

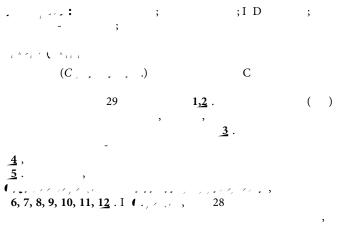
## Development of PCR-based Markers Associated with Powdery Mildew Resistance using Bulked Segregant Analysis (BSA-seq) in Melon

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Powdery mildew (PM) is a fungus that causes disease in both the feld 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 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.



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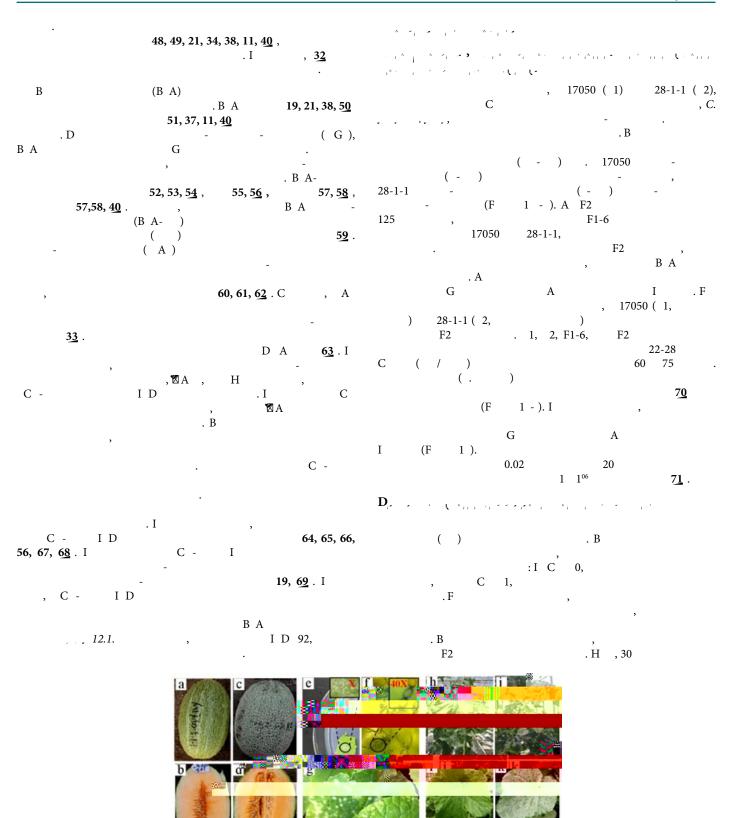
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Fruits morphology and PM disease evaluation. Fruit appearance and fruit longitudinal section of P1 line (a-b) and P2 line (c-d) showing skin and fesh characteristics; Powdery mildew pathogen single spore isolation (e) followed by conidiophore and conidia 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.

Page 3 of 9

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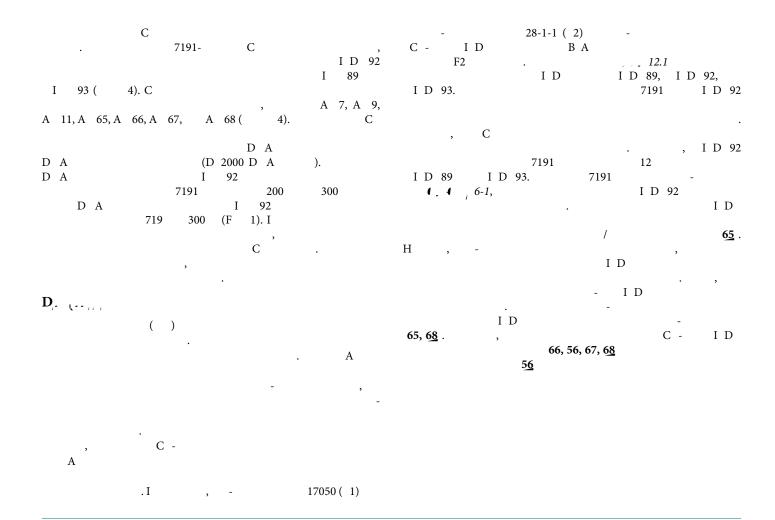
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Page 5 of 9

