

Supplementary Materials

Table S1. Patterns of genetic variation at single-locus level for each sampled subpopulation.

Subpopulation	Genetic parameters	Locus									
		AAT-1	AAT-2	PGI	LAP	GDH	6PGD	MDH-1	MDH-4	IDH	MNR
Mach	Na	1	2	2	2	2	4	2	1	1	1
	Ne	1.000	1.724	1.268	1.083	1.173	3.333	1.771	1.000	1.000	1.000
	H _E	0.000	0.420	0.211	0.077	0.147	0.700	0.435	0.000	0.000	0.000
Lim	Na	1	2	2	1	2	3	2	1	1	2
	Ne	1.000	1.268	1.471	1.000	1.041	2.323	1.814	1.000	1.000	1.083
	H _E	0.000	0.211	0.320	0.000	0.039	0.570	0.449	0.000	0.000	0.077
Aka	Na	1	2	3	2	2	4	2	1	1	2
	Ne	1.000	1.268	1.758	1.173	1.220	3.307	1.523	1.000	1.000	1.173
	H _E	0.000	0.211	0.431	0.147	0.180	0.698	0.343	0.000	0.000	0.147
Ade	Na	2	2	3	2	2	4	2	1	1	2
	Ne	1.127	1.625	1.705	1.041	1.173	3.027	1.855	1.000	1.000	1.173
	H _E	0.113	0.385	0.414	0.039	0.147	0.670	0.461	0.000	0.000	0.147
Tro	Na	1	2	3	2	2	3	2	1	1	1
	Ne	1.000	1.574	1.857	1.041	1.173	2.887	1.771	1.000	1.000	1.000
	H _E	0.000	0.365	0.462	0.039	0.147	0.654	0.435	0.000	0.000	0.000
PaN	Na	2	2	3	2	2	4	2	1	2	3
	Ne	1.024	1.716	1.645	1.097	1.189	2.626	1.644	1.000	1.012	1.194
	H _E	0.023	0.417	0.392	0.089	0.159	0.619	0.392	0.000	0.012	0.163
PaS	Na	2	2	3	2	2	4	2	1	1	2
	Ne	1.046	1.418	1.402	1.131	1.290	3.013	1.678	1.000	1.000	1.169
	H _E	0.044	0.295	0.287	0.116	0.225	0.668	0.404	0.000	0.000	0.145
PaZ.400	Na	2	2	2	2	2	4	2	1	1	2
	Ne	1.041	1.292	1.497	1.083	1.150	2.697	1.724	1.000	1.000	1.268
	H _E	0.039	0.226	0.332	0.077	0.130	0.629	0.420	0.000	0.000	0.211
PaZ.800	Na	2	2	3	2	2	4	2	1	1	3
	Ne	1.083	1.574	1.508	1.173	1.368	2.990	1.814	1.000	1.000	1.129
	H _E	0.077	0.365	0.337	0.147	0.269	0.666	0.449	0.000	0.000	0.114
PaZ.1200	Na	2	2	3	2	2	4	2	1	2	2
	Ne	1.041	1.243	1.532	1.062	1.243	2.483	1.419	1.000	1.020	1.105
	H _E	0.039	0.196	0.347	0.058	0.196	0.597	0.295	0.000	0.020	0.095
Mean over locus	Na	2.000	2.000	2.667	2.000	2.000	4.000	2.000	1.000	1.333	2.333
	Ne	1.055	1.370	1.512	1.106	1.254	2.723	1.652	1.000	1.007	1.167
	H _E	0.052	0.262	0.339	0.094	0.198	0.631	0.388	0.000	0.007	0.140
	F _{ST}	-0.034	0.0296	0.0003	0.0064	0.0119	0.0232	0.0251	0	0.0022	0.0149

Na: Number of alleles per locus; Ne: Effective number of alleles; H_E: Genetic diversity; F_{ST}: Genetic differentiation.

Table S2. Assessment of Mendelian inheritance in *P. brutia* from Cyprus. (For loci where the analysed megagametophytes were lower than 18, the χ^2 was not calculated.)

Isoenzyme	Heterozygous Genotype	Number of Trees [§]	Observed and Expected Allele Observations ^{§§}				χ^2	d.f. n-1 [†]	$\chi^2_{0,05}$	P
			A	B	C	D				
AAT-1	AB	2	10 (6)	2 (6)	-	-	-	-	-	-
AAT-2	AB	12	36 (36)	36 (36)	-	-	0	1	3.84	> 0.99
	AB	1	3 (3)	3 (3)	-	-	-	-	-	-
PGI-2	AC	1	2 (3)	-	4 (3)	-	-	-	-	-
	BC	12	-	35 (36)	37 (36)	-	0,05	1	3.84	0.75 - 0.90
LAP-1	AB	4	14 (12)	10 (12)	-	-	0,66	1	3.84	0.25 - 0.50
GDH-1	AB	9	26 (27)	28 (27)	-	-	0,07	1	3.84	0.75 - 0.90
	AB	8	24 (24)	24 (24)	-	-	0	1	3.84	> 0.99
	AC	13	40 (39)	-	38 (39)	-	0,05	1	3.84	0.75 - 0.90
6PGD-1	BC	3	-	9 (9)	9 (9)	-	0	1	3.84	> 0.99
	BD	2	-	6 (6)	-	6 (6)	0	-	-	-
	CD	3	-	-	7 (9)	11 (9)	0,88	1	3.84	0.25 - 0.50
MDH-1	AB	20	59 (60)	61 (60)	-	-	0,03	1	3.84	0.75 - 0.90
	AB	1	4 (3)	2 (3)	-	-	-	-	-	-
MNR-1	BC	4	-	12 (12)	12 (12)	-	0	1	3.84	> 0.99

[§] number of trees that shows the relative genotypes; ^{§§} the expected value is the one in the parentheses; [†] n = 2, the number of allele in the heterozygous genotype.

