The following supplement accompanies the article

Temporal genetic change in North American Pacific oyster populations suggests caution in seascape genetic analyses of high gene-flow species

Xiujun Sun, Dennis Hedgecock*

*Corresponding author: dhedge@usc.edu

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Supplement 1

HISTORY OF U.S. PACIFIC OYSTER POPULATIONS

The Pacific oyster *Crassostrea gigas*, which is native to coastal areas of the Primorsky Territory of Russia, Japan, Korea, and northern China, has been introduced to all continents but Antarctica and is now one of the most important species in global aquaculture (Ruesink et al. 2005; FAO 2015). Historically, four geographic forms or races of the Pacific oyster—Hokkaido, Miyagi, Hiroshima, and Kumamoto—were recognized in Japan, based on morphological and physiological characteristics (Imai & Sakai 1961). Though these geographical races were initially supported by a study of allozyme variation (Fujio 1979), a later allozyme study found only low levels of genetic differentiation throughout Japan, which was attributed to massive movement of seed among growing areas (Ozaki & Fujio 1985). As the Miyagi type had the most promising results in growth and survival of juveniles and adults (Imai & Sakai 1961), they were imported to the northwestern coast of North America, beginning in the early 20th century, and in massive numbers of spat on shell annually from 1927 to 1977, except during World War II (Mann 1979; Quayle 1988; Boom et al. 1994). Miyagi-type oysters were the only oysters imported into British Columbia (Quayle 1988) and the predominant type introduced into the State of Washington, along with small quantities of Kumamoto oysters, now recognized as a different species *C. sikamea* (Banks et al. 1994; Camara et al. 2008). Large, naturalized populations of the Pacific oyster were subsequently established in several areas of British Columbia (Pendrell Sound, Hotham Sound, Pipestem Inlet, and Ladysmith Harbor, where the first natural spawning was recorded in 1932; Quayle 1988) and in two areas of Washington State (northern Hood Canal and Willapa Bays; Chew 1979), which remain the southern limits of naturalized populations in North America. The history of the U.S. populations of the Pacific oyster suggest the absence of a founder effect or admixture of differentiated stocks.

VARIABILITY OF HRM MARKERS

HRM profiles for 52 HRM markers were obtained from 553 individuals, derived from ten spatial and temporal population samples from North America, with sample sizes ranging from 16 to 148 (See Table S5 at the end of the Supplement). The frequencies of canonical and non-canonical alleles, at each locus in each population, are given in Table S5, along with summary statistics, average numbers of alleles ($\overline{n}_a$), allelic richness (A_r), observed (H_{obs}) and expected ($H_{exp,} H_{nb}$) proportions of heterozygotes, and inbreeding coefficients (F_{IS}).

LINKAGE DISEQUILIBRIUM

Effect of linkage

The 52 HRM markers are spread over nine of the ten linkage groups on the consensus Pacific oyster linkage map presented by Hedgecock et al. (2015; see Table S6 at the end of the Supplement). Because some markers are linked, we need to investigate the potential influence of linkage on the measure of linkage disequilibrium, since the estimate of N_e based on LD assumes that markers are unlinked. Of the 1326 pairs of 52 SNPs distributed over nine linkage groups, 178 pairs comprise SNPs on the same linkage group and 1148 pairs comprise SNPs on different linkage groups. Average LD for linked and unlinked markers is not significantly different in nine of 10 populations and has a borderline significance in Pend90 (Table S1). In four populations, average LD of linked SNPs is less than that for unlinked SNPs. Linked SNPs do not appear to be biasing average LD upward and, thus, biasing LDNe estimates downward.

Table S1 Average LD for linked and unlinked markers, by population

Population	$\overline{LD}$, linked	$\overline{LD}$, unlinked	P [a]
Pend90	0.199	0.185	0.049
Hoth90	0.167	0.178	0.088
Hisn90	0.176	0.185	0.124
Pipe90	0.193	0.197	0.341
Pipe10	0.067	0.066	0.379
Dab85	0.249	0.247	0.446
Dab96	0.089	0.087	0.321*
Dab06	0.087	0.085	0.266
Will96	0.155	0.157	0.361*
Hiro96	0.093	0.092	0.305

[a] Probability of one-tailed *t*-test, assuming equal variances, unless *F*-test is significant (*).

Sharing of SNP pairs with significant LD among populations

An important issue with respect to LD is whether there are pairs of markers that show consistently high LD in multiple population samples, which would suggest maintenance of LD by epistatic natural selection. Nine of 10 populations have significant levels of LD, and in five of those, average LD yielded finitely bounded estimates of N_e. We use these five populations to illustrate the low overlap of high-LD combinations among populations.

Table S2 gives, on the diagonal, the numbers of SNP-pairs in each population with significant LD ($P \leq 0.05$). The body of the table has the number of high-LD SNP pairs that are shared between pairs of populations. These small numbers are consistent with random draws of 100 SNP pairs from a binomial distribution with a high-LD-SNP-pair frequency of 0.075 (100/1326). Our conclusion: the small amount of overlap of high-LD SNP-pairs between populations is attributable to chance.

Table S2 High LD SNP-pairs within five populations of Pacific oyster (diagonal, 490 total); high LD SNP-pairs shared between pairs of populations (off diagonal).

	Hisn90	Pipe90	Dab85	Dab96	Dab06
Hisn90	87	10	8	8	2
Pipe90		105	4	10	7
Dab85			100	8	8
Dab96				101	9
Dab06					97

Classifying high-LD pairs by the number of populations in which they are found, Table S3 shows that the vast majority of high-LD SNPs are found in only a single population and no high-LD pair is shared by all five populations or even by four of them. This argues strongly against the hypothesis that pairs of markers show consistently high LD, owing to global epistatic selection.

Table S3 The number of populations in which high-LD SNP pairs occur.

No. high-LD SNP pairs	No. Pops
354	1
62	2
4	3

SIMULATIONS OF F_S DISTRIBUTIONS UNDER RANDOM GENETIC DRIFT WITH MIGRATION

Simulation parameters

We used SimuPOP (Peng & Kimmel 2005) to explore how a chi-square probability plot of $n\hat{F}/\overline{F}$ might depart from linearity under the influence of migration from a larger metapopulation. The simulation followed 50 biallelic SNPs, each at initial frequencies of 0.5 in a local population of N_e = 100, for 150 generations after a 50-generation burn-in period. We ran two scenarios for the amount of migration and size of the metapopulation: (1) the local population exchanges one migrant per generation with a metapopulation of N_e = 10,000 and (2) the local population exchanges 10 migrants per generation with a metapopulation of N_e = 1,000. Each simulation created an allele-frequency data set every 10 generations, from generation 50 to generation 190; summary genetic statistics were calculated for these 15 population samples, using Genetix, and F_s and N_e were estimated for seven, non-overlapping, 10-generation intervals (i.e. generation 50 to 60, 70 to 80, and so on), using NeEstimator.

Summary genetic statistics for the simulated population

Standard population genetic statistics were calculated for the 15 temporal samples created by each of the simulated scenarios. These statistics were then averaged across generations for each scenario. Similar averages were obtained for the 10 observed populations (data in Table 2 of main article). The average statistics show that, even though the simulated populations had strictly biallelic SNPs, whereas the actual populations were typed for HRM markers, which can have more than two alleles (Sun et al. 2015), the simulated populations had approximately the same level of genetic diversity as the actual populations sampled.

Table S4 Summary statistics for genetic variation in simulated and actual oyster populations.

Statistic	Averages for 15 temporal samples, N_e=10000, N_em=1	Averages for 15 temporal samples, N_e=1000, N_em=10	Averages for 10 observed populations
N_a	2	2	2.92
H_{exp}	0.427	0.404	0.437
H_{nb}	0.430	0.406	0.444
H_{obs}	0.431	0.406	0.451

Distributions of $n\hat{F}/\bar{F}$ in a simulated population evolving under drift and migration

We used NeEstimator to calculate F_s for seven, non-overlapping 10-generation intervals, and we show results for three of those intervals (generations 50 to 60, 110 to 120, and 170 to 180), for each of the two scenarios. We transformed locus-specific F_s values by $50F_S/\bar{F}$, where $\bar{F}$ is the arithmetic average of the locus-specific values (Nei & Tajima 1981). These values are plotted against chi-square values corresponding to the cumulative rank of the locus-specific F_s values. The resulting probability plots (Fig. S1) strongly resemble the probability plot for the observed data in all cases (Fig. 4A in main article), suggesting that the shape of the distribution is not strongly influenced by the population parameters of the simulation.

