

Supplementary Table 2. The oligo sequences used in this study

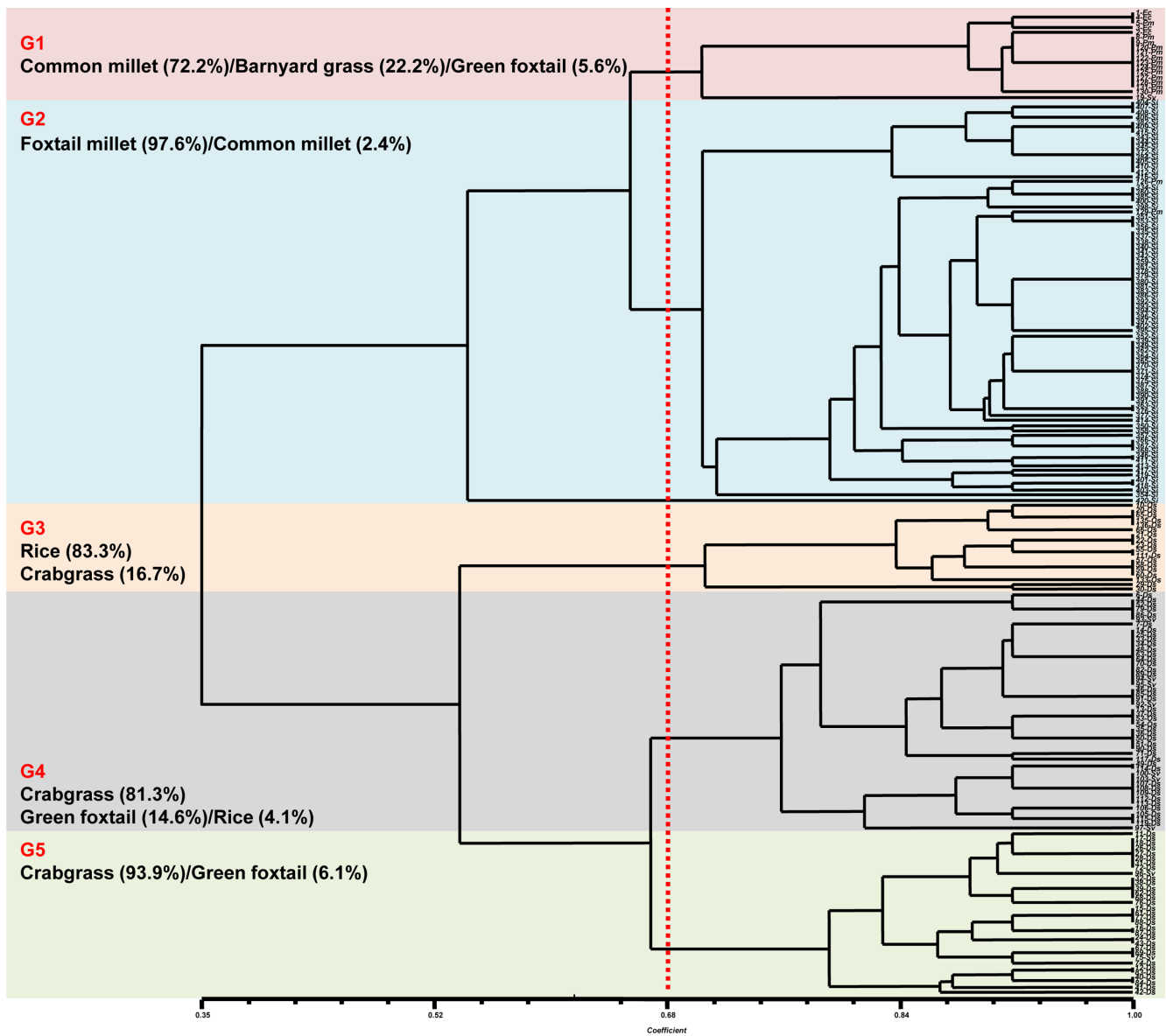
Name	Sequence (5'→3')	Reference
Phylogenetic analysis		
ITS5	GGAAGTAAAAGTCGTAACAAGG	White et al. (1990)
ITS4	TCCTCCGCTTATTGATATGC	White et al. (1990)
<i>Pot2</i> rep-PCR		
Pot2-1	CGGAAGCCCTAAAGCTGTTT	George et al. (1998)
Pot2-2	CCCTCATTCGTCACACGTTT	George et al. (1998)
Avirulence genes		
Avr-Pita_ORF_F	ATGCTTTTTTATTTCATTATTTTTTTTTTTCACAC	Park et al. (2010)
Avr-Pita_ORF_R	TTAACAATATTTATAACGTGCACATTGTG	Park et al. (2010)
Avr-Pita3_F	TTTCTCTCTTTTCGTTTTTCTC	This study
Avr-Pita3_R	TGTGGGTTCTCTCTGGCTTC	This study
Avr-Pia_ORF_F	ATGCATTTTTCGACAATTTTCATCCCC	This study
Avr-Pia_ORF_R	ACCTAGTAAGGCTCGGCAG	This study
Avr-Pii_ORF_F	ATGCAACTTTCCAAAATTACTTTTCGC	This study
Avr-Pii_ORF_R	TTAGTTGCATTTATGATTAAAATACGCGTC	This study
Avr-Pikm_ORF_F	ATGCGTGTACCACITTTAACACA	Park et al. (2010)
Avr-Pikm_ORF_R	TTAAAAGCCGGCCTTTTTTTCC	Park et al. (2010)
AvrPiz-t_ORF_F	ATGCAGTTCTCAACCATCATCACC	This study
AvrPiz-t_ORF_R	CTATTGGCGCTGAGCCTGAG	This study
Avr1-CO39_ORF_F	ATGAAAGTCCAAGCTACATTTCGCC	This study
Avr1-CO39_ORF_R	TCAACAAGACTCATCGTCGTCAGC	This study
PWL2_ORF_F	ATGCAACAACATCATCCTCCCTTTTGC	This study
PWL2_ORF_R	CATAATATGTCAGCCCTCTTCTCGCTG	This study
ACE1_F	GCAGGCTTCCACCATGGACTTTATTT	This study
ACE1_R	CGAATGCCTTTGCCGTGAGTTCAT	This study

