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Sources of resistance of different cotton genotypes against bacterial blight disease incited by *Xanthomonas axonopodis* pv. *malvacearum* under natural epiphytotics

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ABSTRACT

A total thirty-six cotton genotypes were screened in replicated thrice with Randomized Block Design against bacterial blight disease incited by *Xanthomonas axonopodis* pv. *malvacearum* under natural epiphytotics. Results revealed that 3 genotypes showed moderately resistant, 31 showed moderately susceptible and 2 showed susceptible against bacterial blight of cotton. Disease severity at 60 DAS ranged from 2.42 to 27.5 per cent, PH 1009 (2.42 per cent), Paig 29 (2.42 per cent) had shown lowest disease severity. Disease severity at 90 DAS ranged from 9.63 to 58.6 per cent. NH 633 (9.63 per cent) had shown minimum disease severity followed by PH 1062 (9.91 per cent) and PH 1031 (10.37 per cent). Disease severity at 120 DAS ranged from 11.63 to 68.94 per cent. The lowest PDI was recorded by NH 633 (11.63 %) followed by Paig 265 (13.26 %) and NH 637 (13.55 %). Mean disease severity (PDI) of cotton genotypes was recorded in range 9.71 to 51.68 per cent.

1. Introduction

Cotton (*Gossypium* spp.) belongs to family malvaceae is one of the important cash, fibre and oilseed crop commonly grown in many parts of India. Cotton mainly grown for fibre needs of the human. Cotton almost accounts 65 per cent of fibre production in India. Edible oil is extract from cotton seed and de-oiled cakes are used

as a cattle feed, which is a good source of high quality protein for animals. India has the largest acreage 95.5 lakh/ha under cotton at global level and has the productivity of 591 kg lint/ha and ranks second in production 332 lakh bales after China during 2008-09 (Anonymous, 2009). In India, main cotton growing area is seen in the central zone of India comprising of Gujarat, Maharashtra and Madhya Pradesh. Cotton is grown in Maharashtra on an area of 31.24 lakh ha. While, the production is near about 60 lakh bales, with an average productivity of 320 kg lint/ha during 2008-09 (Anonymous, 2009).

Amongst the several factors responsible for reduction in yield and quality deterioration of cotton in India, a disease occupies a vital place. Bacterial blight of cotton caused by *Xanthomonas axonopodis* pv. *malvacearum* is one of the serious diseases of cotton. It is recorded in almost every country in the world which grows cotton. It is an important disease of cotton in India, Pakistan, China, South East Asia, South America, Australia and Europe (Hillocks, 1992). In India, disease observed in Andhra Pradesh, Haryana, Madhya Pradesh, Maharashtra, Punjab, Rajasthan and Tamil Nadu (Verma, 1986; and Shrinivasan, 1994).

Bacterial blight was first reported from Albama (USA) by Atkinson in 1891. However, the disease was introduced in India through exotics in the middle of 19th century. The disease was first reported in India in Madras in 1918. The disease is considered as semi systemic disease. Pathogen infects all the stages of plants. In India, the disease is known to occur in all the cotton growing areas with an annual losses upto 30 per cent (Mishra *et al*. 2001). The pathogen is both externally as well as internally seed borne (Verma and Singh, 1974) which plays important role in primary spread of the disease.

Considering the importance of the bacterial blight in cotton cultivation, resistant varieties have been advocated in past for the management of this disease. Use of resistant cultivars, however remains the most efficient and eco-friendly method, followed by this, the efficient management of the bacterial blight have been obtained by chemical mean.

2. Materials and methods

A field experiment was carried out to study sources of resistance against bacterial blight of cotton replicated thrice with Randomized Block Design (RBD). The available thirty six genotypes of *Gossypium arborium* and *Gossypium hirsutum* were answered for their reaction during the year 2008-09 with plot size 5.4 m x 3.6 m. Spacing maintained for *Gossypium hirsutum* - 60 cm x 60 cm and *Gossypium arborium* - 45 cm x 22.5 cm. Observations on disease incidence and severity were recorded at 60 DAS, 90 DAS and 120 DAS.

Per cent disease evaluation was calculated as per the standard area diagram developed by Mayee and Datar (1986). For recording the disease intensity at field condition, 0 to 9 disease rating scale developed by Mayee and Datar (1986) was used. For this purpose five leaves located at the bottom, five middle and five top of the plant were chosen and scored as per scale given below.

Table 1a
Disease rating scale (Mayee and Datar, 1986).

