

Population Structuring Among Steelhead of the Alsea Basin

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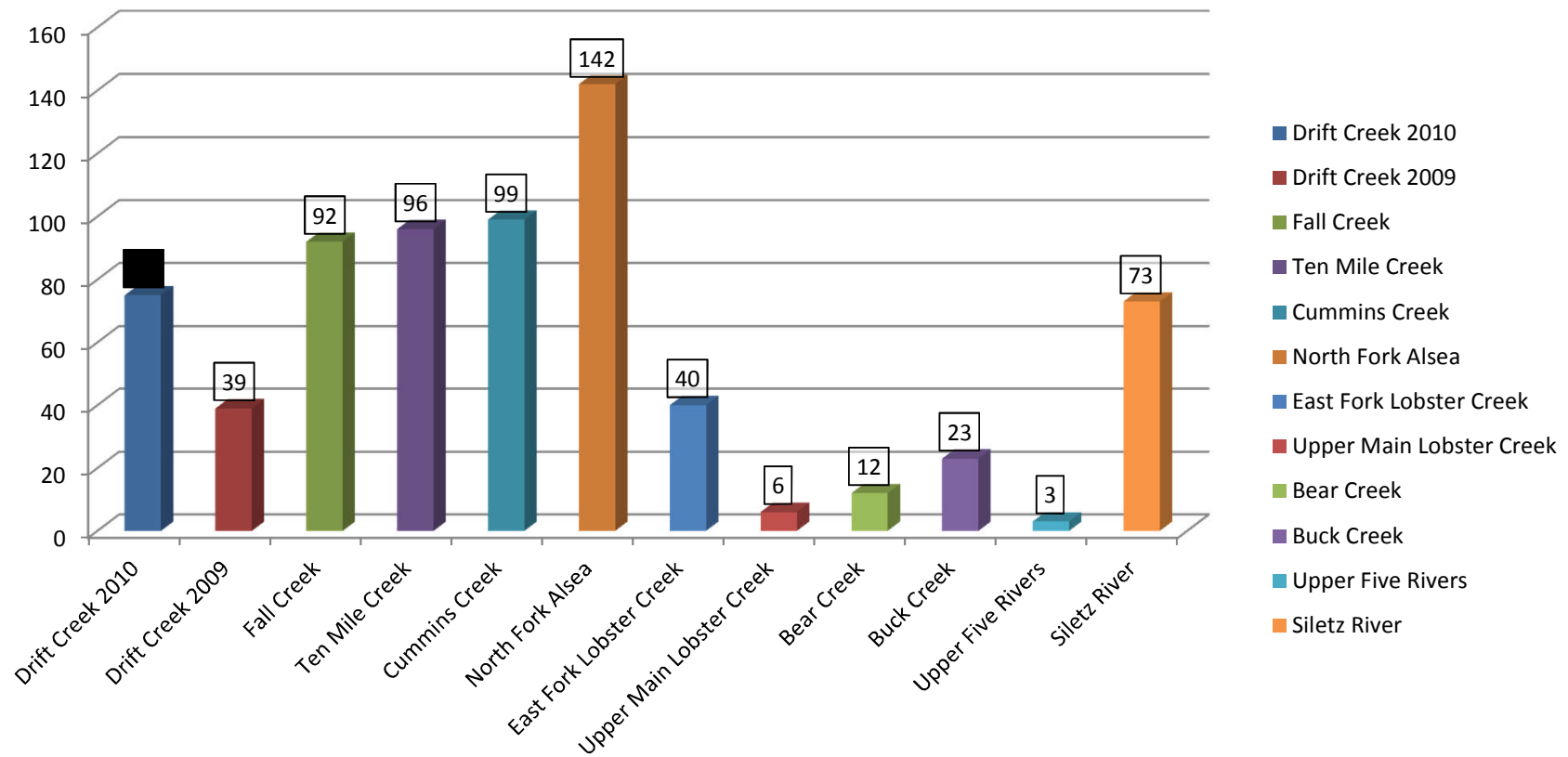
Populations

- 12 populations, 715 individuals.
- Alsea locations: Drift Creek, North Fork Alsea, Five Rivers, Lobster Creek, and Fall Creek.
- Out of basin locations: Siletz River, Ten Mile Creek, Cummins Creek.



