Genetic homology between the CMS (A) and their alloplasmic maintainer (B) line in chilli pepper through SSR markers

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Abstract

The purpose of this study was to assess the genetic similarity between the CMS (A) and the maintainer (B) lines using 120 SSR markers. Almost all the amplified markers showed monomorphic bands between the CMS lines and corresponding B lines. Between CMS463D2A and CMS463D2B (alloplasmic maintainer line) and between CMS463L9A and CMS463L9B, polymorphic banding patterns were observed by a marker (Hpms 2-13) for chromosome 1. After eight cycles of backcrossing (BC_8F_1) and selection, the genome recovery of the recurrent parent in all the CMS lines was estimated to be 100%, except CMS463D2A and CMS463D2B, and between CMS463L9A and CMS463L9B where the recovery was 99.01%, and 98.9%, respectively. Similarly, for the fruit weight, fruit length, fruit width, and pericarp thickness, the paired *t*-test was non-significant for mean value of all the CMS A- and CMS B-lines except CMS4624A and CMS4624B for fruit length, and CMS4626A and CMS4626B for fruit width, where the differences were significant.

Key words: *Capsicum annuum*, CMS, Genetic similarity, SSR markers

Introduction

Chilli, also known as hot pepper, belongs to the genus *Capsicum* of which five species (*C. annuum* L., *C. chinense* Jacq., *C. frutescens* L., *C. baccatum* L. Ruiz. & Pavon, and *C. pubescens* Ruiz. & Pavon) are cultivated (Wei et al. 2019). *C. annuum* is the most widely domesticated species, both in the number of varieties grown as well as being the most commonly cultivated worldwide (Meena et al. 2018). The dry chilli productivity of India has increased by 62.34% from 1.54 tonnes ha^{-1} in 2010 to 2.5 tonnes ha^{-1} in 2017 (FAO 2017). Cultivation of high yielding hybrids has contributed about 50% to the increased productivity. Commercial hybrid chilli seeds are produced either by hand-emasculation and pollination or by exploiting male sterility (MS) systems including CMS lines (Jindal et al. 2020). The use of cytoplasmic male sterility (CMS) reduces hybrid seed costs by up to 50% (Yang et al. 2008). CMS also ensures purity of the F_1 seed as self-pollination is prevented due to the sterile pollen. But the CMS lines in chilli pepper has been influenced by the environmental factors especially the low temperature (Peterson 1958), multi allelic inheritance (Min et al. 2009) and the modifier genes (Lee et al. 2008). Stable CMS lines could be established by selecting maintainer plants tolerant to temperature fluctuations, the incorporation of seedling markers for the early elimination of progenies resulting from self-pollination, and sampling of environmental conditions that produced the highest level of MS (Lee 2001). Recently, we have transferred S-cytoplasm from a source described in Gniffke et al. (2009) into elite breeding lines with diverse genetic backgrounds. The lines have been regarded as completely male sterile, temperature stable and are suitable for hybrid development (Meena et al. 2018). Backcross breeding is a common method of transferring a target trait and the aim of repeated backcrossing with the recipient parent is to increase the contribution of the recurrent parent genome in the progeny. Hence, the purpose of this study was to ascertain whether the genome of the recurrent parent has been fully recovered after eight cycles of backcrossing (BC_8F_1) and selection.

Materials and Methods

Plant materials and SSR markers: The experiment involved 13 CMS (A-) lines and their alloplasmic maintainer (B-) lines of chilli pepper. The CMS source 'CCA 4261' was introduced from the World Vegetable Center, Taiwan, and it was transferred to the locally adapted elite chilli breeding lines (Meena et al. 2018). The CMS and maintainer lines were raised at the Vegetable

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Research Farm, PAU, Ludhiana. To assess the genome recovery of the recurrent parent (after eight cycles of backcrossing and selection) in the following CMS lines, the molecular analysis was conducted at the Molecular Breeding Laboratory of the Department of Vegetable Science, PAU, Ludhiana, India. The screening of the A-lines and the maintainer B-lines was carried out for identification of polymorphism. The DNA from 13 CMS A-lines and their maintainer B-lines were subjected to PCR amplification with the selected 120 PCR based SSR markers, 10 from each linkage group (Table 1). The SSR primers used for this study were selected from the linkage maps developed by Lee et al. (2004), Minamiyama et al. (2006), Yi et al. (2006) and Ince et al. (2010).