FIG 1

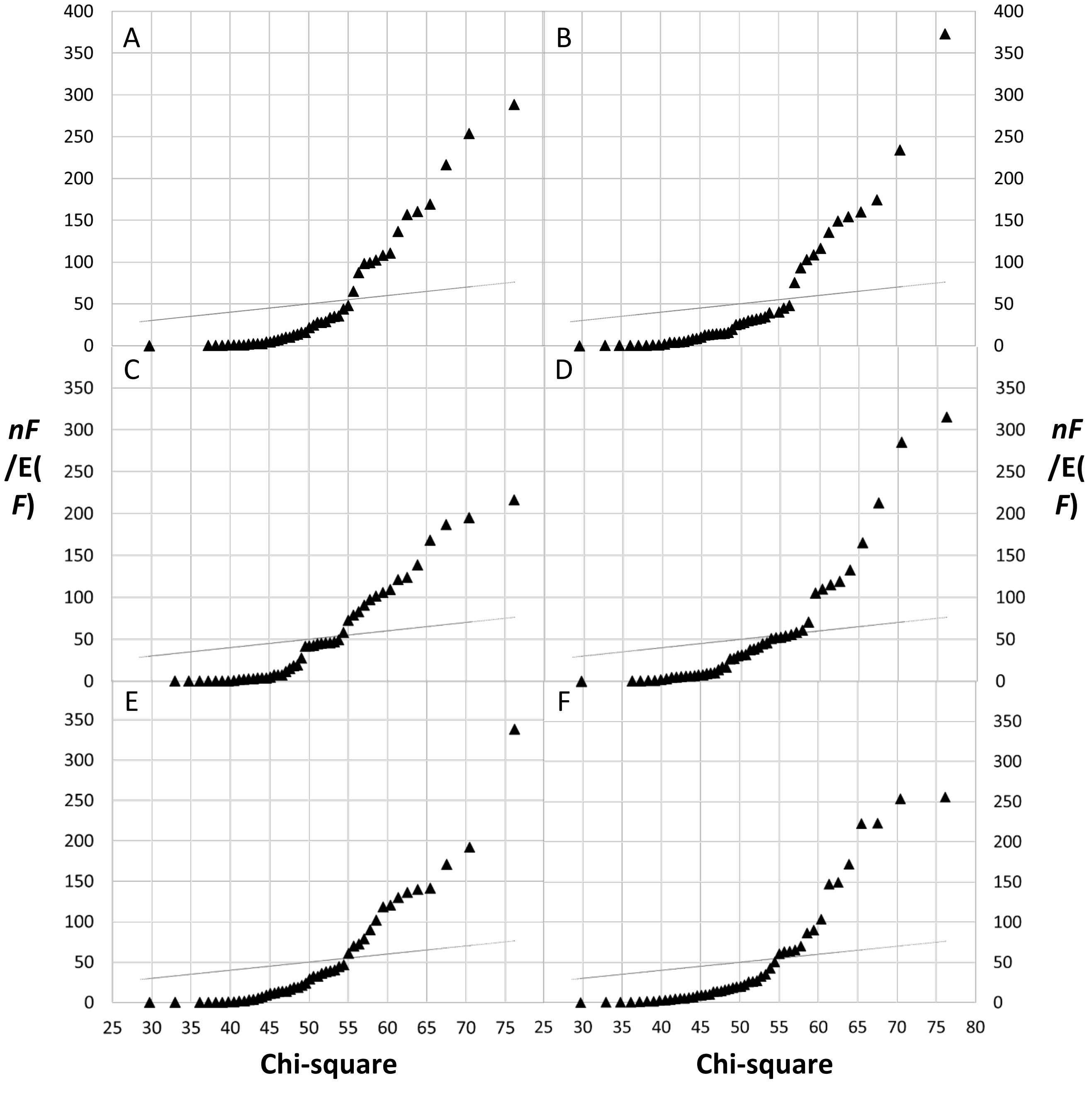

Fig. S1 Chi-square probability plots of transformed locus-specific F_s values from simulations. Temporal variances over non-overlapping, 10-generation intervals (generations 50 to 60, 110 to 120, and 170 to 180). A,C,E: Scenario 1; B,D,F: Scenario2.

EXTRA TABLES AND REFERENCES

Table S5 Summary statistics of genetic variability for 52 HRM markers in 10 populations of the Pacific oyster *Crassostrea gigas*

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
12-431										
(n)	23	24	24	21	148	16	94	92	29	80
A	0.435	0.375	0.500	0.667	0.497	0.625	0.479	0.516	0.552	0.544
C	0.544	0.625	0.500	0.333	0.500	0.375	0.511	0.484	0.448	0.450
X	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000
Y	0.022	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.006
A_r	2.696	2.000	2.000	2.000	2.108	2.000	2.312	2.000	2.000	2.200
H exp.	0.515	0.469	0.500	0.444	0.503	0.469	0.510	0.500	0.495	0.502
H n.b.	0.527	0.479	0.511	0.455	0.505	0.484	0.513	0.502	0.503	0.505
H obs.	0.435	0.417	0.333	0.381	0.466	0.375	0.543	0.554	0.552	0.488
F_{IS}	0.178	0.132	0.352	0.167	0.077	0.231	-0.059	-0.104	-0.098	0.035
150-A337617G										
(n)	23	23	24	22	146	16	94	92	30	80
A	0.435	0.522	0.500	0.500	0.445	0.469	0.511	0.484	0.433	0.600
G	0.565	0.478	0.500	0.477	0.545	0.500	0.489	0.500	0.550	0.381
X	0.000	0.000	0.000	0.023	0.010	0.031	0.000	0.016	0.017	0.019
A_r	2.000	2.000	2.000	2.727	2.373	3.000	2.000	2.438	2.533	2.490
H exp.	0.492	0.499	0.500	0.522	0.505	0.529	0.500	0.516	0.509	0.494
H n.b.	0.502	0.510	0.511	0.534	0.507	0.546	0.502	0.519	0.518	0.497
H obs.	0.522	0.435	0.417	0.455	0.384	0.688	0.489	0.467	0.367	0.413
F_{IS}	-0.039	0.151	0.187	0.152	0.244	-0.269	0.026	0.099	0.296	0.172
1132-A814109G										
(n)	23	24	24	22	148	16	94	92	30	80
A	0.370	0.396	0.417	0.432	0.382	0.469	0.473	0.391	0.367	0.550
G	0.587	0.604	0.563	0.568	0.591	0.469	0.495	0.598	0.633	0.369
X	0.044	0.000	0.021	0.000	0.027	0.063	0.032	0.011	0.000	0.081
A_r	2.912	2.000	2.667	2.000	2.604	3.000	2.679	2.318	2.000	2.952
H exp.	0.517	0.478	0.510	0.491	0.504	0.557	0.530	0.489	0.464	0.555
H n.b.	0.529	0.489	0.520	0.502	0.506	0.575	0.533	0.492	0.472	0.558
H obs.	0.478	0.458	0.542	0.500	0.568	0.563	0.585	0.544	0.467	0.600
F_{IS}	0.097	0.063	-0.042	0.004	-0.123	0.022	-0.098	-0.105	0.012	-0.075
1893-G130921T										
(n)	23	24	24	21	147	16	94	92	30	80
A	0.174	0.063	0.146	0.143	0.157	0.125	0.085	0.082	0.100	0.288
C	0.804	0.938	0.813	0.857	0.833	0.844	0.915	0.902	0.883	0.675
X	0.022	0.000	0.042	0.000	0.010	0.031	0.000	0.016	0.017	0.038
A_r	2.696	1.968	2.893	2.999	2.290	3.000	1.956	2.388	2.526	2.744
H exp.	0.322	0.117	0.317	0.245	0.281	0.272	0.156	0.179	0.209	0.460
H n.b.	0.330	0.120	0.324	0.251	0.282	0.280	0.157	0.180	0.213	0.463