Populations

Locations vs. Samples



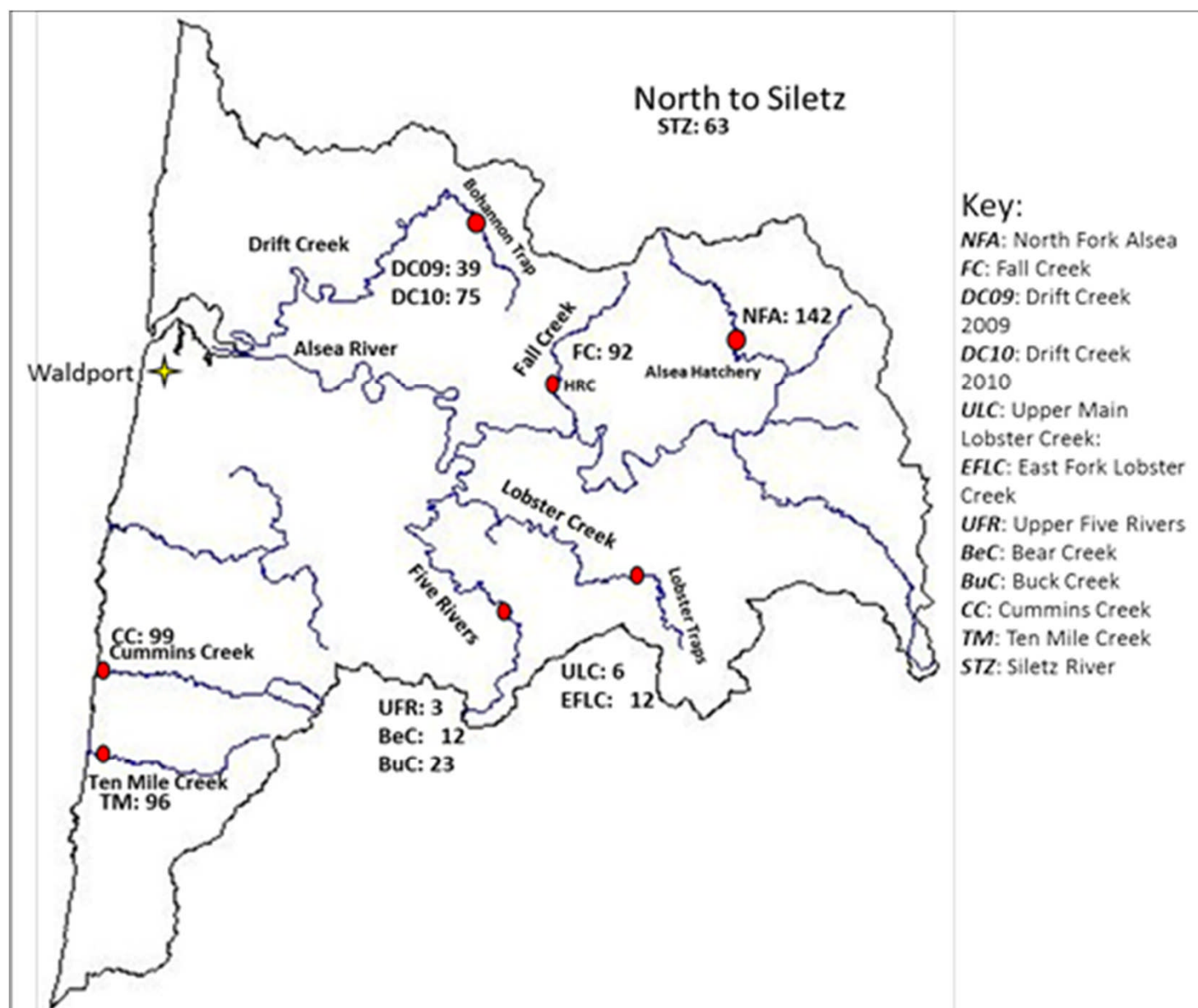


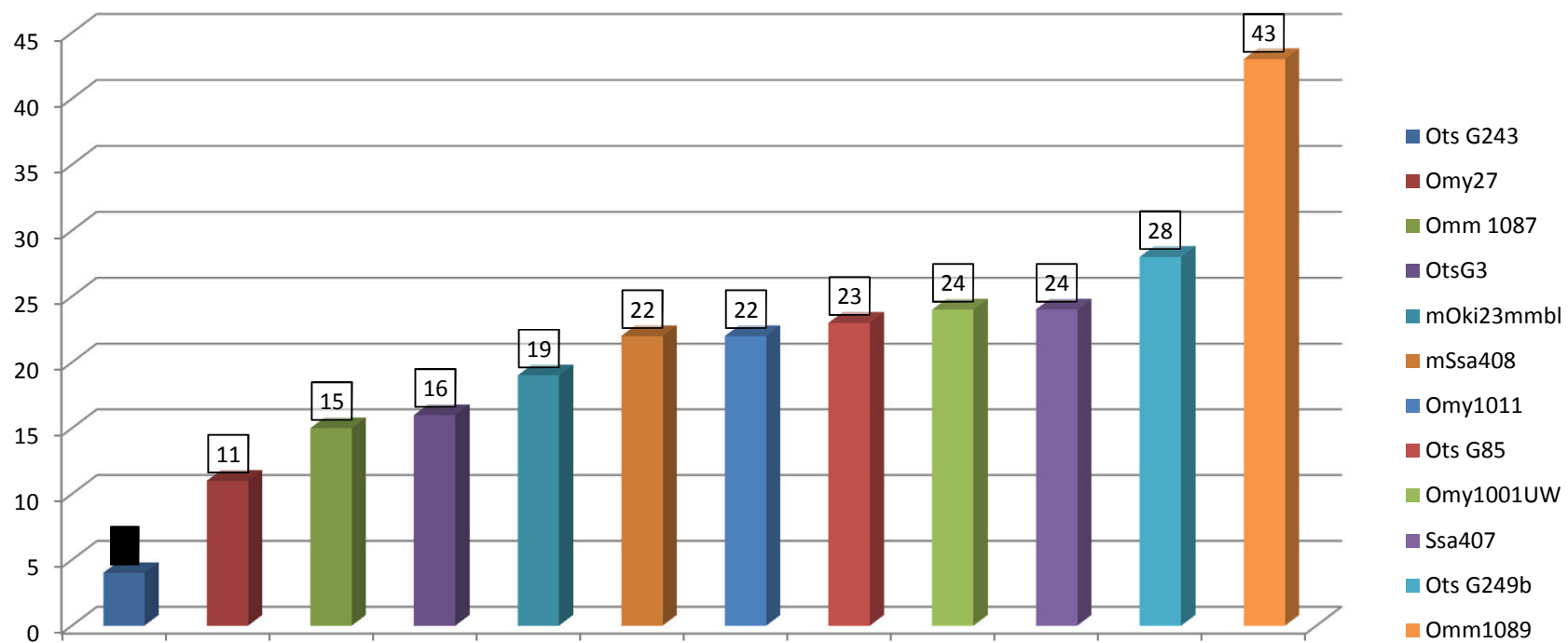
Figure 1: *O. mykiss* sampling locations, with population acronyms right. Sample sizes are listed next to site names.

Loci

- 12 microsatellite loci
- Samples with 7 or more failed amplifications were removed (15 samples).

