

Original Research Article

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## Evaluation of Safflower Genotypes against Major Disease Alternaria Leaf Spot of Safflower

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### ABSTRACT

Safflower (*Carthamus tinctorius* L.) is one of the most important oilseed crops of the world valued for its highly nutritious edible oil. It is a multipurpose crop having various uses like source of edible oil, cattle feed, medicinal and industrial products. The leaf spot disease caused by *Alternaria carthami* Chowdhary is a major destructive disease of safflower (*Carthamus tinctorius* L.) in India. The disease has been reported to cause seed yield losses to the tune of 10 to 25 per cent. Under severe conditions, it has been reported to cause 50 per cent loss in seed yield 34 germplasm accessions were screened for the identification of resistance or even tolerance for the disease. The incidence of *Alternaria* leaf spot was observed in the field under natural conditions. Accessions were grouped based on 0 to 9 disease rating scale. Five accessions showed resistant reaction with grade 3 and eighteen accessions showed moderately resistant (MR) reaction with grade 5 and seven genotypes showed susceptible reaction with grade 7.

#### Keywords

Safflower,  
Alternaria leafspot,  
Genotype

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### Introduction

Safflower (*Carthamus tinctorius* L.) occupies prominent place in the agricultural wealth and economy of India. It belongs to family *Compositae* and believed to be native of Afghanistan. The word *Carthamus* is Arabic word *quartum* (means the colour of dye obtained from florets). It is described as “*Kusumbha*” in ancient Sanskrit literature.

Other Indian names, like *Kusum*, *Karrad* (Hindi), *Kusumpuli* (Bengali), *Kusumbo* (Gujrathi), *Kardi*, *Kurdi* (Marathi), *Sendurakam* (Tamil), *Kusuma* (Telgu), *Kusube*, *Kusume* (Kannada), *Kusumba* (Punjabi) seem to have been derived from “*Kusumbha*”. Presently the most common name being “*Kusum*” or “*Kardi*”. It is a rich source of proteins and edible oil and so many farmers plant it.

Safflower (*Carthamus tinctorius* L.) is one of the most important oilseed crops of the world valued for its highly nutritious edible oil. It is a multipurpose crop having various uses like source of edible oil, cattle feed, medicinal and industrial products.

Safflower is known to suffer from many fungal and bacterial diseases among them seed borne disease viz., *Alternaria* leaf spot/blight (ALS) caused by *Alternaria carthami* and soil borne diseases viz., wilt (*Fusarium oxysporum f.sp. carthami*) and *Phytophthora* blight (*Phytophthora carthami*) are major and attack at different stages of crop growth (Bhale *et al.*, 1998).

The leaf spot disease caused by *Alternaria carthami* Chowdhary is a major destructive disease of safflower (*Carthamus tinctorius* L.) in India. The disease has been reported to cause seed yield losses to the tune of 10 to 25 per cent (Indi *et al.*, 1988). Under severe conditions, it has been reported to cause 50 per cent loss in seed yield (Indi *et al.*, 1986). Safflower plant is also prone to infection by several seed-borne fungi (Ramesh and Avitha, 2005). Seeds also act as carrier in transmission of pathogens and thereby cause economic threat to safflower cultivation. Considering the economic losses in this present investigation attempts were therefore made to screen out the resistant sources against the *Alternaria* leaf spot disease.

### Materials and Methods

The experiment was carried out at Agricultural Research Station, Annigeri, University of Agricultural Sciences, Dharwad during *rabi* 2017-18. The research station is situated in the northern dry zone of Karnataka between 15°8'N latitude, 75°3'E longitude and at an altitude of 624.80 meters above the mean sea level. The experimental material for the present study comprised of 34 safflower germplasm accessions obtained from the

Germplasm Unit of the Directorate of Oilseeds Research, Hyderabad. Disease screening for *Alternaria* was done under field condition. Methodology as followed as below.

The crop was sown using randomized block design with single row system. Each genotype was planted with 45 cm row spacing and 20 cm between the plants. Recommended agronomic practices and insect pest control measures were followed as per the package of practices of University of Agricultural Sciences, Dharwad, Karnataka. The observations were recorded on ten plant basis, selected randomly from each replication of the individual genotype for percent disease index (PDI). The disease severity was recorded at flowering stage and harvesting stage following standard disease scoring scale (Mayee and Datar, 1986). Further, the materials were categorized as highly resistant, resistant, moderately resistant, susceptible and highly susceptible based on 0 to 9 disease scale for *Alternaria* (Table 1).