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
H obs.	0.391	0.125	0.375	0.191	0.299	0.313	0.170	0.174	0.233	0.488
F_{IS}	-0.193	-0.045	-0.163	0.245	-0.062	-0.119	-0.088	0.035	-0.097	-0.053
1893-T131175C										
(n)	23	23	24	22	146	16	93	92	30	79
A	0.304	0.370	0.396	0.341	0.325	0.375	0.312	0.424	0.367	0.120
G	0.609	0.457	0.521	0.523	0.510	0.469	0.457	0.462	0.517	0.798
X	0.087	0.174	0.083	0.136	0.164	0.156	0.231	0.114	0.117	0.082
A_r	2.994	3.000	2.991	2.999	2.997	3.000	3.000	2.986	2.997	2.944
H exp.	0.529	0.625	0.565	0.592	0.607	0.615	0.641	0.594	0.585	0.343
H n.b.	0.541	0.639	0.577	0.606	0.609	0.635	0.644	0.597	0.595	0.345
H obs.	0.348	0.783	0.583	0.636	0.699	0.625	0.753	0.685	0.533	0.329
F_{IS}	0.362	-0.232	-0.011	-0.052	-0.148	0.016	-0.170	-0.148	0.105	0.046
1800-G134541A										
(n)	22	24	24	22	147	16	94	92	29	80
A	0.046	0.083	0.063	0.068	0.075	0.031	0.090	0.065	0.121	0.088
G	0.955	0.917	0.938	0.932	0.925	0.969	0.910	0.935	0.879	0.913
A_r	1.930	1.991	1.968	1.983	1.937	2.000	1.964	1.907	1.998	1.962
H exp.	0.087	0.153	0.117	0.127	0.139	0.061	0.165	0.122	0.212	0.160
H n.b.	0.089	0.156	0.120	0.130	0.139	0.063	0.165	0.123	0.216	0.161
H obs.	0.091	0.167	0.125	0.136	0.136	0.063	0.181	0.130	0.172	0.150
F_{IS}	-0.024	-0.070	-0.045	-0.050	0.021	0.000	-0.094	-0.064	0.205	0.067
210-A16017C										
(n)	23	23	23	22	147	16	94	92	30	80
A	0.435	0.370	0.478	0.432	0.456	0.563	0.426	0.408	0.400	0.531
C	0.522	0.587	0.522	0.500	0.469	0.438	0.527	0.522	0.600	0.450
X	0.022	0.000	0.000	0.000	0.014	0.000	0.011	0.000	0.000	0.019
Y	0.022	0.044	0.000	0.068	0.061	0.000	0.037	0.071	0.000	0.000
A_r	3.391	2.912	2.000	2.999	3.253	2.000	3.048	2.924	2.000	2.490
H exp.	0.538	0.517	0.499	0.559	0.568	0.492	0.540	0.557	0.480	0.515
H n.b.	0.550	0.529	0.510	0.572	0.570	0.508	0.543	0.560	0.488	0.518
H obs.	0.565	0.478	0.348	0.455	0.551	0.500	0.479	0.435	0.467	0.588
F_{IS}	-0.029	0.097	0.323	0.209	0.033	0.016	0.119	0.224	0.045	-0.135
483-A152980G										
(n)	23	24	24	22	148	16	93	92	28	80
A	0.957	0.979	0.875	0.955	0.899	0.750	0.914	0.864	0.893	0.844
G	0.044	0.021	0.125	0.046	0.101	0.250	0.086	0.136	0.107	0.156
A_r	1.912	1.667	1.999	2.000	1.973	2.000	1.958	1.994	1.996	1.998
H exp.	0.083	0.041	0.219	0.087	0.182	0.375	0.157	0.235	0.191	0.264
H n.b.	0.085	0.042	0.223	0.089	0.183	0.387	0.158	0.236	0.195	0.265

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
H obs.	0.087	0.042	0.250	0.091	0.176	0.500	0.172	0.250	0.214	0.263
F_{IS}	-0.023	0.000	-0.122	-0.024	0.039	-0.304	-0.089	-0.059	-0.102	0.011
1736-G550540A										
(n)	23	24	24	22	147	16	93	92	30	79
A	0.630	0.438	0.583	0.273	0.551	0.469	0.543	0.533	0.517	0.443
G	0.370	0.563	0.417	0.727	0.449	0.531	0.457	0.467	0.483	0.557
A_r	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000
H exp.	0.466	0.492	0.486	0.397	0.495	0.498	0.496	0.498	0.499	0.494
H n.b.	0.476	0.503	0.497	0.406	0.497	0.514	0.499	0.501	0.508	0.497
H obs.	0.304	0.375	0.583	0.273	0.463	0.688	0.484	0.478	0.700	0.430
F_{IS}	0.366	0.258	-0.179	0.333	0.068	-0.352	0.030	0.045	-0.387	0.134
471-C853263T										
(n)	22	24	24	22	147	16	93	91	30	80
A	0.659	0.604	0.729	0.682	0.721	0.563	0.694	0.802	0.800	0.744
G	0.273	0.167	0.229	0.205	0.129	0.281	0.172	0.137	0.133	0.131
X	0.068	0.229	0.042	0.114	0.150	0.156	0.134	0.060	0.067	0.125
A_r	2.983	3.000	2.894	2.000	2.987	3.000	2.993	2.883	2.957	2.985
H exp.	0.487	0.555	0.414	0.480	0.441	0.580	0.471	0.334	0.338	0.414
H n.b.	0.498	0.567	0.423	0.492	0.442	0.599	0.474	0.336	0.344	0.417
H obs.	0.318	0.500	0.333	0.500	0.435	0.688	0.495	0.297	0.400	0.375
F_{IS}	0.366	0.120	0.215	-0.018	0.016	-0.154	-0.044	0.117	-0.168	0.100
1715-C587389T										
(n)	23	23	24	21	145	16	91	90	28	79
A	0.174	0.348	0.375	0.238	0.238	0.219	0.352	0.289	0.286	0.234
G	0.761	0.630	0.583	0.643	0.672	0.750	0.615	0.661	0.661	0.709
X	0.044	0.000	0.042	0.119	0.079	0.031	0.022	0.022	0.036	0.051
Y	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.011	0.000	0.000
Z	0.022	0.022	0.000	0.000	0.003	0.000	0.011	0.017	0.018	0.006
A_r	3.608	2.696	2.894	2.000	3.259	3.000	2.863	3.317	3.392	3.046
H exp.	0.389	0.481	0.517	0.516	0.485	0.389	0.497	0.479	0.480	0.440
H n.b.	0.397	0.492	0.528	0.529	0.487	0.401	0.500	0.481	0.489	0.443
H obs.	0.391	0.435	0.833	0.571	0.448	0.375	0.495	0.389	0.536	0.443
F_{IS}	0.015	0.118	-0.597	-0.084	0.079	0.067	0.011	0.193	-0.098	0.000
911-C186663A										
(n)	23	24	24	22	147	16	94	92	29	80
A	0.652	0.708	0.625	0.523	0.674	0.844	0.697	0.685	0.724	0.731
C	0.348	0.292	0.375	0.477	0.327	0.156	0.303	0.304	0.276	0.256
X	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.013
A_r	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.318	2.000	2.361
H exp.	0.454	0.413	0.469	0.499	0.440	0.264	0.423	0.438	0.400	0.400
H n.b.	0.464	0.422	0.479	0.511	0.441	0.272	0.425	0.441	0.407	0.402

