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Short Communication

Breeding bacterial blight resistant rice (*Oryza sativa* L.) hybrids

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Bacterial blight (BB) caused by pathogen *Xanthomonas oryzae* pv. *oryzae* (Dowson) Dye is a major rice (*Oryza sativa* L.) disease especially in the tropics and sub tropics. Since no chemical control is effective against this disease therefore, genetic resistance is the suitable alternative for the disease management. In hybrid breeding programme, resistance governed by dominant gene(s), is desirable because even one parent having dominant resistance will result in the development of resistant hybrids. [1].

A 'WA' cytoplasmic male sterile (CMS) line *viz.*, PMS 12A was derived from our locally developed BB resistant maintainer line PAU 1356-30-4 (Improved Sona / TN1/ Nam Sagui) and has been used in the present study. This CMS line derives its dominant resistance from the Thai variety Nam Sagui. The present paper reports the inheritance pattern of PMS 12A resistance, its expression in a range of test cross F_1's, fertility restoration behaviour of male parents used and further utilization of resistance in strengthening hybrid rice breeding programme.

Both the CMS lines used in the study *viz.*, PMS 11A (BB score = 7, susceptible) and PMS 12A (BB score = 3, resistant) exhibit complete male sterility (100%). The elite and agronomically superior genotypes of diverse origin which are shown as the male parents in Table 2 were planted in the Source Nursery during *kharif* 1996. Hand crosses were attempted using selected lines as pollen parents on a single plant basis to hybridize with PMS 11A and 12A. During *kharif* 1997, the test-cross F_1's were grown as paired rows, each consisting of 12 plants. The corresponding male parent was planted side by side. After every ten test-cross F_1, the hybrid checks were planted. When the crop was at maximum tillering stage, first row of every F_1, its respective male parent, CMS lines, maintainers, yield checks, F_2 and BC_1 populations were artificially inoculated with the bacterial blight suspension culture of I (most prevalent in Punjab) following leaf-clipping method [2]. After 21 days of pathotype inoculation, disease scoring was done following the Standard Evaluation System [3] according to the 1-9 scale, where 1 represents highly resistant and 9 highly susceptible. During flowering, anthers of 5-10 spikelets of each plant in a single row of F_1's were squashed and pollen grains stained with 1% iodine potassium iodide solution and observations for pollen fertility were made from at least 5-6 microscopic fields. Two panicles of each 5 plants in a single row were also bagged to study their spikelet fertility at maturity. Based upon the degree of pollen and spikelet fertility (%) in the test cross F_1's the respective male parents were designated as restorer (>80.0 %), maintainer (0.0 %) and partial (> 0.0 to < 80.0 %).

The CMS lines *viz.*, V20A, PMS 3A, PMS 8A, PMS 10A and PMS 11A are BB susceptible. Therefore, inheritance of BB resistance in PMS 12A was studied in five crosses involving PMS 12B and maintainer lines of above CMS lines (Table 1). As expected, F_1 plants of all crosses were resistant. Segregation pattern in F_2 generation in these crosses exhibited a good fit to 3 resistant: 1 susceptible ratio. Similarly, back cross plants of these crosses involving susceptible maintainer as recurrent parent segregated into good fit of 1 resistant : 1 susceptible ratio. This indicates the presence of single dominant gene governing resistance in PMS 12B. Some of the fertility restorers like PAU 1920-100-1-3-3, PAU 2020-10-3-1-1 and PAU 2064-18-3-3 as identified in this study (Table 2) and developed through over conventional breeding programme also possess resistance. For knowing the allelic relationships for resistance genes in these restorers and PMS12A, the test cross F_1 and F_2 plants of PMS 12 A × PAU 1920 - 100-1-3-3-(PR106///TN_1/Patong 32//PR106 *5), PMS12A × PAU 2020-10-3-1-1 (PR108/TN_1//Patong 32///PR106 * 6//// PR108) and PMS12A × PAU 2064-18-3-3 (TN_1/Patong 32// PR 106 *6 /// PR 103 *4) were studied for disease reaction (Table 1). All the F_2 plants of crosses sampled were found to be resistant and therefore did not segregate for disease reaction.

