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Effects of Aggregating Coastwide Genetic Baselines for Improved Mixture Resolution of High-Seas Caught Salmon

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Abstract

Genetic analysis is used to identify individual stocks in mixed stock fisheries for management purposes. In instances where the number of potential contributing stocks is large and there is limited genetic divergence between populations within areas, baseline populations are often grouped into regional aggregations for analysis. Commonly used stock composition software maximizes the probability that the mixture allele frequencies are derived from specific baseline populations and those probabilities are added to determine the overall contribution from each regional grouping. An assumption with current stock composition methodologies is that the sampled baseline population allele frequency distribution represents the actual population allele frequency distribution, a condition which may be unrealistic especially with multi-allelic markers assayed in a small subset of a baseline stock. Differences between individual baseline and population allele frequency distributions can adversely affect stock composition analyses through misallocation. As a result, we investigated whether there may be instances where it may be advantageous to combine baseline allele counts within a region prior to stock composition rather than sum individual population allocations within regions after allocation. Results show that aggregating allele counts within regional baseline populations prior to mixture stock analysis can be an effective method in certain instances resulting in increased stock accuracy.

Introduction

Statistical methods have been developed to use various genetic, biological, and physical characteristics to identify specific fisheries stock proportions in mixtures (Fournier et al., 1984). Over the years, there have been extensive efforts to develop regional and ocean-wide genetic baselines for Pacific salmon by assaying allele frequency distributions of DNA-based characteristics such as single nucleotide polymorphisms (SNPs) and microsatellite markers. Species-wide baselines are required for analyzing the stock composition of salmon mixture samples taken in both high-seas research and managed fisheries where contributing stocks can originate from a large geographical distribution. Current maximum likelihood and Bayesian approaches for performing stock composition analysis assume a number of conditions including (1) that all contributing mixture stocks are represented in the genetic baseline, (2) that allele frequencies for the baseline samples truly represent the population allele frequencies, (3) that baseline genotypes are in Hardy-Weinberg Equilibrium, and (4) that individual loci within the baseline are not phased or linked. Rarely are these assumptions fully met, so stock composition often relies on a compromise approach that is specific to the question being addressed.

Because of the limited number of independent tests (samples) and the effects of chance, small sample collections represented in a genetic baseline are more likely to show allele frequency differences relative to the true population. While an issue for all marker types, adverse effects of including small sample collections in a genetic baseline are most likely to be pronounced for multi-allelic markers like microsatellites where the number of alleles can sometimes exceed the number of individual samples.

Both conditional maximum likelihood programs SPAM (ADF&G, 2003) and Onchor (Kalinowski, 2008) and the Bayesian programs BAYES (Pella and Masuda, 2001) and cBAYES (Neaves et al., 2005) apply two commonly employed methods for performing stock composition. While there are significant differences, both approaches maximize the probability that the mixture allele frequencies are derived from specific baseline populations. In current practice, control files identify baseline population groups and regional estimates are generated by summing individual baseline population proportions (“allocate-sum”). Baseline populations are generally aggregated based on similarity of genetic characteristics, a process that can minimize the error of misallocation of closely related baseline populations. The “allocate-sum” protocols currently used today were first evaluated 25 years ago (Wood et al., 1987) where simulated mixtures were developed for up to 9 hypothetical stocks with information for 9 biallelic markers and the effects of the “allocate-sum” and “pool-allocate” protocols were compared. “Pool-allocate” is an alternative approach in which the regional population allele counts are combined into aggregations within the baseline before stock composition analysis. Based on known simulated mixture compositions, the “allocate-sum” procedure was found to be more accurate under those study conditions than “pool-allocate.” Since then, a number of Pacific Rim baselines have been assembled representing hundreds of populations assayed for many markers, some with many alleles. This paper is a re-evaluation of the “pool-allocate” method in this new context. The tests selected for this analysis were chosen to highlight issues associated with aggregating baseline populations and don’t necessarily reflect the power of the baselines which have been fully evaluated elsewhere.

Materials and Methods

Microsatellite Baseline

Allele frequency distributions from the Pacific Rim chum salmon microsatellite baseline (Beacham et al., 2009a) were downloaded from the Fisheries and Oceans Canada Molecular Genetics web page (http://www-sci.pac.dfo-mpo.gc.ca/mgl/data_e.htm) and a SPAM baseline file was created within Excel. For this analysis, 11 of the 14 markers were used. The following 3 loci were removed: *Oki2* and *One111* which may be available in future analyses pending optimization and *Oke3* which was not consistently amplified.

SNP Baseline

Baseline allele frequencies from the Pacific Rim chum salmon SNP baseline (Seeb et al., 2011) were downloaded from the DRYAD web site (<http://datadryad.org/using>). To generate SPAM baseline and mixture files, a program was written in C++. For this analysis, 54 of the 58 loci were used as the following 4 linked loci were removed: *CCT3220*, *GHI2943*, *IL8r272*, and *U50787*.

Stock Composition Analysis

SPAM software (ADF&G, 2003) uses a conditional maximum likelihood approach in which the mixture genotypes are compared directly with the baseline to determine the most likely mixture stock composition. In addition to performing stock composition analysis, SPAM also enables the analysis of known mixtures as a method for assaying the effectiveness of the baseline for stock separation. For these analyses, a mixture size of 400 was used with between 500 and 1,000 replicates to identify the 90% non-symmetric confidence interval, a statistic most appropriate for evaluating mixtures containing a high percentage of samples from individual regional aggregations.

Genotyping

DNA was extracted from the axillary process of chum salmon and microsatellite genotyping was performed as described previously (McCraney et al., 2012). Briefly, samples were genotyped for the following 11 microsatellite loci: *Oki100* (Beacham et al., 2009b), *Omm1070* (Rexroad et al., 2001), *Omy1011* (Spies et al., 2005), *One101*, *One102*, *One104*, *One114* (Olsen et al., 2000), *Ots103* (Nelson and Beacham, 1999), *Ots3* (Greig and Banks 1999), *Ots68* (Williamson et al., 2002), and *Ssa419* (Cairney et al., 2000). Thermal cycling for the amplification of DNA fragments with the polymerase chain reaction (PCR) was performed on a dual 384-well GeneAmp PCR System 9700 (Applied Biosystems, Inc.). Samples from the PCR reactions were diluted into 96-well plates for analysis by a 16-capillary, 36 cm array on the ABI 3130xl Genetic Analyzer. Genotypes were double-scored with GeneMapper 4.0 software (Applied Biosystems, Inc.) and exported to Excel spreadsheets (Microsoft, Inc.) for further analysis.