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
H obs.	0.435	0.417	0.500	0.500	0.422	0.313	0.436	0.467	0.414	0.413
F_{IS}	0.064	0.013	-0.045	0.021	0.044	-0.154	-0.027	-0.061	-0.018	-0.026
186-A134353G										
(n)	23	23	24	22	147	16	94	91	30	79
A	0.783	0.848	0.708	0.841	0.742	0.875	0.777	0.753	0.717	0.734
G	0.152	0.087	0.250	0.046	0.129	0.063	0.096	0.115	0.150	0.082
X	0.065	0.065	0.042	0.114	0.129	0.063	0.128	0.132	0.133	0.184
A_r	2.976	2.970	2.894	2.999	2.983	3.000	2.963	2.980	2.998	2.953
H exp.	0.360	0.269	0.434	0.278	0.417	0.227	0.371	0.403	0.446	0.421
H n.b.	0.368	0.275	0.443	0.284	0.418	0.234	0.373	0.405	0.454	0.423
H obs.	0.435	0.304	0.250	0.318	0.415	0.250	0.372	0.451	0.400	0.456
F_{IS}	-0.186	-0.108	0.441	-0.122	0.008	-0.071	0.003	-0.113	0.120	-0.077
452-T87528C										
(n)	23	23	24	22	148	16	94	92	30	79
A	0.913	0.848	0.750	0.909	0.767	0.844	0.745	0.826	0.833	0.804
G	0.087	0.152	0.229	0.091	0.226	0.156	0.250	0.169	0.167	0.196
X	0.000	0.000	0.021	0.000	0.007	0.000	0.005	0.005	0.000	0.000
A_r	1.994	2.000	2.667	2.000	2.205	2.000	2.170	2.172	2.000	2.000
H exp.	0.159	0.258	0.385	0.165	0.361	0.264	0.383	0.289	0.278	0.315
H n.b.	0.162	0.264	0.393	0.169	0.362	0.272	0.385	0.291	0.283	0.317
H obs.	0.174	0.304	0.458	0.182	0.405	0.188	0.372	0.304	0.333	0.317
F_{IS}	-0.073	-0.158	-0.171	-0.077	-0.121	0.318	0.033	-0.047	-0.184	0.003
395-G201684A										
(n)	23	24	24	22	148	16	94	92	30	80
A	0.087	0.146	0.188	0.023	0.091	0.063	0.128	0.114	0.033	0.081
G	0.913	0.854	0.813	0.977	0.909	0.938	0.872	0.886	0.967	0.919
A_r	1.994	2.000	2.000	2.999	1.966	2.000	1.992	1.986	1.786	1.952
H exp.	0.159	0.249	0.305	0.044	0.166	0.117	0.223	0.202	0.064	0.149
H n.b.	0.162	0.254	0.311	0.046	0.166	0.121	0.224	0.203	0.066	0.150
H obs.	0.087	0.125	0.208	0.046	0.182	0.125	0.213	0.228	0.067	0.163
F_{IS}	0.470	0.514	0.335	0.000	-0.097	-0.034	0.050	-0.123	-0.018	-0.082
683-T197693C										
(n)	23	23	24	21	145	16	94	92	30	80
A	0.544	0.500	0.563	0.405	0.479	0.531	0.457	0.467	0.467	0.531
G	0.457	0.457	0.438	0.595	0.479	0.406	0.489	0.473	0.500	0.394
X	0.000	0.022	0.000	0.000	0.021	0.063	0.043	0.044	0.017	0.044
Y	0.000	0.022	0.000	0.000	0.021	0.000	0.011	0.016	0.017	0.031
A_r	2.000	3.391	2.000	2.000	3.015	3.000	3.094	3.228	3.067	3.475
H exp.	0.496	0.541	0.492	0.482	0.540	0.549	0.549	0.556	0.532	0.560
H n.b.	0.507	0.553	0.503	0.494	0.542	0.567	0.552	0.559	0.541	0.563

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
H obs.	0.304	0.652	0.542	0.429	0.538	0.688	0.628	0.565	0.700	0.600
F_{IS}	0.405	-0.185	-0.079	0.135	0.007	-0.222	-0.137	-0.011	-0.301	-0.065
41954-C77670T										
(n)	23	24	24	22	147	16	94	90	29	80
A	0.348	0.396	0.333	0.205	0.303	0.219	0.340	0.289	0.207	0.306
G	0.609	0.604	0.604	0.682	0.643	0.781	0.606	0.678	0.672	0.631
X	0.000	0.000	0.021	0.091	0.044	0.000	0.011	0.033	0.052	0.038
Z	0.044	0.000	0.042	0.023	0.010	0.000	0.043	0.000	0.069	0.025
A_r	2.912	2.000	3.560	2.983	3.077	2.000	3.094	2.697	3.880	3.338
H exp.	0.507	0.478	0.522	0.485	0.493	0.342	0.515	0.456	0.498	0.506
H n.b.	0.518	0.489	0.533	0.496	0.495	0.353	0.517	0.459	0.506	0.509
H obs.	0.435	0.458	0.750	0.455	0.435	0.188	0.649	0.511	0.448	0.538
F_{IS}	0.164	0.063	-0.420	0.085	0.120	0.477	-0.256	-0.115	0.117	-0.057
304-A403683G										
(n)	22	24	23	22	147	16	94	92	30	80
A	0.159	0.104	0.130	0.091	0.184	0.188	0.138	0.103	0.167	0.206
G	0.750	0.833	0.783	0.841	0.735	0.750	0.729	0.799	0.733	0.656
X	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.038	0.000	0.000
Y	0.068	0.042	0.065	0.068	0.068	0.031	0.128	0.060	0.100	0.131
Z	0.023	0.021	0.022	0.000	0.014	0.031	0.005	0.000	0.000	0.006
A_r	3.711	3.558	3.671	2.999	3.278	4.000	3.157	3.608	2.992	3.193
H exp.	0.407	0.293	0.366	0.280	0.422	0.400	0.434	0.346	0.424	0.510
H n.b.	0.417	0.299	0.374	0.287	0.423	0.413	0.436	0.348	0.432	0.513
H obs.	0.455	0.292	0.391	0.318	0.456	0.438	0.479	0.359	0.500	0.600
F_{IS}	-0.094	0.024	-0.048	-0.114	-0.077	-0.061	-0.099	-0.031	-0.162	-0.171
1583-A699270G										
(n)	23	24	24	22	148	16	94	92	30	80
A	0.870	0.813	0.729	0.796	0.737	0.625	0.739	0.723	0.867	0.794
G	0.109	0.167	0.250	0.182	0.247	0.344	0.245	0.239	0.133	0.194
X	0.022	0.021	0.021	0.023	0.017	0.031	0.016	0.038	0.000	0.013
A_r	2.694	2.667	2.667	2.000	2.500	3.000	2.430	2.744	1.999	2.361
H exp.	0.232	0.312	0.405	0.334	0.397	0.490	0.393	0.419	0.231	0.332
H n.b.	0.237	0.318	0.414	0.341	0.398	0.506	0.395	0.421	0.235	0.334
H obs.	0.261	0.250	0.542	0.364	0.405	0.500	0.340	0.402	0.200	0.313
F_{IS}	-0.105	0.218	-0.317	-0.067	-0.019	0.012	0.140	0.045	0.151	0.066
77-T1135452C										
(n)	22	23	24	22	148	16	94	92	30	79
A	0.409	0.500	0.521	0.455	0.527	0.594	0.489	0.467	0.550	0.487
G	0.591	0.478	0.458	0.523	0.416	0.406	0.484	0.505	0.417	0.513
X	0.000	0.022	0.021	0.023	0.057	0.000	0.027	0.027	0.033	0.000
A_r	2.000	2.696	2.667	2.000	2.865	2.000	2.611	2.620	2.786	2.000

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
H exp.	0.484	0.521	0.518	0.520	0.546	0.482	0.526	0.525	0.523	0.500
H n.b.	0.495	0.532	0.529	0.532	0.548	0.498	0.528	0.528	0.532	0.503
H obs.	0.455	0.565	0.625	0.364	0.547	0.688	0.543	0.511	0.567	0.418
F_{IS}	0.083	-0.063	-0.186	0.321	0.002	-0.398	-0.027	0.033	-0.067	0.170
85-C112245T										
(n)	23	24	24	20	147	16	93	92	30	80
A	0.391	0.292	0.417	0.325	0.289	0.438	0.360	0.364	0.267	0.381
G	0.544	0.604	0.438	0.500	0.633	0.531	0.586	0.571	0.683	0.588
X	0.022	0.042	0.063	0.100	0.014	0.000	0.000	0.027	0.000	0.000
Y	0.000	0.042	0.021	0.000	0.034	0.000	0.016	0.027	0.033	0.019
Z	0.044	0.021	0.063	0.075	0.031	0.031	0.038	0.011	0.017	0.013
A_r	3.608	4.454	4.602	2.000	3.712	3.000	3.174	3.558	3.320	2.851
H exp.	0.549	0.546	0.627	0.629	0.514	0.525	0.525	0.540	0.461	0.509
H n.b.	0.561	0.558	0.640	0.645	0.516	0.542	0.528	0.543	0.468	0.512
H obs.	0.348	0.542	0.750	0.750	0.524	0.688	0.538	0.663	0.600	0.638
F_{IS}	0.386	0.029	-0.176	-0.168	-0.016	-0.279	-0.018	-0.222	-0.287	-0.247
12-T353707C										
(n)	23	24	24	22	144	16	94	92	30	80
A	0.391	0.438	0.417	0.500	0.347	0.281	0.362	0.315	0.317	0.406
G	0.609	0.500	0.500	0.477	0.618	0.594	0.596	0.587	0.583	0.525
X	0.000	0.042	0.063	0.023	0.010	0.094	0.027	0.076	0.067	0.013
Y	0.000	0.021	0.021	0.000	0.024	0.031	0.016	0.022	0.033	0.056
A_r	2.000	3.560	3.634	2.727	2.864	4.000	3.041	3.476	3.744	3.234
H exp.	0.476	0.556	0.572	0.522	0.497	0.559	0.513	0.550	0.554	0.556
H n.b.	0.487	0.568	0.584	0.534	0.499	0.577	0.516	0.553	0.563	0.560
H obs.	0.522	0.625	0.750	0.546	0.514	0.750	0.511	0.554	0.567	0.688
F_{IS}	-0.073	-0.102	-0.292	-0.022	-0.031	-0.314	0.011	-0.003	-0.006	-0.231
43084-C115432T										
(n)	23	24	24	22	147	16	94	92	29	80
A	0.326	0.417	0.396	0.659	0.320	0.375	0.335	0.245	0.362	0.300
G	0.674	0.583	0.604	0.341	0.657	0.625	0.633	0.734	0.621	0.694
X	0.000	0.000	0.000	0.000	0.017	0.000	0.005	0.022	0.000	0.006
Y	0.000	0.000	0.000	0.000	0.007	0.000	0.027	0.000	0.017	0.000
A_r	2.000	2.000	2.000	2.983	2.646	2.000	2.781	2.537	2.552	2.200
H exp.	0.440	0.486	0.478	0.449	0.467	0.469	0.486	0.401	0.483	0.429
H n.b.	0.449	0.497	0.489	0.460	0.468	0.484	0.489	0.404	0.492	0.431
H obs.	0.478	0.583	0.458	0.318	0.449	0.625	0.468	0.424	0.448	0.425
F_{IS}	-0.066	-0.179	0.063	0.313	0.041	-0.304	0.043	-0.051	0.090	0.015
1402-T40502G										
(n)	23	24	24	22	148	16	94	92	29	80
A	0.261	0.375	0.313	0.227	0.335	0.344	0.298	0.299	0.241	0.269