### Results and Discussion

In present investigation, 34 germplasm accessions were screened for the identification of resistance or even tolerance for the disease. The incidence of *Alternaria* leaf spot was observed in the field under natural conditions and the results are presented in table 2. Accessions were grouped based on 0 to 9 disease rating scale. Five accessions showed resistant reaction with grade 3 and eighteen accessions showed moderately resistant (MR) reaction with grade 5 and seven genotypes showed susceptible reaction with grade 7.

The similar studies on the safflower germplasm screening against *Alternaria* blight (*Alternaria carthami*) were done earlier by several workers (Akashe, *et al.*, 1994; Desai, 1998; Indi, *et al.*, 2004; Relekar, 2008 and Murumkar *et al.*, 2009).

**Table.1** Disease scoring scale to *Alternaria* leaf spot of safflower

Grade	Description	Category
0	No symptoms on leaves	Immune
1	Small, round brown spots covering 1% or less of the leaf	Highly resistant
3	Brown sunken spots covering 1-10% of the leaf area	Resistant
5	Brown spots enlarging to form circular spots covering 11-25% of the leaf Area	Moderately resistant
7	Circular , brown, sunken spots covering 26-50% of the leaf area	Susceptible
9	Circular to irregular, brown sunken spots covering 51% or more of the leaf Area	Highly susceptible

**Table.2** Reaction of safflower genotypes to *Alternaria* leaf spot during *rabi* 2017-18

Sl.No	Germ plasma	Mean	Reaction
1	SAF-1601	11.35	MR
2	SAF-1603	8.4	R
3	SAF-1606	13.05	MR
4	SAF-1608	9.1	R
5	SAF-1607	10.55	MR
6	SAF-1630	26.8	S
7	SAF-1656	32.2	S
8	SAF-1659	4.11	R
9	SAF-1660	16.1	MR
10	SAF-1685	10.5	MR
11	SAF-1689	30.1	S
12	SAF-1693	27.1	S
13	SAF-1401	26.7	S
14	SAF-1517	14.7	MR
15	SAF-1556	26.25	S
16	GMU-2757	30.25	S
17	SAF-1617	6.25	R
18	SAF-1701	18.9	MR
19	SAF-1710	22.0	MR
20	SAF-1711	10.5	MR
21	SAF-1717	7.8	R
22	SAF-1738	11.7	MR
23	PBNS-153	4.95	R
24	PBNS-154	8.6	R
25	PBNS-170	11	MR
26	PBNS-171	10.8	MR
27	PBNS-172	10.5	MR

28	1749-1	28.1	S
29	3350-8	23.1	MR
30	3350-2	11.8	MR
31	1703-2	10.5	MR
32	3350-3	10.7	MR
33	1749-1-2	15.9	MR
34	DSI-116	6.4	R
35	HUS305	9.05	R
36	Manjira	29.1	S

Awadhiya (1992) identified *A. carthami*, *Fusarium moniliforme*, *Botrytis cinerea*, *Macrophomina phaseolina*, *Stachybotrys* spp. and *Oedocephalum* spp. from seeds of 50 safflower cultivars in states of Maharashtra, Karnataka, Andhra Pradesh and Madhya Pradesh in India. *A. carthami* was the only pathogen found in all varieties tested. In studies of healthy, discoloured, wrinkled and deformed seeds of five varieties (APRR 2, HUS 304, JSF 1, NS 99-A and SF 364) no particular association of the pathogen with the condition of seed was found. Chavan and Kakde (2009) isolated nine fungal species from safflower cultivars. Among these, *Aspergillus* spp. showed dominance, followed by *Fusarium* spp. and *Alternaria* spp. Bhima variety showed maximum susceptibility to fungi and got infected by *Aspergillus niger*. *A. flavus*, *Fusarium oxysporum*, *Alternaria dianthicola* and *Alternaria dianthi* while C1L and C1B varieties were least susceptible to fungi.

This study confirms that differences in resistance to major diseases exist in germplasm of safflower. The resistant nature of elite lines observed in present field trials confirmed the reports by Singh *et al.*, (1987), Borkar and Shinde (1988), Zad (1992), Khanam (1993) and Ismail *et al.*, (2004). These findings suggest that it is possible to improve an existing line through further selection and screening of the progenies of the parental line.

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