

# Genetic profile for Quilcene NFH coho salmon

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# National Fish Hatchery Broodstock Genetic Profile

**Facility:** Quilcene National Fish Hatchery

**Stock:** coho salmon (*Oncorhynchus kisutch*)

**Parental stock:** Primarily from Big Quilcene River, with occasional introductions of other stocks

**Year founded:** 1911

**Generation time:** 3 years. In recent years some 2 year old males (jacks) have been integrated into the broodstock to facilitate gene flow among year classes. In 2003 a target that 10% of males should be jacks was set, and in 2007 the target was increased to 20% of all males  
Ref 1

**Segregation / Integration history:** Segregated.

**Table 1 - Broodstock samples analyzed:**

Description	Year	n	Life stage	Data source
Quilcene NFH broodstock	2000	92	returning adult	AFTC
Quilcene NFH broodstock	2001	94	returning adult	AFTC
Quilcene NFH broodstock	2002	93	returning adult	AFTC
Quilcene NFH broodstock	2007	77	returning adult	AFTC
Quilcene NFH broodstock	2008	65	returning adult	AFTC
Quilcene NFH broodstock	2009	100	returning adult	AFTC
Quilcene NFH broodstock	2010	92	returning adult	AFTC

**Table 2 – Coho salmon samples analyzed for comparison:**

Description	H/W	Year	n	Life stage	Data source
Little Quilcene	W	2005	47	juvenile	AFTC
Little Quilcene	W	2006	47	juvenile	AFTC
Big Beef Creek	W	2003	77	returning adult	NOAA
Big Beef Creek	W	2004	57	juvenile	NOAA
Tarboo Creek	W	2005	47	juvenile	AFTC
Tarboo Creek	W	2006	45	juvenile	AFTC
Thorndyke Creek	W	2005	47	juvenile	AFTC
Thorndyke Creek	W	2006	48	juvenile	AFTC

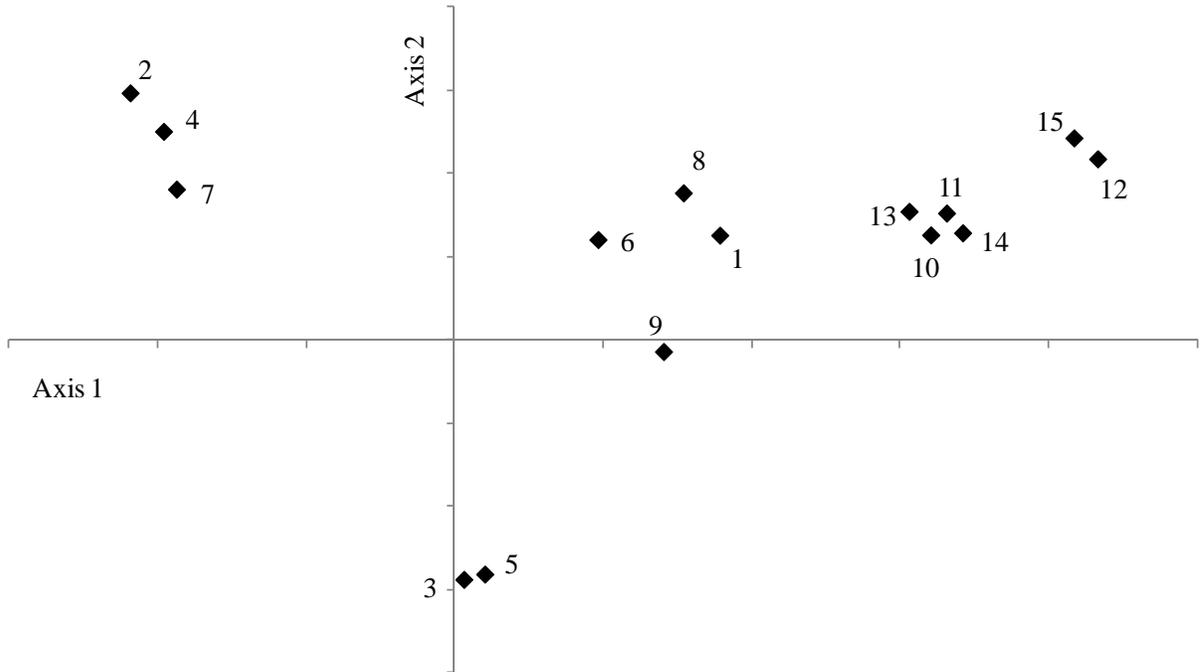
**Genetic markers analyzed:**

11 microsatellites standardized between NOAA Fisheries Manchester Field Station and AFTC<sup>Ref</sup><sup>2</sup> (11 / 11 loci). A complete list of the markers analyzed is provided in Appendix 1. Genotyping success rates are presented in Appendix 2.

