Table S1 Number of maternal trees and natural pollinated seeds used in this study

Seed sampling site	No. pure maternal tree	No. hybrid maternal tree	Total no. maternal tree	No. seeds from pure maternal tree[a]	Total no. seeds[b]
Gn	8	11	19	140	304
Gs	6	8	14	85	201
T	15	3	18	272	322
D	12	0	12	198	207
M	8	5	13	152	226
	49	27	76	847	1260

[a] seeds used in the STRUCTURE analysis; [b] seeds used in the POLDISP analysis.

Table S2 Results of BayeScan and Micro-Checker

Locus	BayeScan			Micro-Checker							
	$\log_{10}$(qval)	F_{ST}	prob	SHHA (n=28)	SHHB (n=34)	SHHC (n=37)	SHHD (n=31)	SHHG (n=37)	SHIA (n=30)	SHIB (n=24)	No. population with null allele
Cal0157	-0.04	0.29	0.05	no	no	no	no	no	no	no	0
Cal0166	-0.03	0.29	0.04	no	no	no	no	no	no	**yes**	1
Cal0219	-0.03	0.29	0.03	no	**yes**	no	no	no	**yes**	**yes**	3
Cal0302	-0.04	0.29	0.05	no	no	no	no	no	no	no	0
Cal0351	-0.04	0.29	0.05	no	**yes**	no	**yes**	no	**yes**	**yes**	4
Cal0800	-0.03	0.29	0.03	no	no	no	no	no	no	no	0
Cal0804	-0.07	0.30	0.10	no	no	no	no	no	no	no	0
Cal0899	-0.03	0.29	0.04	no	no	no	no	no	no	no	0
Cal0952	-0.04	0.29	0.05	no	no	no	no	no	no	no	0
Cal1090	-0.08	0.28	0.12	no	no	no	no	no	no	no	0
Cal1176	-0.04	0.30	0.05	no	no	no	no	no	no	no	0
Cal1290	-0.04	0.29	0.04	no	no	no	no	no	no	**yes**	1
Cal1571	-0.05	0.29	0.07	no	**yes**	no	no	no	no	no	0
Cal1632	-0.11	0.33	0.22	**yes**	**yes**	no	**yes**	no	no	no	3
Cal1639	-0.06	0.28	0.09	no	no	no	no	no	no	no	0
Cal1647	-0.05	0.29	0.05	no	no	no	no	no	**yes**	no	1
Cal1777	-0.06	0.30	0.08	no	no	no	no	no	no	no	0

Table S3 Number of cymes used for inter- and intra-cross pollination, and seeds used in germination experiments, and number of seedlings whose mortality was tracked.

Cross type	Cross pairs		No. cymes	No. seeds sown	No. seedlings tracked
	Maternal	Paternal			
Inter-cross	D4	G2	1	24	10
	D4	G13	2	24	9
	D7	G2	1	24	11
	D7	G13	2	24	11
	D12	G2	2	24	8
	D12	G13	2	24	10
	D14	G2	3	24	8
	D14	G13	2	24	10
	D15	G2	1	24	7
	D15	G13	-	24	12
Total			16	240	96
Intra-cross	D4	D2	-	24	8
	D4	D5	1	24	7
	D4	D9	1	24	8
	D4	D13	1	24	7
	D7	D1	1	0	0
	D7	D2	1	24	4
	D7	D3	1	24	3
	D7	D9	1	24	11
	D7	D16	2	24	6
	D8	D5	1	24	3
	D8	D16	1	24	8
	D14	D2	1	24	7
	D14	D3	-	24	2
	D14	D5	2	24	5
	D14	D9	2	24	3
	D14	D16	1	24	2
	D15	D6	1	24	12
Total			18	384	96

- denotes that artificial crosses were performed, but not included in the calculation of the fruit set rate since the number of flowers in the cymes were not counted.

