

Genetic analysis of blast resistance in rice

Mahendra Persaud*, A. Kumar, R.B.S. Sengar, Abhinav Sao, R.K. Dantre and M.N. Shrivastava

Indira Gandhi Agricultural University, Krishak Nagar, Raipur, Chhattisgarh

ABSTRACT

The genetic analysis of blast (*Pyricularia grisea* Sacc.) resistance in rice was conducted in Chhattisgarh, India. The inheritance studies revealed that, resistant parents RR 166-645 and Bala possessed a single dominant gene, which is effective against one or more races of blast. The resistant line RR 345-2 and moderately resistant lines IAC 25 and IR 42221-2-3-2 possesses two independent dominant genes, each gene providing resistance against a single but different race. Allelic tests showed that, the genes conferring resistance to blast present in RR 166-645 and RR 345-2 are non-allelic. Similarly, the resistance conferring genes in WAB 56-50 and B 61444-F-MR-6-0-0 are also non-allelic.

Key words: rice, blast, resistant donors, inheritance, allelic relationships

Blast disease caused by the fungus *Magnaporthe grisea* (anamorph: *Pyricularia grisea* Sacc.) is the biggest constraint of stable rice production (Reddy and Bentur, 2000). The disease has long been recognized as the most explosive and potentially damaging disease of the rice crop. It limits rice yields in all major rice growing regions of the world, especially in irrigated lowlands and dry upland environments where predisposition factors, favour disease development to epidemic proportions (Babugee and Ganamanickam, 2000). Host-Plant resistance has been recognized as the most economical and viable approach to check the yield losses. The genetics of blast resistance in rice has been extensively studied (Mackill and Bonman, 1992; Chao *et al.*, 1999). About 40 blast resistance genes have been identified in rice and at least 20 loci for complete resistance and 10 QTLs for partial resistance have been genetically mapped (McCouch *et al.*, 1994).

Even though Chhattisgarh region is considered as the “rice bowl” of India and the prevailing physical environment of some areas of such as Bastar plateau, Northern hilly regions and Bilaspur favors the development of blast to epidemic proportions there was no serious attempt to accumulate or generate genetic information on blast in this state. Furthermore, there is

a lack of an organized breeding program with blast resistance as its mainstream objective in the state.

It is almost mandatory to understand the mode of inheritance and the allelic relationships of the genes governing resistance to blast in order to successfully develop resistant varieties with effective and durable resistance. Hence the present study aimed at understanding the inheritance and allelic relationships of gene(s) for blast resistance present in some newly identified donors.

The current studies were conducted in the Department of Plant Breeding and Genetics, Indira Gandhi Agricultural University, Raipur, Chhattisgarh in collaboration with College of Agriculture and Research Station, Ambikapur and over three cropping season's *viz.*, wet season. Hybridization and advancing of various generations were carried out at Raipur during wet season. Screening for disease reaction was done at hot spot for blast Ambikapur.

Seven genotypes, IAC 25, IR 42221-2-3-2, Bala, RR 166-645, RR 345-2, WAB 56-50, and B 61444-F-MR-6-0-0 were used in the study. The first two genotypes were identified as moderately resistant and the others resistant against blast fungus race prevalent in Chhattisgarh (Persaud, 2002). The first five

genotypes were crossed with susceptible parents for inheritance study and the last four were crossed among themselves for the allelic study. The F_1 generation of the crosses was grown in subsequent season for advancing the population to F_2 generation. The seeds of individual F_1 plants were harvested separately. Ten to twenty F_1 seeds from each cross were grown in rows in plastic tray (12cm. x 18 cm.). At 51 days after sowing the trays were placed in an established uniform blast nursery (UBN) bed (25 days old) in such a way that the tray was surrounded by susceptible check. The F_2 populations were sown family wise in the UBN. A population was represented by ten rows (30cm long and 10 cm spacing), each row being a produce of single F_1 plants. Susceptible check cultivar Mahamaya was planted after every row and each population was further surrounded by two rows of the same susceptible check.

The test populations were screened against leaf blast under upland nursery condition at Ambikapur, which are considered as “host spot” in a Uniform Blast Nursery (UBN) as per procedure given by (Ou, 1965). Additional measures for maintaining conducive environment for blast infestation such as dense planting, high rate of nitrogen (120 kg ha⁻¹) application, supplemental overhead sprinkler irrigation 2-3 times on each rainless day were provided.

Observations were recorded following the 0-9 scale of Standard Evaluation System (SES) of IRRI (INGER, 1996) when susceptible check reached 8-9 score. The score of the F_1 plants were noted. In F_2 the plants were uprooted from the nursery and individual score was taken. Plants with score of up to 3 were pooled as resistant and those with scores 4-9 were pooled as susceptible.

The natural occurrence of blast at Ambikapur and Jagdalpur during the seasons under study was very high. The susceptible check attained score of 8 and 9.

