International Journal of Chemical Studies

P-ISSN: 2349–8528 E-ISSN: 2321–4902 IJCS 2019; 7(3): 3274-3277 © 2019 IJCS Received: 13-03-2019 Accepted: 15-04-2019

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Screening of eggplant (Solanum melongena L.) genotypes to isolate the stable source of resistance for bacterial wilt

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Abstract

Eggplant or brinjal (*Solanum melongena* L.) is an important vegetable crop grown in tropical and subtropical parts of world including India. Bacterial wilt (*Ralstonia solanacearum*) is one of the major constraints in brinjal production in these regions and cause the yield loss upto 100 percent under favorable climatic conditions. Due to lack of information about the host, pathogen and environment, limited success is reported to control this disease. Hence, to identify the stable source of resistance, 30 accessions of eggplant (*Solanum melongena* L.) were screened in a sick plot for bacterial wilt (*Ralstonia solanacearum*) resistance at Indian Institute of Horticultural Research, Hessaraghatta, Bengaluru. Among 30 genotypes, IIHR-500A showed maximum resistance with no wilting symptom while eight genotypes namely IIHR-127, IIHR-575, IIHR-584, IIHR-667A, IIHR-766A, IIHR-817, IIHR-874, IIHR-882 showed resistant reaction with good yield potential. Three genotypes viz., IIHR 438-2, IIHR-618, IIHR-766 showed moderately resistant reaction and another three IIHR-576, IIHR-583 and IIHR-798 moderately susceptible reaction. The genotypes IIHR-574, IIHR-692, IIHR-793 and IIHR-871, IIHR-692, IIHR-694, IIHR-694, IIHR-694, IIHR-813, IIHR-813, IIHR-880, IIHR-584, IIHR-569, IIHR-571, IIHR-632, IIHR-711, IIHR-694, IIHR-812, IIHR-813, IIHR-880, IIHR-881 were highly susceptible.

Keywords: Bacterial wilt, eggplant, percent disease incidence, resistant, susceptible

Introduction

Eggplant or brinjal (Solanum melongena L.) is an important vegetable crop grown in India and all the parts of world (Frary et al. 2007, Khapte et al. 2012)^[3,7] belongs to family Solanaceae. The fruits are rich source of vitamin A and B, minerals, phosphorus and protein (Gopalan et al. 2007) ^[5] having various medicinal properties and is good for patients suffering from diabetic. India, the second largest producer of eggplant in the world consists of large number of cultivars according to consumer preference based on fruit colour, size and shape. The production of brinjal has been hindered by several insect pests and devastating diseases. Among these, bacterial wilt disease is the most devastating and a limiting factor caused by Ralstonia solanacearum throughout the tropical, sub-tropical and temperate regions of the world (Gopalakrishnan et al. 2014)^[4]. Many species of plant are being infected by Bacterial wilt especially solanaceae crops (Liu et al. 2016)^[9]. Severity of disease is more in Karnataka, Kerala, Odisha, Maharashtra, Madhya Pradesh, West Bengal, Chhattisgarh and Himachal Pradesh (Rao et al, 1976) ^[10]. In severe condition yield losses ranging from 65 to 70% (Das and Chattopadhyay, 1953)^[2]. The recent studies reported the yield losses for about 4.24 to 86.14 per cent (Sabita et al. 2000)^[12] while in hot and humid climate, the disease can cause up to 100% losses. Recently, this disease has increased to alarming proportion in the plains of India.

This disease is favored by the combination of high temperature and poor drainage and in severe condition yield losses ranges from 65 to 70% (Das and Chattopadhyay, 1953; Rao *et al*, 1976) ^[2, 11]. The pathogen of bacterial wilt is difficult to manage as the pathogen survives in the soil for several years. The disease affects the plant at flowering stage showing symptoms like sudden wilting, yellowing of foliage and stunted plant growth (Kelman, 1953; Rai *et al.*, 1975) ^[7, 10] and finally the vascular tissues show brownish discoloration accompanied by browning and rotting of tissues inside vascular bundles (Smith, 1920) ^[15]. Cultural practices like crop rotation, biological method like use of antagonistic organisms and chemical control

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like application of antibiotics are some of the control measures use for management of bacterial wilt but not so effective. Once the disease symptoms start to appear in the field, application of bactericides and copper fungicides has no effect on the bacterium. At present, the most important goal of any plant breeder is to develop commercial eggplant varieties and hybrids with resistance to bacterial wilt (BW) in oblong fruited brinjals but it seems a difficult task to do so because of non-availability of stable source of resistance in such varieties (Bainsla*et al.*, 2016, Yang *et al.*, 2014) ^[2, 17].

