



Evolution of wheat blast resistance gene Rmg8 accompanied by differentiation of variants recognizing the powdery mildew fungus

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Supplementary Table 1. Primers used in this study

Objectives	Primer name	Sequence(5' > 3')	Description
Mapping of <i>Rmg8</i>	KM9-F	TGATGGTCTGACGTCCGTGC	CAPS marker (<i>Spe</i> I)
	KM9-R	CAATCACTACCAGTAACGTTACACGGTG	
	KM12-F	TAGAGCTCTCAAGCAGCACTCCCTTGAG	CAPS marker (<i>Hinf</i> I)
	KM12-R	GAAGTGGAAAGGTTAGACACTGAGGAAG	
	KM13-F	GTGCCACCAGGGCGACTTGTTC	CAPS marker (<i>Msp</i> I)
	KM13-R	AGTCTCCCCAAAGTCCAGCGG	
	KM25-F	AGGTAGATGCTGCTATGTGACTTGTG	Presence/absence marker (presence in Sch)
	KM25-R	AGACGGAGATTGTGATGAGGAG	
	KM27-F	AGGCACGGAAGGCAATTTCAC	Presence/absence marker (presence in S-615)
	KM27-R	TGCTCGCTGATAGCATCAACAAG	
	KM30-F	AACCGTGAGATTCCACTG	Presence/absence marker (presence in S-615)
	KM30-R	TATCTCCGTAAAGAGCTTCCAAGA	
	KM65-F	ACGATGCATCCTTGATACATCAAC	CAPS marker (<i>Hae</i> III)
	KM65-R	TCCGTGTCACAGTTCAGAAATAGATAG	
	KM109-F	TGGATTGTTCTTCATCGCTTC	CAPS marker (<i>Hae</i> III)
	KM109-R	TGTTGGAACGTAGGGTTCAACC	
	KM138-F	ATAACGCTGAGTCAAAGTCTCCAC	Presence/absence marker (presence in S-615)
	KM138-R	TAGATACGGTTGAAATGCTTCTTCTC	
	KM140-F	AGCATCATCCAAAAGTCCC	Presence/absence marker (presence in S-615)
	KM140-R	TGTATTGAGAAATCGTTACCTGG	
	KM155-F	AGATGGGATTGACAGCTTG	Presence/absence marker (presence in Sch)
	KM155-R	AGAACATGTGCCACTACAAGGC	
Mapping of <i>Rmg8</i>	KM171-F	TGACGCTAGAGACCAACAGATG	Presence/absence marker (presence in S-615)
& Detection of <i>Rmg8</i> variants	KM171-R	ACCATTGGAAGGATGAGCTG	
Mapping of <i>Rmg8</i> and <i>Rmg7</i>	KM200-F	TTCGACGGCATCTGCAAGTGGAAAGACCC	Presence/absence marker (presence in S-615)
& Detection of <i>Rmg8</i> variants	KM200-R	ACTGCGCGCGCTCCCCCTGCAT	
Mapping of <i>Rmg7</i>	KM201-F	AAAAATAGAGGTGCGGTGGTAG	CAPS marker (<i>Mbo</i> I)
	KM201-R	AAAAGAGGGGATTGAAGGAG	
	KM202-F	AAGGGTCAGGCGTTAATGG	CAPS marker (<i>Xho</i> I)
	KM202-R	ATCCAGCATCCTGCACATT	
Transgene detection*	HPT-F	GTGTCACTGTTGCAAGACCTG	for detection of transgene
	HPT-R	GATGTTGGCGACCTCGTATT	
Protoplast assay	InF-Rmg8-V1-F	TGTGTGTCAGATCGGGTTACTGACTGCAAATG	for In-Fusion cloning of <i>Rmg8-V1</i> and <i>Rmg7-V1</i>
& transformation of Fielder	InF-Rmg8-V1-R	GGAAATTGAGCTCGAACACATTCAAGAGAG	
	InF-Rmg8-V2-F	TGTGTGTCAGATCGGGTTACTGACTGCAAATG	for In-Fusion cloning of <i>Rmg8-V2</i> and <i>Rmg7-V2</i>
	InF-Rmg8-V2-R	GGAAATTGAGCTCGCACGTCAATACTTCAT	
	InF-Rmg8-genome-F	TGTGTGTCAGATCGGGTTACTGACTGCAAATG	for In-Fusion cloning of <i>Rmg8</i> -genome
	InF-Rmg8-genome-R	GGAAATTGAGCTCGCACGTCAATACTTCAT	
Protoplast assay	InF-PWT3dSP-F	TGTGTGTCAGATCGATGAGTGACTTTGGAAAGTA	for In-Fusion cloning of <i>PWT3</i> without its signal peptide
	InF-PWT3dSP-R	GGAAATTGAGCTCGTACGGCGATGCAAACAGC	