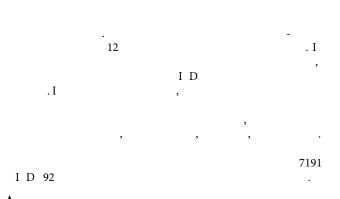
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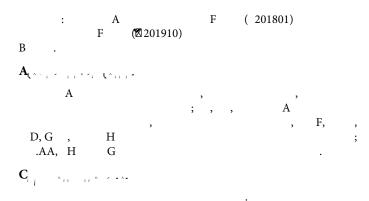
## Page 6 of 9

chr12	MInDel23	20998229	GTGATTCGACCTTTAGTGGCAAAA	ATCTAAACTTGGCCAACTCACTTG	228
chr12	MInDel24	21001671	TGCTGGCGGAAGAAATTAAATGAG	GTCTAGAGCAGGGCAAAGATTTTG	204
chr12	MInDel25	21001071	CCTACAACTTCACCCACTTTTGAG	CGAGAATGTTTTACTAGCTCAACCA	263
chr12	MInDel26	21012231	ACGTGTTTACAATGTACCGTGA	TGGGGATAAAGTGAGGAAGAGTTG	173
chr12	MInDel27	21013801	ACTGGATTACATGACCACTAAGTG	CTAACAACTTATCACAAGTACTCGC	288
chr12	MInDel28	21014354	CGACTTGATAATAAGCACACGTGT	TGTGAACCTATTAGTCCACCAAGT	87
chr12	MInDel29	21016018	AAAATCGACCTACCTTCAACGA	TACTGTTGTTGTCCCACATATCGA	297
chr12	MInDel30	21202574	GTGGGGATTTGATTACGTGTTCAA	CAACTGGGAAGGATGACATGAAAA	273
chr12	MInDel31	21229417	GCGATCATGTTTTCCTCAACCTTC	CTACTTCGAGTGGCCTAAATGACT	250
chr12	MInDel32	21229663	AGTCATTTAGGCCACTCGAAGTAG	TTTCTCCACATGTAACTGTACCCA	174
chr12	MInDel33	21351602	AGCCATCAAAGCCCAAAGTCTATA	TGAATCCTTGAAAGTTTCCGACAC	100
chr12	MInDel34	21362591	CCAGACCCACCATGTAAAATACCA	AAAATCGATTAGCCAAACCTCGTG	217
chr12	MInDel35	21362703	CACGATTGTTTAGATTTGGACCCA	AAAATCGATTAGCCAAACCTCGTG	84
chr12	MInDel36	21363548	GGCCATTGAACCACACTTACAAAT	AATCCATAGACGACCACAAGAGTC	246
chr12	MInDel37	21374693	CAAACGAAGCCTAGACTCAAACTC	TTTTGTGCCGTGGAAAGATAGAGA	285
chr12	MInDel38	21377989	GTGATATGTACCCTTTCTGAACACA	AGTTCAACAATGTATGAGAGGGTGA	145
chr12	MInDel39	21378699	CCCCTTCTCCTTCTCACTTTATTT	TTAAAGGTATATCTAGGGAGGGCC	129
chr12	MInDel40	21382890	CGATTGCAAAACCTACAAGAGAGT	GGGCGTGTTTTAACCTCCTTTTAT	267
chr12	MInDel41	21383696	TGACACTACAAATACGACTCGCTT	AATAACTCTCATCCTCCACTGACG	189
chr12	MInDel42	21402647	CTGCCTAAGATTGCGCTACCTTTT	CAAATCTCGATTACTCTTGCACCC	263
chr12	MInDel43	21424800	ACTCAAAGTGGTGTTCAGATGTGA	GGAAGGTGTGTTGTTTTCTGAGTT	282
chr12	MInDel44	21426178	TGAAGTTGAAGAGGTAAGTTGGGT	CTGCCACGTGTAGAACATTTTAGA	232
