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SCREENING OF TOMATO GENOTYPES AGAINST BACTERIAL WILT (*RALSTONIA SOLANACEARUM*) UNDER FIELD CONDITION FOR CHHATTISGARH

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ABSTRACT
The present investigation was conducted at Department of Plant Breeding and Genetics, Horticulture farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) during Rabi 2008-09. The experimental material comprised of twenty genotypes along with two checks of tomato and the experiment was laid out in Randomized block design with three replication. Result on bacterial wilt showed that genotypes Cherry Jaspur had high resistant reaction (HR); four genotypes viz., ATL-01-19, Pant T-10 and CO-3 recorded moderately resistance in field condition against bacterial wilt.

KEY WORD:- Tomato, *Lycopersicon esculentum*, Bacterial wilt.

INTRODUCTION

Tomato (*Lycopersicon esculentum*) is one of the most important solanaceous vegetable crop grown worldwide due to its acclimatization to a wide variety of environments, as well as its high nutritive value. It remains in the focus of the horticultural industry, as is evidenced by an increasing in its cultivation ever since the mid nineteenth century. World-over, tomato cultivation spans an area of 3.75 million hectare, with a production of 125 million tonnes. In India, tomato is cultivated in an area of 6.1 million hectare with an annual production of 87 million tonnes. In India its average productivity remains low (15.9 t/ha) as against 27.20 t/ha in the world. Whereas, in Chhattisgarh, tomato occupies an area of 37,717 hectare with a production of 404,143.4 MT and productivity of 15.10 t/ha which is very near to national average (http://faostat.fao.org/). Tomato crop has suffered from several biotic and abiotic stresses during its growing season. Among those stresses, bacterial wilt of tomato caused by *Ralstonia solanacearum* (Yabuuchi *et al.,*1995) is one of the most devastating and wide-spread diseases of crops worldwide (Poussier *et al*., 1999). The tomato wilt (*Ralstonia solanacearu*) belongs to a group of ubiquitous and diverse plant pathogen that occurs widely in India as a soil dwelling root pathogen on various crops and also can be isolated from different varieties of the same species. *R. solanacearum* infects more than 200 species in 50 families (Hayward, 1991), including tomato, potato, eggplant, pepper, tobacco, banana, chilli and peanut (French and Sequeira, 1970). The seedling mortality in tomato is the main problem in most of tropical regions like Chhattisgarh. Without clear knowledge of pathotype present in a particular cropping ecosystem it is very difficult to select crop varieties for the area. Thus, progress of breeding programme depends upon up-to-date knowledge of existing of pathotypes of pathogen in a particular ecosystem. Resistance cultivars have been used as an important component of integrated disease management.

MATERIALS & METHODS

The present investigations were conducted at Department of Plant Breeding and Genetics, Horticulture farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) during Rabi 2008-09. The experimental material comprised of twenty genotypes of tomato. Details of treatment are given in Table -1

The genotypes populations were grown on raised bed with three replications. The bacterial solution having 6 x 10^5 cfu/ml concentration was drenched in collar region of three weeks old seedlings of each genotype. The observations were recorded after 21 days after inoculation. The mortality per cent was recorded and further classified into 0-5 scale as under and fit into the formula to work out host reaction.

The location severity index (LSI) was calculated by using the following formula.

$$LSI = \frac{\sum \text{Score x number of genotypes}}{\text{Total number of genotypes observed}} \times 100$$