Evaluation for fruit traits: Thirteen CMS A- and CMS B- lines were grown to evaluate for important fruit traits during the year 2017-18. The lines were sown in finely-prepared nursery beds of 0.15 m height and 1.0 m wide. Seed treated with Captan @ 2-3 g.kg^{-1} of seed were sown on 30th September, 2017 at a depth of 5 cm. The seedlings were transplanted to the field on 03rd November, 2017 on ridges at a spacing of 75 cm between rows × 45 cm among plants. The experiment was laid out in randomized complete block design (RCBD) with two replications. There were ten plants of each genotype on a ridge. Cultural practices such as fertilization, irrigation, weed control, disease and insect-pest control were performed as per the Package of Practices for Cultivation of Vegetable Crops (Anonymous 2017). To assess the fruit trait similarity between the CMS A- and B- lines of chilli, numbers of quantitative traits were studied including fruit weight (g), fruit length (cm), fruit width (mm), and pericarp thickness (mm).

Statistical analysis: Paired *t*-test was used to compare the means of CMS A- and B-lines following SPSS software (Version 22.0).

Results and Discussion

The genetic similarity or homology between the thirteen CMS A- and their corresponding CMS B-lines was examined by using SSR markers. Out of 120 markers screened, 102 markers (85.0%) were amplified in CMS463D2A (both A and B-), 95 markers (79.1%) in CMS463L3 and CMS463L9 (both A and B-), 101 markers (84.1%) in CMS463L11 (both A and B-), 97 markers (80.8%) in CMS463D13 and CMS463D14 (both A and B-), 66 markers (55.0%) in CMS4622 (both A and B-), 82 markers (68.3%) in CMS4623 (both A and B-), 89 markers (74.1%) in CMS4624 and CMS4626 (both A and B-), 77 markers (64.1%) in CMS4627 (both A and B-), and 76 markers (63.3%) in CMS46213 and

CMS4611 (both A and B-). All the amplified markers showed monomorphic bands between the CMS A- and the CMS B- lines on superfine 2.5% agarose gel (Figure 1). Between CMS463D2A and CMS463D2B (alloplasmic maintainer line) and between CMS463L3A and CMS463L3B, polymorphic banding patterns were observed by a marker (Hpms 2-13) for chromosome 1, but the percentage of marker which showed the polymorphic bands, were negligible. The probable reasons could be either some genetic drag between lines or due to the technological limitations. After eight cycles of backcrossing (BC$_8$F$_1$) and selection, the genome recovery of the recurrent parent in all the lines was estimated to be 100%, except CMS463D2A and CMS463D2B (alloplasmic maintainer line) and between CMS463L3A and CMS463L3B where the recovery was 99.01%, and 98.9%, respectively, measured by percentage of the monomorphic marker ratios. These results are in agreement with Meena et al. (2019), who also assessed the genetic similarity between three selected CMS lines in BC$_5$F$_1$ generation and concluded that the genome recovery of the recurrent parent in three selected A and B line pairs was more than 96 percent. The lines are, therefore, genetically stable and are ready for utilization in hybrid breeding programs.

Horticultural performance of CMS A and B lines: The traits like fruit weight, fruit length, fruit width, and pericarp thickness directly contribute towards total yield, among these the fruit weight and length has a key role in acceptance of produce by the consumer. The agronomic traits of CMS A- and B-lines were measured and compared by *t*-test in BC$_8$F$_1$ generation. The observed results for fruit weight (g), fruit length (cm), fruit width (mm), and pericarp thickness (mm) on CMS A- and B-lines showed non-significant as well as significant differences (Table 2). For fruit weight, fruit length, fruit width, and pericarp thickness, the paired *t*-test was non-significant for mean value of all the CMS lines A- and CMS B- lines except CMS4624A and CMS4624B for fruit length, and CMS4626A and CMS4626B for fruit width, where the difference was significant. The reasons for such significant difference between the lines may be due to the temperature fluctuation because it has been reported that CMS system in chilli pepper highly sensitive to temperature (Meena et al. 2018). The results showed that performance of CMS A- and CMS B-lines were statistically at par. The average fruit weight ranged from 2.6 g (CMS4611A) to 7.3 g (CMS4626A) and 2.55 g (CMS4611B) to 6.2 g (CMS463D13B) in A- and B-lines, respectively. In CMS A-line the average fruit length ranged from 5.65 cm in CMS4611A to 10.55 cm in CMS4623A, whereas in CMS B-line the average fruit

