

Supplementary data

Genetic diversity and DNA fingerprinting of indigenous and exotic mandarin genotypes in India using SSR markers

Gurteg Singh*, Pushpinder Singh Aulakh, Navraj Kaur Sarao, Gurupkar Singh Sidhu and Harinder Singh Rattanpal

Supplementary Table1. Primer sequence and other characteristics of sixty SSR markers used in characterization of mandarin genotypes

S. No.	Primer	Sequence 5' to 3'	GC content (%)	Melting temperature (°C)	Annealing temperature (°C)
1	CiBE0447-F	CACAAAGAGAGTAACCCACAA	42.8	55.9	54
	CiBE0447-R	CGTCAAGAAGAGAGAATGATG	42.8	55.9	
2	CiBE0733-F	TCTAAGTTGGTTGGGAGTT	42.1	52.3	49
	CiBE0733-R	TCTTTATGATTGTATTTGATGGA	26	51.7	
3	CiBE1116-F	TAAACCACTGTCACCGCA	50	53.7	52
	CiBE1116-R	AGGAAAGAAAGAAGACGAAGT	38	53.9	
4	CiBE2843-F	TTGAGAGAGGTAGCCATT	44.4	51.4	50
	CiBE2843-R	GCTTTAGACCAACACATACAGA	40.9	56.5	
5	CiBE3298-F	TTCTCCTCCACTACACAACAC	47.6	57.8	51
	CiBE3298-R	CTTGAATCCCATTTC AAC	42.1	52.3	
6	CiBE3397-F	AGGCGGAGATAGAGAAGTAAA	42.8	55.9	54
	CiBE3397-R	ATCACAACACTACGAATACCCAC	42.8	55.9	
7	CiBE3936-F	GTAATGATAGCCGTTGGTCTT	38	55.9	52
	CiBE3936-R	TATGAGATGCCTTGATTGCT	47.6	53.9	
8	CiBE3966-F	CTCTCCTCCATTATCTTCTCC	31.8	57.8	51
	CiBE3966-R	TTCTTTACCTTGATTCTTCTCT	44.4	52.76	
9	CiBE4225-F	GTGGAGCGATTTGACATT	45	51.4	50
	CiBE4225-R	CTCACAGCAACAACAAC	45.4	55.2	
10	CiBE4721-F	TGGATGGGATGGAATGGTTCTT	47.4	58.3	56
	CiBE4721-R	TGCTTGGTTTGGCTTGACTCT	47.6	57.8	
11	CiBE4796-F	GATGAGAACGCTGATGCT	50	53.7	51
	CiBE4796-R	TTCAACCACACTGACGATAA	40	53.2	
12	CiBE5156a-F	GCAGATGTATGGATTGGATT	40	53.2	51
	CiBE5156a-R	AGTGGTTGTGATTATGGTTGA	38	53.9	
13	CiBE5171-F	TTACCCTTGCCGTTTCCGTG	55	59.3	57
	CiBE5171-R	CGTGATTCTGATTGGTTGCTGG	50	60.3	
14	CiBE5720-F	TGAAGGACACTGATGTAGGAC	47.6	57.8	51
	CiBE5720-R	AAACTTGTTGGGAAGGAG	50	53.7	
15	CiBE5866-F	ATCTCGCTCACTTCAGAGTT	45	55.2	53
	CiBE5866-R	GGATTATTGTGTTTCCTCCTC	42.8	55.9	
16	CiBE6006-F	AATGCTACCTTATTCTCATCAA	31.8	52.7	51
	CiBE6006-R	GCACTTTATTTGCCGTTTACT	38	53.9	
17	CiBE6092-F	CGGACAAGGAGATGAAGATAG	47.6	57.8	52
	CiBE6092-R	TTCTAACAGCACCAAGCAG	47.3	54.4	
18	CiBE6256-F	TGTATTTATTTCTGACTACGACC	34.7	55.3	50
	CiBE6256-R	ATGCGTTTGGTGTGTGTT	44.4	51.4	
19	CCSM40-F	ACA AGA GTC GCA ACA ATC	44.4	51.4	50
	CCSM40-R	GAC AAC AGT GGC AAT ACC	50	53.7	
20	CCSM170-F	GCC AAT CAG CTA AGA GGG TT	50	57.3	55
	CCSM170-R	GGA TCT GAG ATG CTC CTG CT	56.5	59.9	
21	CCSM201-F	AGC TAG GGT TCC CCA GAT TC	55	59.3	55