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
C	0.674	0.583	0.688	0.750	0.642	0.625	0.644	0.669	0.672	0.706
X	0.065	0.042	0.000	0.023	0.024	0.031	0.059	0.033	0.086	0.025
A_r	2.976	2.894	2.000	2.727	2.555	3.000	2.879	2.688	2.986	2.594
H exp.	0.474	0.517	0.430	0.385	0.476	0.490	0.494	0.463	0.482	0.428
H n.b.	0.484	0.528	0.439	0.394	0.477	0.506	0.496	0.465	0.491	0.431
H obs.	0.391	0.500	0.542	0.500	0.453	0.500	0.543	0.424	0.517	0.475
F_{IS}	0.195	0.055	-0.241	-0.276	0.051	0.012	-0.094	0.089	-0.055	-0.103
41572-T72531C										
(n)	22	24	24	21	147	16	94	90	29	80
A	0.614	0.625	0.667	0.595	0.571	0.594	0.543	0.583	0.690	0.425
G	0.296	0.292	0.292	0.333	0.323	0.344	0.372	0.344	0.241	0.500
X	0.068	0.021	0.042	0.071	0.041	0.063	0.059	0.022	0.052	0.063
Y	0.000	0.000	0.000	0.000	0.024	0.000	0.000	0.022	0.000	0.006
Z	0.023	0.063	0.000	0.000	0.041	0.000	0.027	0.028	0.017	0.006
A_r	3.711	3.634	2.894	2.983	4.070	3.000	3.490	3.721	3.467	3.300
H exp.	0.531	0.520	0.469	0.530	0.565	0.525	0.563	0.539	0.463	0.565
H n.b.	0.543	0.531	0.479	0.542	0.567	0.542	0.566	0.542	0.471	0.569
H obs.	0.636	0.500	0.667	0.333	0.571	0.500	0.585	0.556	0.310	0.688
F_{IS}	-0.176	0.060	-0.405	0.391	-0.008	0.080	-0.034	-0.025	0.345	-0.210
1101-A416386G										
(n)	23	23	24	22	148	16	94	90	29	80
A	0.326	0.609	0.583	0.682	0.541	0.625	0.500	0.572	0.466	0.619
G	0.435	0.283	0.292	0.114	0.345	0.250	0.303	0.317	0.276	0.194
X	0.022	0.044	0.021	0.091	0.010	0.063	0.059	0.028	0.086	0.050
Y	0.217	0.065	0.104	0.114	0.105	0.063	0.138	0.083	0.172	0.138
A_r	3.696	3.888	3.664	3.995	3.271	4.000	3.874	3.582	3.986	3.834
H exp.	0.657	0.544	0.563	0.501	0.578	0.539	0.636	0.565	0.670	0.558
H n.b.	0.672	0.556	0.575	0.513	0.580	0.557	0.639	0.568	0.682	0.562
H obs.	0.522	0.565	0.583	0.500	0.520	0.438	0.543	0.533	0.517	0.563
F_{IS}	0.227	-0.018	-0.014	0.025	0.103	0.219	0.152	0.061	0.245	-0.001
504-C268597T										
(n)	23	23	24	22	148	16	94	92	30	80
A	0.152	0.217	0.229	0.182	0.277	0.344	0.271	0.283	0.250	0.294
G	0.848	0.739	0.771	0.796	0.686	0.531	0.702	0.674	0.700	0.681
X	0.000	0.022	0.000	0.023	0.034	0.125	0.027	0.038	0.050	0.019
Y	0.000	0.022	0.000	0.000	0.003	0.000	0.000	0.005	0.000	0.006
A_r	2.000	3.391	2.000	2.000	2.831	3.000	2.611	2.918	2.904	2.690
H exp.	0.258	0.406	0.353	0.334	0.452	0.584	0.433	0.465	0.445	0.449
H n.b.	0.264	0.415	0.361	0.341	0.453	0.603	0.435	0.467	0.453	0.452
H obs.	0.217	0.522	0.458	0.227	0.493	0.813	0.404	0.489	0.433	0.513
F_{IS}	0.179	-0.266	-0.278	0.340	-0.088	-0.364	0.071	-0.048	0.043	-0.135

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
42640-C29524T										
(n)	23	23	24	22	148	16	94	92	30	79
A	0.217	0.304	0.250	0.273	0.307	0.250	0.282	0.261	0.300	0.241
G	0.739	0.696	0.708	0.727	0.693	0.750	0.702	0.728	0.683	0.753
X	0.022	0.000	0.042	0.000	0.000	0.000	0.016	0.005	0.017	0.006
Y	0.022	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000
A_r	3.391	2.000	2.894	2.983	2.000	2.000	2.431	2.348	2.533	2.202
H exp.	0.406	0.423	0.434	0.397	0.426	0.375	0.427	0.402	0.443	0.375
H n.b.	0.415	0.433	0.443	0.406	0.427	0.387	0.430	0.404	0.450	0.377
H obs.	0.391	0.435	0.250	0.455	0.291	0.375	0.351	0.283	0.400	0.203
F_{IS}	0.057	-0.005	0.441	-0.123	0.321	0.032	0.184	0.301	0.113	0.465
1497-T149063C										
(n)	23	24	24	22	142	16	93	92	30	79
A	0.435	0.479	0.396	0.477	0.384	0.469	0.403	0.424	0.483	0.411
G	0.500	0.458	0.500	0.477	0.567	0.406	0.452	0.516	0.467	0.487
X	0.065	0.063	0.104	0.046	0.046	0.125	0.129	0.060	0.050	0.101
Y	0.000	0.000	0.000	0.000	0.004	0.000	0.016	0.000	0.000	0.000
A_r	2.976	2.968	2.997	2.930	2.906	3.000	3.427	2.886	2.904	2.978
H exp.	0.557	0.556	0.583	0.542	0.529	0.600	0.617	0.550	0.546	0.583
H n.b.	0.569	0.568	0.595	0.555	0.531	0.619	0.620	0.553	0.555	0.587
H obs.	0.435	0.417	0.625	0.546	0.556	0.813	0.688	0.609	0.600	0.506
F_{IS}	0.240	0.271	-0.052	0.018	-0.048	-0.327	-0.111	-0.101	-0.082	0.138
1836-T763319G										
(n)	23	24	24	22	147	16	94	92	30	80
A	0.870	0.917	0.771	0.841	0.772	0.813	0.787	0.728	0.783	0.713
C	0.130	0.083	0.229	0.159	0.221	0.156	0.207	0.255	0.200	0.150
X	0.000	0.000	0.000	0.000	0.007	0.031	0.005	0.016	0.017	0.138
A_r	2.000	1.991	2.000	2.000	2.206	3.000	2.170	2.438	2.533	2.992
H exp.	0.227	0.153	0.353	0.268	0.355	0.315	0.337	0.404	0.346	0.451
H n.b.	0.232	0.156	0.361	0.274	0.356	0.325	0.339	0.406	0.352	0.454
H obs.	0.261	0.167	0.292	0.318	0.340	0.250	0.298	0.413	0.300	0.525
F_{IS}	-0.128	-0.070	0.195	-0.167	0.045	0.236	0.122	-0.017	0.150	-0.158
1665-C192489T										
(n)	23	24	24	21	148	16	94	92	29	80
A	0.674	0.625	0.521	0.571	0.605	0.563	0.537	0.533	0.483	0.656
G	0.283	0.292	0.438	0.262	0.280	0.406	0.356	0.386	0.379	0.275
X	0.022	0.042	0.000	0.143	0.112	0.000	0.085	0.082	0.103	0.056
Y	0.022	0.042	0.042	0.024	0.003	0.031	0.021	0.000	0.035	0.013
A_r	3.391	3.787	2.894	2.000	3.090	3.000	3.485	2.950	3.798	3.234
H exp.	0.465	0.521	0.536	0.584	0.543	0.518	0.577	0.561	0.611	0.490
H n.b.	0.475	0.532	0.547	0.598	0.545	0.534	0.580	0.564	0.622	0.494