Table S4 Percentage of mating pair in hybrid adult trees and hybrid naturally pollinated seeds

Mating pair	Adult trees (%)	Seeds (%)
G-T	12.5	19.6
G-D	7.4	19.2
G-M	52.3	27.2
T-D	6.0	8.0
T-M	15.7	17.0
D-M	6.0	10.3

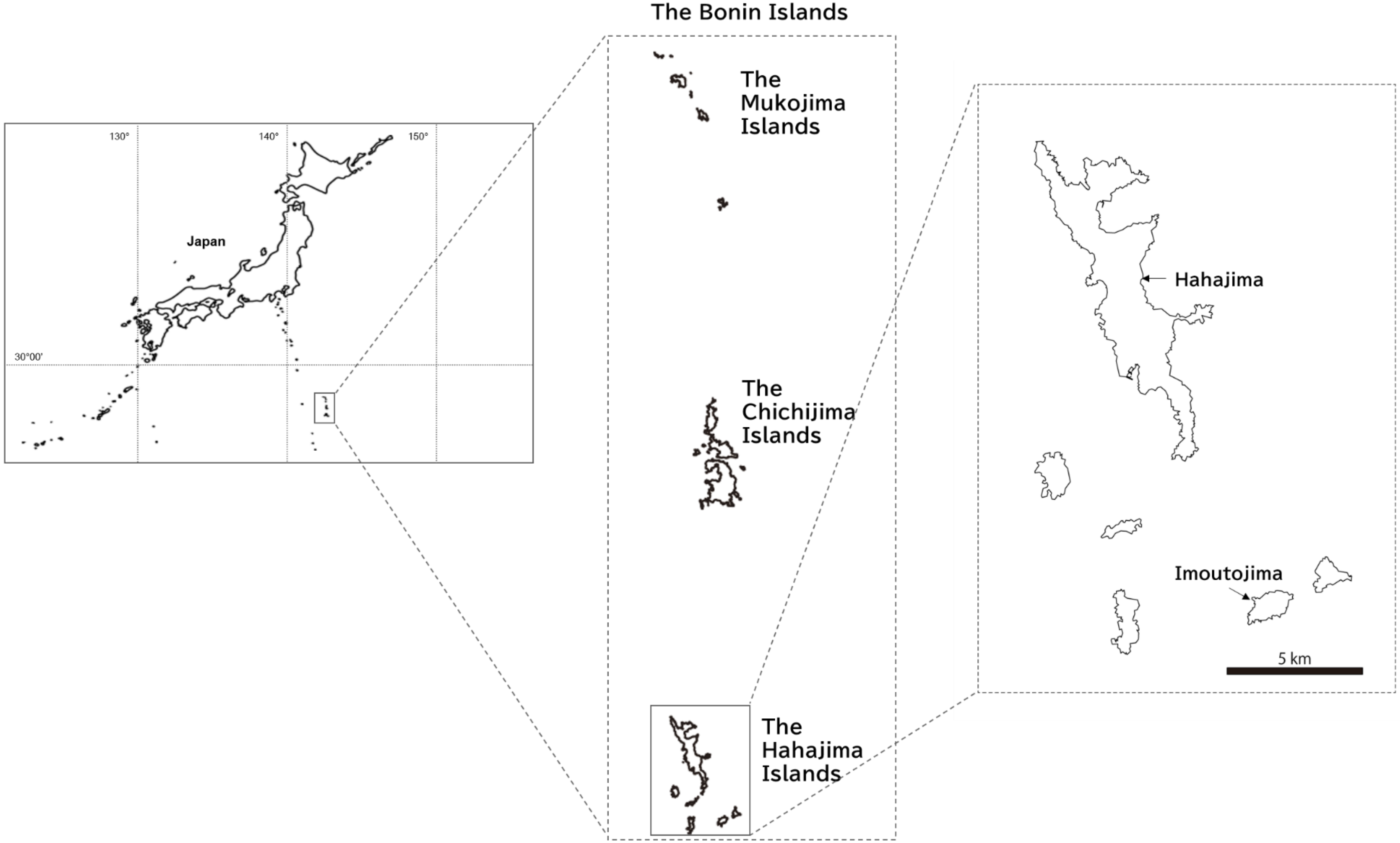

Fig. S1 Location of the Bonin Islands, and the Hahajima and Imoutojima Islands in the Hahajima Islands.

