



Development of PCR-based Markers Associated with Powdery Mildew Resistance using Bulk Segregant Analysis (BSA-seq) in Melon

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Powdery mildew (PM) is a fungus that causes disease in both the field and the greenhouse. Utilizing resistant cultivars is the most effective approach of disease management. To develop insertion-deletion (InDel) marker associated to this trait, whole genome of PM resistant line M17050 (P1) and PM-susceptible line 28-1-1 (P2) were sequenced. A total of 1,200 InDels, with an average of 100 markers per chromosome, were arbitrarily chosen from the sequencing data for experimental validation. One hundred InDel markers were ultimately selected due to their informative genetic bands. Further, an F2 segregating population of melons generated from these two parents was inoculated by PM pathogen. Based on bulk segregant analysis (BSA) using these 100 InDel markers, the powdery mildew resistance was associated with the genomic region *LVpm12.1* on melon chromosome12. This region overlapped the previously described QTL-hotspot area carrying multiple PM-resistance QTLs. Moreover, conventional QTL mapping analysis was done, which located *LVpm12.1* in the region between 22.72 Mb and 23.34 Mb, where three highly polymorphic InDel markers MInDel89, MInDel92, and MInDel93 were detected. Therefore these markers could be used to track this resistance locus in melon while the lines carrying this locus could be employed in PM melon resistance breeding programs after validation test.

Abstract text (partially obscured and illegible)

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48, 49, 21, 34, 38, 11, 40, . I , 32

B (B A) . B A 19, 21, 38, 50 C , 17050 (1) 28-1-1 (2), , C.

. D (G), . B

B A G . B A- (-) . 17050 - ,

57,58, 40 . 52, 53, 54 , 55, 56 , 57, 58 , 28-1-1 - (-) - ,

(B A-) B A - (F 1 -). A F2 F1-6

() 125 , 17050 28-1-1, F2 ,

(A) . B A

60, 61, 62 . C , A G A I . F

33 .) 28-1-1 (2,) , 17050 (1, F2 . 1, 2, F1-6, F2

D A 63 . I C (/) 22-28 60 75 .

C - I D , A , H . I C (.) 70

, B A (F 1 -). I ,

C - I (F 1). G A

0.02 1 1⁰⁶ 20 71 .

D

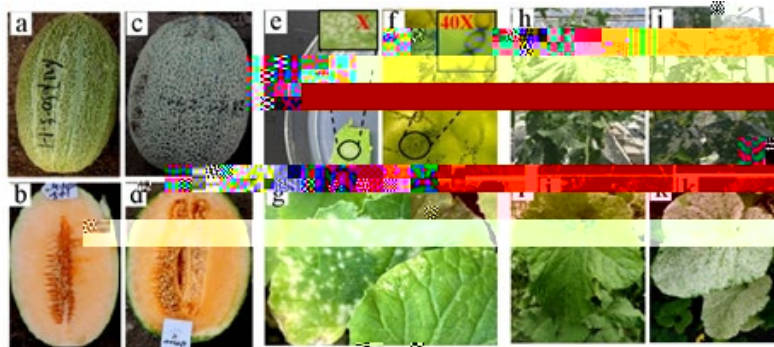
. I , 64, 65, 66, () . B

C - I C - I : I C 0,

19, 69 . I , C 1, . F ,

B A . B

12.1. , I D 92, . B F2 . H , 30



Fruits morphology and PM disease evaluation. Fruit appearance and fruit longitudinal section of P1 line (a-b) and P2 line (c-d) showing skin and flesh characteristics; Powdery mildew pathogen single spore isolation (e) followed by conidiophore and conidia observation under light microscope (f), Maintenance of PM disease on melon leaves using artificial inoculation in growth chamber (g); Leaves from P1 and resistant F2 plant (h-i) and that from P2 and susceptibility F2 plant (j-k); X and 40X, represents high magnification observation.

