

## **Accumulating candidate genes for broad-spectrum resistance to rice blast in a drought-tolerant rice cultivar**

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## Supplementary Materials

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Figure S2. Correlation of Lesion Number (LN) in Ambikapur and lesion number in Hazaribag, India on F<sub>4</sub> lines from intermated BC<sub>3</sub>F<sub>4</sub> families. LN counts at both sites showed a significantly positive correlation ( $r= 0.546^{**}$ ,  $n=80$  2005).

Figure S3. Location of SSR markers and candidate genes (green rectangles) considered in the study. OXLP = GLP.

Figure S4. Diagram representing data from genome-wide scan of parental lines and a selected subset of F<sub>6</sub> intermated lines. Moroberekan (1 - red), and Vandana (2 - blue) genomic regions are shown in three selected lines IR78221-19-6-33-B (3), IR78221-19-6-90-B (4), IR78222-20-7-148-2-B (5) all of which show Resistant phenotype. While most of the genomic background is similar to Vandana, some regions, including QTLs containing CGs, are from Moroberekan. Green regions represent heterozygosity.

Literature Cited in the Supplemental Figures and Tables in Carrillo et al.

**Table S1.** List of intermated<sup>1</sup> lines derived from BC<sub>3</sub>F<sub>4</sub> progenies of Vandana x Moroberekan that were used for this study.

Code	Line	Cross
VM-101	IR78221-19-2-4-2-B	V4M-14-1-B x V4M-5-3-B
VM-102	IR78221-19-2-4-1-B	V4M-14-1-B x V4M-5-3-B
VM-103	IR78221-19-2-13-1-B	V4M-14-1-B x V4M-5-3-B
VM-104	IR78221-19-2-13-2-B	V4M-14-1-B x V4M-5-3-B
VM-105	IR78221-19-2-14-1-B	V4M-14-1-B x V4M-5-3-B
VM-106	IR78221-19-2-14-2-B	V4M-14-1-B x V4M-5-3-B
VM-107	IR78221-19-2-35-B-B	V4M-14-1-B x V4M-5-3-B
VM-108	IR78221-19-3-104-B	V4M-14-1-B x V4M-5-3-B
VM-109	IR78221-19-3-196-B	V4M-14-1-B x V4M-5-3-B
VM-110	IR78221-19-3-222-B	V4M-14-1-B x V4M-5-3-B
VM-111	IR78221-19-6-6-B	V4M-14-1-B x V4M-5-3-B
VM-112	IR78221-19-6-15-B	V4M-14-1-B x V4M-5-3-B
VM-113	IR78221-19-6-16-B	V4M-14-1-B x V4M-5-3-B
VM-114	IR78221-19-6-89-B	V4M-14-1-B x V4M-5-3-B
VM-115	IR78221-19-6-94-B	V4M-14-1-B x V4M-5-3-B
VM-116	IR78221-19-6-99-B	V4M-14-1-B x V4M-5-3-B
VM-167	IR78221-19-4-43-1-B	V4M-14-1-B x V4M-5-3-B
VM-168	IR78221-19-4-43-2-B	V4M-14-1-B x V4M-5-3-B
VM-169	IR78221-19-4-54-B	V4M-14-1-B x V4M-5-3-B
VM-170	IR78221-19-6-3-B	V4M-14-1-B x V4M-5-3-B
VM-171	IR78221-19-6-7-B	V4M-14-1-B x V4M-5-3-B
VM-172	IR78221-19-6-23-B	V4M-14-1-B x V4M-5-3-B
VM-173	IR78221-19-6-33-B	V4M-14-1-B x V4M-5-3-B
VM-174	IR78221-19-6-56-B	V4M-14-1-B x V4M-5-3-B
VM-175	IR78221-19-6-82-B	V4M-14-1-B x V4M-5-3-B
VM-176	IR78221-19-6-90-B	V4M-14-1-B x V4M-5-3-B
VM-177	IR78221-19-6-95-B	V4M-14-1-B x V4M-5-3-B
VM-126	IR78222-20-7-47-B	V4M-14-1-B x V4M-6-1-B
VM-127	IR78222-20-7-50-1-B	V4M-14-1-B x V4M-6-1-B
VM-128	IR78222-20-7-50-2-B	V4M-14-1-B x V4M-6-1-B
VM-129	IR78222-20-7-50-3-B	V4M-14-1-B x V4M-6-1-B
VM-130	IR78222-20-7-199-1-B	V4M-14-1-B x V4M-6-1-B
VM-131	IR78222-20-7-199-2-B	V4M-14-1-B x V4M-6-1-B
VM-132	IR78222-20-7-199-3-B	V4M-14-1-B x V4M-6-1-B
VM-133	IR78222-20-8-33-1-B	V4M-14-1-B x V4M-6-1-B
VM-134	IR78222-20-8-33-2-B	V4M-14-1-B x V4M-6-1-B
VM-135	IR78222-20-8-53-1-B	V4M-14-1-B x V4M-6-1-B
VM-136	IR78222-20-8-53-2-B	V4M-14-1-B x V4M-6-1-B
VM-137	IR78222-20-8-116-1-B	V4M-14-1-B x V4M-6-1-B

<sup>1</sup>The BC<sub>3</sub>F<sub>3</sub> and BC<sub>3</sub>F<sub>4</sub> lines were intermated in all pairwise combinations and advanced to F<sub>6</sub>. At F<sub>6</sub>, 84 progenies were selected based on resistance to blast and morphoagronomic traits similar to Vandana.

