

Inheritance Pattern and Molecular Markers for Resistance to Blackleg Disease in Cabbage

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Supplementary information

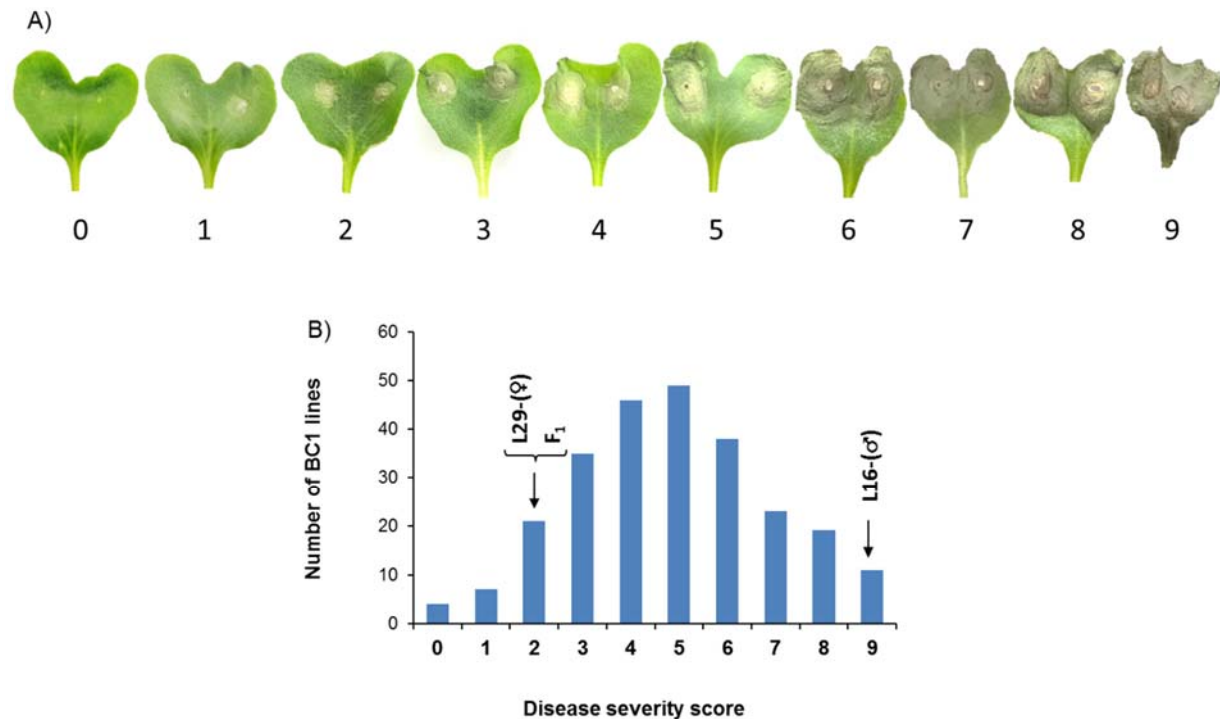


Figure S1: (A) Criteria for scoring the severity of blackleg disease symptoms in *Leptosphaeria maculans* isolate 03-02 s infected cotyledons at 12 days after inoculation (dai). Cotyledons with 0-5 and 6-9 scores were characterized as resistant and susceptible, respectively. (B) Frequency distributions of disease scores of the 253 BC1 population raised from the resistant (R) and susceptible (S) parental lines, L29 (♀) and L16 (♂), respectively.



Figure S2: Domain structures of the putative disease resistance related domain (NB-ARC, LRR, TIR, CC EREB, FBD, RLK etc.) containing genes within the collinear region of *B. napus* blackleg resistant gene *Rlm1* in *B. oleracea*.

Domain analysis was carried out using NCBI conserved domain database (<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>). Domains are indicated by different shapes and colors. NB-ARC. Nucleotide-binding adaptor shared by APAF-1, certain *R-gene* products, and CED-4, LRR. Leucine rich repeat, TIR. Toll/Interleukin-1 receptor, LRP. Receptor-like kinase protein and FBD. F-box domain etc.

