

## Inheritance of Blast Resistance in Pearl Millet (*Pennisetum glaucum* (L.) R. Br.)

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### Abstract

Pearl millet blast, caused by *Pyricularia grisea* (Cooke) Sacc, has recently emerged as a serious disease in India. Two susceptible lines (DHLBI 21B and DHLBI 36B) and two resistant lines (DHLBI 28B and ICMB 10899) were selected and four crosses were made as susceptible x resistance viz., DHLBI 21B X DHLBI 28B, DHLBI 36B X DHLBI 28B, DHLBI 21B X ICMB 10899 and DHLBI 36B X ICMB 10899 and generations viz., P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub> of each cross were used to study the inheritance of blast resistance in pearl millet. These were evaluated for disease reaction with natural inoculation under field condition at Dhule during *kharif* season. All four crosses showed the goodness of fit to 3:1 (R:S) segregation ratio in F<sub>2</sub> population and 1:1 (R:S) ratio was observed in their backcross populations under hotspot field condition. The disease reaction of the F<sub>1</sub>s, and the segregation patterns of resistance in the F<sub>2</sub>s, B<sub>1</sub> and B<sub>2</sub> generations, on inheritance of blast indicated that the resistance is monogenic and a single dominant gene controls resistance to the natural inoculum of *Magnaporthe grisea*.

**Key words : Pearl millet, blast and inheritance.**

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The pearl millet crop is susceptible to various diseases caused by fungal, bacterial, viral, and nematode pathogens. Among the many diseases that plague pearl millet, downy mildew produced by *Sclerospora graminicola* has long been a severe issue for pearl millet hybrids. But in recent years, Blast or leaf spot of pearl millet, caused by *Magnaporthe grisea* (Herbert) Barr [anamorph: *Pyricularia grisea* (Cooke) Sacc.], has recently emerged as a serious disease that threatens both forage and grain production of pearl millet worldwide (Sharma et al., 2013). This disease was initially documented in Kanpur, Uttar Pradesh. (Mehta et al., 1953). The frequency and intensity of blasts have increased in pearl millet growing areas across India, particularly in the regions of Maharashtra, Punjab, Haryana, Uttar Pradesh and Rajasthan. Blast, also known as leaf spot, is a significant disease affecting both forage and grain production in pearl millet (Nayaka et al., 2017). The disease thrives in environments with high

plant density, moderate temperatures (25-30°C), regular rains, gloomy sky and 90% relative humidity (Sharma et al., (2013).

In pearl millet, Tift 85DB that was resistant to pathogen population from Georgia, USA was shown to be sensitive for the Patancheru isolate of pearl millet blast pathogen, suggesting the wide range of pathogen diversity. The only surefire, least expensive, and environmentally benign way to defeat this illness is to breed for blast resistance. Resistance sources have been discovered and blast screening systems for the field and greenhouse have been devised (Thakur et al., 2009). Understanding how resistance is inherited will directly affect how well this disease is bred for genetic management. Thus, it is crucial to design a variety or hybrid for blast resistance in order to boost output and productivity. Knowledge on the inheritance of resistance will have a direct bearing on the breeding efficiency for genetic management of this disease.

Hence, there is a need to study the inheritance of blast resistance in pearl millet. The breeding of blast resistance is still in its infancy in India. A single dominant gene controls the resistance to blast, according to reports from Gupta et al., (2012), Pawar et al., (2016), Singh et al., (2018) and Malik et al., (2021). These were the only research to far that attempted to explain the nature and genetics of resistance to pearl millet blast. In India, the breeding for blast resistance is still in its early stages. Considering the importance of the crop and the above facts, there is a need to generate information on blast inheritance pattern.

### Materials and methods

The parental material used in the current studies include four genetically diverse and good combining inbred lines of pearl millet DHLBI 21B and DHLBI 36B which are susceptible to blast while, DHLBI 28B and ICMB 10899 are resistance to the blast reaction in 0-9 scale under hotspot condition. Four crosses were made as susceptible x resistance viz., DHLBI 21B X DHLBI 28B, DHLBI 36B X DHLBI 28B, DHLBI 21B X ICMB 10899 and DHLBI 36B X ICMB 10899 and backcrossing was also done in Summer 2023. F<sub>1</sub> hybrids along with their both the respective parents were sown in

Summer 2023 to produce seed for F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub> generations. All six populations were evaluated in three replication and the response to blast under field conditions was scored for the P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub> generations at Bajra research scheme, College of agriculture, Dhule during *Kharif* 2023. In single replication one rows each of parents and F<sub>1</sub>'s, three rows of each B<sub>1</sub> and B<sub>2</sub> and six rows of each F<sub>2</sub> were sown with the row length of 4.0 m each. Disease severity was recorded at 30 and 60 DAS stage using a 0-9 progressive scale developed by Thakur et al. (2009).

