Table 1 Primer sequences and characteristics of 4 *Babylonia areolata* single-locus microsatellite markers

Locus	GenBank acc. no.	Repeat motif [§]	Primer sequences (5'-3')	Ta (℃)	MgCl$_2$ (mM)	n	a	as	H_E	H_O	P_{HWE}
HUBA01	FJ594998	(TG)$_n$	F: tgtgacatgaacaagggacttc	62	1.2	30	10	302-340	0.92	0.88	0.056
			R: aggaaactcagagcattcgtg								
HUBA07[†]	FJ595004	(AG)$_N$(TG)$_N$	F: aaaagtgcttctcgtgcattg	60	1.2	27	15	219-309	0.60	0.36	0.006
			R: aacttgtctctttcggggaac								
HUBA10[†]	FJ595007	(TG)$_N$(AG $_n$	F: atctccgtcgtcttgtgattg	58	2.0	31	5	380-450	0.87	0.60	0.023
			R: tgctggtattcagtcctgtcc								
HUBA18	FJ595015	(TC)$_N$(TTC)$_N$(GTG)$_N$	F: tacgacgtgtttgacgtgttg	60	1.5	29	14	390-430	0.76	0.84	0.025
			R: tgacctcacgcaagaaaagag								

Note: The number of individual analyzed (n), number of alleles (a), allele size range in base pairs (as), observed (H_O) and expected (H_E) heterozygosities are presented for each locus. Ta is the annealing temperature and P_{HWE} is the probability of Hardy–Weinberg equilibrium. [§]Repeat motif: N, pure; n, interrupted; Values in bold represent significant probability estimates after correction for Bonferroni multiple tests (initial α< 0.05/5 = 0.01); [†]Loci showing evidence for null alleles suggested by Micro-Checker