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Disease resistance of improved MR220 lines against *Pyricularia oryzae* Cavara and their preliminary agronomic performance

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Electronic Supplementary Material (ESM)

Table S1. Blast disease scoring scale developed by the International Rice Research Institute (IRRI 2013) using a scale of 0–9

Scale	Disease severity	Host response
0	no lesion observed	highly resistant
1	small brown specks (< 0.5 mm in diameter)	resistant
2	small roundish to slightly elongated, necrotic grey spots with a distinct brown margin (0.5–1 mm in diameter)	moderately resistant
3	grey centres and brown margin 1–3 mm in diameter	moderately resistant
4	typical spindle shaped blast lesions, 3 mm or longer in diameter, less than 4% of the leaf area infected	moderately susceptible
5	typical blast lesions, 3 mm or longer in diameter, infected 4–10% of the leaf area	moderately susceptible
6	typical blast lesions, 3 mm or longer in diameter, infected 11–25% of the leaf area	susceptible
7	typical blast lesions, 3 mm or longer in diameter, infected 26–50% of the leaf area	susceptible
8	typical blast lesions, 3 mm or longer in diameter, infected 51–75% of the leaf area	highly susceptible
9	typical blast lesions, 3 mm or longer in diameter, infected more than 75% of the leaf area	highly susceptible

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Table S2. Resistance reaction of the BC_3F_4 lines and their parents following the inoculation with isolate MPO 988.3 of the $P_{0.0}$ pathotype of *Pyricularia oryzae*

Variety/lines	Presence of *Pi9* gene	Resistance reaction			
		DLA (%)	DS	DSe (%)	LR
B220PI9-3-1	*Pi9* gene	0	1	7.4	R
B220PI9-3-4	*Pi9* gene	0	0	4.8	HR
B220PI9-3-9	*Pi9* gene	0	1	13.3	R
B220PI9-3-10	*Pi9* gene	0	0	1.9	HR
B220PI9-3-12	*Pi9* gene	0	0	0	HR
B220PI9-3-24	*Pi9* gene	0	0	5.9	HR
B220PI9-3-48	*Pi9* gene	0	1	10.4	R
B220PI9-3-49	*Pi9* gene	0	0	3.3	HR
B220PI9-3-52	*Pi9* gene	0	0	2.8	HR
B220PI9-3-56	*Pi9* gene	0	0	4.4	HR
B220PI9-3-65	*Pi9* gene	0	1	5.6	R
B220PI9-3-76	*Pi9* gene	0	0	0.4	HR
B220PI9-3-77	*Pi9* gene	0	1	5.9	R
B220PI9-3-79	*Pi9* gene	0	0	3.7	HR
B220PI9-3-81	*Pi9* gene	0	1	7.8	R
B220PI9-3-83	*Pi9* gene	0	0	2.9	HR
B220PI9-3-88	*Pi9* gene	0	0	3.7	HR
B220PI9-3-91	*Pi9* gene	0	0	2.6	HR
B220PI9-3-93	*Pi9* gene	0	1	7.0	R
B220PI9-3-94	*Pi9* gene	0	0	4.1	HR
MR220	none	56.3	8	90.4	HS
MR211	none	56.2	9	100.0	HS
IRTP21683	*Pi9* gene	0.3	1	11.9	HR

DLA – disease leaf area; DS – disease score; DSe – percentage disease severity; LR – line response; HR – highly resistant; R – resistant; HS – highly susceptible; Means within a column with a common letter are not significantly different by Duncan's multiple range test at a level of $P \leq 0.05$

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Table S3. Agronomic traits and yield of twenty BC_3F_4 lines and their parents, off season 2018