	CCSM201-R	GGC CTC CAA GTA CAA CCA AA	50	57.3	
22	CCSM204-F	CTG GCT CAG CTC TGC TCA TT	55	59.3	55
	CCSM204-R	ATG ACA TAA TCG TGC CCT GC	50	57.3	
23	CCSM205-F	CGT TTA TGG CTC TGG TGG AT	50	57.3	55
	CCSM205-R	AAT AGC TCC ACT GCT GCC AC	55	59.3	
24	CCSM 06-F	ATCTGTGTGAGGACTGAA	44.4	51.4	50
	CCSM 06-R	CCTCTATTAATGTGCCTG	44.4	51.4	
25	CCSM 09-F	GACTGGATTAGAGTTCTCTG	45	55.2	51
	CCSM 09-R	ATGGATGTGTTATCTCACTC	40	53.2	
26	CCSM 40-F	ACAAGAGTCGCAACAATC	44.4	51.4	50
	CCSM 40-R	GACAACAGTGGCAATACC	50	53.7	
27	CCSM 68-F	ACATGGACAGGACAATAAG	45	55.2	51
	CCSM 68-R	CACTTCTGCCTTGCTATG	50	53.7	
28	CCSM 69-F	GCAAGGAGTTAGTAATGTGG	45	55.2	53
	CCSM 69-R	CCATTCCTGAGACAGTGAAG	50	57.3	
29	CCSM 70-F	GCAAGGAGTTAGTAATGTGG	45	55.2	52
	CCSM 70-R	CTCGTGTGCAAGTTGCAT	50	53.7	
30	CCSM 77-F	TATCCAACCATGTGTGTCCATA	40.9	56.7	51
	CCSM 77-R	CACTAGGTCACCATTAATTG	40	53.2	
31	CCSM 95-F	AAGAAGCTCTCACCTCTC	50	53.7	50
	CCSM 95-R	TAACGTCTGAACGAACTG	44.4	51.4	
32	CCSM 111-F	TGATACATAATATGGGATAG	30	49.1	47
	CCSM 111-R	TTAGTGATTTCGTGGAGC	47	50.3	
33	CCSM 112-F	ATGCCATTATGTGTGTG	41.1	47.9	46
	CCSM 112-R	CAGACCTGAACATAACTC	44.4	51.4	
34	CCSM 156-F	GTCTCTGTTGTGTGTCGGTT	50	57.3	51
	CCSM 156-R	ACGAAGTGAAGTGTGTAATG	40	53.2	
35	AC01-F	TTTGACATCAACATAAAAACAAG AAA	24	53.1	49
	AC01-R	TTTTAAAATCCCTGACCAGA	35	51.1	
36	AG14-F	AAAGGGAAAGCCCTAATCTCA	42.8	55.9	54
	AG14-R	CTTCCTCTTGCGGAGTGTTC	55	59.3	
37	ATC09-F	TTCCTTATGTAATTGCTCTTTG	31.8	52.7	51
	ATC09-R	TGTGAGTGTTTGTGCGTGTG	50	57.3	
38	CAG01-F	AACACTCGCACCAAATCCTC	50	57.3	55
	CAG01-R	TAAATGGCAACCCAGCTTTG	47.6	57.8	
39	CAT 01-F	GCTTTCGATCCCTCCACATA	50	57.3	55
	CAT 01-R	GATCCCTACAATCCTTGGTCC	52.3	59.7	
40	CCT01-F	TCAACACCTCGAACAGAAGG	50	57.3	55
	CCT01-R	CCCACATGCTAGCACAAAGA	50	57.3	
41	CT02-F	ACGGTGCGTTTTGAGGTAAG	50	57.3	53
	CT02-R	TGACTGTTGGATTTGGGATG	45	55.2	
42	CT19-F	CGCCAAGCTTACCACTCACTAC	57.8	63.4	57
	CT19-R	GCCACGATTTGTAGGGGATAG	52.3	59.7	
43	CT21-F	CGAACTCATTAAGCCGAAAC	40.9	56.5	54
	CT21-R	CAACAACCACCACTCTCACG	55	59.3	
44	CTT01-F	TCAGACATTGAGTTGCTCG	47.3	54.4	52
	CTT01-R	TAACCACTTAGGCTTCGGCA	50	57.3	
45	GT03-F	GCCTTCTTGATTACCGGAC	50	57.3	53
	GT03-R	TGCTCCGAAC TTCATCATTG	45	55.2	
46	CMS4-F	CCTCAAACCTTCTCCAATCC	47.6	57.8	54
	CMS4-R	CTGTAAAGTACATGCATGTTGG	40.9	56.5	
47	CMS7-F	CAGGATGCTTGTGGTGATG	50	57.3	55
	CMS7-R	ACAGTGGATACAAACATGCTGC	45.4	58.3	
48	CMS 16-F	AAAGAAAAATGTTATGTGCATG	27.2	50.9	49
	CMS 16-R	GATGGAGTTTCTCTAGCTCCC	52.3	59.7	
49	CMS 17-F	CTGTGCTCTCAAAGCTCCG	57.8	58.7	56
	CMS 17-R	TCAGATTCAAGTCAATGGAGG	45.4	58.3	
50	CMS 26-F	TGATGTCTTGATCCACACTTCC	45.4	58.3	56
	CMS 26-R	ACTCAAAGCTCCGCTACAGTG	52.3	59.7	

51	CMS30-F	AACACCCCTTGGAGGGAG	61.1	58.2	56
	CMS30-R	GCTGTTCACACACACAACCC	55	59.3	
52	CMS31-F	CGTGCAGAGAAACTCAGATCC	52.3	59.7	52
	CMS31-R	GCTGAAAAAGATTCATTTTGCC	36.3	54.6	
53	CMS39-F	CTCAGCTCTCTGTCTCTCTCC	59	63.9	57
	CMS39-R	CTGGAGCAGGGTGACCTATC	60	61.4	
54	CMS46-F	TCAAACATCAGACGAAGCAA	40	53.2	50
	CMS46-R	TGAATCTTTTGCCGAATTTTG	33.3	52	
55	CMS47-F	GGATCCTCCACCATCTCGTA	55	59.3	53
	CMS47-R	TTCTTCTTCCATGCCGACTT	45	55.2	
56	458-F	CCCCCTCTTTTCTCTTCCA	50	57.3	55
	458-R	TTCTGGGCTGGTAGGTCAG	55	59.3	
57	571-F	TCGCCCTCCCCCTGAAATTA	55	59.3	57
	571-R	GAAAGCCTGGTGGGAGCAGA	60	61.4	
58	497-F	CGCAATTCAATTCCCTGTCT	45	55.2	53
	497-R	CGTCGAGCAACAAATCAAGA	45	55.2	
59	506-F	AGCGGAGGAAAAAGGAAAAG	45	55.2	53
	506-R	CATATGCCATCACCACCAA	45	55.2	
60	495-F	GGCCTTAAACCACCTTGACA	50	57.3	53
	495-R	TGAGGCTTTTGCTGTTGTTG	45	55.2	