

Identification of a locus conferring dominant resistance to maize rough dwarf disease in maize

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Supplementary Information

1. **Supplementary Figure S1** Multiple sequence alignment showing identity between S221-S and RBSDV isolated from different maize planting locations in China. S221-S: parental plant showing MRDD symptoms in the present study. The GenBank accession numbers AJ291706, KC875238 and KM921681, JX421771, KX660762, DQ407917 are rice black streaked dwarf virus isolated from Wuhan, Jiangsu, Shandong, Anhui, Baoding China, respectively.

S221-S	1	GATCATATAAATAGAGAAATTGACAATTAAAAACGACCAACCAATAGAAACACAATTCATCGACTTCTCAATCTAATGAAAATCGTC	90
AJ291706	3	C.....	92
MRDV cDNA	3	C.....	92
KC875238	3	C.....	92
JX421771	3	C.....	92
KX660762	3	C.....	92
KM921681	3	A.....C.....	92
S221-S	91	TTTCAACCAAGAAATCCCCCTACTCGATGACGGCATCTTCGAACCTTCTGAACCTACCTTATTGATGGAAACCACTTCGACAAAACCTTGCT	180
AJ291706	93		182
MRDV cDNA	93	T.....	182
KC875238	93		182
JX421771	93		182
KX660762	93		182
KM921681	93		182
DQ407917	1		54
S221-S	181	ATTGTGGTTTTAATTATCTCATCTCCCTAACCTTGAACGTGACTTTAACGTTGCATCTGTTTATGTCGCGGAGAATTTTG-GTCTATAA	269
AJ291706	183	A.....-AAT...-G	270
MRDV cDNA	183	A.....-G	270
KC875238	183	A.....-G	270
JX421771	183	A.....-G	270
KX660762	183	A.....-AAT...-G	270
KM921681	193	A.....-G	270
DQ407917	55	A.....T.....A.....-G	142
S221-S	270	CATTTCCTG-GAA--AGATTGAAAGATTGGATAGAAAGGCTTGTATTGTTGAAATCTGCTGATTTTACTTTGCTTCTAGAATATAC	355
AJ291706	271	AA..CTT.....AT.....C.....AAA.A..AGCG.....C.....	357
MRDV cDNA	271	AA..CCT.....AT.....A.C.....AAA.A..AGCG.....C.....	357
KC875238	271	AA..CCT.....AT.....C.....AAA.A..AGCG.....C.....	357
JX421771	271	AA..CTT.....AT.....C.....AAA.A..AGCG.....C.....	357
KX660762	271	AA..CTT.....AT.....C.....AAA.A..AGCG.....C.....	357
KM921681	271	AA..CTT.....AT.....C.....AAA.A..AGCG.....C.....	357
DQ407917	143	AA..CTT.....AT.....C.....AAA.A..AGCG.....C.....	229
S221-S	356	TCTTAAACCATCATCAGAAACCGATCTGCTATTCCAGAGAATGAGAAAGAAGAGAAATGCTAAACAGTTACTCTAAAGTTGCTCACTCC	445
AJ291706	358		447
MRDV cDNA	358	T.....	447
KC875238	358		447
JX421771	358	A.....	447
KX660762	358		447
KM921681	358	G.....A.....	447
DQ407917	230	A.....	319
S221-S	446	AAAAGAAGAGAAGAAAACAGTTGAAATGTCATGTTGCGCAATTCTGAACCGTGAATCTGAAGAATCTTTAAGCTCTGAAATTCCTGAAGG	535
AJ291706	448		537
MRDV cDNA	448	G.....	537
KC875238	448		537
JX421771	448		537
KX660762	448	G.....	537
KM921681	448	G.....	537
DQ407917	320		409
S221-S	536	TGAAGCTGC	544
AJ291706	538		94
MRDV cDNA	538		94
KC875238	538		94
JX421771	538		94
KX660762	538		94
KM921681	538		94
DQ407917	410		93

2. **Supplementary Table S1** MRDD disease severity in the parent lines (K36 and S221) and F₁ and F₂ progenies

Disease score	Number of plants in 2015				Number of plants in 2016			
	K36	S221	F ₁	F ₂	K36	S221	F ₁	F ₂
0	40	1	39	368	39	1	37	679
1	0	0	0	56	1	0	1	90
2	0	9	1	29	0	8	0	50
3	0	30	0	60	0	31	2	121
Total number of diseased plants	0	39	1	145	1	39	3	261
Total number of plants	40	40	40	513	40	40	40	940
Disease incidence (%)	0	97.5	2.5	28.27	2.5	97.5	7.5	27.77
Disease severity index (DSI)	0	67.5	1.25	19.10	0.63	68.13	3.13	19.61

3. **Supplementary Table S2** The distribution of markers on each chromosome

Chromosome	Number of SLAFs	Number of SNPs
Chromosome 1	27,423	97,890
Chromosome 2	19,484	83,762
Chromosome 3	19,592	86,975
Chromosome 4	21,635	92,253
Chromosome 5	19,050	69,569
Chromosome 6	13,342	61,784
Chromosome 7	16,145	60,557
Chromosome 8	17,324	40,477
Chromosome 9	13,850	53,106
Chromosome 10	13,390	61,075
Other	897	2,222
Total	182,132	709,670

4. **Supplementary Table S3** Summary of different SNPs in the candidate region between parents