Loci

Loci vs. Alleles

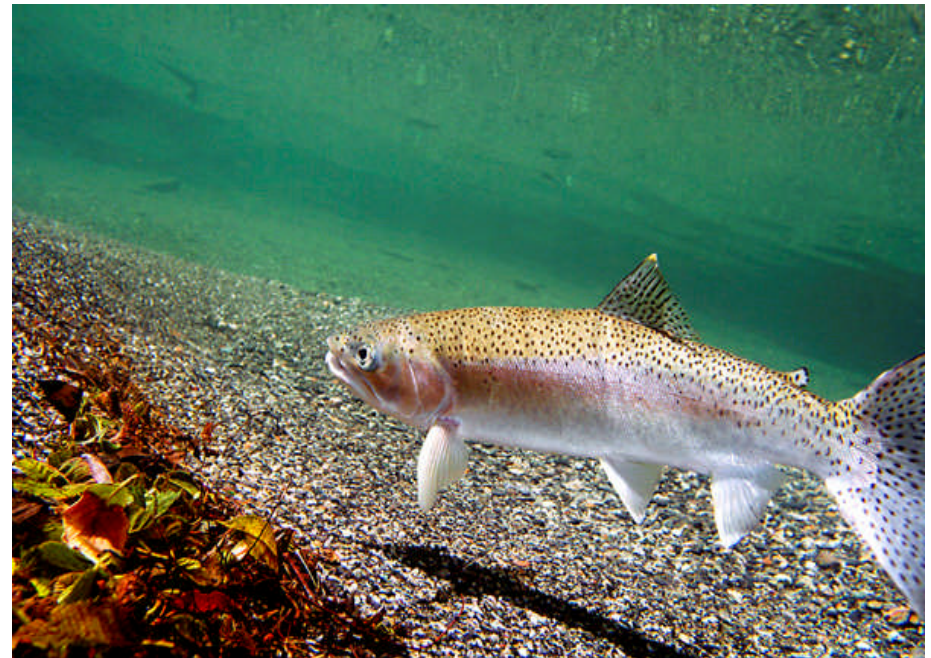


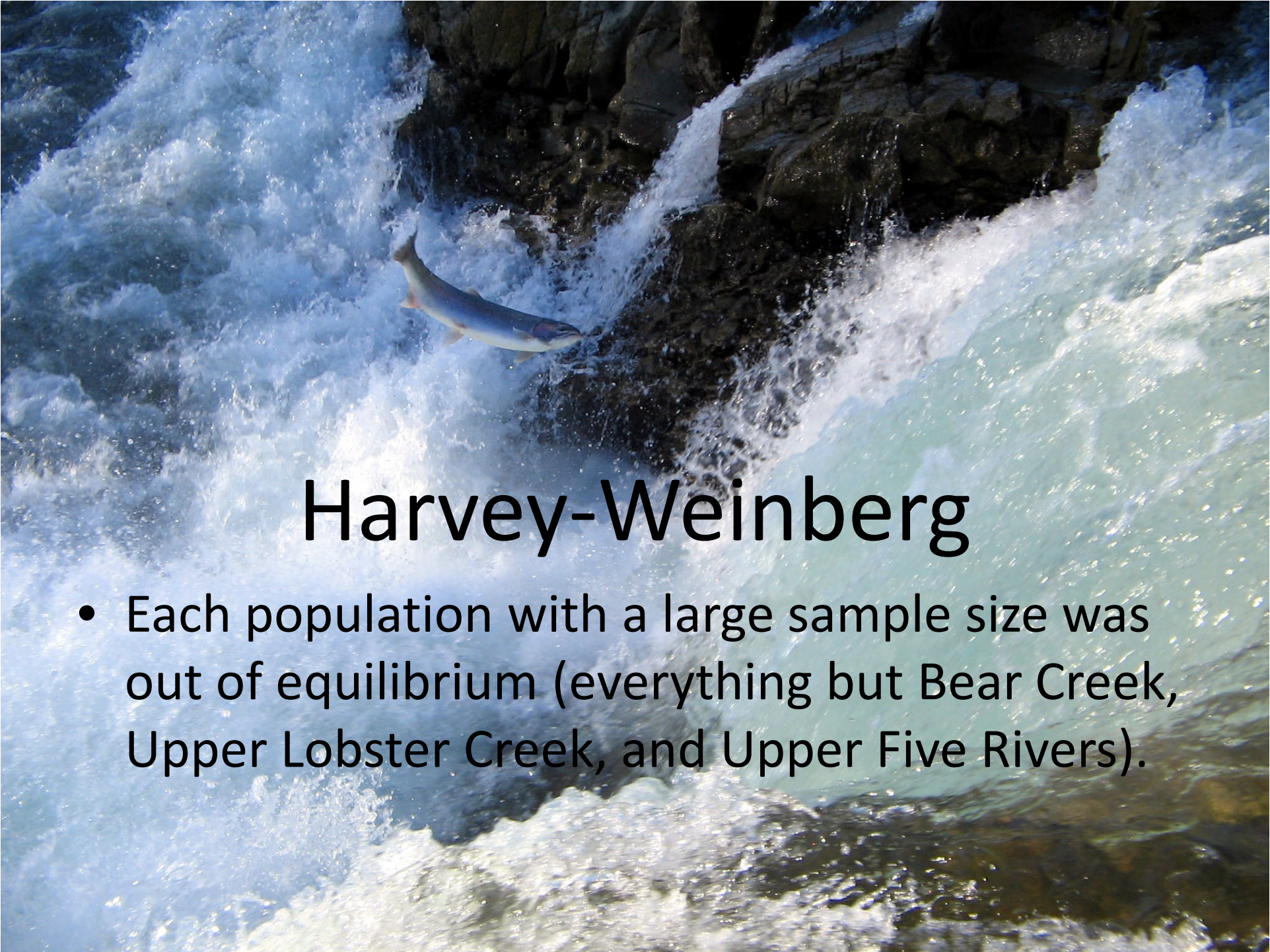
Note:

- Two individuals were removed before further analysis, one from Ten Mile Creek, one from Cummins Creek. Both were strong outliers with bad amplification.
- The Ten Mile individual was unscored on 3 loci, homozygous for several others with poor amplification.
- The Cummins Creek individual was unscored on 6 loci, with poor amplification on the others.
- Only changes “All site” results.

Linkage Disequilibrium

- Populations displaying significant LD (greater 20% of crosses from 100 permutations significant, GENETIX):
 - Cummins Ck (99): 56%
 - N. Fork Alsea (142): 50%
 - Bear Creek(12): 30%
 - E. Fork Lobster Ck (40): 24%
 - Drift Ck 10 (75): 23%



A photograph of a salmon in mid-air, jumping over a rocky waterfall. The water is turbulent and white with foam, and the rocks are dark and jagged. The salmon is silvery with a hint of orange on its tail and belly.

Harvey-Weinberg

- Each population with a large sample size was out of equilibrium (everything but Bear Creek, Upper Lobster Creek, and Upper Five Rivers).

	ADC09	ADC10	ATM	ACC	AEL	AUL	ABC	ABuC	AFR	AFC	Szt	ANF
ADC09		*0.00076	*0.00076	*0.00076	*0.00076	0.02348	*0.00076	*0.00076	0.25985	*0.00076	*0.00076	*0.00076
ADC10	0.0065		*0.00076	*0.00076	*0.00076	0.05833	*0.00076	*0.00076	0.32045	*0.00076	*0.00076	*0.00076
ATM	0.0131	0.0083		*0.00076	*0.00076	0.08409	*0.00076	*0.00076	0.53939	*0.00076	*0.00076	*0.00076
ACC	0.0153	0.0156	0.0105		*0.00076	0.00227	*0.00076	*0.00076	0.375	*0.00076	*0.00076	*0.00076
AEL	0.0128	0.0101	0.0103	0.0208		0.03333	*0.00076	0.00227	0.20682	0.00227	*0.00076	*0.00076
AUL	0.0049	-0.0032	-0.0063	0.009	-0.0058		0.00152	0.06061	0.49015	0.04015	0.06591	0.02576
ABC	0.0492	0.0489	0.0516	0.0597	0.0542	0.0568		*0.00076	0.01894	*0.00076	*0.00076	*0.00076
ABuC	0.0084	0.0078	0.011	0.0184	0.0073	-0.009	0.0624		0.34545	0.03636	*0.00076	0.00303
AFR	0.0197	0.0131	0.0063	0.0241	0.0063	0.0028	0.1227	0.0062		0.79394	0.45076	0.37197
AFC	0.0077	0.0057	0.0079	0.015	0.0046	-0.0049	0.0446	0.0029	0.0037		*0.00076	*0.00076
Szt	0.0128	0.0143	0.0102	0.0195	0.0182	-0.0015	0.0716	0.013	0.0051	0.0165		*0.00076
ANF	0.0121	0.0072	0.0115	0.018	0.0115	-0.0043	0.0534	0.0037	0.0175	0.0029	0.0166	

Table 1: Pairwise F_{ST} s and resultant p values for each pair of *O. mykiss* populations from the Alsea River Basin and neighboring systems. F_{ST} values are on the left, p values on the right. Shaded p values with an asterisk are significant after sequential Bonferroni correction.