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
H obs.	0.478	0.542	0.625	0.619	0.534	0.688	0.628	0.554	0.586	0.525
F_{IS}	-0.006	-0.019	-0.146	-0.036	0.021	-0.299	-0.083	0.017	0.058	-0.064
1665-G158678A										
(n)	23	24	24	21	148	16	94	92	30	80
A	0.022	0.104	0.125	0.071	0.132	0.125	0.122	0.109	0.083	0.081
G	0.978	0.896	0.875	0.929	0.845	0.875	0.878	0.886	0.917	0.919
X	0.000	0.000	0.000	0.000	0.024	0.000	0.000	0.005	0.000	0.000
A_r	1.696	1.997	1.999	2.000	2.596	2.000	1.990	2.157	1.982	1.952
H exp.	0.043	0.187	0.219	0.133	0.269	0.219	0.215	0.203	0.153	0.149
H n.b.	0.044	0.191	0.223	0.136	0.270	0.226	0.216	0.205	0.155	0.150
H obs.	0.044	0.208	0.250	0.143	0.230	0.250	0.245	0.207	0.167	0.163
F_{IS}	0.000	-0.095	-0.122	-0.053	0.148	-0.111	-0.134	-0.010	-0.074	-0.082
1093-G353478T										
(n)	23	23	24	21	147	16	94	92	30	80
A	0.544	0.544	0.583	0.595	0.578	0.563	0.617	0.565	0.683	0.475
C	0.391	0.435	0.375	0.405	0.408	0.438	0.362	0.397	0.283	0.494
X	0.065	0.022	0.042	0.000	0.014	0.000	0.021	0.038	0.033	0.031
A_r	2.976	2.696	2.894	2.000	2.371	2.000	2.529	2.744	2.786	2.678
H exp.	0.547	0.515	0.517	0.482	0.499	0.492	0.488	0.522	0.452	0.530
H n.b.	0.559	0.527	0.528	0.494	0.501	0.508	0.491	0.525	0.459	0.533
H obs.	0.565	0.565	0.583	0.429	0.537	0.750	0.575	0.489	0.333	0.525
F_{IS}	-0.011	-0.075	-0.107	0.135	-0.074	-0.500	-0.172	0.068	0.278	0.015
43426-A48381C										
(n)	23	24	24	22	148	16	94	92	30	80
A	0.609	0.542	0.750	0.614	0.625	0.563	0.697	0.592	0.533	0.506
C	0.391	0.458	0.250	0.386	0.362	0.438	0.303	0.397	0.450	0.494
X	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.011	0.017	0.000
A_r	2.000	2.000	2.000	2.983	2.369	2.000	2.000	2.318	2.533	2.000
H exp.	0.476	0.497	0.375	0.474	0.479	0.492	0.423	0.492	0.513	0.500
H n.b.	0.487	0.507	0.383	0.485	0.480	0.508	0.425	0.494	0.522	0.503
H obs.	0.522	0.500	0.417	0.500	0.439	0.625	0.457	0.544	0.500	0.463
F_{IS}	-0.073	0.014	-0.090	-0.031	0.086	-0.240	-0.077	-0.100	0.042	0.081
156-C164236A										
(n)	23	23	24	22	148	16	94	92	30	80
A	0.174	0.217	0.208	0.227	0.260	0.344	0.234	0.217	0.317	0.300
C	0.826	0.761	0.792	0.750	0.726	0.625	0.745	0.766	0.667	0.688
X	0.000	0.022	0.000	0.023	0.007	0.031	0.021	0.016	0.017	0.013
Y	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000	0.000
A_r	2.000	2.696	2.000	2.000	2.313	3.000	2.529	2.438	2.533	2.361
H exp.	0.287	0.373	0.330	0.385	0.405	0.490	0.390	0.365	0.455	0.437
H n.b.	0.294	0.382	0.337	0.394	0.406	0.506	0.392	0.367	0.463	0.440
H obs.	0.261	0.478	0.417	0.364	0.446	0.500	0.457	0.348	0.500	0.500

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
F_{IS}	0.114	-0.260	-0.243	0.079	-0.099	0.012	-0.167	0.053	-0.082	-0.138
43574-C42733A										
(n)	23	24	24	22	148	16	94	92	30	80
A	0.348	0.250	0.417	0.455	0.314	0.438	0.293	0.304	0.367	0.294
C	0.630	0.708	0.563	0.546	0.676	0.500	0.681	0.674	0.600	0.700
X	0.022	0.042	0.021	0.000	0.010	0.063	0.027	0.022	0.033	0.006
A_r	3.391	3.560	3.333	2.983	2.291	4.000	2.923	2.538	3.573	2.200
H exp.	0.481	0.434	0.510	0.496	0.445	0.555	0.450	0.453	0.504	0.424
H n.b.	0.492	0.443	0.520	0.507	0.446	0.573	0.453	0.455	0.513	0.426
H obs.	0.652	0.542	0.625	0.455	0.588	0.625	0.564	0.554	0.600	0.513
F_{IS}	-0.336	-0.228	-0.206	0.106	-0.319	-0.095	-0.248	-0.219	-0.173	-0.204
358-C158710T										
(n)	23	23	24	22	147	16	94	92	30	80
A	0.674	0.565	0.729	0.682	0.704	0.625	0.777	0.674	0.683	0.719
G	0.304	0.370	0.229	0.273	0.279	0.313	0.207	0.315	0.250	0.275
X	0.022	0.065	0.042	0.046	0.017	0.063	0.016	0.011	0.067	0.006
A_r	2.696	2.976	2.894	2.999	2.440	3.000	2.430	2.318	2.958	2.200
H exp.	0.453	0.540	0.414	0.459	0.426	0.508	0.354	0.446	0.466	0.408
H n.b.	0.463	0.552	0.423	0.469	0.428	0.524	0.356	0.449	0.474	0.410
H obs.	0.478	0.522	0.333	0.409	0.456	0.375	0.319	0.457	0.533	0.500
F_{IS}	-0.034	0.055	0.215	0.131	-0.066	0.291	0.103	-0.017	-0.128	-0.220
1469-T226856C										
(n)	23	23	24	21	148	16	94	92	30	80
A	0.739	0.609	0.667	0.762	0.679	0.656	0.686	0.674	0.783	0.656
G	0.261	0.391	0.333	0.238	0.260	0.313	0.261	0.245	0.117	0.256
X	0.000	0.000	0.000	0.000	0.061	0.031	0.053	0.082	0.100	0.088
A_r	2.000	2.000	2.000	2.000	2.881	3.000	2.853	2.950	2.989	2.962
H exp.	0.386	0.476	0.444	0.363	0.468	0.471	0.458	0.479	0.363	0.496
H n.b.	0.394	0.487	0.454	0.372	0.469	0.486	0.461	0.482	0.369	0.499
H obs.	0.435	0.348	0.333	0.381	0.412	0.188	0.415	0.500	0.367	0.575
F_{IS}	-0.106	0.290	0.270	-0.026	0.122	0.622	0.100	-0.038	0.006	-0.153
67-A25130C										
(n)	23	24	24	22	148	16	94	92	30	80
A	0.652	0.667	0.813	0.614	0.574	0.656	0.628	0.663	0.583	0.544
C	0.348	0.333	0.188	0.386	0.426	0.313	0.372	0.326	0.417	0.456
X	0.000	0.000	0.000	0.000	0.000	0.031	0.000	0.011	0.000	0.000
A_r	2.000	2.000	2.000	2.000	2.000	3.000	2.000	2.318	2.000	2.000
H exp.	0.454	0.444	0.305	0.474	0.489	0.471	0.467	0.454	0.486	0.496
H n.b.	0.464	0.454	0.311	0.485	0.491	0.486	0.470	0.456	0.494	0.499
H obs.	0.522	0.417	0.375	0.409	0.500	0.688	0.617	0.435	0.433	0.538

