

Genetic profile for Makah NFH fall Chinook salmon

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National Fish Hatchery Broodstock Genetic Profile

Facility:	Makah National Fish Hatchery
Stock:	Fall Chinook salmon (<i>Oncorhynchus tshawytscha</i>)
Parental stock:	Sooes River fall Chinook salmon
Year founded:	1981
Generation time:	2-6 years (y) (4.9% 2y, 28.6% 3y, 44.2% 4y, 21.1% 5y, 1.2% 6y) ^{ref 1}

Segregation / Integration history:

All years integrated. Proportion of wild (W) and hatchery (H) fish used for broodstock unknown. Fish released from the hatchery are marked by adipose clip, but the proportion of marked fish used in the broodstock is not recorded.

Table 1 - Broodstock samples analyzed:

Description	Year	n	Life stage	Data source
Makah NFH broodstock	1985	9	returning adult	AFTC
Makah NFH broodstock	1996	15	returning adult	AFTC
Makah NFH broodstock	2001	60	returning adult	AFTC†
Makah NFH broodstock	2003	78	returning adult	GAPS (WDFW)
Makah NFH broodstock	2007	98	returning adult	AFTC

Table 2 - Samples analyzed for comparison:

Description	H / W	Year	n	Life stage	Data source
Quinalt NFH broodstock	H	2001	65	returning adult	AFTC
Quinalt NFH broodstock	H	2006	38	returning adult	GAPS (WDFW)
Forks Creek H broodstock	H	2005	142	returning adult	GAPS (WDFW)
Humptulips H broodstock	H	1990	82	returning adult	GAPS (WDFW)
Hoh River	W	2004	83	returning adult	GAPS (WDFW)
Hoh River	W	2005	37	returning adult	GAPS (WDFW)
Queets River	W	1996	50	returning adult	GAPS (WDFW)
Queets River	W	1997	30	returning adult	GAPS (WDFW)
Quillayute River	W	1995	50	returning adult	GAPS (WDFW)
Quillayute River	W	1996	58	returning adult	GAPS (WDFW)

† Originally included in GAPS, but reanalyzed due to amount of missing data (up to 47% by locus)

Genetic markers analyzed:

GAPS microsatellites^{ref 2} (13 / 13 loci) and GAPS single nucleotide polymorphisms^{ref 3} (67 / 75 loci; <http://www.fws.gov/aftc/gapsSnp.pdf>). 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 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 “-“.

a) microsatellites

Description	H_e	H_o	AR rank	HWE	F_{IS}	LD	N_e
Makah NFH 85	0.85	0.82	11	1	0.04	0	-
Makah NFH 96	0.84	0.81	15	0	0.04	0	216 (48 - infinite)
Makah NFH 01	0.86	0.86	14	1	0.00	6	219 (140 - 449)
Makah NFH 03	0.85	0.87	12	1	-0.02	4	537 (195 - infinite)
Makah NFH 07	0.86	0.86	13	1	0.00	27	256 (170 - 475)
Quinault NFH 01	0.86	0.87	5	1	-0.01	16	112 (83 - 168)
Quinault NFH 06	0.85	0.84	6	0	0.02	5	-
Forks Creek H	0.86	0.86	7	0	0.00	5	652 (365 - 2420)
Humptulips H	0.86	0.87	10	1	0.00	1	-
Hoh River 04	0.86	0.85	2	0	0.01	4	683 (250 - infinite)
Hoh River 05	0.86	0.83	4	2	0.04	4	-
Queets River 96	0.86	0.83	3	0	0.03	2	-
Queets River 97	0.87	0.86	1	0	0.01	0	-
Quillayute River 95	0.86	0.86	9	0	0.00	0	-
Quillayute River 96	0.84	0.83	8	1	0.01	3	-

b) single nucleotide polymorphisms

Description	H_e	H_o	HWE	F_{IS}	LD	N_e
Makah NFH 01	0.33	0.33	2	0.03	105	135 (76 - 417)
Makah NFH 07	0.32	0.32	4	0.05	97	127 (69- 500)
Quinault NFH 01	0.32	0.32	4	0.04	108	194 (101 - 971)

Figure 1 - Correspondence Analysis (CA) of microsatellite genotype data in Chinook salmon from Makah NFH and adjacent populations. Axes 1, 2, and 3 explained 28.29%, 19.35%, and 13.69% of the inertia, respectively.

