

S2 Table. Allelic size range, expected heterozygosity (*He*) and efficiency of MS-PCR amplification of each locus. The allelic size range is described in base pairs (bp). In this table, the level of polymorphism of each locus was described as the expected heterozygosity (*He*) calculated for each marker using pooled samples from all areas. The efficiency of amplification was calculated as the percentage of samples with positive PCR amplification for a specific locus over the total number of analysed samples (n=292).

locus	range (bp)	<i>He</i>	efficiency of amplification
MS1	230-248	0.63	95.5%
MS2	189-237	0.79	93.2%
MS3	181-196	0.63	92.5%
MS4	188-215	0.70	89.7%
MS5	166-229	0.22	92.1%
MS6	209-248	0.86	89.7%
MS7	143-167	0.20	79.5%
MS8	205-340	0.92	84.9%
MS9	144-177	0.82	91.8%
MS10	178-268	0.66	84.6%
MS12	200-332	0.85	81.8%
MS15	232-289	0.85	82.9%
MS16	158-374	0.90	71.6%
MS20	191-254	0.88	84.9%