Table S1. Analysis of variance of fraction of daughters in sympatric and allopatric introgressions (data were arcsin squareroot transformed; see text for details).

	df	Sum of squares	*F* ratio	*P*
SR chromosome	3	0.0077	0.383	0.766
Y chromosome population	3	0.0032	0.159	0.924
Y chrom replicate [Y chrom population]	70	0.4063	0.864	0.780
SR chrom x Y chrom rep [Y chrom population]	210	2.0895	1.481	< 0.0001
SR chrom x Y chromosome population	9	0.0373	0.617	0.784

Table S2. Variability measures for each of the seven microsatellites within each population and across all populations. Shown are the number of sampled alleles (N), the number of different alleles (A), the observed heterozygosity (H_O), and the expected heterozygosity (H_E). The populations are listed in the same order and with the same abbreviations as in Table 1. H_O values in italics show a deficiency of heterozygotes at $P < 0.001$. Populations are listed from North to South, in the same order and with the same abbreviations as in Table 1.

pop:		AB1	MB	AB2	AB3	BC	ON	MT1	ND	ID	MN	MT2	PEI	OR	NY	TN1	TN2	Mean	SD	Total
locus	N	60	60	60	62	68	40	60	60	72	60	82	46	82	60	32	32	58.5	14.85	936
Neo6003	A	14	15	15	15	13	14	15	13	14	15	18	15	19	16	16	13	15.00	1.67	31
	H_O	0.77	0.86	0.73	0.87	0.74	*0.65*	0.77	0.83	*0.69*	*0.72*	0.76	0.96	*0.68*	*0.57*	0.88	0.73	0.76	0.10	0.76
	H_E	0.91	0.92	0.92	0.93	0.88	0.91	0.92	0.90	0.90	0.92	0.93	0.94	0.92	0.92	0.94	0.90	0.92	0.01	0.92
Neo6429	A	14	14	14	16	18	9	12	14	13	17	16	17	16	15	12	11	14.25	2.44	36
	H_O	0.83	0.80	0.80	0.81	0.88	0.85	0.80	0.87	0.77	0.87	0.73	0.78	0.80	*0.63*	1.00	0.93	0.82	0.08	0.81
	H_E	0.89	0.88	0.88	0.88	0.93	0.88	0.89	0.89	0.89	0.93	0.88	0.93	0.91	0.90	0.89	0.90	0.90	0.02	0.91
Neo8380	A	7	8	6	8	10	6	8	10	9	8	8	7	11	9	8	5	8.00	1.59	19
	H_O	0.50	0.37	0.50	0.65	0.56	0.65	0.60	0.60	0.63	0.77	0.66	0.43	0.56	*0.47*	0.69	0.63	0.58	0.10	0.58
	H_E	0.56	0.49	0.46	0.64	0.57	0.64	0.56	0.64	0.70	0.68	0.63	0.53	0.58	0.60	0.63	0.69	0.60	0.07	0.60
Neo8394	A	11	13	14	13	14	11	11	16	11	12	12	11	14	12	9	9	12.06	1.88	29
	H_O	0.70	0.62	0.73	0.68	0.72	*0.70*	0.57	0.83	0.69	0.83	0.76	0.82	0.78	0.70	0.69	*0.63*	0.72	0.08	0.72
	H_E	0.84	0.86	0.89	0.83	0.88	0.86	0.84	0.90	0.82	0.86	0.84	0.86	0.87	0.83	0.87	0.80	0.85	0.03	0.85
Neo7013	A	10	10	12	13	15	8	12	13	13	10	12	10	13	13	7	6	11.06	2.49	27
	H_O	0.87	0.63	0.77	0.61	0.79	0.65	0.87	0.80	0.75	0.90	0.71	0.91	0.83	*0.73*	0.88	0.75	0.78	0.09	0.78
	H_E	0.83	0.71	0.82	0.80	0.89	0.80	0.86	0.86	0.85	0.81	0.84	0.88	0.86	0.83	0.78	0.68	0.82	0.06	0.85
Neo5270	A	18	11	16	13	18	7	14	11	17	14	22	14	15	19	11	7	14.19	4.17	46
	H_O	*0.36*	*0.39*	*0.27*	*0.23*	*0.32*	*0.31*	*0.26*	*0.30*	*0.30*	*0.16*	*0.33*	*0.39*	*0.11*	*0.42*	*0.33*	*0.36*	0.30	0.08	0.29
	H_E	0.91	0.88	0.92	0.86	0.92	0.76	0.89	0.88	0.91	0.92	0.95	0.92	0.89	0.95	0.94	0.87	0.90	0.05	0.92
Neo6428	A	5	5	5	6	10	7	11	7	7	8	6	8	10	12	5	6	7.38	2.28	24
	H_O	*0.35*	*0.24*	*0.26*	*0.30*	*0.42*	*0.26*	*0.46*	*0.23*	*0.26*	*0.17*	*0.31*	*0.41*	*0.43*	0.57	0.44	0.31	0.34	0.11	0.34
	H_E	0.58	0.56	0.69	0.64	0.68	0.55	0.80	0.62	0.64	0.67	0.62	0.58	0.67	0.71	0.61	0.56	0.64	0.07	0.65

Table S3. Pairwise population differentiation at five autosomal microsatellite loci. F_{ST} is above the diagonal, and R_{ST} is below the diagonal. Values in bold are significant at the $P < 0.01$ level, and values in italics are significant at the $P < 0.001$ level, based on 1000 permutations. Populations are listed from North to South, in the same order and with the same abbreviations as in Table 1.

