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### Supplementary Data

**Table S1:** Primer sequences and expected product sizes of SSR and STS markers used for screening 10 rice cultivars for *Xa-R* gene allelic state

Gene	Linked Marker	Primer Forward (5'~ 3' )	Primer Reverse (5'~ 3' )	Expected Product size	Reference
<i>Xa2</i>	RM-317 (SSR)	CATACTTACCAGTTCACCGCC	CTGGAGAGTGTCAGCTAGTTGA	154	(Singh et al., 2015a)
<i>Xa4</i>	RM-224 (SSR)	ATCGATCGATCTTCACGAGG	TGCTATAAAAGGCATTCGGG	160	(Singh et al., 2015a)
<i>xa5</i>	RM-13 (SSR)	TCCAACATGGCAAGAGAGAG	GGTGGCATTTCGATTCCAG	139	(Singh et al., 2015a)
<i>xa13</i>	xa-13-prom (SSR)	GGCCATGGCTCAGTGTTTAT	GAGCTCCAGCTCTCCAAATG	498	(Singh et al., 2015a)
<i>Xa21</i>	pTA248 (STS)	AGACGCGGAAGGGTGGTTCCCGGA	AGACGCGGTAATCGAAGATGAAA	982	(Singh et al., 2015a)

**Table S2:** Information on primer sequences of the genes used for quantitative real-time PCR analysis of resistant and susceptible rice cultivars

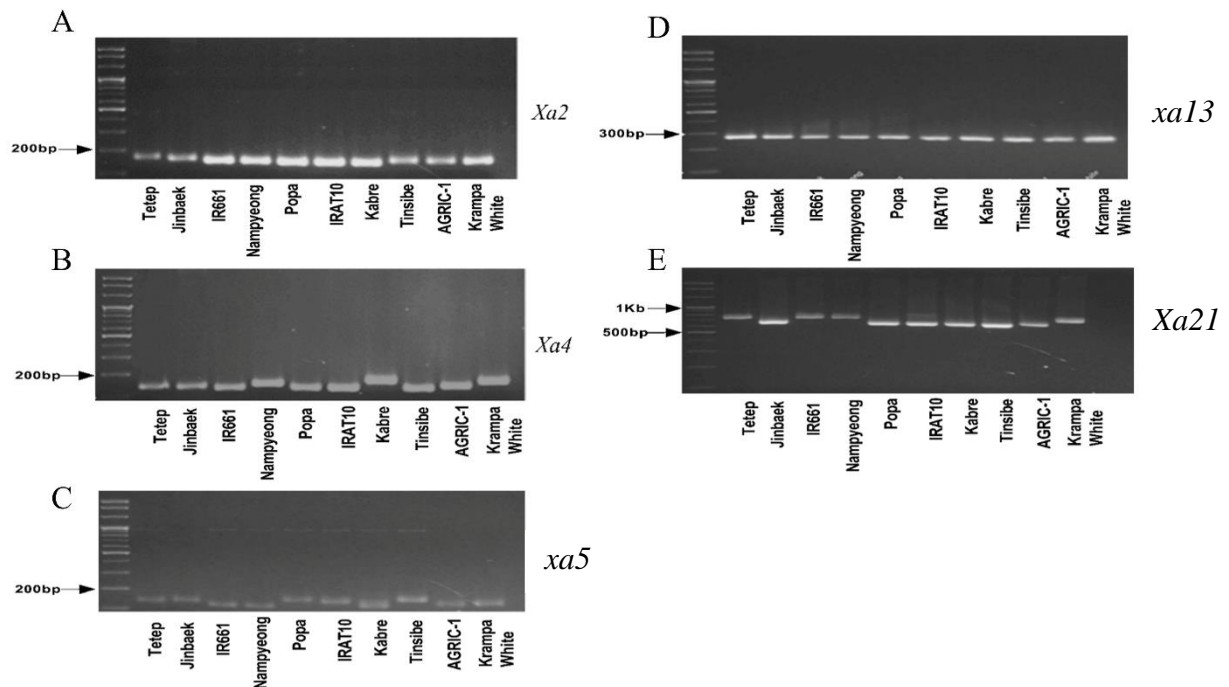
Gene	Primer Forward (5'~ 3')	Primer Reverse (5'~ 3')	Expected size	Product
<i>OsUBI</i>	GACGGACGCACCCTGGCTGA	TGCTGCCAATTACCATATAC	395	
<i>OsJAZ8</i>	GTTACCCACCTCAGCCTCAC	TTTATACGGCGAAACCGAAC	100	
<i>OsPR1a</i>	AGTTCGTCGAGCAGGTTATC	AGATTGGCCGACGAAGTTG	200	
<i>OsPR10b</i>	TGTGGAAGGTCTGCTTGGA	CACTCGTGAAGCAAAAACAC	133	
<i>OsWRKY4</i>	GGACCAGGGCGATGTCACGT	TGTCCATCCATGATTCTTCG	117	