For developing mixture files, microsatellite allele calls were converted to match those in the Fisheries and Oceans Canada chum salmon microsatellite baseline (Beacham et al., 2009a) using a conversion table developed by analyzing known samples shared between the laboratories. Genotypes from converted mixtures were exported from Excel as text files, and C programs were used to format the data into mixture files. Stock compositions were determined using both maximum likelihood and Bayesian approaches by comparing mixture allele frequencies with those from reference baseline populations.

Results

Identification of Regional Stock Groupings for Microsatellite Baseline Analysis

To determine population aggregations for this test, two different descriptive analyses were used. First, regional groupings were approximated using the published neighbor-joining dendrogram (Beacham et al., 2009a). Second, a Principal Coordinate Analysis (PCO) was used based on Cavalli-Sforza Edwards (CSE) genetic distance (Cavalli-Sforza and Edwards, 1967) calculated from the allele frequencies of the baseline populations. A comparison of the PCO plot for the 11 microsatellites (Figure 1 with data from Beacham et al., 2009a) is similar to those produced previously for allozyme (Seeb et al., 2004) and SNP (Seeb et al., 2011) characters suggesting all markers are measuring similar genetic differences. While additional population structure is apparent and quantified elsewhere, we focused on the following 6 large regional groups for this test: East Asia, North Asia, coastal Western Alaska, Upper/Middle Yukon, Southwest Alaska Peninsula, and Eastern Gulf of Alaska/Pacific Northwest (East GOA/PNW). Regional designations for each of the populations are shown in the Appendix.

100% Simulation Analysis for 6 Large Regional Aggregations

As a measure of the ability of the baseline to discriminate the 6 individual regions, 100% simulation studies were completed in SPAM in which all samples of a hypothetical mixture were from one region and that mixture was re-evaluated against the baseline to determine the percentage reallocating back to the correct region. This analysis was completed for all 6 regions using both the “allocate-sum” and “pool-allocate” methodologies (Table 1). For “allocate-sum”, the 381 population baseline for the 11 microsatellite markers was evaluated using regional groupings designated in the SPAM control file. In this instance, the identity of each baseline population was maintained and the stock composition was determined as the sum of the individual stocks within the designated regions. For “pool-allocate”, the 381 population baseline was reconfigured such that allele counts for each of the populations within a region were aggregated into a single large population as a means to both better represent the allele frequency distribution within the region and mitigate effects of having disproportionate numbers of baseline populations within specific regions. The results from the “allocate-sum” methodology show strong stock separation for all 6 aggregations with repartitioning rates ranging from 82% to 98% (Table 1). Stock separation was improved using the “pool-allocate” method where repartitioning rates ranged from 98% to 100%.

Stock Composition Comparison of Samples of Known Geographic Origin Using 6 Aggregated and Regional Baseline Groupings

As part of an ongoing collaboration to develop a combined SNP/microsatellite baseline, additional baseline populations/samples were genotyped for 13 of the microsatellite markers used in the DFO microsatellite chum salmon baseline (Beacham et al., 2009a). Using the 11 markers identified previously, these new samples were grouped as a mixture representing the following regions in the microsatellite baseline: East Asia (120 samples from 3 populations), North Asia (142 samples from 4 populations), Western Alaska (273 samples from 4 populations), Kuskokwim (673 samples from 8 populations), Southwest Alaska (132 samples from 2 populations), and GOA-PNW (1,159 samples from 19 populations). In the microsatellite baseline, Kuskokwim stocks were included with the Western Alaska region, so this represents a second test for that region. Again, stock separation was improved using the “pool-allocate” method where repartitioning rates ranged from 88% to 100% (Table 2).

Comparison of High-seas Stock Composition Results Using 6 Aggregated and Regional Baseline Groupings

As part of the groundfish trawl fishery in the Bering Sea, Chinook and chum salmon are taken as incidental catch and are referred to as salmon bycatch. As a means to both better understand (1) the potential impact of harvest and (2) salmon migration patterns to help mitigate future impacts, the National Marine Fisheries Service’s Alaska Fisheries Science Center developed stock compositions for available bycatch sample sets from previous years. In 2006, genetic samples were collected opportunistically as part of a special project to assay feasibility and may be subject to various biases; consequently, stock composition estimates apply to the sample set and may not represent the composition of the total chum salmon bycatch, but do provide an indication of presence. When stock composition estimates of the 2006 year chum salmon bycatch sample mixture (1,367 samples) were compared using both the “allocate-sum” and “pool-allocate” protocols, the results were similar suggesting the results were not negatively impacted by aggregating the baseline populations (Table 3).

Effects of “Pool-Allocate” for a SNP Baseline

To investigate the effects of aggregating a SNP baseline, an analysis was completed using the chum salmon Pacific Rim SNP baseline (Seeb et al., 2011) and the baseline was aggregated into the 15 regions defined in the manuscript. Test mixtures were developed using a program written in C++ that would (1) randomly take samples from a baseline region at a designated rate (1 in 6 was used), (2) format the selected samples into a mixture file, (3) remove those samples from the baseline file, and (4) reconfigure new individual and aggregated population baseline files. A conditional maximum likelihood estimation was completed in SPAM to repartition the mixture files using both the “allocate-sum” and “pool-allocate” methodologies (Table 4). Since 100% of the samples for each test came from a specific region, it provided a quick measure of the ability of the baseline to reallocate those samples to the region of origin. The results show that the stock composition was generally improved using “pool-allocate” method. The greatest improvement in overall assignment was for the Bristol Bay-South grouping (improvement of 17%) with the average improvement across all regions of 3.5%. The group with the worst performance with the “pool-allocate” method was the Kodiak group which saw a decrease in performance of almost 6%, and could potentially be explained by the uniqueness of individual stocks.

Discussion

There are unique issues inherent to performing genetic stock composition analysis of samples collected on the high-seas, especially in areas in which samples can originate from a wide distribution of stocks. For example, the assumption that all stocks contributing to the mixture are represented in the genetic baseline may not be fulfilled in all instances. As a compromise, mixture allocations to individual baseline populations are often aggregated into large regions based on genetic similarity and stock composition performed using an “allocate-sum” approach.

