SUPPLEMENTARY DATA

Fig. S1. Delta-*K* values from 20 replicates of STRUCTURE analysis calculated by StrutureHarvester, for *K* from 1 to 8.

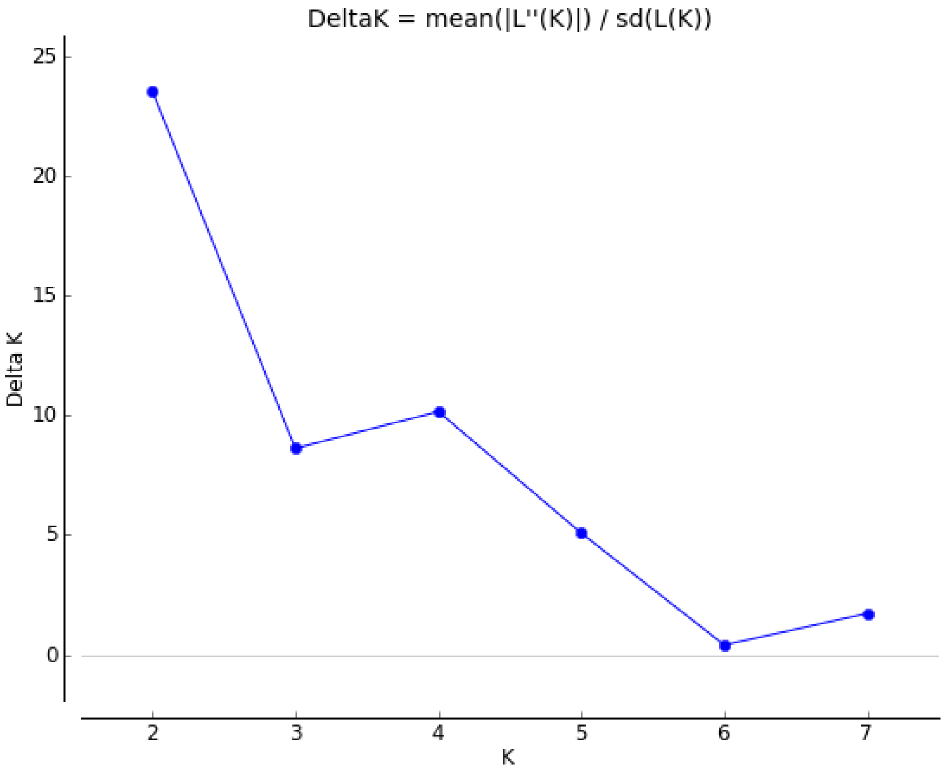

Fig. S2. Probabilities of unassigned pollen genotypes to belong to STRUCTURE-inferred clusters estimated by GeneClass2.