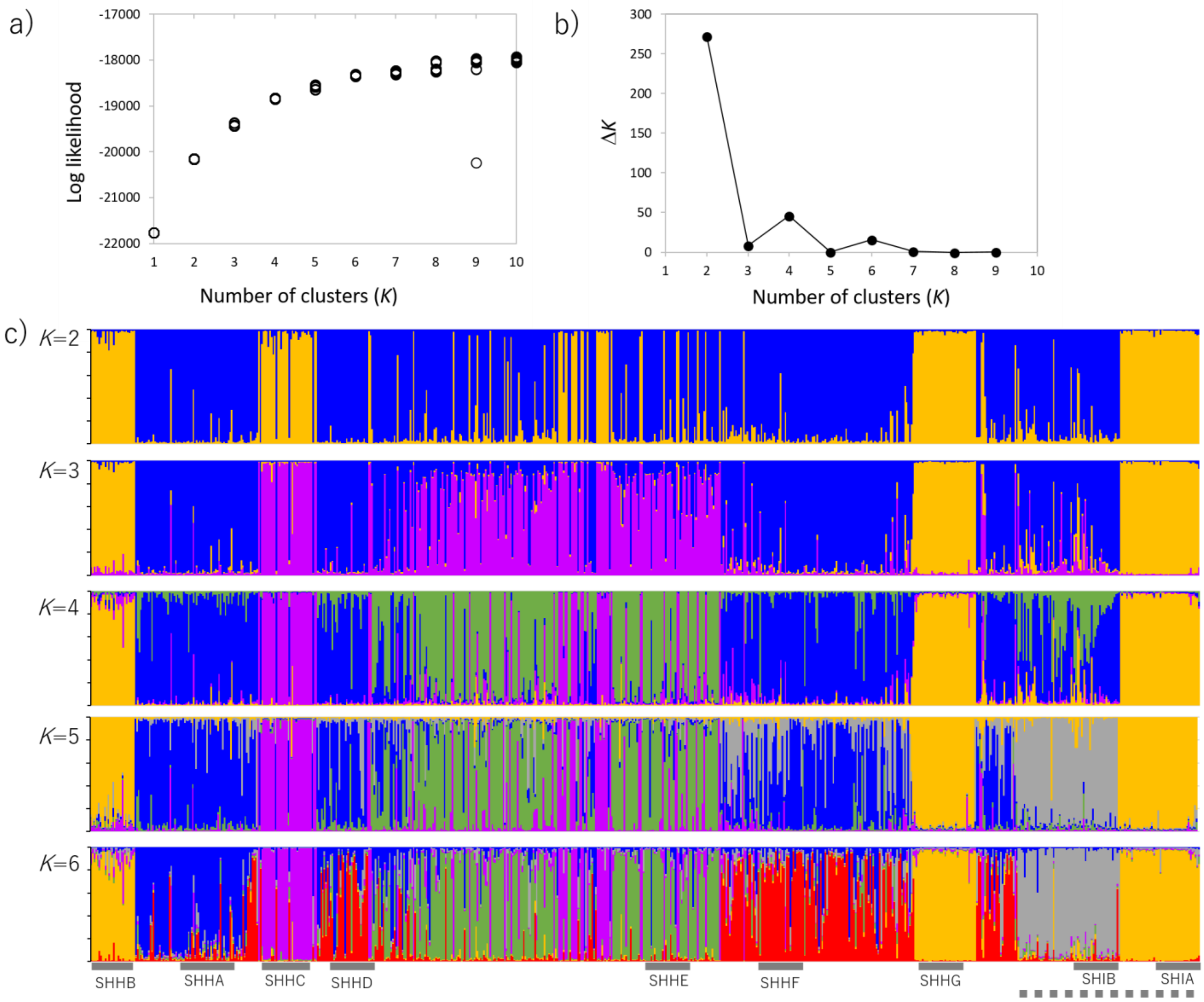

Fig. S2 Results of STRUCTURE analysis. (a) Changes in log likelihood, (b) ΔK, representing the number of clusters ranging 1–10, (c) bar plots showing clustering of all adult trees in the Hahajima Islands. Individuals are aligned roughly from north to south by population. The solid gray lines below the bar plot X-axis indicate populations used in Sugai et al. (2019). The gray dashed line refers to individuals on the satellite Imoutojima Island; all other trees are on Hahajima Island.