**Table S1 continued**

Code	Line	Cross
VM-138	IR78222-20-8-116-2-B	V4M-14-1-B x V4M-6-1-B
VM-139	IR78222-20-8-143-1-B	V4M-14-1-B x V4M-6-1-B
VM-140	IR78222-20-8-143-2-B	V4M-14-1-B x V4M-6-1-B
VM-141	IR78222-20-8-155-1-B	V4M-14-1-B x V4M-6-1-B
VM-142	IR78222-20-8-155-2-B	V4M-14-1-B x V4M-6-1-B
VM-143	IR78222-20-8-155-3-B	V4M-14-1-B x V4M-6-1-B
VM-144	IR78222-20-8-176-1-B	V4M-14-1-B x V4M-6-1-B
VM-145	IR78222-20-8-176-2-B	V4M-14-1-B x V4M-6-1-B
VM-146	IR78222-20-11-62-B	V4M-14-1-B x V4M-6-1-B
VM-147	IR78222-20-17-19-1-B	V4M-14-1-B x V4M-6-1-B
VM-148	IR78222-20-17-19-2-B	V4M-14-1-B x V4M-6-1-B
VM-149	IR78222-20-21-4-B	V4M-14-1-B x V4M-6-1-B
VM-150	IR78222-20-21-71-B	V4M-14-1-B x V4M-6-1-B
VM-117	IR78222-20-1A-7-1-B	V4M-14-1-B x V4M-6-1-B
VM-118	IR78222-20-1A-7-2-B	V4M-14-1-B x V4M-6-1-B
VM-119	IR78222-20-1A-38-1-B	V4M-14-1-B x V4M-6-1-B
VM-120	IR78222-20-1A-38-2-B	V4M-14-1-B x V4M-6-1-B
VM-121	IR78222-20-1A-38-3-B	V4M-14-1-B x V4M-6-1-B
VM-122	IR78222-20-2-36-1-B	V4M-14-1-B x V4M-6-1-B
VM-123	IR78222-20-2-36-2-B	V4M-14-1-B x V4M-6-1-B
VM-124	IR78222-20-6-154-1-B	V4M-14-1-B x V4M-6-1-B
VM-125	IR78222-20-6-154-2-B	V4M-14-1-B x V4M-6-1-B
VM-178	IR78222-20-7-128-B	V4M-14-1-B x V4M-6-1-B
VM-179	IR78222-20-7-140-B	V4M-14-1-B x V4M-6-1-B
VM-180	IR78222-20-7-148-1-B	V4M-14-1-B x V4M-6-1-B
VM-181	IR78222-20-7-148-2-B	V4M-14-1-B x V4M-6-1-B
VM-182	IR78222-20-7-148-3-B	V4M-14-1-B x V4M-6-1-B
VM-183	IR78222-20-8-118-B	V4M-14-1-B x V4M-6-1-B
VM-184	IR78222-20-17-47-B	V4M-14-1-B x V4M-6-1-B
VM-151	IR78222-20-23-29-B	V4M-14-1-B x V4M-6-1-B
VM-152	IR78224-22-2-2-B	V4M-14-1-B x V4M-82-2-B
VM-153	IR78224-22-2-4-B	V4M-14-1-B x V4M-82-2-B
VM-154	IR78224-22-2-15-B	V4M-14-1-B x V4M-82-2-B
VM-155	IR78224-22-2-24-B	V4M-14-1-B x V4M-82-2-B
VM-156	IR78224-22-2-36-B	V4M-14-1-B x V4M-82-2-B
VM-157	IR78224-22-2-50-B	V4M-14-1-B x V4M-82-2-B
VM-158	IR78224-22-2-59-B	V4M-14-1-B x V4M-82-2-B
VM-159	IR78224-22-2-60-1-B	V4M-14-1-B x V4M-82-2-B
VM-160	IR78224-22-2-60-2-B	V4M-14-1-B x V4M-82-2-B
VM-161	IR78224-22-2-74-B	V4M-14-1-B x V4M-82-2-B
VM-162	IR78224-22-2-96-B	V4M-14-1-B x V4M-82-2-B
VM-163	IR78224-22-2-98-B	V4M-14-1-B x V4M-82-2-B
VM-164	IR78224-22-2-104-B	V4M-14-1-B x V4M-82-2-B
VM-165	IR78224-22-2-113-B	V4M-14-1-B x V4M-82-2-B

VM-166

IR78224-22-2-114-B

V4M-14-1-B x V4M-82-2-B

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**Table S2** Candidate genes associated with resistance to rice blast used in this study

Gene	Rice loci	Chr	Bioprocess	Functional evidence
14-3-3	LOC_Os02g36974	2	Primary metabolism/ cellular signal transduction	Disease resistance QTL <sup>1</sup> ; Induced gene in rice- <i>M. oryzae</i> and rice- <i>X. oryzae</i> interactions <sup>2</sup> .
Aldose reductase	LOC_Os05g39690	5	Stress response	Disease resistance QTL <sup>1</sup> ; Associated with stress tolerance in mature seeds of rice <sup>3</sup>
Chitinase	LOC_Os03g04060	2	Chitin degradation	Disease resistance QTL <sup>1</sup> ; Defense response by degrading fungal chitin <sup>4</sup>
Heat shock protein 90 (HSP90)	LOC_Os06g50300	6	Stress response	Pathogen-induced defense gene and chaperoning role in R-gene mediate resistance <sup>5,6</sup>
Oxalate oxidase (OXO)	LOC_Os03g48750	3	Oxidative burst, signaling, structure	Gene cluster as a disease resistance QTL <sup>7-10</sup>
	LOC_Os03g48760	3		
	LOC_Os03g48770	3		
	LOC_Os03g48780	3		
Germin-like proteins (GLP)	LOC_Os08g08920	8	Strengthening of cell wall during papilla formation in barley-powdery mildew interaction	Gene cluster as a disease resistance QTL <sup>7-9</sup> ; Induced expression in rice- <i>M. oryzae</i> interaction <sup>11,12</sup> .
	LOC_Os08g08960	8		
	LOC_Os08g08970	8		
	LOC_Os08g08980	8		
	LOC_Os08g08990	8		
	LOC_Os08g09000	8		
	LOC_Os08g09010	8		
	LOC_Os08g09020	8		
	LOC_Os08g09040	8		
	LOC_Os08g09060	8		
	LOC_Os08g09080	8		
	LOC_Os08g13440	8		
	LOC_Os08g35750	8		

