Genetic profile for Warm Springs NFH spring Chinook salmon

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National Fish Hatchery Broodstock Genetic Profile

Facility: Warm Springs National Fish Hatchery

Stock: Spring Chinook salmon (*Oncorhynchus tshawytscha*)

Parental stock: Wild fish from Warm Springs River

Year founded: 1978

Generation time: 3-5 years (y) (11% 3y, 84% 4y, 5% 5y) [ref 1]

Segregation / Integration history: Integrated. Goal is for a minimum average of 10% of the hatchery broodstock to be derived from natural origin adults, although it has not been possible to incorporate wild fish in some years. Round Butte Hatchery spring Chinook (a segregated stock) have been reared and released at Warm Springs NFH on four occasions when adult returns to Warm Springs NFH were insufficient to meet broodstock needs.

Table 1 - Broodstock samples analyzed:

a) GAPS microsatellites [Ref 2]

Description	Year	n	Life stage	Data source
Warm Springs NFH	2001	92	adult	AFTC
Warm Springs NFH	2002	61	adult	GAPS
Warm Springs NFH	2003	69	adult	GAPS
Warm Springs NFH	2004	94	adult	AFTC

b) Columbia River GSI SNPs v1 [Ref 3]

Description	Year	n	Life stage	Data source
Warm Springs NFH	2001	95	adult	AFTC
Warm Springs NFH	2004	94	adult	AFTC
Warm Springs NFH	2010	236	adult	AFTC
Warm Springs NFH	2011	203	adult	AFTC

Table 2 – Spring Chinook samples analyzed for comparison:

a) GAPS microsatellites

Description	H/W	Year	n	Life stage	Data source
Carson NFH	H	2001	78	adult	GAPS
Carson NFH	H	2004	39	adult	GAPS
Entiat NFH	H	2002	135	juvenile	GAPS
Granite Creek	W	2005	26	adult	GAPS
Granite Creek	W	2006	34	adult	GAPS
John Day River	W	2005	14	adult	GAPS
John Day River	W	2006	35	adult	GAPS
Klickitat Hatchery	H	2002	44	adult	GAPS
Klickitat Hatchery	H	2006	42	adult	GAPS
Klickitat River	W	2005	44	adult	GAPS
Methow River	H	1998	45	juvenile	GAPS
Methow River	H	2000	43	juvenile	GAPS
Naches	W	1993	64	adult	GAPS
Twisp River	W	2001	91	adult	GAPS
Twisp River	W	2005	35	adult	GAPS
Wenatchee Hatchery	H	2000	37	adult	GAPS
Wenatchee River	W	1993	62	adult	GAPS

b) Columbia River GSI SNPs v1

Description	H/W	Year	n	Life stage	Data source
Warm Springs River	W	1976	137	adult	AFTC/ODFW♣
Warm Springs River	W	1977	142	adult	AFTC/ODFW♣
Pelton Trap	mix	1974	83	adult	AFTC/ODFW♣
Pelton Trap	mix	2010	90	adult	AFTC
Pelton Trap	mix	2011	83	adult	AFTC
Big-Creek Spring	W	2001	82	adult	CRITFC
CapeHorn Spring	W	2005	84	juvenile	CRITFC
Carson NFH Spring	H	2007	88	juvenile	CRITFC
Winthrop NFH Spring	H	2001	86	adult	CRITFC
Catherine Spring	W	2003	91	adult	CRITFC
Cle-Elum Spring	H	2006	72	adult	CRITFC
Dworshak NFH Spring	H	2005	92	adult	CRITFC
East Fork Salmon Spring	W	2005	149	adult	CRITFC
Imnaha Spring	W	1998	182	adult	CRITFC
John-Day Spring	W	2005	74	adult	CRITFC
Johnson Creek Spring	W	2002	88	adult	CRITFC
Klickitat Hatchery Spring	H	2002	89	adult	CRITFC
Klickitat Wild Spring	W	2006	92	adult	CRITFC
Lochsa Spring	H	2005	80	adult	CRITFC
Lolo Spring	W	2001	89	juvenile	CRITFC
Lookingglass Spring	H	1994	83	juvenile	CRITFC
Methow Spring	H	1998	93	juvenile	CRITFC
Minam Spring	W	2002	90	juvenile	CRITFC
Newsome Spring	W	2001	78	adult	CRITFC
Pahsimeroi Spring	mix	2004	82	adult	CRITFC
Rapid River Hatchery	H	1999	44	juvenile	CRITFC
Sawtooth Spring	H	2003	46	adult	CRITFC
Secesh Spring	W	2001	81	juvenile	CRITFC
Tucannon Spring	W	2003	75	adult	CRITFC
Wenaha Spring	W	2002	0	juvenile	CRITFC
Camas Spring	W	2006	0	juvenile	CRITFC
Wenatchee Spring	W	1993	0	adult	CRITFC
West Fork Yankee Fork	W	2005	0	juvenile	CRITFC

♣These samples were archived by Oregon Department of Fish and Wildlife (ODFW) and the corresponding genetic data will be presented in a joint report by ODFW and USFWS in 2012.

Genetic markers analyzed:

1) GAPs microsatellites: 13 microsatellites standardized among most agency and academic laboratories [Ref 2].
2) Columbia River GSI SNPs version 1: 92/96 SNP markers used by Columbia River Intertribal Fish Commission (CRITFC), Idaho Department of Fish and Game (IDFG) and Abernathy Fish Technology Center (AFTC) for genetic stock identification (GSI) [Ref 3]. The baseline used by CRITFC and IDFG was recently increased to 192 single nucleotide polymorphism (SNP) markers used for both GSI and parentage-based tagging (PBT).

