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Assessment of seed yield and field screening against fusarium wilt in safflower (*Carthamus tinctorius* L.)

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Abstract

Safflower (*Carthamus tinctorius* L.) is an important oilseed crop valued for its adaptability to drought-prone environments; however, its productivity is severely constrained by low yield potential and *Fusarium* wilt caused by *Fusarium oxysporum* f. sp. *carthami*. In the present study, a total of 75 diverse genotypes along with four yield checks were evaluated in an augmented randomized block design during Rabi 2025-26 at the Agricultural Research Station, Tandur, Telangana, for seed yield and yield attributing traits along with resistance to *Fusarium* wilt. Analysis of variance revealed significant genetic variability among the genotypes for all the traits studied, revealing ample scope for selection and genetic improvement. The *per se* performance of seed yield per plant ranged from 5.88 to 24.48 g and the genotypes viz., TSF-3450, TSF-845, GMU7921, TSF-3439, GMU7919, TSF-3429 and TSF-3444 had shown significantly superior performance over the best yield check RVSAF-18-1 (13.14 g). Screening of same set of genotypes with one resistant and one susceptible check under wilt-sick plot against *Fusarium* wilt showed a wilt incidence ranged from 0 to 87.50%, reflecting substantial diversity in disease response. Four genotypes, namely TSF-3440, TSF-3439, TSF-845 and TSF-3442, exhibited complete immunity to *Fusarium* wilt, while five genotypes showed resistance and eight were categorized as moderately resistant. Notably two genotypes i.e., TSF-845 and TSF-3439 were found to be high yielding coupled with immunity to wilt. The identified high-yielding and disease-resistant genotypes provide valuable genetic resources for developing stable, productive and *Fusarium* wilt resistant safflower cultivars suited to wilt prone areas.

Keywords: Seed yield, *Fusarium* wilt, wilt sick-plot, safflower

Introduction

Safflower (*Carthamus tinctorius* L.) is a valuable oilseed crop belonging to the family Asteraceae and is extensively grown under arid and semi-arid climatic conditions worldwide. Owing to its remarkable tolerance to drought and salinity, safflower is recognized as a versatile crop that provides high quality vegetable oil and natural carthamin dye obtained from its florets (Anon., 2001) ^[1]. In India, safflower is cultivated in an area of 0.64 lakh hectares, with a total production of 0.43 lakh tonnes and an average productivity of 672 kg ha⁻¹ (Indiastat, 2024-25) ^[4]. Maharashtra and Karnataka are the major safflower growing states followed by Telangana. In Telangana, it is cultivated in an area of 0.02 lakh hectares, with a production and productivity of 0.03 lakh tonnes and 1316 kg ha⁻¹ respectively. Despite its potential uses, safflower cultivation area in India has been declining alarmingly due to low seed yield, low oil content and susceptibility to biotic and abiotic stresses such as aphids, wilt and moisture stress (Nimbkar, 2009) ^[9].

Despite its immense agronomic adaptability to marginal environments, the global and national productivity of safflower is severely constrained by a wide array of biotic stresses, particularly fungal pathogens that damage the crop across various growth stages (Prabhavathi *et al.*, 2025 and Reddy *et al.*, 2025) ^[10, 12]. Among the fungal diseases affecting safflower, wilt caused by *Fusarium oxysporum* f. sp. *carthami* is one of the most destructive soil-borne diseases (Klisiewicz and Houston, 1962) and is considered a major economic constraint to safflower production. It causes extensive vascular discoloration, severe chlorosis, acropetal wilting and eventual plant death (Reddy *et al.*, 2025) ^[12]. It is reported to exhibit seed transmission rates of 10-40% (Chakrabarti and Basuchaudhary, 1980) ^[2], facilitating rapid dissemination across geographical borders and resulting in yield losses ranging from 80 to 93% under susceptible cultivars and poorly drained conditions (Sastry and Ramachandram, 1994; Prabhavathi *et al.*, 2025) ^[10, 13].

