

Table S1. Trait heritability and QTL detection

Trait			QTL Analysis											
Experiment ^a	RIL effect ^b	H ^{2c}	Locus	DPI ^d				Chr	Position (cM)	max LOD ^e	Interval (map position) ^f	Var ^g	Effect ^h	Epistasis ⁱ
				3*	5	7	10							
Growth Chamber	<i>P</i> < 0.0001 <i>df</i> = 112 <i>F</i> = 2.19	0.75	<i>QRX1.1</i>	<i>ns</i>	<i>ns</i>	<i>ns</i>	***	I	31.1	2.3	[7 - 47] 1243559 - 13395602	11.1	-0.35	47(1):32(3) 2.8 24(1):21(4) 2
			<i>QRX2</i>	***	<i>ns</i>	<i>ns</i>	<i>ns</i>	II	69.1	2.40	[50 - 77] 9813845 - 18603183	12	-0.08	-
			<i>QRX3</i>	<i>ns</i>	***	***	***	III	104	17.8	[100.6 - 105.6] 18948842 - 22787634	53.7	-0.62	105(3):13(4) 2.8 104(3):27(1) 2.1 & 2.5 104(3):12(4) 3
			<i>QRX5.1</i>	<i>ns</i>	<i>ns</i>	***	***	IV	24	3.4	[14.29 - 37] 1586683 - 9448354	15.9	-0.41	-
			<i>QRX5.2</i>	***	***	<i>ns</i>	<i>ns</i>	IV	34.4	3.77	[17 - 41] 1586683 - 10551891	17.2	-0.22	-
			Greenhouse	<i>P</i> < 0.0001 <i>df</i> = 114 <i>F</i> = 8.16	0.50	<i>QRX1.2</i>	***	***	***	<i>ns</i>	I	106	3.37	[94 - 114.1] 22388396 - 28841663
<i>QRX3</i>	<i>ns</i>	<i>ns</i>				***	***	III	104	5.22	[99 - 105.6] 18780383 - 23042168	22.1	-0.47	104(3):47(3) 2.3 86(1):29(5) 2.4
Bacterial Growth	<i>P</i> = 0.0002 <i>df</i> = 94 <i>F</i> = 1.84	0.17	<i>QRX3</i>	***	<i>epi</i>			III	102	2.63	[69 - 105] 13596040 - 23042168	15.9	-0.58	34(1):47(1) 2.1

^a Three different experiments were conducted: the disease index was measured for both growth chamber and greenhouse grown 28 day-old plants and an IGC (Internal Growth Curve) experiment was conducted using growth chamber grown plants (see materials and methods).

^b The RIL effect at 10 dpi was estimated using GLM procedure (Type III SS) with SAS software version 9.1 (SAS Institute, Cary, NC, USA).

^c H^2 : broad-sense heritability at 10 dpi

^d QTL detection at different days post-inoculation (DPI) using the *scanone* function in Rqtl (www.r-project.org). * The disease index scoring was performed at 3, 5, 7, 10 and 4, 5, 7, 10 days post-inoculation for the growth chamber and greenhouse experiments, respectively. *ns*: no QTL was detected; *** QTL with Log of odds ratio ≥ 2.5 underscored: maximum LOD score; *epi*: significant digenic epistatic interaction detected (see Epistasisⁱ).

^e Maximum Log of odd ratio observed.

^f Support intervals are given in Centimorgans and TAIR 9 coordinates were estimated by dropping 1.5 LOD units.

^g ^h The proportion of phenotypic variance explained by each QTL and the estimated phenotypic effects corresponding to the allelic substitution from Kas-1 allele to Col-5 allele, were calculated in the context of multiple-QTL models using the function *fitqtl* of Rqtl. Values correspond to the results when the LOD is maximum. When a single QTL was considered, the heritability due to the QTL was estimated by $(1 - 10^{-2 \text{ LOD} / n})$, where n is the sample size.

ⁱ Significant pair-wise epistatic interactions were determined using interaction LOD scores from *scantwo* function in Rqtl: marker position in cM with chromosome in brackets for both markers followed by the interaction LOD score; in *italic*: significant interaction between markers outside of QTLs. The time at which the epistatic interaction occurred was indicated in the DPI^d column (*epi*).