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Identification of resistance sources against bacteria blight of cotton caused by Xam race no. 18

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ABSTRACT

Cotton, "king of fibres" enjoys a pre-eminent status among all cash crops in the country, being the principal raw material for a flourishing textile industry. Among the various diseases occurring on cotton, the foliar disease bacterial blight caused by *Xanthomonas axonopodis* pv. *malvacearum* is gaining more importance in recent years because of their increasing incidence. These have been known to occur on all the various cultivated and wild species of cotton in Maharashtra, since many years, in an epiphytotic form on commercially grown varieties, which leads to severe defoliation and substantial yield lossess. Among the 221 cultivated genotypes screened for resistance against bacterial leaf blight disease under field conditions, 80 genotypes showed immune reaction. Further, 69 genotypes were resistant, 13 genotypes were moderately resistant, The 19 entries showed the moderately susceptible reaction and 40 entries showed the susceptible reaction to the bacterial blight disease.

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INTRODUCTION

Cotton, "king of fibres" enjoys a pre-eminent status among all cash crops in the country, being the principal raw material for a flourishing textile industry. It provides livelihood to about sixty million peoples and is an important agricultural commodity providing remunerative income to millions of farmers both in developed and developing countries. Among the various diseases occurring on cotton, the foliar disease bacterial blight caused by *Xanthomonas axonopodis* pv. *malvacearum* is gaining more importance in recent years because of their increasing incidence. These have been known to occur on all the various cultivated and wild species of cotton in Maharashtra, since many years, in an epiphytotic form on commercially grown varieties, which leads to severe defoliation and substantial yield lossess. In nature, some genotypes exhibits the resistance against foliar diseases and the degree of resistance also varies at different stages of crop growth. There are number of cultivated varieties or hybrids of cotton showing variability in reaction (susceptibility/ resistance) to bacterial blight and

therefore, it is almost important to study and find out the sourses of resistance against the race no. 18 which is prevalant in Maharashtra.

MATERIAL AND METHODS

The disease samples showing typical symptoms of bacterial blight of cotton were collected from the field of cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri and National trial of cotton from Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. Seeds of cotton genotypes and varieties were procured from Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri and cotton Improvement Project, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. For identification of races seeds of nine differentials *viz.*, Acala-44, Stonevil 20, Stonevill-2BS9, 1-10B, 101-102B, Mebane B-1, 20-3, Gregg and DPX$_4$were sown in glasshouse in earthen pots and plants maintained in good growth condition. Nutrient agar (NA) was used for isolation of *Xanthomonas axonopodis* pv. *Malvacearum* from diseased samples and further multification, respectively.

Pathogenicity of isolated bacterium :

The pathogenicity of isolated bacterium was tested on Acala-44 cotton cultivar which is susceptible to all the known races of *Xanthomonas axonopodis* pv. *Malvacearum* giving prominent water soaking susceptible reaction.

For this bacterial culture was multiplied on NA slants and 48 hours bacterial growth was used to prepare bacterial suspension by adding 10 ml sterile water in each NA slants. The bacterial cells were allowed to suspend into sterilized water by gentle scrabing with inoculating needle. The optical density of the bacterial suspension was adjusted at 0.1 OD at 620 nm with the help of Spectrophotometer. The bacterial suspension thus, obtained was used for inoculating into the cotton leaves of Acala-44 which was sown in the glasshouse of the Department of Plant Pathology, Mahatma Phule Krishi Vidyapeeth, Rahuri. Three leaf stage plant was used for testing the pathogenicity.

Inoculation was done by syringe infilteration methods, in which bacterial suspension was injected in to the intercellular spaces of Acala-44 leaves. In the glasshouse high humidity was maintained. Observations of inoculated leaves were noted from 3 days onward to record disease symptoms/water soaking.

Race identification of *Xanthomonas axonopodis* pv. *Malvacearum* :

Nine cotton differentials *viz.*,Acala-44, Stonevil 20, Stonevill-2BS9, 1-10B, 101-102B, Mebane B-1, 20-3, Gregg and DP x P_4 were grown in glasshouse for race identification. The leaves of these differentials were inoculated at three leaf stage with individual bacterial suspension by syring infilteration methods as described above. The reaction (susceptible water soaking reaction/ hypersensitive HR reaction) of bacterial isolates on these differential were noted after 3 days for identification of *Xanthomonas axonopodis* pv. *Malvacearum*as described by Verma and Singh (1975).

Screening of the genotypes against the bacterial blight :

140 cotton (Bt and non-Bt) hybrids/varieties / genotypes were screened under field condition against bacterial blight to identify the source of resistance during *Kharif* 2013 at Cotton Improvement Project Mahatma Phule Krishi Vidyapeeth, Rahuri and 10 Bt, 71 non- Bt genotypes were screened at Cotton Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola.

