

Supplementary Materials:

Table S1. SSR Markers for blast resistance alleles detection.

QTLs	Marker	Chr.	Sequence
<i>qBl1</i>	RM319	1	Forward 5' ATCAAGGTACCTAGACCACCAC 3'
			Reverse 3' TCCTGGTGCAGCTATGTCTG 5'
	RM212	1	Forward 5' CCACTTTCAGCTACTACCAG 3'
			Reverse 3' CACCCATTGTCTCTCATTATG 5'
<i>qBl2</i>	RM48	2	Forward 5' TGTCCCACTGCTTCAAGC 3'
			Reverse 3' CGAGAATGAGGGACAAATAACC 5'
	RM207	2	Forward 5' CCATTCGTGAGAAGATCTGA 3'
			Reverse 3' CACCTCATCCTCGTAACGCC 5'
<i>qBl11</i>	RM224	11	Forward 5' ATCGATCGATCTTCACGAGG 3'
			Reverse 3' TGCTATAAAAGGCATTCGGG 5'
	RM144	11	Forward 5' TGCCCTGGCGCAAATTTGATCC 3'
			Reverse 3' GCTAGAGGAGATCAGATGGTAGTGCATG 5'
<i>qBl12</i>	RM27933	12	Forward 5' TCCTCTGTCATATGGCTGTAAACG 3'
			Reverse 3' GGACAAGGAGGAAGTATTGATTGG 5'

SSR= Simple sequence repeat; QTLs= quantitative trait loci.

Table S2. Analysis of variance of BC₂F_{3:2} selected line and check varieties against 4 isolates of *Pyricularia oryza*.

SOV	df	MS
Isolate	3	2.392 ^{ns}
Genotype	10	165.66 ^{**}
Genotype × Isolate	30	2.03 ^{ns}
Error	88	1.42
C.V. (%)		34.55

^{**} significant at $p = 0.05$; ns = not significant different; SOV = Source of variation; df = degree of freedom; MS = mean square; C.V. = Coefficient of variation.