<b>Gene</b>	<b>Rice loci</b>	<b>Chr</b>	<b>Bioprocess</b>	<b>Functional evidence</b>
Pathogenesis related protein 1 (PR1)	LOC_Os10g11500	10	Pathogenesis related protein	Gene cluster as a disease resistance QTL <sup>1</sup> ; Involved in defense response against fungal and bacterial pathogens of plants <sup>13</sup>
Pathogenesis related protein 5 (thaumatin-like proteins)/PR5	LOC_Os06g47600	6	Pathogenesis related protein	Gene cluster as a disease resistance QTL <sup>7, 8, 9</sup> ; Antifungal activity by binding to beta-1,3-glucans <sup>14,15</sup>
	LOC_Os07g23470	7		
	LOC_Os12g43380	12		
Peroxidase	LOC_Os07g48020	7	Oxidative burst, signaling, structure	Gene cluster as a disease resistance QTL <sup>1</sup> . Involved in defense response to bacterial blight of rice <sup>16</sup>
Probenazole-induced protein	LOC_Os12g36880	12	Pathogenesis related protein	Induced expression by probenazole and by <i>M. oryzae</i> <sup>17</sup>
Putative 2-dehydro-3-deoxyphosphoheptonate aldolase (DHAP)	LOC_Os07g42960	7	Aromatic amino acid synthesis	Pathogen-induced defense gene in maize- <i>Puccinia sorghi</i> interaction (Bai et al., unpublished)



**Table S3** - Primer sequences for candidate genes that were used in this study

Gene	Primer name	Chr	Forward Sequence (5'-3')	Reverse Sequence (5'-3')
14-3-3	14-3-3	2	GCTTTCCCGTGAGGAGAATG	GCCACCATGGTATTCTCAGC
Aldose reductase	AR	5	TGCTCACTCCGTTTCAGACAG	CAGGTTCCGCAGCTGTCTAT
Chitinase	CHI	2	CGTCAAAGCCGGATGTCC	GCGGTAAACAACGGTACGATC
Heat shock protein 90 (HSP90)	HSP90	6	TGGTCACCCTTTGATTGACTC	AGATGAGCTCCCTCAGGAAA
Oxalate oxidase	OsOxo1	3	CAAACAAAGCCAGCTTGTC	CCCATAACATGGGAGAAAGTT
	OsOxo2	3	CCAGCTCGTCACTGCTACTG	AGCGAAGAACGGTACGAAAA
	OsOxo3	3	CATAGCTCGATGTGCATGGT	GCCGACATTGAACTGGAAGT
	OsOxo4	3	GCCAGGTGCCATTTTCATTAC	AGTACCCACCGGTGAACTTG
Oxalate oxidase (1 kb upstream)	OsOxo1 UP	3	AGCTTGTCCTGCGCTTCTT	GTGGCAATCTTGGAGGAGAA
	OsOxo2 UP	3	GCCTCTACGGGGTCTTGACT	AGCGAAGAACGGTACGAAAA
	OsOxo3 UP	3	GGACCCTCTCCAGGACTTCT	CACGGACCACCTTGGAAAT
	OsOxo4 UP	3	ACCCTGACCCTCTCCAAGAC	CGGACCACCCTGGAGTAGTA
Germin-like protein	GLP	8	GCAATTAGAACGGTATGAGC	TCGACGACATTGAACTGGAGG
Pathogenesis related protein 1 (PR1)	PR1	10	TTACGCACCCAATTGTAGCA	TCCCAGAGTCACAAACATCG
Pathogenesis related protein 5 (PR5)	PR5_6	6	CAAATTCCACGAATATCCAA	TACCTGAGGTCCTCCCATCA
	PR5_7	7	TCTTGGTTGCTTCCGTTCTT	CGCCTGAAGAGAAATGCAA
	PR5_12	12	TGGATTCACAAACCACGAAA	TTGTCTTCGGGGAACAGGTA
Peroxidase	POX	7	TGATCAGAAGCCATATGTAGC	ATCAGCTGAGCATCTCATATAAGG
Probenazole-induced protein	PR10	12	ATGCCAGGTCTCAAATGTC	TCTCCGTCGAGTGTGACTTG
Putative 2-dehydro-3-deoxyphosphoheptonate aldolase (DHAP)	DHAP	7	GACCGTGTAAGTAATGGGTGGT	GGCTGAGCAGTCATAGAAGAGG

**Table S4** SSR markers co-localizing with candidate genes that map to disease resistance QTL and showing polymorphism between Vandana and Moroberekan

<b>Candidate Gene</b>	<b>Chr</b>	<b>cM</b>	<b>SSR Marker<sup>1</sup></b>
14-3-3	2	88.2	RM6056, RM5363
Chitinase	2	93.2	RM6379
Oxalate oxidase	3	122.8	RM426, RM504, RM168
Aldose Reductase	5	95.8	RM188, RM1187
PR5 (Thaumatococcus-like)	6	113.4	RM340, RM6811
HSP90	6	121.7	RM176, RM6563, RM1150
PR5 (Thaumatococcus-like)	7	50	RM214, RM542
Putative DHAP	7	78.9	RM478, RM234, RM1330
Peroxidase	7	115.5	RM5720
Germin-like protein	8	38.5	RM544, RM310, RM6208, RM547
Germin-like protein	8	48.8	RM6429, RM3215,
Germin-like protein	8	53.7	RM331, RM126
PR1b	10	15.2	RM216, RM5348, RM311
Probenazole-induced protein	12	94.7	RM1015

<sup>1</sup> SSRs were selected based on anchor markers from BAC clones with the candidate gene loci found in [www.gramene.org](http://www.gramene.org). Primer sequences are available at <http://143.48.220.116/microsat/index.html>.

**Table S5.** Correlation coefficients between measured parameters for resistance to blast across screening sites in India and the Philippines

SSR Marker	Trait <sup>1,2</sup>									
	India								Philippines	
	Almora				Hazaribag		Ambikapur	IRRI	Cavinti	
	LN	SB	DLA	SD	PB	YB	LB	PB	LB	SB
<b>India</b>										
<u>Almora</u>										
LN										
SB	0.05									
DLA	0.77 <sup>d</sup>	-0.16								
SD	-0.49 <sup>d</sup>	0.02	-0.47 <sup>d</sup>							
PB	0.78 <sup>d</sup>	0.03	0.79 <sup>d</sup>	-0.65 <sup>d</sup>						
YB	-0.60 <sup>d</sup>	-0.06	-0.60 <sup>d</sup>	0.62 <sup>d</sup>	-0.81 <sup>d</sup>					
<u>Hazaribag</u>										
LB	0.11	-0.02	0.14	-0.11	0.15	-0.32 <sup>b</sup>				
PB	-0.17	-0.12	-0.17	-0.08	-0.19	0.12	0.00			
<u>Ambikapur</u>										
LB	0.21	-0.04	0.20	-0.10	0.23	-0.25 <sup>a</sup>	0.28 <sup>a</sup>	-0.18		
<b>Philippines</b>										
IRRI										
SB	0.30 <sup>b</sup>	0.20	0.20	-0.26	0.37 <sup>b</sup>	-0.32 <sup>a</sup>	0.13	-0.31 <sup>b</sup>	0.28 <sup>a</sup>	
<u>Cavinti</u>										
SB	0.30 <sup>b</sup>	0.10	0.28	-0.27	0.41 <sup>c</sup>	-0.35 <sup>b</sup>	0.16	-0.29 <sup>a</sup>	0.34 <sup>b</sup>	0.95 <sup>d</sup>

