

## Supplementary data

Table S1. The list of [primers](#) used in this study.

Markers	Chr	Primer Forward (5'→3')	Primer Reverse (5'→3')	Motif	Size (bp)*
RM312*	1	GTATGCATATTTGAT AAGAG	AAGTCACCGAGTTTA CCTTC	(ATTT) 4(GT)9	200
RM250*	2	GGTTCAAACCAAGCT GATCA	GATGAAGGCCTTCCA CGCAG	(CT)17	150
RM318*	2	GTACGGAAAACATGG TAGGAAG	TCGAGGGAAGGATCT GGTC	(GT)15	150
RM251*	3	GAATGGCAATGGCGC TAG	ATGCGGTTCAAGATT CGATC	(CT)29	150
RM1369*	6	AACCTGAGAGTGCCA ATTGG	TCCCCTAGTAAAGCG GATTC	(AG)27	120
RM223*	8	GAGTGAGCTTGGGCT GAAAC	GAAGGCAAGTCTTGG CACTG	(CT)25	300
RM6364*	10	GTTCATTTTCGTCCTTC TCGG	TCTCGATTCTTCCTTC TCCG	(GAA)1 3	150
RM202*	11	CAGATTGGAGATGAA GTCCTCC	CCAGCAAGCATGTCA ATGTA	(CT)30	150
RM224*	11	ATCGATCGATCTTCA CGAGG	TGCTATAAAAAGGCAT TCGGG	(AAG)8 (AG)13	157
<i>GT</i> exon1**	11	CTCGATTGCAATCCA CGTTC	TCGAACACGTAGCTG AAGTC	-	624
<i>Rc</i> Exon 1- 2***	7	GATCTCGATCATCCA CGAGC	ATGCGTGGATCAACA CACCG	-	990

\* The SSR primers were derived from (Chen et al., 2017), \*\* *GT* gene primers were designed in exon 1 from the XM015777298.2 sequence, \*\*\**Rc* gene primers were designed in exon 1-exon 2, based on the sequence accession KX549256. Chr is chromosome number.

Table S2. The scoring data used to construct the phylogenetic tree based on the SSR pattern and *GT* and *Rc* gene sequences.

SSR Markers- size	Sample					SSR Markers- size	Sample				
	WRE J	RRE J	BRE J	BRC J	BRW J		WRE J	RRE J	BRE J	BRC J	BRW J
RM1369- 100	-	-	-	1	1	RM250- 200	-	2	-	-	-
RM1369- 120	1	1	1	-	-	RM251- 250	-	-	-	2	-
RM223-150	-	-	-	-	-	RM251- 500	-	-	-	2	-
RM223-200	0	0	0	0	0	RM251- 800	-	-	2	-	-
RM223-300	1	1	-	-	-	RM318- 150	0	0	0	0	0
RM6364- 150	2	-	-	-	-	RM318- 200	-	1	-	-	1
RM6364- 180	0	0	0	0	0	RM224- 250	1	1	1	-	1
RM6364- 200	-	1	1	1	-	RM224- 180	0	0	0	0	0
RM6364- 300	1	1	-	-	-	RM202- 200	0	0	0	0	0

SSR Markers- size	Sample					SSR Markers- size	Sample				
	WRE J	RRE J	BRE J	BRC J	BRW J		WRE J	RRE J	BRE J	BRC J	BRW J
RM6364- 350	-	-	-	-	2	RM202- 300	-	1	1	1	1
RM250-180	0	0	0	0	0	RM202- 350	-	2	-	-	-

Nucleotide number of GT	Sample					Nucleotide number of GT	Sample				
	WREJ	RREJ	BREJ	BRCJ	BRWJ		WREJ	RREJ	BREJ	BRCJ	BRWJ
130	0	0	0	0	2	454	1	1	1	1	1
135	0	0	0	0	2	479	1	1	1	1	1
144	0	0	0	0	2	499	0	0	0	0	2
148	0	0	0	0	2	543	1	1	1	1	1
150	0	0	0	0	2	545	0	2	0	0	0
162	0	0	0	0	2	546	0	2	0	0	0
174	0	0	0	0	2	563	0	2	0	0	0
207	0	0	0	0	2	577	0	2	0	0	0
264	0	0	0	0	2	580	0	2	0	0	0
297	0	0	0	0	2	586	0	2	0	0	0
305	1	1	1	1	1	650	1	1	1	1	1
328	1	1	1	1	1	667	1	1	1	1	1
366	0	0	0	0	2	695	0	0	0	0	2
377	0	0	0	0	2						

Nucleotide number of <i>Rc</i>	Sample					Nucleotide number of <i>Rc</i>	Sample				
	WREJ	RREJ	BREJ	BRCJ	BRWJ		WREJ	RREJ	BREJ	BRCJ	BRWJ
1781	1	0	0	1	0	2352	2	0	0	0	0
1782	0	0	0	2	0	2366	2	0	0	0	0
1784	2	0	0	0	0	2373	2	0	0	0	0
1786	2	0	0	0	0	2382	0	2	0	0	0
1794	2	0	0	0	0	2385	2	0	0	0	0
1796	2	0	0	0	0	2391	1	1	0	0	0
1797	1	1	1	1	1	2394	2	0	0	0	0
1799	2	0	0	0	0	2398	2	0	0	0	0
1800	0	0	0	0	2	2399	2	0	0	0	0
1801	0	2	0	0	0	2400	1	1	0	0	0
1809	2	0	0	0	0	2402	2	0	0	0	0
1810	2	0	0	0	0	2403	2	0	0	0	0
1817	2	0	0	0	0	2404	2	0	0	0	0
1819	2	0	0	0	0	2408	2	0	0	0	0
1822	2	0	0	0	0	2415	2	0	0	0	0
1843	2	0	0	0	0	2416	2	0	0	0	0
1844	2	0	0	0	0	2417	2	0	0	0	0
1856	2	0	0	0	0	2419	2	0	0	0	0
2210	2	0	0	0	0	2420	2	0	0	0	0
2241	2	0	0	0	0	2426	2	0	0	0	0
2277	2	0	0	0	0	2430	2	0	0	0	0
2299	2	0	0	0	0	2431	2	0	0	0	0
2344	2	0	0	0	0	2433	2	0	0	0	0
2346	2	0	0	0	0	2442	2	0	0	0	0
2349	2	0	0	0	0	2445	2	0	0	0	0
2351	2	0	0	0	0						

(-) The band was not detected in the sample, 0 for conserved SSR pattern or sequence, 1 for similarity >variability and 2 for similarity< variability.