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RESEARCH NOTE

Screening of cumin germplasm against *Fusarium* wilt under wilt-sick plot conditions

GANESUNI LAKSHMI PRASANNA[1] **and N. R. PATEL**[2]

Department of Plant Pathology, Sardarkrushinagar, Dantiwada Agricultural University, Sardarkrushinagar, Gujarat-385505, India

[*]**E-mail:** ganesunilakshmiprasanna@gmail.com

ABSTRACT: Wilt caused by *Fusarium oxysporum* f. sp. *cumini* is the most serious disease of cumin (*Cuminum cyminum* L.) in India. Cumin germplasm was screened against *Fusarium* wilt at S. D. Agricultural University, Gujarat, India. Out of 105 genotypes evaluated, none of the genotype was found to be immune to wilt. The genotypes *viz.,* JC-18-11 and GC-5-1 were highly resistant with a minimum wilt incidence of 5.00 per cent while the genotypes *viz*., JC-18-01 (17.25%), JC-18-07 (18.25%), GP-5 (20.05%) and GP-7 (20.00%) were resistant. The genotypes *viz.,* JC-18-03 (25.15%), JC-18-05 (25.00%), JC-18-06 (25.00%), GP-3 (25.00%), GC-3(c) (25.06%), JC-2010-5 (30.25%), Sanand 5 (30.50%), Sanand 6(30.25%) and GP-4 (30.14%) were found moderately resistant. The genotypes *viz.,* JC-18-04 (35%), GP-2 (35%), GC-5-2 (35%), GC-5 (c) (35%) JC-18-02 (40%), JC-2000-28-1 (40%), JC-16-07 (40%), JC-18-08 (45%), GC-4 (c) (45%) and J-Cum-2-2017 (50%) were found susceptible to the pathogen. The remaining germplasm accessions with the wilt incidence of more than 50% were susceptible to highly susceptible.

Keywords: Cumin, germplasms, *Fusarium* wilt, screening, resistant, susceptible

Cumin (*Cuminum cyminum* L.) is a small herbaceous plant in the family Apiaceae (Umbelliferae), commonly called as "zeera". In India, cumin is exclusively cultivated in Gujarat and Rajasthan. The share of Gujarat in total area and production was 36.7 and 46.3 per cent, respectively (Vinod Kumar, 2017). Gujarat produced 319.9 thousand MT from 3.5 lakh hectare area during the year 2018-19(Anonymous, 2020). The main constraint to achieve high productivity is susceptibility of cumin to devastating diseases *viz*., *Fusarium* wilt, *Alternaria* blight and powdery mildew (Pandey *et al*., 2019). Cumin is seriously affected by wilt caused by *Fusarium oxysporum* f. sp. *cumini* which causes up to 80 per cent yield loss (Divakara Sastry and Anandaraj, 2013). Wilt remained a serious, destructive and widespread disease of the crop and has threatened the cumin cultivation in Gujarat and Rajasthan. As *Fusarium* wilt is a soil borne disease, it is difficult to eradicate as the asexual fungal spores such as chamydospores survive up to six years in soil even in the absence of suitable host. As the wilt pathogen is soil borne, it is difficult to manage with fungicides or with any single management tactics. Hence there is a need to explore resistant sources in the existing genotypes. So, present investigation was carried out to find out resistant genotypes for the management of cumin wilt.

A total of one hundred and five (105) cumin genotypes were evaluated in *Fusarium* wilt sick plot at Seed Spices Research Station, Sardarkrushinagar Dantiwada Agricultural University, Jagudan, Gujarat, India. The cumin seeds were sown in wilt affected field having a wilt pathogen population of 1.3×10^4 cfu/g of soil. The infected soil was used because it permits the assessment of field resistance by allowing the infection process to take place under natural conditions, with realistic doses of naturally produced inoculums. Sowing of cumin was done in *rabi* season during the year 2019-2020. The size of each plot was 0.90 m × 4.0 m (2 rows of each genotype) with row spacing of 30cm. Each of the test entries was alternated by susceptible check. The recommended agronomic practices were followed. The statistical design used was augmented method. Based on the proportion of plants exhibiting *Fusarium* wilt symptoms in susceptible germplasm, the data was recorded for healthy and wilted plants from different genotypes and per cent disease incidence was calculated. Germplasm accessions were categorised as highly resistant (0-10% disease), resistant (11-20%), moderately resistant (21-30%), susceptible (31-50%) and highly susceptible (> 50%) as per the scale given by Iqbal *et al.* (2005).