<sup>1</sup> LN = lesion number; SB = seedling blast; DLA = diseased leaf area; SD = start of disease (days after sowing); PB = panicle blast; YB = yield under blast condition; LB = leaf blast

<sup>2</sup> Significance of correlation: a =  $p < 0.05$ ; b =  $p < 0.01$ ; c =  $p < 0.001$ ; d =  $p < 0.0001$

**Table S6.** List of simple sequence repeat (SSR) markers used for a genome scan of 114 intermated progenies of Vandana x Moroberekan that were used in the study.

Marker	Map	Chr	Position cM	Motif	Annealing Tm (°C)	Product Size (bp)	GenBank Accession	References
RM495	IRMI 2003	1	0.3	(CTG)7	55	159	AQ573939	18
RM84	CORNELL SSR 2001	1	26.2	(TCT)10	55	113	AF343869	19
RM220	CORNELL SSR 2001	1	28.4	(CT)17	55	127	AF344041	19
RM1	CORNELL SSR 2001	1	29.7	(AG)26	55	113	AF344003	20
RM581	IRMI 2003	1	49	(GA)12	55	143	AP000969	18
RM490	CORNELL SSR 2001	1	51	CT)13	55	101	AQ510019	18
RM24	CORNELL SSR 2001	1	78.4	(GA)29	55	192	AF343841	19
RM5	IRMI 2003	1	98.5	(GA)14	55	113	AF344007	20
RM246	CORNELL SSR 2001	1	115.2	(CT)20	55	116	AF344066	19
RM302	IRMI 2003	1	135.8	(GT)30(AT)8	55	156	AF344127	21
RM104	IRMI 2003	1	159	(GA)9	55	222		22
RM414	IRMI 2003	1	161.5	(TGCA)6	55	223	AQ158869	18
RM14	CORNELL SSR 2001	1	194.1	(GA)18	55	191	AF344015	
RM109	IRMI 2003	2	0	(AG)16	55	97	D15964	21
RM154	CORNELL SSR 2001	2	4.8	(GA)21	55	183	D39059	22
RM452	CORNELL SSR 2001	2	58.4	(GTC)9	55	209	AQ326476	18
RM27	CORNELL SSR 2001	2	66	(GA)7	55	158	AF343844	19
RM561	CORNELL SSR 2001	2	74.1	(GA)11	55	190	AQ913300	18
RM6843	IRMI 2003	2	88.2	(TCT)25	55	201	AY023517	23
RM5363	IRMI 2003	2	91.8	(TC)13	55	143	AY022038	23
RM526	IRMI 2003	2	109.3	(TAAT)5	55	240	AQ794492	18
RM6	IRMI 2003	2	125.6	(AG)16	55	163	AF344008	20
RM530	IRMI 2003	2	130.2	(GA)23	55	161	AQ840710	18
RM213	IRMI 2003	2	150.5	(CT)17	55	139	AF344034	19
RM208	IRMI 2003	2	154.1	(CT)17	55	173	AF344029	19

Marker	Map	Chr	Position cM	Motif	Annealing Tm (°C)	Product Size (bp)	GenBank Accession	References
RM60	CORNELL SSR 2001	3	0	(AATT)5AATC T(AATT)	55	165	AF343863	19
RM569	IRMI 2003	3	9.3	(GA)30	55	226	AQ864658	18
RM545	IRMI 2003	3	24.7	(CT)16	55	175	AQ916814	18
RM517	CORNELL SSR 2001	3	42.9	(CT)15	55	266	AQ689735	18
RM7	CORNELL SSR 2001	3	64	(GA)19	55	180	AF344009	20
RM487	IRMI 2003	3	87.9	(AC)10	55	176	AQ395854	18
RM473	CORNELL SSR 2001	3	113.2	(TCTA)14	55	97	AQ331312	18
RM426	IRMI 2003	3	122.3	(CA)10	55	150	AQ259184	18
RM168	IRMI 2003	3	122.8	T15(GT)14	55	116		24
RM186	IRMI 2003	3	127.4	(CGG)5	61	124	D39420	21
RM148	CORNELL SSR 2001	3	140.7	(TG)12	55	129		24
RM143	CORNELL SSR 2001	3	207.3	(CGG)7	67	207	D78609	21
RM130	CORNELL SSR 2001	3	208.2	(GA)10	55	85	D40295	21
RM85	CORNELL SSR 2001	3	231	(TGG)5(TCT)12	55	107	AF344087	21
RM537	IRMI 2003	4	3.1	(CCG)9	55	236	AQ860402	18
RM518	IRMI 2003	4	7.9	(TC)15	55	171	AQ690034	18
RM551	CORNELL SSR 2001	4	8.1	(AG)18	55	192	AQ869594	18
RM261	CORNELL SSR 2001	4	35.4	C9(CT)8	55	125	AF344080	19
RM185	CORNELL SSR 2001	4	50.8	(AGG)9	61	197	D24415	21
RM119	IRMI 2003	4	62.6	(GTC)6	67	166		21
RM241	IRMI 2003	4	83	(CT)31	55	138	AF344061	19
RM3092	IRMI 2003	4	85.5	(AT)49	55	181	AY019767	23
RM317	IRMI 2003	4	96	(GC)4(GT)18	55	155	AF344142	21
RM159	IRMI 2003	5	5.4	(GA)19	55	248	D48905	21
RM122	CORNELL SSR 2001	5	10.1	(GA)7A(GA)2A (GA)11	55	227		24
RM413	CORNELL SSR 2001	5	26.7	(AG)11	55	79	AQ157494	18