Table 1: List of SSR primer pairs used in the present study to check genetic similarity between CMS A- and B-lines

S. No.	Marker	Forward sequence	Reverse sequence	Fragment size (bp)	Linkage group
1	AA840689	GACAACATAGGCGGACCTTTGG	TGCTTTAGGTCTACGTCCTTGCAC	267	3
2	AA840692	TGGAAGTGATTACTGGAAACCATGC	GGGGTTTAGTCATGGAATCTTTTGC	202	3
3	asu 7	GTGTCTTCCCTCCTTCACAGTGCTC	TCTCTCTGTTTCTTATGTTTTGCGG	-	6
4	BD 76366	AAAACTCCAAACTACCCCTGG	TTAAGCGTAGCGCTTGTGTG	330	2
5	BM 59622	CGTCTTTCACTTGTCTTTTGTTC	AGTGGGTTCACTGACTTGGG	90	3
6	BM 061910	ATTGTGATAGCAACCCCTGG	CACAGATGAGGGCACAAATG	292	3
7	BM 64867	TCTGGGAATTTTGGAACTGC	TCCAGTTTTGATCATCTCCAAC	138	2
8	BM 67271	GTATGCTGCAACCATCGTTG	ATTGGTTTGGGGAGACACAGC	202	8
9	CA 514621	GTCGAACAAAATGGGGTTTG	GCTGGAGAGTGCTGGTGG	216	2
10	CA 515275	CTCTGCCCTCCTCAACCC	AAAATATGGTCGGAGATCCG	100	12
11	CA 515649	TCTCCAATTTCCATTCGGAG	TAATCGCATTTGCGAACTTG	190	2
12	CA 516334	ACCCACCTTCATCAACAACC	ATTTGTGGCTTTTCGAAACG	248	6
13	CA 516439	GACAGTCTTTCAAGAACTAGAGAGAG	TGGAGCAAACACAGCAGAAC	158	10
14	CA 517699	ACGCCAAGAAAATCATCTCC	CCATTGCTGAAGAAAATGGG	147	3
15	CA 523558	AATCCTCCAAATCCACCCTC	ATTCGATTGCTTGCTCCTTG	176	6
16	CA 526211	TTGGGGACTTCACGTCTCTC	TTGATGATAAATCCTCCCCC	175	8
17	CA 847460	ACGAGGCGCCCTCTCTC	GAGTCCAAACTGAAGCTGCC	178	8
18	CAMS-024	TGTTGAGGCTTGGGAAAAAC	CAAGATAATGGGTAGAAAGGCAAC	219	8
19	CAMS-065	CCAGTCTCATCCAGCAGACA	CATATGCTGCTCCTGCATTC	213	2
20	CAMS-072	CCCGCGAAATCAAGGTAAT	AAAGCTATTGCTACTGGGTTCG	153	5
21	CAMS-090	TCGCTCAAAGCACATCAAAG	CTTGATTGTTCTTCCACTGCTG	243	8
22	CAMS-095	CGCTAGCATGACACTCAAGG	AAACGGCAAGGCTACACATC	228	5
23	CAMS-122	CATCCACGTGCATAGTCAGG	TTCTAAGTGTTGAAATTATGGGATTT	178	5
24	CAMS-163	TCCATATAGCCCGTGTGTGA	GCGTGGGAATACAATGCTAGA	250	5
25	CAMS-177	ATTCTCTACCCCTGCCTGTG	CTCAGGAGATGTCCCACGAT	229	2
26	CAMS-190	TTTCTGCAGTGTTACCAATATTTCA	CCCATGGGTCCTACCTCAG	212	5
27	CAMS-199	CCCTACCTCGGCATGTGATA	TGCATTGCATGGGGATATAA	188	5
28	CAMS-207-2	CTCACGAGCCACTTGAACAC	GCCTTGTTTCCTATCCCAAC	243	5
29	CAMS-301	CTGTCCATGCTTGTGATGCT	TGATTTGTGCCTCGTTTGAG	180	8
30	CAMS-309	GAAAATCGACCCGTTTTGAA	TCAATTCGGACAAAATTAGCAA	235	9
