

Table S1.

Characteristics of the 14 SSRs loci selected for *T. melanosporum* analyses on at each analyses scales (brûlés and truffle ground scale).

SSR	motif	localisation	Size range (bp)	Na*	He**	Retained at brûlé scale	Retained at truffle ground scale
me11	(AG)16	intron	277-308	22	0.441	✓	✓
me13	(AT)13	Intergenic region	81-119	7	0.5	✓	✓
me14	(CT)21	Intergenic region	136-154	8	0.419	✓	✓
me02	(TC)16	Intergenic region	143-177	17	0.556	✓	✓
Tm2	(TAT)15	Intergenic region	129-221	24	0.821	-	-
Tm9	(ATCA)12	Intergenic region	282-338	9	0.547	✓	✓
Tm75	(GAAA)14	Intergenic region	312-352	9	0.528	✓	✓
Tm1	(ATTG)18	Intergenic region	300-361	18	0.601	✓	✓
Tm21	(ATA)26	TE	256-323	17	0.554	✓	-
Tm98	(TAT)15	Intergenic region	199-238	10	0.511	-	✓
Tm127	(TTTA)14	TE	158-222	12	0.257	✓	✓
Tm22	(CCTCAT)17	Intergenic region	291-362	20	0.62	✓	✓
Tm269	(TGTTGC)15	Intergenic region	353-407	14	0.424	✓	✓
me09	(AG)29	Intergenic region	Not clearly lisible	-	-	-	-

*Na: Number of observed alleles and **He: Expected heterozygosity, calculated 1091 samples including ascocarps, ECM and others samples.

SSR name with « me »: Riccioni *et al.*, 2008.

SSR name with « Tm »: Murat *et al.*, 2010.