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
F_{IS}	-0.128	0.084	-0.211	0.160	-0.019	-0.435	-0.315	0.048	0.125	-0.077
301-A1180087G										
(n)	23	24	24	22	146	16	94	92	30	78
A	0.870	0.688	0.708	0.841	0.716	0.656	0.707	0.766	0.750	0.712
G	0.065	0.313	0.250	0.136	0.253	0.313	0.234	0.196	0.250	0.269
X	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.000
Y	0.065	0.000	0.042	0.023	0.003	0.031	0.037	0.033	0.000	0.013
Z	0.000	0.000	0.000	0.000	0.014	0.000	0.021	0.005	0.000	0.006
A_r	2.952	2.000	2.894	2.999	2.856	3.000	3.264	2.861	2.000	2.574
H exp.	0.235	0.430	0.434	0.274	0.423	0.471	0.443	0.373	0.375	0.421
H n.b.	0.241	0.439	0.443	0.280	0.425	0.486	0.445	0.375	0.381	0.424
H obs.	0.261	0.542	0.500	0.227	0.418	0.563	0.468	0.359	0.300	0.423
F_{IS}	-0.086	-0.241	-0.131	0.192	0.016	-0.164	-0.052	0.045	0.216	0.002
1599-G99594T										
(n)	23	24	24	22	148	16	94	92	30	80
A	0.413	0.438	0.354	0.455	0.318	0.344	0.293	0.288	0.383	0.238
C	0.587	0.563	0.625	0.546	0.659	0.656	0.702	0.707	0.567	0.744
X	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.013
Y	0.000	0.000	0.021	0.000	0.020	0.000	0.005	0.005	0.050	0.006
A_r	2.000	2.000	2.667	2.000	2.608	2.000	2.170	2.174	2.904	2.561
H exp.	0.485	0.492	0.484	0.496	0.465	0.451	0.421	0.418	0.529	0.390
H n.b.	0.496	0.503	0.494	0.507	0.466	0.466	0.424	0.420	0.538	0.393
H obs.	0.565	0.375	0.458	0.636	0.405	0.688	0.489	0.424	0.500	0.350
F_{IS}	-0.144	0.258	0.073	-0.262	0.131	-0.500	-0.156	-0.009	0.072	0.109
433-A824952G										
(n)	23	23	23	22	148	16	94	92	30	79
A	0.239	0.304	0.217	0.205	0.355	0.375	0.388	0.380	0.317	0.437
G	0.761	0.696	0.783	0.773	0.635	0.594	0.596	0.576	0.667	0.525
X	0.000	0.000	0.000	0.023	0.003	0.000	0.016	0.022	0.000	0.006
Y	0.000	0.000	0.000	0.000	0.007	0.031	0.000	0.022	0.017	0.032
A_r	2.000	2.000	2.000	2.983	2.313	3.000	2.431	3.075	2.533	2.885
H exp.	0.364	0.423	0.340	0.361	0.471	0.506	0.494	0.522	0.455	0.532
H n.b.	0.372	0.433	0.348	0.369	0.472	0.522	0.497	0.525	0.463	0.536
H obs.	0.304	0.609	0.435	0.409	0.473	0.563	0.489	0.457	0.467	0.557
F_{IS}	0.185	-0.419	-0.257	-0.112	-0.001	-0.080	0.015	0.132	-0.009	-0.040
1862-T254299G										
(n)	23	24	24	22	146	16	93	92	29	78
A	0.391	0.417	0.354	0.477	0.421	0.406	0.398	0.315	0.517	0.474
C	0.565	0.542	0.646	0.500	0.538	0.594	0.565	0.625	0.448	0.455
X	0.022	0.021	0.000	0.000	0.027	0.000	0.016	0.027	0.000	0.019
Y	0.022	0.021	0.000	0.023	0.014	0.000	0.022	0.033	0.035	0.051

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
A_r	3.391	3.333	2.000	2.999	2.983	2.000	2.968	3.307	2.803	3.348
H exp.	0.527	0.532	0.458	0.522	0.533	0.482	0.522	0.508	0.530	0.565
H n.b.	0.538	0.543	0.467	0.534	0.534	0.498	0.525	0.511	0.540	0.569
H obs.	0.565	0.458	0.542	0.546	0.527	0.688	0.495	0.500	0.586	0.551
F_{IS}	-0.051	0.159	-0.163	-0.022	0.013	-0.398	0.058	0.022	-0.088	0.030
41064-C38981T										
(n)	23	24	24	22	148	16	94	92	30	80
A	0.174	0.083	0.167	0.136	0.169	0.094	0.186	0.114	0.150	0.181
G	0.696	0.813	0.729	0.682	0.750	0.781	0.676	0.772	0.800	0.706
X	0.130	0.104	0.104	0.182	0.078	0.125	0.133	0.103	0.050	0.113
Y	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Z	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.011	0.000	0.000
A_r	3.000	2.988	2.997	2.983	3.042	3.000	3.163	3.283	2.904	2.985
H exp.	0.469	0.322	0.430	0.484	0.403	0.365	0.491	0.381	0.335	0.456
H n.b.	0.479	0.329	0.439	0.495	0.404	0.377	0.494	0.383	0.341	0.459
H obs.	0.565	0.375	0.417	0.500	0.385	0.375	0.521	0.435	0.267	0.475
F_{IS}	-0.184	-0.144	0.052	-0.011	0.048	0.006	-0.056	-0.137	0.220	-0.036
536-T78147C										
(n)	23	24	24	22	146	16	92	91	30	80
A	0.565	0.479	0.500	0.409	0.545	0.625	0.511	0.533	0.533	0.513
G	0.413	0.417	0.479	0.546	0.414	0.344	0.429	0.423	0.433	0.444
X	0.000	0.021	0.000	0.000	0.010	0.000	0.027	0.033	0.033	0.013
Y	0.000	0.063	0.000	0.000	0.007	0.000	0.016	0.011	0.000	0.006
Z	0.022	0.021	0.021	0.046	0.024	0.031	0.016	0.000	0.000	0.025
A_r	2.696	4.301	2.667	2.000	3.063	3.000	3.496	3.014	2.786	3.155
H exp.	0.510	0.592	0.520	0.533	0.531	0.490	0.553	0.536	0.527	0.540
H n.b.	0.521	0.605	0.531	0.546	0.533	0.506	0.556	0.539	0.536	0.543
H obs.	0.565	0.667	0.625	0.455	0.507	0.563	0.489	0.681	0.667	0.600
F_{IS}	-0.087	-0.105	-0.182	0.170	0.049	-0.116	0.122	-0.267	-0.250	-0.106
1605-T146035C										
(n)	23	24	24	20	148	16	94	92	30	80
A	0.761	0.625	0.771	0.675	0.716	0.469	0.702	0.777	0.733	0.681
G	0.196	0.292	0.208	0.225	0.220	0.469	0.282	0.174	0.233	0.294
X	0.022	0.063	0.021	0.100	0.051	0.063	0.005	0.027	0.017	0.025
Y	0.022	0.021	0.000	0.000	0.014	0.000	0.011	0.022	0.017	0.000
A_r	3.391	3.634	2.667	2.000	3.197	3.000	2.482	3.156	3.067	2.594
H exp.	0.382	0.520	0.362	0.484	0.436	0.557	0.427	0.365	0.407	0.449
H n.b.	0.390	0.531	0.370	0.496	0.438	0.575	0.430	0.367	0.414	0.452
H obs.	0.348	0.458	0.375	0.450	0.446	0.688	0.415	0.337	0.333	0.463
F_{IS}	0.111	0.139	-0.015	0.095	-0.019	-0.204	0.035	0.081	0.198	-0.024

