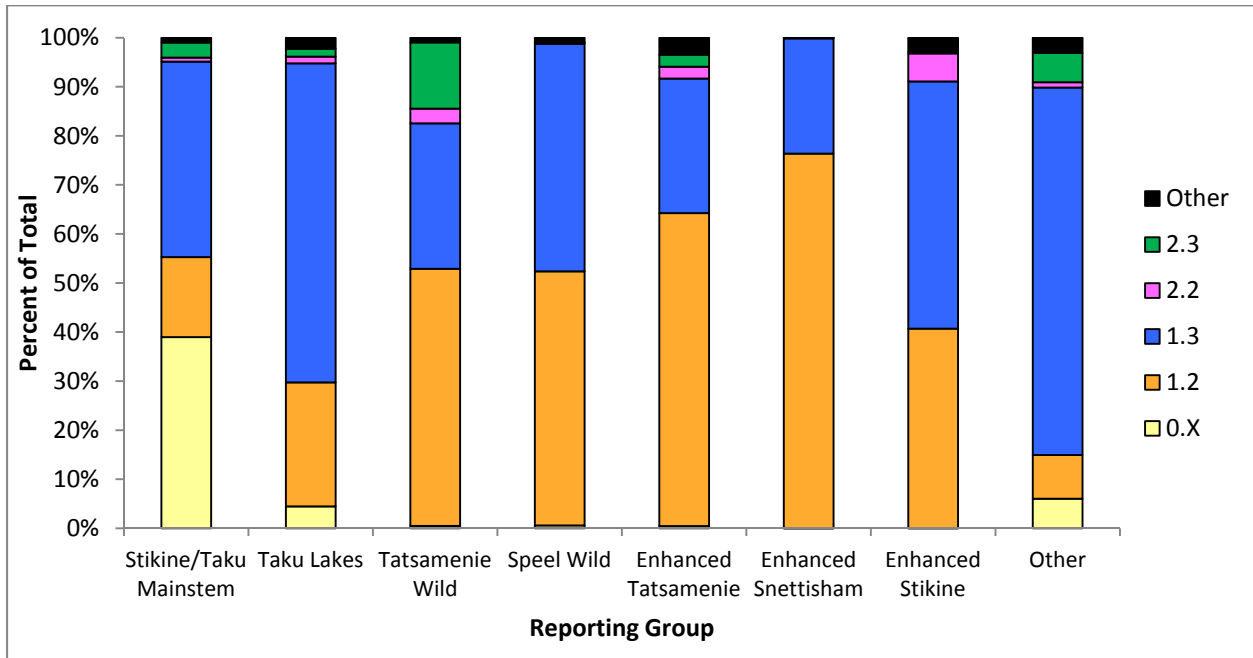


Figure 4. Age composition by reporting group of sockeye salmon caught in the District 111 gillnet fishery in 2014.

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 2014. Wild collections are ordered north to south and followed by enhanced collections.