Marker	Map	Chr	Position cM	Motif	Annealing Tm (°C)	Product Size (bp)	GenBank Accession	References
RM249	CORNELL SSR 2001	5	55.6	(AG)5A2(AG)14	55	121	AF344069	19
RM459	IRMI 2003	5	77.4	(CATC)6	55	63	AQ327864	18
RM188	IRMI 2003	5	95.3	(CA)8	61	210	D22459	21
RM1187	IRMI 2003	5	96.1	(AG)14	50	131	AY017862	23
RM421	IRMI 2003	5	101.5	(AGAT)6	55	234	AQ255791	18
RM178	IRMI 2003	5	104.4	(GA)5(AG)8	67	117	D49132	21
RM26	IRMI 2003	5	111.3	(GA)15	55	112	AF343843	19
RM540	CORNELL SSR 2001	6	0	(AG)16	55	172	AQ861615	18
RM204	IRMI 2003	6	12.9	(CT)44	55	169	AB026295 .001	19
RM225	CORNELL SSR 2001	6	26.2	(CT)18	55	140	AF344046	19
RM253	CORNELL SSR 2001	6	37	(GA)25	55	135		18
RM549	IRMI 2003	6	51.3	(CCG)9	55	148	AQ868278	18
RM1150	IRMI 2003	6	121.7	(AG)13	55	147	AY017825	23
RM494	IRMI 2003	6	124.4	(AGA)16	55	203	AQ573378	18
RM427	IRMI 2003	7	11	(TG)11	55	185	AQ271555	18
RM2	CORNELL SSR 2001	7	36.1	(GA)2A(GA)13	55	150	AF344004	20
RM214	IRMI 2003	7	49.7	(CT)14	55	112	APO04305 .001	19
RM336	CORNELL SSR 2001	7	61	(CTT)18	55	154	AF344160	21
RM182	CORNELL SSR 2001	7	61	(AT)16	67	346	L10346	22
RM10	CORNELL SSR 2001	7	63.5	(GA)15	55	159	AF344012	20
RM1279	IRMI 2003	7	75.6	(AG)17	50	182	AY017954	23
RM3799	IRMI 2003	7	75.9	(GA)19	55	189	AY020474	23
RM234	IRMI 2003	7	93.9	(CT)25	55	156	AF344054	19
RM1330	IRMI 2003	7	96.1	(AG)20	55	161	AY018005	23
RM5720	IRMI 2003	7	115.5	(AAT)22	55	196	AY022395	23
RM248	IRMI 2003	7	118	(CT)25	55	102	AF344068	19

Marker	Map	Chr	Position cM	Motif	Annealing Tm (°C)	Product Size (bp)	GenBank Accession	References
RM408	IRMI 2003	8	0.5	(CT)13	55	128	AQ163658	18
RM152	IRMI 2003	8	3.3	(GGC)10	55	151	D22858	22
RM38	IRMI 2003	8	16.4	(GA)16	55	250	AF343851	19
RM6208	IRMI 2003	8	42.9	(CGG)8	55	143	AY022883	23
RM210	IRMI 2003	8	53.7	(CT)23	55	140	AF344031	19
RM331	IRMI 2003	8	54.3	[(CTT)4GTT]2 (CTT)11	55	176	AF344155	21
RM547	CORNELL SSR 2001	8	58.1	(ATT)19	55	235	AQ866086	18
RM137	CORNELL SSR 2001	8	60.9	(CT)7	55	218	D47598	21
RM80	CORNELL SSR 2001	8	103.7	(TCT)25	55	142	AF343865	19
RM308	CORNELL SSR 2001	8	104.8	(AT)4-6- (GT)2T2(GT)7	55	132	AF344133	21
RM281	IRMI 2003	8	119.9	(GA)21	55	138	AF344107	21
RM219	CORNELL SSR 2001	9	75.6		55			18
RM257	CORNELL SSR 2001	9	75.9		55			18
RM201	CORNELL SSR 2001	9	93.9	(CT)17	55	158	AF344023	19
RM205	IRMI 2003	9	96.1	(CT)25	55	122	AF344026	19
RM215	IRMI 2003	9	115.5	(CT)16	55	148	AF344036	19
RM245	IRMI 2003	9	118		55			23
RM222	IRMI 2003	10	0.5	(CT)18	55	213	AF344043	19
RM2504	IRMI 2003	10	3.3	(AT)28	55	184	AY019179	23
RM5348	IRMI 2003	10	16.4	(TC)13	55	183	AY022023	23
RM216	IRMI 2003	10	42.9	(CT)18	55	146	AF344037	19
RM171	IRMI 2003	10	48.8	(GATG)5	55	328	D84275	22
RM229	CORNELL SSR 2001	10	58.1	(TC)11(CT)5C3 (CT)5	55	116	AF344049	19
RM457	IRMI 2003	11	52.2	(TTAA)5	55	228	AQ327602	18
RM21	IRMI 2003	11	53.7	(GA)18	55	157	AF344021	20

**Table S7.** Correlation of SSR markers to trait means for Vandana, Moroberekan and intermated BC<sub>3</sub>F<sub>4</sub> lines screened for resistance to rice blast at multi-location trials in India and the Philippines.

