Genetic profile for Carson NFH Spring Chinook salmon

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Prepared by

Applied Research Program in Conservation Genetics

Abernathy Fish Technology Center

U.S. Fish and Wildlife Service

Longview, WA 98632

(360) 425-6072

National Fish Hatchery Broodstock Genetic Profile

Facility: Carson National Fish Hatchery

Stock: spring Chinook salmon (*Oncorhynchus tshawytscha*)

Parental stock: Natural-origin spring Chinook salmon collected at Bonneville Dam during upstream migration in 1955-1964 [Ref 1].

Year founded: 1955

Generation time: 3 years (1.7%), 4 years (89.2%) or 5 years (9.1%) [Ref 2].

Segregation / Integration history: Segregated. Spring Chinook salmon were historically excluded from most of the Wind River system by Shipherd Falls, approximately 2 miles from the confluence with the Columbia River [Ref 1].

Table 1 - Broodstock samples analyzed:

Description	Year	n	Life stage	Data source
Carson NFH	2001	78	returning adult	GAPS
Carson NFH	2004	39	returning adult	GAPS
Carson NFH	2007	89	returning adult	AFTC
Carson NFH	2011	95	returning adult	AFTC

Table 2 – Spring Chinook salmon samples analyzed for comparison:

Description	H/W	Year	n	Life stage	Data source
Little White Salmon NFH	H	2001	99	returning adult	AFTC
Little White Salmon NFH	H	2007	96	returning adult	AFTC
Little White Salmon NFH	H	2011	91	returning adult	AFTC
Granite Creek	W	2005	26	returning adult	GAPS
Granite Creek	W	2006	34	returning adult	GAPS
John Day River	W	2005	14	returning adult	GAPS
John Day River	W	2006	35	returning adult	GAPS
Methow Hatchery	H	1998	45	juvenile	GAPS
Methow Hatchery	H	2000	43	juvenile	GAPS
Naches River	W	1993	64	returning adult	GAPS
Twisp River	W	2001	91	returning adult	GAPS
Twisp River	W	2005	35	returning adult	GAPS
Wenatchee Hatchery	H	2000	37	returning adult	GAPS
Wenatchee River	W	1993	62	returning adult	GAPS
Winthrop NFH	H	1992	106	returning adult	AFTC
Winthrop NFH	H	2010	95	returning adult	AFTC

Genetic markers analyzed:

GAPS microsatellites [ref 3] (13 / 13 loci). A complete 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 (AR), number of loci exhibiting departures from Hardy-Weinberg Equilibrium (HWE), F_{IS} (a measure of departure from random mating), percent of pairwise tests for linkage disequilibrium yielding significant results (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	HWE	F_{IS}	LD	N_e
1	Carson NFH 2001	0.79	0.81	8.11	1	-0.02	15.7	185 (96 - 1,015)
2	Carson NFH 2004	0.77	0.82	7.05	8	-0.06	18.0	11 (9 - 15)
3	Carson NFH 2007	0.80	0.79	8.28	5	0.01	23.5	80 (64 - 103)
4	Carson NFH 2011	0.81	0.81	8.56	1	0.00	2.3	5,811 (397 - Infinite)
5	Little White Salmon NFH 2001	0.79	0.78	8.37	1	0.02	7.4	256 (158 - 583)
6	Little White Salmon NFH 2007	0.79	0.78	7.98	8	0.01	20.3	61 (50 - 77)
7	Little White Salmon NFH 2011	0.79	0.78	8.41	0	0.01	2.8	306 (185 - 763)
8	Granite Creek 2005	0.77	0.76	8.10	1	0.02	0.0	104 (50 - 2,505)
9	Granite Creek 2006	0.76	0.73	8.08	0	0.04	0.0	-
10	John Day River 2005	0.74	0.77	7.26	1	-0.04	0.0	-
11	John Day River 2006	0.76	0.73	7.48	1	0.05	0.5	640 (125 - Infinite)
12	Methow Hatchery 1998	0.79	0.79	8.44	0	0.01	1.8	420 (139 - Infinite)
13	Methow Hatchery 2000	0.80	0.79	8.32	2	0.00	2.3	220 (102 - Infinite)
14	Naches 1993	0.82	0.81	8.72	1	0.02	0.9	-
15	Twisp River 2001	0.76	0.74	7.29	5	0.03	13.4	82 (62 - 114)
16	Twisp River 2005	0.77	0.75	7.56	5	0.03	6.0	76 (49 - 147)
17	Wenatchee Hatchery 2000	0.79	0.79	8.40	1	0.00	8.3	28 (22 - 37)
18	Wenatchee River 1993	0.79	0.81	8.47	1	-0.02	1.4	318 (152 - 38,750)
19	Winthrop NFH 1992	0.79	0.78	8.21	2	0.02	6.5	85 (70 - 104)
20	Winthrop NFH 2010	0.78	0.77	8.07	2	0.01	7.4	172 (118 - 291)