The “allocate-sum” and “pool-allocate” methodologies were first evaluated 25 years ago using a theoretical baseline of 9 populations assayed for 9 biallelic markers (Wood et al., 1987). While it concluded the “allocate-sum” methodology was most accurate, it’s unclear how that analysis would be affected by contemporary baselines with hundreds of populations assayed for markers with many alleles. This analysis shows that the “pool-allocate” methodology for stock composition can be more accurate in certain instances potentially because (1) the larger numbers of samples within an aggregated baseline “population” may better represent the overall allele frequency distribution within a region and (2) the aggregation approach limits bias associated with differences in total numbers of populations within regions. In addition to improvements in accuracy, the stock composition software realized its likelihoods much quicker, an improvement which could help decrease the computing time required for Bayesian stock composition analyses (data not shown).

While there are situations where the “pool-allocate” methodology would be preferred, it is simply a balance between competing limitations. For example, potential improvements in the allele frequency distributions of aggregated baselines can be offset by potential violations of Hardy-Weinberg Equilibrium (HWE) conditions due to combining samples from non-mating populations. HWE conditions are often assumed in stock composition software to expand baseline allele frequencies to expected genotypes which are then used to compare with the

mixture for stock composition. In a test of the Pacific Rim chum salmon SNP baseline, the number of significant HWE tests increased from 4% to 10% (data not shown) when the baseline was aggregated, but this also correlated with an increase in accuracy suggesting some degree of compromise between the various conditions. While the increase of significant HWE tests could be reflective of aggregating dissimilar populations, it could also be influenced by the increased statistical power associated with increasing sample numbers in each test. These results suggest that aggregating populations within regions should be done with caution, especially in instances where the conditions for HWE are compromised.

While the advantages of the “pool-allocate” method were apparent for biallelic markers like SNPs (Table 4), it was more pronounced for stock composition with baselines using multiallelic markers (Tables 1-2). Improvements in accuracy may help improve stock composition analyses of salmon mixtures collected in the high-seas, where stocks from throughout the Pacific Rim may be encountered (Table 3).

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References

- ADF&G (Alaska Department of Fish and Game). 2003. SPAM Version 3.7: Statistics program for analyzing mixtures. Alaska Department of Fish and Game, Commercial Fisheries Division, Gene Conservation Laboratory, Anchorage, Alaska.
- Beacham, T.D., Candy, J.R., Le, K.D. and M. Wetklo. 2009a. Population structure of chum salmon (*Oncorhynchus keta*) across the Pacific Rim, determined from microsatellite analysis. Fish. Bull., U.S. 107: 244-260.
- Beacham, T.D., Le, K.D., Wetklo, M., McIntosh, B., Ming, T. and K.M. Miller. 2009b. Population structure and stock identification of chum salmon from western Alaska determined with microsatellite and major histocompatibility complex variation, p. 141-160. In C. C. Krueger and C. E. Zimmerman (eds.), Pacific salmon: ecology and management in western Alaska's populations. American Fisheries Society, Symposium 70, Bethesda, Maryland.
- Cairney, M., Taggart, J.B. and B. Hoyheim. 2000. Characterization of microsatellite and minisatellite loci in Atlantic salmon (*Salmo salar* L.) and cross-species amplification in other salmonids. Mol. Ecol. 9: 2175-2178.

- Cavalli-Sforza, L. L., and A. W. F. Edwards. 1967. Phylogenetic analysis: models and estimation procedures. *Evolution* 21:550–570.
- Fournier, D.A., Beacham, T.D., Riddell, B.E., and C.A. Busack. 1984. Estimating stock composition in mixed stock fisheries using morphometric, meristic, and electrophoretic characteristics. *Can. J. Fish. Aquat. Sci.* 41: 400-408.
- Greig, C. and M.A. Banks. 1999. Five multiplexed microsatellite loci for rapid response run identification of California's endangered winter chinook salmon. *Anim. Genet.* 30: 318-320.
- Kalinowski, S. T. 2008. ONCOR: Software for genetic stock identification. Available at: <http://www.montana.edu/kalinowski/Software.htm>.
- McCraney, W.T., Farley, E.V., Kondzela, C.M., Naydenko, S.V., Starovoytov, A.N., and J.R. Guyon. 2012. Genetic stock identification of overwintering chum salmon in the North Pacific Ocean. *Environ. Biol. Fish* 94: 663-668.
- Neaves, P.I., Wallace, C.G., Candy, J.R., T.D. Beacham. 2005. cBayes: computer program for mixed stock analysis of allelic data. Version 3.0. Available at www.pac.dfompo.gc.ca/sci/mgl/Cbayes_e.htm
- Nelson, R.J., and T.D. Beacham. 1999. Isolation and cross species amplification of microsatellite loci useful for study of Pacific salmon. *Anim. Genet.* 30: 228-229.
- Olsen, J.B., Wilson, S.L., Kretschmer, E.J., Jones, K.C. and J.E. Seeb. 2000. Characterization of 14 tetranucleotide microsatellite loci derived from sockeye salmon. *Mol. Ecol.* 9: 2,185-2,187.
- Pella, J., and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. *Fish. Bull., U.S.* 99: 151-167.
- Rexroad, C.E., Coleman, R.L., Martin, A.M., Hershberger, W.K. and J. Killefer. 2001. Thirty-five polymorphic microsatellite markers for rainbow trout (*Oncorhynchus mykiss*). *Anim. Genet.* 32: 317-319.
- Seeb, L.W., Templin, W.D., Sato, S., Abe, S., Warheit, K., Park, J.Y., and J.E. Seeb. 2011. Single nucleotide polymorphisms across a species' range: implications for conservation studies of Pacific salmon. *Mol. Ecol. Res.* 11:195-217.
- Seeb, L.W., Crane, P.A., Kondzela, C.M., Wilmot, R.L., Urawa, S., Varnavskaya, N.V., and J.E. Seeb. 2004. Migration of Pacific Rim chum salmon on the high seas: insights from genetic data. *Env. Biol. Fish.* 69:21–36.

