

5' TGCTCACATGTCTTCGAGAAGGAA 3' MaYMV-F primer

1 50
BR1A (MG570476) TGCTCACATGTCTTCGAGAAGGAATACCTCGCACGCCCGGTTAACCAAAA
KU248489 TGCTCACATGTCTTCGAGAAGGAACACCTCGCACGCCCGGTTAACCAAAA
BR1B.MaYMV.F -----
BR1B.MaYMV.R -----TTCGAGAAGGAATACCTCGCACGCCCGGTTAACCAAAA

51 100
BR1A (MG570476) CAAAATGATTTACAAATTGGTTTATGGTTACAACCCGGCGAACGGTTCAT
KU248489 CAAAATGATCTATAAAATTGGTTTATGGTTATAACCCGGCGAACGGTTCAT
BR1B.MaYMV.F --AAATGATTTACAAATTGGTTTATGGTTACAACCCGGCGAACGGTTCAT
BR1B.MaYMV.R CAAAATGATTTACAAATTGGTTTATGGTTACAACCCGGCGAACGGTTCAT
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101 150
BR1A (MG570476) CGGAGGTCTTGCAGCGTTATCTTGACGCCTGTATGAGCGTGCTTCACGAG
KU248489 CGGAGGTCTTGCAGCGCTATCTTGACGCCTGCATGAGCGTGCTTCACGAG
BR1B.MaYMV.F CGGAGGTCTTGCAGCGTTATCTTGACGCCTGTATGAGCGTGCTTCACGAG
BR1B.MaYMV.R CGGAGGTCTTGCAGCGTTATCTTGACGCCTGTATGAGCGTGCTTCACGAG
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151 200
BR1A (MG570476) CTACGCCATGACCCCGAAAACCGTGGAGCTTCTGTACAAGTGGCTGGTATC
KU248489 CTACGCCATGACCCCGAAAACCGTGGAGCTTCTGTACAAGTGGCTGGTATC
BR1B.MaYMV.F CTACGCCATGACCCCGAAAACCGTGGAGCTTCTGTACAAGTGGCTGGTATC
BR1B.MaYMV.R CTACGCCATGACCCCGAAAACCGTGGAGCTTCTGTACAAGTGGCTGGTATC

201 250
BR1A (MG570476) TCCAGTCCAGCAACAAAAGGTTTGAAAACAGAAGTTTCAAAGGTAGCCAG
KU248489 TCCAGTCCAGCAACAAAAGGTTTGAAACACAGAAGTTTCAAAGGTAGCCAG
BR1B.MaYMV.F TCCAGTCCAGCAACAAAAGGTTTGAAAACAGAAGTTTCAAAGGTAGCCAG
BR1B.MaYMV.R TCCAGTCCAGCAACAAAAGGTTTGAAAACAGAAGYTTCAAAGGTAGCCAG
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251 300
BR1A (MG570476) ACACACGTGAGTTGCAAGTGCTGGAATCCTAGTCTCACACATAAGCAGCC
KU248489 ACACACGTGAGTTGCAAGTGCTGGAATCCTAGTCTCACACATAAGCAGCC
BR1B.MaYMV.F ACACACGTGAGTTGCAAGTGCTGGAATCCTAGTCTCACACATAAGCAGCC
BR1B.MaYMV.R ACACACGTGAGTTGCAAGTGCTGGAATCCTAGTCTCACACATAAGCAGCC
* *

301 350
BR1A (MG570476) ATAGATTGAAACTCTTTTGCGGGGTTCTTATAGGGATCCTCGTTGCTGT
KU248489 ATAGATTGAAACTCTTTTGCGGGGTTCTCATAGGGATCCTCGTTGCTGT
BR1B.MaYMV.F ATAGATTGAAACTCTTTTGCGGGGTTCTTATAGGGATCCTCGTTGCTGT
BR1B.MaYMV.R ATAGATTGAAACTCTTTTGCGGGGTTCTTATAGGGATCCTCGTTGCTGT
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351 400
BR1A (MG570476) CCCCGTAACCATCTTTGGCTTGTACAAGATCTACCTATCTATCTCCTCGA
KU248489 CCCCGTAACCATCTTTGGCTTGTACAAGATCTACCTATCTATCTCCTCGA
BR1B.MaYMV.F CCCCGTAACCATCTTTGGCTTGTACAAGATCTACCTATCTATCTCCTCGA
BR1B.MaYMV.R CCCCGTAACCATCTTTGGCTTGTACAAGATCTACCTATCTATCTCCTCGA