Figure 1 – Correspondence Analysis (CA) of allele frequencies observed in samples from Carson NFH and other middle and upper Columbia River spring Chinook salmon populations. Sample numbers are those listed in Table 3. Axis 1 and 3 accounted for 13.6%, and 9.7% of the variance, respectively.

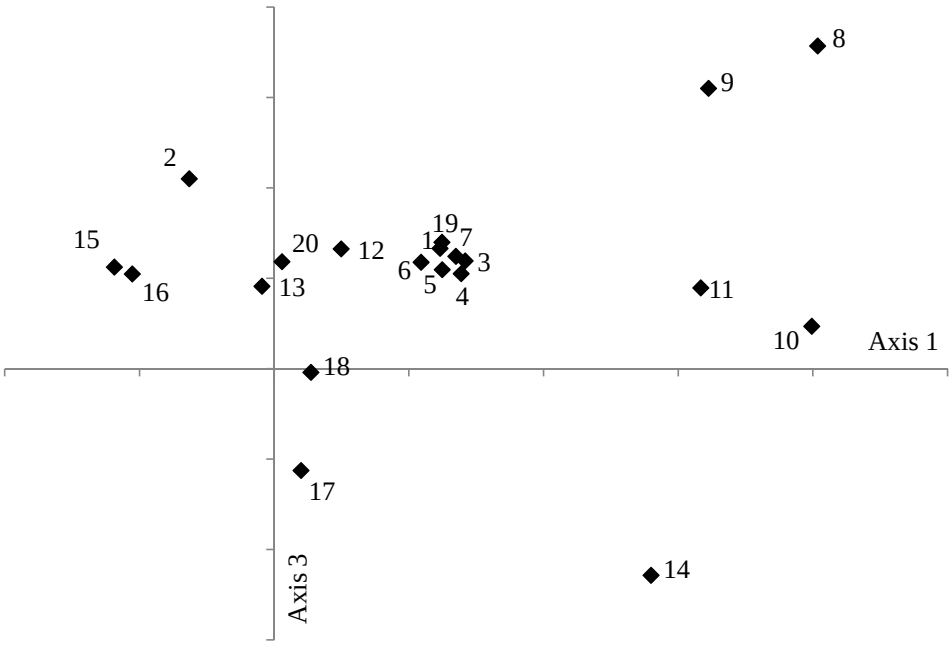
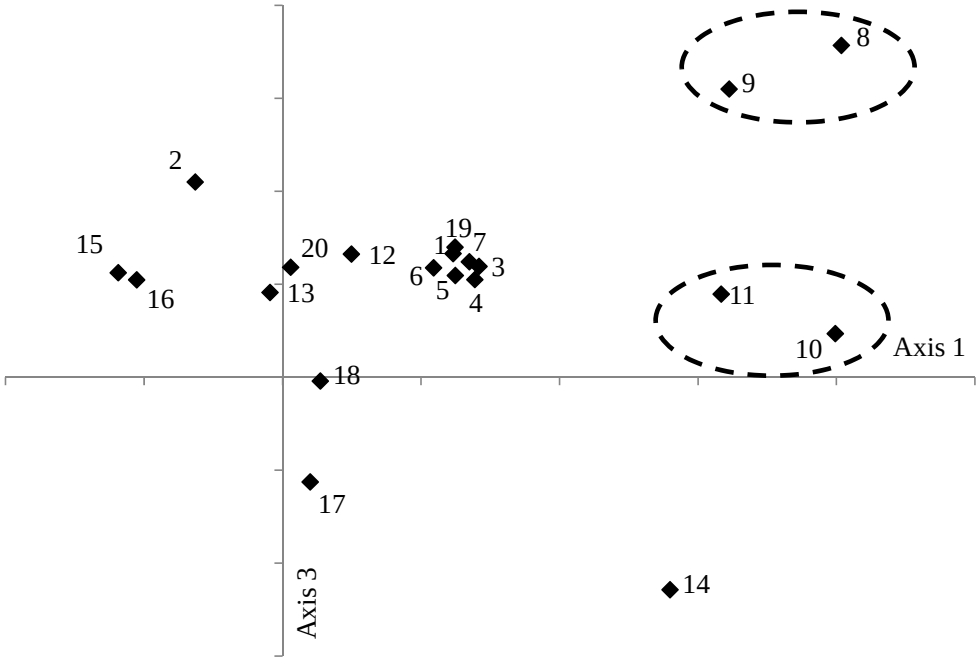
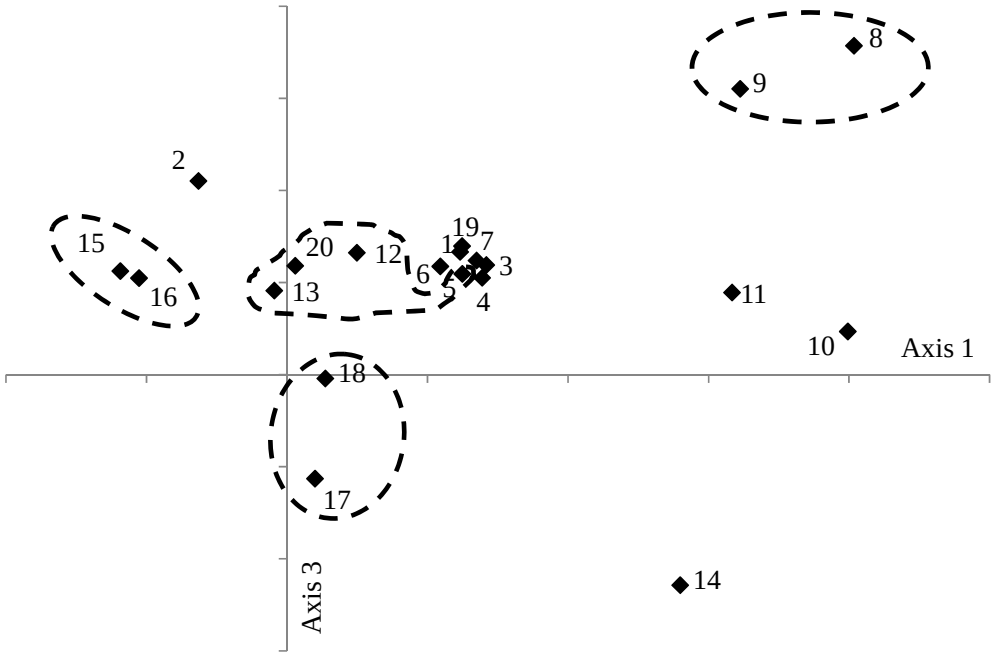