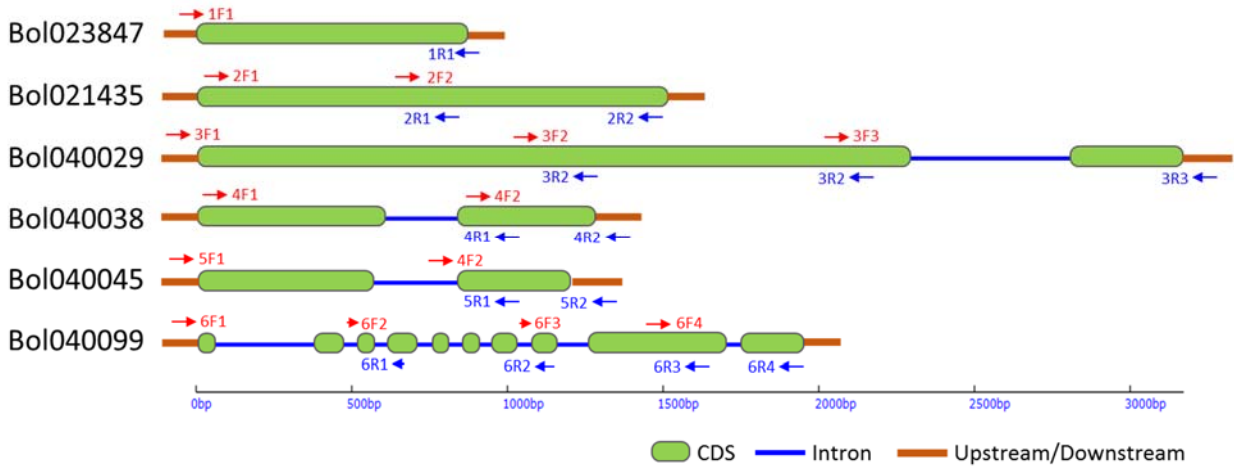


Figure S3: Exon-intron structures and primer positions on the selected six putative R-genes for detecting length polymorphism between blackleg resistant and susceptible cabbage lines.

Primer specifications are shown in Table 3 and the detected polymorphism is shown in Figure 3.

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*      20      *      40      *      60      *      80      *      100
Bol040029 : ggttggttctttgctgagagtctcaacATGCTTGAGAATCTCACTGAGTTGTCGTTGGTAACAACACCTAACCAGGACCGGTTTCGTTTCGGTTCAGAA : 100
L16- (♂) -S : ggttggttctttgctgagagtctcaacATGCTTGAGAATCTCACTGAGTTGTCGTTGGTAACAACACCTAACCAGGACCGGTTTCGTTTCGGTTCAGAA : 100
L29- (♀) -R : ggttggttctttgctgagagtctcaacATGCTTGAGAATCTCACTGAGTTGTCGTTGGTAACAACACCTAACCAGGACCGGTTTCGTTTCGGTTCAGAA : 100
3F1

*      120     *      140     *      160     *      180     *      200
Bol040029 : AACTGCAAGAACTTGCTGACTTTAGAGTTGTCTTACAACGAATTCGAAGTGGTGTCTCTGAGTTAGGGAACCTAGTAGCCTTGACGCTCTGGTGA : 200
L16- (♂) -S : AACTGCAAGAACTTGCTGACTTTAGAGTTGTCTTACAACGAATTCGAAGTGGTGTCTCTGAGTTAGGGAACCTAGTAGCCTTGACGCTCTGGTGA : 200
L29- (♀) -R : AACTGCAAGAACTTGCTGACTTTAGAGTTGTCTTACAACGAATTCGAAGTGGTGTCTCTGAGTTAGGGAACCTAGTAGCCTTGACGCTCTGGTGA : 200

*      220     *      240     *      260     *      280     *      300
Bol040029 : TTGTGAGTGGAACCTTGTCAGGCACGATCCCTGCCTCGTAGGTATGTTAAAGAAGCTCACGGTTATTATCTCTCAGAGAATCGTCTCTCTGGGCTGT : 300
L16- (♂) -S : TTGTGAGTGGAACCTTGTCAGGCACGATCCCTGCCTCGTAGGTATGTTAAAGAAGCTCACGGTTATTATCTCTCAGAGAATCGTCTCTCTGGGCTGT : 300
L29- (♀) -R : TTGTGAGTGGAACCTTGTCAGGCACGATCCCTGCCTCGTAGGTATGTTAAAGAAGCTCACGGTTATTATCTCTCAGAGAATCGTCTCTCTGGGCTGT : 300
Region encoding LRR-1 domain

*      320     *      340     *      360     *      380     *      400
Bol040029 : CCTTCAGAGATTGGTAACCTGCTAGTTTAAACAGTTTAAAGCTCAACAAACACAGCTTGAGGAGAGATACCGAGTTCGTTAGGTAGCTGAGGAAG : 400
L16- (♂) -S : CCTTCAGAGATTGGTAACCTGCTAGTTTAAACAGTTTAAAGCTCAACAAACACAGCTTGAGGAGAGATACCGAGTTCGTTAGGTAGCTGAGGAAG : 400
L29- (♀) -R : CCTTCAGAGATTGGTAACCTGCTAGTTTAAACAGTTTAAAGCTCAACAAACACAGCTTGAGGAGAGATACCGAGTTCGTTAGGTAGCTGAGGAAG : 400
Region encoding LRR-2 domain