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 higher numbers representing less 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; given 78 potential pairs between microsatellites and 4,186 potential pairs between SNPs), 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) GAPS microsatellites

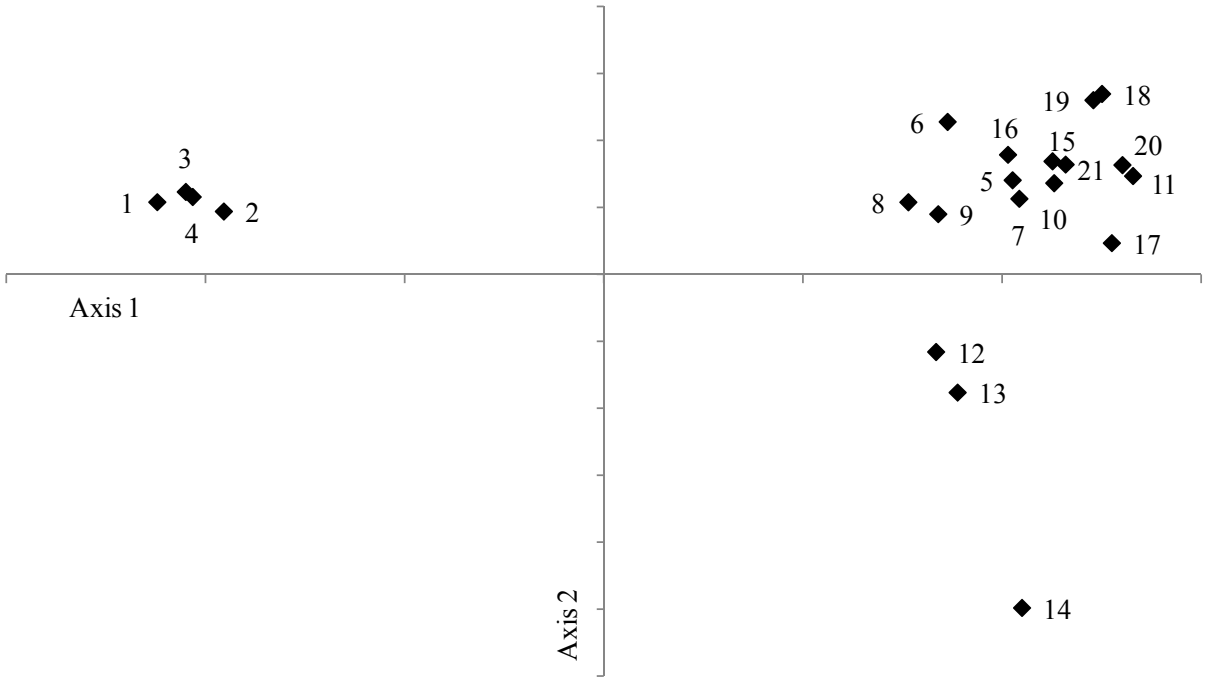
No	Description	H_e	H_o	AR rank	HWE	F_{IS}	LD	N_e
1	Warm Springs NFH 2001	0.74	0.74	16	1	-0.01	8	609 (252 - Infinite)
2	Warm Springs NFH 2002	0.72	0.72	19	1	0.03	6	216 (112 - 1274)
3	Warm Springs NFH 2003	0.72	0.73	18	0	-0.04	4	164 (106 - 328)
4	Warm Springs NFH 2004	0.73	0.73	19	0	0.00	8	1,769 (326 - Infinite)
5	Carson NFH 2001	0.79	0.79	9	1	-0.02	36	185 (96 - 1,042)
6	Carson NFH 2004	0.77	0.77	21	8	-0.06	39	11 (9 - 15)
7	Entiat NFH 2002	0.78	0.78	12	9	-0.01	76	25 (22 - 28)
8	Granite Creek 2005	0.77	0.77	9	1	0.02	0	104 (50 - 2,505)
9	Granite Creek 2006	0.76	0.76	11	0	0.04	4	-
10	John Day River 2005	0.74	0.74	15	1	-0.04	0	-
11	John Day River 2006	0.76	0.76	13	1	0.05	1	640 (125 - Infinite)
12	Klickitat Hatchery 2002	0.82	0.82	8	3	0.01	31	33 (26 - 43)
13	Klickitat Hatchery 2006	0.83	0.83	3	0	0.00	7	155 (82 - 764)
14	Klickitat River 2005	0.86	0.86	1	1	0.02	18	44 (32 - 68)
15	Methow River 1998	0.79	0.79	5	2	0.01	5	420 (139 - Infinite)
16	Methow River 2000	0.80	0.80	6	2	0.00	6	220 (102 - Infinite)
17	Naches 1993	0.82	0.82	2	1	0.02	2	-
18	Twisp River 2001	0.76	0.76	17	5	0.03	28	82 (62 - 114)
19	Twisp River 2005	0.77	0.77	14	5	0.03	14	76 (49 - 147)
20	Wenatchee Hatchery 2000	0.79	0.79	6	1	0.00	18	28 (22 - 37)
21	Wenatchee River 1993	0.79	0.79	3	1	-0.02	5	318 (152 - 38,750)