Variety/lines	No.	Group	TN	PH (cm)	MAT (days)	LOP (cm)	FSPP (%)	WOS (g)	CCT (kg/ha)
B220PI9-3-1	1	4	12.3	87.0	103.0	25.6	75.0	23.2	3 968.0
B220PI9-3-4	2	2	13.7	91.3	101.3	23.8	85.3	23.7	4 698.7
B220PI9-3-9	3	4	12.2	96.4	98.7	27.4	80.8	24.0	3 328.0
B220PI9-3-10	4	2	11.8	93.8	96.7	24.0	71.6	24.9	4 336.0
B220PI9-3-12	5	4	12.5	97.4	98.0	24.5	76.8	25.0	3 837.3
B220PI9-3-24	6	2	12.4	97.6	100.3	23.8	72.8	25.1	4 708.7
B220PI9-3-48	7	1	10.6	98.7	100.7	24.4	71.6	22.3	5 010.7
B220PI9-3-49	8	4	14.1	94.0	96.3	22.5	67.8	27.2	3 770.7
B220PI9-3-52	9	4	13.2	96.0	98.0	24.5	74.3	21.9	3 720.0
B220PI9-3-56	10	2	12.3	91.8	100.3	25.5	74.7	26.6	4 437.3
B220PI9-3-65	11	4	13.8	99.8	98.3	25.7	81.8	25.6	3 488.0
B220PI9-3-76	12	1	13.1	92.2	101.3	24.5	76.3	26.5	5 664.0
B220PI9-3-77	13	1	11.5	90.8	102.3	25.7	74.9	23.5	5 344.0
B220PI9-3-79	14	1	11.5	95.2	102.3	26.2	75.8	23.3	5 157.3
B220PI9-3-81	15	1	12.5	89.2	101.3	26.6	86.3	26.6	5 029.3
B220PI9-3-83	16	1	13.4	93.4	108.7	24.2	71.3	24.8	5 786.7
B220PI9-3-88	17	1	13.3	94.2	103.7	24.9	79.4	24.9	5 322.7
B220PI9-3-91	18	2	12.9	95.2	98.0	23.5	73.4	24.0	4 656.0
B220PI9-3-93	19	2	11.2	89.1	98.3	24.9	67.9	24.7	4 741.3
B220PI9-3-94	20	4	12.5	88.4	97.3	25.1	77.2	26.8	3 925.3
IRTP21683	21	3	9.8	91.3	90.7	19.5	68.9	19.3	1 600.0
MR220	22	2	14.6	91.6	107.3	27.2	86.9	25.6	4 315

TN – number of tillers; PH – plant height; MAT – 80% maturing; LOP – length of panicle; FSPP – filled spikelet % per panicle; WOS – weight of 1000 spikelets; CCT – crop cutting test yield

Table S4. List of seven characteristics used for the cluster analysis and their significance levels from the univariate test statistics using the CANDISC procedure (SAS software)

Characters	TN	PH (cm)	MAT (days)	LOP (cm)	FSPP (%)	WOS (%)	CCT (kg/ha)
R^2	0.335	0.040	0.528	0.504	0.081	0.400	0.941
$R^2/(1 - R^2)$	0.503	0.041	1.117	1.015	0.088	0.667	16.052
F-value	3.020	0.250	6.700	6.090	0.530	4.000	96.310
Pr > F	0.057	0.863	0.003	0.005	0.668	0.024	< 0.0001

TN – number of tillers; PH – plant height; MAT – 80% maturing; LOP – length of panicle; FSPP – filled spikelet % per panicle; WOS – weight of 1000 spikelets; CCT – crop cutting test yield; R^2 – R-square; Pr > F – significant value test