*      420     *      440     *      460     *      480     *      500
Bol040029 : CTGAGAGTCTTGAGCTTTTCGAGAACCGGTTCTCCGGTGAGATACCTATAGAGTGTGGAAGATTACCTCTTTCTCAGCTTCTGGTGTATCAAAACA : 500
L16- (♂) -S : CTGAGAGTCTTGAGCTTTTCGAGAACCGGTTCTCCGGTGAGATACCTATAGAGTGTGGAAGATTACCTCTTTCTCAGCTTCTGGTGTATCAAAACA : 500
L29- (♀) -R : CTGAGAGTCTTGAGCTTTTCGAGAACCGGTTCTCCGGTGAGATACCTATAGAGTGTGGAAGATTACCTCTTTCTCAGCTTCTGGTGTATCAAAACA : 500

*      520     *      540     *      560     *      580     *      600
Bol040029 : ACCTCACAGGAGCTCTCTGGAGATGACAGAGTTAAAGCATCTGAAGAAAGTTACTCTCTTCAACAACGGCTTCTACGGAGAGATACCATCGCTTT : 600
L16- (♂) -S : ACCTCACAGGAGCTCTCTGGAGATGACAGAGTTAAAGCATCTGAAGAAAGTTACTCTCTTCAACAACGGCTTCTACGGAGAGATACCATCGCTTT : 600
L29- (♀) -R : ACCTCACAGGAGCTCTCTGGAGATGACAGAGTTAAAGCATCTGAAGAAAGTTACTCTCTTCAACAACGGCTTCTACGGAGAGATACCATCGCTTT : 600
3sF2      3sR1

*      620     *      640     *      660     *      680     *      700
Bol040029 : AGGTGTGCAAGCAGCTTGAAGAGATTGACTTTATTAGCAACAACTCACGGGAGAGATACCGCGGAATCTCTGCCATGGGAAGAAGCTGACAGTGCTT : 700
L16- (♂) -S : AGGTGTGCAAGCAGCTTGAAGAGATTGACTTTATTAGCAACAACTCACGGGAGAGATACCGCGGAATCTCTGCCATGGGAAGAAGCTGACAGTGCTT : 700
L29- (♀) -R : AGGTGTGCAAGCAGCTTGAAGAGATTGACTTTATTAGCAACAACTCACGGGAGAGATACCGCGGAATCTCTGCCATGGGAAGAAGCTGACAGTGCTT : 700

*      720     *      740     *      760     *      780     *      800
Bol040029 : AACTTGGGCTCTAACCAGCTCCACGGGAAGATACCGACGCTCTATCGGTCGCTGCAAGAGCATGAGAGGTTTCATCCTCAGAGAGAACCACTCACAGGCC : 800
L16- (♂) -S : AACTTGGGCTCTAACCAGCTCCACGGGAAGATACCGACGCTCTATCGGTCGCTGCAAGAGCATGAGAGGTTTCATCCTCAGAGAGAACCACTCACAGGCC : 800
L29- (♀) -R : AACTTGGGCTCTAACCAGCTCCACGGGAAGATACCGACGCTCTATCGGTCGCTGCAAGAGCATGAGAGGTTTCATCCTCAGAGAGAACCACTCACAGGCC : 800

*      820     *      840     *      860     *      880     *      900
Bol040029 : CTCTCCCTGAGTTTCTCAAGATCATAGTATCTCGTTTCTTGATTTTAAATACAAACAGCTTCGAAGGACCGATCCCGAGAAGCTTTGGAAGCTCTAGGAA : 900
L16- (♂) -S : CTCTCCCTGAGTTTCTCAAGATCATAGTATCTCGTTTCTTGATTTTAAATACAAACAGCTTCGAAGGACCGATCCCGAGAAGCTTTGGAAGCTCTAGGAA : 900
L29- (♀) -R : CTCTCCCTGAGTTTCTCAAGATCATAGTATCTCGTTTCTTGATTTTAAATACAAACAGCTTCGAAGGACCGATCCCGAGAAGCTTTGGAAGCTCTAGGAA : 900

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Bo1040029 : tgtttgtcacgcataaagactgactatacatattacaaaaccggttaaaactcggttaaattctataccgaactacaccaagtctaatagtattgtgt : 2500
L16- (♂) -S : tgtttgtcacgcataaagactgactatacatattacaaaaccggttaaaactcggttaaattctataccgaactacaccaagtctaatagtattgtgt : 2500
L29- (♀) -R : tgtttgtcacgcataaagactgactatacatattacaaaaccggttaaaactcggttaaattctataccgaactacaccaagtctaatagtattgtgt : 2500
                                     BLR-C-InDel_F

          *          2520          *          2540          *          2560          *          2580          *          2600
Bo1040029 : agtttagaataaagaacagaacaaagcctaacaatcacaacggtaactaaatcggttaactctaaaccagactatccaaatcctaacagatta : 2600
L16- (♂) -S : agtttagaataaagaacagaacaaagcctaacaatcacaacggtaactaaatcggttaactctaaaccagactatccaaatcctaacagatta : 2600
L29- (♀) -R : agtttagaataaagaacagaacaaagcctaaca-----ggtaactaaatcggttaactctaaaccagactatccaaatcctaacagatta : 2589