Sr. No.	Leaf area infected (%)	Score
1.	Zero	0
2.	Less than 1%	1
3.	1 to 10%	3
4.	11 to 25%	5
5.	26 to 50%	7
6.	More than 50%	9

The average intensity of each plot was worked out by using following formula.

$$PDI = \frac{\text{Sum of observed numerical ratings}}{\text{Number of leaves observed x maximum of grade scale}} \times 100$$

Measurement of disease intensity (severity) was carried out on five randomly selected plants in each plot.
Per cent incidence was calculated from the number of infected plants against the total number of plants at the time of observation by using following formula.

$$\text{Per cent incidence (PI)} = \frac{\text{No. of plants diseased}}{\text{Total number of plants observed}} \times 100$$

Table 1b
Disease rating scale suggested by IPM project (2006-07).

Grade	Disease reaction	Description
0	Disease free (DF)	Plants completely free from infection
I	Resistant (R)	Spots few scattered, nearly 1 mm dia coalescing spots seen, infected area covers upto 5 %
II	Molderately resistant (MR)	Whitish lesions covers upto 6-10 % leaf area
III	Moderately susceptible (MS)	Spots turning brown and black coalescing and spreading, 11-20 % leaf area covered
IV.	Susceptible (S)	Longer lesions, spots covering more than 20% leaf area, lesions turn brown to black. In several cases branches and stems also seen infected

3. Results and discussion

Results (Table 2 and 3) revealed that out of 36 genotypes of cotton were screened under natural condition of infection none showed immune, none showed resistant, while 3 genotypes were moderately resistant, 31 were moderately susceptible and 2 were susceptible against bacterial blight of cotton.

Disease severity at 60 DAS ranged from 2.42 to 27.5 per cent. Highest PDI was recorded by LRA 5166 (27.5 %) followed by NH 619 (15.59 %), MCU 5 (11.11 %) and PA 646 (11.11 %). Lowest PDI was recorded by PH 1009 (2.42 %) and Paig 29 (2.42 %).

Disease severity at 90 DAS ranged from 9.63 to 58.6 per cent. Highest PDI was recorded by LRA 5169 (58.6 %) followed by NH 619 (20.3 %) and NHH 44 (17.9 %). Lowest PDI was recorded by NH 633 (9.63 %) followed by PH 1062 (99.91 %) and PH 1031 (10.37 %).

Disease severity at 120 DAS ranged from 11.63 to 68.94 per cent. Highest PDI was recorded by LRA 5166 (68.94 %) followed by NH 619 (33.33 %). The lowest PDI was recorded by NH 633 (11.63 %) followed by Paig 265 (13.26 %) and NH 637 (13.55 %).

Mean disease severity ranged from 9.71 to 51.68 per cent. Highest mean disease severity recorded in LRA 5166 (51.68 %) followed by NH 619 (22.07 %) and PA 686 (19.28 %). Lowest mean disease severity recorded in NH 633 (9.71 %), Pa 532 (9.75 %) and Paig 265 (9.75 %). Total 3 genotypes showed moderately resistance to the disease (NH 633, PA 532 and Paig 265). However, total 31 genotypes showed moderately susceptible to the disease (NHH 44, NH 640, NH 634, NH 615, NH 635, NH 637, NH 630, NH 632, MCU 5, DCH 32, PH 1062, PH 1029, PH 1031, PH 1004, PH 1047, PH 1009, PH 1052, PH 348, PA 541, PA 405, PA 687, PA 528, PA 304, PA 693, PA 646, PA 653, PA 08, PA 686, Paig 29, Paig 8/1 and Paig 255) and 2 genotypes *viz*., NH 619 and LRA 5166 (SC) showed susceptible to bacterial blight disease. Thus the promising high yielding bacterial blight of cotton resistant genotypes identified through this investigation can be deployed in disease endemic areas to aim for sustainable productivity.

Similar type of work was also undertaken by several workers previously against bacterial blight of cotton and reported disease reaction of cotton varieties by Poswal (1994), Cook *et al*. (1997), Patil and Ghodere (1998), Singh *et al*. (2002), Khodke *et al*. (2003), Singh (2003) and Singh Astha *et al*. (2007). The present field screening of cotton genotypes in this study indicates resistance to bacterial blight is inheritable as the resistant character is passable from the parental inbred lines to their hybrids. Thus, screening cotton genotypes for resistance to bacterial blight

is of paramount importance and it should be part of the efforts in the development of commercial hybrids with high yield potential and superior resistance to *X. axonopodis* pv. *malvacearum*.

Table 2
Screening of different genotypes of cotton to bacterial blight disease.