	InF-avr-Rmg8dSP-F	TGTGTGTCAGATCGATGCTGCCTGCGCCGAG	for In-Fusion cloning of <i>avr-Rmg8</i> without its signal peptide
	InF-avr-Rmg8dSP-R	GGAAATTGAGCTCGCTACTGCCTCTAGTACCG	
<i>Rmg8</i> variant analysis	Rmg8-E5-F	GGTTCTACTGACTGCAAATGGA	for amplification of Exon 1-5 of <i>Rmg8</i> variants in <i>Triticum</i> spp.
	Rmg8-E5-R	TGTAGCAACCCAATTAAAGGAAG	and <i>Ae. speltoides</i> from genomic DNA
	Rmg8-V1V2-F	GAAACGTGCTACCAGACAGAAATC	for amplification of Exon 6 (V1) and Exon 7 (V2) of <i>Rmg8</i> variants
	Rmg8-V1V2-R	CAACATGAAGAAATTATCGTCA	in <i>Triticum</i> spp. and <i>Ae. speltoides</i> from genomic DNA
	Rmg8U-V1-1R	ATTTCACAAAGAGAGCTAGCGG	for amplification of <i>AeuRmg8</i> V1 variant from cDNA of <i>Ae. umbellulata</i> accessions in combination with Rmg8-E5-F
	Rmg8U-V2-1R	AAATTCCATCATCACAGGAGCAC	for amplification of <i>AeuRmg8</i> V2 variant from cDNA of <i>Ae. umbellulata</i> accessions (KU-4026, KU-4103, KU-5934, KU-12198) in combination with Rmg8-E5-F
	Rmg8U-V2-2R	AAGTAATTGCAACATGAAGAAATT	for amplification of <i>AeuRmg8</i> V2 variant from cDNA of <i>Ae. umbellulata</i> accessions (KU-8-5, KU-4035, KU-4043, KU-5954) in combination with Rmg8-E5-F
	Rmg8M-V1-1R	GTCAGGTCAAGCAGGTGG	for amplification of <i>AecRmg8</i> V1 variant from cDNA of <i>Ae. comosa</i> (KU-17-2) with Rmg8-E5-F
	Rmg8M-V2-1R	AAATTCCATCGTCACAGGAGC	for amplification of <i>AecRmg8</i> V2 variant from cDNA of <i>Ae. comosa</i> (KU-17-2) with Rmg8-E5-F
	M13_fwd	GTAAAACGACGGCCAGT	for sanger sequencing
	T3_promoter	ATTAACCCCTCACTAAAGGGAA	for sanger sequencing
	Rmg8-seq-F1	GAAACCCGCCAATATACTGCTC	for sanger sequencing
	Rmg8-seq-F2	ATGCTATGAGACAGCTTAGAGTGC	for sanger sequencing
	Rmg8-seq-F3	GAAACGTGCTACCAGACAGAAATC	for sanger sequencing
	Rmg8-seq-F4	AAGTGGTCAGCCTGTTGGTG	for sanger sequencing
	Rmg8-seq-F5	ATGACGCTAGAGACCAACAGATG	for sanger sequencing
	Rmg8-seq-F6	AGTATGCCAAACCGCAGCTC	for sanger sequencing
	Rmg8-seq-F7	ATCCTTCAATGGTGTACTGTG	for sanger sequencing
	Rmg8-seq-R1	TCCATAAGAGCATTGGACATCC	for sanger sequencing
	Rmg8-seq-R2	TTTGTCCGGTCAGTATTCTAGG	for sanger sequencing
	Rmg8-seq-R3	CACGACCTTGAGGTACATGAGTT	for sanger sequencing
	Rmg8-seq-R4	TCCGTCTCAAGGCTCAGATG	for sanger sequencing
	Rmg8-seq-R5	GGACATGAAGCGGTAGAAGTT	for sanger sequencing
	Rmg8-seq-R6	TGTTGTCCATTTGGAGC	for sanger sequencing
	Rmg8-seq-R7	CAACATGAAGAAATTATCGTCA	for sanger sequencing
	Rmg8U_V1_seq_F1	ACCTTCATGATAATCATATTATT	for sanger sequencing
	Rmg8U_V1_seq_R1	TTGGCGGGTTTAGATCCAAGTG	for sanger sequencing
	Rmg8U_V2_seq_F1	GCCGTGAAAGGATGTCATCCAG	for sanger sequencing
	Rmg8U_V2_seq_F2	AGCGCTGACTTGTATAGTCTGG	for sanger sequencing
	Rmg8U_V2_seq_R1	AGCGGCGGGTCGGCCTGCTCCAG	for sanger sequencing
	Rmg8U_V2_seq_R2	CGAGCTCGGCGTGTGACAGCGTC	for sanger sequencing

* Refer to Abe, F. et al. Genome-edited triple recessive mutation alters seed dormancy in wheat. *Cell Rep.* **28**, 1362-1369 (2019).