          *          2620          *          2640          *          2660          *          2680          *          2700
Bo1040029 : gactgggtataatttggttttagagtttaaccggtttataatctgttagggcttggtttggtgtaaatatcgtctgtttctgtttgtcacgcgtgaaa : 2700
L16- (♂) -S : gactgggtataatttggttttagagtttaaccggtttataatctgttagggcttggtttggtgtaaatatcgtctgtttctgtttgtcacgcgtgaaa : 2700
L29- (♀) -R : gactgggtataatttggttttagag-----gttagggcttggtttggtgtaaatatcgtctgtttctgtttgtcacgcgtgaaa : 2613

          *          2720          *          2740          *          2760          *          2780          *          2800
Bo1040029 : ctgcattatacgtattagacttggtatagtttgcctatagaatttaaccggtttataatctcttagggcttggtttggtgtaaatatctctgtttct : 2800
L16- (♂) -S : ctgcattatacgtattagacttggtatagtttgcctatagaatttaaccggtttataatctcttagggcttggtttggtgtaaatatctctgtttct : 2800
L29- (♀) -R : -----ttaaaccggtttataatctcttagggcttggtttggtgtaaatatctctgtttctcttagggcttggtttggtgtaaatatctctgtttct : 2672
                                     BLR-C-2808_F

          *          2820          *          2840          *          2860          *          2880          *          2900
Bo1040029 : gtttctcacgcatgaaactgtgctgAAAACGCTTTAGACGGTGAGCGGAAGAGAATCAGACGTTTACAGTTACGGAGTTGTGTTGCTAGAGCTG : 2900
L16- (♂) -S : gtttctcacgcatgaaactgtgctgAAAACGCTTTAGACGGTGAGCGGAAGAGAATCAGACGTTTACAGTTACGGAGTTGTGTTGCTAGAGCTG : 2900
L29- (♀) -R : gtttctcacgcatgaaactgtgctgAAAACGCTTTAGACGGTGAGCGGAAGAGAATCAGACGTTTACAGTTACGGAGTTGTGTTGCTAGAGCTG : 2772
                                     BLR-C-2808_P
                                     BLR-C-InDel_R
                                     BLR-C-2808_R

          *          2920          *          2940          *          2960          *          2980          *          3000
Bo1040029 : CGAGGAAGAGAGCGGTGGACAAGTCCTTCCCGGACAGTACTGATATACTAGCTGGGTGAGATCTATGTTGAGCAGCAGCAGCGTACACACATGGTGTC : 3000
L16- (♂) -S : CGAGGAAGAGAGCGGTGGACAAGTCCTTCCCGGACAGTACTGATATACTAGCTGGGTGAGATCTATGTTGAGCAGCAGCAGCGTACACACATGGTGTC : 3000
L29- (♀) -R : CGAGGAAGAGAGCGGTGGACAAGTCCTTCCCGGACAGTACTGATATACTAGCTGGGTGAGATCTATGTTGAGCAGCAGCAGCGTACACACATGGTGTC : 2872

          *          3020          *          3040          *          3060          *          3080          *          3100
Bo1040029 : AACCAATTGTTGATCCGTTCTTCCGGACGAGCTTCTTAATTCGGATCTTAGGGAACAGATAGTTGAGGTGACTGAATTGGCACTGAGTTGTACGGAGAGA : 3100
L16- (♂) -S : AACCAATTGTTGATCCGTTCTTCCGGACGAGCTTCTTAATTCGGATCTTAGGGAACAGATAGTTGAGGTGACTGAATTGGCACTGAGTTGTACGGAGAGA : 3100
L29- (♀) -R : AACCAATTGTTGATCCGTTCTTCCGGACGAGCTTCTTAATTCGGATCTTAGGGAACAGATAGTTGAGGTGACTGAATTGGCACTGAGTTGTACGGAGAGA : 2972

          *          3120          *          3140          *          3160          *          3180          *          3200
Bo1040029 : GATCCAGCGAGGAGACCGACGATGAGAGAGGTGGTGAAATGTGTTGCGATGCGCAAGGTCTTGTAAAGATGCCCTCGGGTTCAAGTTCCGTAATcttttac : 3200
L16- (♂) -S : GATCCAGCGAGGAGACCGACGATGAGAGAGGTGGTGAAATGTGTTGCGATGCGCAAGGTCTTGTAAAGATGCCCTCGGGTTCAAGTTCCGTAATcttttac : 3200
L29- (♀) -R : GATCCAGCGAGGAGACCGACGATGAGAGAGGTGGTGAAATGTGTTGCGATGCGCAAGGTCTTGTAAAGATGCCCTCGGGTTCAAGTTCCGTAATcttttac : 3072

