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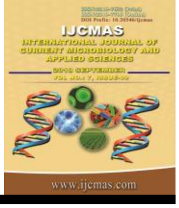

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Identification of Sources of Resistance against Wilt (*Fusarium oxysporum* f. sp. *ciceri*) in Chickpea Genotypes under Temperate Agro-Climatic Conditions of Kashmir

Shifa Showket[1], Sabiya Bashir[2*], Mohammad Najeeb Mughal[1], Reyaz-ul-Raouf Mir[1], F.A. Bhatt[1] and T.A. Shah[1]

[1]Division of Plant Pathology, Faculty of Agriculture, [2]Dryland Agriculture Research Station, S. K. University of Agricultural Sciences and Technology of Kashmir, Budgam-191132, India

**Corresponding author*

ABSTRACT

Keywords

Chickpea, *Fusarium* wilt, Genotype screening, Kashmir, Temperate agro-climatic conditions

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Thirty five chickpea genotypes in Chickpea International Elite Nursery Winter 2018 (CIEN-W-18), procured from ICARDA were evaluated against wilt caused by *Fusarium oxysporum* f. sp *ciceri* during Rabi 2018 under temperate agro-climatic conditions of Kashmir. None of the genotypes were found highly resistant, while only three genotypes *viz*., FLIP10-355C, FLIP11-40C and FLIP11-45C were Resistant. Seven genotypes *viz*., FLIP10-332C, FLIP10-343C, FLIP11-125C, FLIP11-163C, FLIP11-175C, FLIP11-190C and FLIP11-231C were moderately resistant while fourteen genotypes *viz*., FLIP10-318C, FLIP10-333C, FLIP10-364C, FLIP11-05C, FLIP11-06C, FLIP11-09C, FLIP11-11C, FLIP11-22C, FLIP11-32C, FLIP11-58C, FLIP11-134C, FLOP11-151C, FLIP11-193C and FLIP93-93C were moderately susceptible. Eight genotypes *viz*., FLIP10-337C, FLIP10-345C, FLIP11-21C, FLIP11-102C, FLIP11-66C, FLIP11-158C, FLIP82-150C and FLIP88-85C were found susceptible and three genotypes (ILC482, FLIP11-08C and FLIP10-338C) were highly susceptible.

Introduction

Chickpea (*Cicer arietinum* L.) is an important pulse crop, which rank third after dry beans (*Phaseolus vulgaris* L.) and dry peas (*Pisum sativum* L.) (Dhar and Gurha, 1998). India is largest producer of chickpea in the world contributing 65.49 per cent in production and 65.25 per cent in area. In India chickpea is grown on 81.17 lakh hectare of land, producing 59.01 lakh tonnes with a productivity of 727 kg ha^{-1}(Anonymous, 2015). *Fusarium oxysporum* f. sp. *ciceri* (Foc, Padwick) is a serious soil borne disease of chickpea (Hossain *et al.*, 2013) and was first reported in Indo-Pak sub-continent by Butler in 1918. It is one of the major constraints in chickpea cultivation throughout the world especially in Indian sub-continent where chickpea is a commonly grown as pulse crop. Nema and Khare (1973) reported yield loss due to wilt upto 61 per cent if the infection occurs at seedling stage and 43 per cent if the infection occurs at flowering stage. In India, at National level, the yield loss due to wilt may vary between 5 to 10 per cent (Singh and Dahiya, 1973). However, under congenial weather conditions for disease, it may cause complete (100 %) yield loss (Pande *et al.*, 2010; Kumari and Khanna, 2014).

Though reports on different aspects of the disease are available from India and abroad, very scanty information is available on this disease from Jammu and Kashmir. Although various chemical fungicides are available for management of disease but they incur high cost and cause environmental hazards and deleterious effects on human health. Identification of resistant genotypes is one of the most suitable, cheap and eco-friendly method of management of disease and improving the farmers returns. Keeping in view the importance of disease, socio-economic status of the crop and inadequate research work carried out, an attempt was made to identify sources of resistance to the disease in the genotypes procured from ICARDA.

Materials and Methods

Thirty five genotypes, including four Checks *viz*., ILC482, FLIP-82-150C, FLIP88-85C and FLIP 93-93C, procured from ICARDA were screened against the wilt under natural epiphytotic conditions in Chickpea International Elite Nursery 2018 (CIEN-W-18) at FOA, Wadura during Rabi 2017-18. The genotypes were classified into Highly Resistant (HR), Resistant (R), Moderately Resistant (MR), Moderately Susceptible (MS), Susceptible (S) and Highly Susceptible (HS) groups on the basis of their response to disease under natural epiphytotic conditions. All the entries were planted in two replications. Susceptible checks were planted in separate plots. The length of each row was 4m and width was 0.45m. The observation on wilt was recorded as percentage of disease incidence calculated by following formula:

$$\text{Disease incidence (\%)} = \frac{\text{No. of plants exhibiting wilt symptoms}}{\text{Total of total plants observed}} \times 100$$

A scale (0 – 5 point) was used for categorization of genotypes.

