Western Alaska Salmon Stock Identification Program **Technical Document:**[1] 2

Version : 1.0

Title: Investigation of temporal variation in sockeye and chum salmon baselines
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Introduction

During the initial review of the Western Alaska Salmon Stock Identification Program (WASSIP) study plan, the Technical Committee (TC) commented on the potential for fluctuation in allele frequencies (as a result of natural processes) to have an effect on the utility of the baselines for mixed stock analysis (MSA; Technical Document 1). The recommendation by the TC was "*At a minimum,* [the baselines] *should be evaluated to determine 1) the magnitude of allele frequency change over time; and 2) the relative magnitude of temporal and geographic differences in allele frequency.*"

There are two forces capable of changing allele frequencies over time: drift and selection. Traditionally, drift has been the primary force studied because most loci were thought to be neutral to selection. However, for some loci, selection may also play an important role (see Technical Document 5). This distinction is important because it will guide how we look for changes in allele frequencies through time. Drift changes allele frequencies at a rate inverse to the effective population size and has the same force on all loci. On the other hand, selection could change allele frequencies quickly even if the effective population sizes are large.

In the preliminary baselines destined for use in the WASSIP analysis for both sockeye salmon and chum salmon, numerous spawning locations were represented by collections taken in two or

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more years during approximately the same calendar times. For sockeye salmon, the baseline used in this analysis contained 127 repeat collections (that contained at least 30 fish each) representing 62 putative populations (subset of the baseline in Technical Document 5). For chum salmon the baseline contained 53 repeat collections representing 26 putative populations (Technical Document 4). We used these repeat collections to investigate the magnitude of temporal variation in allele frequencies. The baselines will continue to be updated with additional collections and additional loci through the spring and summer of 2010 and the analyses presented here (Version 1) will need to be repeated on the final datasets.

Methods

Variation in allele frequency over time within and between populations was measured in three ways: 1) a hierarchical log-likelihood ratio test (modified from Sokal and Rohlf 1995), 2) a hierarchical Analysis of Variance (Weir 1990), and 3) a graphical representation of pair-wise F_{ST} (Weir and Cockerham 1984). Separate analyses were done for each species.

Placing the log-likelihood ratio statistic into a hierarchical framework enables assessment of the relative effect of allele frequency differences within and between populations from samples taken in more than one year. However, interpretation of p-values calculated on these statistics is not straight-forward since the null hypothesis of homogeneity is typically violated due to genetic drift (Waples and Teel 1989). Log-likelihood ratio statistics were calculated using S-plus (TIBCO Software Inc., Palo Alto, CA).

Perhaps a more appropriate approach is a three-level Analysis of Variance (ANOVA) treating the temporal samples as sub-populations based on the method described in Weir (1990). Use of this method allows the quantification of the sources of total allelic variation and permits the calculation of the between-collection component of variance and the assessment of its magnitude relative to the between-population component of variance. This analysis was conducted using the software package GDA (Lewis and Zaykin 2001).

Pairwise F_{ST} values were calculated between all temporal collections using GDA. Patterns of variation within and between populations were visualized with two methods. First, the pairwise F_{ST} matrix was plotted as an image plot in the statistical package R (R Development Core Team 2008). The resulting plot is a grid where each "pixel" is a comparison between a pair of collections. A darker color indicates a larger F_{ST} between collections and, thus, larger differences between the collections. The information in the rows is exactly the same as that contained in the columns. Pixels directly on the diagonal are comparisons of collections with themselves and therefore represent zero, whereas pixels just off the diagonal indicate comparisons between collections from the same location in different years. Ideally, the pixels that indicate temporal comparisons would be white while and all others would be dark. This would indicate nicely that differences between temporal collections were small relative to differences between populations.

Second, the pairwise F_{ST} matrix was used as a dissimilarity matrix in the unweighted pair group method with arithmetic mean (UPGMA) algorithm to draw a tree. This allowed for grouping of collections into successive clusters based on the magnitude of the F_{ST} values between pairs or groups of collections. The expectation was that collections from the same population would have lower F_{ST} between them than they would with any collection from another population and would therefore be combined at the lowest level of the tree.

Results

Sockeye salmon

In the range-wide baseline for sockeye salmon 62 of the 375 populations represented had collections taken in more than a single year which had been assayed for genotypes (Table 1). These populations were centered in the Bristol Bay and Kuskokwim areas.

Log-likelihood ratio statistics, in a hierarchical framework, indicated that only seven of the 62 repeat collections showed heterogeneity within populations among years after adjusting for multiple tests (Table 2). For each region and overall regions, significant heterogeneity among populations was detected. The seven populations that showed significant heterogeneity among years after adjusting for multiple tests included: Elovka River, Goodnews River - Middle Fork, West Fork, Hewitt Lake, Larson Lake, Birch Creek, and Tatsamenie Lake. An additional four populations had significant deviations before adjusting for multiple tests: Goodnews River – North Fork, Idavain Creek, Fish Creek, and Skilak Lake. The three-level ANOVA indicated that the variation among populations was 41 times the amount of variation among repeat collections across years within populations (between collections, σ_S = 0.038; between populations, σ_P = 1.552; ratio 41.239).

Pairwise F_{ST} values showed that generally the variation among collections within populations (collections made across years) was smaller than the variation among populations (Figures 1 and 2). In the color-coded pair-wise F_{ST} plots (Figure 1), a white diagonal line through a field of reds and pinks is apparent which visually demonstrates the among-population variation relative the within-population variation.

In the UPGMA tree (Figure 2), most temporal collections paired together. The temporal collections within populations that did not group included: Elovka River from Russia where one collection paired with the other Russian population, but the second temporal collection paired with Big Lake in Cook Inlet; Spink Creek which paired with the geographic proximate population of Byers Lake in Cook Inlet; Clark River which is closely related to other Chignik drainage collections; Kogrukluk and Kanektok rivers, which are both from the Kuskokwim River drainage; and Lower and Upper Talarik creeks which are next to each other and drain into Iliamna Lake.