          *          3220          *          3240          *          3260          *          3280          *          3300
Bo1040029 : taaggctctttactaagggaagggccgaaggggatgttattagtaagtagtaagtgtaagtgttttggttaactagaagtaatectaactcgccctataatgggc : 3302
L16- (♂) -S : taaggctctttactaagggaagggccgaaggggatgttattagtaagtagtaagtgtaagtgttttggttaactagaagtaatectaactcgccctataatgggc : 3302
L29- (♀) -R : taaggctctttactaagggaagggccgaaggggatgttattagtaagtagtaagtgtaagtgttttggttaactagaagtaatectaactcgccctataatgggc : 3174
                                     3R5

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Figure S4: Alignment of nucleotide sequences of the gene *Bol040029* from the susceptible (L16) and resistant lines (L29) using Clustal Omega showing the positions of the developed InDel and high resolution melting (HRM) Markers, *BLR-C-InDel-F/R* and *BLR-C-2808*, respectively.

The positions are mentioned including the UTR regions.

The polymorphic primer set (3F3-3R3, Figure 3) is shown in box and the InDel (*BLR-C-InDel-F/R*) and the HRM (*BLR-C-2808*) marker developed for detecting blackleg resistant and susceptible genotypes are presented as yellow and green highlighted text, respectively. The 128 bp deleted region of the resistant line is highlighted gray and the C²⁸⁰⁸T SNP within the HRM probe *BLR-C-2808-P* is shown in green highlighted text.

The SNPs that generated two LRR domains in the resistant line (L29) is highlighted in white text and red background and the genome regions encoding these two LRR domains, LRR-1 and LRR-2 are blue and red underlined, respectively.

Light blue text = 5' and 3' UTR region; bold, red and underlined text = start and stop codons; black text = exon; red and lower case text = intron; shaded single nucleotides = SNPs. The six set of primers (Table S2) used for cloning the six fragments of this gene are underlined.

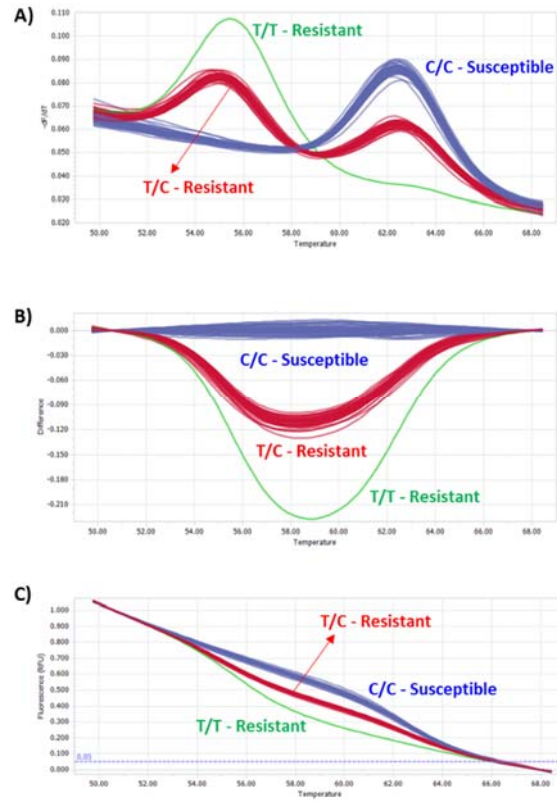


Figure S6. Normalized melting peaks (A), the difference plots (B) and normalized melting curves (C) of the high resolution melting analysis of 253 BC1 lines generated from the resistant (R) and susceptible (S) parental lines, L29 (♀) and L16 (♂), respectively using the developed HRM marker BLR-C-2808 (forward and reverse primers and C2808T SNP based probe).

Only the plots of representative 96 samples are shown here. The genotyping results of all 253 BC1 lines are shown in Figure 6 and Table S1 and of 30 commercial inbred lines are shown in Figure 7.

Table S1: Disease scores against the *Leptospira maculans* isolate 03-02s and prediction of resistance by developed InDel and HRM markers in the 253 BC1 population raised from resistant and susceptible parental lines L29 (♀) and L16 (♂), respectively. R. Resistant, S. Susceptible, Hetero. Heterozygous, InDel. Insertion-Deletion, HRM. High Resolution Melting.