31	CAMS-311	GGTGCGCTAGAGATGGAGAG	TTTGAGTGTTCGGGGACTGGT	234	6
32	CAMS-330	GGCTACCGCCTTCTGACTTA	TTCGTATCTGGGGTGTCAAA	208	4
33	CAMS-336	GGTGGAAACTTGCTTGGAGA	CCCAGAACCATCCACCTACT	157	3
34	CAMS-340	TTTATGCCCATTCACAAAATAA	GGACGAATTCACCGAGTGC	250	10
35	CAMS-361	TTGGTGTGGTTAGGGGAGAG	GGCGTTCGAACTTGTGAAAT	207	4
36	CAMS-373	GGTTGATGGTCCATGTTCAA	CCTCCTACCCTATCCCCAAG	230	12
37	CAMS-405	TTCTTGGGTCCCACACTTTC	AGGTTGAAAGGAGGGCAATA	241	11
38	CAMS-420	CAGCGTTCTATCGTCTCAAATG	TTGACAAACCAGAAATTGATCG	200	5
39	CAMS-456	ATGGAGCTGGGGCTAAAAAT	GCTCAGCAAATTGAGGAGAAG	153	1
40	CAMS-460	CCTTTCACTTCAGCCCACAT	ACCATCCGCTAAGACGAGAA	215	7
41	CAMS-492	GTTCAAACACTTCCCCCTCA	TGTCATCGTTGGTCGTTACC	250	12
42	CAMS493	TCGATGACGAAAAAGTGTGAA	AGGGCAAAAGACCCATTCTT	223-225	8
43	CAMS-494	GGTAGGTGAGGACCCACAGA	AACTATACCCCCGCTGCTCT	247	4
44	CAMS-606	GACTAGTCCCCGTTCAACCA	TTTGCGAGAAGATGCTTCAG	208	7
45	CAMS-647	CGGATTCGGTTGAGTCGATA	GTGCTTTGGTTCGGTCTTTC	221	3
46	CAMS-655-2	CCTTGCTGCTACCTATTGAAGA	TCCAATCGTCGATATGTTTGTT	224	4
47	CAMS-668-2	ATCGTCCATTTGTGGGAAAA	TGTGGTCGGAAATAGGAAGAA	158	10
48	CAMS-679	TTTGCATGTTTTACCCATTCC	ATGTGAAACACATAGGTAGCACTGA	200	1
49	CAMS-826	CTTGATCTCAAGAACCAGCTACAA	TGTACATTGAAGACACGGAAGAA	244	8
50	CAMS-838	CCAGGATGGTGTTAAGGGTTT	GTCGCATCAATGAGCATAGG	229	6
51	CAMS-844	GCAAAGAAAAAGAAAAGCCTGA	CTGCAACTGCTGCTTCATTC	223	1
52	CAMS-855	AAGTGTCAAGGAAGGGGACA	CCTAACCACCCCCAAAAGTT	243	8
53	CAMS-876	TGTGTCTGAAGCGGAACAAA	AAGCAGTGAGCGACGAAGA	243	9
54	CAMS-880	GAGCCAAGAAAAAGGTGGAA	CAACTCATCGTTCAACAACACA	237	6
55	GPMS 93	ATCCTTGGCGTATTTTGCAC	TTCACTTTGCACACAGGCTT	202-268	3
56	GPMS 100	TCCATACGGTTGGAGGAGAG	ACTATGCTCTGCTGTGCCCT	141-169	2
57	GPMS 103	TGGCAGTTGCAATATCAATCTC	AAACCTTGTCACGCATCCAT	134-149	7
58	GPMS 109	ATCTATGCATGCCATCACCG	TGGGCTAAAGGCCATGTTAC	165-183	10
59	GPMS 156	GATATAGAACCACACAAGACTGGG	TATGGCTCTTGCGGGAATAC	228-232	10
60	GPMS 159	AAGAACATGAGGAACTTTAACCATG	TTCACCCTTCTCCGACTCC	281-317	10
61	GPMS 164	AATGAAATCAATCGGGCTTG	ACCTCGCACCAATTCTTTTG	230-259	12
62	GPMS 169	TCGAACAAATGGGTCATGTG	GATGAGGGTCCTGTGCTACC	176-220	2