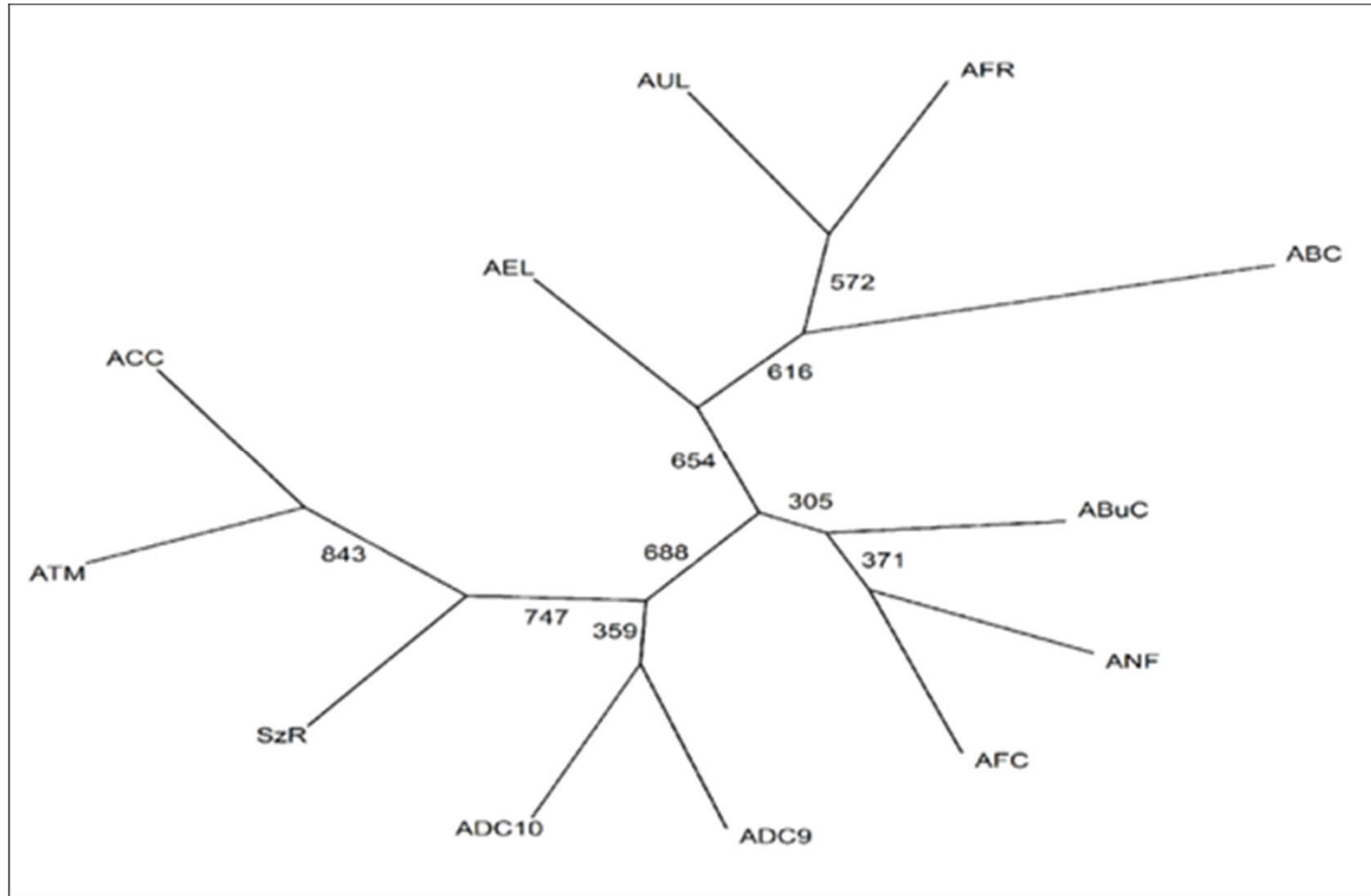


Figure 3: Unrooted trees of *O. mykiss* populations from the Alsea River Basin and neighboring systems generated using the neighbor-linking method from Cavalli-Sforza and Edwards chord distances