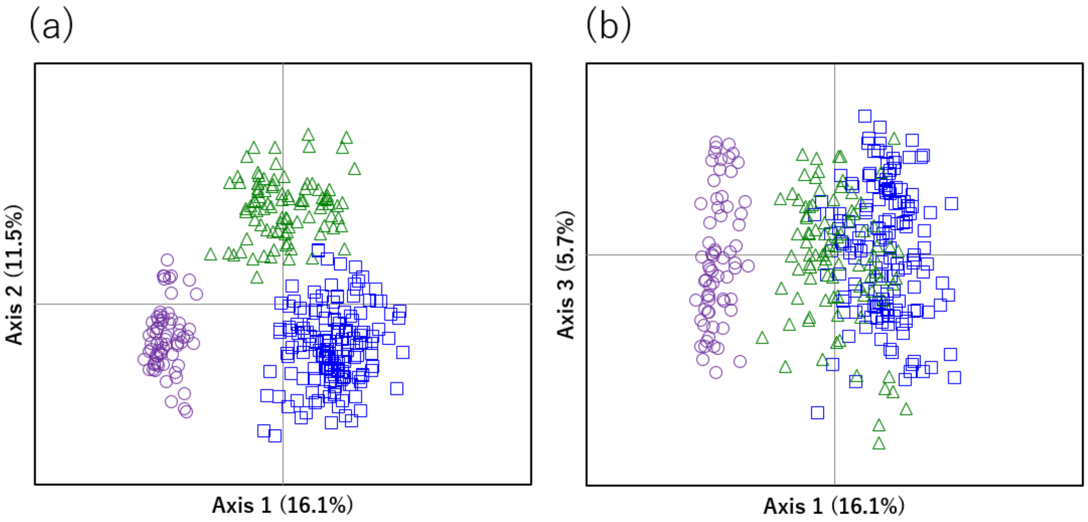

Fig. S3 Principal coordinate analysis (PCoA) scatter plots of pure adults from ecotypes G (blue squares), T (purple circles), and M (green triangles) for the 1st and 2nd principal coordinate axes (a) and the 2nd and 3rd principal coordinate axes (b).