Chum salmon

In the range-wide baseline for chum salmon, 26 of the 153 populations represented had collections taken in more than a single year which had been assayed for genotypes (Table 3). These sets of collections were heavily weighted toward Western Alaska (12 populations) and Washington and Idaho (7 populations).

Three of the 26 within-population log-likelihood ratio tests were significant at $\alpha=0.05$ after accounting for multiple tests (Table 4). These included Amur River, Snake River, and Lilliwaup River - Summer. One additional collection was significant before accounting for multiple tests (George River). These four significant results were enough to drive the significance of the total within-population log-likelihood ratio test (Table 4). Despite these significant differences among temporal collections within populations, the three-level ANOVA shows that the among-population component of total allelic variation is 38.98 times greater than the among temporal collections within populations component (between collections, $\sigma_S = 0.040$; between populations, $\sigma_P = 1.541$; ratio 38.983).

The plot of pairwise F_{ST} values (Figure 3) visually shows that the differences between temporal collections within populations are in general relatively small. However, the large white patch in the lower, left-hand side of Figure 3 shows the lack of variation among the Western Alaska populations and the smaller white patch in the upper, right-hand side show similar lack of variation among populations within Washington and Idaho. These white patches demonstrate the lack of differentiation among populations within these regions relative to the differences between temporal collections within populations, which is problematic for distinguishing these populations in mixed stock analyses.

The UPGMA tree of pairwise F_{ST} values provides another visual way to see that there is little among-population variation relative to the variations among temporal collections within populations in the Western Alaska and the Washington/Idaho regions (Figure 4). Outside of these regions the temporal collections for populations pair together. Within these regions, some of the temporal collections pair together within populations. The pairing of some temporal collections of populations provides some hope that with additional targeted markers, there is potential to increase resolution among populations.

Conclusions

Other baselines containing relative temporal variation higher than observed in these baselines have been used successfully for MSA applications. For example, Beacham et al. (2005b) used a microsatellite baseline for sockeye salmon from British Columbia that yielded high resolution in MSA applications. In their baseline, they found variation among populations was approximately 13 times greater than annual variation. In our baseline, the variation among populations relative to the annual variation was much higher in both the chum and sockeye salmon baselines; 39 times higher for chum salmon and 41 times higher for sockeye salmon. In other words, the proportion of the total variation accounted for by variation among years was much smaller in our baselines than in the baseline used successfully for MSA by Beacham et al. (2005b).

The ratio of variation within populations (among years) relative to the variation among populations was similar or lower in our baseline than has been reported in other baselines covering similar geographic distributions (Pacific rim). The variation among populations was 13 times higher and 42 times higher than the variation among populations for chum salmon and sockeye salmon, respectively, from throughout the Pacific rim (Beacham et al. 2006; Beacham et al. 2009). The sockeye salmon baseline was determined to be useful for Pacific rim-wide MSA analyses (Beacham et al. 2005a).

The partitioning of variation within and between populations across baselines will be affected by three sources. First, the populations that are included in the baseline will have an effect. For example, if baseline collections represent higher proportions of populations from areas with more variation, then the proportion of variation accounted for by differences among years is going to be relatively smaller and vice-versa. Second, the number of years separating temporal collections will also have an effect on the among-year variation that is measured. In these species, samples separated by 3 to 5 years will generally measure intra-generational variation, while samples separated by longer periods will measure inter-generational variation. Third, differences in the characteristics of the marker type could affect the measurement of this ratio. For instance, Beacham et al. (2005a and 2009) used fewer microsatellite loci, but across all loci there were more alleles assayed than in the baselines used in this analysis.

One immediate concern that rises from this analysis is the lack of variation measured among populations from Western Alaska for chum salmon. The results presented here indicate that there is some signal for among-population differences, but that the signal is weak. This pattern is similar to the pattern seen earlier in sockeye salmon from the Meshik, Ugashik and Egegik drainages in Bristol Bay before the MHC locus was screened (Habicht et al. 2007). After the addition of the MHC loci to the baseline it was possible to segregate the populations and MSA simulations improved drastically. MHC appears to be a locus under selection (Technical Document 5), and the hope is that the new loci being developed for chum salmon based on cDNA and using Western Alaska populations as ascertainment (Technical Document 6) will provide loci that allow MSA to distinguish among populations in western Alaska.

In summary, temporal variation in allele frequencies within populations does not appear to be a major concern in these baselines. However, this analysis will be repeated when the full baseline sets are completed and many new temporal comparisons will be possible.

Future Directions

Sockeye salmon

1. Additional collections exist (many collected in 2009) that represent repeat temporal collections in the ADFG archive. Laboratory analysis of these collections has begun and will be used to expand the analysis of temporal variation.
2. Investigation of temporal variation at selected loci identified in Technical Document 5. For loci under selection, it will be important to look for Hardy-Weinberg disequilibrium as a sign of transition in the selected allele and then following up with new temporal collections to determine contemporary allele frequencies.
3. Investigation of the power of markers in development (Technical Document 6) to discriminate among populations.
4. Investigate the magnitude of intra- and inter-generational variation in allele frequencies in sockeye populations coastwide.

Chum salmon

1. Additional collections exist (some collected in 2009) that represent repeat temporal collections in the ADFG archive. Laboratory analysis of these collections has begun and will be used to expand the analysis of temporal variation.
2. Investigation of within-year run timing variation as noted in several populations during the baseline evaluation (Technical Document 4).
3. Investigation of the power of markers in development (Technical Document 6) to discriminate among populations especially in Western Alaska and Bristol Bay.
4. Investigate the magnitude of intra- and inter-generational variation in allele frequencies in chum populations coastwide.

Literature cited

Beaumont, M. A., and D. J. Balding. 2004. Identifying adaptive genetic divergence among populations from genome scans. Molecular Ecology 13(4):969-980.

Beacham, T. D., J. R. Candy, B. Mcintosh, C. MacConnachie, A. Tabata, K. Kaukinen, L. Deng, K. M. Miller, R. E. Withler, and N. Varnavskaya. 2005a. Estimation of stock composition and individual identification of sockeye salmon on a Pacific rim basis using microsatellite and major histocompatibility complex variation. Transactions of the American Fisheries Society 134:1124–1146.