Lines	Disease Score	Resistance Status	InDel (BLR-C-F/R)	HRM (BLR-C-2808)
L16 (♂)	9	S	S	CC_S
L29 (♀)	2	R	Hetero_R	TT_R
F1	2	R	Hetero_R	Hetero-R
BC1_1	2	R	Hetero_R	Hetero-R
BC1_2	4	R	Hetero_R	Hetero-R
BC1_3	6	S	S	CC_S
BC1_4	8	S	S	CC_S
BC1_5	5	R	S	CC_S
BC1_6	6	S	S	CC_S
BC1_7	3	R	Hetero_R	Hetero-R
BC1_8	9	S	S	CC_S
BC1_9	6	S	S	CC_S
BC1_10	6	S	Hetero_R	Hetero-R
BC1_11	1	R	Hetero_R	Hetero-R
BC1_12	2	R	Hetero_R	Hetero-R
BC1_13	8	S	S	CC_S
BC1_14	6	S	S	CC_S
BC1_15	7	S	Hetero_R	Hetero-R
BC1_16	8	S	S	CC_S
BC1_17	4	R	Hetero_R	Hetero-R
BC1_18	2	R	Hetero_R	Hetero-R
BC1_19	8	S	S	CC_S
BC1_20	6	S	S	CC_S
BC1_21	4	R	S	CC_S
BC1_22	5	R	S	CC_S
BC1_23	9	S	S	CC_S
BC1_24	8	S	S	CC_S
BC1_25	4	R	Hetero_R	Hetero-R
BC1_26	2	R	Hetero_R	Hetero-R
BC1_27	6	S	S	CC_S
BC1_28	6	S	Hetero_R	Hetero-R
BC1_29	9	S	S	CC_S
BC1_30	0	R	Hetero_R	Hetero-R
BC1_31	9	S	S	CC_S
BC1_32	8	S	S	CC_S
BC1_33	2	R	Hetero_R	Hetero-R
BC1_34	6	S	Hetero_R	Hetero-R
BC1_35	7	S	S	CC_S
BC1_36	4	R	S	CC_S
BC1_37	8	S	S	CC_S
BC1_38	6	S	S	CC_S
BC1_39	9	S	S	CC_S
BC1_40	7	S	S	CC_S
BC1_41	5	R	S	CC_S
BC1_42	3	R	Hetero_R	Hetero-R
BC1_43	6	S	S	CC_S
BC1_44	6	S	Hetero_R	Hetero-R
BC1_45	7	S	S	CC_S
BC1_46	6	S	S	CC_S
BC1_47	4	R	Hetero_R	Hetero-R
BC1_48	8	S	S	CC_S
BC1_49	3	R	Hetero_R	Hetero-R
BC1_50	7	S	Hetero_R	Hetero-R
BC1_51	6	S	S	CC_S
BC1_52	8	S	S	CC_S
BC1_53	5	R	Hetero_R	Hetero-R
BC1_54	5	R	Hetero_R	Hetero-R
BC1_55	9	S	S	CC_S
BC1_56	5	R	Hetero_R	Hetero-R
BC1_57	6	S	Hetero_R	Hetero-R
BC1_58	5	R	S	CC_S

Lines	Disease Score	Resistance Status	InDel (BLR-C-F/R)	HRM (BLR-C-2808)
BC1_61	3	R	Hetero_R	Hetero-R
BC1_62	9	S	S	CC_S
BC1_63	5	R	Hetero_R	Hetero-R
BC1_64	9	S	S	CC_S
BC1_65	6	S	S	CC_S
BC1_66	4	R	Hetero_R	Hetero-R
BC1_67	5	R	S	CC_S
BC1_68	6	S	S	CC_S
BC1_69	6	S	S	CC_S
BC1_70	8	S	S	CC_S
BC1_71	6	S	S	CC_S
BC1_72	3	R	Hetero_R	Hetero-R
BC1_73	4	R	Hetero_R	Hetero-R
BC1_74	9	S	S	CC_S
BC1_75	9	S	S	CC_S
BC1_76	5	R	S	CC_S
BC1_77	5	R	Hetero_R	Hetero-R
BC1_78	6	S	Hetero_R	Hetero-R
BC1_79	5	R	Hetero_R	Hetero-R
BC1_80	6	S	S	CC_S
BC1_81	5	R	Hetero_R	Hetero-R
BC1_82	6	S	Hetero_R	Hetero-R
BC1_83	7	S	S	CC_S
BC1_84	5	R	Hetero_R	Hetero-R
BC1_85	8	S	S	CC_S
BC1_86	4	R	Hetero_R	Hetero-R
BC1_87	5	R	Hetero_R	Hetero-R
BC1_88	3	R	Hetero_R	Hetero-R
BC1_89	5	R	Hetero_R	Hetero-R
BC1_90	4	R	S	CC_S
BC1_91	5	R	Hetero_R	Hetero-R
BC1_92	5	R	Hetero_R	Hetero-R
BC1_93	6	S	S	CC_S
BC1_94	5	R	Hetero_R	Hetero-R
BC1_95	5	R	S	CC_S
BC1_96	5	R	Hetero_R	Hetero-R
BC1_97	6	S	Hetero_R	Hetero-R
BC1_98	5	R	Hetero_R	Hetero-R
BC1_99	4	R	Hetero_R	Hetero-R
BC1_100	5	R	Hetero_R	Hetero-R
BC1_101	8	S	S	CC_S
BC1_102	7	S	S	CC_S
BC1_103	4	R	Hetero_R	Hetero-R
BC1_104	8	S	S	CC_S
BC1_105	8	S	S	CC_S
BC1_106	6	S	Hetero_R	Hetero-R
BC1_107	3	R	Hetero_R	Hetero-R
BC1_108	6	S	S	CC_S
BC1_109	7	S	S	CC_S
BC1_110	7	S	S	CC_S
BC1_111	5	R	S	CC_S
BC1_112	7	S	S	CC_S
BC1_113	6	S	S	CC_S
BC1_114	7	S	S	CC_S
BC1_115	7	S	Hetero_R	Hetero-R
BC1_116	4	R	Hetero_R	Hetero-R
BC1_117	7	S	S	CC_S
BC1_118	0	R	Hetero_R	Hetero-R
BC1_119	7	S	S	CC_S
BC1_120	2	R	Hetero_R	Hetero-R
BC1_121	4	R	Hetero_R	Hetero-R

