Genetic profile for Spring Creek NFH fall Chinook salmon

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National Fish Hatchery Broodstock Genetic Profile

Facility: Spring Creek National Fish Hatchery

Stock: Fall Chinook salmon (*Oncorhynchus tshawytscha*)

Parental stock: Tule Fall Chinook salmon from White Salmon River

Year founded: 1901

Generation time: 2-5 years (y) (14% 2y, 64% 3y, 21% 4y, <1% 5y) [ref 1]

Segregation / Integration history:

The vast majority of fish that approach the hatchery are probably of hatchery origin, however, it is possible that some wild fish (e.g. from White Salmon River, Hood River or Klickitat River) are incorporated.

Table 1 - Broodstock samples analyzed:

Description	Year	n	Life stage	Data source
Spring Creek NFH broodstock	2001	56	returning adult	GAPS
Spring Creek NFH broodstock	2002	62	returning adult	GAPS
Spring Creek NFH broodstock	2006	84	returning adult	AFTC

Table 2 - Samples analyzed for comparison:

Description	H/W	Year†	n	Life stage	Data source
Hood River	W	2002	33	returning adult	AFTC
Hood River	W	2006	33	returning adult	AFTC
Cowlitz Hatchery	H	2004	128	returning adult	GAPS
Lewis River	W	2003	91	returning adult	GAPS
Little White Salmon NFH	H	2001	93	returning adult	AFTC
Little White Salmon NFH	H	2006	94	returning adult	GAPS
White Salmon River	W	2006e	291	smolt	AFTC
White Salmon River	W	2006l	22	smolt	AFTC
White Salmon River	W	2007e	400	smolt	AFTC
White Salmon River	W	2007l	207	smolt	AFTC
White Salmon River	W	2008e	378	smolt	AFTC
White Salmon River	W	2008l	248	smolt	AFTC

†The suffix “e” indicates early migrant and “l” indicates late migrant.

Genetic markers analyzed:

GAPS microsatellites [ref 2] (13 / 13 loci). A list of the markers analyzed is provided in Appendix 1. Genotyping success rates are presented in Appendix 2.

Table 3 - Diversity within samples. Expected (H_e) and observed (H_o) heterozygosity, allelic richness rank (AR rank, with 1 representing the most diversity and 15 representing the least diversity), number of loci exhibiting departures from Hardy-Weinberg Equilibrium (HWE), F_{IS} (a measure of departure from random mating), number of pairs of loci exhibiting linkage disequilibrium (LD), and effective population size (N_e) based on LD are listed for each sample. Samples in which we observed no evidence for any disequilibrium caused by genetic drift due to a finite number of parents (i.e. those with an estimated N_e of infinity) have N_e marked by "-".

No	Description	H_e	H_o	AR rank	HWE	F_{IS}	LD	N_e
1	Spring Creek NFH 2001	0.83	0.83	13	2	0.01	2	-
2	Spring Creek NFH 2002	0.83	0.83	15	2	0.01	3	-
3	Spring Creek NFH 2006	0.83	0.83	12	2	0.01	0	-
4	Hood River 2002	0.86	0.86	8	3	0.06	1	163 (75 - Infinite)
5	Hood River 2006	0.88	0.88	7	7	-0.02	49	10 (8 - 12)
6	Cowlitz Hatchery	0.87	0.87	9	1	0.00	7	-
7	Lewis River	0.89	0.89	5	2	0.01	4	885 (306 - Infinite)
8	Little White Salmon NFH 2001	0.87	0.87	4	1	-0.01	3	-
9	Little White Salmon NFH 2006	0.88	0.88	5	3	-0.01	21	181 (135 - 263)
10	White Salmon River 2006e	0.85	0.85	10	6	0.01	42	214 (162 - 297)
11	White Salmon River 2006l	0.88	0.88	3	0	-0.01	0	-
12	White Salmon River 2007e	0.85	0.85	11	12	0.01	73	89 (79 - 100)
13	White Salmon River 2007l	0.88	0.88	2	8	0.00	31	185 (141 - 254)
14	White Salmon River 2008e	0.83	0.83	14	5	0.02	53	199 (165 - 244)
15	White Salmon River 2008l	0.88	0.88	1	3	0.00	39	212 (172 - 269)

Figure 1 - Correspondence Analysis (CA) of allele frequencies observed in fall Chinook salmon from Spring Creek NFH and adjacent collection sites. Sample numbers are those listed in Table 3. The primary (horizontal) axis accounted for 42.33% of the inertia and the secondary (vertical) axis accounted for 11.11% of the inertia.