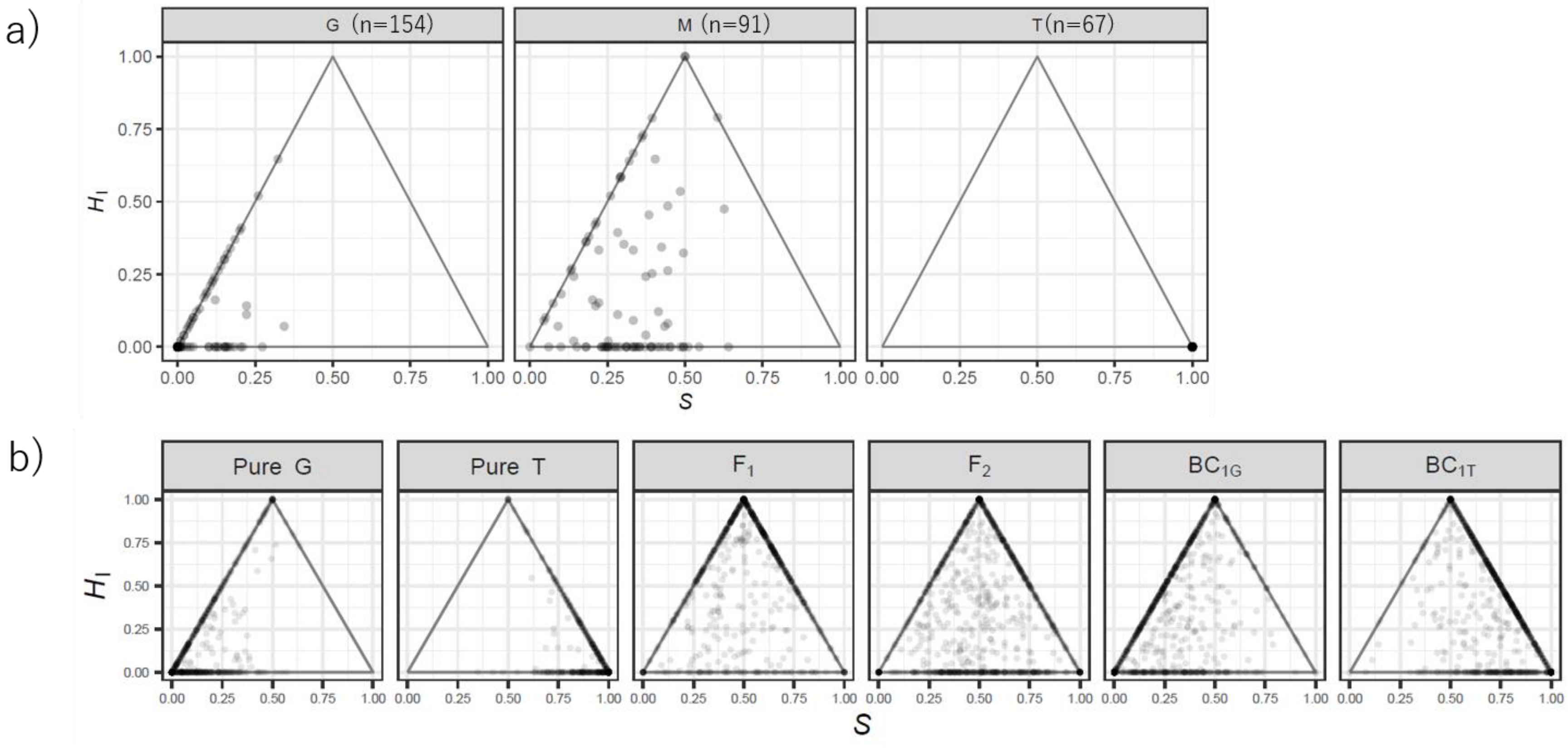

Fig. S4 Triangular plots depicting the ancestry of T (S) and interclass heterozygosity (H_I) for observed (a) and simulated data (b) as estimated by HIest. F_1, first filial hybrids; F_2, second filial hybrids; BC_{1G}, first-generation backcross hybrids to G; BC_{1T}, first-generation backcross hybrids to T.

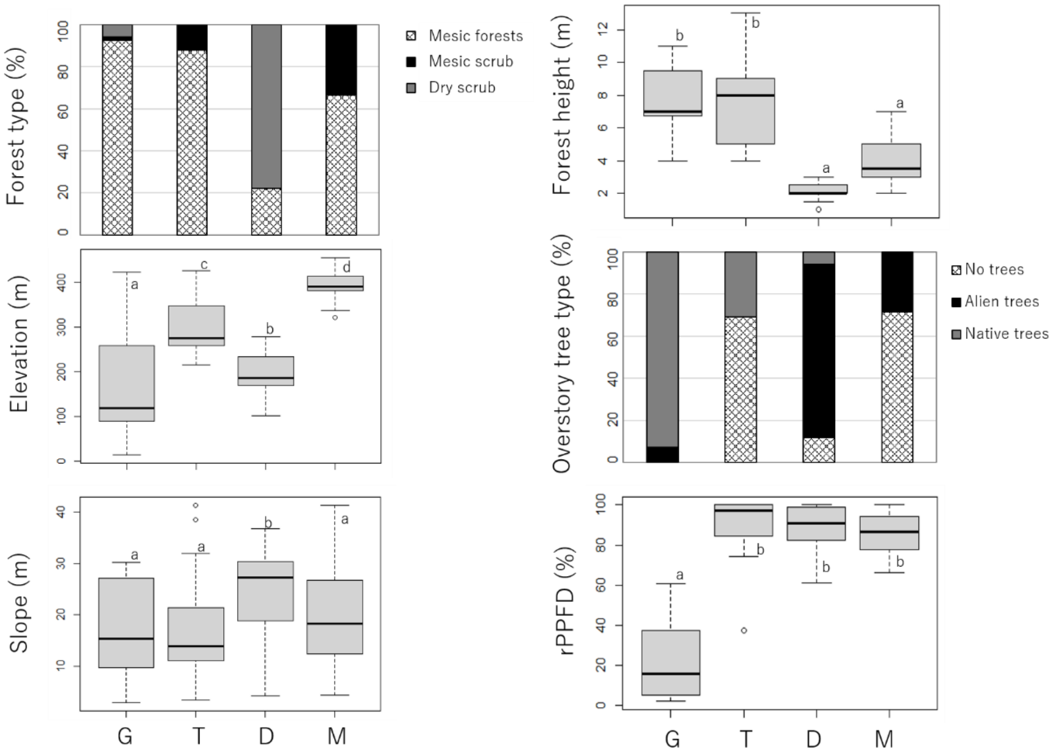

Fig. S5 Forest type, elevation, slope, forest height, overstory tree type, and rPPFD (relative photosynthetic photon flux density) of pure adult trees of each ecotype. Different letters indicate significant differences among ecotypes ($p < 0.05$, pairwise t-test with Bonferroni correction).