SSR Marker	Chr	cM	Trait <sup>1,2</sup>											
			India								Philippines			
			<u>Almora</u>				<u>Hazaribag</u>		<u>Ambikapur</u>		<u>IRRI</u>	<u>Cavinti</u>		
			LN	SB	DLA	SD	PB	YB	LB	PB	LB	SB	SB	
RM109	2	0	-	-	-	-	0.30 <sup>b</sup>	-0.34 <sup>b</sup>	0.17	-0.13	0.06	0.52 <sup>d</sup>	0.50 <sup>d</sup>	
RM154	2	4.8	-	-	-	-0.26 <sup>a</sup>	-	-	-	-	-	-	-	
RM452	2	58.4	0.36 <sup>c</sup>	0.42 <sup>c</sup>	0.31 <sup>b</sup>	-0.26 <sup>a</sup>	0.46 <sup>d</sup>	-0.46 <sup>c</sup>	-	-	-	0.34 <sup>c</sup>	0.34 <sup>b</sup>	
RM545	3	24.7	0.26 <sup>a</sup>	-	-	-	-	-	-0.25 <sup>a</sup>	-	-	0.28 <sup>a</sup>	-	
RM517	3	42.9	-	-	0.26 <sup>a</sup>	-	0.38 <sup>b</sup>	-0.28 <sup>a</sup>	-	-	-	-	0.25 <sup>a</sup>	
RM473D	3	113.2	-0.35 <sup>b</sup>	0.32 <sup>b</sup>	-0.29 <sup>b</sup>	0.37 <sup>c</sup>	-0.53 <sup>d</sup>	0.55 <sup>d</sup>	-	-	-	-0.32 <sup>b</sup>	-0.31 <sup>b</sup>	
RM426	3	122.3	-	0.32 <sup>b</sup>	-	-	0.26 <sup>a</sup>	-0.28 <sup>a</sup>	-	-0.26 <sup>a</sup>	-	0.32 <sup>b</sup>	0.31 <sup>b</sup>	
RM168	3	122.8	0.34 <sup>c</sup>	-	0.36 <sup>c</sup>	-0.31 <sup>b</sup>	0.52 <sup>d</sup>	-0.44 <sup>c</sup>	-	-	-	0.25 <sup>a</sup>	0.25 <sup>a</sup>	
RM186	3	127.4	0.26 <sup>a</sup>	-	0.25 <sup>a</sup>	-0.29 <sup>a</sup>	0.25 <sup>a</sup>	-0.38 <sup>b</sup>	0.35 <sup>c</sup>	-	0.30 <sup>b</sup>	0.26 <sup>a</sup>	0.33 <sup>b</sup>	
RM143	3	207.3	-0.28 <sup>a</sup>	0.25 <sup>a</sup>	-0.33 <sup>a</sup>	-	-	0.26 <sup>a</sup>	-	-	-	-	-	
RM85	3	231	0.29 <sup>a</sup>	-	-	-0.25 <sup>a</sup>	0.37 <sup>b</sup>	-0.32 <sup>b</sup>	-	-	-	0.29 <sup>a</sup>	0.30 <sup>b</sup>	
RM413	5	26.7	-	-	-	-	-	-	-	-	-	-0.25 <sup>a</sup>	-	
RM421	5	101.5	0.30 <sup>a</sup>	-	0.28 <sup>a</sup>	-0.27 <sup>a</sup>	0.41 <sup>c</sup>	-0.33 <sup>b</sup>	-	-	-	-	-	
RM178	5	104.4	-	-	-	-	0.33 <sup>b</sup>	-0.34 <sup>b</sup>	-	-	-	-	-	
RM26	5	111.3	-	-	0.33 <sup>b</sup>	-	-	-	-	-	-	-	-	
RM2	7	36.1	0.33 <sup>b</sup>	0.35 <sup>c</sup>	0.26 <sup>a</sup>	0.39 <sup>c</sup>	0.46 <sup>c</sup>	-0.43 <sup>c</sup>	-	-	-	0.39 <sup>b</sup>	0.37 <sup>b</sup>	
RM1330	7	96.1	-	-	-	-	-	-	-	0.31 <sup>b</sup>	-	-	-	
RM408	7	118.0	0.32 <sup>b</sup>	-	0.31 <sup>b</sup>	-0.29 <sup>b</sup>	0.48 <sup>d</sup>	-0.52 <sup>d</sup>	-	-	-	0.24 <sup>a</sup>	0.25 <sup>a</sup>	
RM152	8	3.3	0.28 <sup>a</sup>	0.33 <sup>b</sup>	-0.29 <sup>b</sup>	-0.29 <sup>a</sup>	0.37 <sup>b</sup>	-0.45 <sup>c</sup>	-	-	-	0.37 <sup>c</sup>	0.37 <sup>c</sup>	
RM3215	8	49.5	-	-	-	-	-	-	-	-	-	-	-0.25 <sup>a</sup>	



**Table S7** (continued)

SSR Marker	Chr	cM	Trait <sup>1,2</sup>											
			India									Philippines		
			Almora						Hazaribag		Ambikapur	IRRI	Cavinti	
			LN	SB	DLA	SD	PB	YB	LB	PB	LB	SB	SB	
RM25	8	52.2	-	-	0.25 <sup>a</sup>	-0.25 <sup>a</sup>	-	-	-	-	-	-	-	-
RM331	8	54.3	-	-	-	-	-	-	-	-0.55 <sup>d</sup>	-	-	-	-
RM137	8	58.1	-	-	-	-	-	-	-	-	0.35 <sup>b</sup>	-	-	-
RM547	8	58.1	-	-	-	-	-	-0.30 <sup>a</sup>	-	-	-	-	-	-
RM308	8	104.7	-	-	-	-	-	-	-	-0.26 <sup>a</sup>	-	0.26 <sup>a</sup>	-0.26 <sup>a</sup>	-
RM281	8	119.9	0.27 <sup>a</sup>	0.27 <sup>a</sup>	0.27 <sup>a</sup>	-	0.43 <sup>c</sup>	-0.43 <sup>c</sup>	-	-	-	0.26 <sup>a</sup>	0.27 <sup>a</sup>	-

<sup>1</sup>LN = lesion number; SB = seedling blast; DLA = diseased leaf area; SD = start of disease (days after sowing); PB = panicle blast; YB = yield under blast condition; LB = leaf blast

<sup>2</sup>Significance of correlation is: a =  $p < 0.05$ ; b =  $p < 0.01$ ; c =  $p < 0.001$ ; d =  $p < 0.0001$

**Table S8.** SSR markers correlated with resistance to rice blast in India and the Philippines that co-localize with known QTL for resistance to biotic stress<sup>1</sup>.