b) Columbia River GSI SNPs v1

No	Description	H_e	H_o	AR rank	HWE	F_{IS}	LD	N_e
1	Warm Springs NFH 2001	0.24	0.24	13	2	-0.01	117	478 (216 - Infinite)
2	Warm Springs NFH 2004	0.23	0.24	19	1	-0.02	136	284 (167 - 772)
3	Warm Springs NFH 2010	0.24	0.24	15	5	0.00	328	115 (93 - 145)
4	Warm Springs NFH 2011	0.24	0.24	16	6	0.02	175	213 (143 - 364)
5	Warm Springs River 1976	0.24	0.19	7	41	0.19	289	53 (41 - 70)
6	Warm Springs River 1977	0.24	0.21	4	17	0.10	211	139 (103 - 201)
7	Pelton Trap 1974	0.24	0.23	8	4	0.07	264	41 (34 - 50)
8	Pelton Trap 2010	0.25	0.25	10	5	0.00	314	64 (55 - 76)
9	Pelton Trap 2011	0.25	0.25	22	5	0.00	254	55 (46 - 69)
10	Big-Creek Spring	0.20	0.21	18	7	-0.01	198	35 (29 - 43)
11	CapeHorn Spring	0.20	0.20	3	0	0.02	169	59 (47 - 76)
12	Carson NFH Spring	0.23	0.23	14	1	0.01	162	131 (94 - 202)
13	Winthrop NFH Spring	0.23	0.23	17	4	0.00	192	77 (59 - 105)
14	Catherine Spring	0.23	0.23	37	2	0.01	155	108 (82 - 153)
15	Cle-Elum Spring	0.27	0.27	33	2	0.02	136	468 (203 - Infinite)
16	Dworshak NFH Spring	0.23	0.23	21	1	-0.01	109	202 (125 - 446)
17	East Fork Salmon Spring	0.21	0.22	27	4	-0.02	136	87 (64 - 130)
18	Imnaha Spring	0.22	0.23	23	2	-0.02	102	671 (245 - Infinite)
19	John-Day Spring	0.24	0.24	5	7	0.01	130	265 (146 - 994)
20	Johnson Creek Spring	0.21	0.21	24	3	0.01	126	152 (99 - 282)
21	Klickitat Hatchery Spring	0.29	0.29	34	3	0.01	229	124 (99 - 161)
22	Klickitat Wild Spring	0.31	0.30	25	5	0.03	316	74 (64 - 87)
23	Lochsa Spring	0.23	0.22	6	1	0.02	109	137 (92 - 243)
24	Lolo Spring	0.22	0.23	35	2	-0.01	131	132 (89 - 230)
25	Lookingglass Spring	0.23	0.23	2	3	0.00	239	38 (31 - 47)
26	Methow Spring	0.23	0.22	1	5	0.05	257	53 (42 - 68)
27	Minam Spring	0.24	0.24	26	2	0.02	163	112 (82 - 166)
28	Newsome Spring	0.23	0.22	29	2	0.02	122	176 (112 - 360)
29	Pahsimeroi Spring	0.21	0.22	20	2	-0.02	132	76 (56 - 109)
30	Rapid River Hatchery	0.22	0.22	12	3	0.01	104	429 (186 - Infinite)
31	Sawtooth Spring	0.21	0.21	11	3	0.00	114	191 (112 - 497)
32	Secesh Spring	0.21	0.20	30	2	0.02	85	146 (95 - 277)
33	Tucannon Spring	0.25	0.26	36	3	-0.04	236	52 (42 - 64)
34	Wenaha Spring	0.24	0.25	28	1	-0.02	129	79 (56 - 127)
35	Camas Spring	0.20	0.20	31	4	-0.02	113	33 (26 - 43)
36	Wenatchee Spring	0.22	0.22	32	1	0.01	144	103 (75 - 156)
37	West Fork Yankee Fork	0.21	0.21	9	5	0.02	227	26 (22 - 31)

Figure 1 - Graphical representations of genetic data observed in Warm Springs NFH and adjacent spring Chinook salmon populations. For microsatellite data, correspondence analysis was performed on microsatellite allele frequencies (a) and for SNP data, principal component analysis was performed on genetic chord distances. Sample numbers are those listed in Table 3.

a) Correspondence analysis of GAPS microsatellite allele frequencies - Axis 1 and 2 accounted for 21.58% and 13.14% of the inertia, respectively.



b) Principal component analyses of genetic chord distances based on Columbia River GSI SNPs v1 - Axis 1 and 2 accounted for 57.14% and 20.64% of the inertia, respectively.