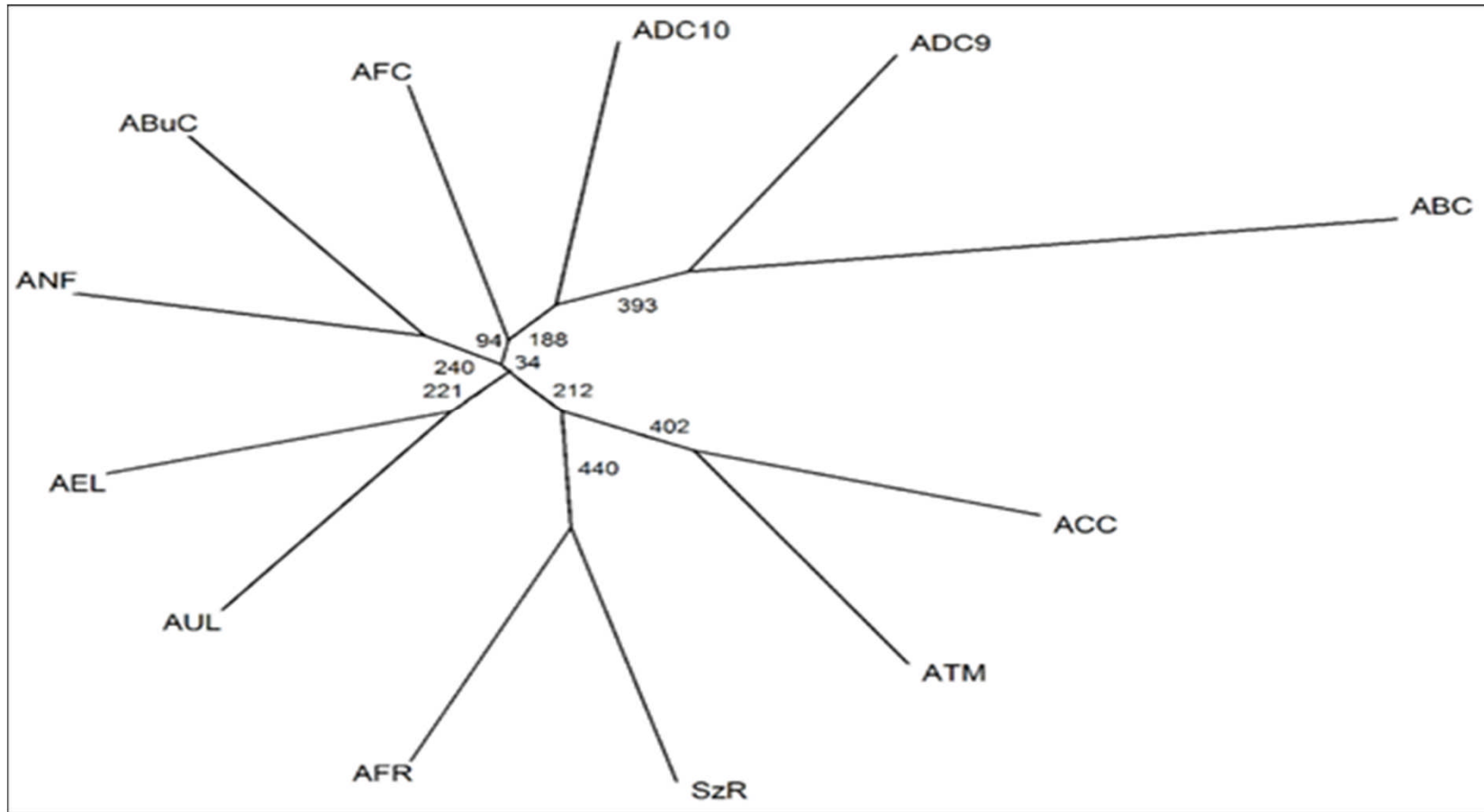


Figure 3: Unrooted trees of *O. mykiss* populations from the Alsea River Basin and neighboring systems generated using the neighbor-linking method from Nei's genetic distance (b). Numbers indicate the number of bootstrapped replicates that contained the labeled branch.

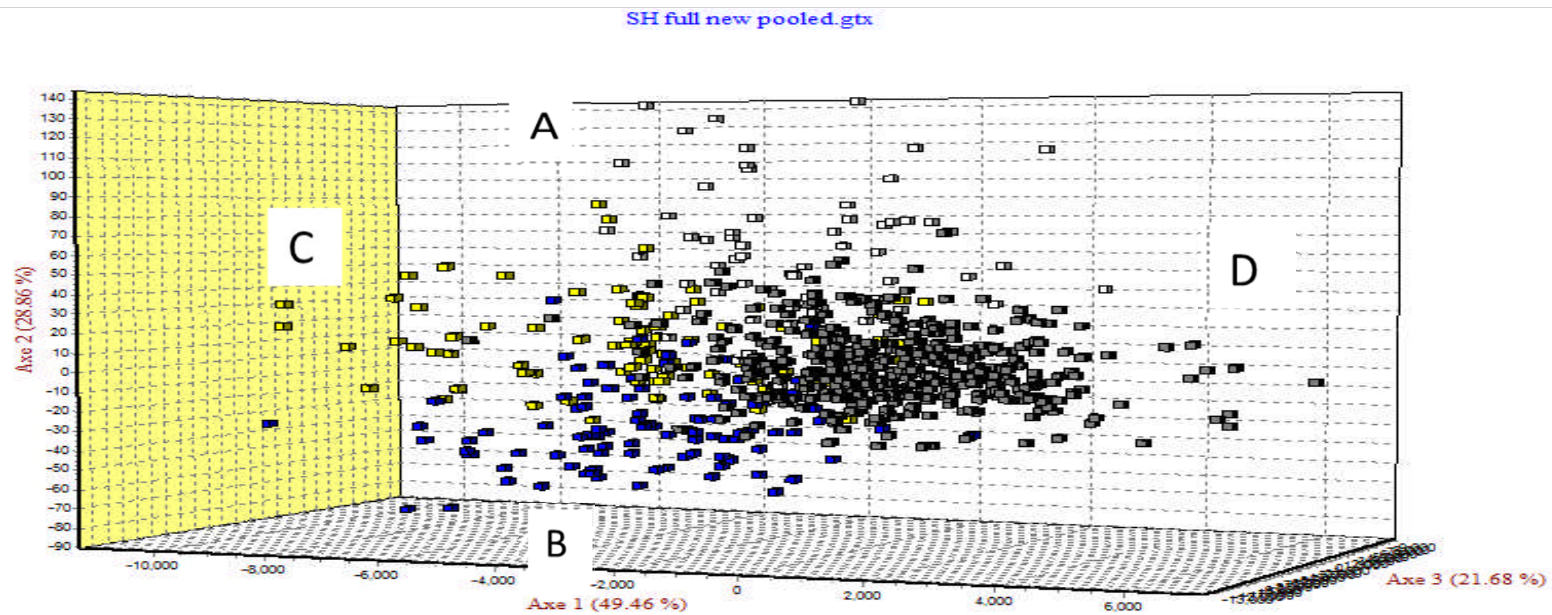
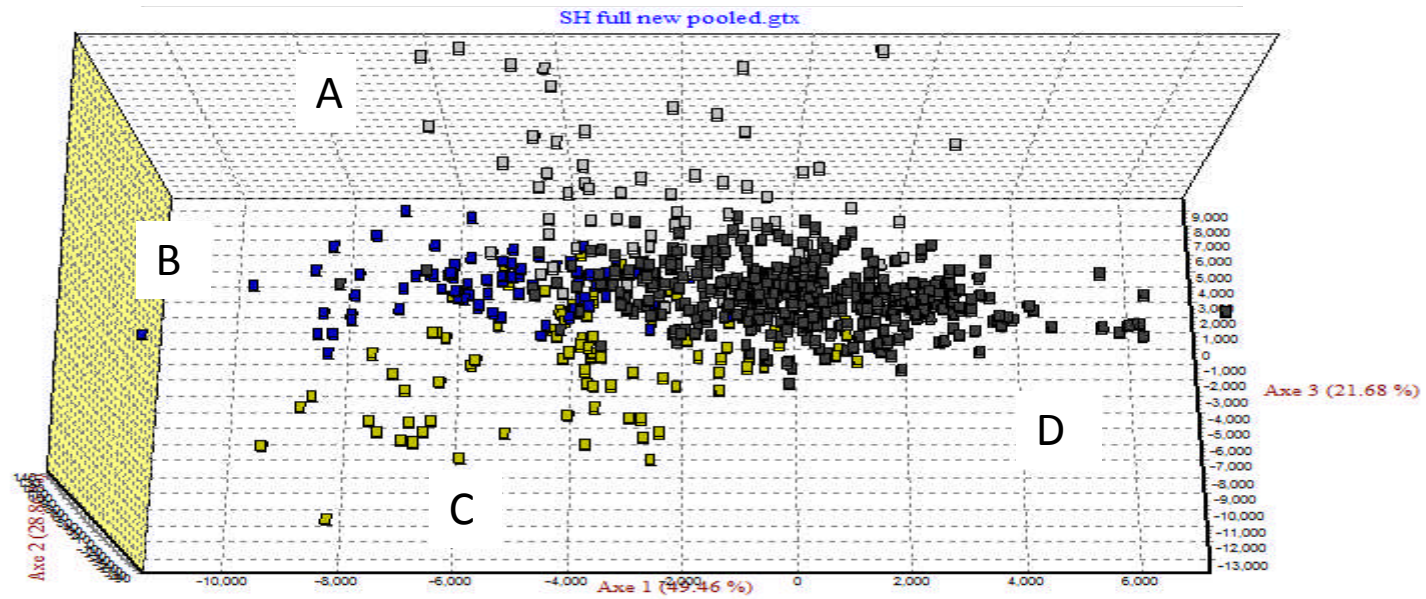


