

DNA markers to study genetic diversity and fingerprinting in *Arbutus unedo* L. (strawberry tree)

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PURPOSE OF THE STUDY



What are the genetic distances and the level of diversity among 27 Portuguese *Arbutus unedo* genotypes ?

RESULTS

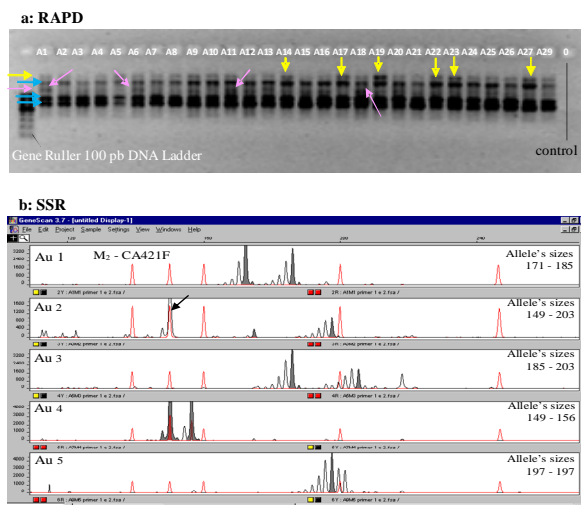


Fig. 1. RAPD (OPC9), 2 polymorphic (yellow and rose arrows) and 3 monomorphic bands (blue arrows) (a); M2 SSR automatic sequencer output. Sample number in the left upper corner. Red peak=ROX marker (b).

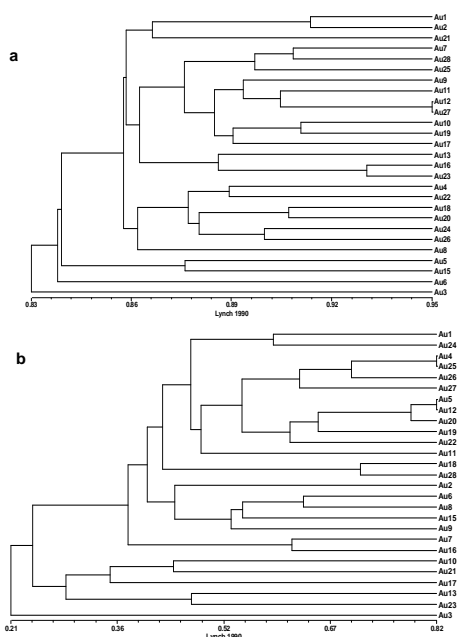
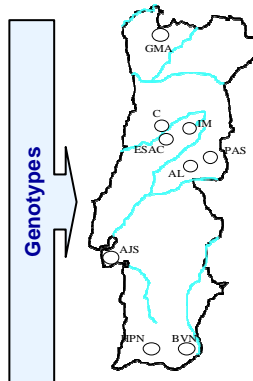


Fig. 2. UPGMAs based on a band similarity coefficient Lynch (1990): RAPD (a) and SSR (b).

MATERIAL AND METHODS



Region	Code	Local name
GMA	Au 7	Gerês Mata de
	Au 10	Albergaria
	Au 22	
C	Au 3	Coimbra
	Au 11	
	Au 15	
ESAC	Au 21	Coimbra (ESAC)
	Au 23	
	Au 27	
IM	Au 13	
	Au 16	Alva e Alvoco
	Au 24	
PAS	Au 6	Serra da Gardunha
	Au 9	
	Au 19	
AL	Au 2	Serra Alvêlos e
	Au 5	Muradal
	Au 17	
AJS	Au 1	Serra da Arrábida
	Au 20	(Portinho)
	Au 25	
HPN	Au 4	Algarve /Silves
	Au 8	/Herdade da Parra
	Au 28	
BVN	Au 12	Algarve/Serra do
	Au 18	Caldeirão/
	Au 26	Barranco Velho

Molecular markers: 19 RAPDs (OPC) and 5 SSRs from *Vaccinium* (Ericaceae)

RAPDs			
Parameter	value	Parameter	value
Nº of bands	124	Polymorphic level	57.3%
Nº of polymorphic bands	71	He	0.27 ± 0.014

SSR								
Locus	Na	He	Ho	Fis	P-value	Sig.	F (null)	PIC
M2	22	0.90	0.85	0.05	0.2018	NS	0.0546	0.88
M4	9	0.79	0.78	0.02	0.0146	NS	0.0534	0.75
M7	7	0.78	0.69	0.11	0.0159	NS	0.0985	0.73
M10	6	0.57	0.56	0.03	0.004	NS	0.0868	0.51
M11	14	0.73	0.62	0.16	0.0007	*	0.0887	0.70
Mean	11.6	0.75	0.70	0.07	0.0474		0.0764	0.71

Tab. 1. Genetic diversity parameters estimates: N° of alleles/locus (Na), expected heterozygosity (He), observed heterozygosity (Ho), fixation index (Fis), polymorphic information content (PIC). Sig. refers to the Sig. resulting from the HWE test (after Bonferroni correction), and F(null) refers to null allele frequency.

CONCLUSIONS

RAPD: some genotypes shared up to 95% of the bands. The tree topology (fig. 2a) was supported by a moderate correlation (r=0.63; P<0.001).

SSR: the UPGMA showed a degree of band similarity between genotypes up to 82% (fig. 2b). The Mantel test validated the tree topology (r=0.75; P<0.001). Finally, no correlation was found between the SSR and the RAPD pair-wise similarity matrices.

The diversity with SSRs (He=75%) was much higher than the 27% uncovered with the RAPDs, in agreement with the high microsatellites polymorphism, though monomorphic bands were used in the latter (Tab 1).

Mantel tests unfolded the lack of correlation between genetic and geographical distance matrices, for both SSRs and RAPDs. Indeed, the genotypes did not group according to their geographical origin, in both cases. Reduced gene flow, due to fragmentary distribution of the species in the country, together with the type of mating system (pollination by small insects), are plausible explanations for these results.