Contd.. Table 1

S. No.	Marker	Forward sequence	Reverse sequence	Fragment size (bp)	Linkage group
63	GPMS 171	TCCACCACAATATTTCGAAGG	TGGCTGTCCAACACTGTGAG	288-346	9
64	GPMS 183	GAGCTTCATAGATGATATGCAAGAG	TCCCAAGCTAACCCATTTACTG	195-227	12
65	GPMS 187	TTTAGAATCCTCACCACGGG	TCAATGCACAAACTTTAATTTGC	219-246	6
66	GPMS 191	AGGTCAGCGACGGCAAC	ATTTTAGGAGCCGACCTTCC	261-286	1
67	Hpms 1–139	CCAACAGTAGGACCCGAAAATCC	ATGAAGGCTACTGCTGCGATCC	299	1
68	Hpms 1–148	GGCGGAGAAGAACTAGACGATTAGC	CCACCCAATCCACATAGACG	197	1
69	Hpms 1–155	ACGAGGCCCAAGCTGTTATGTC	TTGTCCCGACTCTCCATTGACC	207	1
70	Hpms 1-165	GGCTATTTCCGACAAACCCTCAG	CCATTGGTGTTTTCACTGTTGTG	213	4
71	Hpms 1–172	GGGTTTGCATGATCTAAGCATTTT	CGCTGGAATGCATTGTCAAAGA	344	11
72	Hpms 1–173	TGCTGGGAAAGATCTCAAAAGG	ATCAAGGAAGCAAACCAATGC	163	3
73	Hpms 1–227	CGTGGCTTCAAGTATGGACTGC	GGGGCGGAACTTTTCTTATCC	237	7
74	Hpms 1–274	TCCCAGACCCCTCGTGATAG	TCCTGCTCCTTCCACAACTG	174	7
75	Hpms 1–281	TGAGGCAGTGGTATGGTCTGC	CCCGAGTTCGTCTGCCAATAG	132	1
76	Hpms 2–2h	GCAAGGATGCTTAGTTGGGTGTC	TCCCAAAATTACCTTGCAGCAC	146	11
77	Hpms 2–13	TCACCTCATAAGGGCTTATCAATC	TCCTTAACCTTACGAAACCTTGG	259	1
78	Hpms 2–21	TTTTTCAATTGATGCATGACCGATA	CATGTCATTTTGTCATTGATTTGG	295	10
79	Hpms 2–23	CCCTCGGCTCAGGATAAATACC	CCCCAGACTCCCACTTTGTG	126	5
80	Hpms 2–24	TCGTATTGGCTTGTGATTTACCG	TTGAATCGAATACCCGCAGGAG	205	9
81	HpmsAT2–20	TGCACTGTCTTGTGTTAAAATGACG	AAAATTGCACAAATATGGCTGCTG	148	6
82	HpmsE003	TTTCTGCAATTCCCCTTGTTCA	CAGCAGAGCCTTCAGTAGCAGC	164	2
83	HpmsE006	GCTGACCGTTTTCGTTTTGGG	CAAAATTCAACCGCACCAACA	243	4
84	HpmsE012	AAACGCTGAAAAAGGCGTTGAC	TGCACCAACTTCTTCCATGCAC	208	11
85	HpmsE020	CCCCCGAGAGGAACAGAATCAT	TTCCATTTTGGTCCAGCTACCA	200	7
86	HpmsE024	CGAGCCTAACCACCCAAATCAG	AAGGGAACGGAGGGACGACTAC	212	12
87	HpmsE025	TGAGCATCCCGTTATCTCAAATCA	CCCAATTCTTCAGGCAATCTCC	213	9
88	HpmsE031	CCCTAAATCAACCCCAAATTCAA	CCCCCATTACCTGACTGCAAAA	167	10
89	HpmsE049	CACTCCAACAGCAGCAGCAAAC	CCTTGCCGATGTTGAAGCTTTT	247	4
90	HpmsE050	CCCCACCTTCCATCATCAGCTA	TGGTAATTCTGCGGTCGATTCC	247	3