Lines	Disease Score	Resistance Status	InDel (BLR-C-F/R)	HRM (BLR-C-2808)
BC1_59	9	S	S	CC_S
BC1_60	5	R	Hetero_R	Hetero-R
BC1_124	5	R	Hetero_R	Hetero-R
BC1_125	6	S	S	CC_S
BC1_126	7	S	Hetero_R	Hetero-R
BC1_127	4	R	Hetero_R	Hetero-R
BC1_128	2	R	Hetero_R	Hetero-R
BC1_129	5	R	Hetero_R	Hetero-R
BC1_130	4	R	Hetero_R	Hetero-R
BC1_131	5	R	S	Hetero-R
BC1_132	5	R	Hetero_R	Hetero-R
BC1_133	5	R	Hetero_R	Hetero-R
BC1_134	8	S	S	CC_S
BC1_135	6	S	Hetero_R	Hetero-R
BC1_136	6	S	S	CC_S
BC1_137	3	R	Hetero_R	Hetero-R
BC1_138	1	R	Hetero_R	Hetero-R
BC1_139	5	R	Hetero_R	Hetero-R
BC1_140	5	R	S	CC_S
BC1_141	5	R	Hetero_R	Hetero-R
BC1_142	6	S	S	CC_S
BC1_143	6	S	Hetero_R	Hetero-R
BC1_144	3	R	Hetero_R	Hetero-R
BC1_145	5	R	Hetero_R	Hetero-R
BC1_146	7	S	S	CC_S
BC1_147	3	R	Hetero_R	Hetero-R
BC1_148	2	R	Hetero_R	Hetero-R
BC1_149	4	R	Hetero_R	Hetero-R
BC1_150	4	R	Hetero_R	Hetero-R
BC1_151	7	S	S	CC_S
BC1_152	5	R	S	CC_S
BC1_153	8	S	S	CC_S
BC1_154	5	R	Hetero_R	Hetero-R
BC1_155	7	S	Hetero_R	Hetero-R
BC1_156	8	S	S	CC_S
BC1_157	6	S	S	CC_S
BC1_158	7	S	S	CC_S
BC1_159	4	R	Hetero_R	Hetero-R
BC1_160	6	S	S	CC_S
BC1_161	7	S	S	CC_S
BC1_162	3	R	Hetero_R	Hetero-R
BC1_163	5	R	Hetero_R	Hetero-R
BC1_164	6	S	Hetero_R	Hetero-R
BC1_165	6	S	S	CC_S
BC1_166	4	R	Hetero_R	Hetero-R
BC1_167	7	S	S	CC_S
BC1_168	6	S	Hetero_R	Hetero-R
BC1_169	2	R	Hetero_R	Hetero-R
BC1_170	5	R	S	CC_S
BC1_171	7	S	S	CC_S
BC1_172	6	S	S	CC_S
BC1_173	4	R	Hetero_R	Hetero-R
BC1_174	8	S	S	CC_S
BC1_175	3	R	Hetero_R	Hetero-R
BC1_176	7	S	S	CC_S
BC1_177	5	R	Hetero_R	Hetero-R
BC1_178	6	S	S	CC_S
BC1_179	7	S	S	CC_S
BC1_180	4	R	S	CC_S
BC1_181	4	R	Hetero_R	Hetero-R
BC1_182	4	R	Hetero_R	Hetero-R
BC1_183	7	S	Hetero_R	Hetero-R
BC1_184	2	R	Hetero_R	Hetero-R
BC1_185	3	R	Hetero_R	Hetero-R
BC1_186	6	S	Hetero_R	Hetero-R
BC1_187	7	S	S	CC_S
BC1_188	6	S	S	CC_S