Supplementary Table 4. Proportions of isolates from rice and crabgrass before and after inoculation

Tested host	Original host	Isolate	Before inoculation (%)	After inoculation (%)
Rice	Rice-origin	W11-21	10.00	27.94
		W11-54	10.00	2.21
		W11-58	10.00	16.18
		W11-65	10.00	4.41
		W11-145	10.00	19.85
		W11-165	10.00	2.94
	Crabgrass-origin	W11-62	10.00	4.41
		W11-110	10.00	4.41
		W11-111	10.00	13.24
		W11-394	10.00	4.41
Crabgrass	Rice-origin	W11-21	12.50	0.00
		W11-58	12.50	0.00
		W11-65	12.50	0.00
		W11-141	12.50	0.00
	Crabgrass-origin	W11-11	12.50	41.46
		W11-12	12.50	4.88
		W11-62	12.50	41.46
		W11-76	12.50	12.20

References

- George, M. L. C., Nelson, R. J., Zeigler, R. S. and Leung, H. 1998. Rapid population analysis of *Magnaporthe grisea* by using rep-PCR and endogenous repetitive DNA sequences. *Phytopathology* 88:223-229.
- Park, S.-Y., Chi, M.-H., Milgroom, M. G., Kim, H., Han, S.-S., Kang, S. and Lee, Y.-H. 2010. Genetic stability of *Magnaporthe oryzae* during successive passages through rice plants and on artificial medium. *Plant Pathol. J.* 26:313-320.
- White, T. J., Bruns, T., Lee, S. and Taylor, J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: *PCR protocols: a guide to methods and applications*, eds. by M. A. Innis, D. H. Gelfand, J. J. Sninsky and T. J. White, pp. 315-322. Academic Press, San Diego, CA, USA.



Supplementary Fig. 1. *Magnaporthe* clades based on the similarity of avirulence genes. Abbreviations for the Poaceae species are as follows: Ec, *Echinochloa crus-galli*; Pm, *Panicum miliaceum*; Sv, *Setaria viridis*; Si, *Setaria italica*; Os, *Oryza sativa*; Ds, *Digitaria sanguinalis*.