Sr. No.	Name of genotypes	Mean per cent disease intensity of bacterial blight on cotton			Mean	Disease reaction
		60 DAS	90 DAS	120 DAS		
1	NHH 44	10.64	17.9	19.62	16.05	MS
2	NH 619	15.59	20.3	33.33	22.07	S
3	NH 640	9.36	15.31	20.51	15.06	MS
4	NH 634	10.62	16.9	18.82	15.44	MS
5	NH 615	6.12	10.91	15.81	10.96	MS
6	NH 635	7.65	19.36	21.55	16.19	MS
7	NH 637	7.65	11.34	13.55	10.85	MS
8	NH 633	8.15	9.63	11.63	9.71	MR
9	NH 630	5.73	10.78	14.5	10.34	MS
10	NH 632	8.67	11.11	13.13	10.97	MS
11	MCU 5	11.11	16.9	26.81	18.27	MS
12	DCH 32	6.38	12.1	17.57	12.02	MS
13	PH 1062	5.12	9.91	15.81	10.28	MS
14	PH 1029	10.21	16.54	22.86	16.54	MS
15	PH 1031	6.13	10.37	14.27	10.26	MS
16	PH 1004	6.13	11.1	15.15	10.79	MS
17	PH 1047	7.54	12.84	18.89	13.09	MS
18	PH 1009	2.42	13.1	15.65	10.39	MS
19	PH 1052	4.53	14.38	17.57	12.16	MS
20	PH 348	4.78	11.11	15.42	10.44	MS
21	PA 532	5.34	10.64	13.26	9.75	MR
22	PA 541	9.36	12.8	20.52	14.22	MS
23	PA 405	5.54	12.42	14.38	10.78	MS
24	PA 687	7.38	10.56	17.47	11.8	MS
25	PA 528	6.66	11.11	14.35	10.7	MS
26	PA 304	4.44	10.63	16.39	10.49	MS
27	PA 693	5.54	11.52	14.52	10.53	MS
28	PA 646	11.11	16.37	25.17	17.55	MS
29	PA 653	4.53	12.83	15.38	10.91	MS
30	PA 08	6.66	16.35	27.71	16.91	MS
31	PA 686	10.21	16.09	31.55	19.28	MS
32	Paig 29	2.42	14.96	30.86	16.08	MS
33	Paig 265	5.34	10.64	13.26	9.75	MR
34	Paig 8/1	4.44	10.63	16.39	10.49	MS
35	Paig 255	6.66	11.11	14.35	10.7	MS
36	LRA 5166 (SC)	27.5	58.6	68.94	51.68	S

Cotton genotypes NH 619 and LRA 5166 were rated as susceptible and NHH 44, NH 640, NH 634, NH 615, NH 635, NH 637, NH 630, NH 632, MCU 5, DCH 32, PH 1062, PH 1029, PH 1031, PH 1004, PH 1047, PH 1009, PH 1052, PH 348, PA 541, PA 405, PA 687, PA 528, PA 304, PA 693, PA 646, PA 653, PA 08, PA 686, Paig 29, Paig 8/1, Paig 255 were rated as moderately susceptible based on the tests against *X. axonopodis* pv. *malvacearum,* containing protein toxins so they were rated as susceptible to bacterial blight based on the test against the pathogen under field conditions. The different results between the test against the rust toxins of *X. axonopodis* pv. *malvacearum* and the test against the pathogen suggest that the severity of bacterial blight of cotton is a complex syndrome

affected by the toxic substances such as proteins and the degradation of the tissues by the enzymes produced by *X. axonopodis* pv. *malvacearum.* A high level of resistance to common rust can only be achieved if a maize plant is susceptible by the bacterial blight toxin, the cell wall degradation enzymes, and the germ tube prolification of *X. axonopodis* pv. *malvacearum* in infected tissues. Therefore, screening maize genotypes for resistance to *X. axonopodis* pv. *malvacearum* by artificially inoculation of the pathogen would be more effective than the tests against the rust toxin produced by the pathogen.

Table 3

Reaction of maize genotypes against *X. axonopodis* pv. *malvacearum* under field conditions.

Disease grade	Code	Disease reaction	Name of genotypes	No. Of genotypes
0	DF	Disease free	None	--
I	R	Resistant	None	--
II	MR	Moderately resistant	NH 633, PA 532, Paig 265	3
III	MS	Moderately susceptible	NHH 44, NH 640, NH 634, NH 615, NH 635, NH 637, NH 630, NH 632, MCU 5, DCH 32, PH 1062, PH 1029, PH 1031, PH 1004, PH 1047, PH 1009, PH 1052, PH 348, PA 541, PA 405, PA 687, PA 528, PA 304, PA 693, PA 646, PA 653, PA 08, PA 686, Paig 29, Paig 8/1 and Paig 255	31
IV	S	Susceptible	NH 619, LRA 5166(SC)	2
			Total	36

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