

Table 2 Information and characteristics of 20 microsatellite loci in a wild *P. lutea* population (n=16)

Locus GenBank No.	Motif	Primer sequence (5'-3')	Ta(°C)	a	Size (bp)	H_o	H_e	P_{HWE}
<i>plo7</i> HQ435873-HQ435879	(TTG) ₆ (TTTA) ₆	F: agcactgtctgtaacaagcgaag R: tattggaaggaggctctaaattg	50	4	206-225	0.75	0.75	0.568
<i>plo10</i> § HQ435880-HQ435883	(AAT) ₉ (AGA) ₈	F: caagctatagccatgtgataccc R: gtagtcctctcaggggatttg	50	4	204-249	0.06	0.63	0.004
<i>plo37</i> § HQ435922-HQ435924	(ATG) ₁₁	F: tcccttatacatgcaagggaagtg R: ttccagtcctcctgtctctccag	55	6	388-423	0.38	0.75	0.031
<i>plo42</i> § HQ435936-HQ435939	(GAC) ₄ (CAA) ₃	F: taattaggctaccagggagttcg R: atcacttgagttgtgggatgg	55	2	196-199	0.00	0.38	0.001
<i>plo66</i> HQ435976-HQ435980	(TGA) ₃ (TGA) ₅	F: ttttgatagtgatcgctgtagtgg R: gctatcacctcaccaccat	55	2	187-196	0.56	0.53	0.592
<i>plo68</i> § HQ435985	(TCA) ₈ (ATC) ₆	F: tcttaattctcaataattccttgg R: cacagggaaccttccttgc	55	7	354-433	0.13	0.83	0.000
<i>plo74</i> § HQ435986-HQ435990	(CATC) ₁₆	F: gctattggaagcgtgtttt R: tccgtataactatgccagaaa	55	5	186-202	0.19	0.72	0.002
<i>plo78</i> GU137158 *	(AC) ₆	F: actgtttacaatacacgacggaag R: gcctgttaagtacaagtcacc	50	3	115-124	0.81	0.56	0.074
<i>pasE005</i> KP407156	(AT) ₆	F: gtctgagtcctggttacatc R: gagttttccatcagccaacag	53	2	202-204	0.38	0.48	1.000
<i>pasE016</i> KP407157	(GA) ₇	F: ttgtccaaccggcaactac R: ttctgttctctgtggctttc	53	2	209-211	0.13	0.29	1.000
<i>pasE021</i> KP407158	(CAT) ₈	F: atgattttgcacggctctc R: aacacctcgaactctggatctg	48	6	221-247	0.94	0.78	0.033
<i>pasE030</i> KP407159	(AT) ₆	F: gtctgaatcccgtggttacatc R: catcagccaacagcaatgc	53	1	195	0.00	0.18	- #
<i>pasE041</i> KP407160	(AAACA) ₃ (AAAC) ₄	F: agtgcctgtaacctctccttg R: ctgaggtcaaagtgttggtgag	48	3	220-235	0.38	0.66	0.212
<i>pasE042</i> § KP454004	(ACC) ₅	F: atctttttcccaacctaacag R: cgtgtgaacgtagctttgtag	48	3	226-248	0.13	0.67	0.002
<i>pasE056</i> KP407161-KP407162	(AAC) ₆	F: ctttggttaaagctggccaat R: ttggttatttctgctgtggt	50	3	290-298	0.25	0.52	0.147
<i>pasE060</i> KP407163-KP407164	(CT) ₁₀	F: tcgtaagagcacaataaagc R: ccagtaaatgacccagaca	50	7	272-298	0.50	0.81	0.012
<i>pasE062</i> KP407165-KP407166	(AG) ₆	F: tgatcctggcctatcaaaatg R: gacttgagaagagcatgctg	53	2	290-294	0.38	0.48	1.000
<i>pasE065</i> KP407167-KP407168	(TTA) ₄ (AT) ₄	F: gactaacccttttgaactgc R: aaggcaggttagatggttaagt	53	2	395-399	0.06	0.24	- #
<i>pasE073</i> KP407169-KP407170	(AAC) ₄	F: gcgagaagcaacacaatccta R: tcttgctttgtcacagttt	48	4	329-342	0.75	0.73	0.013
<i>pasE099</i> KP407171-KP407171	(CA) ₅	F: gcttcgccaatattcttgc R: ttggcagtgaagaagagtg	53	2	202-288	0.06	0.34	- #
Average±SD across loci						3.5±1.8	0.34±0.29	0.57±0.20

Note: Values in bold represent significant ($P<0.05$) deviation from HWE; # no enough allele information for HWE test; § Loci showing evidences of null; * The *P. lutea*'s sequences resulted from amplification of primer pair *Plo78* were too short to submit to GenBank and get an access number. GU137158 is the GenBank number of original *P. lobata* microsatellite sequence