Lines	Disease Score	Resistance Status	InDel (BLR-C-F/R)	HRM (BLR-C-2808)
BC1_122	6	S	Hetero_R	Hetero-R
BC1_123	4	R	Hetero_R	Hetero-R
BC1_189	4	R	Hetero_R	Hetero-R
BC1_190	8	S	S	CC_S
BC1_191	5	R	S	CC_S
BC1_192	6	S	S	CC_S
BC1_193	7	S	S	CC_S
BC1_194	6	S	S	CC_S
BC1_195	3	R	Hetero_R	Hetero-R
BC1_196	1	R	Hetero_R	Hetero-R
BC1_197	4	R	Hetero_R	Hetero-R
BC1_198	6	S	S	CC_S
BC1_199	7	S	S	CC_S
BC1_200	6	S	Hetero_R	Hetero-R
BC1_201	7	S	S	CC_S
BC1_202	4	R	Hetero_R	Hetero-R
BC1_203	7	S	S	CC_S
BC1_204	3	R	Hetero_R	Hetero-R
BC1_205	3	R	Hetero_R	Hetero-R
BC1_206	5	R	S	CC_S
BC1_207	7	S	S	CC_S
BC1_208	7	S	S	CC_S
BC1_209	8	S	S	CC_S
BC1_210	7	S	Hetero_R	Hetero-R
BC1_211	2	R	Hetero_R	Hetero-R
BC1_212	4	R	Hetero_R	Hetero-R
BC1_213	8	S	S	CC_S
BC1_214	5	R	Hetero_R	Hetero-R
BC1_215	3	R	Hetero_R	Hetero-R
BC1_216	7	S	S	CC_S
BC1_217	5	R	Hetero_R	Hetero-R
BC1_218	7	S	S	CC_S
BC1_219	6	S	Hetero_R	CC_S
BC1_220	6	S	Hetero_R	CC_S
BC1_221	2	R	Hetero_R	Hetero-R
BC1_222	6	S	Hetero_R	Hetero-R
BC1_223	6	S	S	CC_S
BC1_224	1	R	Hetero_R	Hetero-R
BC1_225	5	R	Hetero_R	Hetero-R
BC1_226	2	R	Hetero_R	Hetero-R
BC1_227	6	S	S	CC_S
BC1_228	4	R	Hetero_R	Hetero-R
BC1_229	6	S	Hetero_R	Hetero-R
BC1_230	7	S	S	CC_S
BC1_231	4	R	Hetero_R	Hetero-R
BC1_232	7	S	S	CC_S
BC1_233	6	S	Hetero_R	Hetero-R
BC1_234	4	R	S	CC_S
BC1_235	8	S	S	CC_S
BC1_236	7	S	S	CC_S
BC1_237	2	R	Hetero_R	Hetero-R
BC1_238	5	R	Hetero_R	Hetero-R
BC1_239	8	S	S	CC_S
BC1_240	3	R	Hetero_R	Hetero-R
BC1_241	7	S	S	CC_S
BC1_242	5	R	Hetero_R	Hetero-R
BC1_243	5	R	S	CC_S
BC1_244	4	R	Hetero_R	Hetero-R
BC1_245	5	R	Hetero_R	Hetero-R
BC1_246	7	S	S	CC_S
BC1_247	6	S	S	CC_S
BC1_248	5	R	S	Hetero-R
BC1_249	3	R	Hetero_R	Hetero-R
BC1_250	2	R	Hetero_R	Hetero-R
BC1_251	7	S	Hetero_R	Hetero-R
BC1_252	8	S	S	CC_S
BC1_253	6	S	S	CC_S

R. Resistant, S. Susceptible, Hetero. Heterozygous, InDel. Insertion-Deletion, HRM. High Resolution Melting.

Table S2. Specifications of primers designed for cloning the six consecutive fragments covering the entire length of the gene *Bol040029*.

Cloning Fragments	Forward Primer (5'-3')	Reverse Primer (5'-3')	Length (bp)
Fragment-1	3F1: GGTTGGTTCTTTGCCTGAGA	3sR1: AGAAGCCGTTGTTGAAGAGAGT	578
Fragment-2	3sF2: ACTCTCTTCAACAACGGCTTCT	3sR2: GTTAAACCCAACGTCAAAACGC	514
Fragment-3	3F2: GCGTTTTGACGTTGGGTTTAAC	3sR3: TATAAGCACGATCTTCCAGGTG	571
Fragment-4	3sF3: CACCTGGAAGATCGTGCTTATA	3R3: CTGTGACCGTTGCAGTTGAG	683
Fragment-5	3F4: CTCAACTGCAACGGTCACAG	3R4: GAGTTGTGTGCTAGAGCTG	634
Fragment-6	3F5: CAGCTCTAGCAACACAACCTC	3R5: GCCCATTATAGGCCGAGTTA	414

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