Beacham T.D., B. McIntosh, and C. MacConnachie. 2005b. Population structure and stock identification of sockeye salmon (*Oncorhynchus nerka*) in coastal lakes in British Columbia, Canada. Canadian Journal of Zoology 83: 834–844.

Beacham. T. D., B. Mcintosh, C. MacConnachie, K. M. Miller, R. E. Withler, and N. Varnavskaya. 2006. Pacific rim population structure of sockeye salmon as determined from microsatellite analysis. Transactions of the American Fisheries Society 135:174–187.

Beacham, T. D., J. R. Candy, K. D. Le, and M. Wetklo. 2009. Population structure of chum salmon (*Oncorhynchus keta*) across the Pacific Rim, determined from microsatellite analysis. Fishery Bulletin 107: 244-260.

Habicht, C., L. W. Seeb, and J. E. Seeb. 2007. Genetic and ecological divergence defines population structure of sockeye salmon populations returning to Bristol Bay, Alaska, and provides a tool for admixture analysis. Transactions of the American Fisheries Society 136:82–94,

Lewis, P.O. and D. Zaykin. 2001. Genetic data analysis: computer program for the analysis of allelic data. Version 1.0. URL http://lewis.eeb.uconn.edu/lewishome/software.html.

R Development Core Team (2008). R: A language and environment for statistical computing. R

Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org.

Sokal, R.R. and F.J. Rohlf. 1995. Biometry. 3rd Edition. Freeman, San Francisco, CA.

Waples, R. S., and D. J. Teel. 1990. Conservation genetics of Pacific salmon. I. Temporal changes in allele frequency. Conservation Biology. 4: 144-156.

Waples, R. S. 1990. Temporal changes of allele frequency in Pacific salmon - implications for mixed-stock fishery analysis. Canadian Journal of Fisheries and Aquatic Sciences 47(5):968-976.

Weir, B. S. 1990. Genetic data analysis. Sinauer Associates, Sunderland, Massachusetts.

Weir, B.S. and C.C. Cockerham. 1984. Estimating F-statistics for the analysis of population structure. Evolution 38. 1358-1370.

Technical Committee review and comments

Document 2: Investigation of temporal variation in sockeye and chum salmon baselines

Line 18: migration also can affect allele frequencies

23: drift might have the same 'force' on all loci but the consequences vary among loci due to chance

45: is this a G test?

59: *FST* refers to differences among geographic subpopulations; temporal F should be used for temporal comparisons

88-90: care should be used in applying a multiple testing adjustment for large datasets like this, as the adjusted critical P value can be so low that meaningful differences are obscured. If an explicit adjustment is made for multiple tests, it is preferable to also report results of the unadjusted tests so the reader can better evaluate how well results compare with null expectations.

176-177: actually, comparison of parents and offspring (~3-5 years apart) should produce the smallest genetic differences, while samples taken 1-2 years apart share no parents and should be relatively more divergent. See Waples 1990 J. Heredity.

[*Unedited comments from "Panel comments October 2009.doc" related to Technical Document 2*.]

Table 1. Collections of sockeye salmon sampled from the same location at approximately the same time in the calendar year but in multiple years organized by region used to examine within-population and among population genetic variability. Sample year and sample sizes are provided.

Region	Population	Collection	Year	N
Western Kamchatka				
	Ozernaya River	Ozernaya River	2000	50
		Ozernaya River	2002	50
	Elovka	Elovka	1994	69
		Elovka	1995	40
NW Bristol Bay - Yukon Kuskokwim				
	Andreafsky River	Andreafsky River weir	2006	48
		Andreafsky River weir	2008	47
	Necons River	Necons River	2006	55
		Necons River	2007	93
	Kogrukluk River	Kogrukluk River weir	2001	95
		Kogrukluk River weir	2007	48
	Kanektok River	Kanektok River weir	2002	95
		Kanektok River weir	2007	48
	Goodnews River - North Fork	Goodnews River - North Fork	2002	95
		Goodnews River - North Fork	2006	48
	Goodnews River - Middle Fork	Goodnews River weir - Middle Fork	2007	47
		Goodnews River weir - Middle Fork	2001	96
		Goodnews River weir - Middle Fork	1991	48
	Togiak Lake	Togiak Lake, Sunday Creek	2000	95
		Togiak Tower	2006	95
	Silver Horn	Silver Horn beaches	2008	124
		Silver Horn beaches	2007	95
	Hardluck Bay	Hardluck Bay	2008	157
		Hardluck Bay beaches	2007	95
	Little Togiak Lake	A Beach - Little Togiak Lake	2004	65
		A Beach - Little Togiak Lake	2005	30
	Pick Creek	Pick Creek	2001	95

Region	Population	Collection	Year	N
		Pick Creek	2008	93
Eastern Bristol Bay				
	Tomkok Creek	Tomkok Creek	2000	95
		Tomkok Creek	2002	48
	Tommy Creek	Tommy Creek	2002	48
		Tommy River	2000	96
	Copper River	Copper R. (Iliamna Lk. System)	1999	47
		Copper River	2000	96
	Gibralter River	Gibralter R. (Iliamna Lk. System)	1999	48
		Gibralter River	2000	96
	Upper Talarik	Upper Talarik	2004	95
		Upper Talarik	2006	95
	Lower Talarik	Lower Talarik	2001	70
		Lower Talarik Creek	2000	95
	Moraine Creek	Moraine Creek	2004	95
		Moraine/Funnel Creek	2001	96
	Battle River	Battle River	2004	96
		Battle Creek	2001	96
	Kulik River	Kulik River	2001	96
		Kulik River	2004	96
	Americian River	American River, Naknek Lake	2000	92
		American River	2001	95
	Idavain Creek	Idavain Creek	2000	95
		Idavain Creek	2006	48
	Kejulik River	Upper Kejulik River	2000	48
		Kejulik River	2001	96
Alaska Peninsula				
	Sandy Lake	Sandy Lake	2000	96
		Sandy River weir	2007	95
	Hoodoo Lake	Hoodoo Lake - Sapsuk shoal spawners	2005	95
		Hoodoo Lake	2001	95
	Chiaktuak Creek	Chiaktuak Creek	2008	174