401 450
BR1A (MG570476) ACGTGC GTTCAATTGTGAATGAATACGGGAGGTAGAAATGGACGCAGAGC
KU248489 ACGTGC GTTCAATTGTGAATGAATACGGGAGGTAGAAATGGACGCAGAGC
BR1B.MaYMV.F ACGTGC GTTCAATTGTGAATGAATACGGGAGGTAGAAATGGACGCAGAGC
BR1B.MaYMV.R ACGTGC GTTCAATTGTGAATGAATACGGGAGGTAGAAATGGACGCAGAGC

451 500
BR1A (MG570476) TAGGAACCGCCGACGCGCTCGCAATAATAACCGGGCCCAGCCAGTGGTTG
KU248489 TAGGAACCGCCGACGCGCTCGCAATAATAACCGGGCCCAGCCAGTGGTTG
BR1B.MaYMV.F TAGGAACCGCCGACGCGCTCGCAATAATAACCGGGCCCAGCCAGTGGTTG
BR1B.MaYMV.R TAGGAACCGCCGACGCGCTCGCAATAATAACCGGGCCCAGCCAGTGGTTG

	501	550
BR1A (MG570476)	TTGTCGCGGCAAATCCGCGTCGAGGACGCCCTCGAAGACGAAGACGACCA	
KU248489	TTGTCGCGGCAAATCCGCGTCGAGGACGCCCTCGAAGACGAAGACGACCA	
BR1B.MaYMV.F	TTGTCGCGGCAAATCCGCGTCGAGGACGCCCTCGAAGACGAAGACGACCA	
BR1B.MaYMV.R	TTGTCGCGGCAAATCCGCGTCGAGGACGCCCTCGAAGACGAAGACGACCA	
	551	600
BR1A (MG570476)	AGTGGAAACACTGCAGGAAGACCTGGAGTCAGACGAGGCTCGCGGGAGAC	
KU248489	AGTGGAAACACTGCAGGAAGACCTGGAGTCAGACGAGGCTCGCGGGAGAC	
BR1B.MaYMV.F	AGTGGAAACACTGCAGGAAGACCTGGAGTCAGACGAGGCTCGCGGGAGAC	
BR1B.MaYMV.R	AGTGGAAACACTGCAGGAAGACCTGGAGTCAGACGAGGCTCGCGGGAGAC	
	601	650
BR1A (MG570476)	TTTTGTATTTTCAAAGGACTCTCTCACGGGCAATGCCTCCGAAAAGTCA	
KU248489	TTTTGTATTTTCAAAGGACTCTCTCACGGGCAATGCCTCCGAAAAGTCA	
BR1B.MaYMV.F	TTTTGTATTTTCAAAGGACTCTCTCACGGGCAATGCCTCCGAAAAGTCA	
BR1B.MaYMV.R	TTTTGTATTTTCAAAGGACTCTCTCACGGGCAATGCCTCCGAAAAGTCA	
	651	700
BR1A (MG570476)	CCTTCGGGCCGTCTTTATCAGAGTGTGCAGCATTCAGTGGCGGAATTCTC	
KU248489	CCTTCGGGCCGTCTTTATCAGAGTGTGCAGCATTCAGTGGCGGAATTCTC	
BR1B.MaYMV.F	CCTTCGGGCCGTCTTTATCAGAGTGTGCAGCATTCAGTGGCGGAATTCTC	
BR1B.MaYMV.R	CCTTCGGGCCGTCTTTATCAGAGTGTGCAGCATTCAGTGGCGGAAT-CTC	*
	701	753
BR1A (MG570476)	AAGGCCTACCATGAGTATAAGATCTCAAAGATCATACTGGAGTTCATCTCCGA	
KU248489	AAGGCCTACCATGAGTATAAGATCTCAAAGATCATACTGGAGTTCATCTCCGA	
BR1B.MaYMV.F	AAGGCCTACCATGAGTATAAGATCTCAAAGATCATACTGGA-----	
BR1B.MaYMV.R	AAGGCCTACC-----	

MaYMV-R primer 3' TCTAGTATGACCTCAAGTAGAGGCT 5'

Online Resource 6. Confirmation by Sanger sequencing that the expected maize yellow mosaic virus RT-PCR product was amplified from maize inbred B73 sample BR1B. Sequences derived from sequencing the 753bp RT-PCR product with the MaYMV-F or MaYMV-R primers were named BR1B.MaYMV.F or BR1B.MaYMV.R, respectively. These sequences were aligned to the corresponding sequence from the assembled MaYMV RSA BR1A genome sequence determined by 5'RACE, 3'RACE, RT-PCR and Sanger sequencing [BR1A (MG570476)], and the reference sequence MaYMV Yunnan 11 from China [KU248489]. The MaYMV-F and MaYMV-R primer sequences are reported in Chen *et al.* (2016). Non-consensus sites are shown by an asterisk.

Chen S, Jiang G, Wu J, Liu Y, Qian Y, Zhou X (2016) Characterization of a Novel Polerovirus Infecting Maize in China. *Viruses* 8 (5):120