TABLE-1: The experimental material comprised of twenty genotypes of tomato

S.No.	Treatments/ Genotypes	Source
1	ATL-01-19	GAU ANAND, (GUJRAT)
2	HADT-294	HARP, RANCHI (JHARKHAND)
3	VR-35	IIVR, VARANASI (UTTER PRADESH)
4	PAU-2371	PAU LUDHIANA, (PANJAB)
5	VTG-89	VPKAS ALMORA, (UTTARANCHAL)
6	VTG-90	VPKAS ALMORA, (UTTARANCHAL)
7	DVRT-2 (C)	IIVR, VARANASI (UTTER PRADESH)
8	CO-3 (C)	TNAU COIMBATORE, (TAMILNADU)
9	VTG-85	VPKAS ALMORA, (UTTARANCHAL)
10	VTG-86	VPKAS ALMORA, (UTTARANCHAL)
11	VR-415	IIVR, VARANASI (UTTER PRADESH)
12	PANT-T-10	GBPAU&T PANT NAGAR, (UTTARANCHAL)
13	PANT-T-11	GBPAU&T PANT NAGAR, (UTTARANCHAL)
14	VTG-93	VPKAS ALMORA, (UTTARANCHAL)
15	VTG-106	VPKAS ALMORA, (UTTARANCHAL)
16	PAU-2374	PAU LUDHIANA, (PANJAB)
17	NDT-9	NDUA&T FAIZABD, (UTTER PRADESH)
18	ARKA VIKAS	IIHR, (BANGLORE)
19	H-24	CCSHAU HISSAR, (HARYANA)
20	CHERRY JASHPUR	JASHPUR, (CHHATISHGARH)

TABLE-2: The mortality per cent and classification

Score	Per cent mortality	Reaction
0	0	Highly resistant
1	1-10	Resistant
2	11-25	Moderately resistant
3	26-50	Moderately susceptible
4	51-75	Susceptible
5	76-100	Highly susceptible

RESULT:

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 incalculatable 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 season winter 2008-09.

Data in table indicates that during *Rabi* 2008 none of genotypes were, found to be immune against tomato bacterial wilt. Only one genotype Cherry Jashpur was found to be highly resistant. Three genotypes (ALT-01-19, Pant T-10, CO-3) were found susceptible genotypes and sixteen (VTG-86, VR-415, VTG-93, DVRT-2, HADT-294,Pant T-11, Arka Vikash, VTG-89, VR-35, PAU2371, PAU2374, VTG-90, H-24, NDT-9, VTG-106, VTG-85) showed high susceptibility location severity index of 4.04.

TABLE: 3 screening of tomato genotypes against bacterial wilt (*Ralstonia solanacearum*) under field condition

Scale	Mortality (%)	Reaction	Number of genotypes	*Rabi* 2008
0	0	Immune	0	-
1	1-10	Highly Resistant (HR)	1	Cherry Jashpur
2	11-25	Moderatly Resistant (MR)	0	-
3	26-50	Moderately Susceptible (MS)	0	-
4	51-75	Susceptible(S)	3	ALT-01-19, Pant T-10, CO-3
5	76-100	Highly Susceptible(HS)	16	VTG-86, VR-415, VTG-93, DVRT-2, HADT-294, PANT T-11, Arka Vikash, VTG-89, VR-35, PAU 2371, PAU 2374, VTG-90, H-24, NDT-9, VTG-106, VTG-85
Location Severity Index (LSI)			4.04	

DISCUSSION

Tikoo *et al.* (1990) recorded that simple genetic control may underlie the bacterial wilt resistance in some resistance stocks originating from the tropical areas. Grimault *et al*. (1995) reported that the inheritance o resistance to bacterial wilt in tomato by a single dominant gene. Oliveira *et al.* (1999) observed that the importance of additive gene effects on the resistance against bacterial wilt, while, Monma *et al.* (1997) reported that the bacterial wilt resistance is partially recessive. Sharma, *et al.* (2006) at Jharkhand, eight tomato parental lines and 28 F_1 crosses developed at the station were tested in bacteria (*R. solanacearum*) sick plot during 2000-01 to 2002-03, in Jharkhand, India. Finally, five most promising parental lines and four F_1 crosses were tested during rainy season during 2005-06 to evaluate the fruit yield and resistance. The F_1 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) have also used such technique for identification of resistant host genotype(s) and its utilization in breeding horticulturally improved bacterial wilt resistant cultivars development.

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