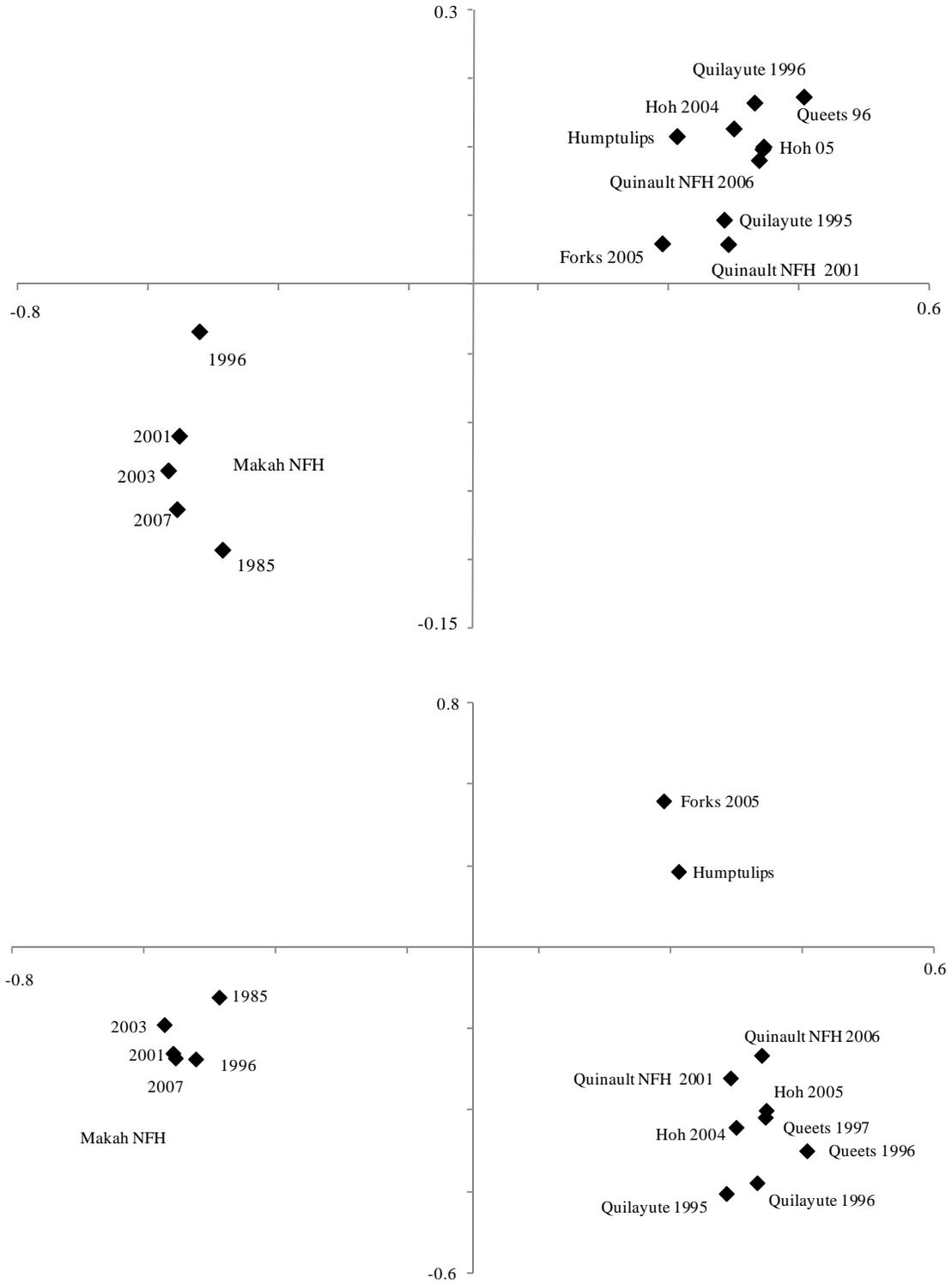
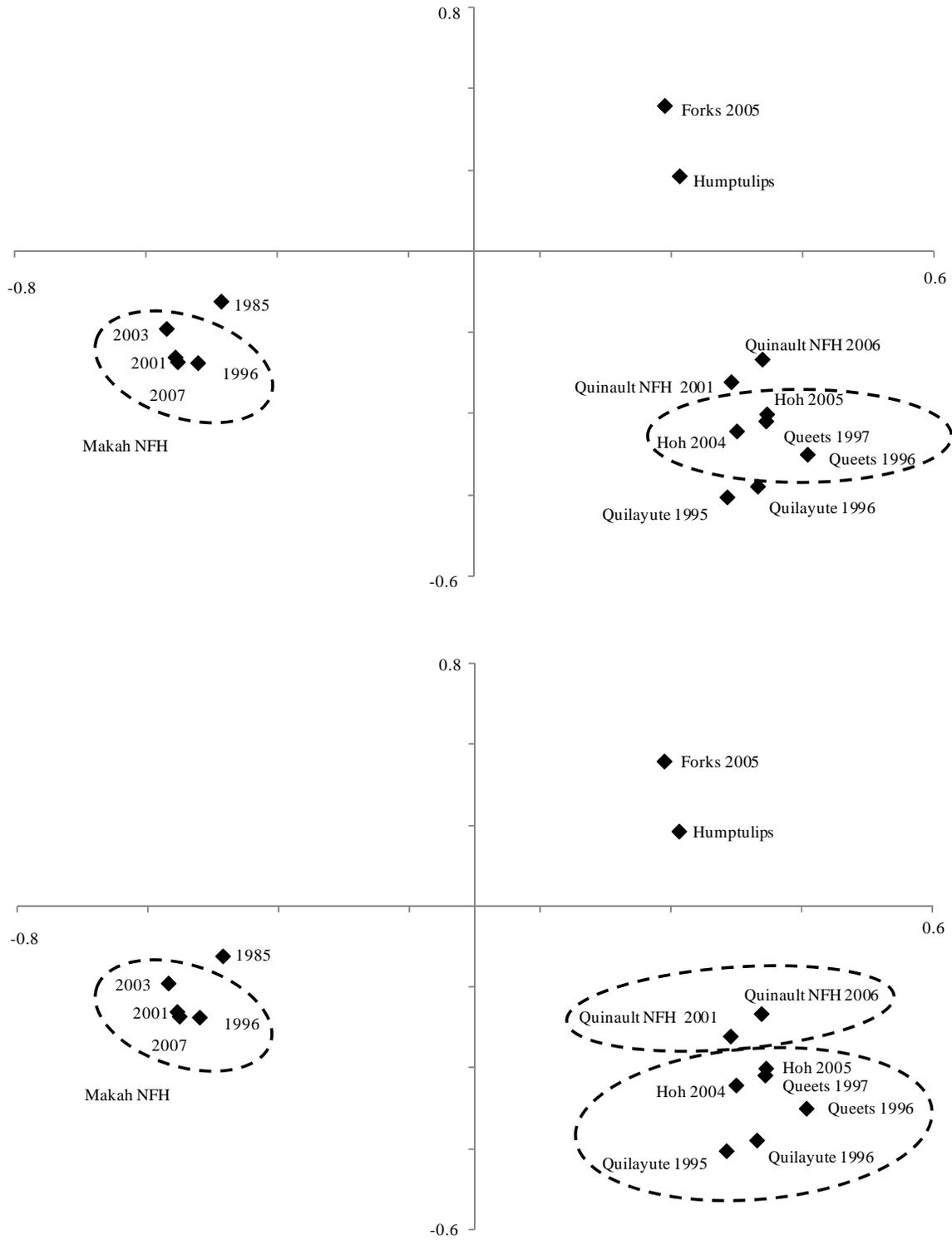