Figure 4: Two views of a 3D AFC plot for populations of Siletz River (A), Ten Mile Creek (B), Cummins Creek (C), and Alsea River Basin (D) *O. mykiss* populations.

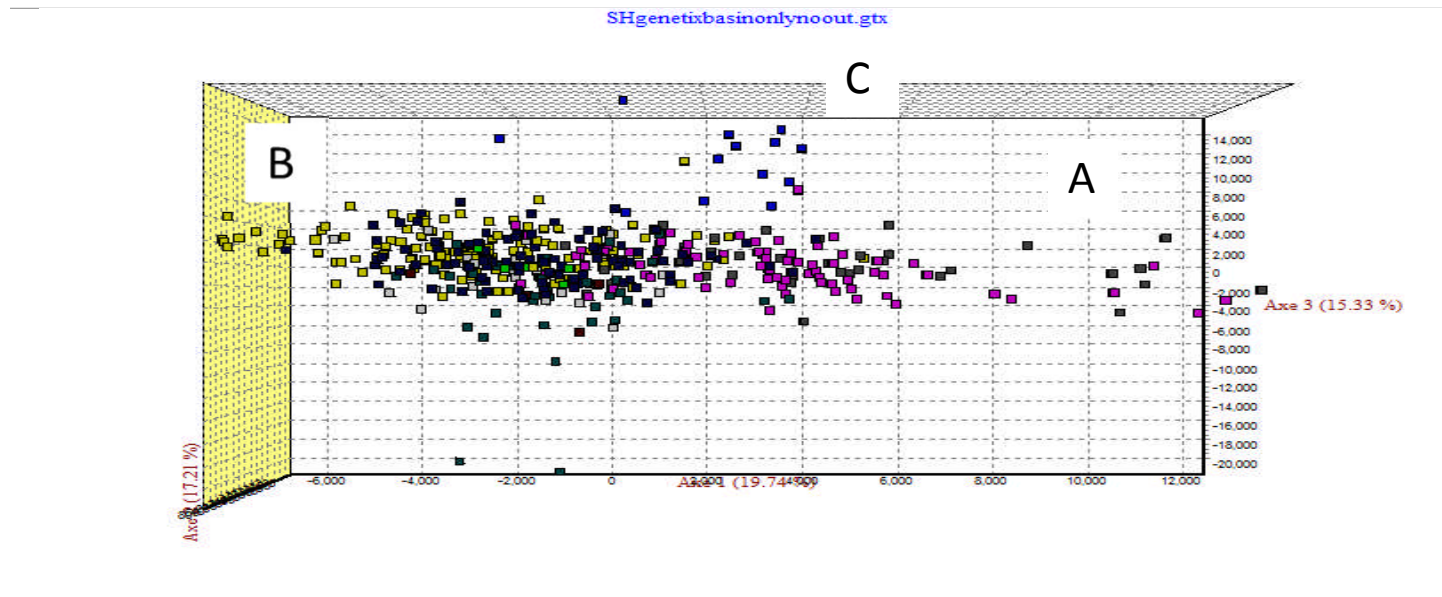
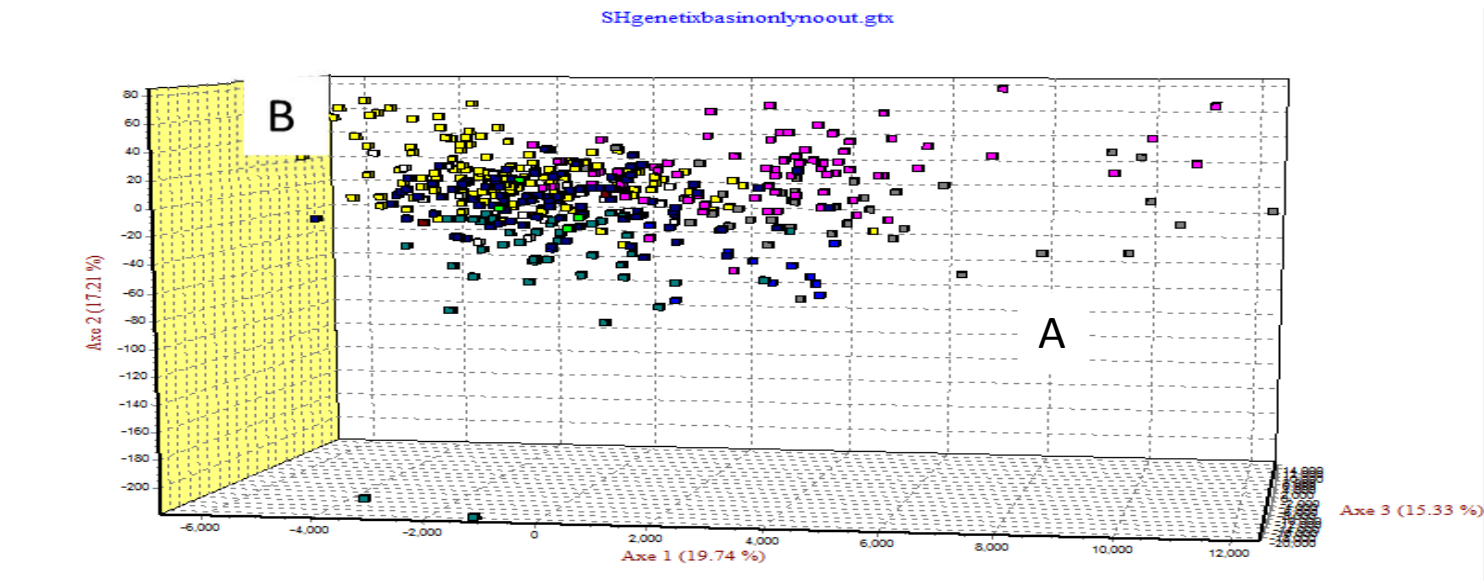