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
42684-C117024T										
(n)	23	24	24	22	148	16	94	92	30	80
A	0.674	0.688	0.604	0.591	0.612	0.594	0.649	0.663	0.567	0.388
G	0.326	0.313	0.396	0.409	0.389	0.406	0.346	0.337	0.433	0.613
X	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
A_r	2.000	2.000	2.000	2.983	2.000	2.000	2.170	2.000	2.000	2.000
H exp.	0.440	0.430	0.478	0.484	0.475	0.482	0.459	0.447	0.491	0.475
H n.b.	0.449	0.439	0.489	0.495	0.477	0.498	0.462	0.449	0.499	0.478
H obs.	0.391	0.375	0.542	0.455	0.561	0.688	0.436	0.457	0.400	0.500
F_{IS}	0.132	0.148	-0.112	0.083	-0.177	-0.398	0.056	-0.016	0.202	-0.047
917-A14399G										
(n)	23	24	24	22	148	16	94	91	29	79
A	0.348	0.354	0.354	0.273	0.291	0.375	0.303	0.297	0.276	0.361
G	0.652	0.604	0.583	0.682	0.686	0.594	0.686	0.676	0.707	0.519
X	0.000	0.042	0.063	0.046	0.024	0.031	0.011	0.028	0.017	0.120
A_r	2.000	2.894	2.968	2.000	2.555	3.000	2.312	2.624	2.552	2.990
H exp.	0.454	0.508	0.530	0.459	0.445	0.506	0.437	0.455	0.424	0.586
H n.b.	0.464	0.519	0.542	0.469	0.446	0.522	0.440	0.457	0.431	0.590
H obs.	0.609	0.292	0.625	0.318	0.385	0.563	0.372	0.451	0.448	0.633
F_{IS}	-0.322	0.443	-0.158	0.327	0.137	-0.080	0.153	0.014	-0.040	-0.074
62-A277284G										
(n)	23	24	24	21	148	16	94	92	30	80
A	0.609	0.688	0.667	0.714	0.682	0.813	0.734	0.690	0.700	0.706
G	0.326	0.292	0.313	0.286	0.297	0.188	0.255	0.288	0.283	0.244
X	0.044	0.021	0.021	0.000	0.020	0.000	0.000	0.005	0.000	0.044
Y	0.022	0.000	0.000	0.000	0.000	0.000	0.011	0.016	0.017	0.006
A_r	3.608	2.667	2.667	2.000	2.500	2.000	2.312	2.612	2.533	2.997
H exp.	0.521	0.442	0.458	0.408	0.446	0.305	0.396	0.440	0.429	0.440
H n.b.	0.532	0.451	0.467	0.418	0.447	0.315	0.398	0.443	0.437	0.443
H obs.	0.565	0.458	0.500	0.381	0.500	0.125	0.447	0.413	0.500	0.488
F_{IS}	-0.063	-0.016	-0.072	0.091	-0.119	0.610	-0.123	0.067	-0.148	-0.102
39884-C5114T										
(n)	23	24	24	22	148	16	93	92	29	78
A	0.500	0.688	0.604	0.523	0.591	0.469	0.608	0.609	0.535	0.506
G	0.457	0.313	0.354	0.409	0.385	0.469	0.323	0.370	0.466	0.436
X	0.044	0.000	0.042	0.068	0.024	0.063	0.065	0.022	0.000	0.045
Y	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.013
A_r	2.912	2.000	2.894	2.983	2.555	3.000	3.076	2.538	2.000	3.176
H exp.	0.540	0.430	0.508	0.555	0.502	0.557	0.523	0.492	0.498	0.551
H n.b.	0.552	0.439	0.519	0.568	0.503	0.575	0.526	0.495	0.506	0.555
H obs.	0.478	0.375	0.458	0.500	0.541	0.688	0.591	0.489	0.655	0.590
F_{IS}	0.136	0.148	0.118	0.122	-0.074	-0.204	-0.126	0.012	-0.301	-0.063

Locus, alleles, statistics	Population									
	Pend90	Hoth90	Hisn90	Pipe90	Pipe10	Dab85	Dab96	Dab06	Will96	Hiro96
43954-G96199A										
(n)	23	24	24	21	148	16	94	92	29	80
A	0.196	0.167	0.125	0.191	0.112	0.063	0.160	0.169	0.155	0.200
G	0.804	0.833	0.875	0.810	0.882	0.938	0.819	0.821	0.828	0.781
X	0.000	0.000	0.000	0.000	0.007	0.000	0.021	0.011	0.017	0.019
A_r	2.000	2.000	1.999	2.000	2.189	2.000	2.527	2.317	2.551	2.490
H exp.	0.315	0.278	0.219	0.308	0.210	0.117	0.303	0.298	0.291	0.349
H n.b.	0.322	0.284	0.223	0.316	0.211	0.121	0.305	0.300	0.296	0.352
H obs.	0.304	0.250	0.250	0.381	0.210	0.125	0.330	0.337	0.345	0.350
F_{IS}	0.055	0.121	-0.122	-0.212	0.006	-0.034	-0.083	-0.125	-0.169	0.004
728-C136683T										
(n)	23	24	24	22	148	16	93	91	30	80
A	0.478	0.479	0.604	0.500	0.503	0.500	0.554	0.495	0.500	0.506
G	0.522	0.521	0.375	0.500	0.493	0.500	0.446	0.506	0.500	0.494
X	0.000	0.000	0.021	0.000	0.003	0.000	0.000	0.000	0.000	0.000
A_r	2.000	2.000	2.667	2.000	2.108	2.000	2.000	2.000	2.000	2.000
H exp.	0.499	0.499	0.494	0.500	0.503	0.500	0.494	0.500	0.500	0.500
H n.b.	0.510	0.510	0.504	0.512	0.505	0.516	0.497	0.503	0.509	0.503
H obs.	0.522	0.792	0.667	0.727	0.682	0.375	0.570	0.571	0.800	0.638
F_{IS}	-0.023	-0.572	-0.331	-0.436	-0.353	0.280	-0.148	-0.138	-0.589	-0.269

Table S6 SNP markers and their map positions (Hedgecock et al. 2015)

SNP name from Sun et al. 2015	New SNP name from Hedgecock et al. 2015	Linkage group	Position
12-431		1	2.0
150-T337619C	150-A337617G	1	6.8
1132-G814109A	1132-A814109G	1	14.9
1893-G130921T		1	14.9
1893-A131177G	1893-T131175C	1	20.8
1800-C134543T	1800-G134541A	1	23.3
210-A16017C		1	23.9
483-T152982C	483-A152980G	1	24.9
1736-A550540G	1736-G550540A	1	33.7
471-C853263T		1	37.3
1715-G587404A	1715-C587389T	1	40.8
911-A186663C	911-C186663A	1	42.2
186-G134353A	186-A134353G	1	43.2
452-T87528C		1	44.1
395-G201684A		3	0.9
683-A197695G	683-T197693C	3	32.8
41954-C77670T		3	90.0
304-G403683A	304-A403683G	3	91.0
1583-T699272C	1583-A699270G	3	103.1
77-A1135454G	77-T1135452C	4	11.3
85-T112248C	85-C112245T	4	21.2
12-G353709A	12-T353707C	4	46.2
43084-A115434G	43084-C115432T	4	93.3
1402-C40504A	1402-T40502G	5	17.4
41572-G72533A	41572-T72531C	5	21.2
1101-A416390G	1101-A416386G	5	46.8
504-C268597T		5	76.3
42640-T29524C	42640-C29524T	5	80.2
1497-T14903C	1497-T149063C	6	11.1
1836-T763319G		6	11.1
721-G697985A	1665-C192489T	6	15.6
1665-G158678A		6	21.6
1093-G353478T		6	43.9
43426-A48381C		6	45.2
156-C164236A		6	67.7
43574-C42808A	43574-C42733A	7	0.4
358-A158712G	358-C158710T	7	0.9
1469-C226856T	1469-T226856C	7	15.6
67-G25132T	67-A25130C	7	47.3
301-T1180089C	301-A1180087G	7	49.2
1599-G99594T		7	55.0
433-C824954T	433-A824952G	7	64.6
1862-T254299G		7	73.8
41064-A38983G	41064-C38981T	8	8.9
536-T78147C		8	18.0

SNP name from Sun et al. 2015	New SNP name from Hedgecock et al. 2015	Linkage group	Position
1605-T146035C		8	58.9
42684-G117026A	42684-C117024T	8	59.7
917-G14399A	917-A14399G	9	6.4
62-T277286C	62-A277284G	10	18.3
39884-A5116G	39884-C5114T	10	18.8
43954-C96201T	43954-G96199A	10	31.9
728-C112704T	728-C136683T	10	46.3

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