Chi square test ( $P \leq 0.05$ ) was used to compare the ratio of observed resistant to susceptible plants in the segregating populations in field condition.

### Results and discussion

Among parents, the susceptible parents DHLBI 21B and DHLBI 36B showed susceptibility to blast (score>5), while resistant parent DHLBI 28B and ICMB 10899 showed all resistant plants (score of  $\leq 3$ ). All F<sub>1</sub>s (S x R) and B<sub>2</sub>S [(S x R) X R] of four crosses were resistant (score of  $\leq 3$ ) under field conditions. In F<sub>2</sub>s (S x R) and B<sub>1</sub>s [(S x R) X S] of four crosses there was a clear-cut segregation either for resistant plants (score of  $\leq 3$ ) or for susceptible

#### Blast severity rating scale (1-9) recorded as per Thakur et al. (2009).

Rating Scale	Symptoms and lesions	Disease reaction
1	No lesion to small brown specks of pinhead size	HR
2	Large brown specks	R
3	Small, roundish to slightly elongated, necrotic gray spots, about 1-2 mm in diameter with brown margin	R
4	Typical blast lesions, elliptical, 1-2 cm long, usually confined to the between main veins, covering <2% of leaf area	MR
5	Typical blast lesions covering<10% of the leaf area	MR
6	Typical blast lesions covering 10-25% of the leaf area	S
7	Typical blast lesions covering 26-50% of the leaf area	S
8	Typical blast lesions covering 51-75% of the leaf area and many leaves dead	HS
9	All leaves dead	HS

HR: Highly resistant, R: Resistant, MR: Moderately resistant, S: Susceptible, HS: Highly susceptible.

plants (score > 5) and no plant had a score of above 3 and below 5 for blast reaction in field conditions.

In the cross, DHLBI 21B x DHLBI 28B, 22 plants of P<sub>1</sub> DHLBI 21B, 20 plants of P<sub>2</sub> DHLBI 28B, 24 F<sub>1</sub> plants, 135 F<sub>2</sub> plants, 62 B<sub>1</sub> (backcross with DHLBI 21B) plants and 71 B<sub>2</sub> (backcross with DHLBI 28B) plants were screened in field conditions. All of the P<sub>2</sub>, F<sub>1</sub> and B<sub>2</sub> plants exhibited resistance. In the F<sub>2</sub> population, out of 135 plants 97 were resistant and 38 were susceptible which fitted well to

expected monogenic ratio of 3:1 (R:S) with  $\chi^2$  value of 0.71 with P-value of 0.40. Among the B<sub>1</sub> population, out of 62 plants 33 were resistant and 29 plants exhibited the susceptible reaction which fitted with the expected ratio of 1:1(R:S) with the  $\chi^2$  value 0.26 and P-value 0.61.

In the cross, DHLBI 36B x DHLBI 28B, 23 plants of P<sub>1</sub> DHLBI 36B, 20 plants of P<sub>2</sub> DHLBI 28B, 23 F<sub>1</sub> plants, 149 F<sub>2</sub> plants, 70 B<sub>1</sub> (backcross with DHLBI 36B) plants and 65 B<sub>2</sub> (backcross with DHLBI 28B) plants were

**Table 1.** Segregation for blast resistant (R) and susceptible (S) plants in P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub> generations and  $\chi^2$  test in pearl millet

