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Debanjana Debnath
Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, West Bengal, India

M Divya
Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, West Bengal, India

Suraj Golder
Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, West Bengal, India

Imtinungsang Jamir
Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, West Bengal, India

Tridip Bhattacharjee
Department of vegetable science, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, West Bengal, India

Correspondence
Debanjana Debnath
Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, West Bengal, India

Screening of different genotypes/ crosses of tomato (*Lycopersicon esculentum*) for resistance to bacterial wilt (*Ralstonia solanacearum*) under field condition

Debanjana Debnath, M Divya, Suraj Golder, Imtinungsang Jamir and Tridip Bhattacharjee

Abstract
The present investigation was conducted at Department of Plant Pathology, C-block, Bidhan Chandra Krishi Vishwavidyalaya, Kalyani (W.B.) during 2017-08. The experimental material comprised of twenty genotypes of tomato and the experiment was laid out in Randomized block design with three replications. Result on bacterial wilt showed that five genotypes found to be highly resistant, eight genotypes found to be resistant, one genotype found to be moderately susceptible, one genotype found to be susceptible and five genotypes were found to be highly susceptible in field condition against bacterial wilt.

Keywords: Tomato, *Lycopersicon esculentum*, bacterial wilt

Introduction
Tomato (*Solanum lycopersicon*) is one of the most important solanaceous vegetable that cultivated worldwide for its wider environmental adoptability, higher is nutrition value and industrial use. But tomato production hampered by different biotic and abiotic factors. Among these bacterial wilt of tomato caused by *Ralstonia solanacearum*is one of the most devastating disease (Poussier *et al*., 1999) [8]. In India bacterial wilt of tomato was first reported in Solan area of Himachal Pradesh (Gupta *et al*., 1998). A huge loss of 10 to 100% in plant mortality and 10.83 to 92.62% yield reduction was recorded. (Mishra *et al*., 1995) [5]. The pathogen have a wide host range of solanaceous crops such as tomato, potato, brinjal, chilli and non solanaceous crop such as ginger, banana and groundnut. The symptoms of tomato bacterial wilt disease started as drooping of lower leaves, followed by wilting of whole plants within a few days which leads to complete collapse of the plants (McCarter, 1991) [4]. After a cross section of stem white or yellowish bacterial ooze comes out. The pathogen is a soil borne and can be spread over the field by thin film of water, irrigation or rainfall. If once the disease symptoms appears after that application of bactericide and any other chemical is not fruitful and also the crop rotation is not a effective control measures as because the pathogen is soil borne and can persist indefinitely in infested fields (Jaworski and Morton, 1964; Sonoda, 1978) [3, 10]. So, the cultivation of resistant variety can be the most effective and logical way of suppressing the pathogen. In this direction, 20 number of accessions of tomato were screened against bacterial wilt resistance which can be used in breeding programme in the development of bacterial wilt resistant hybrids of tomato.

Material and methods
The present investigation was carried out at C-Block (Lat: 22.99841, Lng: 88.45912), Bidhan Chandra Krishi Viswavidhyalaya, Kalyani, W.B. The experimental material comprised of twenty genotypes and hybrids and the seedlings were transplanted at four weeks after sowing (4 WAS). They were grown on raised sick bed with three replications containing 10 plants each in a Randomized Block Design (RBD). The bacterial solution having 6 x 10^5 cfu/ml was drenched in the collar region of each seedling at two weeks after transplanting (2 WAT). The observations were recorded from 7 days after inoculation. The mortality per cent was recorded and further classified into 0-5 scale proposed by Kelman and fit into the following formula to work out disease incidence and percent disease index (PDI).

Table 1: Disease scale for Bacterial wilt disease

Scale	Description
0	No symptom
1	One leaf partially wilted
2	One to two leaves wilted
3	All leaves except uppermost 2-3 leaves wilted
4	All leaves wilted
5	Death of whole plant

$$\text{Disease Incidence (DI)} = \frac{\text{Number of wilted plants}}{\text{Total number of plants}} \text{X } 100$$

$$\text{PDI} = \frac{\text{Sum of all the numerical ratings}}{\text{Number of observations} \times \text{Maximum disease grade}} \times 100$$

And the genotype reaction identified by using the scale given by Winstead and Kelman (1952) modified by Hussain *et al*. (2005). The scale is given below:

Table 2: Reaction scale for Bacterial wilt disease

Reaction	Percentage Disease Incidence
Highly resistant(HR)	No wilt symptom
Resistant(R)	1-20% plants wilted
Moderately Resistant(MR)	21-40% plants wilted
Moderately Susceptible(MS)	41-60% plants wilted
Susceptible(S)	61-80% plants wilted
Highly Susceptible(HS)	More than 80% plants wilted