	AB1	MB	AB2	AB3	BC	ON	MT1	ND	ID	MN	MT2	PEI	OR	NY	TN1	TN2
AB1		0.003	-0.006	-0.002	0.008	-0.002	*0.019*	0.001	*0.015*	-0.003	*0.019*	0.005	0.005	0.002	0.015	**0.021**
MB	-0.003		0.004	0.012	*0.019*	0.002	*0.032*	0.016	*0.032*	0.009	*0.033*	0.011	*0.022*	0.005	0.017	*0.029*
AB2	-0.009	-0.010		-0.002	*0.013*	0.008	*0.025*	0.005	*0.021*	0.007	*0.025*	0.009	0.012	0.011	*0.027*	*0.044*
AB3	-0.004	0.003	-0.005		-0.002	*0.013*	0.008	*0.025*	0.005	*0.021*	0.007	*0.025*	0.009	0.012	0.011	*0.027*
BC	0.009	0.018	0.008	-0.004		0.003	0.007	0.005	**0.012**	0.009	*0.011*	0.007	0.003	0.006	0.012	*0.027*
ON	0.025	0.037	0.020	-0.004	-0.017		0.011	0.002	0.009	0.000	*0.019*	0.006	0.013	0.000	0.011	0.014
MT1	**0.068**	*0.079*	**0.053**	0.023	0.025	0.028		0.015	0.009	0.013	0.000	*0.018*	0.010	0.010	*0.024*	*0.037*
ND	0.006	0.011	-0.002	-0.006	-0.012	-0.009	0.020		0.011	0.000	*0.020*	0.004	0.006	0.005	**0.022**	*0.039*
ID	0.030	0.020	0.018	0.004	0.017	0.025	0.016	0.008		0.007	0.009	0.010	0.008	*0.021*	*0.028*	*0.040*
MN	0.020	0.018	0.007	-0.004	0.000	-0.002	0.001	-0.009	-0.012		*0.010*	0.001	0.002	-0.003	0.008	0.015
MT2	0.010	0.028	0.013	0.002	-0.007	-0.008	0.029	-0.008	0.024	0.003		0.014	0.006	0.014	0.016	*0.033*
PEI	0.007	0.003	0.002	-0.011	-0.003	-0.002	0.010	-0.008	-0.018	-0.013	0.007		-0.001	0.010	0.010	*0.031*
OR	0.009	0.024	0.005	-0.002	-0.003	-0.001	0.007	-0.009	0.013	-0.004	-0.005	0.001		0.008	0.013	*0.040*
NY	-0.013	-0.013	-0.015	-0.005	0.012	0.020	0.054	0.005	0.012	0.012	0.017	0.001	0.011		0.006	0.014
TN1	-0.002	0.014	0.003	-0.013	-0.018	-0.023	0.025	-0.009	0.013	0.001	-0.014	-0.005	-0.006	0.001		0.008
TN2	0.015	0.037	0.032	0.013	0.008	0.031	0.058	0.024	0.037	0.020	0.004	0.007	0.012	0.014	-0.020	

Table S4. Proportion of membership of each population into each of the three clusters, as defined by the Structure analyses. One of five runs of $K=3$ is shown here; the results were consistent among runs. Population is as defined in Table 1; populations are listed here in the rank order of the probability of each cluster assignment, and in the same order as in Figure 6. N is the number of individuals genotyped at each microsatellite locus.

Population	N	**Cluster 1**	Cluster 2	Cluster 3
TN2	16	**0.95**	0.034	0.016
MB	30	**0.942**	0.041	0.018
AB1	30	**0.911**	0.075	0.015
AB2	30	**0.86**	0.046	0.094
ON	20	**0.836**	0.085	0.079
AB3	31	**0.806**	0.170	0.024
NY	30	**0.692**	0.162	0.145
MN	30	**0.690**	0.193	0.117
ND	30	**0.662**	0.293	0.046
TN1	16	**0.604**	0.320	0.076
BC	34	**0.534**	0.256	0.210
PEI	23	0.425	**0.557**	0.018
OR	41	0.317	**0.476**	0.207
MT1	30	0.305	0.036	**0.659**
MT2	41	0.222	0.127	**0.651**
ID	36	0.414	0.09	**0.496**

Table S5. Results of the Structure analyses to infer the number of genetic clusters (K). Shown here for value of K is the average and standard deviation of the likelihood of the data given that value of K, as well as each value of ΔK.