Material and Methods

The present study was carried out at ICAR-IIHR, Bengaluru, India. Thirty different eggplant genotypes were used as experimental material for screening of bacterial wilt, including resistant and susceptible checks (Table 1) during the year 2017-2018 in bacterial-wilt sick plot of Horticultural Research farm, Hessaraghatta, Bengaluru. The seedlings were raised in pro trays and transplanted in the main sick plot after 35 days of sowing where sick plot soil had pathogen population of less than 1.0 x 10^8 cfu/gm soil. Artificial inoculation was carried out to maintain required pathogen population to get sufficient wilting. All necessary recommended package of practices for growing brinjal crop were followed from transplanting upto harvest. The experiment layout was prepared in Randomized Complete Block Design (RCBD), with three replications. A total of 12 plants were planted in each treatment at the spacing of 60 x 45 cm and the plants were inoculated with bacterium culture twice by following soil drenching and pin prick method. First inoculation was carried out after 20 days of planting whereas second inoculation was taken up 40 days after transplanting. All the 30 genotypes including resistant (IIHR-127) and susceptible (IIHR-812) check were subjected to artificial inoculation at 20 and 40 days after transplanting. Symptoms of wilting appeared after six days of inoculation. Observations were recorded by adopting disease scoring the scale 0 to 5, as given by Winstead and Kelman, (1952) ^[16] with little modification for genotype evaluation. Modification in scale rating was done in such a way that scale 0 - Highly Resistant (HR) with no wilt symptom; 1 - Resistant (R), with 1 - 20% wilted plants; 2 - Moderately Resistant (MR) with 21 -40% wilted plants; 3 - Moderately Susceptible (MS) with 41-60% wilted plants; 4 - Susceptible (S) with 61-80% wilted plants, and, 5 - Highly Susceptible (HS) with > 80% wilted plants. The experimental data were statistically analyzed by using SAS software. Data on per cent incidence of wilt were transformed into arc sine and analysis of variance and which were carried out with transformed values. All 30 accessions

were categorized as highly resistant to highly susceptible,

depending on the percentage of wilted plants.

Table 1: List of 30 genotypes used for screening along with their characteristics.