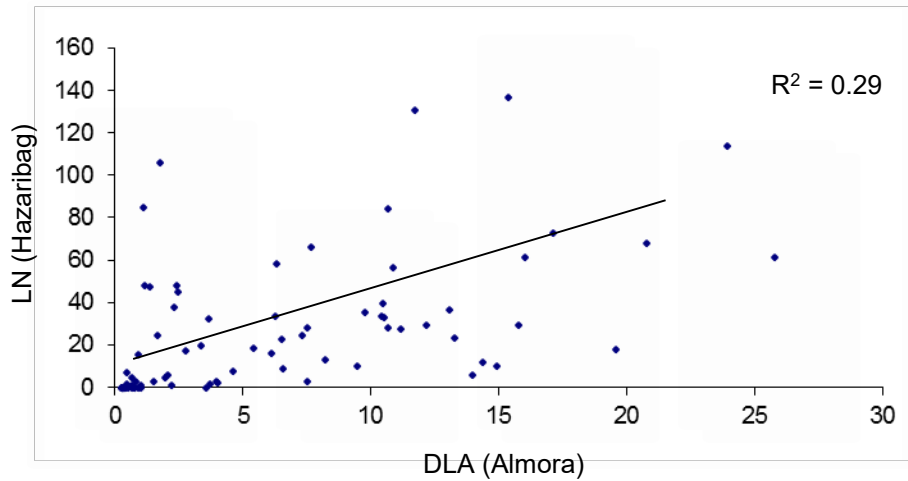
Marker	Chr	cM	BB	RB	BPH	SB	References
RM109	2	0	X	X			1,25
RM154	2	4.8	X	X			1
RM452	2	58.4				X	26
RM545	3	24.7		X	X		1,26 2
RM517	3	42.9		X	X		2,26
RM473D	3	113.2					1
RM143	3	207.3				X	27
RM85	3	231					1
RM413	5	26.7		X			1,28
RM421	5	101.5		X		X	25,29
RM178	5	104.4				X	29
RM2	7	36.1		X			25,30
RM408	7	118.0		X		X	27,30
RM152	8	3.3		X		X	28,30,31
RM3215	8	49.5		X	X	X	28,30,31
RM25	8	52.2	X	X	X	X	1,28,30-32
RM331	8	54.3	X	X		X	1,28,30-32
RM137	8	58.1	X	X		X	1,28,30-32
RM547	8	58.1	X	X		X	1,28,30,32
RM308	8	104.7			X		33
RM281	8	119.9	X		X		1,26,32

<sup>1</sup> BB = bacterial blight; RB = rice blast; BPH = brown plant hopper; SB = sheath blight

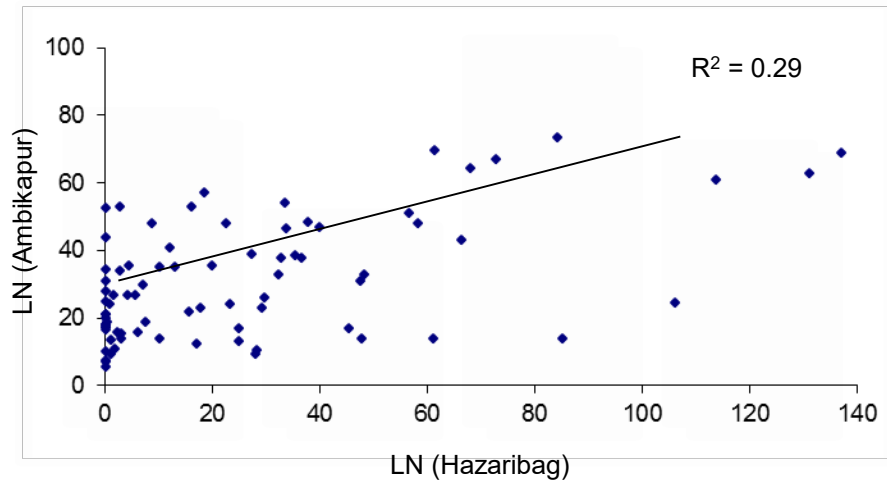
**Table S9.** Field performance of Vandana, Moroberekan and selected intermated BC<sub>3</sub>F<sub>4</sub> lines screened for resistance to rice blast at multi-location trials in India and the Philippines.

Line	Trait/Location										
	India									Philippines	
	Almora						Hazaribag		Ambikapur	IRRI	Cavinti
	LN	SB	DLA	SD	PB	YB	LB	PB	LB	SB	SB
Moroberekan	0.70	3.5	1.5	20	3.2	-	0	0	1.5	1.0	1.0
IR78221-19-6-7-B-B	1.1	2.5	1.0	25	3.3	15.35	2.0	20.8	4.0	1.0	1.0
IR78221-19-6-33-B-B	1.4	5.0	2.0	15	3.9	105.0	2.0	2.4	4.0	1.0	1.0
IR78221-19-4-54-B-B	1.2	4.5	1.5	15	3.5	152.5	2.0	51.3	2.0	1.0	1.0
IR78221-19-6-56-B-B	0.9	4.0	1.0	25	3.1	80.0	2.0	1.3	2.5	1.0	1.0
IR78221-19-6-82-B-B	0.5	3.0	1.0	20	3.4	165.0	2.0	7.5	1.0	1.0	1.0
IR78221-19-6-90-B-B	0.3	6.0	1.0	20	3.0	112.5	3.0	5.0	2.5	1.0	1.0
IR78221-19-6-99-B-B	0.9	6.0	1.0	25	3.3	170.5	2.0	10.2	4.0	1.0	1.0
IR78222-20-7-148-2-B	1.2	5.0	1.5	20	5.1	70.5	2.0	3.0	4.0	4.0	4.0
IR78221-19-3-196	2.4	2.5	57.5	15	8.3	5.0	3.0	10.0	4.0	4.0	4.0
Vandana	3.3	8.5	65.0	15	8.3	5.0	4.0	10.0	5.0	7.0	8.0