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The management of *Fusarium* wilt using conventional chemical or cultural practices is generally ineffective and economically unviable due to its soil-borne nature. Therefore, the identification of resistant host plants represents the most effective strategy for the long-term management of this disease (Murumkar *et al.*, 2008 and Reddy *et al.*, 2025)^[8, 12]. Screening under field conditions in uniformly infected environments using specialized wilt-sick plots are considered the most dependable method for confirming resistance under natural disease pressure (Prabhavathi *et al.*, 2025)^[10]. The objective of the study is to identify high-yielding safflower genotypes with resistance to *Fusarium* wilt among diverse genotypes. Accordingly, this investigation was designed to evaluate the diverse panel of safflower genotypes for seed and oil yield, along with screening for resistance to *Fusarium* wilt.

Material and Methods

In the present study, 75 diverse safflower genotypes were evaluated for seed yield along with screening for resistance to *Fusarium* wilt. The experiment was conducted at the Experimental Farm of the Agricultural Research Station, Tandur, Telangana, during Rabi 2025-26. Two sets of experiments were carried out separately for evaluation of yield and its components and screening against *Fusarium* wilt under wilt-sick conditions. In the first experiment, 75 safflower genotypes were evaluated for seed yield and its components with four checks. The trial was laid out in Augmented Randomized Block Design in five blocks, each block consists of 15 genotypes and checks were repeated in each block. The genotypes were sown in a row of 5 m length with a spacing of 45 cm between rows and 20 cm between plants within a row. Recommended package of practices were followed to raise the crop.

The observations were recorded on five randomly selected plants for the traits viz., plant height (cm), number of capitula plant⁻¹, diameter of primary capitulum, number of seeds primary capitulum⁻¹, 100 seed weight (g) and seed yield plant⁻¹ (g), while days to 50% flowering and days to maturity were recorded on a plot basis. The mean data was subjected to statistical analysis as per the Augmented Randomized Block Design suggested by Federer (1956).

In the second set of experiment, the same 75 safflower genotypes, along with one resistant and one susceptible check, were screened against *Fusarium* wilt under wilt-sick plot by ensuring consistent disease pressure with a pathogen Foc population of 3.5×10^3 cfu/g. To monitor disease pressure and ensure uniformity of wilt incidence across the experimental area, a susceptible check (NIRA) and a resistant check (TSF-1) were included after every five test entries. All the recommended agronomic practices were followed except for the application of plant protection measures against *Fusarium* wilt. The genotypes were sown in a row of 5 m length with a spacing of 45 cm between rows and 15 cm plant-to-plant distance. Wilt observations were recorded starting from 30 days after sowing (DAS) and subsequently at 15 days intervals, with observations taken at 30, 45, 60, 75, 90, 105 and a final observation at 120 DAS. The *Fusarium* wilt incidence (%) for each genotype was calculated using the following formula:

$$\text{Percentage wilt incidence (\%)} = (\text{Number of wilted plants} / \text{Total plant population}) \times 100$$

The final disease response of each genotype was assessed based on the cumulative wilt incidence recorded up to 120 days after sowing. The genotypes were categorized according to the *Fusarium* wilt disease rating scale of the All India Coordinated Research Project (AICRP) on Safflower. Disease severity was also evaluated using a 0-9 disease rating scale (Mayee and Datar, 1986)^[7] as presented below.

Disease scale	Particulars	Reaction
0	No wilting symptoms	Immune
1	<1% plants wilted	Highly Resistant
3	1 - 10% plants wilted	Resistant
5	11-20% plants wilted	Moderately resistant
7	21-50% plants wilted	Susceptible
9	>51% plants wilted	Highly susceptible

Results and Discussions

Study of mean performances for seed yield and its components

The analysis of variance (ANOVA) revealed significant differences among the safflower genotypes for all the eight yield and yield contributing traits, indicating the existence of substantial genetic variability in the material under study (Table-1). Highly significant variation was observed for days to 50% flowering, days to maturity, plant height, number of capitula per plant, number of seeds per capitulum, 100-seed weight, seed yield per plant, volume weight, hull content and oil content, while the diameter of the primary capitulum showed significant variation.

Mean performance of 79 safflower genotypes including four checks for seed yield and yield components revealed that six genotypes (GMU7915, GMU7919, GMU7886, GMU7908, GMU7892 and GMU7914) exhibited significant early flowering, whereas seven genotypes (GMU7914, GMU7915, GMU7908, GMU7892, GMU7886, GMU7918 and GMU7919) showed significantly early maturity over the earliest check ISF-764, indicating their potential as valuable sources for developing early duration cultivars (Table-2).