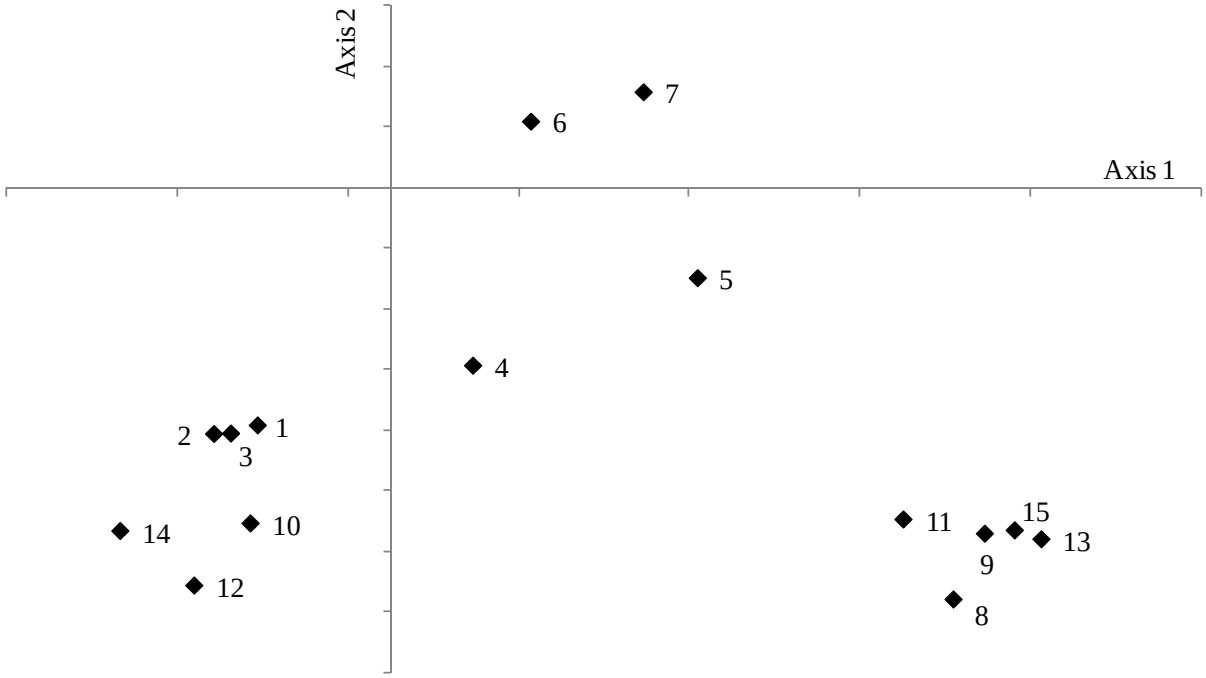
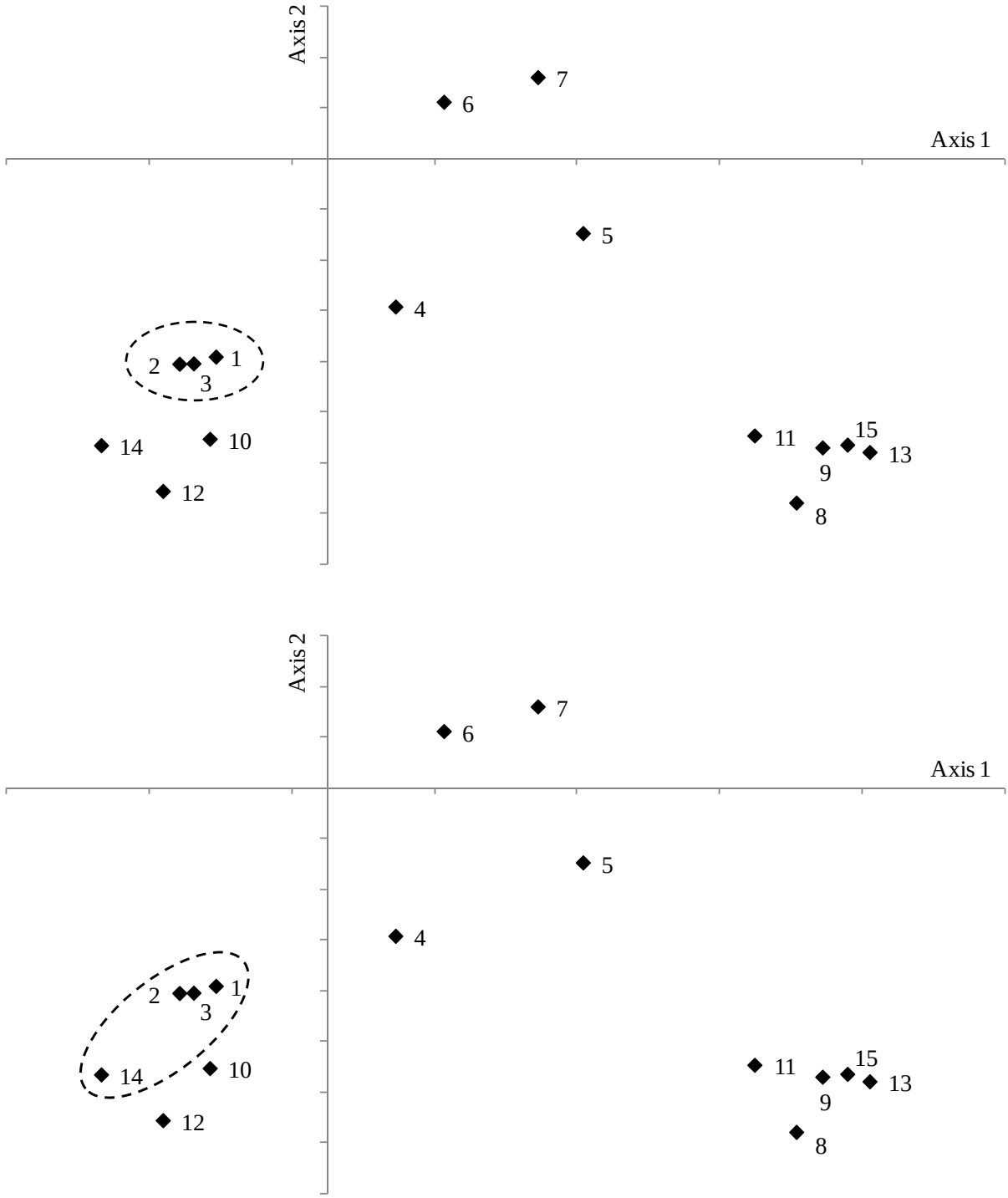