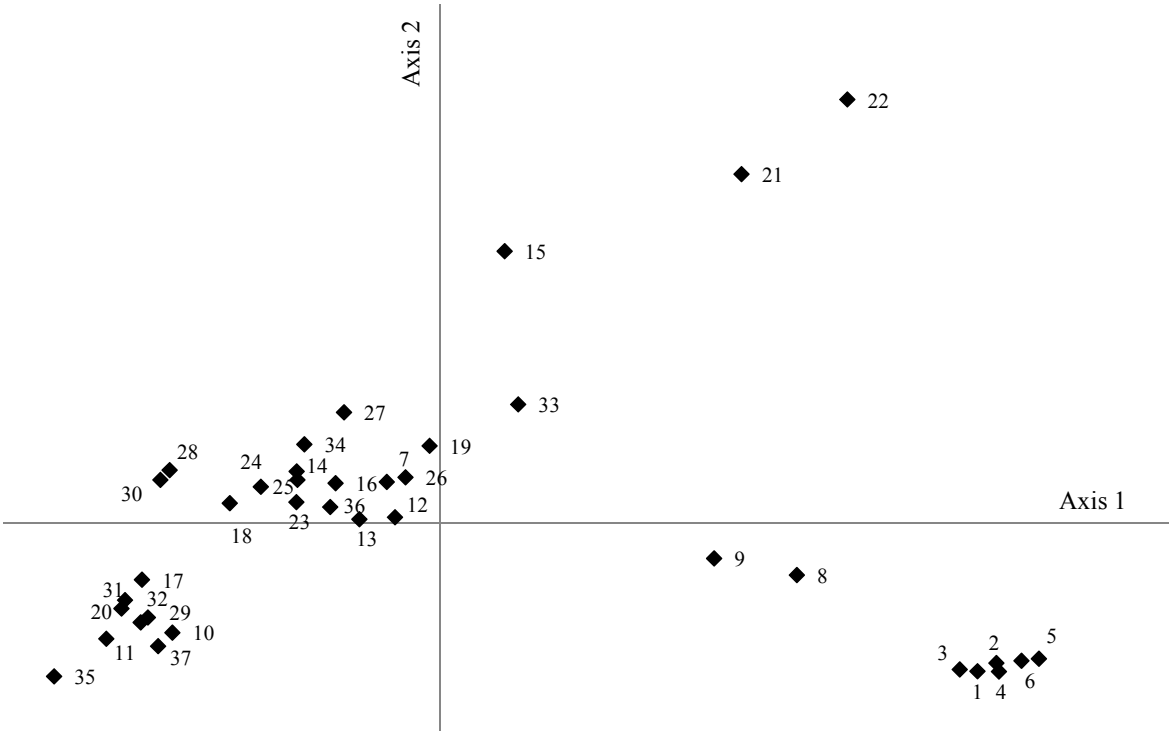
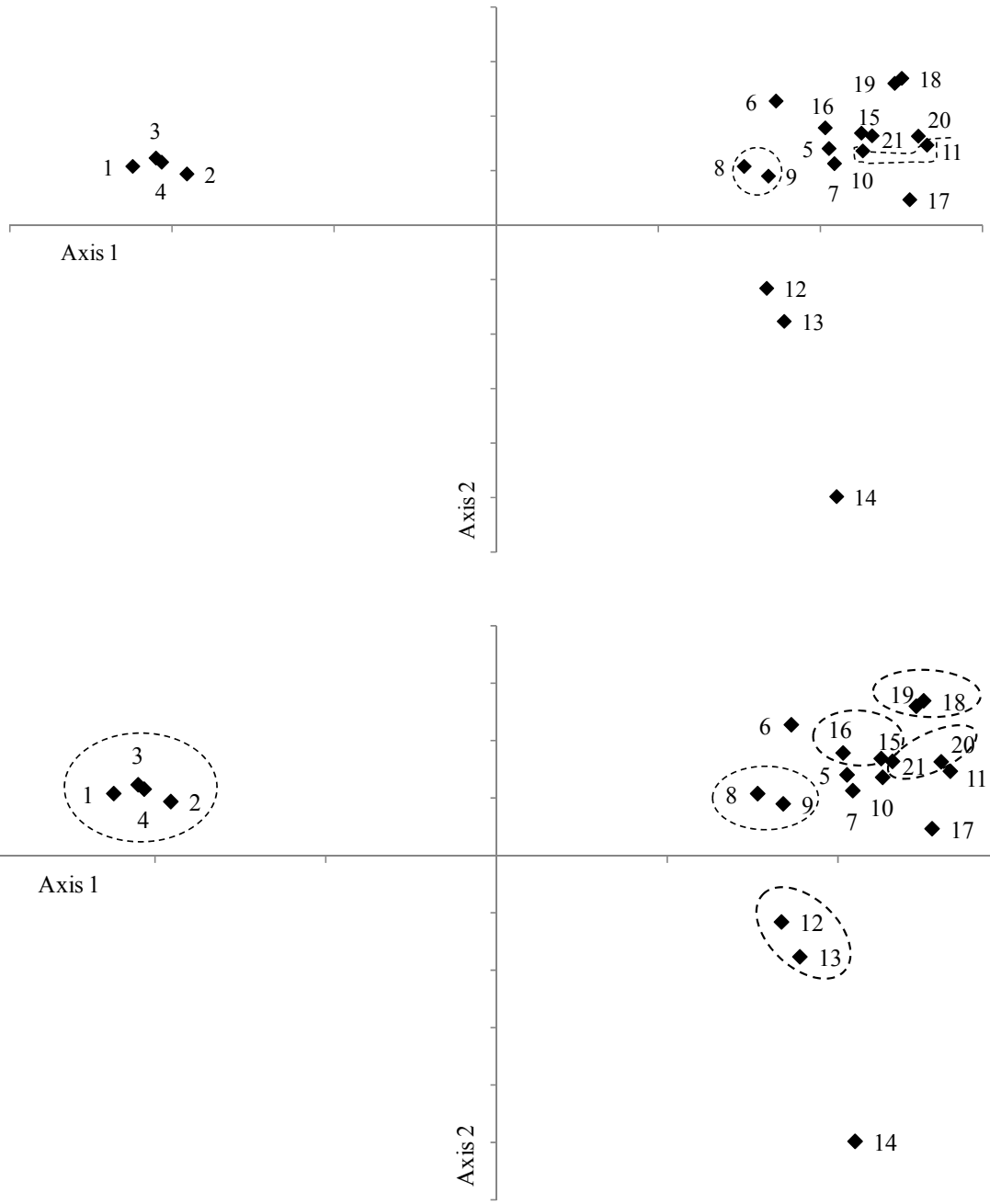
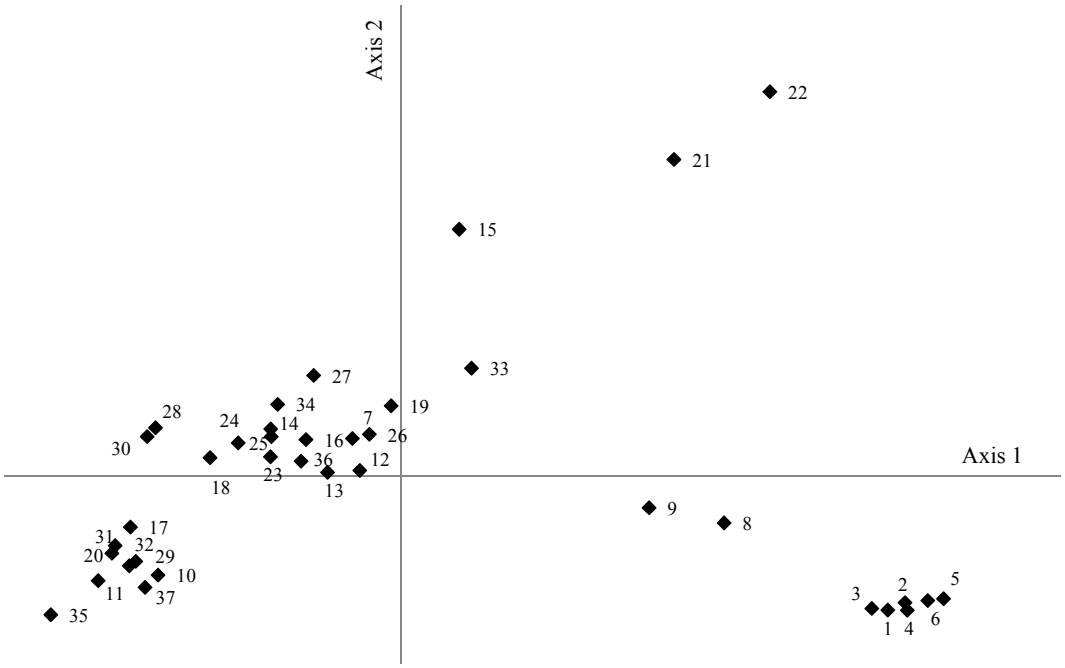