Chromosome	Position (bp)	Ref (B73)	S221	K36	Codon change	Amino acid ^a change	Gene ID
6	62,078,047	G	T	G	tGg/tTg	W/L	GRMZM2G444383
6	62,112,558	C	C	A	Ctt/Att	L/I	AC186583.3_FG004
6	64,074,905	A	A	G	aTt/aCt	I/T	GRMZM2G124972
6	67,811,315	G	C	G	Gtg/Ctg	V/L	GRMZM2G700955
6	69,248,287	A	A	G	Atg/Gtg	M/V	GRMZM2G384564
6	69,248,324	C	C	T	cCa/cTa	P/L	GRMZM2G384564
6	69,248,432	T	T	C	cTc/cCc	L/P	GRMZM2G384564

AA: amino acid

5. Supplementary Table S4 Information on the SSR markers used in linkage analysis in this study

Marker name	Position on chromosome 6 (bp)	Forward primer (5'-3')	Reverse primer (5'-3')
6F4R4	55,822,325-55,822,566	CACTCAGGGTCTGCTTGGAG	CTCTCTCTATCCTAAAATAGTAGTCGT
6F5R5	55,950,898-55,951,240	CAAAGGGTCGTTTGGGCCA	TTCAACCCGAGGTTTGGAGC
6F6R6	56,058,408-56,058,549	TCTATGACACGTGTGGGCAC	TGTGTTTGTATGACTCCCCCT
6F7R7	56,335,833-56,335,956	ACTACACGACTCCGACTCGA	TTGAACCAGTTTGCAGGGGT
6F8R8	56,452,804-56,452,977	CTACACAGCTTCAAGGCCCA	CCGCTGTTGTTTCTGGCTTC
6F9R9	57,019,210-57,019,447	TGATGCTGCTGCTGCTTTTG	AGCCGAAAAATTCATCACCGA
6F10R10	57,130,660-57,130,868	TGGCCTAGTTTAGAAAAAGAGCT	TCGGTGCAAAGTGGTTTTCC
6F11R11	57,647,144-57,647,245	TCATGGCCGCTTGTGTGTAT	CATCACAAGCAGCACGTACG
6F12R12	57,772,604-57,772,757	TATGTGTGTGCCCTCCTTGC	TTGGCCCACTTTGTTTTGGC
6F13R13	58,683,686-58,683,872	TCCTCCCAATGCAAGGTGTC	CGTAGGGTTGGTTCCGAACA
6F14R14	59,920,064-59,920,534	CTATTCAACCGCCCCCTGTT	ACCGGATCGTTCTCTATGCG
6F15R15	60,113,527-60,113,742	TGCTTGATTGAAGTGCTTGCT	ATGGGCAGTGATGACTCCAT
6F16R16	60,416,993-60,417,205	GTGGGTGTTGCTCAGCATTG	GCAGCGGTAACAACGAAGC
6F17R17	61,191,473-61,191,687	GGCAGTGCCTGATAGCAAGA	ACCAGTCAACTGCTACGAGC
6F18R18	61,533,190-61,533,389	GAAGCTTGGAGGTAGCGACA	AGCTGTATTACGCGTCGACT
6F19R19	62,656,610-62,656,791	TGCTTTCGCTCTCCAGCTAGG	GGCTTCTGACTTTCGGACGA
6F20R20	62,777,760-62,777,922	AGTCAGCAAAGGCCACAGAA	CGAACTGGTGTAACTGTGTC
6F21R21	63,654,542-63,654,669	TCGTTATGAGGGTGATAACCAGC	CGTCGTAGCTCGCGAAAATG
6F22R22	64,384,982-64,385,168	ACACAGAGCAACAACATACTCA	TGTCCTTGGATGGTCATGCC
6F23R23	65,076,565-65,076,772	CCGCTGCTTGTGAATCCATG	AACATAACGTAGGTCCGCCC
6F24R24	65,407,726-65,407,919	CTTTACGCTGAAATCCGCCG	GCACCAGATCGCTTGATTGC
6F25R25	65,526,472-65,526,648	CATAGGGGATGAGTTGGGCC	TGCCATGCCGATGTTTTTGT
6F26R26	66,095,500-66,095,709	GGGGTGGTGATCACTCTCAC	AAAATGGAGACGACGGCAGT
6F27R27	66,591,888-66,592,187	TGCTGGAGTTTGTGTTGTGCA	GCCCAAGCGGTGTTTCTTA
6F28R28	67,437,844-67,437,998	CACCGGGGTGCTTGTAGTAG	CACACACACACGTTGACGAC
6F29R29	68,396,487-68,396,671	CACGGACTTAAGGAGCCATGT	CACTCTGAGCTGTGCACTGT
6F30R30	69,764,319-69,764,546	GGTGCAATTTAGTAGCGCCG	TGGGACTAAAAGGCTACCGA
6F31R31	70,996,239-70,996,423	ACTGTGAGGTGGTCAGGACT	AAGCGTTGCTTCTCAGAGGT
6F32R32	72,227,569-72,227,886	AACTTCAACAACGCTTGGGC	CATGGACCCGATCTAGTGCC
6F33R33	72,887,108-72,887,316	TCCGACCATCGTTACATTGGT	ACGTTGAAAAGAACACGCGG
6F34R34	73,915,399-73,915,578	GCCGTGGCTGTAAGAAAAGC	TATGCCGCGAAGTAAAGGCA
6F35R35	74,480,444-74,480,662	TTCATCAACCGCACATACGT	CGCACGTCTCCTTTTCACTTC