Figure 2 - Statistical tests of divergence among samples from Carson NFH and other middle and upper Columbia River spring Chinook salmon populations. Sample numbers are those listed in Table 3. Dashed lines indicate groups of samples lacking statistically different allele frequencies (top) and statistically 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 2004 sample from Carson NFH appeared divergent from the other Carson NFH samples, exhibited substantial departures from HWE and LD, and also exhibited the greatest genotyping failure rate of any sample. These results suggest a potential problem with the sample, so any interpretation of the results for this sample should be done with caution.
- Correspondence Analysis revealed a pattern of divergence that was dominated by samples from wild populations (Twisp River, Granite Creek, Naches River and John Day River). Samples from Carson NFH and sites which have received eggs and fish from Carson NFH (Little White Salmon NFH, Winthrop NFH) were clustered in the center of the plot. Hatchery and Wild samples from the Wenatchee River were also near the center.
- Samples from Carson NFH were statistically different from each other and from samples from other sites, including sites to which Carson NFH fish have been planted. It is important to note, however, that many of the p-values were marginal and F_{ST} estimates were often lower between sites than between years within sites. For example the range of F_{ST} values between Carson NFH and Little White Salmon NFH was identical to the range of F_{ST} values among years at these two sites (0.002-0.006).
- Genetic diversity (H_e, H_o and AR) observed in the Carson NFH samples was comparable to that observed in samples from other sites.
- LD was relatively high in three of the four samples from Carson NFH, and was generally higher in hatchery samples than in wild samples (except the Twisp River). High LD often indicates an increased level of inbreeding in a population (reduced effective size), or that the sample being analyzed contains individuals from more than one population.
- The USFWS Columbia Basin Hatchery Review Team (HRT) identified transfer of Carson NFH fish to other basins as a genetic risk to populations of spring Chinook salmon endemic to those basins [Ref 1]. Such transfers are thought to impede the ability of

populations to adapt to local environments e.g. [Ref 4]. The present results confirm that sites which have received Carson strain produce samples of spring Chinook salmon which are genetically similar to those taken from Carson NFH. These results are thus consistent with the HRTs finding of genetic risks associated with translocations.