Table 3: Screening of tomato genotypes for Bacterial wilt disease incidence

S. No.	Genotypes	Disease Incidence of Bacterial wilt						Reaction at 42 DAI
		7 DAI	14 DAI	21 DAT	28 DAI	35 DAI	42 DAI	
1	2016 cherry	0.00 (0.00)*	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	HR
2	2016 cherry X Cherry round yellow (F1)	10.00 (18.43)	33.33 (35.22)	70.00 (56.79)	76.67 (61.22)	93.33 (77.41)	96.67 (83.86)	HS
3	CLN 2764 A	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	6.67 (12.29)	10.00 (1843)	10.00 (18.43)	R
4	DG Variant	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	HR
5	Pattar kuchi	0.00 (0.00)	23.33 (28.78)	56.67 (48.85)	83.33 (66.14)	96.67 (83.46)	100.00 (90.00)	HS
6	F1 X 2016 cherry	10.00 (18.43)	10.00 (18.43)	23.33 (28.78)	63.33 (52.78)	76.67 (61.22)	80.00 (63.43)	S
7	CLN 27777E	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	10.00 (18.43)	10.00 (18.43)	10.00 (18.43)	R
8	CLN 27777E X CLN 2777F	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	HR
9	CLN 2777F	0.00 (0.00)	0.00 (0.00)	33.33 (35.22)	56.67 (48.85)	83.33 (66.14)	100.00 (90.00)	HS
10	AFT X 2764AF3P2F4P1F5P1F6P1	20.00 (26.57)	20.00 (26.57)	63.33 (52.78)	73.33 (59.00)	86.67 (68.86)	90.00 (71.57)	HS
11	Cherry round yellow	20.00 (26.07)	20.00 (26.57)	56.67 (48.85)	76.67 (61.22)	93.33 (77.71)	100.00 (90.00)	HS
12	2764 A X AFT F3P3F4P1F5P1F6P1	0.00 (0.00)	0.00 (0.00)	6.67 (12.29)	10.00 (18.43)	10.00 (18.43)	10.00 (18.43)	R
13	AFT X 2764 A F3P2F4P1F6P1	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	10.00 (18.43)	10.00 (18.43)	10.00 (18.43)	R
14	Utkal Kumari	0.00 (0.00)	0.00 (0.00)	10.00 (18.43)	10.00 (18.43)	10.00 (18.43)	10.00 (18.43)	R
15	Utkal Raja	10.00 (18.43)	13.33 (21.14)	50.00 (45.00)	53.33 (46.92)	56.67 (48.85)	60.00 (50.77)	MS
16	Utkal Deepti	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	HR
17	2777C X Kumari F2	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	6.67 (12.29)	10.00 (18.43)	10.00 (18.43)	R
18	2777F X Kumari	16.67 (23.86)	20.00 (26.57)	20.00 (26.57)	23.33 (28.78)	20.00 (26.57)	20.00 (26.57)	R
19	244D X Kumari X Kumari BCF 2	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	HR
20	2498 D X Deepti F3	10.00 (18.43)	10.00 (18.43)	10.00 (18.43)	13.33 (21.14)	16.67 (23.86)	20.00 (26.57)	R
	SEM	1.13	0.9	1.7	2.46	2.73	1.37	
	CD	3.24	2.58	4.87	7.04	7.81	3.93	
	CV	26.12	15.48	15.03	15.66	14.65	6.76	

*Figures in parentheses are arc sine transformed values

Table 4: Screening of tomato genotypes for Bacterial wilt percent disease index (PDI)