K	Mean ln Pr(X|K)	Standard deviation of ln Pr(X|K)	ΔK
1	-10684.24	0.21	
2	-10640.02	14.09	0.04
3	**-10595.26**	12.44	**13.59**
4	-10719.48	36.31	0.85
5	-10812.80	127.32	1.32
6	-11074.62	107.40	0.31
7	-11302.80	179.96	0.56
8	-11631.68	123.91	0.92
9	-12074.80	576.78	0.85
10	-12025.50	417.03	0.22
11	-11882.98	453.36	0.70
12	-12058.32	439.24	0.29
13	-12107.24	651.48	0.24
14	-11997.36	425.30	1.11
15	-12359.02	269.29	2.22
16	-12123.26	345.97	0.68

Figure S1. Crossing scheme to extract a *sex-ratio* chromosome into laboratory culture. Females are shown as circles, and males as squares. To maintain the stock after it is in pure culture, the two crosses shown here in G6/G7 are completed each generation.
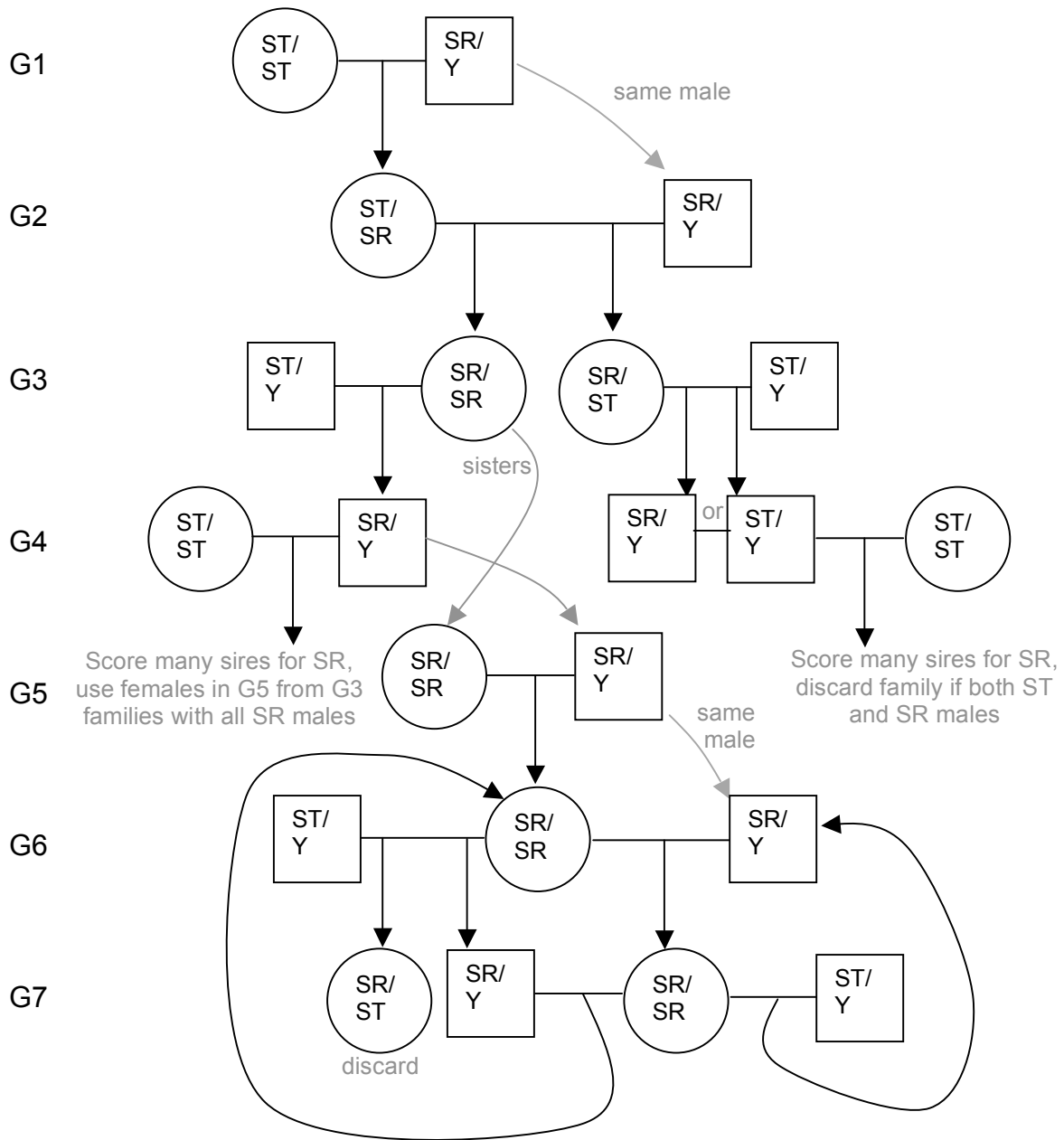
Figure S2. Distribution of offspring sex ratio in each of the sampled 15 populations.

Populations shown in the same order as in Table 1, from North to South.