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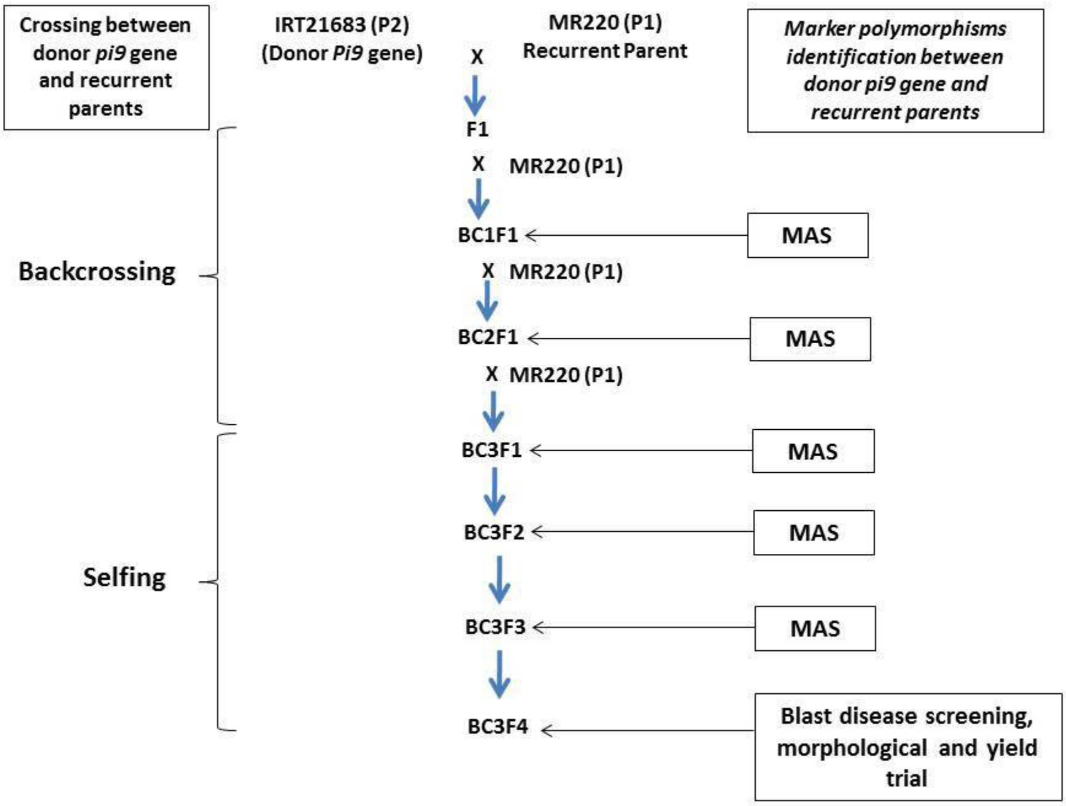

Figure S1. Backcrossing breeding scheme using marker-assisted selection as a tool for the development of the BC_3F_4 lines carrying *Pi9* gene from the cross of IRTP21683 and MR220

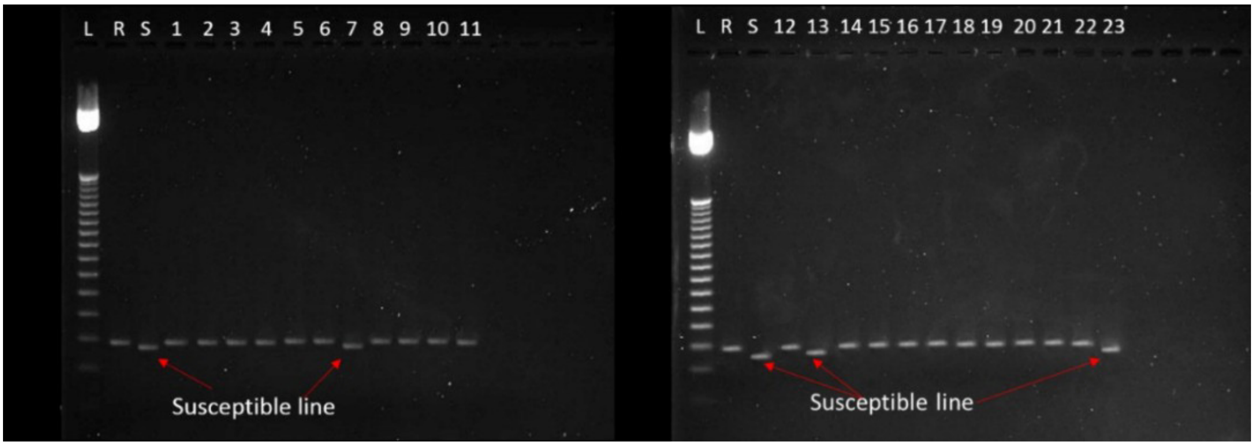

Figure S2. Allele banding patterns of the PCR products as amplified by marker RM7311 on the genomic DNA of the BC_3F_4 lines derived from the cross of IRTP21683 and MR220

Lanes labelled as R and S represent the alleles of the resistant (IRTP21683) and susceptible (MR220) parents, respectively; lane 23 is the susceptible control (MR211); lanes labelled as 1 to 22 represent the BC_3F_4 lines; L – 50 bp-ladder

REFERENCES

IRRI (2013): Standard Evaluation System for Rice. 5th Ed. Manila, International Rice Research Institute.