Sources cited

1. USFWS Columbia Basin Hatchery Review Team. 2007. Columbia Gorge NFHs Review (Final Report). Available: http://www.fws.gov/pacific/Fisheries/Hatcheryreview/Reports/columbiagorge/GorgeNFHReview_19Dec2007_FINAL.pdf

2. Based on BY1995-2005 returns to hatchery as documented in the CRIS database, provided by Steve Pastor and Rod Engle, Columbia River Fisheries Program Office.

3. 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.

4. Utter, F.M., Chapman, D.W., and Marshall, A.R. 1995. Genetic population structure and history of Chinook salmon of the upper Columbia River. American Fisheries Society Symposium 17: 149-165.

Availability

Genotype data and allele frequencies for NFH stocks are 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 Carson NFH spring 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). Shaded cells indicate data that are <90% complete.

Description	Year	Microsatellite call rate
Carson NFH	2001	0.893
Carson NFH	2004	0.882
Carson NFH	2007	0.978
Carson NFH	2011	1.000
Little White Salmon NFH	2001	1.000
Little White Salmon NFH	2007	0.998
Little White Salmon NFH	2011	0.996
Granite Creek	2005	0.923
Granite Creek	2006	0.980
John Day River	2005	0.934
John Day River	2006	0.978
methow98	1998	0.961
methow00	2000	0.966
Naches	1993	0.918
Twisp River	2001	0.973
Twisp River	2005	0.982
Wenatchee Hatchery	2000	0.967
Wenatchee River	1993	0.952
Winthrop NFH	1992	0.993
Winthrop NFH	2010	0.994

Appendix 3. Pairwise F_{ST} values between collections of spring 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).

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	0.023	0.006	0.006	0.005	0.006	0.002	0.013	0.013	0.029	0.026	0.005	0.008	0.016	0.021	0.019	0.015	0.012	0.004	0.007
2	-	0.025	0.024	0.023	0.025	0.021	0.030	0.036	0.061	0.045	0.018	0.022	0.039	0.032	0.029	0.027	0.023	0.022	0.022
3		-	0.002	0.004	0.005	0.002	0.013	0.014	0.027	0.026	0.004	0.007	0.015	0.021	0.021	0.014	0.008	0.004	0.008
4			-	0.003	0.005	0.003	0.013	0.014	0.028	0.023	0.004	0.008	0.009	0.020	0.017	0.012	0.006	0.004	0.010
5				-	0.002	0.002	0.013	0.013	0.029	0.030	0.002	0.008	0.012	0.018	0.019	0.014	0.008	0.004	0.007
6					-	0.005	0.016	0.016	0.035	0.034	0.004	0.012	0.017	0.022	0.023	0.016	0.010	0.005	0.010
7						-	0.011	0.012	0.026	0.023	0.002	0.005	0.017	0.019	0.018	0.012	0.009	0.003	0.004
8							-	0.001	0.021	0.025	0.012	0.018	0.021	0.031	0.027	0.026	0.018	0.013	0.019
9								-	0.025	0.031	0.015	0.020	0.025	0.033	0.030	0.027	0.019	0.011	0.021
10									-	0.009	0.032	0.036	0.024	0.048	0.049	0.032	0.030	0.029	0.035
11										-	0.026	0.027	0.029	0.042	0.040	0.027	0.026	0.025	0.030
12											-	0.003	0.017	0.011	0.012	0.011	0.006	0.003	0.002
13												-	0.020	0.011	0.009	0.010	0.004	0.007	0.004
14													-	0.031	0.026	0.020	0.017	0.016	0.022
15														-	0.003	0.025	0.018	0.024	0.013
16															-	0.025	0.017	0.022	0.013
17																-	0.001	0.015	0.014
18																	-	0.009	0.008
19																		-	0.009

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.

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.

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

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”).