Figure 2 - Statistical tests of divergence among samples from Spring Creek NFH and adjacent populations. Sample numbers are those listed in Table 3. Dashed lines indicate groups of samples lacking statistically different allele frequencies (top) and statistically significant F_{ST} values (bottom).



Comments

- The goals of this report series are 1) to summarize available genetic information for NFH broodstocks and make that information available to hatchery managers, and 2) to make sure that data for the NFH broodstocks are available for internal hatchery reviews and HET meetings, as well as to our partners.
- The fall Chinook salmon stocks examined here belong to two different return types; Tule (Spring Creek NFH, Hood River, Cowlitz Hatchery, Lewis River, and White Salmon River early smolts) and Upriver Bright (URB; all other samples). These two return types are fairly distinct, but both spawn naturally in White Salmon River adjacent to Spring Creek NFH and thus both were considered here.
- Previous work has demonstrated that there are two populations of fall Chinook smolts that leave White Salmon River each year: a Tule population that leaves in March - April, and a URB population that leaves in May – June [Ref 3].
- Tule fall Chinook samples generally exhibited less diversity (lower allelic richness) than URB samples, and the Spring Creek NFH samples exhibited the lowest diversity of the Tule samples. This was unexpected given the large number of individuals used in the broodstock each year (target of 7,000 adults). Low allelic richness was consistent across years, suggesting that this result was not an artifact of the sample of individuals analyzed. Given the lack of evidence of LD in this the Spring Creek NFH samples, a possible explanation for this result is a bottleneck in the early years of propagation. Egg take records going back to 1980 [Ref 4] suggest that greater than 2,000 females have been used every year since then, so if there was a substantial bottleneck it likely occurred prior to 1980.
- Spring Creek NFH Chinook salmon were significantly divergent from all other Tule and URB populations sampled based on allele frequency heterogeneity, and divergent from all other populations except for one sample from White Salmon River based on F_{ST}. The three samples from Spring Creek NFH did not reveal substantial year-to-year variation in this stock.
- Spring Creek NFH Chinook salmon were the most similar stock to naturally produced Tule fall Chinook in the White Salmon River. This similarity likely reflects the fact that

White Salmon River was the source of the Spring Creek NFH stock, and may also reflect an ongoing hatchery influence on the population in White Salmon River. Similarity based on shared ancestry is difficult to distinguish from similarity based on ongoing gene flow, but it is likely that both factors have contributed to the present similarity of these two populations.

Sources cited

1. Average numbers from 1981-2009 taken from 2009 Hatchery Update for Spring Creek National Fish Hatchery. Provided by Larry Marchant, Project Leader, Spring Creek NFH.

2. Information regarding the microsatellite markers used and the inter-agency baseline in which they are used may be found in the following article:

Seeb LW, Antonovich A, Banks MA, Beacham TD, Bellinger MR, Campbell M, Garza JC, Guthrie CM III, Moran P, Narum SR, Stephenson JJ, Supernault KJ, Teel DJ, Templin WD, Wenburg JK, Young SF, Smith CT. 2007. Development of a Standardized DNA Database for Chinook salmon. Fisheries 32: 540 - 552.