chr12	MInDel45	21426418	CCACAAAAGCGGCTGATGATATTA	TCTCTCTCTCTATCTACCAGCTCA	130
chr12	MInDel46	21427266	AAAATACTCCGTCAACCATGCATC	TGACCGTGTACCAAAAGAATCTTG	107
chr12	MInDel47	21429242	GCAATGATCCTTTGAAACTCACATC	ATAAGGTTGTGGTTTGGGTTTGTC	270
chr12	MInDel48	21430150	TGATGGGGAAGAGATCAGAAAGTG	AACAAGAAACAAAATAGGTCGGCC	281
chr12	MInDel49	21430740	GAGCATTGAGGTTAACGTAAAGACA	GACTTTGCAAAAGAACGTGTAGAC	219
chr12	MInDel50	21440365	TGGTTAGAATAGTTTGTGTTGGAGG	TTGGGGCAAAGATTATCTAGGACT	270
chr12	MInDel51	21441123	CACAAAAGCGAAGATGACAACCTT	TTGGCTTGAATGATCTGGTTGTTC	139
chr12	MInDel52	21443795	AGAAGAAGGAGAAGAGAGAAGGGA	CCCTCCTTCTCTTGATCACTTTCA	113
chr12	MInDel53	21443959	TGAAAGTGATCAAGAGAAGGAGGG	TATTGGAAGAGGCATTAGAAGGGG	180
chr12	MInDel54	21445083	TGTACTTCCTTCTACCTAAAGCGA	CGTGGTTAGATTTGTTGTTGCA	248
chr12	MInDel55	21445095	TGTACTTCCTTCTACCTAAAGCGA	CGTGGTTAGATTTGTTGTTGCA	248
chr12	MInDel56	21445714	TGTAAAGAGAGGCACATGTGTTAGA	TGTCTATCATCTTGCCATCATAGTC	86
chr12	MInDel57	21446584	ATTGGGTTGGGCTCTTTTATTTGG	AAGAGACAGGCCGGAACTTCAATA	300
chr12	MInDel58	21449903	CCCCAACCTATAATGATCAACACC	ATATAGGTGGAAAGAAGAGGGGCTA	191
chr12	MInDel59	21450126	TCTAGCCCTCTTCTTTCCACCTAT	CCAAAAGTGTTGCAATAGGAGTTCA	296
chr12	MInDel60	21453528	AGAGATCGCATGTGTGTATGGTTA	TAGACAAAGTTAACAGAACGCCCA	263
chr12	MInDel61	21453748	TGTCTATTAGAGCCGTACCACATG	AGGAAACACTAAGACAATCGAGCT	155
chr12	MInDel62	21459671	AAAGGCGATAAGTAGTGGTGAAGT	ATGTCCGTCGTCAAAACTTTCTTC	234
chr12	MInDel63	21459939	GAAGAAAGTTTTGACGACGGACAT	GGTTTGCCTTGTGAAAATGAGCTT	177
chr12	MInDel64	21460111	ACAACTACACTCCAAATTCCCCAT	TGAGAGAGAGAGAGAGAGAGAGAG	248
chr12	MInDel65	21468921	ACCCACGAGCATGTAGAAATAAGA	GCAAGGTGATATAAATGGTTGGAGC	258
chr12	MInDel66	21469302	ACACACACACACACACACTTTT	TGGCAATCAACAAAAGGGATGA	294
chr12	MInDel67	2147		&930¾ 2	
	294				



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Page 9 of 9

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