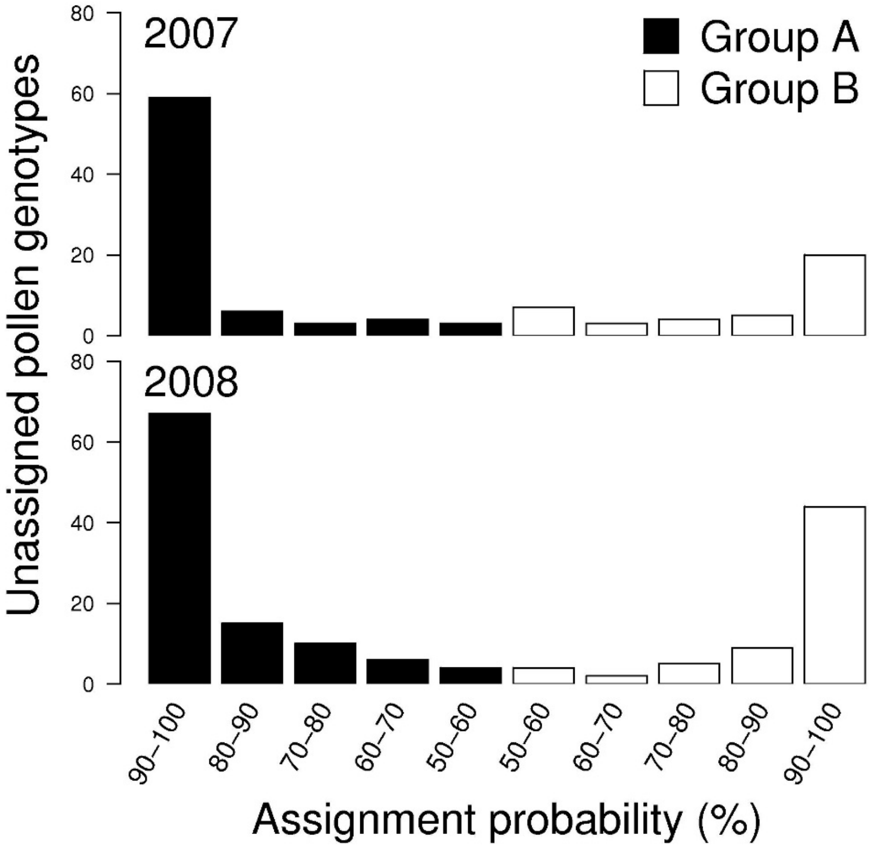

Table S1. Characteristics of the marker set.

Locus	Primer sequence	Repeat motif	T_a	Dye	Reference
UR123	F:AGCAATAAACCTTGTGTCGTG R: GAGCTTGCTATGCTTCGTCTC	$(CA)_4CG\ (CA)_5$ $(TTA)_5$	60°C	HEX	Zalapa *et al.* 2008
UR138	F: CTAGAACCCCCTTCGAAACC R: ACAAAAAGCCCACACACCTC	$(GA)_8$	60°C	TAMRA	Zalapa *et al.* 2008
UR158	F: TTCTTCATAGGCGCTGAGGT R: TGCACCCTGTCAAAGCTAAA	$(TGTA)_5$	55°C	TAMRA	Zalapa *et al.* 2008
UR188a	F: AAAACTAACGCGTCCCTTCC R: ATTTCGCTTCAATTGCGAG	$(AC)_{15}$	55°C	TAMRA	Zalapa *et al.* 2008
Ulmi1-21	F: GCGGTCTTACGTGAGCTTTC R: AAAGAGGCAGACGAAGATGG	$(CT)_{10}$	55°C	FAM	Collada *et al.* 2004
Ulmi1-165	F: CTCTTCCATTCGTCCTCACC R: GAGGTGCCATAAGCCAAGAA	$(CT)_9$	55°C	FAM	Collada *et al.* 2004

T_a, annealing temperature.

Table S2. Correspondence between morphological classification and genetic clustering. The number of individuals morphologically classified as *U. minor*, *U. pumila* and hybrids assigned to each STRUCTURE cluster is reported for the Porporana stand and the surrounding area.

	Porporana stand			Surrounding area		
STRUCTURE clusters	Hybrids	*U. minor*	*U. pumila*	Hybrids	*U. minor*	*U. pumila*
A	0	69	0	8	32	17
B	0	191	0	0	4	2
M	0	90	0	3	20	3

Table S3. Hybrid detection analysis with STRUCTURE. Probabilities that a tree is from, or has ancestry in, the clusters inferred by first STRUCTURE analysis aimed at investigating the genetic structure in the study population.

STRUCTURE clusters	Ancestry in A	Ancestry in B
A	0.994	0.006
B	0.005	0.995
M	0.494	0.506

Table S4. Hybrid detection analysis with NEWHYBRIDS. Number of individuals assigned to purebreds (P0 and P1) or to hybrid categories.

Analysis	STRUCTURE clusters	P0	P1	Hybrids	Unassigned
NEWHYBRIDS Prior information	A	120	0	0	6
	B	0	197	0	0
	M	1	59	1	55
NEWHYBRIDS No prior information	A	41	34	9	42
	B	0	196	0	1
	M	0	91	9	16

Table S5. Genetic diversity parameters locus by locus for the entire dataset (439 individuals) and the Porporana stand only (350 individuals) calculated by GenAlEx (Peakall and Smouse, 2012). EP was calculated accoding to Jamieson and Taylor (1997) formulae by FaMoz (Gerber *et al*., 2003). Mean inbreeding coefficient in brackets was estimated by InEST (Chybicki and Burczyk, 2009) as well as the frequencies of null alleles.

Population	All				Porporana stand					
Locus	N_a	H_O	H_E	EP	Na	H_O	H_E	F_{IS}	null$_{IIM}$	s.e.
UR123	4	0.460	0.532	0.372	4	0.429	0.489	0.124	0.056	0.020
UR138	16	0.573	0.828	0.557	14	0.596	0.847	0.296	0.125	0.017
UR158	7	0.707	0.751	0.580	7	0.775	0.726	-0.068	0.012	0.009
UR188A	7	0.746	0.588	0.337	5	0.796	0.581	-0.370	0.004	0.004
Ulmi1-21	13	0.647	0.735	0.646	13	0.621	0.701	0.115	0.046	0.014
Ulmi1-165	18	0.395	0.705	0.542	16	0.402	0.682	0.411	0.170	0.021
Mean	10.833	0.588	0.690		9.833	0.603	0.671	0.1013 (0.002 ± 0.002 s.e.)		
Overall				0.987						

N_a, number of alleles; H_O, observed heterozygosity; H_E, expected heteozygosity; EP, exclusion probability for paternity analysis; F_{IS}, inbreeding coefficient; null$_{IIM}$, frequency of null allele.