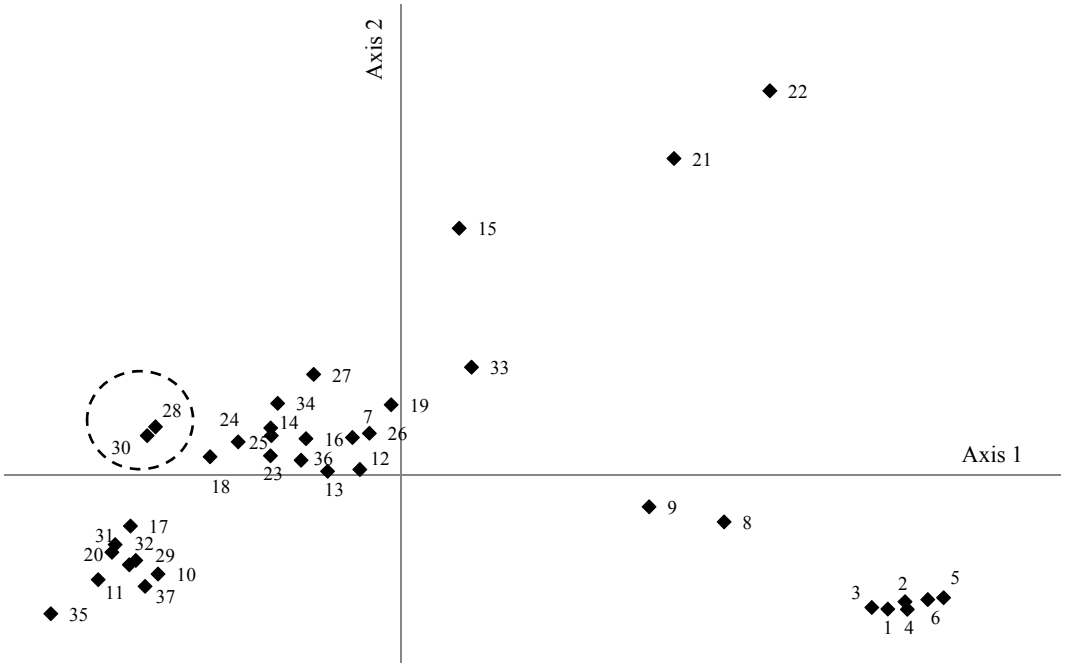
Figure 2 - Statistical tests of divergence among samples from Warm Springs NFH and adjacent spring Chinook salmon populations. Sample numbers are those listed in Table 3. Dashed lines indicate groups of samples lacking statistically different allele frequencies (top) and statistically significant F_{ST}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

a) GAPS microsatellites



b) Columbia River GSI SNPs v1





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.
- Microsatellite data indicated that genetic diversity (indicated by AR and H_o) was low in the Warm Springs NFH samples relative to most other spring Chinook salmon collections. Comparison of the historical (5-6) and contemporary (1-4) collections from Warm Springs River revealed higher AR in historical collections but higher H_o in contemporary collections. These results thus do not provide clear evidence of a loss or increase in genetic diversity since the introduction of Warm Springs NFH.
- High LD (based on SNP data) observed in the Warm Springs NFH 2010 sample (7.8% of tests were significant at α=0.05) may reflect the presence of Round Butte fish inadvertently incorporated in the broodstock in that year, or disproportionate representation of a small number of families in that collection. Similarly, the LD observed in the Warm Springs River 1976 sample based on SNP data (6.9% of tests were significant at α=0.05) may reflect the presence of individuals from multiple populations in the collection. Relatively low N_e estimates for these collections might thus reflect low effective size in the populations, or collections that are not representative of single populations.
- The first two axes in the correspondence analysis and principal component analysis (Figure 1) identified the Deschutes River collections and Klickitat River collections as the most divergent among the populations considered here. The amount of divergence between temporal samples from the Warm Springs NFH and the samples from Warm Springs River based on SNP data was relatively small and similar among all collections, which resulted in these collections clustered relatively close to one another. A finer-scale analysis further indicated strong similarity between contemporary hatchery-origin and wild-origin fish collected at Warm Springs NFH [Ref 4].
- The SNP data revealed that contemporary collections from Warm Springs NFH are most similar to those collected from Warm Springs River in 1976-1977 (prior to return of the