S. No.	Genotypes	Percent Disease Index (PDI) of Bacterial wilt					
		7 DAI	14 DAI	21 DAI	28 DAI	35 DAI	42 DAI
1	2016 cherry	0.00 (0.00)*	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
2	2016 cherry X Cherry round yellow (F1)	4.00 (11.54)	11.33 (19.66)	28.00 (31.94)	46.00 (42.70)	53.33 (46.91)	62.00 (51.97)
3	CLN 2764 A	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	2.67 (7.69)	3.33 (10.40)	6.00 (14.05)
4	DG Variant	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
5	Pattar kuchi	0.00 (0.00)	9.33 (17.71)	22.00 (27.92)	61.33 (51.63)	64.00 (53.17)	69.33 (56.42)
6	F1 X 2016 cherry	4.00 (11.54)	4.00 (11.54)	7.33 (15.68)	37.33 (37.64)	39.33 (38.83)	48.67 (44.24)
7	CLN 27777E	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	2.67 (9.27)	3.33 (10.40)	6.00 (14.05)
8	CLN 27777E X CLN 2777F	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
9	CLN 2777F	0.00 (0.00)	0.00 (0.00)	20.67 (26.96)	32.67 (34.74)	40.00 (39.22)	52.67 (46.53)
10	AFT X 2764AF3P2F4P1F5P1F6P1	6.67 (14.93)	6.67 (14.93)	40.67 (39.60)	56.00 (48.45)	62.67 (52.37)	68.00 (55.58)
11	Cherry round yellow	6.00 (14.05)	7.33 (15.68)	34.00 (35.65)	52.00 (46.14)	58.00 (49.64)	61.33 (51.63)
12	2764 A X AFT F3P3F4P1F5P1F6P1	0.00 (0.00)	0.00 (0.00)	2.00 (6.56)	2.67 (9.27)	3.33 (10.40)	6.00 (14.05)
13	AFT X 2764 A F3P2F4P1F6P1	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	2.67 (9.27)	3.33 (10.40)	4.67 (12.42)
14	Utkal Kumari	0.00 (0.00)	0.00 (0.00)	2.67 (9.27)	3.33 (10.40)	4.00 (11.54)	8.67 (17.10)
15	Utkal Raja	3.33 (10.40)	4.67 (12.42)	16.67 (24.09)	15.33 (22.98)	15.33 (22.98)	20.00 (26.55)
16	Utkal Deepti	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
17	2777C X Kumari F2	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	3.33 (10.40)	4.00 (11.54)	6.00 (14.18)
18	2777F X Kumari	4.67 (12.42)	5.33 (13.30)	7.33 (15.68)	10.00 (18.38)	14.67 (22.47)	18.67 (25.57)
19	244D X Kumari X Kumari BCF 2	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
20	2498 D X Deepti F3	2.67 (9.27)	3.33 (10.40)	4.00 (11.54)	4.67 (12.42)	8.67 (17.10)	14.00 (21.94)
	SEM	0.55	0.53	1.12	1.8	1.21	1.24
	CD	1.57	1.51	3.21	5.15	3.46	3.54
	CV	22.69	15.8	15.84	16.8	10.27	9.18

*Figures in parentheses are arc sine transformed values

Results and discussion

Bacterial wilt (*Ralstonia solanacearum*) is considered as the most serious disease of tomato and other solanaceous crop (Kehnan, 1953). It is especially devasting during the warm wet months in the tropics and subtropics and causes in calculatable losses to many host (Yang, 1979). Twenty genotypes of tomato were screened under field condition against tomato wilt caused by *Ralstonia solanacearum* in artificially inoculated plant during 2017-18.

With respect to disease resistance large variability was observed in each line/genotype. The results showed that, among 20 genotypes tested, five genotypes found to be highly resistant (2016 cherry, DG Variant, CLN 27777E X CLN 2777F, Utkal Deepti, 244D X Kumari X Kumari BCF 2), eight genotypes found to be resistant (CLN 2764 A, CLN 27777E, 2764 A X AFT F3P3F4P1F5P1F6P1, AFT X 2764 A F3P2F4P1F6P1, Utkal Kumari, 2777C X Kumari F2, 2777F X Kumari, 2498 D X Deepti F3), one genotype found to be moderately susceptible (Utkal Raja) one genotype found to be susceptible (F1 X 2016 cherry) and five genotypes were found to be highly susceptible (2016 cherry X Cherry round yellow (F1), F1 X 2016 cherry, CLN 2777F, AFT X 2764AF3P2F4P1F5P1F6P1, Cherry round yellow). With respect to disease severity (PDI) large variability was observed in each line/genotype. The results showed that, percent disease index ranged from 0.00 (2016 cherry, DG Variant, CLN 27777E X CLN 2777F, Utkal Deepti, 244D X Kumari X Kumari BCF 2) to 69.33 (Pattar kuchi).

The simple genetic control may trigger the bacterial wilt resistance in some resistance stocks originating from the tropical areas (Tikoo *et al.*, 1990) [11]. Grimault *et al*. (1995) [1] reported that the inheritance of resistance to bacterial wilt in tomato by a single dominant gene. Oliveira *et al.* (1999) [7] observed that the importance of additive gene effects on the resistance against bacterial wilt, while, Monma *et al*. (1997) [6] reported that the bacterial wilt resistance is partially recessive. Eight tomato parental lines and 28 F1 crosses developed at the station were tested in bacteria (*R. solanacearum*) sick plot during 2000-01 to 2002-03, in Jharkhand, India (Sharma, *et al.*, 2006) [9]. Finally, five most promising parental lines and four F1 crosses were tested during rainy season during 2005-06 to evaluate the fruit yield and resistance. The F1 cross viz., EC-339074 x EC-386021 (Swarna Sampada), was found superior to the others in terms of resistance and fruit yield in a sick plot. Oliveira *et al.*, (1999) [7] have also used such technique for identification of resistant host genotype(s) and its utilization in breeding horticulturally improved bacterial wilt resistant cultivars development.

The line/ genotypes 2016 cherry, DG Variant, CLN 27777E X CLN 2777F, Utkal Deepti and 244D X Kumari X Kumari BCF 2 can be used in breeding programme for development of variety resistant to bacterial wilt. Even development of resistance variety with high yield and good quality is a challenging task since from many years. But even several scientists have developed many numbers of varieties by using the stable sources of resistance.

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