

# Genetic profile for Quinault NFH fall Chinook salmon

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# National Fish Hatchery Broodstock Genetic Profile

- Facility:** Quinault National Fish Hatchery
- Stock:** Fall Chinook salmon (*Oncorhynchus tshawytscha*)
- Parental stock:** Fall Chinook salmon from lower Quinault River, as well as other Washington coastal stocks including Nemah and Willapa, and the Green River. Import of out of basin stocks ended in approximately 1985. Presently, broodstock are captured from adult returns to the hatchery and individuals captured in Lake Quinault. Collection from both sources is generally required to meet broodstock goal.
- Year founded:** 1968
- Generation time:** 2-6 years (y) (1.5% 2y, 7.4% 3y, 48.0% 4y, 42.0% 5y, 0.5% 6y)<sup>ref 1</sup>

**Segregation / Integration history:**

Integrated. All individuals released are marked by adipose clip, and both clipped and unclipped adults are used in broodstock.

**Broodstock samples analyzed:**

Description	Year	n	Life stage	Data source
Quinault NFH broodstock	2001	65	returning adult	AFTC
Quinault NFH broodstock	2006	38	returning adult	GAPS (WDFW)

**Samples analyzed for comparison:**

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

**Genetic markers analyzed:**

GAPS microsatellites<sup>ref 2</sup> (13 / 13 loci) and GAPS single nucleotide polymorphisms<sup>ref 3</sup> (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.

