

Table S1. The information of 15 pair primers for SSR analysis

Locus code	Primer sequence (5'-3')	T <sub>m</sub> (°C)	Repeat motif	Expected allele size range(bp)	Number of alleles	Genbank accession no.
SSR2	F: GATAGCGGAGCCGGTGATT R: GGATGGAAGGCTCAAGATTCG	60	(AG)12 TT(AG)7	242-284	21	HM041034
SSR29	F: ATGGATGAGTGTGCGATAGG R: TGTGATGTAGGAGTCTGAAC	60	(TC)7	168-184	9	DQ453912
SSR54	F: GAGAAGAGAAGGCTGTGTGC R: GAAACCTGATTCGTCGTCGT	62	(CT)47	146-170	14	GQ254833
SSR59	F: CTCCTCGTTTGCCACTCATT R: AAACAGAGGGTTTTCGGTGC	56	(CT)20	196-330	25	GQ254847
SSR74	F: GTCCACGCAAACAGAGACAC R: TTGGCTTGGCTTTCTCTTTC	58	(CT)10	204-240	14	FM161912
SSR111	F: CCCTATTCATTGTCCCTCCA R: GTCCTCCTGGAATTCTGTGC	60	(CT)19	126-164	20	AB674473
SSR113	F: CAACCATGGTGTGCGAGAAGA R: TGCTTAATTTGCCTGTGCAT	60	(AG)23	168-192	11	AB674475
SSR114	F:CTAGACCAGCCCCAAGAACA R: TTCAAGGGCTTCTTCTGAATC	60	(AC)9	204-232	15	AB674476
SSR116	F: GGAACCCCAATTTAGGAACT R: TGCTTGGTGAAAACCATAGA	58	(AC)11	180-214	18	AB674478
SSR117	F: CCGTGTAAGAGTGCCAAATC R: TCTTGAGGTGAGATCAAGTG	60	(TA)5(TG)17	86-188	10	AB674479
SSR118	F:TCTGTTGGTGGTGTGTCAC R:TAATGTGGATGCAAGCAGTG	58	(TC)22(AC)10	148-182	18	AB674480
SSR119	F: CAAGCACACACAAGGATTTG R: TGGCAACTCTCAGGTATCAA	52	(GA)21	200-236	18	AB674481
SSR120	F: GTTGTTTGTGGGTGTGTGTT R: GAGAGAGAACCCAAAGGAAAA	60	(TC)7(AC)12	260-312	27	AB674482
SSR122	F: GTGCAGTGTCCATGTTGAAG R: GACATTTTCTCTGCAAGGTCA	60	(TG)14	158-260	32	AB674484
SSR123	F: TTCCCTCAGCATTAAGGTGT R: CAGGCAAAGGAAGGTAGGTA	60	(TA)9(TG)8	84-112	8	AB674485