

Table S1. Characteristics of ten microsatellite markers used in the genotyping of *Campomanesia adamantium*

Locus	Motif	Primers sequences	AN	TA
CAMP 1	(TG) ₁₆	F 5'-TATCAAGTCACGAAGGTGGG-3' R 5'-TGGCAAGTATATCCTGCTCA-3'	MF280931.1	128-172
CAMP 3	(TG) ₈	F 5'-GTTGGCTCAACAGTTAGCAG-3' R 5'-TCTAGAACTCGGCATTTCCC-3'	MF280933.1	144-178
CAMP 4	(GA) ₁₀ (CA) ₆	F 5'-CTTAATGCACATCCGCAACA-3' R 5'-GGATGAATTATGTACGACACA-3'	MF280934.1	202-240
CAMP 8	(TC) ₂₄	F 5'-AATAGCTTCCAGACTGCTCC-3' R 5'-AAAAGAGAATTTGGAGCGCC-3'	MF280938.1	228-266
CAMP 13	(TG) ₈	F 5'-AGTCGAGTGGGCTCTAGTAT-3' R 5'-ATGTGCTGCTCAGAAAGAGT-3'	MF280943.1	210-240
CAMP 17	(AC) ₉	F 5'-TCATCTTCGGCTACATAACGT-3' R 5'-TCCATGCCTTTTCCTCTTTAGA-3'	MF280947.1	112-138
CAMP 24	(TG) ₇	F 5'-CAAGTCCTACATGGCTGGAT-3' R 5'-AGTGCACGAAAAGTGGTCTA-3'	MF280954.1	222-264
CAMP 25	(TG) ₉	F 5'-TCCATGCCTTTTCCTCTTTAGA-3' R 5'-TCATCTTCGGCTACATAACGT-3'	MF280955.1	118-138
CAMP 28	(GA) ₂₁	F 5'-CGTGATGAAGAGTGATGGGA-3' R 5'-TCATTGATAACTGCGGGTGA-3'	MF280958.1	190-226
CAMP 36	(CA) ₅	F 5'-TCCCAAACACTTCTGTATGCT-3' R 5'-TGGTTCCTAAGATCTCCCA-3'	MF280966.1	108-128

AN: accession number of microsatellite loci available on GenBank at NCBI (National Center for Biotechnology Information); TA: allele size (pb) obtained through the genotyping on Fragment Analyzer (Advanced Analytical Technologies. Inc.)

Table S2 Genetic diversity for *Campomanesia adamantium* using ten specific microsatellite loci

Locus	N	A	A _R	PIC	H _E	H _O	F _{IS}	HWE
CAMP1	259	23	22.57	0.90	0.91	0.44	0.51	0.000*
CAMP3	246	17	16.46	0.88	0.89	0.63	0.29	0.000*
CAMP4	277	20	18.40	0.86	0.87	0.72	0.16	0.000*
CAMP8	251	20	19.84	0.87	0.88	0.31	0.65	0.000*
CAMP13	247	16	15.76	0.90	0.91	0.30	0.67	0.000*
CAMP17	274	14	13.79	0.80	0.83	0.70	0.15	0.000*
CAMP24	267	18	17.57	0.90	0.91	0.49	0.46	0.000*
CAMP25	272	12	11.59	0.82	0.81	0.65	0.21	0.000*
CAMP28	188	20	20.00	0.93	0.92	0.24	0.73	0.000*
CAMP36	194	11	10.99	0.83	0.82	0.59	0.28	0.000*
Mean ± SD	247.5 ± 10.06	17.10 ± 1.22	16.70 ± 3.75	0.97 ± 0.04	0.87 ± 0.01	0.51 ± 0.06	0.41 ± 0.07	0.000

N: number of sampled individuals; A: number of alleles by locus; A_R: allelic richness; PIC: polymorphic information content; H_E: expected heterozygosity; H_O: observed heterozygosity; F_{IS}: inbreeding coefficient; HWE: Hardy-Weinberg equilibrium test; SD: standard deviation

* Fisher's exact test significant for the Hardy-Weinberg equilibrium proportions

TableS3 Estimating global F_{ST} of Weir (1996) both using and without using the ENA correction to evaluate the effect of null alleles per locus and all loci

	F_{ST} without ENA correction	F_{ST} with ENA correction
Locus		
1	0.017	0.012
2	0.017	0.015
3	0.026	0.025
4	0.053	0.036
5	0.026	0.018
6	0.024	0.024
7	0.029	0.023
8	0.021	0.022
9	0.047	0.030
10	0.028	0.028
All Loci	0.028	0.023

F_{ST} estimatives calculated by FreeNA using and without using the ENA correction described in Chapuis and Estoup (2007)

Weir BS (1996) Genetic data analysis II: methods for discrete population genetics. 2ed. Sunderland: Sinauer Associates, 445 p.

Chapuis MP, Estoup A (2007) Microsatellite null alleles and estimation of population differentiation. Mol Biol Evol 24(3): 621-631.