Region	Population	Collection	Year	N
		Chiaktuak Creek	1997	94
	West Fork	West Fork	2008	184
		West Fork	1997	95
	Clark River	Clark River	2008	122
		Clark River September	1997	94
Western GOA				
	Ayakulik River	Ayakulik River weir	2000	96
		Ayakulik River Weir - Late	2008	95
	Saltery Lake	Saltery	1994	95
		Saltery Lake	1999	95
	Chilligan River	Chilligan River	1992	95
		Chilligan River	1994	48
	Lone King Creek	Lone King Creek	2006	30
		Lone King Creek	2008	30
	Packers Lake	Packers Lake	1992	95
		Packers Lake, Kalgin Island	1993	48
	Judd Lake	Judd - Susitna weir	2006	94
		Judd Lake, Talachulitna R.	1993	95
	Shell Lake	Shell - Susitna weir	2006	95
		Shell Lake, Skwentna R.	1993	94
	Hewitt Lake	Hewitt - Susitna weir	2006	65
		Hewitt Lake	1992	49
	West Fork Yentna River	Unnamed Slough, W. Fork	1992	96
		West Fork Yentna River	1993	100
	Chelatna Lake	Chelatna - Susitna weir	2006	95
		Chelatna Lake, Yentna R.	1993	95
	Swan Lake	Swan Lake	2006	95
		Swan Lake - Susitna weir	2007	47
	Byers Lake	Byers - Susitna weir	2007	95
		Byers Lake	1993	95
	Spink Creek	Spink Creek	2007	30
		Spink Creek - Mouth	2008	95

Region	**Population**	**Collection**	**Year**	**N**
	Stephan Lake	Stephan - Susitina weir	2007	95
		Stephan Lake	1993	95
	Larson Lake	Larson Lake	2006	94
		Larson Lake	1993	95
	Birch Creek	Birch Creek	2007	133
		Birch Creek	1993	67
	Big Lake	Big Lake	1992	95
		Fish Creek weir	1994	94
		Fish Creek	1993	95
	Williwaw Creek	Williwaw Creek	2006	39
		Williwaw Creek	2007	69
	Moose Creek	Moose Creek Kenai	1994	95
		Moose Creek, Kenai R.	1993	47
	Ptarmigan Creek	Ptarmigan Creek	1992	47
		Ptarmigan Creek	1993	95
	Tern Lake	Tern Lake	1992	48
		Tern Lake	1993	95
	Skilak Lake	Skilak Lake	1995	48
		Skilak Lake	1992	96
	Eshamy Creek	Eshamy Creek	2008	95
		Eshamy Lake	1991	96
Eastern GOA				
	Windfall Lake	Windfall Lake	2003	48
		Windfall Lake	2007	48
	Nahlin River	Nahlin River	2003	50
		Nahlin River	2007	34
	Tatsamenie Lake	Tatsamenie	1992	95
		Tatsamenie Lake	2005	95
	Iskut River	Iskut River	2002	31
		Iskut River	1985	30
	McDonald Lake	McDonald Lake - Hatchery Creek	2007	93
		Hatchery Creek - McDonald Lake	2001	96

Region	Population	Collection	Year	N
		Hatchery Creek - McDonald Lake	2003	96
	Heckman Lake	Heckman Lake	2004	95
		Heckman Lake - Naha River	2007	95
	Red Bay Lake	Red Bay Lake	2004	95
		Red Bay Lake	1992	50
	Sweetwater Lake	Hatchery Creek - Sweetwater	2007	95
		Hatchery Creek - Sweetwater Lake	2003	47
	Meziadin Lake	Meziadin Beach	2006	95
		Meziadin Lake	2001	95

Table 2. Hierarchical test for temporal variation in sockeye salmon using the log-likelihood ratio test of population homogeneity based on 44 SNP loci. Comparisons are limited to populations where samples from multiple years exist in the current coastwide SNP baseline. Collections years are incorporated at the end of the population names.

Region	Populations	p-value		G	DF
Western Kamchatka					
Between Pops		0.000	**	565.0	54
Within Pops		0.000	**	392.8	108
	Ozernaya.00.02	0.080		69.2	54
	Elovka.94.95	0.000	**	323.6	54
NW Bristol Bay-Yukon Kuskokwim					
Between Pops		0.000	**	10100.0	540
Within Pops		0.041	*	712.1	648
	Andreafsky.06.08	0.803		45.0	54
	Necons.06.07	0.877		42.3	54
	Kogrukluk.01.07	0.242		60.9	54
	Kanektok.02.07	0.258		60.3	54
	GoodnewsNorth.02.06	0.003	**	87.8	54
	GoodnewsMid.07.01.91	0.000	**	181.2	108
	TogiakLake.00.06	0.424		55.4	54
	SilverHorn.08.07	0.427		55.3	54
	Hardluck.08.07	0.950		38.1	54
	LittleTogiak.04.05	0.964		36.9	54
	Pick.01.08	0.662		49.1	54
Eastern Bristol Bay					
Between Pops		0.000	**	6159.0	594
Within Pops		0.441		652.7	648
	Tomkok.00.02	0.925		39.8	54
	Tommy.02.00	0.006		83.8	54
	Copper.99.00	0.722		47.5	54
	Gibralter.99.00	0.108		67.1	54
	UpTalarik.04.06	0.031		75.1	54
	LowTalarik.01.00	0.874		42.4	54
	Moraine.04.01	0.956		37.6	54
	Battle.04.01	0.896		41.4	54
	Kulik.01.04	0.677		48.7	54
	American.00.01	0.987		33.7	54
	Idavain.00.06	0.003	**	87.5	54
	Kejulik.00.01	0.702		48.1	54
Alaska Peninsula					
Between Pops		0.000		2656.0	216
Within Pops		0.001		345.7	270
	Sandy.00.07	0.189		63.0	54
	Hoodoo.05.01	0.637		49.8	54
	Chiaktuak.08.97	0.739		47.0	54