The *per se* performance of plant height ranged from 61.22 to 110.92 cm and the genotypes TSF-3442, TSF-860, GMU993-1 and TSF-3430 were found to be significantly taller than the best check PBNS-12. Among the genotypes studied, only two genotypes, TSF-3452 (24.40) and GMU7904 (24.00) exhibited significant superiority over the best check RVSAF-18-1 (17.92) for the character number of capitula per plant. This trait also showed a considerable range of mean performance varies from 8.45 to 24.40. The genotypes such as TSF-3440 (4.68 cm), TSF-3454 (4.63 cm), TSF-3452 (4.63 cm) and TSF-860 (4.48 cm) were found to have greater primary capitulum diameter compared to the check PBNS-12 (3.86 cm). Though the number of seeds per primary capitulum registered a wide range of variation from 7.07 (GMU893) to 27.02 (TSF-3435) none of the genotypes significantly exceeded the best check PBNS-12 (24.24). The genotypes TSF-3435 (27.02) and TSF-3449 (26.42) were significantly superior over the check ISF-764 (21.08) for seed per primary capitulum.

The 100-seed weight ranged from 3.19 (GMU7865) to 6.29 g (GMU7911) with an average of 4.46 g and the genotypes GMU7911 (6.29 g), TSF-3437 (5.84 g), TSF-860 (5.74 g) and GMU7870 (5.59 g) recorded significantly higher values than the best check RVSAF-18-1 (4.92 g). The *per se* performance of seed yield per plant varied widely from 5.88 (GMU1184) to 24.48 g (TSF-3450). The genotypes viz.,

TSF-3450 (24.48 g), TSF-845 (22.63 g), GMU7921 (21.96 g), TSF-3439 (21.23 g), GMU7919 (20.56 g), TSF-3429 (18.23 g) and TSF-3444 (16.78 g) significantly outperformed over the best check RVSAF-18-1 (13.14 g) highlighting their superiority for yield improvement.

The study demonstrated the presence of considerable diversity among the safflower genotypes for seed yield and its contributing traits. Several genotypes significantly outperformed over the best checks for various traits highlighting their breeding potential and these could be further utilized in crop improvement programmes for development of high yielding varieties.

Screening of safflower genotypes against *Fusarium* wilt

Host plant resistance is widely recognized as the most effective, economical and sustainable strategy for management of soil borne diseases. In the present study, 75 diverse safflower genotypes along with one resistant check (TSF-1) and one susceptible check (NIRA) were evaluated in a wilt-sick plot as per the standard procedure. The genotypes exhibited wilt incidence ranged from 4.35 to 87.50 per cent plant mortality (Table-3), indicating a broad range of disease responses and confirming strong and consistent disease pressure in the sick plot. The screening of 75 test entries revealed high genetic variability in terms of disease reaction.

The 75 genotypes were categorized based on per cent wilt incidence. Among the genotypes evaluated, four genotypes were categorized as immune (0%), five as resistant (1-10%), eight as moderately resistant (11-20%), 41 as susceptible (21-50%) and 17 as highly susceptible (>51%) using disease rating scale (Table 4). The predominance of susceptible and highly susceptible reactions highlights the persistent threat posed by *Fusarium* wilt in safflower cultivation and the limited availability of resistance in existing breeding material.

Four genotypes, namely TSF-3440, TSF-3439, TSF 845 and TSF-3442, were identified as immune, exhibiting a 0% wilt

incidence throughout the entire crop growth cycle. Identification of immune lines from the array of genotypes is very useful in crop improvement programmes. Rajendraprasad *et al.* (2021)^[11] and Reddy *et al.* (2025)^[12] also identified immune donors in their wilt screening studies under high disease pressure. Five genotypes viz., TSF-3426, TSF-3437, TSF-3430, TSF-3450 and TSF-3431 exhibited a resistant (R) reaction, with a wilt incidence of 1-10%. These entries represent valuable genetic sources for developing high yielding *Fusarium* wilt resistant cultivars.