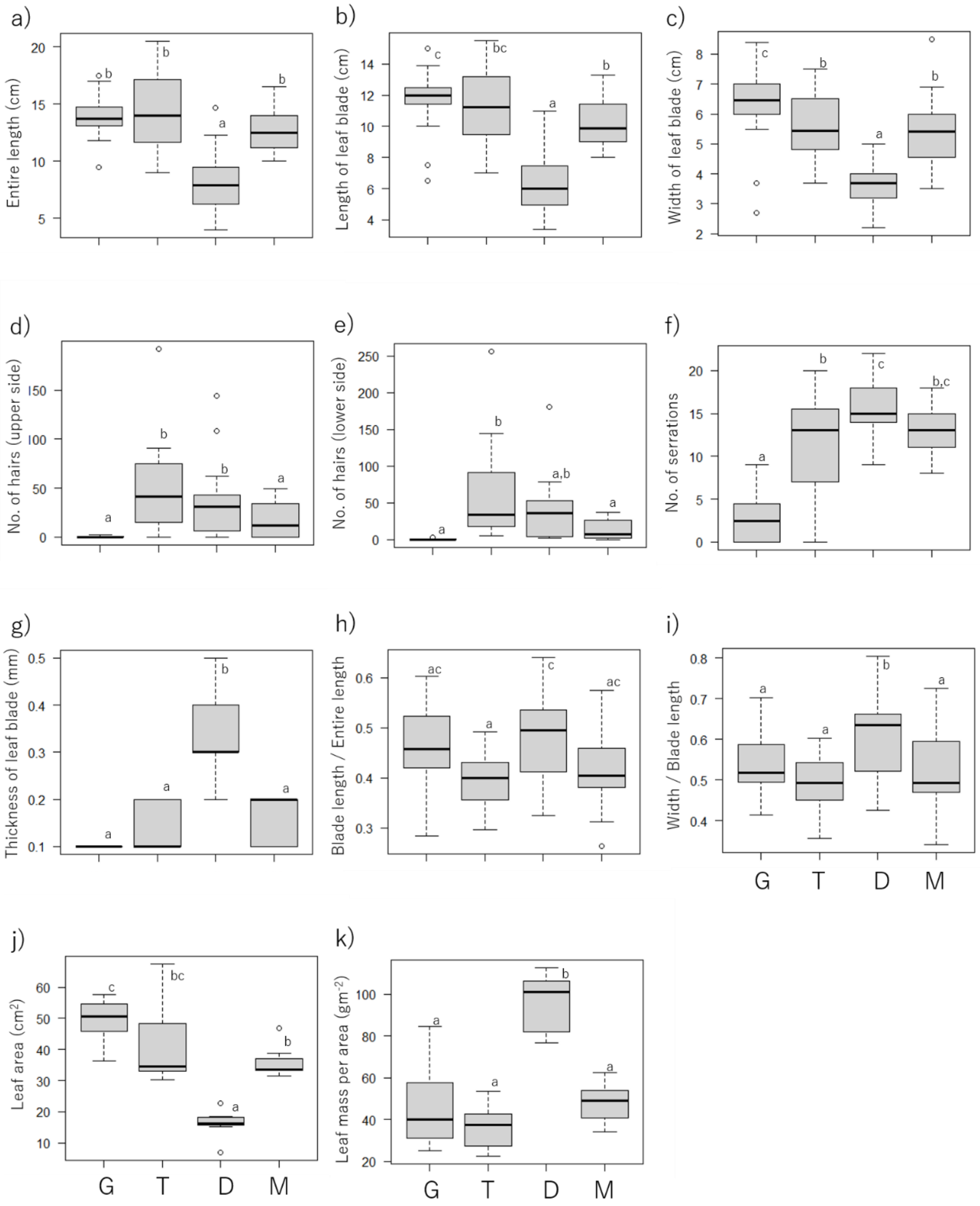

Fig. S6 Eleven leaf morphological traits for each ecotype. Different letters indicate significant differences among ecotypes ($p < 0.05$, pairwise t-test with Bonferroni correction).