Region	Populations	p-value		G	DF
	WestFork.08.97	0.000	**	135.8	54
	Clark.08.97	0.624		50.1	54
Western GOA					
Between Pops		0.000	**	38420.0	1188
Within Pops		0.000	**	1581.9	1242
	Ayakulik.00.08	0.106		67.3	54
	Saltery.94.99	0.227		61.5	54
	Chilligan.92.94	0.970		36.2	54
	LoneKing.06.08	0.111		66.9	54
	Packers.92.93	0.775		45.9	54
	Judd.06.93	0.385		56.4	54
	Shell.06.93	0.075		69.6	54
	Hewitt.06.92	0.000	**	132.9	54
	WestYentna.92.93	0.556		51.9	54
	Chelatna.06.93	0.376		56.7	54
	Swan.06.07	0.789		45.5	54
	Byers.07.93	0.263		60.1	54
	Spink.07.08	0.177		63.5	54
	Stephan.07.93	0.022		76.8	54
	Larson.06.93	0.000	**	108.4	54
	Birch.07.93	0.000	**	155.8	54
	FishCr.94.93.92	0.009	**	145.5	108
	Williwaw.06.07	0.519		52.9	54
	Moose.94.93	0.787		45.5	54
	Ptarmigan.92.93	0.650		49.5	54
	Tern.92.93	0.401		56.0	54
	Skilak.95.92	0.020	*	77.3	54
Eastern GOA					
Between Pops		0.000	**	13060.0	432
Within Pops		0.052		651.0	594
	Eshamy.08.91	0.763		46.3	54
	Windfall.03.07	0.210		62.1	54
	Nahlin.03.07	0.078		69.3	54
	Tatsamenie.92.05	0.000	**	108.8	54
	Iskut.02.85	0.266		60.1	54
	McDonald.07.03.01	0.063		131.3	108
	Heckman.04.07	0.813		44.7	54
	RedBay.04.92	0.774		45.9	54
	Sweetwater.07.03	0.757		46.5	54
	Meziadin.06.01	0.972		36.0	54
Total					
Between Pops		0.000	**	70960.0	3024
Within Pops		0.000	**	4336.2	3510
Between Regions		0.000	**	31184.0	270
Overall		0.000	**	106480.2	6804

Table 3. Collections of chum salmon sampled from the same location at approximately the same time in the calendar year but in multiple years organized by region used to examine within-population and among population genetic variability. Sample year and sample sizes are provided.

Region	Population	Collection	Year	N
Japan				
	Tokachi River	Tokachi River	2002	79
		Tokachi River	1990	80
Russia				
	Amur River	Amur River - summer	1997	60
		Amur River - summer	2001	99
	Anadyr River	Anadyr River - early	2000	28
		Anadyr River - early	1993	31
	Kamchatka	Kamchatka - early	2003	50
		Kamchatka - early	1990	50
Kotzebue Sound				
	Kobuk River	Kobuk River	2005	95
		Kobuk - Salmon River	1991	95
Norton Sound				
	Pilgrim River	Pilgrim River	1994	90
		Pilgrim River	2005	94
	Snake River	Snake River	1993	35
		Snake River	1995	58
		Snake River	2005	95
	Unalakleet River	Unalakleet River	1992	48
		Unalakleet River	2004	95
Yukon Alaska Early				
	Andreafsky River	East Fork Andreafsky River	1993	95
		Andreafsky River - East Fork weir	2004	94
Yukon Alaska Late/Mid				
	Delta River	Delta River	1992	95
		Delta River	1994	95
Yukon Canada				
	Kluane River	Kluane River	2001	93

Region	Population	Collection	Year	N
		Kluane River	2007	33
Kuskokwim				
	Goodnews River	Goodnews River - North Fork	2006	46
		Goodnews Weir	1991	100
	Holokuk River	Holokuk River	1995	48
		Holokuk River	2007	62
	Kogrukluk River	Kogrukluk River	1992	44
		Kogrukluk River	1993	50
	Kwethluk River	Kwethluk River	2007	198
		Kwethluk River	1994	96
	George River	George River	1996	95
		George River	2007	289
Bristol Bay				
	Stuyahok River	Stuyahok River	1992	31
		Stuyahok River	1993	56
Cook Inlet West				
	McNeil River	McNeil River Lagoon	1994	60
		McNeil River	1996	49
Northern SE Alaska				
	Long Bay	Long Bay	1991	66
		Long Bay	1992	95
Washington/Idaho				
	Big Mission Creek	Big Mission Creek - fall	2003	47
		Big Mission Creek - fall	2002	47
	Hamma Hamma River	Hamma Hamma River - summer	2001	47
		Hamma Hamma River - summer	2003	48
	Jimmy Creek	Jimmy Creek - summer	2000	46
		Jimmy Creek - summer	2001	49
	Lilliwaup River - fall	Lilliwaup River - fall	2005	45
		Lilliwaup River - fall	2006	48
	Lilliwaup River - summer	Lilliwaup River - summer	2002	43
		Lilliwaup River - summer	2001	48

Region	Population	Collection	Year	N
	North Creek	North Creek - fall	1994	47
		North Creek - fall	1998	48
	Union River	Union River - summer	2004	42
		Union River - summer	2003	53

Table 4. Hierarchical test for temporal variation in chum salmon using the log-likelihood ratio test of population homogeneity based on 52 SNP loci. Comparisons are limited to populations where samples from multiple brood years exist in the current coast-wide SNP baseline. Collections years are incorporated at the end of the population names.