- Spies, I.B., Brasier, D.J., O'Reilly, T.L., Seamons, T.R. and P. Bentzen. 2005. Development and characterization of novel tetra-, tri-, and dinucleotide microsatellite markers in rainbow trout (*Oncorhynchus mykiss*). Mol. Ecol. Notes 5: 278-281.
- Wood, C.C., McKinnell, S., Mulligan, T.J., and D.A. Fournier. 1987. Stock identification with the maximum-likelihood mixture model: sensitivity analysis and application to complex problems. Can. J. Fish. Aquat. Sci. 44:866-881.
- Williamson, K.S., Cordes, J.F. and B. May. 2002. Characterization of microsatellite loci in chinook salmon (*Oncorhynchus tshawytscha*) and cross-species amplification in other salmonids. Mol. Ecol. Notes 2:17-19.

Table 1. Chum salmon microsatellite baseline simulation analyses. Results from simulation studies using the 381 population Pacific Rim chum salmon microsatellite baseline with 6 regional groups in which 100% of a hypothetical mixture of 400 fish were derived from one region (columns) and reallocated back to the region (rows) with SPAM software. The fraction of fish from each region is designated.

Allocate-Sum	<i>E. Asia</i>	<i>N. Asia</i>	<i>W. Alaska</i>	<i>Upper Yukon</i>	<i>S.W. AK</i>	<i>GOA/PNW</i>
<i>East Asia</i>	0.887	0.028	0.002	0.001	0.008	0.001
<i>North Asia</i>	0.026	0.852	0.011	0.002	0.056	0.008
<i>Western Alaska</i>	0.005	0.048	0.959	0.058	0.040	0.002
<i>Upper/Middle Yukon</i>	0.000	0.002	0.010	0.935	0.001	0.000
<i>SW Alaska</i>	0.001	0.007	0.003	0.001	0.817	0.003
<i>East GOA/PNW</i>	0.011	0.043	0.011	0.002	0.071	0.977

Pool-Allocate	<i>E. Asia</i>	<i>N. Asia</i>	<i>W. Alaska</i>	<i>Upper Yukon</i>	<i>S.W. AK</i>	<i>GOA/PNW</i>
<i>East Asia</i>	0.991	0.005	0.000	0.000	0.001	0.000
<i>North Asia</i>	0.004	0.979	0.003	0.001	0.011	0.001
<i>Western Alaska</i>	0.000	0.004	0.993	0.005	0.002	0.000
<i>Upper/Middle Yukon</i>	0.000	0.000	0.002	0.993	0.000	0.000
<i>SW Alaska</i>	0.000	0.004	0.001	0.000	0.981	0.001
<i>East GOA/PNW</i>	0.002	0.006	0.001	0.001	0.005	0.997

Table 2. Chum salmon microsatellite baseline sample test. Samples collected from known spawning locations were genotyped, combined into regional mixtures as outlined in the text, and allocated to stocks using both the “allocate-sum” and “pool-allocate” baseline protocols. Derived mixtures are designated in the columns and the resulting stock allocation to each baseline groupings designated by rows. Stock composition analysis was performed in SPAM using the Pella-Masuda method for Bayesian modeling of baseline allele frequencies.

Allocate-Sum	<i>E.Asia</i>	<i>N. Asia</i>	<i>Kuskokwim</i>	<i>W. Alaska</i>	<i>S.W. AK</i>	<i>GOA/PNW</i>
<i>East Asia</i>	0.929	0.010	0.000	0.000	0.000	0.001
<i>North Asia</i>	0.049	0.920	0.000	0.000	0.039	0.015
<i>Western Alaska</i>	0.000	0.050	0.906	0.980	0.014	0.001
<i>Upper/Middle Yukon</i>	0.000	0.000	0.092	0.012	0.000	0.001
<i>SW Alaska</i>	0.014	0.003	0.001	0.003	0.732	0.035
<i>East GOA/PNW</i>	0.007	0.017	0.002	0.005	0.216	0.945

Pool-Allocate	<i>E.Asia</i>	<i>N. Asia</i>	<i>Kuskokwim</i>	<i>W. Alaska</i>	<i>S.W. AK</i>	<i>GOA/PNW</i>
<i>East Asia</i>	0.949	0.023	0.000	0.000	0.000	0.000
<i>North Asia</i>	0.049	0.977	0.000	0.000	0.000	0.044
<i>Western Alaska</i>	0.003	0.000	0.906	0.998	0.000	0.000
<i>Upper/Middle Yukon</i>	0.000	0.000	0.094	0.002	0.000	0.000
<i>SW Alaska</i>	0.000	0.000	0.000	0.000	0.919	0.077
<i>East GOA/PNW</i>	0.000	0.001	0.000	0.000	0.081	0.878

Table 3. Regional SPAM stock composition estimates for 1,367 chum salmon samples from the bycatch of the 2006 season Bering Sea groundfish trawl fishery. Standard error and 90% nonsymmetric upper and lower confidence intervals for the SPAM estimates were determined by the analysis of 500 bootstrapping resamplings of the mixture.

Allocate-Sum	Estimate	Std.Dev.	Lower	Upper	Confidence Interval
<i>East Asia</i>	0.262	0.012	0.243	0.284	0.041
<i>North Asia</i>	0.271	0.014	0.251	0.299	0.048
<i>Western Alaska</i>	0.108	0.010	0.090	0.123	0.033
<i>Upper/Middle Yukon</i>	0.056	0.007	0.046	0.068	0.022
<i>SW Alaska</i>	0.019	0.005	0.010	0.026	0.016
<i>Eastern GOA/PNW</i>	0.275	0.013	0.253	0.294	0.041

Pool-Allocate	Estimate	Std.Dev.	Lower	Upper	Confidence Interval
<i>East Asia</i>	0.264	0.013	0.242	0.283	0.041
<i>North Asia</i>	0.292	0.015	0.267	0.317	0.050
<i>Western Alaska</i>	0.107	0.011	0.090	0.126	0.036
<i>Upper/Middle Yukon</i>	0.058	0.007	0.047	0.069	0.023
<i>SW Alaska</i>	0.025	0.007	0.014	0.039	0.024
<i>Eastern GOA/PNW</i>	0.254	0.013	0.233	0.274	0.040

Table 4. 114 population Pacific Rim chum salmon SNP baseline with 15 regional groups. Results from mixtures of samples taken from the individual (top) and aggregated (bottom) Pacific Rim SNP baseline without replacement. Mixture samples were randomly selected at a rate of 1 of 6 samples using a random number generator for each sample and the number of fish in each mixture file (and consequently removed from the baseline) for each region is indicated under “Num”. Baseline regions are designated by rows and the mixture designated by columns labeled by the number from which the mixture was derived. Stock composition analysis was performed in SPAM using the Pella-Masuda method for Bayesian modeling of baseline allele frequencies.