Eight genotypes viz., GMU916, TSF-3429, TSF 861, TSF-3449, TSF-3455, TSF-3454, TSF-3452 and TSF-3457 were categorized as moderately resistant (MR) with wilt incidence ranging from 11-20%. Identification of these lines holds considerable value for safflower improvement programmes as resistant sources typically carry polygenic, partial resistance that provides more durable protection across fluctuating agro-climatic conditions. However, the vast majority of the evaluated lines were highly vulnerable to the pathogen, which falls into the susceptible (21-50% PWI) and highly susceptible (>51% PWI) categories. 41 genotypes showed susceptible reactions, with wilt incidences reaching up to 47.62% (GMU893). Furthermore, seventeen genotypes were placed in a highly susceptible category with severe plant mortality, among which the entries such as GMU7556 (87.50%), GMU7553 (86.36%) and GMU7892 (78.26%) demonstrated severe susceptibility. The high disease incidence observed in the susceptible check, NIRA (77.95%), confirmed the severe and uniform distribution of the pathogen across the experimental plots.

Continuous field screening is imperative due to the variable nature of *F. oxysporum* f. sp. *carthami*. As recommended by Kalpana Sastry and Chattopadhyay (2003)^[5], the immune, resistant and moderately resistant identified donor parents could be directly utilized in introgression programs aiming to enhance the yield stability of safflower cultivars in wilt prone areas.

Table 1: Analysis of variance for seed yield and its attributing characters in safflower

Source of variation	d.f.	Mean sum of squares							
		DFF	DM	PH	NCP	DPC	NSPC	HSW	SYP
Block (Ignoring Treatments)	4	48.31**	21.25**	554.64**	10.56*	0.34**	8.8	0.62**	28.62**
Treatment (Eliminating Blocks)	78	12.67**	13.33**	56.81*	12.11**	0.10*	16.14**	0.41**	13.96**
Checks	3	51.80**	48.98**	43.99	8.04	0.06	34.00**	0.62**	1.89
Checks +Var vs. Var.	75	11.11**	11.90**	57.32*	12.28**	0.10*	15.43**	0.40**	14.45**
Block (Eliminating Check +Var.)	4	1.073	0.669	3.655	1.315	0.035	7.733	0.067	3.752
Entries (Ignoring Blocks)	78	15.10**	14.38**	85.07**	12.59**	0.11*	16.19**	0.44**	15.24**
Varieties	74	13.81**	13.06**	87.74**	12.84**	0.11*	14.05**	0.43**	15.77**
Checks vs. Var.	1	0.16	8.11**	10.08	7.47	0.24*	121.21**	0.56**	15.71**
Error	12	0.51	0.61	18.54	3.07	0.03	3.94	0.03	1.63

*, ** Significant at 5% and 1% level, respectively

DFF- Days to 50% flowering, DM-Days to maturity, PH-Plant height, NECP-No. of capitula per plant, DPC- Diameter of primary capitulum, NSPC-No. of seeds per primary capitulum, HSW-100-Seed weight, SYP-Seed yield per plant.

Table 2: Mean performance of seed yield and its components in safflower genotypes

S. No.	Genotype	DFF	DM	PH	NCP	DPC	NSPC	HSW	SYP
1	GMU7887	83.35	125.45	61.22	18.05	4.05	12.52	3.69	8.46
2	GMU7553	84.35	125.45	68.12	9.75	3.95	14.92	5.09	7.26
3	GMU7556	84.35	127.45	67.22	8.45	3.45	13.32	3.59	6.16
4	GMU7915	75.35	117.45	74.52	14.45	3.55	14.82	5.39	9.26
5	GMU7522	87.35	130.45	72.62	9.05	3.65	20.32	4.59	7.56
6	GMU7909	83.35	125.45	78.52	14.05	3.95	16.12	5.39	10.56
7	GMU7868	80.35	123.45	82.92	20.05	3.95	11.12	5.19	11.36
8	GMU7908	76.35	117.45	73.52	20.25	4.15	9.22	3.79	11.06