Region		Populations	p-value		G	DF
Japan						
		Tokachi.90.02	0.134		65.6	54
Russia						
	Between pops		0.000	**	1272.0	108
	Within pops		0.000	**	233.8	162
		Amur.97.01	0.000	**	194.3	54
		Anadyr.93.00	0.985		33.9	54
		Kamchatka.90.03	1.000		5.6	54
Kotzebue Sound						
		Kobuk.91.05	0.307		58.7	54
Norton Sound						
	Between pops		0.002	*	154.2	108
	Within pops		0.000	**	341.5	216
		Pilgrim.94.05	0.429		55.2	54
		Snake.93.95.05	0.000	**	215.6	108
		Unalakleet.92.04	0.063		70.7	54
Yukon Alaska, early						
		Andreafsky.93.04	0.441		54.9	54
Yukon Alaska, late						
		Delta.92.94	0.908		40.8	54
Yukon Canada						
		Kluane.01.07	0.788		45.5	54
Kuskokwim						
	Between pops		0.000	**	305.9	216
	Within pops		0.137		295.6	270
		Goodnews.91.06	0.232		61.3	54
		Holokuk.95.07	0.260		60.3	54
		Kogrukluk.92.93	0.929		39.6	54
		Kwethluk.94.07	0.226		61.5	54
		George.96.07	0.044		73.0	54
Bristol Bay						
		Stuyahok.92.93	0.175		63.6	54
Cook Inlet, west						
		McNeil.94.96	0.266		60.1	54
Northern Southeast						
		LongBay.91.92	0.318		58.4	54

Region	Populations	p-value		G	DF
Washington					
	Between pops	0.000	**	2405.0	324
	Within pops	0.005	*	451.7	378
	BigMission.02.03	0.464		54.3	54
	HammaHamma.01.03	0.465		54.2	54
	Jimmy.00.01	0.314		58.5	54
	LilliwaupFall.05.06	0.459		54.4	54
	LilliwaupSum.01.02	0.000	**	120.9	54
	NorthCreek.94.98	0.491		53.6	54
	Union.03.04	0.407		55.8	54
Total					
	Between regions	0.000	**	31868	594
	Between pops	0.000	**	4137.1	756
	Within pops	0.000	**	1769.9	1458
	Overall	0.000	**	377774.8	2808

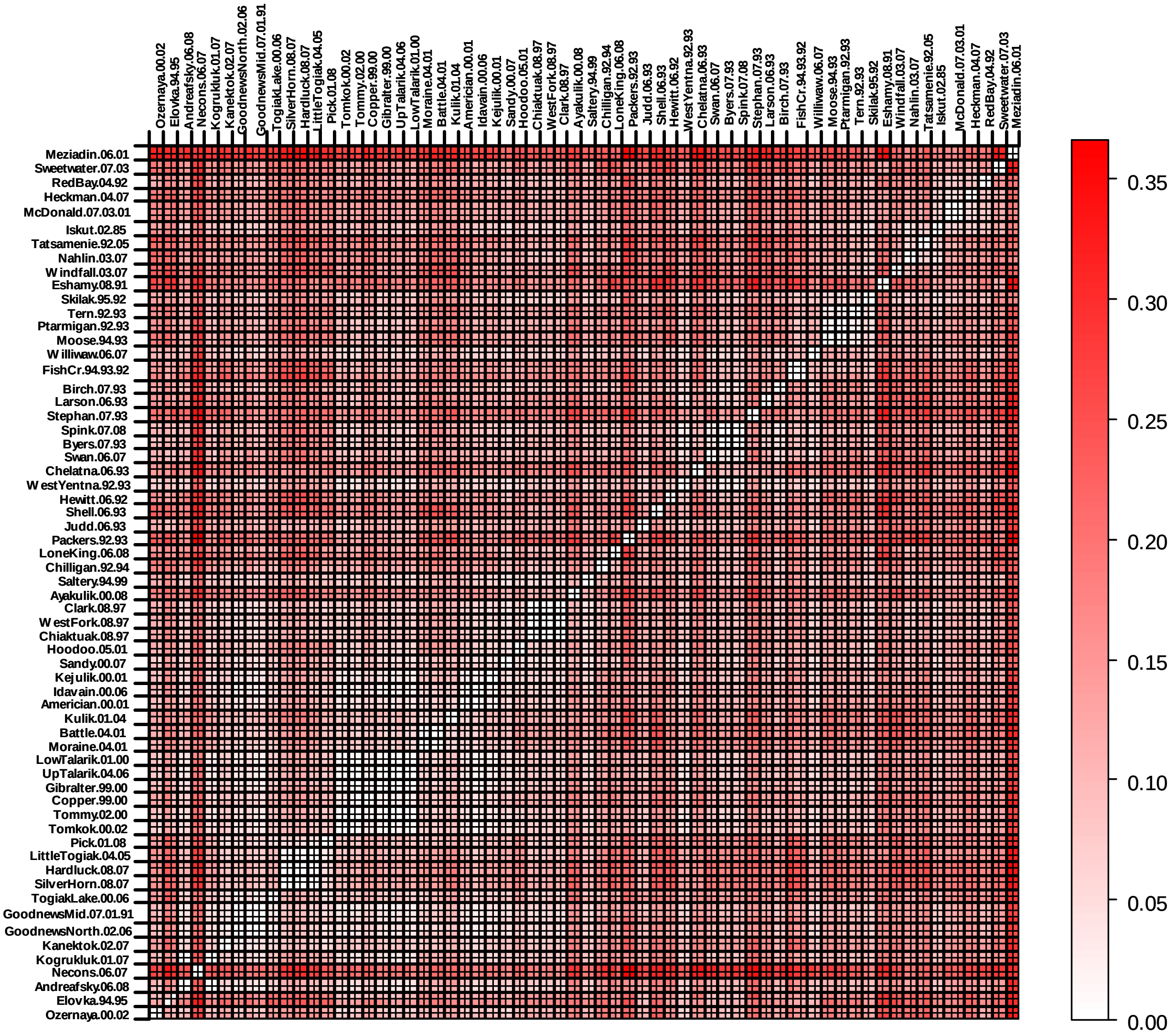

Figure 1. Color-coded pair-wise F_{ST} plots for the inter-annual baseline collections for sockeye salmon. Darker colors indicate higher differences among collections. The diagonal line is white because pair-wise F_{ST} values between the collection and itself is zero. Cells close to the diagonal represent pair-wise F_{ST} values among collections taken in different years for the same population.