91	HpmsE051	TGGCCAGCTTCACACAGAGGTA	TGTCACAATATTGGAGGCCAGAA	262	9
92	HpmsE054	GCCACCCCTCACCTCTCTCTCT	GTTGTTCGCTGGGCTCTTTCTC	219	12
93	HpmsE056	TCCGATTCAATCACTCCCAACA	GTATCGGCAATACGGGCAGAAG	214	1
94	HpmsE061	CCCAAGAAAGAAGTTGGGAATGG	TTCGACGAGCTTGGAAGGTGAT	249	11
95	HpmsE064	CCCTCCTTTTACCTCGTCAAAAA	ATGCCAAGGAGCAATGAGAACC	221	12
96	HpmsE065	TGAAATAGGCCAATCCCTTTGC	ATTCCCTGGGATTCCTGCATTA	199	10
97	HpmsE068	TGTTCCTTTTGTTGTTACCTTTTG	CGTCTAGGAATGGAAGAAGAGC	232	7
98	HpmsE071	CCCCTTCTCCTCCCTCATAAGC	TTCCATGATGTTACCGGAGCAA	188	4
99	HpmsE082	TTTTTCCCACTTTGCCCTTTCC	CAACCCAAGAAAACCCATTGGA	232	9
100	HpmsE084	GCCAGAAGATCCATACTCTCATCA	GGAATGAGCAAAAACAAGAGTCC	220	9
101	HpmsE092	CTCTGGCCCTTTTGTTCTTTCTTG	ACGCCTATTGCGAATTTCAGGA	180	11
102	HpmsE094	CCAGTTGAGAGCTGCTGCAAAA	CACCAACAAAACAAAGGCCACA	241	12
103	HpmsE095	TGCTTAAACCCACTTGCGTCTTG	TCTGCACAGCACAAGACATTCG	184	7
104	HpmsE096	CGGGTCAAACAAAAACCGAAGT	GCTTGTGGTTGAGCTCGCTCTT	237	10
105	HpmsE103	ATTGTGACCCGACTCCTCCAT	TGCTAATGGTGCTAATGCGGTA	177	7
106	HpmsE105	CAACCAAATTGAAACCCCTCCA	CGTCCACCTAATAATGCGACCA	238	12
107	HpmsE113	CCCTAAAGCTCGAGAAATTGAAGC	GAATGCTGTTGCTGGGGTTGTT	225	6
108	HpmsE114	GGTGAGGGAGGTGTGAGCAAA	GATCCACATACGCCATCACTGC	190	7
109	HpmsE116	CATCTCTCCGTTGAATCTATTTCC	ACGGTCATCCATTAGAACCGTA	189	5
110	HpmsE120	GGGGGAGGAAGAGAAGAAGTCG	CCGGACTTTACGAGCACAACCT	209	6
111	HpmsE124	TCGTTAGCAGCAACAACAACAA	CTGCTTCCTGTACATGGCTGTC	227	11
112	HpmsE125	AGGGAGTTCACGCCATTTTTGA	GCGATAACCCACCGGAGAAAAT	204	11
113	HpmsE132	ACATCCACAGCAAAAGGAAAAA	GTGGAAAGTTTGGTGGATCAGA	197	11
114	HpmsE140	GGCTCTGCCTCTCGTCTCCTC	AGGATCAGAAGCAGCGCATTTC	225	4
115	HpmsE141	TCCCAACAACTCAAATGGCTTC	TGGAGGTGCCCTTCTGGTAAAG	206	2
116	HpmsE143	CCATTCAGCTAGGGTTCAGTCCA	CGACCAAATCGAATCTTCGTGA	107	9
117	HpmsE145	TGAGGGTATTTTCGTCATTTCAC	GAAAGCGGAAAACATTAAGAGTCA	222	8
118	HpmsE146	CCCTTCTTCCTTTCCACCATCA	AGGCGTGAAAGGGTTA TGAGGA	227	4
119	HpmsE149	CGGAAACTAAACACACTTTCTCTC	GACTGGACGCCAGTTTGATT	198	11
120	HpmsE150	CCCTCTTCCCCGACTCTCTCTT	AAGCCAATGACTGCATGACCAC	219	9