S. No.	Genotypes	Characters			
1	ППБ 127	Plants are tall and compact, bearing medium long fruits in clusters. Blue black glossy fruit skin with green purple calyx. Dark green leaves with purple leaf base and purple veins when young. Deep purple -green stem. Fruits tender with slow seed maturity with no bitter principle. Crop duration is 150 days. It is resistant to bacterial wilt.			
2	IIHR-228	The plants are dwarf, spiny, and highly branched. The fruits are round in shape, light purple and calyx highly spiny			
3	IIHR 438-2	The plants are tall. The fruits are oval to oblong in shape, dark purple in colour with white stripe.			
4	IIHR -500- A	The plants are tall. The fruits are oblong in shape, light purple in colour with white stripe.			
5	IIHR- 534	Plants are tall erect having dark green foliage with dark green stem. Fruits are born in clusters having fleshy green calyx purple with white			
6	IIHR -569	The plants are tall. The fruits are round to oval in shape, medium purple in colour with white stripe.			
7	IIHR -571	The plants are medium tall. The fruits are round in shape, medium purple in colour with white stripe.			
8	IIHR -574	The plants are medium tall and bushy. The fruits are oval in shape, light purple in colour.			
9	IIHR-575	The plants are tall and bushy. The fruits are oval with flat base, dark purple in colour with white stripe.			
10	IIHR-576	The plants are medium tall and densely covered with foliage. Fruits having solitary bearing habit and purple long or ol in shape.			
11	IIHR-583	The plants are dwarf and spreading. Fruits born in clusters oval in shape and having dark green with white patches.			
12	IIHR-584	The plants tall and spreading. Fruits born in clusters oval in shape and having dark green with white patches.			
13	IIHR-618	The plants tall and spreading. Fruits having solitary bearing habit purple long or oblong in shape.			
14	IIHR-632	The plants tall and spreading. Fruits having solitary bearing habit purple round in shape with big sized fruits with fleshy purple calyx.			
15	IIHR-667 A	The plants tall and spreading. Fruits having solitary bearing habit purple round in shape with fleshy purple calyx.			
16	IIHR-692	The plants tall and spreading dwarf and spreading. Fruits having solitary bearing habit and bell-shaped fruits purple long in shape.			
17	ШПК-/11	Plants tall and spreading, Foliage dark green with purple tinge on stem and mid ribs. Fruits born in clusters with fleshy green calyx with solitary bearing.			
18	IIHR-766	Plants tall and spreading, Foliage dark green Fruits have solitary bearing habit. Fruits green with white patches			
19	IIHR-766 A	Plants tall and spreading, Foliage dark green Fruits have solitary bearing habit. Fruits green with white patches?			
20	IIHR-793	Plants tall and spreading, Foliage dark green Fruits have solitary bearing habit. Fruits purple oblong with big sized fru with fleshy green calyx.			
21	IIHR-794	Plants tall and spreading, Foliage dark green Fruits have solitary bearing habit. Fruits purple oblong with big sized fruits with fleshy purple calyx.			
22	IIHR-798	Plants tall and spreading, Foliage dark green Fruits have solitary bearing habit. Fruits purple oblong with big sized fruits with fleshy purple calyx.			
23	IIHR-812 (SC)	Plants tall and spreading, Foliage dark green Fruits have solitary bearing habit. Fruits purple oblong with very big sized fruits with fleshy purple calyx.			
24	IIHR-813	Plants tall and spreading, Foliage dark green with purple ting on the stem and mid ribs. Fruits born in clusters. Fruits purple oblong with very big sized fruits with fleshy purple calyx.			
25	IIHR-817	The plants tall and spreading with dark stem with dark green foliage, fruits born in clusters and dark purple with white strips.			

26	IIHR-857	Plants tall and spreading, Foliage dark green fruits have solitary bearing habit. Fruits purple oblong with big sized fruits with fleshy purple calyx.
27	IIHR-874	Plants tall and spreading, dark green foliage. Fruits have solitary bearing habit. Fruits purple long with fleshy green calyx.
28	IIHR-880	Plants tall and spreading, dark green foliage. Fruits have solitary bearing habit. Fruits purple long with fleshy green calyx.
29	IIHR-881	Plants tall and spreading, dark green foliage. Fruits have solitary bearing habit. Fruits purple long with fleshy green calyx.
30	IIHR-882	Plants tall and spreading, dark green foliage, Fruits have solitary bearing habit. Fruits purple long with fleshy green calyx.

Results and Discussion

The results of experiment are presented in Table 2 and 3. The results showed that out of 30 genotypes only one genotype viz., IIHR-500A was highly resistant with no wilting symptoms on plant even at the end of crop duration while eight genotypes namely IIHR-127, IIHR-575, IIHR-584, IIHR-667A, IIHR- 766A, IIHR-817, IIHR-874 and IIHR-882 showed resistant reaction with good yield. These results were similar to findings of Gopalkrishnan et al. (2014)^[4]. Similar results were also reported by Santhosha et al. (2015)^[13] and Sharma et al. (2018)^[14]. IIHR-127 showed highly resistance reaction (Gopalkrishnanet al., 2014)^[4] in Indian condition, while, IIHR-589 showed susceptible reaction in Bangladesh condition as reported by Hussain et al. (2015). Breakdown of resistance in this genotype may be due to change in climatic factor or occurrence of more virulent bacterium isolate as this region having high temperature and high humidity which are more congenial for disease severity. Among these eight genotypes minimum wilt incidence was recorded in IIHR-127 (3.33 %) followed by IIHR -667A (9.11%) whereas maximum in IIHR-817 (19.51%) and IIHR-882 (18.69%). The resistant genotypes showed delayed wilting symptoms in one or two plants out of twelve after second inoculation. Three genotypes namely IIHR 438-2, IIHR-618 and IIHR-766 were moderately resistant with wilting incidence of 35.02%, 30.52% and 22.81 %, respectively whereas three lines viz., IIHR-576, IIHR-583, IIHR-798 showed wilt incidence of 45.93%, 54.94 % and 43.86% respectively, and categorized as moderately susceptible. The genotypes IIHR -574, IIHR-692, IIHR-793, IIHR-857 were susceptible to bacterial wilt with wilt incidence varying from 64.28 to 78.15%. Eleven genotypes namely IIHR-228, IIHR- 534, IIHR-569, IIHR-571, IIHR-632, IIHR-711, IIHR-694, IIHR-812, IIHR-813, IIHR-880 and IIHR-881 were classified as highly susceptible class based on wilt incidence which ranged from 81.21 to 95.78%. Similar results were reported by Gopalkrishnan *et al.* (2014)^[4], Santhosha *et al.* (2015) ^[13] and Sharma *et al.* (2018) ^[14]. The results also indicate that the highly susceptible line (IIHR-711) took minimum duration for incubation *i.e.* 6 days whereas resistant line (IIHR-127) took longer duration for incubation *i.e.* 20 days. These findings were in agreement with Gopalkrishnan *et al.* (2014) ^[4] in eggplant.