The results presented in Table 1 revealed that out of one hundred and five cumin genotypes tested, two were highly resistant (HR), four were resistant (R), nine were moderately resistant (MR), ten were susceptible (S) and eighty were found highly susceptible (HS). None of the genotypes was immune to wilt. The germplasm accessions *viz.,* JC-18-11 and GC-5-1 were highly resistant with a

Table 1. Per cent wilt incidence in different germplasm accessions of cumin

Entry	Wilt incidence (%)	Reaction	Entry	Wilt incidence (%)	Reaction
JC-18-01	17.25	R	Sanand 5	30.50	MR
JC-18-02	40.00	S	Sanand 6	30.25	MR
JC-18-03	25.15	MR	GP-1	65.12	HS
JC-18-04	35.12	S	GP-2	35.44	S
JC-18-05	25.00	MR	GP-3	25.00	MR
JC-18-06	25.00	MR	GP-4	30.14	MR
JC-18-07	18.25	R	GP-5	20.05	R
JC-18-08	45.50	S	GP-6	90.62	HS
JC-18-09	90.75	HS	GP-7	20.00	R
JC-18-10	60.14	HS	GP-8	95.00	HS
JC-18-11	5.00	HR	GP-9	100.00	HS
JC-17-08	60.32	HS	GP-10	100.00	HS
CUM-40	70.50	HS	GP-12	100.00	HS
CUM-41	90.68	HS	GP-13	100.00	HS
CUM-42	70.25	HS	GP-14	100.00	HS
CUM-43	65.41	HS	GP-15	100.00	HS
JC-16-03	75.20	HS	GP-16	100.00	HS
JC-16-10	80.72	HS	GP-17	100.00	HS
JC-16-07	40.11	S	GP-18	100.00	HS
JC-2010-5	30.25	MR	GP-19	100.00	HS
GP-20	100.00	HS	JC-2000-28-2	70.33	HS
GP-21	100.00	HS	JC-2000-57	80.27	HS
GP-22	100.00	HS	JC-2002-09	95.00	HS
GP-23	100.00	HS	JC-14-2	90.25	HS
GP-24	100.00	HS	J-Cum-1-2017	95.04	HS
GP-25	100.00	HS	J-Cum-2-2017	50.41	S
GP-26	100.00	HS	JC-2010-05	90.62	HS
GP-27	100.00	HS	GC-5-1	5.00	HR
GP-28	100.00	HS	GC-5-2	35.13	S
GP-29	100.00	HS	Mutation-2	95.24	HS
GP-30	100.00	HS	Mutation-3	100.00	HS
GP-31	100.00	HS	Mutation-4	100.00	HS
GP-32	100.00	HS	Mutation-5	95.25	HS
GP-33	100.00	HS	Mutation-6	95.36	HS
GP-34	100.00	HS	Mutation-7	95.12	HS
GP-35	100.00	HS	Mutation-8	95.48	HS
GP-36	100.00	HS	Mutation-9	95.26	HS
GP-37	100.00	HS	Mutation-10	95.26	HS
GP-38	100.00	HS	Mutation-11	100.00	HS
GP-39	100.00	HS	Mutation-12	100.00	HS

GP-40	100.00	HS	Mutation-13	100.00	HS
GP-41	85.25	HS	Mutation-14	100.00	HS
GP-42	90.12	HS	Mutation-15	100.00	HS
GP-43	80.24	HS	Mutation-17	100.00	HS
GP-44	100.00	HS	Mutation-18	100.00	HS
GP-45	100.00	HS	Mutation-19	100.00	HS
GP-46	100.00	HS	Mutation-20	100.00	HS
GP-47	100.00	HS	GC-1 (c)	70.15	HS
GP-48	100.00	HS	GC-2 (c)	73.28	HS
GP-49	100.00	HS	GC-3 (c)	25.06	MR
GP-50	100.00	HS	GC-4 (c)	45.14	S
JC-2000-5	95.17	HS	GC-5 (c)	35.04	S
JC-2000-28-1	40.21	S			

