

Online Resource 1

Article title: The effect of the *Rht1* haplotype on Fusarium head blight resistance in relation to type and level of background resistance and in combination with *Fhb1* and *Qfhs.ifa-5A*

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Table S1 Analysis of variance table for *Rht1*-NIL groups RE-NIL1, CM, FRxRE and MI across greenhouse and across field experiments

		Green house experiments			Field experiments		
Trait	NIL group	Mean square ^a	F value	p value	Mean square ^a	F value	p value
Plant height (cm)							
	RE-NIL1	2201.4	298.6	0.001	226.3	57.5	0.001
	CM	1930.7	116.3	< 2.2e-16	275.0	21.9	0.002
	FRxRE	6412.7	212.8	< 2.2e-16	1022.6	65.3	0.001
	MI	4187.7	497.2	< 2.2e-16	1107.1	186.5	0.000
Anther retention (%)							
	RE-NIL1	5065.6	43.1	0.005	9671.4	63.5	0.004
	CM	2298	17.1	0.000	988.2	16	0.011
	FRxRE	5010	20.2	0.003	536.1	5	0.086
	MI	422	3.2	0.052	213.6	7.6	0.025
Number of infection sites per head				FHB incidence (%)			
	RE-NIL1	1.38	17.2	0.000	7214.9	68.3	0.000
	CM	0.01	0.9	0.390	1660.1	17.8	0.000
	FRxRE	0.33	11.7	0.000	10717.0	93.4	< 2.2e-16
	MI	0.34	3.0	0.062	936.8	6.4	0.003
Area under the disease progress curve (AUDPC)							
	RE-NIL1	973509	7.8	0.035	249607	30.7	0.003
	CM	273	0.4	0.700	2644.6	6.4	0.045
	FRxRE	393173	3.6	0.110	72574.0	9.2	0.033
	MI	411761	2.9	0.260	270626	19.9	0.008

^a Source of variance: *Rht1* haplotype

Table S2 Analysis of variance table of RE and CM *QTL*-by-*Rht1* groups across field experiments

Source	RE			CM		
	Mean square	F value	p value	Mean square	F value	p value
Plant height (cm)						
<i>Rht1</i> haplotype	101.0	20.2	0.047	150.8	21.4	0.019
<i>QTL</i> haplotype	30.8	6.2	0.074	41.7	5.9	0.078
<i>QTL</i> -by- <i>Rht1</i> haplotype	9.9	2.0	0.070	35.3	5.0	0.000
Anther retention (%)						
<i>Rht1</i> haplotype	17434.1	107.1	< 2.2e-16	1402.3	15.2	0.062
<i>QTL</i> haplotype	14946.4	91.8	0.001	3138.4	34.0	0.000
<i>QTL</i> -by- <i>Rht1</i> haplotype	532.6	3.3	0.004	371.3	4.0	0.034
FHB incidence (%)						
<i>Rht1</i> haplotype	4607.3	55.0	< 2.2e-16	8861.2	38.6	0.000
<i>QTL</i> haplotype	3021.1	36.0	< 2.2e-16	14802.5	64.4	< 2.2e-16
<i>QTL</i> -by- <i>Rht1</i> haplotype	606.1	7.2	0.000	813.6	3.5	0.003
Area under the disease progress curve (AUDPC)						
<i>Rht1</i> haplotype	435233	40.3	0.000	42493	8.4	0.107
<i>QTL</i> haplotype	387997	35.9	0.007	15418	3.0	0.192
<i>QTL</i> -by- <i>Rht1</i> haplotype	6273	0.6	0.738	8146	1.6	0.293

Table S3 Best linear unbiased estimators (BLUEs) across field experiments of NILs grouped by NIL group and *Rht1* haplotype for plant height (PH (cm)), anther retention (AR(%)), Fusarium head blight (FHB) incidence and area under the disease progress curve (AUDPC)

NIL group	<i>Rht1</i> haplotype	PH (cm) ^a	AR (%) ^a	FHB incidence ^a	AUDPC ^a
		BLUEs	BLUEs	BLUEs	BLUEs
RE-NIL1	<i>B1aD1a</i>	86 cd	33.1 ab	63.6 d	261 bc
RE-NIL1	<i>B1bD1a</i>	71 a	47.2 abc	90.4 ef	468 cd
RE-NIL1	<i>B1aD1b</i>	70 a	70.9 cde	93.9 ef	608 d
CM	<i>B1aD1a</i>	92 de	13.1 a	12.7 a	26 a
CM	<i>B1bD1a</i>	81 bc	27.9 ab	20.4 ab	38 ab
CM	<i>B1aD1b</i>	80 bc	28.7 ab	26.9 b	56 ab
FRxRE	<i>B1aD1a</i>	100 f	58.1 bd	50.7 c	251 ac
FRxRE	<i>B1bD1a</i>	74 ab	75.0 cde	86.5 ef	576 d
FRxRE	<i>B1aD1b</i>	74 ab	86.9 de	82.9 e	618 d
MI	<i>B1aD1a</i>	95 ef	92.9 de	88.2 ef	696 d
MI	<i>B1bD1a</i>	69 a	96.1 e	98.1 f	942 e
MI	<i>B1aD1b</i>	71 a	97.1 e	96.8 f	940 e

^a BLUEs of groups with different letters are significantly different (Bonferroni *p*-value adjustment, *p* < 0.05)