Table 2: Comparison of CMS A- and CMS B- lines of chilli pepper for fruit traits by paired *t*- test

Pairs	CMS lines	Fruit weight (g)	Fruit length (cm)	Fruit width (mm)	Pericarp thickness (mm)
1	CMS4611A	2.6[ns]	5.65[ns]	9.55[ns]	0.61[ns]
	CMS4611B	2.55[ns]	6.86[ns]	8.72[ns]	1.08[ns]
2	CMS463D2A	6[ns]	7.51[ns]	13.33[ns]	1.78[ns]
	CMS463D2B	4.55[ns]	7.06[ns]	11.89[ns]	1.46[ns]
3	CMS463D13A	6.85[ns]	8.85[ns]	14.19[ns]	1.61[ns]
	CMS463D13B	6.2[ns]	8.68[ns]	13.5[ns]	1.65[ns]
4	CMS463D14A	5.8[ns]	7.77[ns]	12.58[ns]	1.8[ns]
	CMS463D14B	5.9[ns]	8.46[ns]	13.80[ns]	1.72[ns]
5	CMS463L3A	4.9[ns]	10.05[ns]	12.83[ns]	1.52[ns]
	CMS463L3B	5.4[ns]	9.94[ns]	12.50[ns]	1.40[ns]
6	CMS463L9A	5.1[ns]	6.9[ns]	10.73[ns]	1.78[ns]
	CMS463L9B	4[ns]	7.68[ns]	11.1[ns]	1.27[ns]
7	CMS463L11A	4.27[ns]	9.02[ns]	11.9[ns]	1.4[ns]
	CMS463L11B	3.95[ns]	8.18[ns]	11.40[ns]	1.25[ns]
8	CMS4622A	4.25[ns]	7.76[ns]	11.04[ns]	1.42[ns]
	CMS4622B	4.2[ns]	8.06[ns]	11.26[ns]	1.36[ns]
9	CMS4623A	5.65[ns]	10.55[ns]	11.81[ns]	1.28[ns]
	CMS4623B	3.45[ns]	8.98[ns]	10.17[ns]	1.47[ns]
10	CMS4624A	3.4[ns]	6.87[*]	11.48[ns]	1.26[ns]
	CMS4624B	4.35[ns]	7.94[*]	11.59[ns]	1.36[ns]
11	CMS4626A	7.3[ns]	9.01[ns]	15.2[*]	2.0[ns]
	CMS4626B	5.75[ns]	7.62[ns]	12.56[*]	1.64[ns]
12	CMS4627A	4.67[ns]	8.5[ns]	12.21[ns]	1.64[ns]
	CMS4627B	4.25[ns]	8.26[ns]	11.86[ns]	1.31[ns]
13	CMS46213A	6.02[ns]	9.15[ns]	12.3[ns]	1.42[ns]
	CMS46213B	5.55[ns]	8.96[ns]	11.99[ns]	1.18[ns]

*Significant at the 5% level of significance (*p*<0.05); ns: non-significant at 5%level of significance

length varied from 6.86 cm (CMS4611B) to 9.94 cm (CMS463L3B). Meena et al. (2018) also recorded varied fruit length and fruit weight among the CMS A- lines ranging from 4.28 to 8.29 cm and 2.81 to 7.48 g, respectively.