**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 “-”.

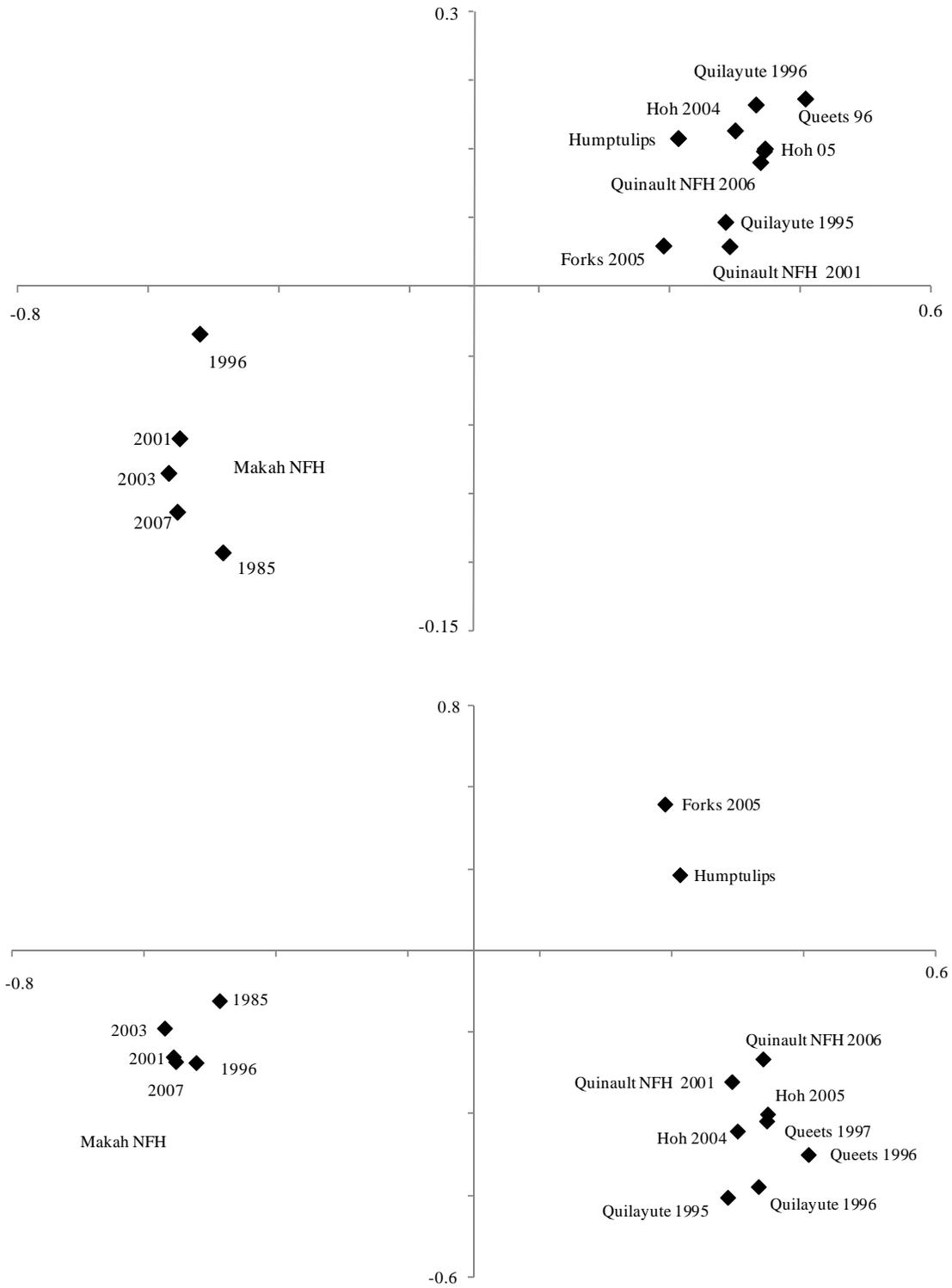
a) microsatellites

Description	$H_e$	$H_o$	AR rank	HWE	$F_{IS}$	LD	$N_e$
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	-
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)
Forks Creek H	0.86	0.86	7	0	0.00	5	652 (365 - 2420)
Humtulpis 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	-

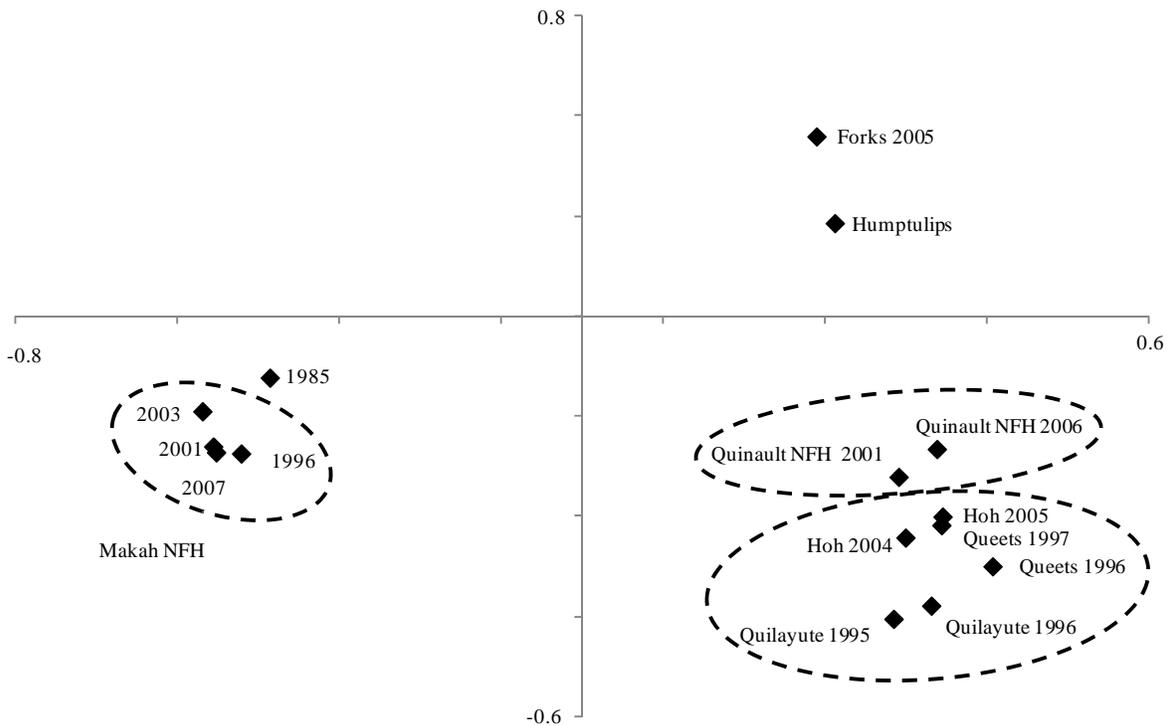
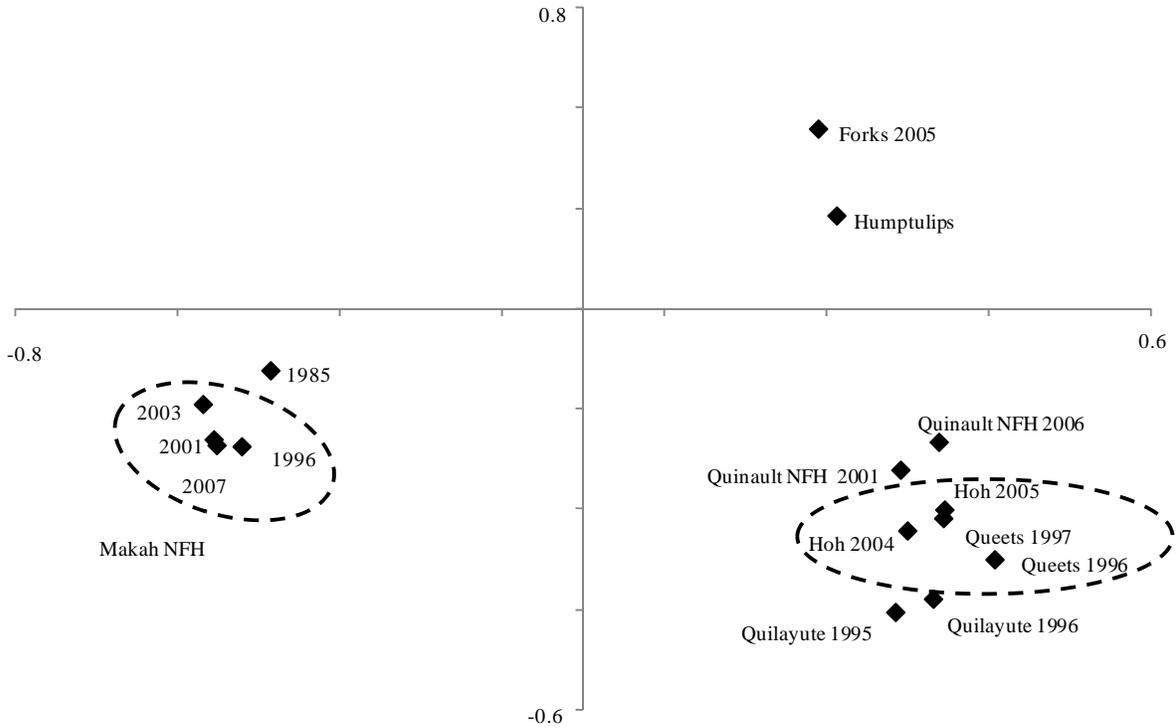
b) single nucleotide polymorphisms

