

Supplementary Material

Tab. S1 - Number of ramets of the parent trees included in the orchard and progeny analysed in each field trial (n=324). (*): Extra parents that had an offspring sampled due to the existence of abnormal phenotypes. This progeny was not included in the mixed linear model.

Parent ID	Number of ramets	Field trial location				
		Fundão	Abrantes	Oleiros	Gorda	Nisa
M74	37	9	15	12	10	9
M18	40	18	1	-	2	-
M49	24	-	19	8	11	10
M28	39	-	-	17	11	10
M07	14	13	24	7	6	9
M13	33	15	20	14	10	10
M89	24	-	-	-	13	11
1552*	1	-	-	6	-	-
100840012*	11	-	-	1	-	-
100841010*	28	-	1	-	1	-
100890020*	7	-	-	-	1	-

Tab. S2 - Field trials brief characterization, including year of establishment, lithology, soil classification according to FAO, range of annual precipitation (mm) and temperatures (mean, minimum and maximum, in °C).

Trial Location	Installation date	Lithology	Soil classification (FAO)	Annual precipitation (mm)	Mean T	Min T	Max T
Fundão	26/11/2015	schists,	Skeletal Leptosol (Humic)	1400-1600	13.39	8.09	18.87
Abrantes	31/12/2016	poorly consolidated sandstones	Leptic Skeleptic Regosol	800-900	15.1	8.49	21.82
Oleiros	28/03/2017	schists	Dystric Skeleptic Leptosol (Humic)	1200-1400	13.17	8.13	18.59
Gorda	15/12/2017	sandstones, loamy limestones	Endoleptic Skeleptic Regosol (Arenic)	700-900	15.24	8.93	21.84
Nisa	15/12/2017	schists	Dystric Skeleptic Leptosol	800-900	15.65	10.06	21.21

Tab. S3 - Microsatellite identification, forward (F) and reverse (R) primer sequences, fragment size and multiplexing.

Microsatellite	Primer Sequence	Fragment size (bp)	Multiplex
Embra11F¹	GCTTAGAATTTGCCTAAACC	94-147	1
Embra11R¹	GTAAAATCCATGGGCAAG		
Embra119F¹	GGAATTTCCCGTCAAATC	117-224	1
Embra119R¹	CTGAAGCTTGACAATCAGG		
Emerc8F²	CCAGATTGTAGCCCTTATGTG	229-263	1
Emerc8R²	CATCCCAATCAAACGAAC		
Emerc7F²	CGAATCAAGTCGACATGTGTG	265-317	1
Emerc7R²	CCGTCGACCGCCCTAT		
Embra23F¹	GGTTGTTTCATCTTTTCCATG	114-150	2
Embra23R¹	AGCGAAGGCAATGTGTTT		
Embra41F¹	ATGATTTTGTGCGTGGAC	174-210	2
Embra41R¹	TCAGGTGAAAGGATGGAG		
Embra227F¹	CGAATGCCATAGATTGTCAG	300-324	2
Embra227R¹	CAGGCATCTCGTACGTGGA		
En15F⁵	TCCTCGTGCTCATACTCAAA	70-104	3
En15R⁵	ATGGCTGGAAGTAACCGAGA		
Es76F³	AATGCTGCTGTAGACGATGC	125-177	3
Es76R³	AAGACAAATCAAGCAAGTCAGC		
Eg65F⁴	CGGCCTCATTCTCTAGGTG	228-291	3
Eg65R⁴	GGCTAGACTAGGGGAAAGCG		
Embra37F¹	CACCTCTCCAAACTACACAA	114-170	4
Embra37R¹	CTCCTCTCTTTCACCATTC		
En12F⁵	CAGAACCCAGCGGAGGA	210-252	4
En12R⁵	GGAAACGCCAATGTAGCTCT		

¹ Brondani et al (2006). BMC Plant Biology. 6: 20. <https://doi.org/10.1186/1471-2229-6-20>

² Steane et al (2001). Silvae Genetica 50: 89-91.

³ Glaubitz et al (2001). Genome. 44: 1041–1045. <https://doi.org/10.1139/g01-106>

⁴ Thamarus et al (2002). Theoretical and Applied Genetics. 104: 379–387. <https://doi.org/10.1007/s001220100717>

⁵ Developed by CSIRO, Division of forestry and forest products, Canberra, Australia
(<http://www.ffp.csiro.au/tigr/molecular/eucmsps.html>)

Tab. S4 - Contingency table with the number of normal and abnormal phenotypes per class of inbreeding coefficient (F), used as input for the chi-square test of independence (n=324).

Inbreeding coefficient (F)	Normal Phenotype	Abnormal Phenotype
0	160	17
0.063	33	2
0.125	11	0
0.25	3	0
0.5	87	11
Total plant number	294	30

Tab. S5 - Values of within family group co-ancestry and corresponding intraclass correlation for the seven open pollinated families sampled in the *E. globulus* seed orchard.

OP Family	Θ	1/r	R
M74	0.214276961	2.333428653	0.428553922
M18	0.161002604	3.10553983	0.322005208
M49	0.415909091	1.202185792	0.831818182
M28	0.298387097	1.675675676	0.596774194
M07	0.168359102	2.969842402	0.336718204
M13	0.184795673	2.705691057	0.369591346
M89	0.335714286	1.489361702	0.671428571