9	GMU7870	78.35	121.45	76.72	17.25	3.85	14.32	5.59	12.66
10	GMU7882	88.35	130.45	83.22	13.85	3.65	15.12	4.29	10.46
11	GMU7875	85.35	127.45	90.72	10.85	4.25	22.72	3.59	9.96
12	GMU7862	86.35	129.45	86.82	10.75	4.35	23.12	4.29	10.86
13	GMU7919	75.35	119.45	90.92	17.75	3.85	24.12	4.59	20.56
14	GMU7892	76.35	117.45	83.72	18.65	3.65	8.52	3.49	7.66
15	GMU7914	76.35	116.45	81.92	17.95	3.95	14.12	5.19	14.56
16	GMU7911	78.60	123.20	88.34	9.20	4.23	13.57	6.29	10.56
17	GMU7871	85.60	129.20	99.74	13.10	4.13	21.57	4.29	12.66
18	GMU7918	77.60	119.20	81.04	15.00	3.83	19.77	4.89	13.06
19	GMU7907	86.60	129.20	89.24	18.10	3.83	14.07	3.79	8.36
20	GMU7518	89.60	132.20	81.54	20.00	2.93	21.37	3.89	15.56
21	GMU7901	79.60	123.20	83.04	16.60	3.93	23.37	3.79	14.06
22	GMU7904	76.60	121.20	81.44	24.00	3.73	14.37	4.69	15.86
23	GMU7894	77.60	121.20	71.24	13.90	3.93	15.17	4.19	8.46
24	GMU7905	84.60	128.20	75.14	12.50	3.23	21.97	4.29	12.96
25	GMU7913	80.60	123.20	85.64	14.30	3.73	15.57	4.39	9.16
26	GMU7865	84.60	129.20	89.14	17.10	4.33	15.57	3.19	14.96
27	GMU7920	83.60	125.20	84.14	17.90	3.83	16.77	4.69	13.96
28	GMU7886	75.60	118.20	77.44	15.50	3.73	17.77	4.29	11.26
29	GMU7861	85.60	130.20	89.34	11.90	3.73	19.17	4.29	8.16
30	GMU7921	78.60	120.20	77.04	21.10	3.93	19.37	4.79	21.96
31	GMU7879	76.60	121.70	91.47	10.20	3.53	21.87	3.81	6.18
32	GMU7872	77.60	122.70	88.37	16.60	3.93	11.67	4.71	7.48
33	GMU880	84.60	128.70	90.97	17.20	3.43	12.87	4.11	9.18
34	GMU993-1	84.60	127.70	108.37	11.00	3.83	18.07	4.21	10.08
35	GMU1579	84.60	126.70	86.97	14.40	3.53	12.27	5.01	6.68
36	GMU884	84.60	127.70	99.87	14.00	3.43	13.97	4.81	5.98
37	GMU914	83.60	127.70	86.37	12.40	3.53	18.87	4.11	9.18
38	GMU1184	84.60	126.70	95.57	14.80	3.73	15.07	5.21	5.88
39	GMU916	83.60	125.70	88.47	18.80	3.23	14.07	4.01	6.88
40	GMU893	84.60	124.70	84.47	19.20	3.53	7.07	3.91	7.08
41	GMU891	84.60	126.70	86.57	18.20	3.83	18.07	4.31	13.88
42	GMU942	83.60	126.70	93.47	13.40	4.23	17.47	4.71	8.78