Table S6. Comparison of pollen immigration estimates obtained by varying FaMoz settings about genotyping error values (*e*: 0.01, 0.05 and 0.10) and inbreeding coefficient values (F_{IS}: 0 and 0.10) on the original and transformed datasets. The pollen immigration estimate from the scenario selected for analyzing pollen dispersal patterns (original dataset, $F_{IS} = 0.10$, $e = 0.05$) is highlighted in bold.

		Genotyping error		
Dataset	Inbreeding coefficient	$e = 0.01$	$e = 0.05$	$e = 0.1$
Original	$F_{IS} = 0.10$	87.56	**77.72**	62.43
	$F_{IS} = 0$	79.79	62.18	59.07
Transformed	$F_{IS} = 0.10$	88.60	80.83	76.16
	$F_{IS} = 0$	85.23	80.05	63.21

Table S7. Pollen immigration rate for each mother tree in 2007 and 2008. For each mother tree, the number of sampled seeds, its geographical location (in the central Porporana stand or in the surrounding agricultural area) and the genetic cluster to which it was assigned by STRUCTURE analysis are also reported.

Year	Tree ID	*N*	Morphological classification	Porporana stand	Genetic cluster	Pollen immigration rate
2007	PO001	9	*U. minor*	yes	A	0.89
	PO125	9	*U. pumila*	no	A	0.67
	PO126	10	*U. minor*	no	A	0.70
	PO129	9	*U. minor*	no	M	1.00
	PO139	10	*U. minor*	no	A	0.90
	PO147	10	*U. pumila*	no	B	0.70
	PO148	4	*U. pumila*	no	A	0.75
	PO149	6	*U. pumila*	no	M	1.00
	PO150	4	Hybrid	no	M	0.75
	PO152	6	*U. pumila*	no	A	1.00
	PO157	8	*U. minor*	no	M	0.88
	PO170	8	*U. minor*	no	M	1.00
	PO173	10	*U. minor*	no	A	0.90
	PO174	6	*U. minor*	no	M	1.00
	PO175	8	*U. minor*	no	A	0.63
	PO182	10	*U. pumila*	no	A	0.50
	PO187	8	*U. pumila*	no	A	0.63
	PO193	8	hybrid	no	A	0.75
	PO198	4	*U. minor*	no	B	0.75
	PO204	10	*U. minor*	no	M	0.60
2008	PO001	7	*U. minor*	yes	A	1.00
	PO101	9	*U. minor*	yes	A	1.00
	PO116	9	*U. minor*	yes	M	0.67
	PO126	10	*U. minor*	no	A	0.60
	PO129	8	*U. minor*	no	M	1.00
	PO131	10	*U. minor*	no	M	0.70
	PO133	9	*U. minor*	no	M	0.67
	PO134	8	*U. pumila*	no	A	1.00
	PO139	9	*U. minor*	no	A	0.44
	PO147	7	*U. pumila*	no	B	1.00
	PO148	5	*U. pumila*	no	A	1.00
	PO149	8	*U. pumila*	no	M	1.00
	PO150	8	hybrid	no	M	0.75
	PO152	2	*U. pumila*	no	A	1.00
	PO157	9	*U. minor*	no	M	0.89
	PO170	9	*U. minor*	no	M	0.89
	PO173	8	*U. minor*	no	A	0.38
	PO174	6	*U. minor*	no	M	1.00
	PO175	9	*U. minor*	no	A	0.44
	PO182	10	*U. pumila*	no	A	0.20
	PO183	9	*U. pumila*	no	M	1.00
	PO185	8	*U. minor*	no	A	1.00
	PO193	10	hybrid	no	A	0.90
	PO195	9	*U. minor*	no	M	0.89
	PO198	9	*U. minor*	no	B	0.89
	PO200	9	hybrid	no	A	0.56
	PO202	8	*U. minor*	no	M	0.50
	PO204	7	*U. minor*	no	M	0.71

N, number of sampled seeds.

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