HR- Highly resistant, R- Resistance, MR- Moderately resistance, S- Susceptible
HS- Highly susceptible

minimum wilt incidence of 5.00 per cent. The genotypes *viz*., JC-18-01 (17.25%), JC-18-07 (18.25%), GP-5 (20.05%) and GP-7 (20.00%) were found resistant. The genotypes *viz.,* JC-18-03 (25.15%), JC-18-05 (25.00%), JC-18-06 (25.00%), GP-3 (25.00%), GC-3(c) (25.06%), JC-2010-5 (30.25%), Sanand 5 (30.50%), Sanand 6 (30.25%) and GP-4 (30.14%) were found moderately resistant. The germplasms *viz.,* JC-18-04 (35.12%), GP-2 (35.44%), GC-5-2 (35.13%), GC-5 (c) (35.04%) JC-18-02 (40.00%), JC-2000-28-1 (40.21%), JC-16-07 (40.11%), JC-18-08 (45.50%), GC-4 (c) (45.14%) and J-Cum-2-2017 (50.41%) were found susceptible to the pathogen.

The remaining genotypes *viz.,* JC-18-10 (60.14%), JC-17-08 (60.32%), CUM-43 (65.41%), GP-1 (65.12%), CUM-40 (70.50%), CUM-42 (70.25%), GC-1 (c) (70.15%), JC-2000-28-2 (70.33%), GC-2 (c) (73.28%), JC-16-03 (75.20%), JC-16-10 (80.72%), GP-43 (80.24%), JC-2000-57 (80.27%), GP-41 (85.25%), GP-6 (90.62%), JC-18-09 (90.75%), CUM-41 (90.68%), GP-42 (90.12%), JC-14-2 (90.25%), JC-2010-05 (90.62%), GP-8 (95.00%), JC-2000-5 (95.17%), JC-2002-09 (95.00%), J-Cum-1-2017 (95.04%), Mutation-2 (95.24%), Mutation-5 (95.25%), Mutation-6 (95.36%), Mutation-7 (95.12%), Mutation-8 (95.48%), Mutation-9 (95.07%) and Mutation-10 (95.26%) were found highly susceptible. The genotypes *viz.,* GP-9, GP-10, GP-11, GP-12, GP-13, GP-14, GP-15, GP-16, GP-17, GP-18, GP-19, GP-20, GP-21, GP-22, GP-23, GP-24, GP-25, GP-26, GP-27, GP-28, GP-29, GP-30, GP-31, GP-32, GP-33, GP-34, GP-35, GP-36, GP-37, GP-38, GP-39, GP-40, GP-44, GP-45, GP-46, GP-47, GP-48, GP-49, GP-50, Mutation-3, Mutation-4, Mutation-11, Mutation-12, Mutation-13, Mutation-14, Mutation-15, Mutation-17, Mutation-18, Mutation-19 and Mutation-20 recorded cent per cent wilt incidence and were categorized as highly susceptible.

Twelve lines of cumin were screened against wilt pathogen *F. oxysporum* f. sp. *cumini* and highest resistance was recorded in UC-220 and UC-231 Arora *et al.*, (2004). Deepak *et al.,* (2008) screened 25 cumin germplasms but, none them shown resistant to wilt and found that the maximum resistance to wilt was observed in UC- 220, EC-220, EC- 232684 and UC-63 lines. The lines JC-2000-21 and JC-2000-22 were found moderately susceptible. The findings of Deepak and his co-workers match with the result of present study. The lines JC-2000-21 and JC-2000-22 in both the investigations are reported as moderately susceptible to *F. oxysporum* f. sp. *cumini*.

The genotypes *viz.,* JC-18-11 and GC-5-1 were found highly resistant with a minimum wilt incidence of 5.00 per cent. The genotypes *viz*., JC-18-01 (17.25%), JC-18-07 (18.25%), GP-5 (20.05%) and GP-7 (20.00%) were found resistant. The genotypes *viz.,* JC-18-03 (25.15%), JC-18-05 (25.00%), JC-18-06 (25.00%), GP-3 (25.00%), GC-3(c) (25.06%), JC-2010-5 (30.25%), Sanand 5 (30.50%), Sanand 6(30.25%) and GP-4 (30.14%) were found moderately resistant. The varieties GC-2 and GC-3 which are recommended to cultivate in Gujarat state were found to be highly susceptible to *F. oxysporum* f. sp. *cumini* under field screen studies.

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