

Genetic profile for Quinault NFH coho salmon

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National Fish Hatchery Broodstock Genetic Profile

- Facility:** Quinalt National Fish Hatchery
- Stock:** coho salmon (*Oncorhynchus kisutch*)
- Parental stock:** Natural-origin (wild) coho trapped in Cook Creek. Gametes from Skagit River coho were integrated in 1975. Queets River stock was introduced in 1983^{Ref 1}.
- Year founded:** 1968
- Generation time:** 2 years (10% of males) to 3 years (100% of females and 90% of males) for past several generations. Early generations (pre-1990) may have included fewer 2 year old males.
- Segregation / Integration history:** Segregated, however, natural origin fish trapped at the hatchery are included in the broodstock.

Table 1 - Broodstock samples analyzed:

Description	Year	n	Life stage	Data source
Quinalt NFH broodstock	2000	44	returning adult	NOAA
Quinalt NFH broodstock	2001	44	returning adult	NOAA
Quinalt NFH broodstock	2002	47	returning adult	NOAA
Quinalt NFH broodstock	2007	93	returning adult	AFTC
Quinalt NFH broodstock	2008	94	returning adult	AFTC
Quinalt NFH broodstock	2009	89	returning adult	AFTC
Quinalt NFH broodstock	2010	83	returning adult	AFTC

Table 2 – Coho salmon samples analyzed for comparison:

Description	H/W	Year	n	Life stage	Data source
Makah NFH broodstock	H	2001	46	returning adult	NOAA
Makah NFH broodstock	H	2002	45	returning adult	NOAA
Makah NFH broodstock	H	2003	43	returning adult	NOAA
Makah NFH broodstock	H	2007	89	returning adult	NOAA
Makah NFH broodstock	H	2008	94	returning adult	NOAA
Makah NFH broodstock	H	2009	99	returning adult	NOAA
Makah NFH broodstock	H	2010	92	returning adult	NOAA
Clearwater	H	1995-2002	112	juvenile	NOAA
Queets	H	1995-2002	132	juvenile	NOAA
Humtulpis	H	2003	48	juvenile	NOAA
Bingham	W	1995	69	juvenile	NOAA
Hope	W	1999	45	juvenile	NOAA

Genetic markers analyzed:

11 microsatellites standardized between NOAA Fisheries Manchester Field Station and AFTC^{Ref}
² (11 / 11 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 rank (AR rank, with 1 representing the most diversity and 19 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	Quinault NFH broodstock 2000	0.87	0.86	8	2	0.08	3	142 (77 - 532.3)
2	Quinault NFH broodstock 2001	0.85	0.85	14	3	0.08	5	115 (62 - 433.8)
3	Quinault NFH broodstock 2002	0.85	0.85	10	1	0.03	3	108 (47 - Infinite)
4	Quinault NFH broodstock 2007	0.84	0.84	17	1	0.05	12	126 (75 - 288)
5	Quinault NFH broodstock 2008	0.86	0.86	4	1	0.01	10	124 (67 - 382.8)
6	Quinault NFH broodstock 2009	0.87	0.87	6	5	0.04	17	127 (72 - 338.7)
7	Quinault NFH broodstock 2010	0.85	0.85	3	2	0.04	12	206 (97 - 3009.1)
8	Makah NFH broodstock 2001	0.84	0.84	18	2	0.03	7	81 (48 - 192.4)
9	Makah NFH broodstock 2002	0.85	0.85	11	2	0.02	9	72 (45 - 145.3)
10	Makah NFH broodstock 2003	0.87	0.87	19	1	0.02	7	81 (46 - 229.1)
11	Makah NFH broodstock 2007	0.86	0.86	7	3	0.02	13	169 (73 - 89387)
12	Makah NFH broodstock 2008	0.85	0.85	13	2	0.02	15	89 (61 - 143.2)
13	Makah NFH broodstock 2009	0.87	0.87	12	2	0.04	17	91 (58 - 167)
14	Makah NFH broodstock 2010	0.86	0.86	8	2	0.02	14	109 (56 - 396.8)
15	Clearwater	0.87	0.87	2	2	0.01	3	356 (186 - 1875.1)
16	Queets	0.88	0.88	1	3	0.04	31	204 (138 - 356.2)
17	Humptulips	0.86	0.86	5	2	0.04	3	1018 (171 - Infinite)
18	Bingham	0.85	0.85	16	3	0.05	4	427 (132 - Infinite)
19	Hope	0.83	0.83	15	3	0.01	11	66 (37 - 194.8)

Figure 1 - Correspondence Analysis (CA) of allele frequencies observed in Quinault NFH and adjacent coho salmon populations. Sample numbers are those listed in Table 3. Axis 1 and 2 accounted for 18.1% and 14.1% of the variance, respectively.