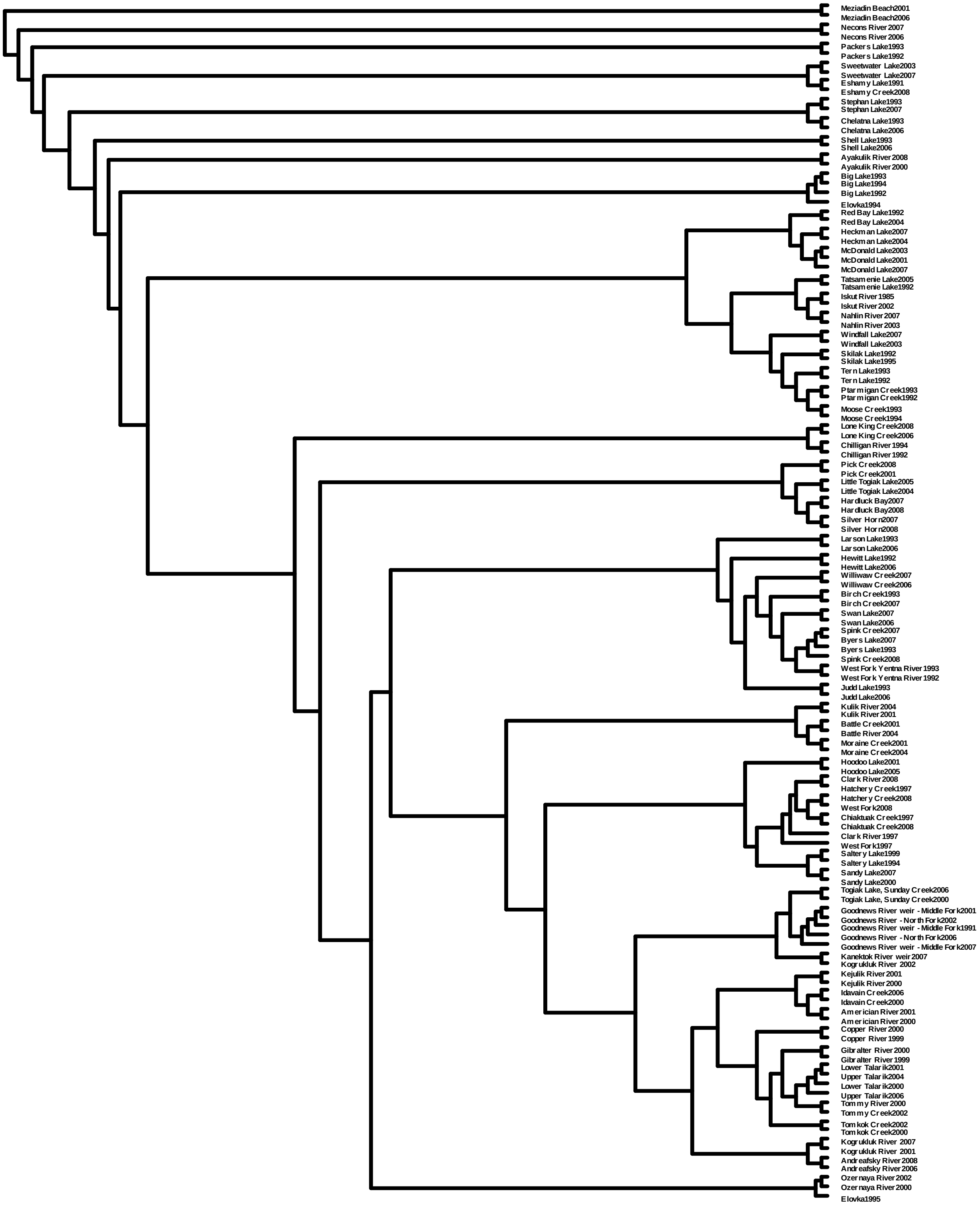

Figure 2. Unweighted pair-group method (UPGMA) tree of pair-wise F_{ST} values for sockeye salmon populations that are represented by two or more collections taken in different years. Generally, collections taken over different years at the same location pair together.