The details of the experiment is below :

Design : Randomized Block Design

Replication : Two

Plot size : 6 test rows of 10 m length each were alternated by LRA 5166 and also surrounded by check.

Row spacing : 90 × 60 cm^2

Date of sowing : 13.06.2013

Fertilizer dose : 100:50:50 NPK kg/ha

Inoculum sprays :

The genotypes were sprayed during evening hr with inoculum of the pathogen at 40 and 80 days after sowing. Inoculation was also done in field by preparing bacterial culture by chaffing the infected leaves. The leaves showing typical spots were chaffed into small pieces with sterilized razor in sterile distilled water. The suspension was allowed to stand for an hour to get bacterial ooze and then filtered through muslin cloth. Inoculum was sprayed on the plants by knapsack sprayer.

Observation :

Ten plants and 6 leaves per plant were selected from

each plot. Observations were recorded at weekly interval from the first appearance of disease upto harvest of crop. Disease incidence was recorded on the basis of number of infected and healthy leaves on each plant and disease

Table 1 : Screening of cotton genotypes in field to the bacterial blight

Sr. No.	Scale	Name of genotype
1.	0 grade (80)	GJHV 514, CNHO 12, GISV 267, P 5430, BS 39, GISV - 272, GSHV - 162, RHH – 0917, DHH 1201, GTHH 194, BHH24, RHH – 0924, GSHH 2646, RHH 0707, ARCHH 9191, MRC 7091, SHH 801, GTHH 193, TCH 1705, LH 2298, ARBC 19, GTHV 04/13, CCB 30, ARBD 27, DB 16, GSB 21, RAB 8, Phule 492, MRC 7388,ARBHH-1301, ARBHH-1302, ARCH 3244, BGDHH 807, BGDHH 821, CSHG-1729, CSHH-2012, DHH-1301, DHH-1302, FHH 231, FHH 234, GSGHH-412, GSHH-2599, GTHH-208, HHH 494, RHH-1007, RHH-1014, RHH-1015, SHH 808,SHH 818,TCHH160161, DSC-1302, CNH121, ARBC-1302, F2617, GSH-4, ARBC-1301, CSH-3178, G.Cot. 100, BPCH-1101, DSC-1301, SCS 1206, CNH 3, H 1465, DB-1301, ARBB-1302, Suvin , GSB-44, DB-1302,ARBB-1301, GSHB-989, BPHB-1207, ARBHB-1302, TCHB 13526, DHB-130,RHB-1014, RHB-1005, ARBHB-1301, DCH 32, DHB-1301,RHB-0922
2.	1 grade (69)	101-102 B, JLA - 0614, RAH-1065, AKA - 2010 - 6, RHcb-001, CNA 1016, NDLA 2985, RHC- 0688, PA - 760, GBHV-170, AKA - 2010 - 4, PH 1075, FMDH 40, P2151, RAJDH 444, FMDH 25, AKDH - 96, GSB 43, ARBB 20, GSB 41, RHB - 0713, ARBHB 701, RHB - 0708, ARBHB 702, RHB - 0812, ARBHB - 1011, RHB - 0711, ARBHB - 1053, KH-1301,ARBH-1301, ARBH-1302, Bihani 301, BPHI-537, BS 1, BS 51-1, CCH 13-1, CCH 13-2, CNH 1116, CNH 19, CPD-1301, CPD-1302, CSH-2931, CSH-3175, F 2451, F 2454, GJHV-511, GJHV-516, GSHV-164, GSHV-169, H 1476, HS 292, HS 293, L-1011, L-804, LH 2255, LH 2307, NDLH 1975,NDLH 1976,P 5629,RS 2728,RS 2733, SCS1211, TCH 1742, TCH 1777, TSH 04/115,
3.	2 grade (13)	SCS 793, ADB 542, DHH 1251, SCS 1214, CCH-12-3, NH615, GBHV- 177, GBHV- 180, DB 39, DB 40, Shaki-9, SCS 1210,SCS 1213
4.	3 grade (19)	SHH 802, DHH 1252, GSHH 2646, Banny, GSHH 2639, Ankur 651, FMDH 36, RAJDH 623, RHAH-1040, NCS1911,FMDH29, Mohini, NACH 433, AAH 35, Tulasi 162, CISAA-27, Ankur 238,GSGDH- 223, Jai, AKDH – 98
5.	4 grade (40)	Akala 44, SCS 1062, BGDS 1063, Sarju (Bt), RCH- 2B, Malika, LRA-5166, DB 139, BS 2, GBHV-181, SCS 1210, CPD-1352, CNH 7008, Ankur 3028, CNH 2001, SCS 1213, CCH 13-4, BPHR-617, H 1236, CCH 13-3, NDLH 1976, CSH 1115, GBHV-182, SCS 1211, ARBH-1351, SP 7007,Gk 218,P 5643, CSH 95, SCS 1214, Akka, NDLH 1975, BS 55, CPD-1351, IH 11, BPHR-621, ARBH-1352, NH 662, AKH 09-05