Allocate			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
-Sum	Population	Num															
1	Hokkaido	214	0.951	0.267	0.000	0.009	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	Honshu/Korea	79	0.049	0.721	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
3	Amur	31	0.000	0.000	0.980	0.000	0.018	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
4	Anadyr/Kamchatka	109	0.000	0.000	0.000	0.946	0.032	0.000	0.000	0.000	0.001	0.000	0.001	0.000	0.001	0.005	0.000
5	Kotzebue	55	0.000	0.000	0.000	0.000	0.842	0.027	0.002	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000
6	Western AK Summer	589	0.000	0.000	0.000	0.014	0.086	0.931	0.008	0.063	0.150	0.007	0.018	0.000	0.000	0.000	0.000
7	Yukon Fall/Mid Summer	266	0.000	0.000	0.000	0.003	0.001	0.010	0.989	0.133	0.025	0.000	0.000	0.000	0.000	0.000	0.000
8	Kuskokwim Fall	39	0.000	0.000	0.000	0.000	0.020	0.004	0.000	0.804	0.025	0.000	0.002	0.000	0.000	0.000	0.000
9	Bristol Bay South	84	0.000	0.000	0.020	0.000	0.000	0.025	0.001	0.000	0.766	0.001	0.008	0.004	0.000	0.000	0.000
10	N AK Peninsula	93	0.000	0.000	0.000	0.016	0.000	0.000	0.000	0.000	0.014	0.959	0.010	0.052	0.000	0.000	0.000
11	S AK Peninsula	95	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.005	0.018	0.923	0.077	0.000	0.000	0.000
12	Kodiak	51	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.015	0.819	0.000	0.007	0.000	0.000
13	Susitna	53	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	0.000
14	GOA/SE AK/BC	224	0.000	0.000	0.000	0.008	0.000	0.002	0.000	0.000	0.003	0.004	0.023	0.048	0.000	0.987	0.001
15	Washington	34	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.999

Pool- Allocate			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	Hokkaido	214	0.960	0.113	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	Honshu/Korea	79	0.040	0.872	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
3	Amur	31	0.000	0.000	0.989	0.000	0.018	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
4	Anadyr/Kamchatka	109	0.000	0.000	0.000	0.949	0.006	0.000	0.000	0.000	0.001	0.000	0.001	0.000	0.001	0.006	0.000
5	Kotzebue	55	0.000	0.000	0.000	0.001	0.965	0.025	0.003	0.002	0.000	0.000	0.000	0.000	0.000	0.001	0.000
6	Western AK Summer	589	0.000	0.000	0.000	0.000	0.003	0.939	0.005	0.023	0.039	0.000	0.002	0.000	0.000	0.000	0.000
7	Yukon Fall/Mid Summer	266	0.000	0.000	0.000	0.001	0.000	0.002	0.992	0.108	0.000	0.000	0.000	0.000	0.000	0.000	0.000
8	Kuskokwim Fall	39	0.000	0.000	0.000	0.000	0.005	0.004	0.000	0.867	0.021	0.000	0.006	0.000	0.000	0.000	0.000
9	Bristol Bay South	84	0.000	0.000	0.011	0.000	0.003	0.027	0.000	0.000	0.938	0.017	0.000	0.000	0.000	0.000	0.000
10	N AK Peninsula	93	0.000	0.000	0.000	0.031	0.000	0.000	0.000	0.000	0.000	0.954	0.000	0.010	0.000	0.000	0.002
11	S AK Peninsula	95	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.029	0.979	0.211	0.000	0.000	0.000
12	Kodiak	51	0.000	0.015	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.757	0.000	0.006	0.000
13	Susitna	53	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.999	0.000	0.000

14	GOA/SE AK/BC	224	0.000	0.000	0.000	0.010	0.000	0.002	0.000	0.000	0.000	0.000	0.000	0.008	0.022	0.000	0.985	0.000
15	Washington	34	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.997

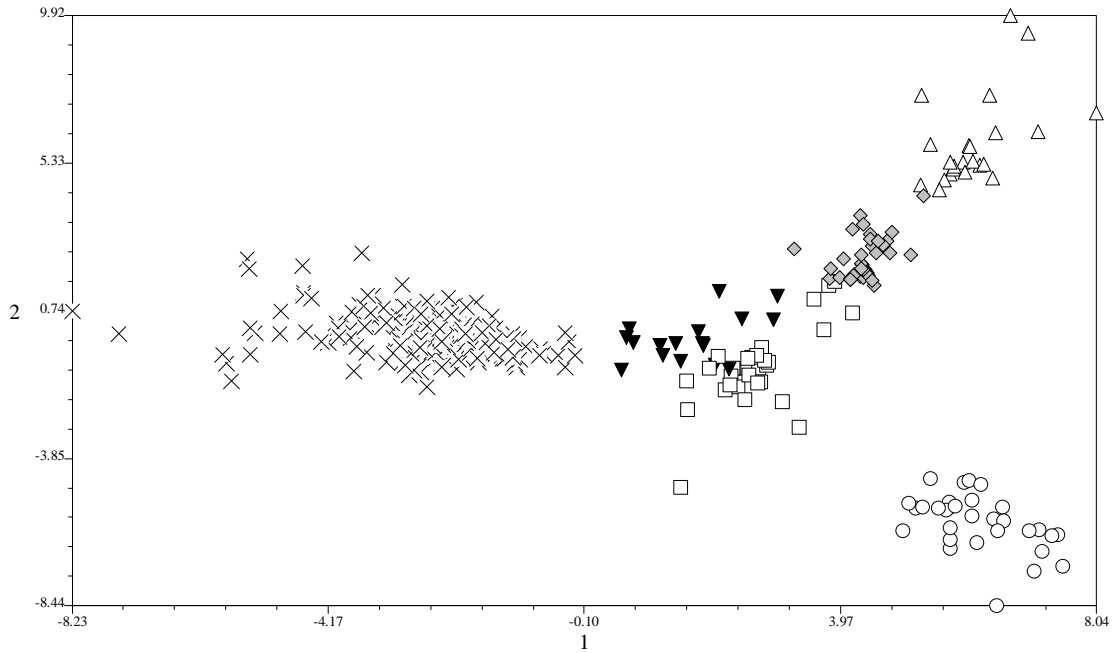


Figure 1. Principal coordinate analysis of 381 chum populations analyzed for 11 microsatellite markers. Eigenvectors were plotted in 2-dimensional space with “1” on the x-axis being the most informative (34.8% of the variation) and “2” on the y-axis the second most (16.9%). Populations are designated with the following symbols: East Asia (open circles), North Asia (open squares), Upper/Middle Yukon (open triangles), Western Alaska (grey diamonds), Southwest Alaska (black upside-down triangles), and Eastern GOA/PNW (X).