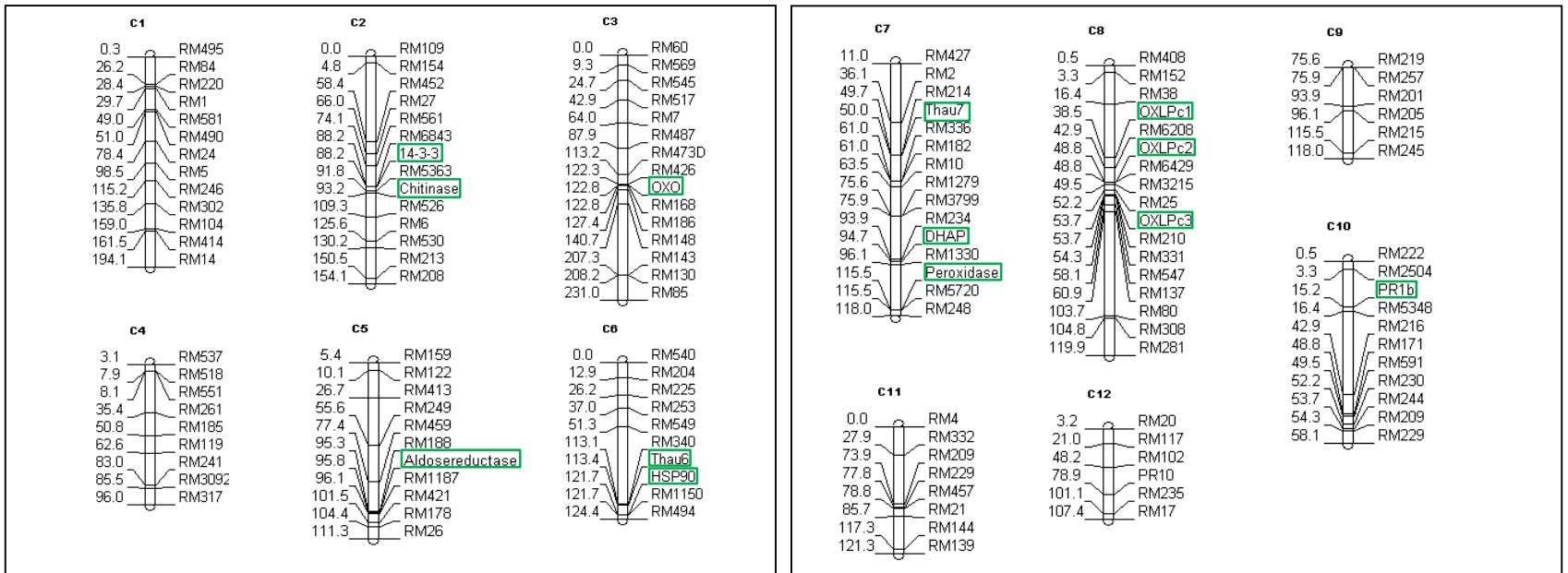
LN = lesion number; SB = seedling blast (Scale 0-9); DLA = % diseased leaf area; SD = start of disease (days after sowing); PB = panicle blast (Scale 0-9); YB = yield under blast condition (grams/plot); LB = Leaf blast



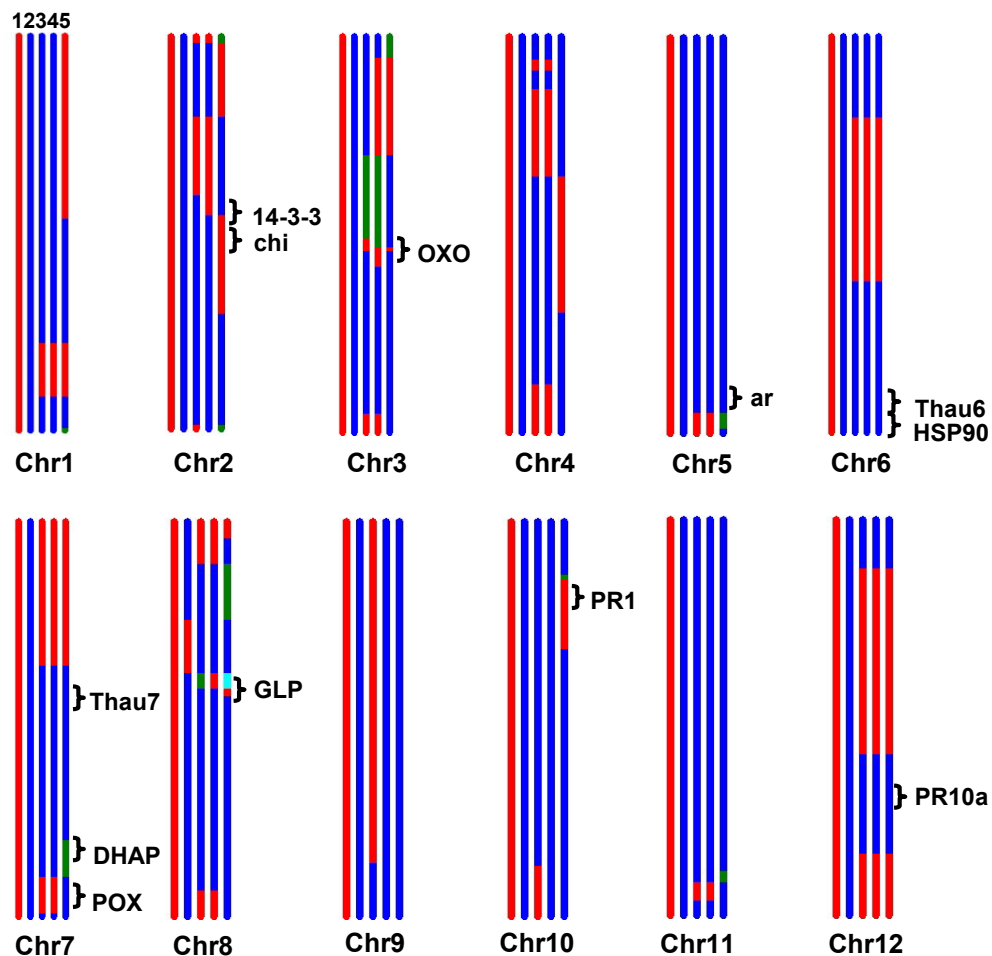
**Fig. S1.** Correlation of disease leaf area at Almora and lesion number at Hazaribag, India on  $F_4$  lines from intermated  $BC_3F_4$  families. Measurements showed a positive correlation ( $r = 0.54^{**}$ ,  $n = 80$  2005). LN = Lesion number, DLA = Disease leaf area.



**Figure S2.** Correlation of Lesion Number (LN) in Ambikapur and lesion number in Hazaribag, India on F<sub>4</sub> lines from intermated BC<sub>3</sub>F<sub>4</sub> families. LN counts at both sites showed a significantly positive correlation ( $r= 0.546^{**}$ ,  $n=80$  2005).



**Figure S3.** Location of SSR markers and candidate genes (green rectangles) considered in the study. OXLP = GLP.



**Figure S4.** Diagram representing data from genome-wide scan of parental lines and a selected subset of F<sub>6</sub> intermated lines. Moroberekan (1- red), and Vandana (2 – blue) genomic regions are shown in three selected lines IR78221-19-6-33-B (3), IR78221-19-6-90-B (4), IR78222-20-7-148-2-B (5) all of which show Resistant phenotype. While most of the genomic background is similar to Vandana, some regions, including QTLs containing CGs, are from Moroberekan. Green regions represent heterozygosity.

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