Table 2 : Reaction of the differential host to races of *Xanthomonas axonopodis* pv. *malvacearum.* (Hunter *et al.,* 1968 and El-Zik and Thaxton 1995)

Race No.	Akala 44	Stonevile 2B-S9	Stonevile	Mebae B-1	1-10B	20-3	101-102B	Gregg	$DPxP_4$
1	+	+	-	-	-	-	-	-	-
2	+	+	+	-	-	-	-	-	-
3	+	+	-	-	+	-	-	N/A	N/A
4	+	+	-	-	-	+	-	N/A	N/A
5	+	+	-	-	+	+	-	N/A	N/A
6	+	+	-	+	+	-	-	+	-
7	+	+	-	+	+	+	-	+	-
8	+	+	+	+	+	-	-	+	-
9	+	-	+	-	-	+	-	N/A	N/A
10	+	+	+	+	+	+	-	+	-
11	+	+	-	-	-	-	-	+	-
12	+	+	+	-	-	-	-	+	-
13	+	-	-	-	-	-	-	N/A	N/A
14	+	+	+	-	+	+	-	+	-
15	+	+	+	-	+	-	-	N/A	N/A
16	+	+	+	+	-	+	-	N/A	N/A
17	+	+	+	-	-	+	-	N/A	N/A
18	+	+	+	+	+	+	-	+	+

"+" = Susceptible reaction, "-" = Resistant reaction, "N/A"=Not available

intensity was recorded by using 0-4 point prescribed grade scale (Sheo Raj, 1988) and incidence and intensity was calculated by following formulas.

$$\text{Per cent disease incidence} = \frac{\text{No. of leaves infected}}{\text{Total number of leaves}} \times 100$$

$$\text{Per cent disease intensity} = \frac{\text{Sum of all the ratings}}{\text{Total number of ratings x max. grade}} \times 100$$

RESULTS AND DISCUSSION

The findings of the present study as well as relevant discussion have been presented under the following heads:

Screening of cotton genotypes for bacterial bilight disease :

Evaluation of Bt and non-Bt cotton hybrids/ varieties /genotypes against bacterial blight was carried out to identify the source of resistance under field conditions. 140 cotton hybrids/ varieties/genotypes screened under field conditions during *Kharif* 2013 at Cotton Improvement Project MPKV, Rahuri and 10 Bt, 71 genotypes were screened at Cotton Research Unit, Dr. PDKV, Akola (Table 1). The incidence of the bacterial blight disease was recorded on 90 and 120 days after sowing using 0-4 scale (Sheo Raj, 1988)

Out of these cotton genotypes, 80 genotypes were free from bacterial blight disease. Further, 69 entries showed the resistant reaction and 13 entries recorted moderately resistant reaction. Where as 19 entries were the moderately susceptible reaction and 40 entry showed the susceptible to the bacterial blight disease. Similarly, Shastry and Tomar (2006) reported that cotton genotype HD-2582 was resistant to bacterial blight among 29 genotypes. Eleven germplasm lines were found moderately resistant. Remaining fifteen were categorized as moderately susceptible to the disease. Chattannavar *et al.* (2004) screened 20 coded Bt cotton genotypes for reaction to foliar diseases of cotton. Eleven, seventeen and one coded entries exhibited resistance reaction to *Alternaria* blight, bacterial blight and grey mildew, respectively. The per cent disease index varied from 22.88 to 32.58, 13.58 to 21.09 and 27.74 to 57.28 to *Alternaria*blight, bacterial blight and grey mildew, respectively Suriachandraselvan *et al*. (2004) screen 84 cotton entries for resistance to bacterial blight disease. Among these none of the entry was found immune to bacterial blight of cotton. SVR-3 was resistant, eleven were moderately resistant and remaining entries were susceptible or highly susceptible.

Identification of races of *Xanthomonas axonopodis* pv. *malvacearum* :

The bacterial blight infected cotton samples were collected from the experimental cotton fields of Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri and Dr. Panjabrao Deshmukh Krishi Vidyapeeth Akola and used for isolation of pathogen. The race identification were tested for their race number of isolated pathogen was carried on nine cotton differentials by following method of Verma and Singh (1974).

Based on the reaction of the nine cotton lines used as differentials hosts inoculated with *Xanthomonas axonopodis* pv. *malvacearum*, the bacterium was identified as Race 18 (Table 2) Verma and singh (1975) determined race composition of Xam in different parts of India and reported distribution of races, *viz*., 1, 2, 2A, 8, 9, 10, 18, 19, 20, 27, 28, 29, and 32. Talib Hussain *et al.* (1979) also identified race 18 from two locations from Pakistan.

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