The highly resistant and resistant line reported during the present experiment are being used in further breeding programmes for developing bacterial wilt resistant eggplant hybrids. These can also be use as one of the donor parents in population genetics as a part of marker assisted selection programme where highly contrasting parent is of prime requirement in resistant breeding.

Table 2: Rating scale for bacterial wilt in eggplant

Rating Bacterial wilt incidence (%)	
1	Highly resistant with no wilt symptom
2	Resistant with 1 - 20% wilted plants
3	Moderately resistant with 21 -40% wilted plants
4	Moderately susceptible, with 41-60% wilted plants
5	Susceptible with 61-80% wilted plants
6	Highly susceptible with >80% wilted plants

Sl No.	Genotypes	Mean percent Disease incidence	Disease reaction	Score
1	IIHR-127 (RC)	3.33 (6.14)	R	1
2	IIHR-228	84.94 (67.21)	HS	5
3	IIHR 438-2	35.02 (36.15)	MR	2
4	IIHR -500-A	0.00 (0.00)	HR	0
5	IIHR- 534	86.28 (68.85)	HS	5
6	IIHR -569	86.26(68.84)	HS	5
7	IIHR -571	89.33(70.51)	HS	5
8	IIHR -574	64.28(53.31)	S	4
9	IIHR-575	16.6(23.97)	R	1
10	IIHR-576	45.93(42.51)	MS	3
11	IIHR- 583	54.94(47.83)	MS	3
12	IIHR-584	11.09(19.07)	R	1
13	IIHR-618	30.52(33.51)	MR	2
14	IIHR-632	81.21(64.33)	HS	5
15	IIHR -667 A	9.11(17.51)	R	1
16	IIHR-692	75.86(60.81)	S	4
17	IIHR-711	95.78(81.21)	HS	5
18	IIHR-766	22.81(27.80)	MR	2
19	IIHR-766 A	18.21(25.02)	R	1
20	IIHR-793	67.20(55.25)	S	4
21	IIHR-794	85.74(67.71)	HS	5
22	IIHR-798	43.86(41.44)	MS	3
23	IIHR-812 (SC)	90.66(75.93)	HS	5
24	IIHR-813	92.09(73.72)	HS	5
25	IIHR-817	19.51(26.17)	R	1
26	IIHR-857	78.15(62.52)	S	4
27	IIHR-874	15.82(23.34)	R	1
28	IIHR -880	89.04(71.96)	HS	5

Table 3: Field screening of 30 eggplant genotypes for reaction against bacterial wilt

29	IIHR -881	89.61(71.44)	HS	5
30	IIHR -882	18.69(25.18)	R	1
	CD (5%)	10.62	-	-
	CV (%)	13.84	-	-

Table 3: Grouping of genotypes based on disease reaction to bacterial wilt incidence.