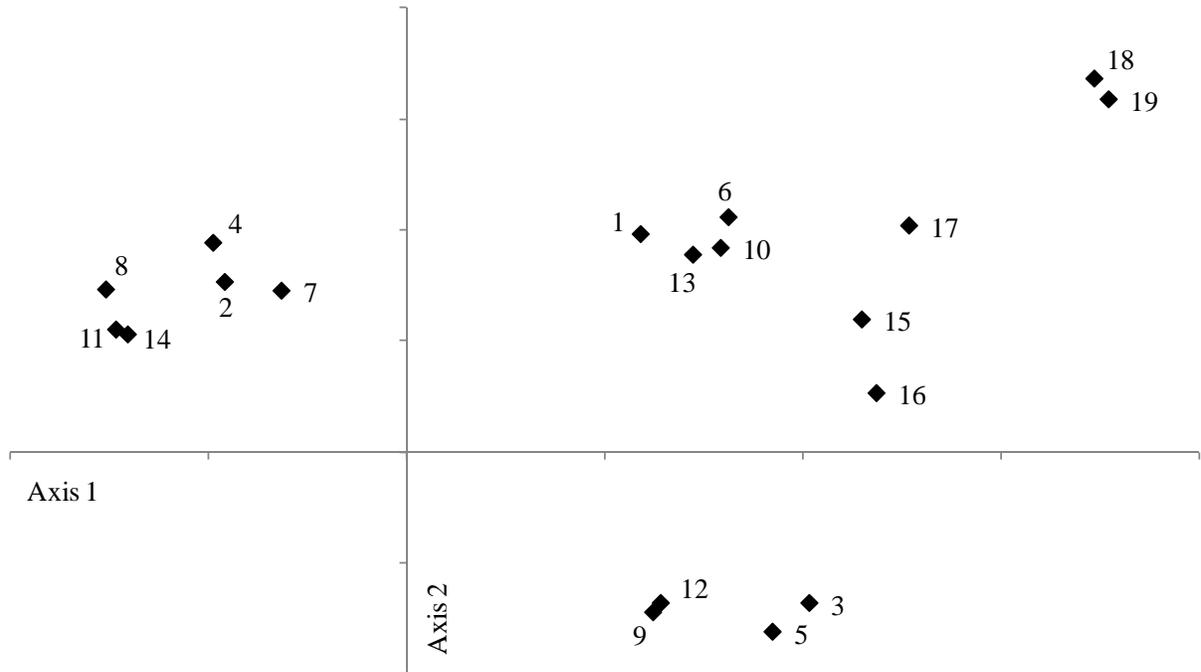
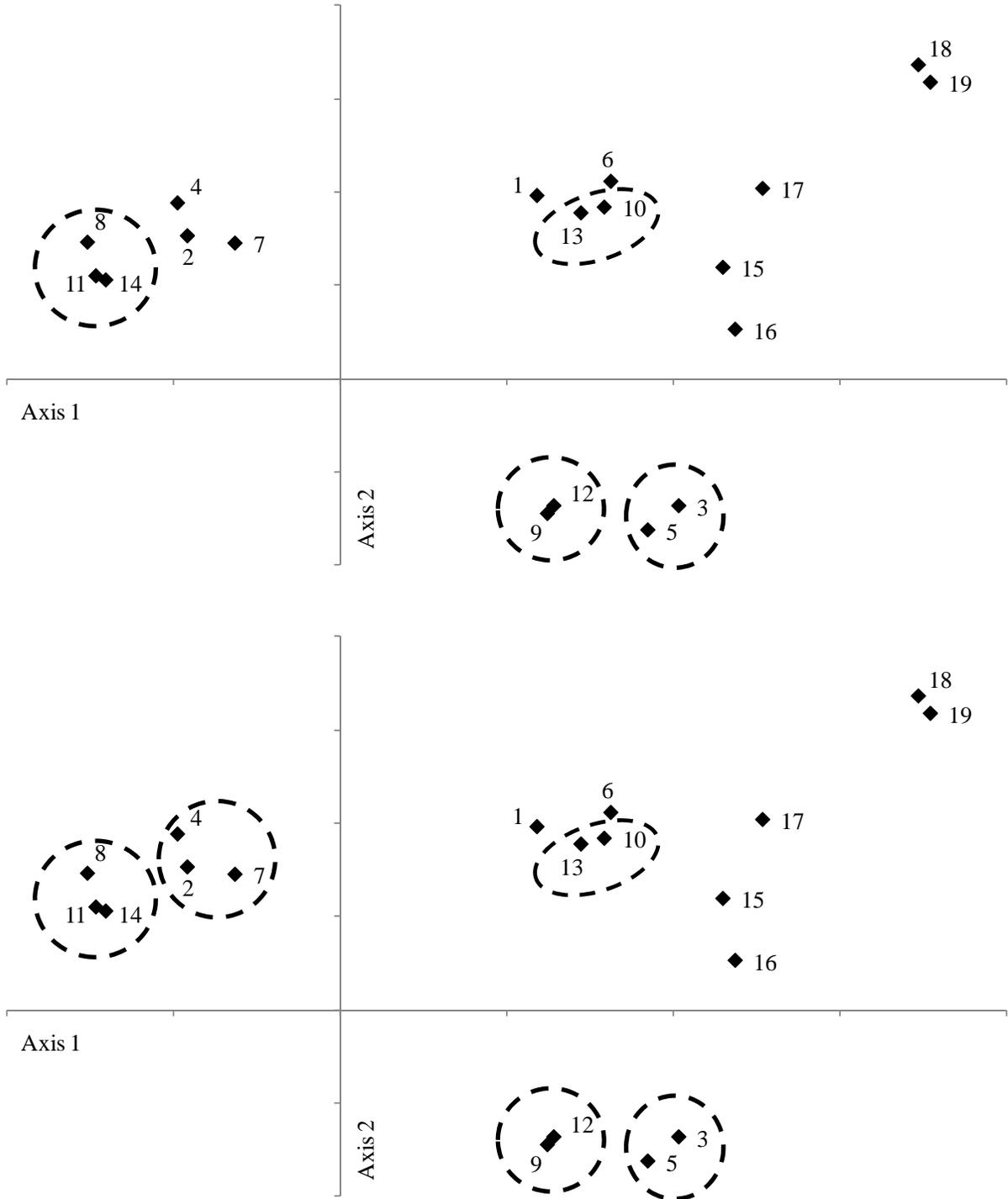