Figure 2 - Statistical tests of divergence among samples from Makah NFH and adjacent populations. Circles indicate groups of samples lacking statistically different allele frequencies (top) and having low pairwise F_{ST} values (i.e. values not >95% of a null distribution in which individuals were permuted among samples) (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.
- Diversity **within** the Makah NFH fall Chinook salmon broodstock samples, as indicated by allelic richness rank, was lower than in the samples representing other hatchery and wild populations examined here. No clear trend of increasing or decreasing diversity was observed among the annual samples (brood years 1985-2007). While the large number of pairs of microsatellites in LD observed in the 2007 Makah NFH sample is interesting, samples from subsequent years would need to be analyzed in order to interpret this result.
- The pattern of divergence **among** samples revealed that Makah NFH fall Chinook salmon are significantly divergent from all other populations sampled. Annual samples of the Makah NFH fall Chinook salmon were generally similar to each other, with only a single (small) sample (1985 broodstock sample; n=9) showing statistical differentiation from the others.
- The distinctiveness of Sooes River fall Chinook salmon might have been caused by a historical separation of this population from its neighbors or from one or more past bottleneck events. The former would indicate increased possibilities of unique adaptive potential, whereas the latter would not. The relatively low diversity in the Makah NFH samples make a bottleneck hypothesis seem more likely; however, I am not aware of studies that have examined the adaptive potential of this population. While a reduction in neutral diversity resulting from a bottleneck may indicate a reduction in the future adaptive potential of this stock, it would not indicate that the stock possesses no unique adaptations to the present environment.

Sources cited

1. Numbers taken from 2009 Sooes Chinook salmon return forecast report prepared by Hap Leon for The Makah tribe.

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. Details regarding the SNP markers included in the GAPS consortium baseline are available at <http://www.fws.gov/aftc/gapsSnp.pdf>

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. Seventy two single nucleotide polymorphism (SNP) markers and thirteen microsatellite markers used to analyze Makah NFH fall Chinook salmon.