3. Smith C, Baker S, Engle R, Olson D. 2009. Genetic analysis of juvenile Chinook salmon collected in White Salmon River. U.S. Fish & Wildlife Service Abernathy Fish Technology Report.

4. Egg take and fecundity data provided by Mark Ahrens, Deputy Project Leader, Spring Creek NFH.

Availability

All data generated for this report will be included in the next builds of the shared GAPS consortium baselines (hosted by NOAA Fisheries). Allele frequencies for NFH stocks are also available from Abernathy Fish Technology Center upon request.

Disclaimer

The findings and conclusions in this report are those of the author and do not necessarily represent the views of the U.S. Fish and Wildlife Service.

Appendix 1. Thirteen microsatellite markers used to analyze Spring Creek NFH fall Chinook salmon.

Microsatellite Markers	
1	Ogo2
2	Ogo4
3	Oki100
4	Omm1080
5	Ots201b
6	Ots208b
7	Ots211
8	Ots212
9	Ots213
10	Ots3M
11	Ots9
12	OtsG474
13	Ssa408

Appendix 2. Genotype call rates (completeness of data).

Description	Year	Microsatellite call rate
Spring Creek NFH broodstock	2001	0.935
Spring Creek NFH broodstock	2002	0.934
Spring Creek NFH broodstock	2006	0.988
Hood River	2002	0.972
Hood River	2006	0.986
Cowlitz Hatchery	2004	0.925
Lewis River	2003	0.927
Little White Salmon NFH broodstock	2001	0.998
Little White Salmon NFH broodstock	2006	1.000
White Salmon River	2006e	0.987
White Salmon River	2006l	0.944
White Salmon River	2007e	0.987
White Salmon River	2007l	0.971
White Salmon River	2008e	0.995
White Salmon River	2008l	0.999

Appendix 3. Pairwise F_{ST} values between collections of fall Chinook salmon. Sample numbers are those listed in Table 3. Shaded cells indicate non-significant results (pairwise F_{ST} values not >95% of a null distribution in which individuals were permuted among samples).

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	-	0.003	0.002	0.004	0.023	0.020	0.029	0.038	0.040	0.003	0.032	0.004	0.038	0.003	0.034
2		-	0.001	0.004	0.029	0.019	0.028	0.045	0.044	0.003	0.031	0.002	0.043	0.001	0.039
3			-	0.004	0.027	0.021	0.029	0.040	0.041	0.002	0.030	0.003	0.039	0.001	0.036
4				-	0.009	0.008	0.015	0.023	0.021	0.002	0.013	0.002	0.021	0.005	0.019
5					-	0.017	0.019	0.019	0.021	0.019	0.018	0.021	0.018	0.028	0.018
6						-	0.006	0.028	0.024	0.016	0.016	0.015	0.025	0.021	0.023
7							-	0.025	0.022	0.023	0.015	0.022	0.022	0.030	0.019
8								-	0.002	0.031	0.007	0.036	0.001	0.043	0.001
9									-	0.032	0.007	0.035	0.003	0.044	0.003
10										-	0.023	0.003	0.030	0.004	0.027
11											-	0.022	0.009	0.029	0.007
12												-	0.034	0.004	0.030
13													-	0.043	0.001
14														-	0.038
15															-

Appendix 4. Glossary

Allele – A unique genetic character state. Each locus has two alleles.

Allelic richness – The number of alleles observed in a sample of individuals, corrected for unequal sample sizes by rarefaction.

Effective population size (N_e) – The number of individuals in a model population which would lose genetic variation at the same rate as an observed population. Deviations from model behavior in real populations (e.g. unequal sex ratios, some individuals reproducing more than others, etc…) tend to make N_e lower than census size (N).

F_{IS} - Correlation of alleles in an individual relative to the subpopulation in which it occurs. Commonly used as a measure of departure from random mating within a subpopulation.

F_{ST} – Correlation of alleles within the same subpopulation relative to the entire population. Commonly used as a measure of divergence between subpopulations.

Gene flow – Movement of genetic material from one population to another. Implies both physical movement and successful integration into the recipient population.

Linkage Disequilibrium (LD) – A measure of departure from independence of alleles in a pair of loci.

Genetic Drift – Process of genetic divergence between populations based on random sampling of alleles each generation.

Heterozygosity – Proportion of individuals in a population that are heterozygotes (i.e. do not have two identical alleles at a locus).

Hardy-Weinberg Equilibrium (HWE) – Genotype ratios expected under a random mating model.

Locus – A physical location on the DNA of an organism. The term "locus" is often used synonymously with "marker" or with any type of marker (e.g., "SNP" or "microsatellite").