The F_1 s of all the crosses studied were resistant indicating the involvement of dominant resistant gene in the parent. The observed frequencies of resistant and susceptible plants in F_2 population of crosses RR 166-645/CR 306-37-13, RR 166-645/RR 165-1160, RR 166-645/CR 143-2-2, RR 166-645 / CR 314-5-10, RR 348-5/RR 166-645, VL 16/RR 166-645 and C101 A 51/Bala (Table 1) fitted well in three resistant and one susceptible (3 R: 1 S) ratio. This indicated control of blast resistance by single dominant gene in the resistant parents, RR 166-645 and Bala.

The F_2 populations of crosses RR 345-2/CR 306-37-13, RR 345-2/CR 143-2-2 and RR 348-5/RR 345-2 segregated in a nine resistant and seven

Table 1. Inheritance and allelic relationships of gene(s) for resistance against blast (*Pyricularia grisea* Sacc) in some new donors

S.N.	Cross Combinations	Reaction of F_1 plants	Reaction of F_2 plants					
			No. of plants			Ratio	χ^2 value	P value
			R	S	Total			
						R : S		
	RR 166-645 / CR 306-37-13	R	250	89	339	3 : 1	0.284	0.70 - 0.50
	RR 166-645 / RR 165-1160	R	291	96	387	3 : 1	0.008	0.98 - 0.95
	RR 166-645 / CR 143-2-2	R	278	102	380	3 : 1	0.688	0.50 - 0.30
	RR 166-645 / CR 314-5-10	R	276	88	364	3 : 1	0.132	0.80 - 0.70
	RR 348-5 / RR 166-645	R	248	95	343	3 : 1	1.331	0.30 - 0.20
	VL-16 / RR 166-645	R	212	66	278	3 : 1	0.764	0.50 - 0.30
	C 101 A 51 / Bala	R	234	86	320	3 : 1	0.600	0.50 - 0.30
	RR 345-2 / C-R 306-37-13	R	143	106	249	9 : 7	0.141	0.70 - 0.60
	RR 345-2 / CR 143-2-2	R	110	95	205	9 : 7	0.595	0.50 - 0.30
	RR 348-5 / RR 345-2	R	158	103	261	9 : 7	0.860	0.50 - 0.30
	IAC 25 / RR 348-5	R	170	115	285	9 : 7	1.338	0.30 - 0.20
	C101 A51 / IR 42221-2-3-2	R	150	140	290	9 : 7	2.44	0.20 - 0.10
	RR 345-2 / RR 166-645	R	218	37	255	57 : 7	3.340	0.10 - 0.05
	WAB 56-50 / B 6144-F-MR-6-0-0	R	270	80	350	51 : 13	1.400	0.30 - 0.20

R = Resistance S = Susceptibility

susceptible (9R : 7S) ratio (Table 1). This can be explained by assuming presence of either two independent dominant genes when present together providing resistance against the races existing at Ambikapur. Alternatively, each of the two dominant genes separately providing resistance to one of the two races existing at Ambikapur, plant exhibits resistance only when it possesses both the genes. In the later case, which appears to be more likely that, the single dominant genes present in each of RR 166-645 and Bala is capable of providing resistance to both races postulated to be existing at Ambikapur. A single gene providing resistant against two races of blast has also been reported by Rath and Padmanabhan (1972) and Atkins and Jonston (1965). A single dominant gene provides resistance to blast have been well documented (Mohanty and Gangopadhyay, 1982 and Mackill *et al.*, 1985).

The F₂ population of crosses of moderately resistant cultivars IAC 25 and IR42221-2-3-2 (IAC25/RR348-5, CA 101A51/IR42221-2-3-2) with susceptible strains segregated in nine resistant and seven susceptible (9 R : 7 S) ratio. This also suggested two independently dominant genes in each resistant parent against two races of fungus, identical to the inheritance of RR 345-2. Many workers have also reported the control of blast by two independent dominant gene (Mohanty and Gangopadhyay, 1982, Mackill *et al.*, 1985 and Shi *et al.*, 1994).

Resistance in RR 345-2 is governed by two independent dominant gene and RR 166-645 by one dominant gene. The F₂ population of a cross between these two parents showed a 57 R: 7 S ratio. The ratio indicated that the population is segregating for three pairs of independently dominant genes. This suggested that the genes in both parents are segregating independently of each other, hence, they are non-allelic. When resistant cultivars WAB 56-50 and B 6144-F-MR-6-0-0 were crossed the F₂ population segregated in 51 R: 13 S ratio. This suggested that three pairs of genes are involved: two independent dominant and one inhibitory dominant gene. One parent possessing one dominant gene and the other contain one dominant along with one inhibitory gene. Thus, the resistance genes in WAB 56-50 and B 6144-F-MR-6-0-0 are non allelic.

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