first releases from Warm Springs NFH; Figure 1). As mentioned above, observed heterozygosity was also comparable between contemporary and historical samples. Use of a local broodstock, incorporation of wild fish (in some years), and limiting escapement of hatchery-origin fish to wild spawning grounds were all undertaken as measures to avoid replacing the native population with a domesticated hatchery population, and all three may have contributed to preservation of the existing population structure. Of course, it is not possible to assess the relative fitness of contemporary hatchery and wild fish in the Warm Springs River based on the samples analyzed here.

Sources cited

1. Average of age structure estimates by brood year at mouth of Deschutes River from 1978 - 2004, provided by David Hand, USFWS Columbia River Fisheries Program 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. Information regarding the single nucleotide polymorphism markers used may be found in the following article:

Matala AP, Hess JE, Narum SR. 2011. Resolving Adaptive and Demographic Divergence among Chinook Salmon Populations in the Columbia River Basin. Transactions of the American Fisheries Society 140: 783-807.

4. A finer-scale analysis of the microsatellite data is presented in:

Smith CT, VonBargen J (2011) Genetic connectivity among hatchery and wild spring Chinook salmon collected at Warm Springs National Fish Hatchery. AFTC Final Report.

Availability

All data generated for this report will be included in the next builds of the shared GAPS consortium baseline (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. Thirteen microsatellite markers (a) and 92 single nucleotide polymorphism (SNP) markers (b) used to analyze spring Chinook salmon.

a) GAPS microsatellites

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

b) Columbia River GSI SNPs v1

1	Ots_102414-395	33	Ots_GDH-81x	65	Ots_Prl2
2	Ots_105105-613	34	Ots_GH2	66	Ots_RAG3
3	Ots_106747-239	35	Ots_GnRH-271	67	Ots_RAS1
4	Ots_110064-383	36	Ots_GPDH-338	68	Ots_RFC2-558
5	Ots_113242-216	37	Ots_GPH-318	69	Ots_S7-1
6	Ots_113457-40R	38	Ots_GST-207	70	Ots_SClkF2R2-135
7	Ots_123048-521	39	Ots_GST-375	71	Ots_SL
8	Ots_128757-61R	40	Ots_GTH2B-550	72	Ots_SWS1op-182
9	Ots_94857-232R	41	Ots_hsc71-3'-488	73	Ots_TAPBP
10	Ots_94903-99R	42	Ots_hsc71-5'-453	74	Ots_TGFB
11	Ots_96222-525	43	Ots_hsp27b-150	75	Ots_TLR3
12	Ots_96500-180	44	Ots_HSP90B-100	76	Ots_TNF
13	Ots_96899-357R	45	Ots_IGF-I.1-76	77	Ots_Tnsf
14	Ots_97077-179R	46	Ots_Ikaros-250	78	Ots_u07-07.161
15	Ots_AldB1-122	47	Ots_IL11	79	Ots_u07-17.135
16	Ots_aldb-177M	48	Ots_IL8R_C8	80	Ots_u07-18.378
17	Ots_ARNT	49	Ots_LWSop-638	81	Ots_u07-20.332
18	Ots_arp-436	50	Ots_mapK-3'-309	82	Ots_u07-25.325
19	Ots_AsnRS-60	51	Ots_mapKpr-151	83	Ots_u07-49.290
20	Ots_aspat-196	52	Ots_MHC1	84	Ots_u07-53.133
21	Ots_Cath_D141	53	Ots_MHC2	85	Ots_u07-57.120
22	Ots_CCR7	54	Ots_mybp-85	86	Ots_u07-64.221
23	Ots_CD59-2	55	Ots_Myc-366	87	Ots_u202-161
24	Ots_CD63	56	Ots_myo1a-384	88	Ots_u211-85
25	Ots_cox1-241	57	Ots_myoD-364	89	Ots_u4-92
26	Ots_CRB211	58	Ots_nkef-192	90	Ots_u6-75
27	Ots_E2-275	59	Ots_NOD1	91	Ots_unk526
28	Ots_EndoRB1-486	60	Ots_nramp-321	92	Ots_zP3b-215
29	Ots_ETIF1A	61	Ots_Ots311-101x		
30	Ots_FARSLA-220	62	Ots_P450		
31	Ots_FGF6A	63	Ots_P53		
32	Ots_FGF6B_1	64	Ots_PGK-54		