Figure 2 - Statistical tests of divergence among samples from Quinault NFH and adjacent coho salmon populations. Sample numbers are those listed in Table 3. Dashed lines indicate groups of samples lacking statistically different allele frequencies (top) and statistically significant F_{ST} values (bottom).



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.
- Makah NFH coho were derived from the Quinault NFH population ~10 generations ago (1981)^{Ref 1}. Further, in 1989 returning adults to Makah NFH were not spawned, and eyed eggs from Quinault NFH were raised at Makah NFH instead (Y. Dettlaff-Polenz, USFWS, personal communication).
- Genetic diversity (measured by allelic richness) in the Quinault NFH samples was not consistently lower or higher than in the other samples examined here.
- Quinault NFH coho appeared distinct from all other populations examined. The three run years were highly divergent from one another. Heterogeneity tests within run years at Quinault NFH yielded non-significant results in one of three run years, and F_{ST} was non-significant among collections from two of three run years.
- While all pairs of samples from Quinault and Makah NFH were significantly different from each other, the CA plot revealed similarity among corresponding run years from these two hatcheries.
- Departures from HWE and LD, in association with positive F_{IS} values, suggest that collections might include individuals from multiple populations. For example, increasing LD in recent years for Quinault NFH broodstock may be due to an increase in the use of 2-year old males. Under this scenario we would expect LD to gradually decrease as the brood years become increasingly similar to one another.

Sources cited

1. United States Fish and Wildlife Service. 2009. Quilcene, Quinault and Makah National Fish Hatcheries Assessments and Recommendations. Final Report by the USFWS Olympic Peninsula Hatchery Review Team. Available at:
http://www.fws.gov/pacific/fisheries/hatcheryreview/Reports/olympen/Olympic_PeninsulaNFHReview_FinalReport_May2009_FINAL.pdf

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

Van Doornik, D. M., D. J. Teel, D. R. Kuligowski, C. A. Morgan, and E. Casillas. 2007. Genetic analyses provide insight into the early ocean stock distribution and survival of juvenile coho salmon off the coasts of Washington and Oregon. *North American Journal of Fisheries Management* 27:220-237.

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. Eleven microsatellite markers used to analyze Quinault NFH coho salmon.

Microsatellite markers	
1	Ots213
2	OtsG42
3	Oki23
4	Ots505
5	Ocl8
6	Oki10
7	One13
8	Oki1
9	Ots103
10	P53
11	Ots3

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

Description	Year	Microsatellite call rate
Quinalt NFH broodstock	2000	0.988
Quinalt NFH broodstock	2001	0.969
Quinalt NFH broodstock	2002	0.971
Quinalt NFH broodstock	2007	0.986
Quinalt NFH broodstock	2008	0.999
Quinalt NFH broodstock	2009	0.994
Quinalt NFH broodstock	2010	0.970
Makah NFH broodstock	2001	0.978
Makah NFH broodstock	2002	0.952
Makah NFH broodstock	2003	0.966
Makah NFH broodstock	2007	0.988
Makah NFH broodstock	2008	0.993
Makah NFH broodstock	2009	0.993
Makah NFH broodstock	2010	0.983
Clearwater	1995-2002	0.955
Queets	1995-2002	0.932
Humptulips	2003	0.989
Bingham	1995	0.959
Hope	1999	0.903

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”).