Figure 5: Two views of a 3D AFC plot for populations of Alsea Basin *O. mykiss*. The positions Drift Creek 2009/2010, north fork Alsea river, and Buck Creek populations are marked (A through C, respectively) as the most distinct clusters.

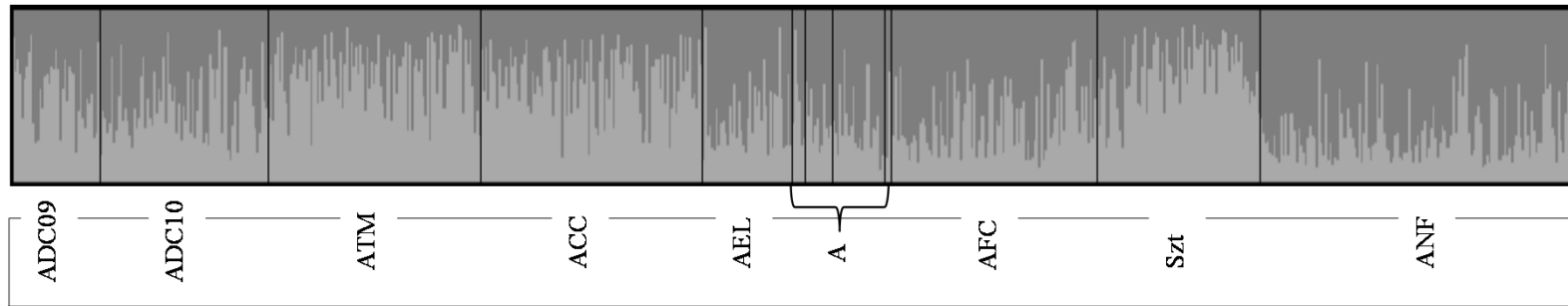


Figure 6: CLUMPP bar plot of Alsea Basin, Ten Mile Creek, Cummins Creek, and Siletz river *O. mykiss* populations. The populations labeled “A” are, left to right, AUL, ABC, ABuC, and AFR. Names correspond to identifiers in Figure 1. Each bar corresponds to one individual, and each color represents the portion of the individual’s alleles which are drawn from a clump or putative population.