Sl No.	Rating	Disease Reaction	Genotype	Total
1.	0	HR	IIHR -500-A	1
2.	1	R	IIHR-127, IIHR-575, IIHR-584, IIHR -667 A, IIHR- 766A, IIHR-817, IIHR-874, IIHR-882.	8
3.	2	MR	IIHR 438-2, IIHR-618, IIHR-766	3
4.	3	MS	IIHR-576, IIHR- 583, IIHR-798	3
5.	4	S	IIHR -574, IIHR-692, IIHR-793, IIHR-857	
6.	5	HS	IIHR-228, IIHR- 534, IIHR-569, IIHR-571, IIHR-632, IIHR-711, IIHR-694, IIHR-812, IIHR-813, IIHR-880, IIHR-881	11

References

- 1. Bainsla NK, Singh S, Singh PK, Kumar K, Singh AK, Gautam R. Genetic behaviour of bacterial wilt resistance in eggplant (*Solanum melongena* L.) in tropics of Andaman and Nicobar Islands of India. American Journal of Plant Science. 2016; 7:333-8.
- 2. Das CR, Chattopadhyay SB. Bacterial wilt on eggplant. Indian Phytopathology. 1953; 8:130-135.
- Frary A, Doganlar S, Daunay MC. Eggplant. (In) Vegetables SE - 9, Genome Mapping and Molecular Breeding in Plants, Kole C (Ed). Springer, Berlin. 2007; pp.287-313.
- 4. Gopalakrishnan C, Singh TH, Artal RB. Evaluation of eggplant accessions for resistance to bacterial wilt caused by *Ralstonia solanacearum* (E.F. Smith) Yabuuchi *et al.* Journal Horticultural Sciences. 2014; 9:202-5.
- 5. Gopalan C, Rama Sastri BV, Balasubramanian S. Nutritive Value of Indian Foods. National Institute of Nutrition (NIN), ICMR, 2007.
- Hossain ZM, Rahman MA, Bashar MA, Screening of brinjal accessions for bacterial wilt caused by *Ralstonia solanacearum*. Bangladesh Journal of Botany. 2005; 34(1):53-58.
- Kelman A. The bacterial wilt caused by *Pseudomonas* solanacearum: A literature review and bibliography. North Carolina Agril. Expt. Stn. Technical bulletin. 1953; 99:194-197.
- 8. Khapte PS, Singh TH, Sadashiva AT, Reddy KM. Performance of parents and hybrids for yield and yield attributing characters in manjarigota type of brinjal (*Solanum melongena* L.). Madras Agricultural Journal. 2012; 99:438-41.
- Liu T, Yu Y, Cai X, Tu W, Xie C, Liu J. Introgression of bacterial wilt resistance from *Solanum melongena* to *Solanum tuberosum* through asymmetric protoplast fusion. Plant Cell Tissue and Organ Culture. 2016; 125:433-43.
- 10. Rai PV, Shivappasetty KKA, Vasanthasetty KP. Bacterial wilt of petunia and its source of inoculum. Current Research. 1975; 4:173-174.
- 11. Rao MVB, Sohi HS, Vijay, OP. Reaction of some varieties of brinjal to *Pseudomonas solanacearum*. Vegetable Science. 1976; 3:61-64.
- 12. Sabita JN, Boruah BM, Rachid HA. Yield Potentiality of Some Brinjal Cultivars in Severely Bacterial Wilt Infected Condition. Vegetable Science. 2000; 27:76-77.
- Santhosha HM, Indiresh KM, Gopalakrishnan C, Singh TH. Evaluation of Brinjal Genotypes against Bacterial Wilt Caused by *Ralstonia solanacearum*. Journal of Horticultural Science. 2005; 10(1):74-78.

- Sharma R, Razdan VK,Dorjey S, Gupta P, Mahajan S. Screening of Brinjal Germplasm against Wilt Complex Disease. International Journal of Current Microbiology and Applied Sciences. 2018; 7(8):1534-1539.
- Smith EF. Brown rot of *Pseudomonas solanacearum*. An introduction to bacterial diseases of plants. W.B. Saunder Co., Phildelphia, U.S.A. 1920; pp.177-201.
- Winstead NN, Kelman A. Inoculation techniques for evaluating resistance to *Pseudomonas solanacearum*. Phytopathology. 1952; 42:628-634.
- 17. Yang X, Cheng Y, Deng C, Ma Y, Wang Z, Chen X and Xue L. Comparative transcriptome analysis of eggplant (*Solanum melongena* L.) and turkey berry (*Solanum torvum* Sw.): Phylogenomics and disease resistance analysis. BMC Genomics. 2014; 15:412.