Table S3. Pairwise genetic distance among sampled subpopulations based on Nei's minimum distance (below the diagonal) and pairwise morphoanatomical Euclidean distance (above diagonal).

	Mach	Lim	Ade	Tro	Aka	PaN	PaS	PaZ.400	PaZ.800	PaZ.1200
Mach	0.0000	1.794	0.896	1.334	2.532	1.252	1.615	1.496	1.388	1.408
Lim	0.0086	0.0000	1.876	1.151	2.389	0.958	1.477	1.161	1.098	1.528
Ade	0.0080	0.0070	0.0000	1.357	2.389	0.958	1.477	1.161	1.098	1.528
Tro	0.0044	0.0083	0.0026	0.0000	2.620	0.968	0.958	0.882	1.080	1.288
Aka	0.0054	0.0057	0.0055	0.0040	0.0000	3.013	2.867	2.613	3.188	2.995
PaN	0.0062	0.0063	0.0051	0.0052	0.0072	0.0000	1.149	1.067	0.292	1.207
PaS	0.0033	0.0047	0.0038	0.0048	0.0030	0.0040	0.0000	0.718	1.148	1.052
PaZ.400	0.0072	0.0016	0.0058	0.0051	0.0033	0.0048	0.0020	0.0000	1.052	1.482
PaZ.800	0.0045	0.0091	0.0034	0.0066	0.0071	0.0035	0.0024	0.0064	0.0000	1.324
PaZ.1200	0.0106	0.0044	0.0095	0.0075	0.0041	0.0048	0.0035	0.0030	0.0072	0.0000

Table S4. Assessment of correlation (Spearman correlation test) signal among the investigated morphological and anatomical traits.

<i>Traits</i>	NShLen	NLen	NWid	NThic	NResIn	NResDo	NResTot	NStomDo	NStomIn	NStoRow	NSto/Row	NStom	NTeh	CLen	CWid	CLen/CWid	SLen	SWid	Swing	SLenWing
NShLen	1.00																			
NLen	0.03	1.00																		
NWid	0.42	-0.27	1.00																	
NThic	0.32	-0.30	0.94**	1.00																
NResIn	0.62	0.09	0.84**	0.80**	1.00															
NResDo	0.68*	0.09	0.79**	0.81**	0.96**	1.00														
NResTot	0.66*	0.09	0.81**	0.81**	0.98**	0.99**	1.00													
NStomDo	0.47	-0.46	0.08	-0.03	-0.13	-0.08	-0.10	1.00												
NStomIn	0.00	-0.40	-0.30	-0.25	-0.47	-0.36	-0.41	0.53	1.00											
NStoRow	0.40	-0.39	-0.05	-0.17	-0.26	-0.19	-0.22	0.97**	0.68*	1.00										
NSto/Row	-0.08	0.25	-0.06	-0.06	-0.15	-0.16	-0.16	0.08	-0.20	0.03	1.00									
NStom	0.14	0.88**	-0.30	-0.36	-0.04	-0.02	-0.03	-0.08	-0.19	-0.01	0.54	1.00								
NTeh	0.29	-0.31	0.68*	0.65*	0.58	0.47	-0.52	0.03	-0.40	-0.13	0.37	-0.23	1.00							
CLen	-0.33	0.53	-0.74*	-0.76*	-0.62	-0.60	-0.61	-0.18	0.36	0.01	0.14	0.56	-0.64*	1.00						
CWid	0.08	0.51	-0.72*	-0.80**	-0.49	-0.45	-0.47	0.10	0.38	0.27	0.08	0.60	-0.61	0.87**	1.00					
CLen/CWid	-0.54	-0.12	0.48	0.56	0.24	0.14	0.19	-0.51	-0.41	-0.58	0.05	-0.30	0.38	-0.35	-0.74*	1.00				
SLen	0.01	0.51	-0.79**	-0.82**	-0.58	-0.51	-0.54	0.13	0.34	0.27	0.33	0.68*	-0.52	0.84**	0.94**	-0.71*	1.00			
SWid	0.24	0.53	-0.58	-0.66*	-0.37	-0.30	-0.33	0.20	0.34	0.34	0.29	0.71*	-0.44	0.79**	0.95**	-0.76*	0.94**	1.00		
SWing	-0.03	0.56	-0.70*	-0.74*	-0.48	-0.45	-0.47	-0.03	0.33	0.13	0.29	0.67*	-0.48	0.91**	0.95**	-0.60	0.95**	0.94**	1.00	
SLenWing	-0.01	0.55	-0.73*	-0.77**	-0.52	-0.47	-0.49	0.01	0.33	0.17	0.30	0.68*	-0.49	0.90**	0.95**	-0.64*	0.97**	0.95**	0.99**	1.00

Significant level: *, $p < 0.05$; **, $p < 0.01$; no symbol: non-significant.