, 50

F1-6,

125

F2

0

I 89, I D 92 D A I D 93 .
1, 2, 1 2
20 . F1-6, 17050 28-1-1,
(D). F2 ,
1 -). , 1 (F
1

15.75 I D / 2.66 I D / 09
06 (3). I
, (1-10), (11-
30), (>30). I D
2.62 , 8.58 , 88.80 ,
- I D 1 2.
B *LV 12.1*
B (B A)
D A ,

chr12	MInDel23	20998229	GTGATTGACCTTTAGTGCCAAAA	ATCTAAACTTGGCCAACCTCACTTG	228
chr12	MInDel24	21001671	TGCTGGCGGAAGAAATTAATGAG	GTCTAGAGCAGGGCAAAGATTTTG	204
chr12	MInDel25	21012231	CCTACAACCTTCACCCACTTTTGAG	CGAGAATGTTTTACTAGCTCAACCA	263
chr12	MInDel26	21012734	ACGTGTTTACAATGTACCGTGA	TGGGGATAAAGTGAGGAAGAGTTG	173
chr12	MInDel27	21013801	ACTGGATTACATGACCACTAAGTG	CTAACAACCTATCACAAAGTACTCGC	288
chr12	MInDel28	21014354	CGACTTGATAATAAGCACACGTGT	TGTGAACCTATTAGTCCACCAAGT	87
chr12	MInDel29	21016018	AAAATCGACCTACCTTCAACGA	TACTGTTGTTGTCCCACATATCGA	297
chr12	MInDel30	21202574	GTGGGGATTTGATTACGTGTTCAA	CAACTGGGAAGGATGACATGAAAA	273
chr12	MInDel31	21229417	GCGATCATGTTTTCTCAACCTTC	CTACTTCGAGTGGCCTAAATGACT	250
chr12	MInDel32	21229663	AGTCAATTAGGCCACTCGAAGTAG	TTTCTCCACATGTAACTGTACCCA	174
chr12	MInDel33	21351602	AGCCATCAAAGCCCAAAGTCTATA	TGAATCCTTGAAAAGTTTCGGACAC	100
chr12	MInDel34	21362591	CCAGACCCACCATGTAAAATACCA	AAAATCGATTAGCCAAACCTCGTG	217
chr12	MInDel35	21362703	CACGATTGTTTAGATTTGGACCCA	AAAATCGATTAGCCAAACCTCGTG	84
chr12	MInDel36	21363548	GGCCATTGAACACACTTACAAAT	AATCCATAGACGACCACAAGAGTC	246
chr12	MInDel37	21374693	CAAACGAAGCCTAGACTCAAACCTC	TTTTGTGCCGTGGAAGATAGAGA	285
chr12	MInDel38	21377989	GTGATATGTACCCTTCTGAACACA	AGTTCAACAATGTATGAGAGGGTGA	145
chr12	MInDel39	21378699	CCCCTTCTCCTTCTCACTTTATT	TTAAAGGTATATCTAGGGAGGGCC	129
chr12	MInDel40	21382890	CGATTGCAAAACCTACAAGAGAGT	GGGCGTGTTTAACCTCCTTTTAT	267
chr12	MInDel41	21383696	TGACACTACAAATGACTCGCTT	AATAACTCTCATCCTCCAATGACG	189
chr12	MInDel42	21402647	CTGCCTAAGATTCGCCTACTTTT	CAAATCTCGATTACTCTTGCACCC	263
chr12	MInDel43	21424800	ACTCAAAGTGGTGTTCCAGATGTGA	GGAAGGTGTGTTGTTTTCTGAGTT	282
chr12	MInDel44	21426178	TGAAGTTGAAGAGGTAAGTTGGGT	CTGCCACGTGTAGAACATTTTGA	232
chr12	MInDel45	21426418	CCACAAAAGCGGCTGATGATATTA	TCTCTCTCTATCTACCAGCTCA	130
chr12	MInDel46	21427266	AAAATACTCCGTCAACCATGCATC	TGACCGTGTACCAAAAAGAACTTTG	107
chr12	MInDel47	21429242	GCAATGATCCTTTGAAACTCACATC	ATAAGGTTGTGGTTTGGGTTTGTG	270