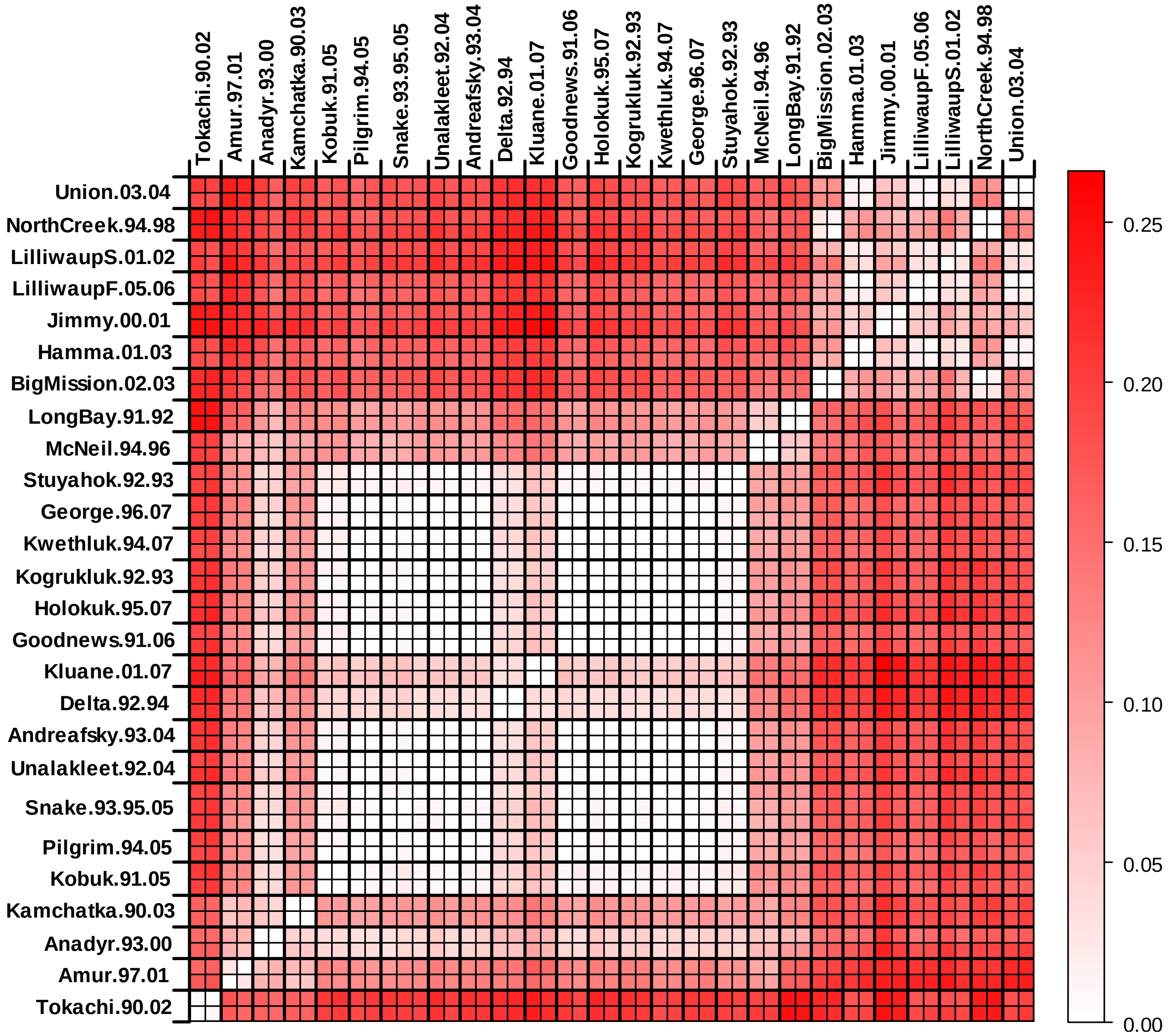

Figure 3. Color-coded pair-wise F_{ST} plots for the inter-annual baseline collections for chum salmon. Darker colors indicate higher differences among collections. The diagonal line is white because pair-wise F_{ST} values between the collection and itself is zero. Cells close to the diagonal represent pair-wise F_{ST} values among collections taken in different years for the same population. The large white patch in the lower, left-hand side of the figure shows the lack of variation among the Western Alaska populations and the smaller white patch in the upper, right-hand side show similar lack of variation among populations within Washington.

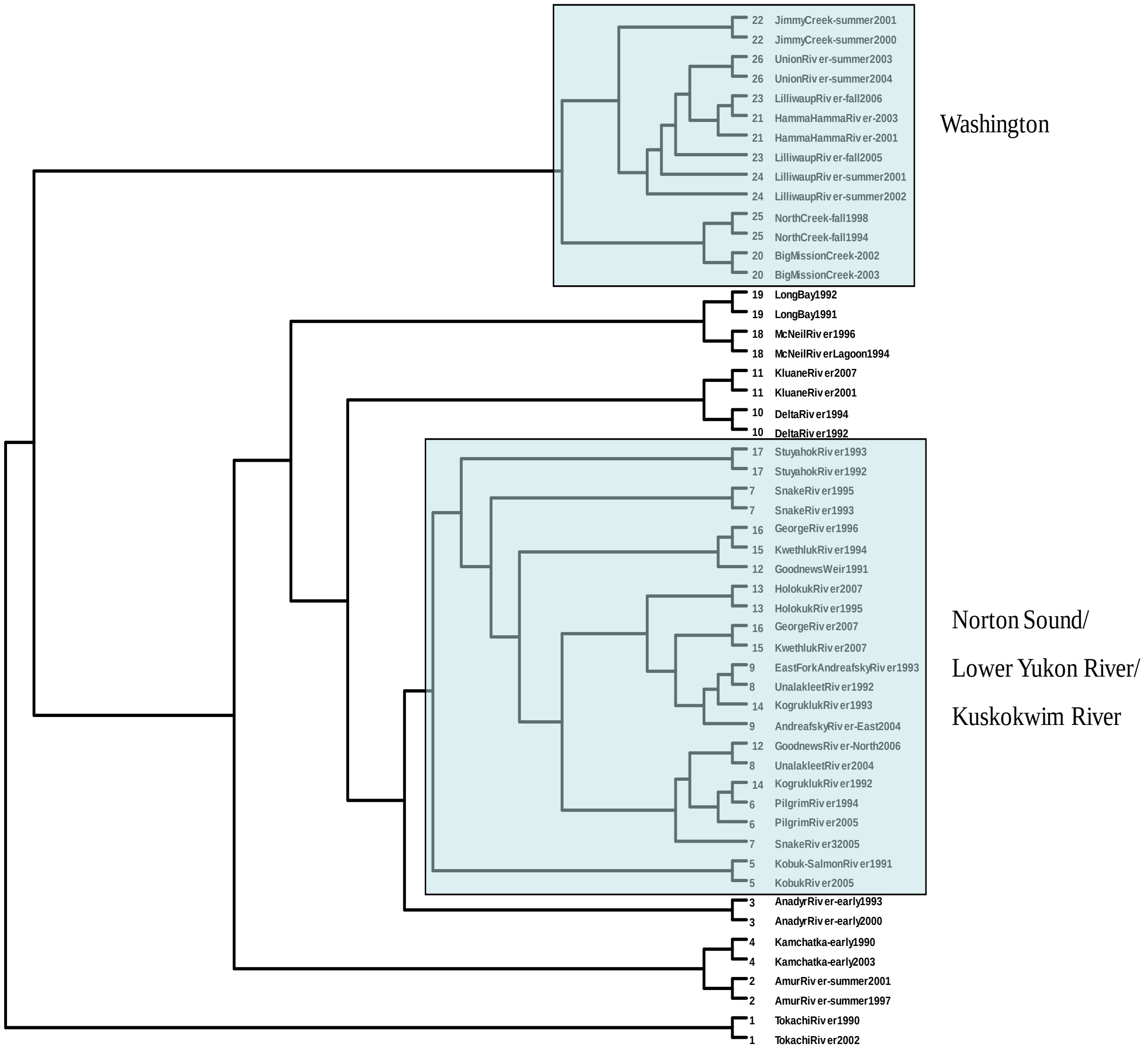

Figure 4. Unweighted pair-group method (UPGMA) tree of pair-wise F_{ST} values for chum salmon populations that are represented by two or more collections taken in different years. Generally, collections taken over different years at the same location pair together except in the areas highlighted in green which include Western Alaska and Washington/Idaho.