In our study, the average fruit width ranged from 9.55 mm (CMS4611A) to 15.2 mm (CMS4626A) and from 8.72 mm (CMS4611B) to 13.8 mm (CMS463D14B) in CMS A- and B-line, respectively. In a study of Singh et al. (2014), the fruit width of hot pepper genotypes varied from 0.91 cm to 1.44 cm. In CMS A-line pericarp thickness ranged from 0.61 mm (CMS4611A) to 2.0

Figure 1: SSR markers showing genetic similarity between the A and B- lines
Where, 1. CMS4611A, 2.CMS4611B, 3.CMS463D2A, 4.CMS463D2B, 5.CMS463D13A, 6.CMS463D13B, 7.CMS463D14A, 8.CMS463D14B, 9.CMS463L3A, 10.CMS463L3B, 11.CMS463L9A, 12.CMS463L9B, 13.CMS463L11A, 14.CMS463L11B, 15.CMS4622A, 16.CMS4622B, 17.CMS4623A, 18.CMS4623B, 19.CMS4624A, 20.CMS4624B, 21.CMS4626A, 22.CMS4626B, 23.CMS4627A, 24.CMS4627B

mm (CMS4626A). On the other hand, the CMS B-line (maintainer) gave range of pericarp thickness from 1.08 mm (CMS4611B) to 1.72 (CMS463D14B). This indicated genetic diversity among the CMS lines that can be exploited for breeding of different segment hybrids.

Conclusion

Based on the marker analysis, the recovery of the genetic material in the CMS A- and the CMS B-line pairs was more than 98%. Based on horticultural performance, it was concluded that the A- and B-lines are statistically at par, indicated that the complete genome of B-line has been transfer or recovered in CMS lines for fruit traits or genetic background of these A- and B-lines became identical. The lines are, therefore, genetically stable and are ready for utilization in hybrid breeding programs.

सारांश

वर्तमान अध्ययन का मुख्य उद्देश्य मिर्च के सी.एम.एस. (ए) एवं अनुरक्षक (बी) वंशक्रमों का 120 एस.एस.आर. मार्कर के माध्यम से अनुवांशिक समानता को ज्ञात करना है। लगभग सभी विस्तारित मार्कस ने सी.एम.एस वंशक्रमों एवं इसी के सापेक्ष की वंशक्रमों में मोनोमार्फिक बैंड्स स्पष्ट किये। सी.एम.एस.–463 डी.2ए. सी.एम. एस.–463 डी2बी (एलोप्लास्मीक अनुरक्षक वंशक्रम) तथा सी.एम.एस. –463 एल9ए एवं सी.एम.एस.–463 एल9बी के मध्य पालीमार्फिक बैन्डिग प्रतिमान क्रोमोजोम–1 पर एक मार्कर (एच.पी.एम.एस.–2–13) का ए स्पष्ट किया गया। आठ प्रतीप संकरणों (बीसी 8 एफ1) तथा चयन के उपरान्त सभी सी.एम.एस. वंशक्रमों में शत–प्रतिशत जीनोम रिकवरी केवल सी.एम.एस.–463 डी.–2ए व सी.एम.एस–463 डी–2बी के अलावा पाया गया तथा सी.एम.एस.–463 एल9ए व सी.एम.एस. –463 एल.9बी. के मध्य रिकवरी क्रमशः 99.01 प्रतिशत व 98.9 प्रतिशत पाया गया। इसी प्रकार फल भार की लम्बाई, फल की चौड़ाई तथा फल भित्ति की मोटाई हेतु सभी सी.एम.एस.–ए व सी. एम.एस.–बी. वंशक्रमों के मध्य मूल्य वेयर्ड टी टेस्ट द्वारा असार्थक पाया गया जबकि सी.एम.एस. 4624 ए व सी.एम.एस.–4624 बी फल की लम्बाई के लिये तथा सी.एम.एस. 4624 ए व सी.एम.एस. 4626 बी फल की चौड़ाई के लिये अन्तर सार्थक पाया गया।

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