Cross	Generation	No of plant observed			No of plants expected		Expected ratio	$\chi^2$	P
		Total	R	S	R	S			
DHLBI 21B x DHLBI 28B	DHLBI 21B (P <sub>1</sub> )	22	0	22					
	DHLBI 28B (P <sub>2</sub> )	20	20	0					
(S x R)	F <sub>1</sub>	24	24	0	24	0	1:0	-	-
	F <sub>2</sub>	135	97	38	101.25	33.75	3:1	0.71	0.40
	B <sub>1</sub>	62	33	29	31	31	1:1	0.26	0.61
	B <sub>2</sub>	71	71	0	71	0	1:0	-	-
DHLBI 36B x DHLBI 28B	DHLBI 36B (P <sub>1</sub> )	23	0	23					
	DHLBI 28B (P <sub>2</sub> )	20	20	0					
(S x R)	F <sub>1</sub>	23	23	0	23	0	1:0	-	-
	F <sub>2</sub>	149	117	31	111.75	37.25	3:1	1.45	0.23
	B <sub>1</sub>	70	32	28	35	35	1:1	1.66	0.20
	B <sub>2</sub>	65	65	0	65	0	1:0	-	-
DHLBI 21B x ICMB 10899	DHLBI 21B (P <sub>1</sub> )	22	0	22					
	ICMB 10899 (P <sub>2</sub> )	19	19	0					
(S x R)	F <sub>1</sub>	25	25	0	25		1:0	-	-
	F <sub>2</sub>	152	109	43	114	38	3:1	0.88	0.35
	B <sub>1</sub>	67	32	35	33.5	33.5	1:1	0.13	0.71
	B <sub>2</sub>	62	62	0	62		1:0	-	-
DHLBI 36B x ICMB 10899	DHLBI 36B (P <sub>1</sub> )	23	0	23					
	ICMB 10899 (P <sub>2</sub> )	19	19	0					
(S x R)	F <sub>1</sub>	22	22	0	22		1:0	-	-
	F <sub>2</sub>	143	99	44	107.25	35.75	3:1	2.54	0.11
	B <sub>1</sub>	59	33	26	29.5	29.5	1:1	0.83	0.36
	B <sub>2</sub>	69	69	0			1:0	-	-

screened in field conditions. All of the  $P_2$ ,  $F_1$  and  $B_2$  plants exhibited resistance. In the  $F_2$  population, out of 149 plants 117 were resistant and 31 were susceptible which fitted well to expected monogenic ratio of 3:1 (R:S) with  $\chi^2$  value of 1.45 with P-value of 0.23. Among the  $B_1$  population, out of 70 plants 32 were resistant and 28 plants exhibited the susceptible reaction which fitted with the expected ratio of 1:1(R:S) with the  $\chi^2$  value 1.66 and P-value 0.20.

In the cross, DHLBI 21B x ICMB 10899, 22 plants of  $P_1$  DHLBI 21B, 19 plants of  $P_2$  ICMB 10899, 25  $F_1$  plants, 152  $F_2$  plants, 67  $B_1$  (backcross with DHLBI 21B) plants and 62  $B_2$  (backcross with ICMB 10899) plants were screened in field conditions. All of the  $P_2$ ,  $F_1$  and  $B_2$  plants exhibited resistance. In the  $F_2$  population, out of 152 plants 109 were resistant and 43 were susceptible which fitted well to expected monogenic ratio of 3:1 (R:S) with  $\chi^2$  value of 0.88 with P-value of 0.35. Among the  $B_1$  population, out of 67 plants 32 were resistant and 35 plants exhibited the susceptible reaction which fitted with the expected ratio of 1:1(R:S) with the  $\chi^2$  value 0.13 and P-value 0.71.

In the cross, DHLBI 36B x ICMB 10899, 23 plants of  $P_1$  DHLBI 36B, 19 plants of  $P_2$  ICMB 10899, 22  $F_1$  plants, 143  $F_2$  plants, 59  $B_1$  (backcross with DHLBI 21B) plants and 69  $B_2$  (backcross with ICMB 10899) plants were screened in field conditions. All of the  $P_2$ ,  $F_1$  and  $B_2$  plants exhibited resistance. In the  $F_2$  population, out of 143 plants 99 were resistant and 44 were susceptible which fitted well to expected monogenic ratio of 3:1 (R:S) with  $\chi^2$  value of 2.54 with P-value of 0.11. Among the  $B_1$  population, out of 59 plants 33 were resistant and 26 plants exhibited the susceptible reaction which fitted with the expected ratio of 1:1(R:S) with the  $\chi^2$  value 0.83 and P-value 0.36.

These ratios revealed best goodness of fit ratio of 3:1 and 1:1 in  $F_2$  and  $B_1$  respectively. These results showed that resistance is monogenic and control by single dominant gene. In contrast, blast resistance genes reported by Wilson et al., (1989) were of nonallelic nature in pearl millet landraces from Burkina Faso and Tift 85DB. The similar results were obtained are in accordance with the results reported by Gupta et al., (2012), Pawar et al., (2016), Singh et al., (2018) and Malik et al., (2021). The identified blast resistant plants could be used to develop blast resistant variety/hybrid and efforts should be made to study pathogenic variability in *P. grisea* isolates from different pearl millet growing areas in India and identify resistant sources to different pathotypes for utilizing them in breeding program to manage this disease through host plant resistance.

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