43	GMU992	83.60	126.70	91.27	14.40	3.93	18.87	4.61	10.68
44	GMU1000	84.60	124.70	86.67	11.60	4.03	18.87	3.91	8.18
45	GMU998	84.60	125.70	88.77	14.00	3.73	15.27	3.31	7.98
46	TSF-3426	85.10	125.45	85.57	16.65	3.68	12.82	4.44	8.83
47	TSF-3436	86.10	129.45	91.87	20.75	3.48	11.82	3.74	10.43
48	TSF-3437	78.10	123.45	88.87	16.05	3.58	18.42	5.84	10.03
49	TSF-3430	84.10	126.45	104.17	13.65	3.98	21.62	5.34	13.33
50	TSF-3435	83.10	126.45	101.87	12.65	3.78	27.02	4.54	12.83
51	TSF-3429	81.10	126.45	89.57	18.85	3.58	20.72	5.24	18.23
52	TSF-3440	85.10	125.45	97.87	11.25	4.68	20.62	3.94	6.93
53	TSF-3428	84.10	126.45	90.77	13.05	3.48	19.62	4.64	9.53
54	TSF-3439	84.10	127.45	91.87	19.85	4.18	21.62	5.14	21.23
55	TSF-3441	84.10	124.45	97.87	16.25	3.88	19.62	4.74	12.43
56	TSF 845	80.10	122.45	100.97	19.25	4.18	20.42	5.34	22.63
57	TSF 860	85.10	125.45	108.67	14.95	4.48	18.72	5.74	11.73
58	TSF 861	86.10	127.45	90.97	14.05	3.98	19.22	4.74	11.93
59	TSF 862	85.10	127.45	86.37	12.05	3.78	18.82	4.34	6.83
60	TSF 870	86.10	129.45	92.77	18.05	3.88	19.42	4.34	12.93
61	TSF-3450	77.35	120.20	89.72	21.60	3.83	21.42	4.59	24.48
62	TSF-3451	85.35	128.20	89.22	21.40	4.03	19.22	3.89	14.18
63	TSF-3442	86.35	129.20	110.92	18.40	4.23	19.22	3.69	9.88
64	TSF-3447	86.35	131.20	82.12	16.20	3.63	15.22	4.49	9.58
65	TSF-3456	85.35	126.20	86.22	17.40	3.83	17.62	3.89	10.38
66	TSF-3449	83.35	126.20	85.62	13.10	3.83	26.42	4.19	12.08
67	TSF-3453	84.35	126.20	87.52	12.30	3.73	21.02	3.69	11.08
68	TSF-3455	85.35	130.20	82.12	14.00	3.73	24.22	4.49	12.78
69	TSF-3454	86.35	130.20	91.62	13.60	4.63	20.82	3.19	8.08
70	TSF-3446	86.35	126.20	85.32	15.00	4.13	21.02	5.09	10.58
71	TSF-3452	84.35	127.20	87.02	24.40	4.63	25.22	3.39	16.08
72	TSF-3457	85.35	127.20	86.82	12.50	4.13	22.42	5.29	7.78
73	TSF-3443	84.35	128.20	79.72	10.40	3.73	21.42	4.39	6.18
74	TSF-3444	85.35	130.20	79.92	18.20	3.63	21.22	4.69	16.78
75	TSF-3431	85.35	131.20	81.22	16.00	3.83	21.02	4.49	13.08
76	A-1 (C)	84.60	127.60	85.24	15.00	3.76	18.36	4.88	12.14

