

Table S3. Information of 18 pairs of simple sequence repeat (SSR) primers

SSR primers	Forward//Reserve primer sequence (5'-3')	Polymorphic fragments	Size range of amplified fragments (bp)	PIC	NA	NE	H	I
BrgMS135	GCATCACCCCTAGTTAATCGAA // AAGAAGGGAGAAAACCTGAAACC	8	200-600	0.843	1.8283	1.717	0.378	0.536
BrgMS13	CCACCCCTAAGTTTTACTCCAA // AGGTTGAGTGAGAGGGAAGAGA	3	100-600	0.559	1.919	1.850	0.439	0.616
BrgM33	GATCACGTCGCAGTATATCCA // TTGGTTCCCCATCTACCATATC	3	300-500	0.579	1.424	1.272	0.160	0.237
BrgMS202	ATCGCCTCAACACACAGTAAAA // TTAGCAAGCATTGATGAAGAGC	6	200-500	0.781	1.960	1.845	0.444	0.628
BrgMS204	TCTGTGTGCAGGAGAACTGTA // AGATCGTGAGTTCTTGGATGAC	6	200-300	0.792	1.879	1.740	0.395	0.561
BrgMS217	CATTCCGCCTAAGCTCATTAAC // CAATTTACCTGCACCTAGTCA	5	100-200	0.650	1.980	1.717	0.406	0.590
BrgMS268	TCACCATGTGTAAAAGACTCGG // TTGGCTTATCTTCTTGGGATTG	6	300-500	0.790	1.828	1.647	0.357	0.513
BrgMS287	TGGGTCTCAGTTTCCATTTTCT // TGCTTGTGAATCTTTGTGTGTG	6	400-500	0.797	1.758	1.655	0.346	0.491
BrgMS318	AACGAAAGACTCGACAGAAAGG // GTGAAGGTCAGGCGAATTTAAG	8	100-500	0.851	1.980	1.773	0.427	0.613
BrgMS343	CCCAAATATCAATCTCAAAGCC // TCGTTTCTCATCAATCTGTTGG	3	300-500	0.592	1.131	1.099	0.055	0.079
BrgMS383	TCGGGCAGATAAAGTAATCCAT // AGAAACCCCTTCACAACAATGA	8	300-400	0.850	1.970	1.831	0.441	0.624
BrgMS479	AGTTGGAACCCCTATCCATTTT // TCTTTGCTTTCTTCTCCTTTTCG	7	100-500	0.828	1.818	1.717	0.380	0.536
BrgMS513	TCTCAGCCTTTAACTTCTCCCA // AACTTTGTTTCAGCTCCTGCTC	4	300-400	0.701	1.303	1.236	0.126	0.182

Table S3. Continued

SSR primers	Forward//Reserve primer sequence (5'-3')	Polymorphic fragments	Size range of amplified fragments (bp)	PIC	NA	NE	H	I
BrgMS629	GTGCTTTCTGCGTTATTTCTCA // TTACGACCACCAACTAGCAAAA	6	300-500	0.807	1.616	1.530	0.282	0.399
BrgMS635	GTGTTTCTCTTCAACGCCTTTT // CACAAAGAATCCCCACAGATTT	5	300-500	0.748	1.869	1.600	0.310	0.499
BrgMS801	ACAAACCTTCTTGTCCTGTCGT // ATATCTTAGCTCTCCACGATGC	5	200-300	0.693	1.970	1.779	0.424	0.608
BrgMS4508	AAAGAAGCTGCTCTTGTTGAGG // TACCCATGAATCTCCGTCTTCT	5	200-600	0.760	1.636	1.570	0.296	0.417
BRAS078	ATTGGGTCTGACCTTTTCTC // CTTTCCTCATCGCTACCAC	7	100-500	0.835	1.859	1.688	0.375	0.538
Total		101						
Average		5.61		0.747	1.673	1.626	0.333	0.496

PIC, Polymorphic information content; NA, Observed number of alleles; NE, Effective number of alleles; H, Nei's gene diversity; I, Shannon's information index.