Appendix. Chum salmon populations in the coastwide chum salmon microsatellite baseline with the 6 regional designations used in the analyses of this report.

DFO Number	Population Name	Region Number	Region
41	Abashiri	1	East Asia
215	Avakumovka	1	East Asia
40	Chitose	1	East Asia
315	Gakko_River	1	East Asia
292	Hayatsuki	1	East Asia
44	Horonai	1	East Asia
252	Kawabukuro	1	East Asia
313	Koizumi_River	1	East Asia
300	Kushiro	1	East Asia
37	Miomote	1	East Asia
391	Namdae_R	1	East Asia
231	Narva	1	East Asia
298	Nishibetsu	1	East Asia
293	Ohkawa	1	East Asia
297	Orikasa	1	East Asia
214	Ryazanovka	1	East Asia
312	Sakari_River	1	East Asia
311	Shari_River	1	East Asia
36	Shibetsu	1	East Asia
299	Shikiu	1	East Asia
253	Shiriuchi	1	East Asia
310	Shizunai	1	East Asia
217	Suifen	1	East Asia
35	Teshio	1	East Asia
39	Tokachi	1	East Asia
38	Tokoro	1	East Asia
314	Tokushibetsu	1	East Asia
291	Toshibetsu	1	East Asia
296	Tsugaruishi	1	East Asia
316	Uono_River	1	East Asia
309	Yurappu	1	East Asia
218	Amur	2	North Asia
207	Anadyr	2	North Asia
384	Apuka_River	2	North Asia
382	Bolshaya	2	North Asia
380	Dranka	2	North Asia
223	Hairusova	2	North Asia
378	Ivashka	2	North Asia
213	Kalininka	2	North Asia
225	Kamchatka	2	North Asia
219	Kanchalan	2	North Asia

DFO Number	Population Name	Region Number	Region
379	Karaga	2	North Asia
294	Kikchik	2	North Asia
209	Kol_	2	North Asia
233	Magadan	2	North Asia
211	Naiba	2	North Asia
295	Nerpichi	2	North Asia
381	Okhota	2	North Asia
212	Oklan	2	North Asia
222	Ola_	2	North Asia
386	Olutorsky_Bay	2	North Asia
228	Ossora	2	North Asia
224	Penzhina	2	North Asia
385	Plotnikova_R	2	North Asia
221	Pymta	2	North Asia
220	Tauy	2	North Asia
383	Tugur_River	2	North Asia
226	Tym_	2	North Asia
230	Udarnitsa	2	North Asia
290	Utka_River	2	North Asia
208	Vorovskaya	2	North Asia
387	Zhypanova	2	North Asia
348	Agiapuk	3	Western Alaska
376	Alagnak	3	Western Alaska
3	Andreafsky	3	Western Alaska
357	Aniak	3	Western Alaska
301	Anvik	3	Western Alaska
80	Chulinak	3	Western Alaska
347	Eldorado	3	Western Alaska
358	George	3	Western Alaska
307	Gisasa	3	Western Alaska
371	Goodnews	3	Western Alaska
288	Henshaw_Creek	3	Western Alaska
339	Imnachuk	3	Western Alaska
361	Kanektok	3	Western Alaska
362	Kasigluk	3	Western Alaska
328	Kelly_Lake	3	Western Alaska
340	Kobuk	3	Western Alaska
343	Koyuk	3	Western Alaska
363	Kwethluk	3	Western Alaska
336	Kwiniuk_River	3	Western Alaska
303	Melozitna	3	Western Alaska
373	Mulchatna	3	Western Alaska
372	Naknek	3	Western Alaska
330	Niukluk	3	Western Alaska
329	Noatak	3	Western Alaska

DFO Number	Population Name	Region Number	Region
345	Nome	3	Western Alaska
302	Nulato	3	Western Alaska
374	Nunsatuk	3	Western Alaska
13	Peel_River	3	Western Alaska
322	Pikmiktalik	3	Western Alaska
331	Pilgrim_River	3	Western Alaska
346	Shaktoolik	3	Western Alaska
341	Snake	3	Western Alaska
368	Stuyahok_River	3	Western Alaska
375	Togiak	3	Western Alaska
154	Tozitna	3	Western Alaska
342	Unalakleet	3	Western Alaska
344	Ungalik	3	Western Alaska
8	Big_Creek	4	Upper/Middle Yukon
89	Big_Salt	4	Upper/Middle Yukon
86	Black_River	4	Upper/Middle Yukon
87	Chandalar	4	Upper/Middle Yukon
28	Chandindu	4	Upper/Middle Yukon
82	Cheena	4	Upper/Middle Yukon
81	Delta	4	Upper/Middle Yukon
7	Donjek	4	Upper/Middle Yukon
5	Fishing_Br	4	Upper/Middle Yukon
88	Jim_River	4	Upper/Middle Yukon
85	Kantishna	4	Upper/Middle Yukon
2	Kluane	4	Upper/Middle Yukon
59	Kluane_Lake	4	Upper/Middle Yukon
181	Koyukuk_late	4	Upper/Middle Yukon
90	Koyukuk_south	4	Upper/Middle Yukon
10	Minto	4	Upper/Middle Yukon
6	Pelly	4	Upper/Middle Yukon
439	Porcupine	4	Upper/Middle Yukon
83	Salcha	4	Upper/Middle Yukon
4	Sheenjek	4	Upper/Middle Yukon
1	Tatchun	4	Upper/Middle Yukon
9	Teslin	4	Upper/Middle Yukon
84	Toklat	4	Upper/Middle Yukon
360	Alagoshak	5	Southwest Alaska
333	American_River	5	Southwest Alaska
366	Big_River	5	Southwest Alaska
354	Coleman_Creek	5	Southwest Alaska
355	Delta_Creek	5	Southwest Alaska
359	Egegik	5	Southwest Alaska
332	Frosty_Creek	5	Southwest Alaska
365	Gertrude_Creek	5	Southwest Alaska
370	Joshua_Green	5	Southwest Alaska