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

a) GAPS microsatellites

Description	Year	Microsatellite call rate
Warm Springs NFH broodstock	2001	0.991
Warm Springs NFH broodstock	2002	0.963
Warm Springs NFH broodstock	2003	0.930
Warm Springs NFH broodstock	2004	0.998
Carson NFH	2001	0.893
Carson NFH	2004	0.882
Entiat NFH	2002	0.953
Granite Creek	2005	0.923
Granite Creek	2006	0.980
John Day River	2005	0.934
John Day River	2006	0.978
Klickitat Hatchery	2002	0.972
Klickitat Hatchery	2006	0.962
Klickitat River	2005	0.942
Methow River	1998	0.961
Methow River	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

b) Columbia River GSI SNPs v1

Description	Year	SNP call rate
Warm Springs NFH	2001	0.989
Warm Springs NFH	2004	0.992
Warm Springs NFH	2010	0.993
Warm Springs NFH	2011	0.994
Warm Springs River	1976	0.931
Warm Springs River	1977	0.939
Pelton Trap	1974	0.980
Pelton Trap	2010	0.998
Pelton Trap	2011	0.989
Big-Creek Spring	2001	0.997
CapeHorn Spring	2005	0.996
Carson NFH Spring	2007	0.998
Winthrop NFH Spring	2001	0.997
Catherine Spring	2003	0.996
Cle-Elum Spring	2006	0.994
Dworshak NFH Spring	2005	0.998
East Fork Salmon Spring	2005	1.000
Imnaha Spring	1998	0.998
John-Day Spring	2005	0.995
Johnson Creek Spring	2002	0.999
Klickitat Hatchery Spring	2002	0.995
Klickitat Wild Spring	2006	0.998
Lochsa Spring	2005	0.995
Lolo Spring	2001	0.997
Lookingglass Spring	1994	0.999
Methow Spring	1998	0.997
Minam Spring	2002	0.996
Newsome Spring	2001	0.999
Pahsimeroi Spring	2004	0.999
Rapid River Hatchery	1999	0.998
Sawtooth Spring	2003	0.996
Secesh Spring	2001	0.995
Tucannon Spring	2003	0.995
Wenaha Spring	2002	0.998
Camas Spring	2006	0.999
Wenatchee Spring	1993	0.996
West Fork Yankee Fork	2005	0.999

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).

a) GAPS microsatellites

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1	0.003	0.002	0.001	0.041	0.051	0.047	0.035	0.039	0.056	0.062	0.045	0.041	0.053	0.039	0.043	0.052	0.060	0.058	0.047	0.039
2	-	0.002	0.003	0.039	0.056	0.047	0.033	0.036	0.056	0.062	0.046	0.044	0.055	0.041	0.042	0.052	0.058	0.057	0.053	0.041
3		-	0.000	0.038	0.052	0.044	0.034	0.035	0.057	0.064	0.048	0.045	0.059	0.036	0.038	0.053	0.053	0.054	0.046	0.035
4			-	0.040	0.051	0.046	0.033	0.035	0.056	0.062	0.048	0.043	0.055	0.039	0.041	0.051	0.059	0.057	0.046	0.038
5				-	0.023	0.013	0.013	0.013	0.029	0.026	0.028	0.024	0.034	0.005	0.008	0.016	0.021	0.019	0.015	0.012
6					-	0.031	0.030	0.036	0.061	0.045	0.047	0.045	0.048	0.018	0.022	0.039	0.032	0.029	0.027	0.023
7						-	0.022	0.024	0.030	0.028	0.034	0.031	0.039	0.011	0.016	0.021	0.031	0.032	0.023	0.018
8							-	0.001	0.021	0.025	0.029	0.025	0.039	0.012	0.018	0.021	0.031	0.027	0.026	0.018
9								-	0.025	0.031	0.030	0.027	0.042	0.015	0.020	0.025	0.033	0.030	0.027	0.019
10									-	0.009	0.047	0.044	0.057	0.032	0.036	0.024	0.048	0.049	0.032	0.030
11										-	0.049	0.042	0.049	0.026	0.027	0.029	0.042	0.040	0.027	0.026
12											-	0.000	0.012	0.026	0.030	0.026	0.043	0.039	0.039	0.030
13												-	0.008	0.025	0.028	0.023	0.045	0.039	0.034	0.027
14													-	0.036	0.038	0.028	0.060	0.053	0.040	0.038
15														-	0.003	0.017	0.011	0.012	0.011	0.006
16															-	0.020	0.011	0.009	0.010	0.004
17																-	0.031	0.026	0.020	0.017
18																	-	0.003	0.025	0.018
19																		-	0.025	0.017
20																			-	0.001
21																				-