Results and Discussion

The persual of data (Table 1 and 2) revealed that in Chickpea International Elite Nursery 2018 (CIEN-W-18), none of the genotypes recorded zero disease incidence and no genotype was found Highly Resistant (HR). However, three genotypes *viz*., FLIP10-355C, FLIP11-40C and FLIP11-45C were Resistant (R) with disease incidence ranging from 4.75 (FLIP10-355C) to 8.75 (FLIP11-45C) per cent and seven genotypes *viz*., FLIP10-332C, FLIP10-343C,FLIP11-163C, FLIP11-175C, FLIP11-190C and FLIP11-231C were Moderately Resistant (MR) with disease incidence varying from 12.50 in genotype FLIP11-125C to 18.00 per cent in genotype FLIP11-163C and fourteen genotypes *viz*., FLIP10-318C, FLIP10-333C, FLIP10-364C, FLIP11-05C, FLIP11-06C, FLIP11-09C, FLIP11-11C, FLIP11-22C, FLIP11-32C, FLIP11-58C, FLIP11-134C, FLOP11-151C, FLIP11-193C and FLIP93-93C were designated as moderately susceptible with disease incidence ranging from 21.00 (FIP11-22C) to 28.00 (FLIP11-151C) per cent. Eight genotypes FLIP10-337C, FLIP10-345C, FLIP11-21C, FLIP11-102C, FLIP11-66C, FLIP11-158C, FLIP82-150C and FLIP88-85C were susceptible. Among the susceptible genotypes, the lowest disease incidence (35.00%) was recorded in genotype FLIP10-337C while highest disease incidence (49.00%) was recorded in FLIP11-150C genotype.

Table.1 Reactions of genotypes in Chickpea International Elite Nursery 2018 (CIEN-W-18)

S. No	Genotype	Per cent wilt incidence
01	FLIP10-355C	4.75
02	FLIP11-40C	7.75
03	FLIP11-45C	8.75
04	FLI10-332C	15.75
05	FLIP10-343C	13.00
06	FLIP11-125C	12.50
07	FLIP11-163C	18.00
08	FLIP11-175C	17.75
09	FLIP11-190C	11.00
10	FLIP11-231C	16.25
11	FLIP10-318C	23.50
12	FLIP10-333C	25.00
13	FLIP10-364C	25.00
14	FLIP11-05C	27.75
15	FLIP11-06C	22.25
16	FLIP11-09C	21.00
17	FLIP11-11C	24.75
18	FIP11-22C	21.25
19	FLIP11-32C	24.75
20	FLIP11-58C	24.00
21	FLIP11-134C	22.50
22	FLIP11-151C	28.00
23	FLIP11-193C	21.00
24	FLIP93-93C	23.00
25	FLIP10-337C	35.00
26	FLIP10-345C	38.25
27	FLIP11-21C	40.50
28	FLIP11-102C	42.00
29	FLIP11-66C	43.50
30	FLIP11-158C	45.00
31	FLIP11-150C	49.00
32	FLIP88-85C	43.75
33	ILC482	53.00
34	FLIP11-08C	55.75
35	FLIP10-338C	52.75

Table.2 Categorization of chickpea genotypes / lines in CIEN-W-18

Category	Reaction	Average wilt incidence (%)	Genotypes/ Lines
0	Highly resistant (none)	0	-
1	Resistant (3)	1-10	FLIP10-355C, FLIP11-40C and FLIP11-45C
2	Moderately resistant (7)	10-20	FLIP10-332C, FLIP10-343C, FLIP11-125C, FLIP11-163C, FLIP11-175C, FLIP11-190C and FLIP11-231C
3	Moderately susceptible (14)	20-30	FLIP10-318C, FLIP10-333C, FLIP10-364C, FLIP11-05C, FLIP11-06C, FLIP11-09C, FLIP11-11C, FLIP11-22C, FLIP11-32C, FLIP11-58C, FLIP11-134C, FLOP11-151C, FLIP11-193C and FLIP93-93C
4	Susceptible (8)	30-50	FLIP10-337C, FLIP10-345C, FLIP11-21C, FLIP11-102C, FLIP11-66C, FLIP11-158C, FLIP82-150C and FLIP88-85C
5	Highly susceptible (3)	50 & above	ILC482, FLIP11-08C and FLIP10-338C

Categorization scale (0 – 5)

Grade	Per cent mortality	Disease reactions
0	No disease	Highly resistant (HR)
1	1 to 10	Resistant(R)
2	10.1 to 20	Moderately Resistant (MR)
3	20.1 to 30	Moderately Susceptible (MS)
4	30.1 to 50	Susceptible (S)
5	50 and above	Highly Susceptible (HS)

(IIPR, 1999)

Three genotypes were found Highly Susceptible and among them lowest disease incidence (53.00%) was recorded in ILC482 followed by FLIP10-338C with disease incidence of 52.75 while genotype FLIP11-08C recorded the highest disease incidence of 56.75 per cent.

In the present investigation the selection for the resistance was based on the reaction of the genotypes to wilt pathogen, *Fusarium oxysporum* f. sp. *ciceri* under natural epiphytotic conditions and the result indicated that three genotypes were Resistant (R) and which could be used as direct introductions or sources of resistance in hybridization programme.

Korde, (2011), Mandhare *et al.*, (2011) and Kumar *et al.*, (2012) gave been screened number of chickpea genotypes and identified promising cultivars in India.

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