77	ISF-764 (C)	78.40	121.80	85.22	16.32	3.60	21.08	4.16	12.16
78	PBNS-12 (C)	85.60	128.60	91.12	15.56	3.86	24.24	4.58	11.68
79	RVSAF-18-1 (C)	83.80	127.80	89.28	17.92	3.68	19.20	4.92	13.14
	Mean	83.01	125.77	86.96	15.55	3.84	18.09	4.46	11.33
	CD @5%	1.90	2.08	11.49	4.68	0.52	5.30	0.48	3.41

DFF- Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm) NCP-No. of capitula per plant, DPC- Diameter of primary capitulum (cm), NSPC-No. of seeds per primary capitulum, HSW-100-Seed weight (g), SYP-Seed yield per plant (g).

Table 3: Wilt incidence of safflower genotypes screened against *Fusarium* wilt at wilt sick plot

S. No.	Genotype	Wilt incidence (%)	Wilt reaction	S. No.	Genotype	Wilt incidence (%)	Wilt reaction
1	NIRA (SC)	77.95	HS	40	GMU1184	37.5	S
2	TSF-1 (RC)	6.57	MR	40	GMU916	16.67	MR
3	GMU7887	66.67	HS	42	GMU893	47.62	S
4	GMU7553	86.36	HS	43	GMU891	36.84	S
5	GMU7556	87.5	HS	44	GMU942	35	S
6	GMU7915	28	S	45	GMU992	27.27	S
7	GMU7522	58.33	HS	46	GMU1000	34.78	S
8	GMU7909	63.64	HS	47	GMU998	30	S
9	GMU7868	56.52	HS	48	TSF-3426	5.26	R
10	GMU7908	40.91	S	49	TSF-3436	33.33	S
11	GMU7870	37.5	S	50	TSF-3437	8	R
12	GMU7882	68	HS	51	TSF-3430	8.7	R
13	GMU7875	62.5	HS	52	TSF-3435	34.78	S
14	GMU7862	60	HS	53	TSF-3429	13.64	MR
15	GMU7919	76	HS	54	TSF-3440	0	Immune
16	GMU7892	78.26	HS	55	TSF-3428	42.86	S
17	GMU7914	37.5	S	56	TSF-3439	0	Immune
18	GMU7911	54.17	HS	57	TSF-3441	25	S
19	GMU7871	32	S	58	TSF 845	0	Immune
20	GMU7918	40	S	59	TSF 860	36.36	S
21	GMU7907	28.57	S	60	TSF 861	16	MR
22	GMU7518	34.78	S	61	TSF 862	32	S
23	GMU7901	76	HS	62	TSF 870	24	S
24	GMU7904	66.67	HS	63	TSF-3450	4.35	MR
25	GMU7894	70	HS	64	TSF-3451	33.33	S
26	GMU7905	28.57	S	65	TSF-3442	0	Immune
27	GMU7913	32	S	66	TSF-3447	28	S
28	GMU7865	56.52	HS	67	TSF-3456	43.48	S
29	GMU7920	43.48	S	68	TSF-3449	15.79	MR
30	GMU7886	40	S	69	TSF-3453	32	S
31	GMU7861	44	S	70	TSF-3455	15	MR
32	GMU7921	36	S	71	TSF-3454	13.64	MR
33	GMU7879	42.11	S	72	TSF-3446	35	S
34	GMU7872	52	HS	73	TSF-3452	19.05	MR
35	GMU880	32	S	74	TSF-3457	17.39	MR
36	GMU993-1	44	S	75	TSF-3443	24	S
37	GMU1579	41.67	S	76	TSF-3444	29.41	S
38	GMU884	33.33	S	77	TSF-3431	9.09	R
39	GMU914	32	S				

Table 4: Reaction of safflower genotypes screened against *Fusarium* wilt at sick plot

Disease scale	Wilt incidence (%)	Wilt Reaction	Genotype	No. of Genotypes
0	No wilting symptoms	Immune (I)	TSF-3440, TSF-3439, TSF 845, TSF-3442	4
1	<1% plants wilted	Highly Resistant (HR)	-	0
3	1 - 10% plants wilted	Resistant (R)	TSF-3426, TSF-3437, TSF-3430, TSF-3450, TSF-3431	5
5	11-20% plants wilted	Moderately Resistant (MR)	GMU916, TSF-3429, TSF 861, TSF-3449, TSF-3455, TSF-3454, TSF-3452, TSF-3457	8
7	21-50% plants	Susceptible (S)	GMU7915, GMU7908, GMU7870, GMU7914, GMU7871, GMU7918, GMU7907, GMU7518, GMU7905, GMU7913, GMU7920, GMU7886, GMU7861, GMU7921,	41

	wilted		GMU7879, GMU880, GMU993-1, GMU1579, GMU884, GMU914, GMU1184, GMU893, GMU891, GMU942, GMU992, GMU1000, GMU998, TSF-3436, TSF-3435, TSF-3428, TSF-3441, TSF 860, TSF 862, TSF 870, TSF-3451, TSF-3447, TSF-3456, TSF-3453, TSF-3446, TSF-3443, TSF-3444	
9	>51% plants wilted	Highly susceptible (HS)	GMU7887, GMU7553, GMU7556, GMU7522, GMU7909, GMU7868, GMU7882, GMU7875, GMU7862, GMU7919, GMU7892, GMU7911, GMU7901, GMU7904, GMU7894, GMU7865, GMU7872	17
Total				75

Conclusion

The present study revealed the existence of significant genetic variability for both seed yield and yield contributing traits and resistance to *Fusarium* wilt. Several genotypes were found significantly superior in performance over the superior checks for seed yield and its components. Even though, majority of the accessions were found highly vulnerable to wilt under wilt screening, four genotypes viz., TSF-3440, TSF-3439, TSF 845 and TSF-3442 were identified as immune and five genotypes viz., TSF-3426, TSF-3437, TSF-3430, TSF-3450, TSF-3431 were resistant. Notably, two genotypes TSF-845 and TSF-3439 were found promising with high seed yield and immune reaction to wilt. These genotypes can be utilized in future breeding programmes to develop stable, high yielding and *Fusarium* wilt resistant safflower cultivars specifically tailored for wilt-endemic regions. These genotypes can be further evaluated in multilocation trials or AICRP trials to further validate their yield stability and disease reaction.

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