>[ref|NR\\_026319.1](#) *Xanthomonas oryzae* strain LMG 5047 16S ribosomal RNA gene, partial sequence  
Length=1502

Score = 2641 bits (1430), Expect = 0.0  
Identities = 1430/1430 (100%), Gaps = 0/1430 (0%)  
Strand=Plus/Plus

K1 (qry) 10	AGTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAACGGCAGCACAGTAAGAGCTTG	69
K1 (sbj) 1	AGTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAACGGCAGCACAGTAAGAGCTTG	60
K1 (qry) 70	CTCTTATGGGTGGCGAGTGGCGGACGGGTGAGGAATACATCGGAATCTACTCTTTCGTGG	129
K1 (sbj) 61	CTCTTATGGGTGGCGAGTGGCGGACGGGTGAGGAATACATCGGAATCTACTCTTTCGTGG	120
K1 (qry) 130	GGGATAACGTAGGGAACTTACGCTAATACCGCATACGACCTACGGGTGAAAGCGGAGGA	189
K1 (sbj) 121	GGGATAACGTAGGGAACTTACGCTAATACCGCATACGACCTACGGGTGAAAGCGGAGGA	180
K1 (qry) 190	CCTTCGGGCTTCGCGCGATTGAATGAGCCGATGTCGATTAGCTAGTTGGCGGGGTAAAG	249
K1 (sbj) 181	CCTTCGGGCTTCGCGCGATTGAATGAGCCGATGTCGATTAGCTAGTTGGCGGGGTAAAG	240
K1 (qry) 250	GCCCACCAAGGCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGAAGTGA	309
K1 (sbj) 241	GCCCACCAAGGCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGAAGTGA	300
K1 (qry) 310	GACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGC	369
K1 (sbj) 301	GACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGC	360
K1 (qry) 370	CTGATCCAGCCATGCCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTTTTGTGG	429
K1 (sbj) 361	CTGATCCAGCCATGCCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTTTTGTGG	420
K1 (qry) 430	GAAAGAAAAGCAGTCGGTTAATACCCGATTGTTCTGACGGTACCCAAAGAATAAGCACCG	489
K1 (sbj) 421	GAAAGAAAAGCAGTCGGTTAATACCCGATTGTTCTGACGGTACCCAAAGAATAAGCACCG	480
K1 (qry) 490	GCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTTACTCGGAATTACT	549
K1 (sbj) 481	GCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTTACTCGGAATTACT	540
K1 (qry) 550	GGGCGTAAAGCGTGCCTAGGTGGTGGTTTAAGTCTGTTGTGAAAGCCCTGGGCTCAACCT	609
K1 (sbj) 541	GGGCGTAAAGCGTGCCTAGGTGGTGGTTTAAGTCTGTTGTGAAAGCCCTGGGCTCAACCT	600
K1 (qry) 610	GGGAATTGCAGTGGATACTGGGTCACTAGAGTGTGGTAGAGGGTAGCGGAATCCCGGTG	669
K1 (sbj) 601	GGGAATTGCAGTGGATACTGGGTCACTAGAGTGTGGTAGAGGGTAGCGGAATCCCGGTG	660
K1 (qry) 670	TAGCAGTGAAATGCGTAGAGATCGGGAGGAACATCAGTGGCGAAGGCGGCTACCTGGACC	729
K1 (sbj) 661	TAGCAGTGAAATGCGTAGAGATCGGGAGGAACATCAGTGGCGAAGGCGGCTACCTGGACC	720

**Fig. S1:** 16srRNA alignment of sequencing results confirming the K1 strain of *Xoo*



**Fig. S2:** STS/SSR marker analysis of 10 rice cultivars. A 3% agarose gel was used to visualize absence or presence of selected markers. If a marker was visible, the exact size of the band was marked as present, and if not then absent. (A) *Xa2* BLB resistant marker is present if above 154 bp. (B) *Xa4* present above 160 bp (C) *xa5* present above 139 bp, (D) *xa13* present above 498bp and (E) *Xa21* present above 982bp.



**Fig. S3:** Phenotypic evaluation of symptoms of different cultivars after inoculation with *Xoo*