DFO Number	Population Name	Region Number	Region
364	Meshik	5	Southwest Alaska
283	Moller_Bay	5	Southwest Alaska
369	Pumice_Creek	5	Southwest Alaska
367	Stepovak_Bay	5	Southwest Alaska
335	Sturgeon	5	Southwest Alaska
350	Uganik	5	Southwest Alaska
334	Volcano_Bay	5	Southwest Alaska
356	Westward_Creek	5	Southwest Alaska
239	Ahnuhati	6	Pacific Northwest
69	Ahta_____	6	Pacific Northwest
155	Ain_	6	Pacific Northwest
183	Algard	6	Pacific Northwest
58	Alouette	6	Pacific Northwest
325	Alouette_North	6	Pacific Northwest
270	Andesite_Cr	6	Pacific Northwest
428	Arnoup_Cr	6	Pacific Northwest
153	Ashlulm	6	Pacific Northwest
156	Awun	6	Pacific Northwest
133	Bag_Harbour	6	Pacific Northwest
164	Barnard	6	Pacific Northwest
16	Bella_Bell	6	Pacific Northwest
79	Bella_Coola	6	Pacific Northwest
49	Big_Qual	6	Pacific Northwest
201	Big_Quilcene	6	Pacific Northwest
281	Bish_Cr	6	Pacific Northwest
198	Bitter_Creek	6	Pacific Northwest
103	Blackrock_Creek	6	Pacific Northwest
390	Blaney_Creek	6	Pacific Northwest
138	Botany_Creek	6	Pacific Northwest
264	Buck_Channel	6	Pacific Northwest
169	Bullock_Chann	6	Pacific Northwest
61	Campbell_River	6	Pacific Northwest
323	Carroll	6	Pacific Northwest
78	Cascade	6	Pacific Northwest
76	Cayeghle	6	Pacific Northwest
42	Cheakamus	6	Pacific Northwest
398	Cheenis_Lake	6	Pacific Northwest
51	Chehalis	6	Pacific Northwest
19	Chemainus	6	Pacific Northwest
47	Chilliwack	6	Pacific Northwest
392	Chilqua_Creek	6	Pacific Northwest
117	Chuckwalla	6	Pacific Northwest
139	Clapp_Basin	6	Pacific Northwest
107	Clatse_Creek	6	Pacific Northwest
118	Clyak	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
62	Cold_Creek	6	Pacific Northwest
77	Colonial	6	Pacific Northwest
353	Constantine	6	Pacific Northwest
168	Cooper_Inlet	6	Pacific Northwest
197	County_Line	6	Pacific Northwest
12	Cowichan	6	Pacific Northwest
414	Crag_Cr	6	Pacific Northwest
161	Dak_	6	Pacific Northwest
259	Dana_Creek	6	Pacific Northwest
123	Date_Creek	6	Pacific Northwest
250	Dawson_Inlet	6	Pacific Northwest
91	Dean_River	6	Pacific Northwest
261	Deena	6	Pacific Northwest
170	Deer_Pass	6	Pacific Northwest
46	Demamiel	6	Pacific Northwest
210	Dipac_Hatchery	6	Pacific Northwest
319	Disappearance	6	Pacific Northwest
269	Dog-tag	6	Pacific Northwest
177	Draney	6	Pacific Northwest
114	Duthie_Creek	6	Pacific Northwest
427	East_Arm	6	Pacific Northwest
266	Ecstall_River	6	Pacific Northwest
94	Elcho_Creek	6	Pacific Northwest
193	Ellsworth_Cr	6	Pacific Northwest
203	Elwha	6	Pacific Northwest
276	Ensheshese	6	Pacific Northwest
263	Fairfax_Inlet	6	Pacific Northwest
32	Fish_Creek	6	Pacific Northwest
429	Flux_Cr	6	Pacific Northwest
102	Foch_Creek	6	Pacific Northwest
179	Frenchman	6	Pacific Northwest
227	Gambier	6	Pacific Northwest
96	Gill_Creek	6	Pacific Northwest
166	Gilttoyee	6	Pacific Northwest
145	Glendale	6	Pacific Northwest
135	Gold_Harbour	6	Pacific Northwest
11	Goldstream	6	Pacific Northwest
66	Goodspeed_River	6	Pacific Northwest
136	Government	6	Pacific Northwest
205	Grant_Creek	6	Pacific Northwest
100	Green_River	6	Pacific Northwest
450	GreenRrHatchery	6	Pacific Northwest
237	Greens	6	Pacific Northwest
141	Harrison	6	Pacific Northwest
438	Harrison_late	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
64	Hathaway_Creek	6	Pacific Northwest
234	Herman_Creek	6	Pacific Northwest
17	Heydon_Cre	6	Pacific Northwest
407	Hicks_Cr	6	Pacific Northwest
400	Homathko	6	Pacific Northwest
411	Honna	6	Pacific Northwest
204	Hoodsport	6	Pacific Northwest
185	Hooknose	6	Pacific Northwest
406	Hopedale_Cr	6	Pacific Northwest
412	Hutton_Head	6	Pacific Northwest
278	Illiance	6	Pacific Northwest
152	Inch_Creek	6	Pacific Northwest
146	Indian_River	6	Pacific Northwest
92	Jenny_Bay	6	Pacific Northwest
115	Kainet_River	6	Pacific Northwest
144	Kakweiken	6	Pacific Northwest
268	Kalum	6	Pacific Northwest
395	Kanaka_Cr	6	Pacific Northwest
402	Kano_Inlet_Cr	6	Pacific Northwest
162	Kateen	6	Pacific Northwest
389	Kawkawa	6	Pacific Northwest
95	Kemano	6	Pacific Northwest
192	Kennedy_Creek	6	Pacific Northwest
238	Kennell	6	Pacific Northwest
351	Keta_Creek	6	Pacific Northwest
101	Khutze_River	6	Pacific Northwest
126	Khutzeymateen	6	Pacific Northwest
282	Kiltuish	6	Pacific Northwest
93	Kimsquit	6	Pacific Northwest
187	Kimsquit_Bay	6	Pacific Northwest
419	Kincolith	6	Pacific Northwest
273	Kispiox	6	Pacific Northwest
106	Kitasoo	6	Pacific Northwest
99	Kitimat_River	6	Pacific Northwest
275	Kitsault_Riv	6	Pacific Northwest
163	Kitwanga	6	Pacific Northwest
271	Kleanza_Cr	6	Pacific Northwest
437	Klewnuggit_Cr	6	Pacific Northwest
21	Klinaklini	6	Pacific Northwest
418	Ksedin	6	Pacific Northwest
125	Kshwan	6	Pacific Northwest
423	Kumealon	6	Pacific Northwest
112	Kwakusdis_River	6	Pacific Northwest
436	Kxngeal_Cr	6	Pacific Northwest
127	Lachmach	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
262	Lagins	6	Pacific Northwest
131	Lagoon_Inlet	6	Pacific Northwest
448	LagoonCr	6	Pacific Northwest
167	Lard	6	Pacific Northwest
160	Little_Goose	6	Pacific Northwest
50	Little_Qua	6	Pacific Northwest
413	Lizard_Cr	6	Pacific Northwest
119	Lockhart-Gordon	6	Pacific Northwest
176	Lower_Lillooet	6	Pacific Northwest
137	Mace_Creek	6	Pacific Northwest
242	Mackenzie_Sound	6	Pacific Northwest
116	MacNair_Creek	6	Pacific Northwest
55	Mamquam	6	Pacific Northwest
121	Markle_Inlet_Cr	6	Pacific Northwest
27	Martin_Riv	6	Pacific Northwest
338	Mashiter_Creek	6	Pacific Northwest
109	McLoughin_Creek	6	Pacific Northwest
178	Milton	6	Pacific Northwest
194	Minter_Cr	6	Pacific Northwest
254	Mountain_Cr	6	Pacific Northwest
111	Mussel_River	6	Pacific Northwest
157	Naden	6	Pacific Northwest
337	Nahmint_River	6	Pacific Northwest
444	Nakut_Su	6	Pacific Northwest
14	Nanaimo	6	Pacific Northwest
122	Nangeese	6	Pacific Northwest
422	Nass_River	6	Pacific Northwest
399	Necleetsconnay	6	Pacific Northwest
113	Neekas_Creek	6	Pacific Northwest
321	Neets_Bay_early	6	Pacific Northwest
320	Neets_Bay_late	6	Pacific Northwest
173	Nekite	6	Pacific Northwest
104	Nias_Creek	6	Pacific Northwest
143	Nimpkish	6	Pacific Northwest
53	Nitinat	6	Pacific Northwest
191	Nooksack	6	Pacific Northwest
186	Nooseseck	6	Pacific Northwest
318	NorrishWorth	6	Pacific Northwest
159	North_Arm	6	Pacific Northwest
377	Olsen_Creek	6	Pacific Northwest
184	Orford	6	Pacific Northwest
287	Pa-aat_River	6	Pacific Northwest
260	Pacofi	6	Pacific Northwest
56	Pallant	6	Pacific Northwest
65	Pegattum_Creek	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
48	Puntledge	6	Pacific Northwest
98	Quaal_River	6	Pacific Northwest
147	Quap	6	Pacific Northwest
108	Quartcha_Creek	6	Pacific Northwest
199	Quinault	6	Pacific Northwest
110	Roscoe_Creek	6	Pacific Northwest
397	Salmon_Bay	6	Pacific Northwest
195	Salmon_Cr	6	Pacific Northwest
134	Salmon_River	6	Pacific Northwest
200	Satsop	6	Pacific Northwest
236	Sawmill	6	Pacific Northwest
410	Seal_Inlet_Cr	6	Pacific Northwest
158	Security	6	Pacific Northwest
130	Sedgewick	6	Pacific Northwest
393	Serpentine_R	6	Pacific Northwest
317	Shovelnose_Cr	6	Pacific Northwest
249	Shustnini	6	Pacific Northwest
206	Siberia_Creek	6	Pacific Northwest
25	Silverdale	6	Pacific Northwest
196	Skagit	6	Pacific Northwest
274	Skeena	6	Pacific Northwest
171	Skowquiltz	6	Pacific Northwest
447	SkykomishRiv	6	Pacific Northwest
132	Slatechuck_Cre	6	Pacific Northwest
43	SlIAMmon	6	Pacific Northwest
15	Smith_Cree	6	Pacific Northwest
54	Snootli	6	Pacific Northwest
180	Southgate	6	Pacific Northwest
26	Squakum	6	Pacific Northwest
142	Squamish	6	Pacific Northwest
128	Stagoo	6	Pacific Northwest
265	Stanley	6	Pacific Northwest
52	Stave	6	Pacific Northwest
396	Stawamus	6	Pacific Northwest
409	Steel_Cr	6	Pacific Northwest
424	Stewart_Cr	6	Pacific Northwest
416	Stumaun_Cr	6	Pacific Northwest
327	Sugsaw	6	Pacific Northwest
324	Surprise	6	Pacific Northwest
75	Taaltz	6	Pacific Northwest
30	Taku	6	Pacific Northwest
18	Takwahoni	6	Pacific Northwest
251	Tarundl_Creek	6	Pacific Northwest
149	Theodosia	6	Pacific Northwest
22	Thorsen	6	Pacific Northwest