b) Columbia River GSI SNPs v1

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37
1	0.003	0.004	0.003	0.002	0.008	0.067	0.019	0.023	0.094	0.124	0.065	0.068	0.082	0.090	0.074	0.108	0.091	0.063	0.110	0.069	0.079	0.081	0.087	0.081	0.071	0.087	0.107	0.096	0.107	0.101	0.112	0.061	0.078	0.119	0.084	0.103
2	-	0.003	0.004	0.002	0.007	0.070	0.021	0.026	0.094	0.124	0.064	0.070	0.082	0.089	0.076	0.111	0.091	0.065	0.113	0.073	0.081	0.083	0.088	0.085	0.072	0.088	0.109	0.098	0.109	0.104	0.113	0.063	0.079	0.116	0.087	0.110
3		-	0.004	0.004	0.007	0.064	0.019	0.027	0.089	0.111	0.061	0.064	0.077	0.088	0.071	0.104	0.087	0.060	0.105	0.077	0.087	0.077	0.081	0.078	0.069	0.082	0.102	0.094	0.101	0.097	0.107	0.061	0.076	0.109	0.083	0.098
4			-	0.003	0.003	0.067	0.020	0.030	0.096	0.119	0.065	0.070	0.084	0.095	0.076	0.110	0.091	0.064	0.107	0.077	0.084	0.083	0.086	0.083	0.071	0.088	0.109	0.099	0.109	0.103	0.110	0.063	0.082	0.115	0.086	0.107
5				-	0.002	0.073	0.021	0.031	0.105	0.131	0.072	0.075	0.090	0.096	0.084	0.114	0.099	0.072	0.117	0.079	0.085	0.089	0.093	0.090	0.078	0.092	0.116	0.106	0.116	0.109	0.118	0.067	0.084	0.125	0.093	0.112
6					-	0.072	0.022	0.033	0.102	0.125	0.069	0.074	0.087	0.095	0.079	0.117	0.097	0.070	0.114	0.079	0.085	0.086	0.090	0.087	0.077	0.092	0.114	0.106	0.116	0.108	0.114	0.066	0.085	0.123	0.092	0.112
7						-	0.036	0.027	0.020	0.033	0.012	0.009	0.011	0.031	0.011	0.018	0.014	0.009	0.017	0.041	0.058	0.015	0.011	0.017	0.014	0.012	0.022	0.020	0.023	0.013	0.023	0.027	0.008	0.029	0.031	0.027
8							-	0.013	0.064	0.083	0.037	0.038	0.047	0.057	0.039	0.070	0.055	0.035	0.073	0.052	0.064	0.044	0.047	0.045	0.040	0.050	0.065	0.065	0.065	0.066	0.073	0.038	0.043	0.074	0.054	0.072
9								-	0.050	0.071	0.030	0.031	0.036	0.047	0.032	0.056	0.045	0.026	0.064	0.043	0.057	0.035	0.038	0.038	0.035	0.038	0.050	0.046	0.055	0.050	0.060	0.042	0.030	0.067	0.048	0.057
10									-	0.036	0.032	0.029	0.034	0.058	0.028	0.038	0.036	0.035	0.027	0.071	0.093	0.036	0.036	0.042	0.044	0.046	0.044	0.039	0.046	0.030	0.033	0.050	0.037	0.031	0.057	0.042
11										-	0.040	0.041	0.045	0.066	0.039	0.053	0.041	0.041	0.031	0.086	0.107	0.041	0.032	0.044	0.062	0.046	0.048	0.046	0.047	0.037	0.040	0.082	0.044	0.044	0.072	0.058
12											-	0.006	0.011	0.035	0.005	0.042	0.020	0.012	0.032	0.045	0.065	0.016	0.015	0.021	0.010	0.020	0.028	0.034	0.032	0.030	0.036	0.032	0.013	0.042	0.024	0.051
13												-	0.012	0.028	0.004	0.038	0.015	0.016	0.033	0.043	0.067	0.013	0.013	0.019	0.008	0.019	0.025	0.030	0.029	0.025	0.030	0.024	0.012	0.043	0.013	0.040
14													-	0.026	0.006	0.036	0.013	0.008	0.033	0.047	0.065	0.013	0.007	0.014	0.015	0.006	0.010	0.034	0.015	0.030	0.040	0.031	0.004	0.045	0.022	0.041
15														-	0.030	0.052	0.040	0.028	0.059	0.028	0.039	0.036	0.033	0.040	0.037	0.027	0.043	0.061	0.046	0.050	0.055	0.036	0.023	0.066	0.039	0.065
16															-	0.042	0.014	0.009	0.033	0.041	0.064	0.007	0.007	0.014	0.008	0.012	0.017	0.034	0.020	0.028	0.038	0.029	0.006	0.035	0.017	0.043
17																-	0.032	0.033	0.033	0.072	0.091	0.036	0.030	0.040	0.048	0.035	0.038	0.020	0.036	0.013	0.041	0.058	0.030	0.050	0.068	0.034
18																	-	0.014	0.030	0.058	0.078	0.011	0.009	0.015	0.022	0.013	0.012	0.026	0.012	0.022	0.043	0.030	0.009	0.044	0.028	0.041
19																		-	0.030	0.039	0.053	0.012	0.008	0.012	0.018	0.007	0.016	0.029	0.018	0.024	0.043	0.028	0.007	0.041	0.028	0.036
20																			-	0.084	0.101	0.036	0.028	0.034	0.047	0.032	0.037	0.034	0.038	0.026	0.019	0.058	0.031	0.036	0.062	0.039
21																				-	0.006	0.053	0.053	0.057	0.044	0.045	0.063	0.074	0.066	0.072	0.078	0.044	0.039	0.086	0.054	0.093
22																					-	0.074	0.073	0.075	0.064	0.058	0.080	0.097	0.085	0.094	0.099	0.057	0.056	0.104	0.076	0.110
23																						-	0.002	0.006	0.026	0.015	0.007	0.038	0.007	0.025	0.045	0.036	0.005	0.043	0.032	0.033
24																							-	0.004	0.022	0.008	0.004	0.028	0.006	0.021	0.036	0.035	0.003	0.038	0.028	0.035
25																								-	0.029	0.019	0.008	0.034	0.007	0.030	0.044	0.037	0.008	0.051	0.034	0.042
26																									-	0.022	0.036	0.037	0.041	0.037	0.042	0.023	0.019	0.051	0.007	0.054
27																										-	0.010	0.037	0.015	0.028	0.048	0.032	0.003	0.046	0.030	0.038
28																											-	0.038	0.001	0.032	0.053	0.046	0.007	0.050	0.039	0.038
29																												-	0.040	0.014	0.037	0.056	0.033	0.045	0.052	0.040
30																													-	0.031	0.059	0.052	0.009	0.048	0.046	0.036
31																														-	0.033	0.053	0.026	0.041	0.052	0.020
32																															-	0.061	0.038	0.049	0.055	0.052
33																																-	0.029	0.067	0.034	0.060
34																																	-	0.042	0.028	0.040
35																																		-	0.067	0.064
36																																			-	0.062

Appendix 4. Glossary

Allele – A unique genetic character state. Each locus has two alleles.

Allelic richness (AR) – 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").