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Table 1. Genetics of B B resistance in rice CMS lines

Cross/ Generation	No. of plants observed	Disease reaction Resistant	Disease reaction Susceptible	Expected ratio	χ^2	P-range
1. V20B × PMS 12B						
F_1	15	15	0	-	-	-
F_2	497	367	130	3:1	0.39	0.70-0.50
F_1 × V20B	23	10	13	1:1	0.39	0.70-0.50
2. PMS 11 B × PMS 12 B						
F_1	16	16	0	-	-	-
F_2	23	17	6	3:1	0.23	0.02-0.01
3. PMS 12B × PMS 10 B						
F_1	14	14	0	-	-	-
F_2	164	126	48	3:1	0.77	0.50-0.30
F_1 × PMS 10B	74	34	40	1:1	0.49	0.50-0.30
4. PMS 12B × PMS 3 B						
F_1	25	25	0	-	-	-
F_1 × PMS 3B	29	14	15	1:1	0.03	0.95-0.80
5. PMS 12B × PMS 8B						
F_1	21	21	0	-	-	-
F_2	36	25	11	3:1	0.59	0.50-0.30

This reveals that the resistance in above 3 restorers is conveyed by a single dominant gene which is allelic to that in PMS 12A. All the above restorers derive their resistance form Patong 32, a native of Malaysia.

Of the 53 male parents test-crossed with PMS 12A, 18 were resistant (3-5 score) whereas, the remaining were susceptible (Table 2). The F_1s of the resistant males with 12A as expected were also resistant. The F_1 between resistant male PAU 1920- 100-1-3-3 and susceptible PMS 11A also showed resistance. All the F_2s involving PMS 12A as the female parent were resistant to the BB isolate inoculated except those which involved UPR 1154-1-2-1, RP 3238-14-7-6-1, Pusa 44, PNA 714-F4-108, CNA 3891 and PSP 087 as pollen parents. Our experience of test cross nursery in *kharif* 1998 also showed non uniformity of resistance expression in the F_1s of PMS 12A with a few male parents. The reduced level of resistance expression in these F_1s could be due to the absence and/or presence respectively of modifier and/or inhibitor gene complex in the above mentioned male parents, which however requires further genetic analysis. It has been indicated that some of the varieties such as TKM6, W 1263, Sigadis and Tadukan carrying major resistance gene *Xa4* also possess minor gene complex for the expression of resistance [4]. Similarly, the resistance in IR 28 rice variety possessing *Xa4* is also reported to be polygenically governed [5].

Table 2. Disease reaction of the test cross F_1's and corresponding male parents and fertility restoration behaviour of the male parents

Combination/variety	Origin of parent	BB score F_1	BB score ♂	Restoration behaviour of male parent
PMS11A/IR13538-48-2-3-2	IRRI	9	7	R
/PAU1920-100-1-3-3	India	3	3	R
/KAUM-6 1-6-1 -1-2	India	9	9	M
/MTU 1009	India	9	7	R
PMS12A/IR74	IRRI	3	9	P
/IR58100-62-3-2	IRRI	3	5	P
/IR58749-52-1-3-2-2	IRRI	3	9	P
/IR58799-50-3-3-3	IRRI	3	9	M
/IR63873-45-2-1-2-3	IRRI	3	9	R
/PAU1920-100-1-3-3	India	3	3	R
/PAU2020-10-3-1-1	India	3	3	R
/PAU2061-9-2-1	India	3	3	R
/PAU2061-19-2-2	India	3	3	R
/PAU2064-18-3-3	India	3	3	R
/PAU2073-42-1-1	India	3	7	P
/PAU2082-79-1-3-2	India	3	9	R
/PAU2335-51-11-2	India	3	3	R
/PAU2335-64-4-2	India	3	3	R
/PAU2341-13-1-2	India	3	9	M
/UPR 189-6	India	3	5	M
/UPR 1138-14-1	India	3	9	P
/UPR 1154-1-2-1	India	3/7	9	P
/UPR1425-1-4-1	India	3	7	M
/UPR 1616-9-2	India	3	9	P
/RP2724-436-15-2	India	3	9	M
/RP3 125-90-12-1-4	India	3	9	P
/RP3238-14-7-6-1	India	5/7	9	P
/HKR93-1	India	3	3	P
PMS12A/Pusa44	India	5/7	9	R
/PNA714-F4-108	Peru	3/5	9	M
/PNA1022-F4-110-1	Peru	3	7/9	P
/CNA3891	Brazil	3/5	9	P
/EBAO AI	China	3	7	M
/Tallan	-	3	7/9	M
/TOX3133-59-1-2-4	Nigeria	3	9	R
/PSP-087	India	5/7	9	P
Checks (hybrids)				
PMS3A/CT8470-15-17-1	Colombia	9	9	R
PMS10A/CT8470-15-17-1	Colombia	9	9	R
PMS11A/CT8470-15-17-1	Colombia	9	9	R

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