Single Nucleotide Polymorphism Markers		Microsatellite Markers			
1	<i>ALDB-177M</i>	38	<i>ASPAT</i>	1	<i>Ogo2</i>
2	<i>Ots_u202-161</i>	39	<i>CD63</i>	2	<i>Ogo4</i>
3	<i>Ots_U211-85</i>	40	<i>CH113457-40R</i>	3	<i>Oki100</i>
4	<i>Ots_U4-92</i>	41	<i>CH128757-61R</i>	4	<i>Omm1080</i>
5	<i>PGK-54</i>	42	<i>CH94903-99R</i>	5	<i>Ots201b</i>
6	<i>RAG3</i>	43	<i>Ch96222-525</i>	6	<i>Ots208b</i>
7	<i>TLR3</i>	44	<i>Ch96500-180</i>	7	<i>Ots211</i>
8	<i>ZR-575</i>	45	<i>CH97077-179R</i>	8	<i>Ots212</i>
9	<i>Ots_113242-216</i>	46	<i>COX1</i>	9	<i>Ots213</i>
10	<i>Ots_123048-521</i>	47	<i>FGF6B_1</i>	10	<i>Ots3M</i>
11	<i>Ots_94857-232R</i>	48	<i>GTH2B-550</i>	11	<i>Ots9</i>
12	<i>Ots_96899-357R</i>	49	<i>IL11</i>	12	<i>OtsG474</i>
13	<i>Ots_ALDB1-122</i>	50	<i>IL8R-C8</i>	13	<i>Ssa408</i>
14	<i>Ots_AsnRS-60</i>	51	<i>mybp-85</i>		
15	<i>Ots_CD59-2</i>	52	<i>MYOD</i>		
16	<i>Ots_EP-529</i>	53	<i>NKEF</i>		
17	<i>Ots_u07-57.120</i>	54	<i>Ots_U07-25.325</i>		
18	<i>Ots_GDH-81x</i>	55	<i>NOD1</i>		
19	<i>Ots_GnRH-271</i>	56	<i>OPLW173_1</i>		
20	<i>Ots_GPDH-338</i>	57	<i>Ots_C3N3</i>		
21	<i>Ots_GPH-318</i>	58	<i>Ots_ETIF1A</i>		
22	<i>Ots_GST-375</i>	59	<i>Ots_FARSLA-220</i>		
23	<i>Ots_Ikaros-250</i>	60	<i>Ots_FGF6A</i>		
24	<i>Ots_myo1a-384</i>	61	<i>Ots_HSP90B-100</i>		
25	<i>Ots_Ots311-101x</i>	62	<i>Ots_IGF-1.1-76</i>		
26	<i>Ots_P53</i>	63	<i>Ots_MHC1</i>		
27	<i>Ots_Prl2</i>	64	<i>Ots_MHC2</i>		
28	<i>Ots_S7-1</i>	65	<i>Ots_P450</i>		
29	<i>Ots_SERPC1-209</i>	66	<i>Ots_RFC2-558</i>		
30	<i>Ots_SWS1op-182</i>	67	<i>Ots_SClkF2</i>		
31	<i>Ots_TGFB</i>	68	<i>Ots_SL</i>		
32	<i>Ots_u07-49.290</i>	69	<i>Ots_TAPBP</i>		
33	<i>Ots_u6-75</i>	70	<i>Ots_Tnsf</i>		
34	<i>Ots_GH2_1</i>	71	<i>Ots_U07-07.161</i>		
35	<i>Ots_unk526</i>	72	<i>NRAMP</i>		
36	<i>Ots_u07-53.133</i>	73	<i>Ots_zP3b-1</i>		
37	<i>Ots_u07-18.378</i>				

Appendix 2. Genotype call rates (completeness of data). Shaded cells highlight data that are <90% complete.

Description	Year	Microsatellite call rate	SNP call rate
Makah NFH broodstock	1985	0.940	
Makah NFH broodstock	1996	0.959	
Makah NFH broodstock	2001	0.999	0.950
Makah NFH broodstock	2003	0.938	
Makah NFH broodstock	2007	0.996	0.943
Quinalt NFH broodstock	2001	0.992	0.954
Quinalt NFH broodstock	2006	0.735	
Forks Creek H. Broodstock	2005	0.980	
Humptulips H. broodstock	1990	0.876	
Hoh River	2004	0.963	
Hoh River	2005	0.977	
Queets River	1996	0.825	
Queets River	1997	0.910	
Quillayute River	1995	0.848	
Quillayute River	1996	0.777	

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”).