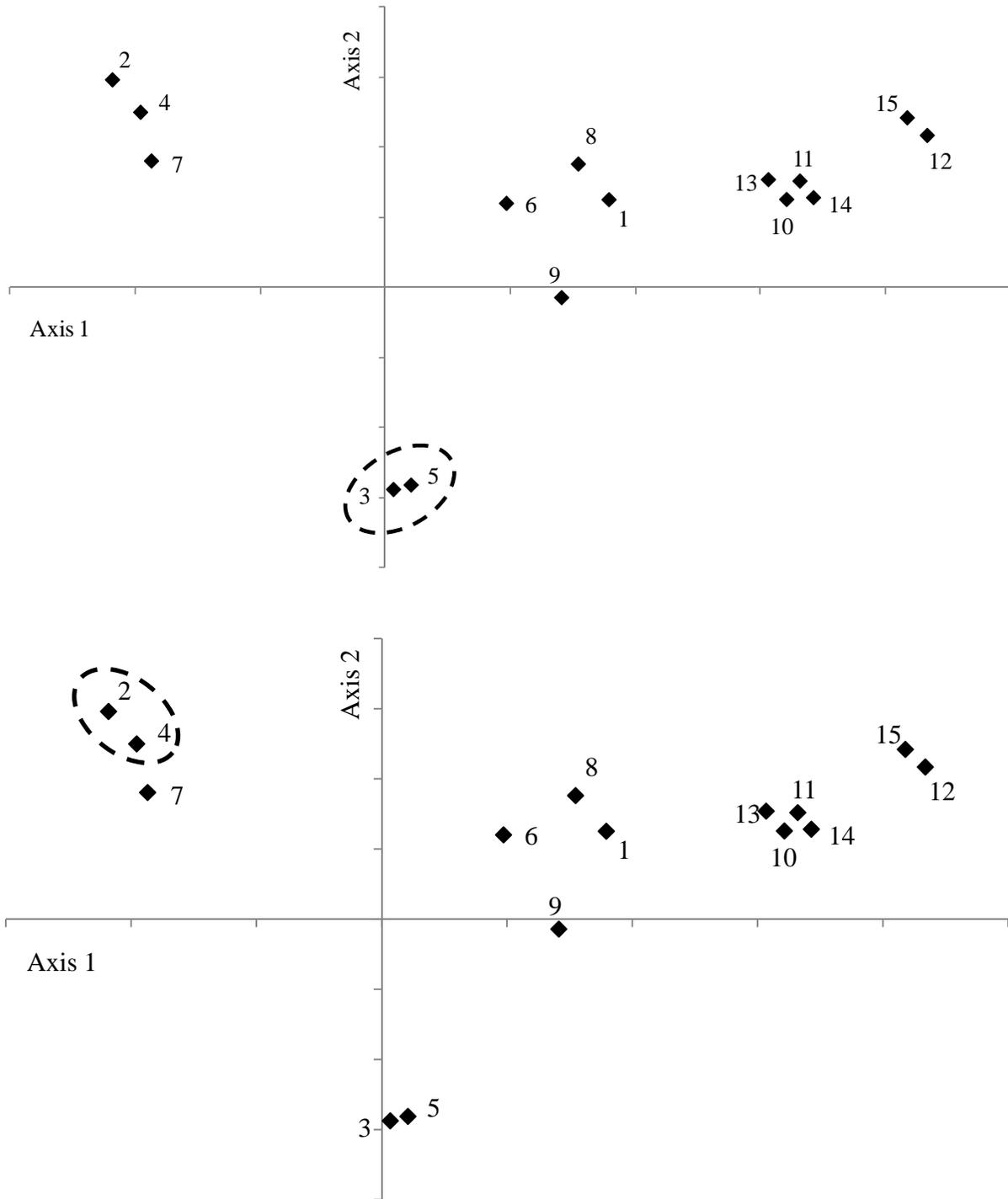
**Table 3 - Diversity within samples.** Expected ( $H_e$ ) and observed ( $H_o$ ) heterozygosity, allelic richness rank (AR rank, with 1 representing the most diversity and 15 representing the least diversity), number of loci exhibiting departures from Hardy-Weinberg Equilibrium (HWE),  $F_{IS}$  (a 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	Quilcene NFH broodstock 2000	0.86	0.86	10	3	0.03	26	100 (61 - 208.4)
2	Quilcene NFH broodstock 2001	0.81	0.81	15	2	0.02	12	125 (77 - 263.8)
3	Quilcene NFH broodstock 2002	0.80	0.80	14	1	0.04	9	109 (51 - 589.7)
4	Quilcene NFH broodstock 2007	0.81	0.81	12	3	0.03	22	103 (64 - 208.1)
5	Quilcene NFH broodstock 2008	0.79	0.79	12	2	0.06	5	207 (76 - Infinite)
6	Quilcene NFH broodstock 2009	0.87	0.87	8	1	0.04	15	101 (64 - 194.5)
7	Quilcene NFH broodstock 2010	0.82	0.82	11	2	0.03	9	167 (104 - 353.7)
8	Little Quilcene 2005	0.87	0.87	2	2	0.03	4	143 (80 - 477.6)
9	Little Quilcene 2006	0.85	0.85	5	3	0.04	1	277 (121 - Infinite)
10	Big Beef Creek 2003	0.86	0.86	1	1	0.01	1	341 (184 - 1586.7)
11	Big Beef Creek 2004	0.86	0.86	2	3	0.04	1	862 (194 - Infinite)
12	Tarboo Creek 2005	0.87	0.87	7	4	0.04	22	17 (14 - 20)
13	Tarboo Creek 2006	0.85	0.85	9	8	-0.04	54	10 (8 - 10.9)
14	Thorndyke Creek 2005	0.85	0.85	4	3	0.04	14	54 (39 - 84.4)
15	Thorndyke Creek 2006	0.86	0.86	6	1	0.01	15	51 (33 - 91.9)