DFO Number	Population Name	Region Number	Region
129	Toon	6	Pacific Northwest
279	Tseax	6	Pacific Northwest
202	Tulalip	6	Pacific Northwest
97	Turn_Creek	6	Pacific Northwest
430	Turtle_Cr	6	Pacific Northwest
247	Tuskwa	6	Pacific Northwest
165	Tyler	6	Pacific Northwest
33	Tzoonie	6	Pacific Northwest
124	Upper_Kitsumkal	6	Pacific Northwest
140	Vedder	6	Pacific Northwest
70	Viner_Sound	6	Pacific Northwest
45	Wahleach	6	Pacific Northwest
172	Walkum	6	Pacific Northwest
73	Waump	6	Pacific Northwest
232	Wells_Bridge	6	Pacific Northwest
352	Wells_River	6	Pacific Northwest
105	West_Arm_Creek	6	Pacific Northwest
267	Whitebottom_Cr	6	Pacific Northwest
326	Widgeon_Slough	6	Pacific Northwest
277	Wilauks_Cr	6	Pacific Northwest
120	Wilson_Creek	6	Pacific Northwest
401	Worth_Creek	6	Pacific Northwest
60	Wortley_Creek	6	Pacific Northwest
248	Yellow_Bluff	6	Pacific Northwest
434	Zymagotitz	6	Pacific Northwest