chr12	MInDel48	21430150	TGATGGGGAAGAGATCAGAAAGTG	AACAAGAAAACAAAATAGGTCGGCC	281
chr12	MInDel49	21430740	GAGCATTGAGGTTAACGTAAGACA	GACTTTGCAAAAAGACGTGTAGAC	219
chr12	MInDel50	21440365	TGGTTAGAATAGTTTGTGTTGGAGG	TTGGGGCAAAGATTATCTAGGACT	270
chr12	MInDel51	21441123	CACAAAAGCGAAGATGACAAACCTT	TTGGCTTGAATGATCTGGTTGTTT	139
chr12	MInDel52	21443795	AGAAGAAGGAGAAGAGAGAAGGGA	CCCTCCTTCTCTTGTACTTTTCA	113
chr12	MInDel53	21443959	TGAAAGTGATCAAGAGAAGGAGGG	TATTGGAAGAGGCATTAGAAGGGG	180
chr12	MInDel54	21445083	TGTACTTCTTCTACCTAAAGCGA	CGTGGTTAGATTTGTTGTTGCA	248
chr12	MInDel55	21445095	TGTACTTCTTCTACCTAAAGCGA	CGTGGTTAGATTTGTTGTTGCA	248
chr12	MInDel56	21445714	TGTAAAGAGAGGCACATGTGTAGA	TGTCTATCATCTTGCCATCATAGTC	86
chr12	MInDel57	21446584	ATTGGGTTGGGCTCTTTATTTGG	AAGAGACAGGCCGGAACCTCAATA	300
chr12	MInDel58	21449903	CCCAACCTATAATGATCAACACC	ATATAGGTGGAAGAAGAGGGCTA	191
chr12	MInDel59	21450126	TCTAGCCCTCTCTTTCCACCTAT	CCAAAAGTGTGCAATAGGAGTTCA	296
chr12	MInDel60	21453528	AGAGATCGCATGTGTGTTGGTTA	TAGACAAAGTTAACAGAACGCCCA	263
chr12	MInDel61	21453748	TGTCTATTAGAGCCGTACACATG	AGGAAACACTAAGACAATCGAGCT	155
chr12	MInDel62	21459671	AAAGGCGATAAGTAGTGGTGAAGT	ATGTCCGTGTCAAAACCTTCTTC	234
chr12	MInDel63	21459939	GAAGAAAAGTTTGGACGACGGACAT	GGTTTGCCTTGTGAAAATGAGCTT	177
chr12	MInDel64	21460111	ACAACCTACACTCCAAATCCCCAT	TGAGAGAGAGAGAGAGAGAGAGAG	248
chr12	MInDel65	21468921	ACCCACGAGCATGTAGAATAAGA	GCAAGGTGATATAAATGGTTGGAGC	258
chr12	MInDel66	21469302	ACACACACACACACACTTTT	TGGCAATCAACAAAAGGATGA	294
chr12	MInDel67	2147		8930%	2
	294				

C 7191- C , I D 92 , C - I D 28-1-1 (2) B A -
I 93 (4). C I 89 F2 . 12.1 I D 89, I D 92,
A 11, A 65, A 66, A 67, A 68 (4). A 7, A 9, I D 93. 7191 I D 92
D A (D 2000 D A). I D 92 7191 12 , I D 92
D A I 92 7191 200 300 I D 89 I D 93. 7191 -
D A 719 300 (F 1).I 6-1, I D 92 I D
C , H , - / **65** .
D () I D - I D
65, 68 . I D - I D
A **66, 56, 67, 68**
56
C -
A
.I , - 17050 (1)

40, C, -12 -6 22.00 22.90
 24.25 12.1 6 22.36
 39.
 12.1 6, H, 12.1, C, -12,
 12.1.

12 . I
 ,
 I D
 ,
 . I , , , .

7191
 I D 92 .

A : A F (201801)
 F (201910)

B
 A
 A , , A ,
 ; , , F, ,
 D, G , H ;
 .AA, H G .

C

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