**Figure 1 - Correspondence Analysis (CA) of allele frequencies observed in Quilcene NFH and adjacent coho salmon populations.** Sample numbers are those listed in Table 3. Axis 1 and 2 accounted for 25.0% and 17.1% of the variance, respectively.



**Figure 2 - Statistical tests of divergence among samples from Quilcene 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.
- Genetic diversity (measured by allelic richness) was generally lower in the Quilcene NFH samples than in the adjacent wild samples. One exception was the Quilcene NFH 2009 sample which exhibited greater allelic richness than the Tarboo Creek 2006 sample. The high levels of LD and departures from HWE in Tarboo Creek 2006 (which was a juvenile collection) indicated that some families may have been over-represented in this collection.
- Quilcene NFH coho appeared distinct from all other populations examined. Tests for allele frequency heterogeneity and  $F_{ST}$  significance indicated that a few pairs from Quilcene NFH yielded non-significant ( $P > 0.05$ ) results, however a different pair was indicated by each test.
- Three distinct broodlines of coho have been observed at Quilcene NFH. The late broodline arrives at about the same time as the wild fish, the early broodline appears ~ 1 month early, and the middle broodline arrives between these two. The primary and secondary axes of the CA plot revealed divergence of the “early” and “middle” broodlines, respectively, from the late broodline and wild fish. This result documents a pattern of genetic divergence which mirrors the observed pattern of phenotypic divergence between the wild and hatchery populations.
- The USFWS Olympic Peninsula Hatchery Review Team identified the relatively high level of divergence among the three broodlines as a Genetic Risk of the Quilcene NFH coho program. They recommended that the proportion of jacks in the Quilcene NFH broodstock be increased to 20% of all males for at least two generations. Pairwise  $F_{ST}$ 's between the collections from 2000-2002 (0.053 – 0.072) were higher than those between collections from 2008-2010 (0.036 - 0.053), indicating a reduction in the level of divergence among the broodlines.



## **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/olypen/Olympic\\_PeninsulaNFHReview\\_FinalReport\\_May2009\\_FINAL.pdf](http://www.fws.gov/pacific/fisheries/hatcheryreview/Reports/olypen/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 Quilcene NFH coho salmon.

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

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

Description	Year	Microsatellite call rate
Quilcene NFH broodstock	2000	0.990
Quilcene NFH broodstock	2001	0.992
Quilcene NFH broodstock	2002	0.992
Quilcene NFH broodstock	2007	0.994
Quilcene NFH broodstock	2008	0.993
Quilcene NFH broodstock	2009	0.996
Quilcene NFH broodstock	2010	0.987
Little Quilcene	2005	0.990
Little Quilcene	2006	0.971
Big Beef Creek	2003	0.976
Big Beef Creek	2004	0.973
Tarboo Creek	2005	0.986
Tarboo Creek	2006	0.986
Thorndyke Creek	2005	0.994
Thorndyke Creek	2006	0.992



#### **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”).