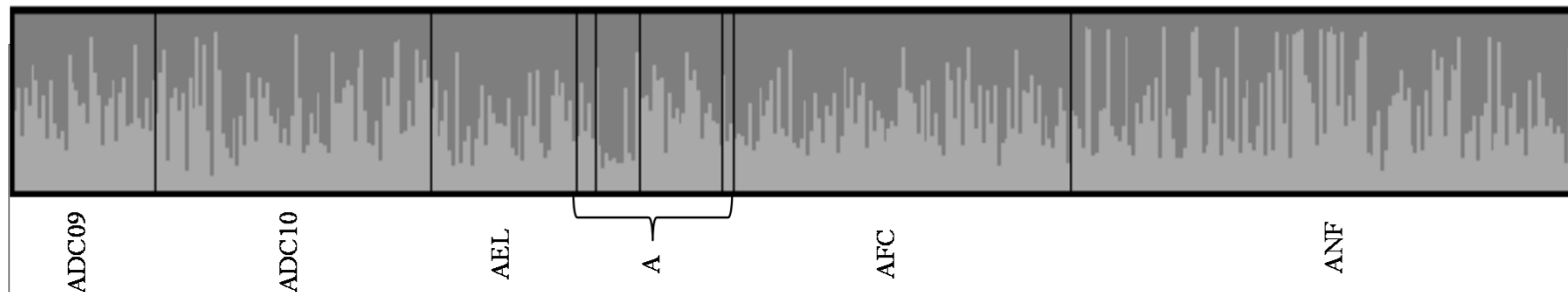
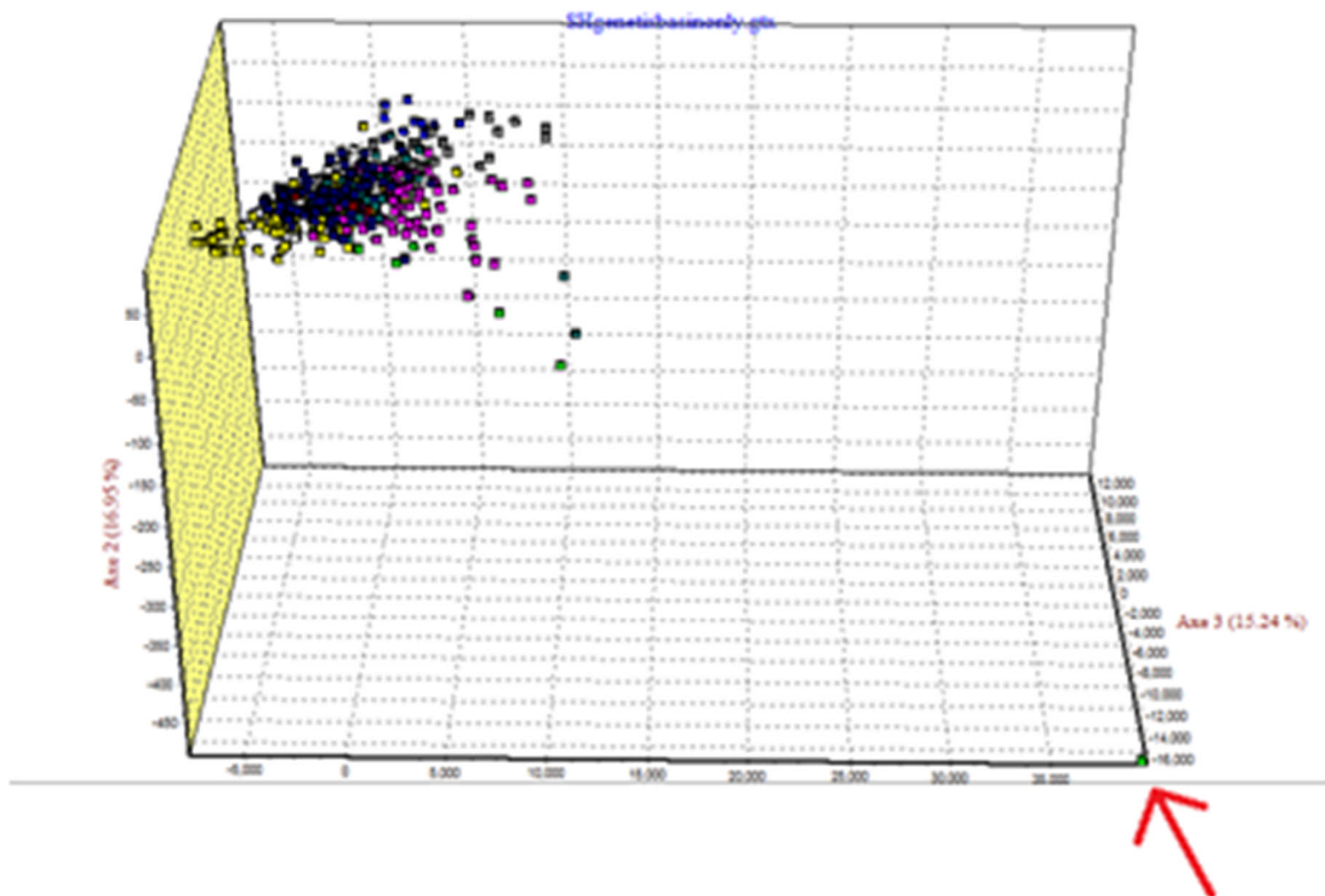
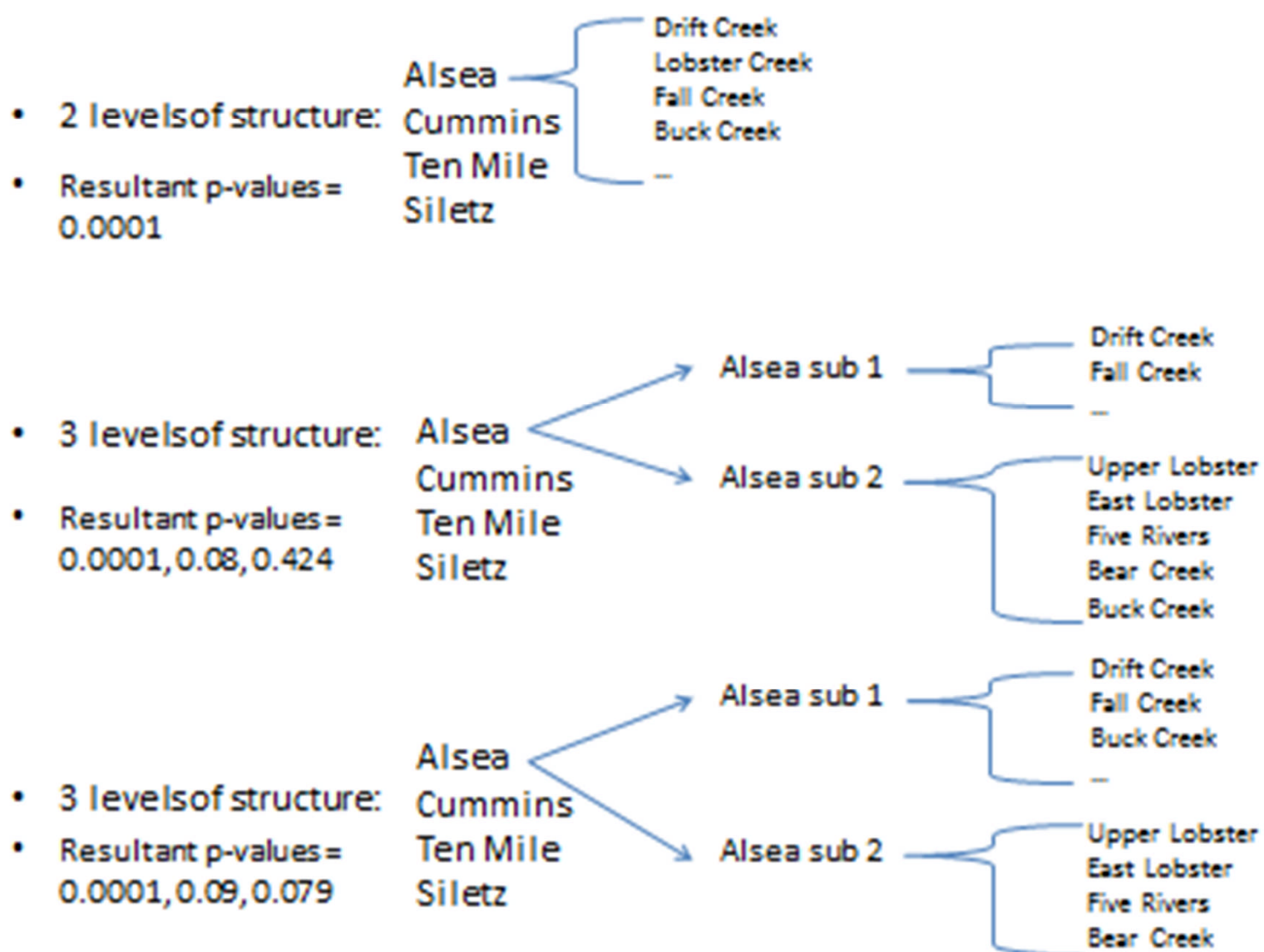


Figure 7: CLUMPP bar plot of Alsea Basin *O. mykiss* populations. The populations labeled “A” are, left to right, AUL, ABC, ABuC, and AFR. Names correspond to identifiers in Figure 1. Each bar corresponds to one individual, and each color represents the portion of the individual’s alleles which are drawn from a clump or putative population.

Basin Outlier



Heirarchical F-statistics: heirfstat results



Conclusions

Although most pairwise F_{st} tests for population samples within the Alsea are determined statistically significant, we question whether this distinction has biological meaning.

Our reasoning for this conclusion are as follows:

1. Pairwise F_{st} values are small (generally 0.01 or less)
2. No bootstrap values for tree branches within the Alsea are significant (all <700)
3. FCA is only able to distinguish DC, FC and BC (marginally)
4. Only compelling distinction discerned by STRUCTURE is Alsea vs neighboring watershed samples where $K = 2$ has the highest likelihood
5. Hierarchical F_{st} tests are not able to distinguish any hierarchy within the Alsea Basin