Reporting Group	Collection Location	Reporting Group	Collection Location	
<i>Other</i>	Bainbridge Lake	<i>Other (cont.)</i>	Chilkat River - Mule Meadows	
	Coghill Lake		Chilkoot Lake - Beaches	
	Eshamy Lake		Chilkoot Lake - Bear Creek	
	Main Bay		Chilkoot River	
	Miners Lake		Berners Bay	
	Bering Lake		Lace River	
	Clear Creek at 40 Mile		Steep Creek	
	Eyak - Hatchery Creek		Windfall Lake	
	Eyak - Middle Arm		Lake Creek - Auke Creek Weir	
	Eyak - South beaches		Crescent Lake	
	Gulkana - Fish Creek		<i>Speel Wild</i>	Speel Lake
	Gulkana - East Fork			Snettisham
	Klutina Lake - inlet		<i>Other (cont.)</i>	Vivid Lake
	Klutina - Mainstem			Bartlett River - Creel survey
	Klutina - Banana Lake			North Berg Bay Inlet
	Klutina - Bear Hole			Hoktaheen Lake
	Kushtaka Lake			Neva Lake
	Long Lake weir	Sitkoh Lake		
	Mahlo River	Lake Eva		
	Martin Lake	Kook Lake		
	Martin River Slough	Pavlof Lake		
	McKinley Lake 2007	Hasselborg Lake		
	McKinley Lake 2008	Kanalku Lake ¹		
	McKinley Lake 1991	Kutlaku Lake		
	Salmon Creek - Bremner	Falls Lake		
	Mendeltna Creek	Ford Arm Creek		
	Mentasta Lake	Klag Bay Stream outlet		
	Paxson Lake - outlet	Redfish Lake Beaches		
	St. Anne Creek	Salmon Lake weir		
	Steamboat Lake - Bremner	Redoubt Lake - outlet		
	Swede Lake	Benzeman Lake		
	Tanada Creek weir	<i>Taku Lakes</i>	King Salmon Lake	
	Tanada Lk - lower outlet		Little Tatsamenie	
	Tanada Lk - shore		Little Trapper Lake	
	Tebay River - Outlet	<i>Tatsamenie Wild Stikine/Taku Mainstem</i>	Kuthai Lake	
	Tokun Lake		Tatsamenie Lake	
	Tonsina Lake		Hackett River	
	Ahrnklin River		Nahlin River	
	Akwe River		Tulsequah River	
	Dangerous River		Yellow Bluff Slough	
	East Alsek River		Sustahine Slough	
	Lost/Tahwah Rivers		Taku River	
	Old Situk River		Takwahoni/Sinwa Creek	
	Mountain Stream		Tuskwa/Chunk/Bear Slough	
	Situk Lake		Fish Creek	
	Blanchard River		Yehring Creek	
	Border Slough		Shakes Slough	
Klukshu River	Iskut River			
Upper Tatshenshini/Kudwat	Verrett River			
Tatshenshini - Kwatini River	Scud River			
Neskataheen Lake	Andy Smith/Porcupine/Fowler			
Tweedsmuir River	Devil's Elbow			
Vern Ritchie	Chutine River			
Chilkat Lake	Chutine Lake			
Chilkat River - Mosquito Lake	Christina Lake			
Chilkat River - Bear Flats	<i>Other (cont.)</i>	Little Tahltan River		

-continued-

Table 1 (cont.)

Reporting Group	Collection Location	Reporting Group	Collection Location
<i>Other (cont.)</i>	Tahltan Lake	<i>Other (cont.)</i>	Alastair Lake
	Hugh Smith Lake		Four Mile Creek/Pierre Creek
	McDonald Lake		Fulton River/Morrison Creek
	Hatchery Creek - Sweetwater		Kitsumkalum Lake
	Kah Sheets Lake		Lower Tahlo River
	Kunk Lake		McDonell Lake - Zymoetz R
	Luck Lake		Nangeese River
	Big Lake		Nanika River
	Mill Creek Weir		Slamgeesh River
	Petersburg Lake		Sustut River - Johanson Lake
	Red Bay Lake		Swan Lake
	Salmon Bay Lake		Upper Babine River
	Shipley Lake		Naden River
	Thoms Lake		Kitlope Lake
	Sarkar Lakes		Baker Lake
	Heckman Lake		Issaquah Creek
	Helm Lake		Cedar River
	Karta River/McGilvery Creek		Adams R - Shuswap Lake
	Kegan Lake		Birkenhead River
	Mahoney Creek		Chilko Lake
	Unuk River - Gene's Lake		Gates Creek
	Fillmore Lake - Hoffman Creek		Harrison River
	Klakas Lake		Horsefly River
	Bar Creek - Essowah Lake		Raft River
	Eek Creek		Stellako River
	Hetta Creek - Middle run		Enhanced - Burnett Inlet
	Hetta Creek - Early run		Enhanced - Main Bay
	Hetta Lake		Enhanced - McDonald
	Klawock River	<i>Enhanced Tatsamenie</i>	Enhanced - Sweetheart
	Bowser Lake	<i>Enhanced Snettisham</i>	Enhanced - Tatsamenie
	Damdochax Creek	<i>Enhanced Stikine</i>	Enhanced - Speel Arm
	Meziadin Lake		Enhanced - Tahltan
	Tintina Creek		Enhanced - Tuya
	Weaver Creek		

Table 2. Number of sockeye salmon sampled from District 111 sockeye gillnet harvests during each statistical week in 2014, samples genotyped, and otolith-marked or aged samples not genotyped for each statistical week.

District	Statistical Week	Total Samples Collected	Genotypes Used in Analysis	Not Genotyped (otolith-marked or aged or both)
111	25	350	150	200
	26	375	159	216
	27	615	213	402
	28	651	207	444
	29	619	193	426
	30	775	171	604
	31	890	188	702
	32	520	136	384
	33	0	0	0
	34	160	15	145
Totals		4,955	1,432	3,523