Description	$H_e$	$H_o$	HWE	$F_{IS}$	LD	$N_e$
Quinault NFH 01	0.35	0.34	0	0.03	106	288 (109 - infinite)
Makah NFH 01	0.35	0.35	0	0.02	114	104 (60 - 284)
Makah NFH 07	0.34	0.33	0	0.03	98	143 (70 - 1484)

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



**Statistical tests of divergence among samples from Quinault NFH and adjacent populations.** Circles indicate groups of samples lacking statistically different allele frequencies (top) and pairwise  $F_{ST}$  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 Quinault NFH fall Chinook salmon broodstock samples exhibited an intermediate level of genetic diversity, with allelic richness values greater than those observed in other hatcheries but lower than those in most wild stocks (Quillayute River was an exception). High LD and the corresponding low  $N_e$  observed in the 2001 Quinault NFH sample might reflect family structure among the individuals sampled. Sampling of individuals from different populations (in the broodstock) could also yield this result. Data from additional broodstock years could help reveal the level of LD in the hatchery population.
- Quinault NFH fall Chinook salmon are significantly divergent from all other populations sampled. Annual samples of the Quinault NFH fall Chinook salmon were similar to each other. Allele frequencies were different between the 2001 and 2006 samples, but  $F_{ST}$  between those samples was not significant.
- Adults constituting the broodstock each year are not randomly mated but are spawned separately according to trapping location and questions have been raised regarding creation of two spatially segregated “broodlines”. If the samples analyzed here did represent two divergent populations or lineages, then we would expect substantial departures from HWE. Neither SNPs nor microsatellites revealed such departures. The LD observed among microsatellite loci in the 2001 sample could be indicative of a mixing of two lineages, but could also have other causes. An important assumption we need to make is that the samples analyzed are representative of fish returning to both Lake Quinault and Quinault NFH. Results based on the presently available samples do not indicate that the hatchery population is a mixture of two discrete populations.
- The *Olympic Peninsula NFHs Assessments and Recommendations Report* indicated that stray rates of Quinault NFH and Lake Quinault pen-reared fall Chinook to locations outside the Quinault River drainage are presumed to be low. The genetic data presented here revealed persistent genetic divergence between Quinault NFH broodstock samples and adjacent wild populations. This result supports the hypothesis that gene flow from

the hatchery to adjacent wild populations is low relative to the level of gene flow among wild populations.

## **Sources cited**

1. Numbers are from tagged Chinook Salmon released and returned at Quinault NFH. Percentages are from brood years 1999 to 2005 based on data in the Regional Mark Information System, and were summarized by Yvonne Dettlaff (Washington Fish and Wildlife Office).

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 Quinault 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
Quinault NFH broodstock	2001	0.992	0.954
Quinault NFH broodstock	2006	0.735	
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
Forks Creek H. Broodstock	2005	0.980	
Humtulpis 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”).