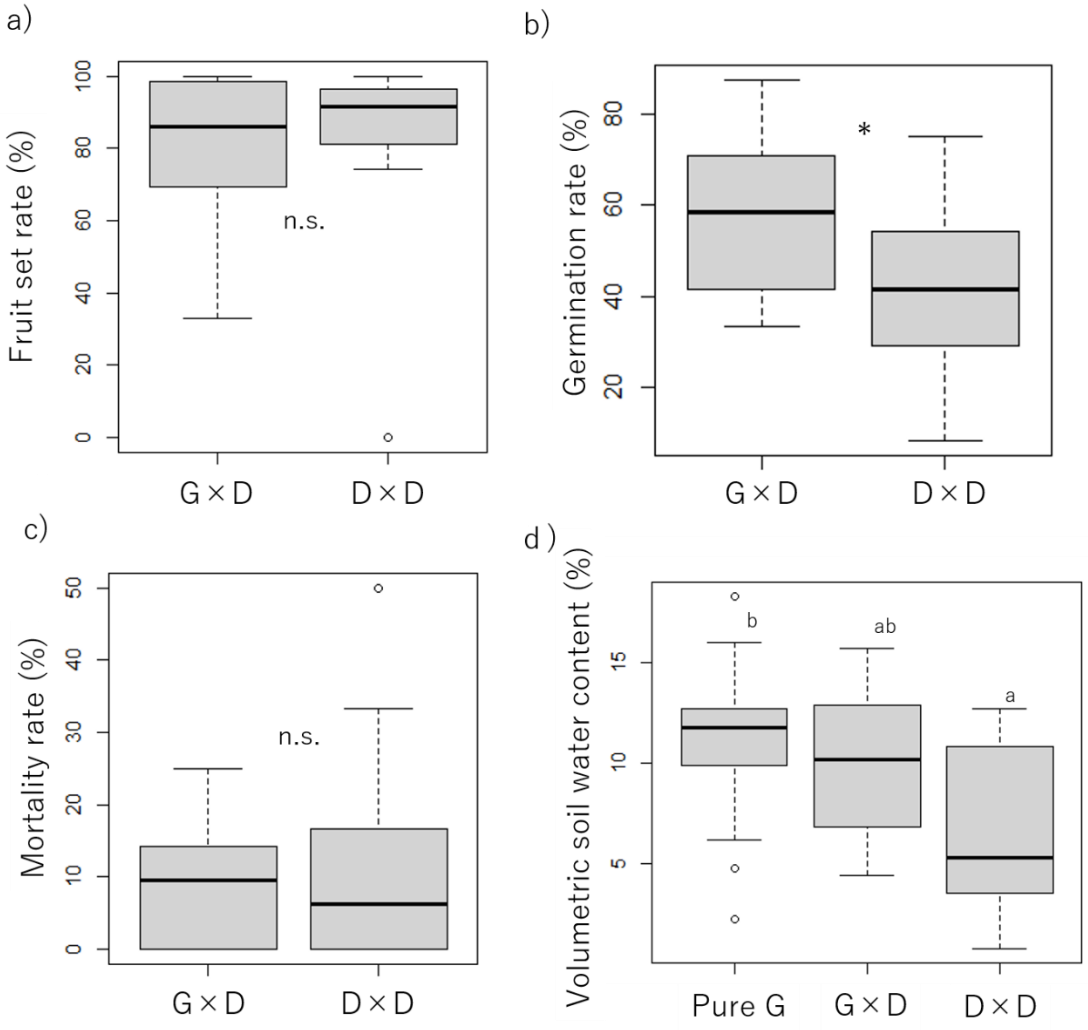

Fig. S7 The results of artificial inter-cross pollination between ecotypes G and D (i.e., G × D), and intra-cross pollination within ecotype D (i.e., D × D). Shown are: a) Fruit set rate, b) germination rate, and c) mortality rate of one-year old seedlings of each cross type as well as d) volumetric soil water content when seedlings begin to wilt for each cross type and pure ecotype G. For panels a-c * indicates a significant difference ($p < 0.05$), n.s. indicates no significant difference. For panel d: different letters indicate significant differences ($p < 0.05$, pairwise t-test with Bonferroni correction).