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Identification of resistant sources through field evaluation of soybean genotypes against anthracnose caused by *Colletotrichum truncatum* (Andrus and Moore)

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Abstract
Soybean (*Glycine max* (L.) Merr.) is an important oilseed and protein crop, yet its productivity is severely constrained by anthracnose/pod blight caused by *Colletotrichum truncatum*, particularly under warm and humid conditions. The present study was undertaken to evaluate the response of forty soybean genotypes to anthracnose under natural epiphytotic field conditions during the *Kharif* season of 2024-25 at the Regional Sugarcane and Rice Research Station, Rudrur, Telangana. The results revealed significant variation in disease incidence and severity among the genotypes with PDI ranging from 46.7 to 100.0 percent. None of the genotypes exhibited complete resistance to anthracnose. Three genotypes, namely Basara, ASB 206 and RSB 1070 showed a moderately resistant reaction recording comparatively lower disease severity and restricted symptom development. Seven genotypes were categorized as moderately susceptible, while the majority of the entries were classified as susceptible to highly susceptible exhibiting severe stem, pod and foliar infections. The wide variability in disease response reflected differences in host-pathogen interactions under field conditions. The identification of moderately resistant genotypes highlights the presence of partial resistance within the evaluated germplasm which can contribute to reduced disease impact and yield loss. These genotypes represent valuable donor sources for breeding programs aimed at developing anthracnose-tolerant soybean cultivars. The study emphasizes the need for continued screening of diverse germplasm to identify stable and durable sources of resistance for sustainable management of soybean anthracnose.

Keywords: Soybean, anthracnose, *Colletotrichum truncatum*, disease resistance, genotype screening, kharif season

Introduction
Soybean is a major source of high-quality protein and oil and the quality of soybean seed is largely determined by its nutritional and anti-nutritional constituents. *Glycine max* (L.) Merr. is regarded as a high-value crop with wide applications in food, fodder and industrial sectors, owing to its unique chemical composition that includes medicinally important compounds such as tocopherols, isoflavones and lecithin in addition to approximately 40% protein and 20% oil content (Sharma *et al.*, 2011, Rajput *et al.*, 2021) [13, 11]. In India, soybean was cultivated on approximately 11.46 million hectares with an estimated production of about 10.54 million metric tonnes and an average productivity of around 920 kg/ha (SOPA, 2025) [16].

Plants exposed to environmental stresses, such as extreme temperatures and fluctuating moisture levels, become more prone to disease development when conditions are favorable for pathogens. Plant diseases are a major constraint on the productivity of economic crops, often leading to substantial losses in both yield and quality (Gupta and Paul, 2002) [5]. Numerous pathogens affect soybean *viz*., anthracnose pod blight, Rhizoctonia aerial blight, frogeye leaf spot and Alternaria leaf spot pose severe threats to profitable cultivation in Telangana. Among the various diseases affecting soybean, anthracnose/pod blight caused by *Colletotrichum* spp. is regarded as one of the most destructive as it infects nearly all above-ground plant parts, including seedlings, stems, petioles, leaves and pods leading to considerable yield losses across major soybean-growing regions worldwide (Khare and Chacko, 1983; Singh *et al.*, 2021, Sharma *et al.*, 2021; Amrate *et al.*, 2022) [6, 15, 11, 1].

This disease inflicts heavy economic damage even 1% severity can cut yields by 115 kg/ha with losses reaching 64.8% on average and upto 100% under wet, conducive conditions in India and worldwide. Synthetic fungicides provide quick relief but breed resistance in pathogens, leave harmful residues and endanger health and ecosystems (Reimann and Deising 2000; Unnikrishnan and Nath 2000; Sharma *et al.*, 2021; Mathpal *et al.*, 2020) [12, 17, 14, 8]. Breeding resistant varieties offers the most sustainable, cost-effective solution, yet Indian reports on anthracnose-resistant sources remain sparse and location-specific (Rajput *et al.*, 2021) [11].

Host plant resistance is recognized as the most economically viable, environmentally safe and sustainable strategy for managing anthracnose/pod blight. However, few soybean cultivars with durable resistance have been widely released, particularly under natural epiphytotic conditions (Zhu *et al.*, 2022) [19]. Therefore, systematic evaluation of soybean varieties to identify resistant donors is essential to support breeding programs aimed at developing anthracnose resistant cultivars. The present study was undertaken to evaluate the response of diverse soybean varieties to anthracnose/pod blight under natural field conditions with the objective of identifying potential resistance sources for future genetic enhancement.

Materials and Methods

During the *Kharif* season of 2024-25, the field experiment was carried out the agricultural farm of Regional Sugarcane and Rice Research Station, Rudrur (18°56′N, 77°87′E), Nizamabad district, Professor Jayshankar Telangana Agricultural University. The climate of Nizamabad is tropical in nature and characterized by hot and dry with most rainfall. The soil type in the experimental plot was heavy textured clay soil. To locate the source of resistance against anthracnose/pod blight, forty germplasms of soybean were screened out which is given in (Table 1).

Table 1: List of soybean genotypes used in study

S. No	Genotypes
1	ASB 15
2	ASB 101
3	ASB 104
4	ASB 107
5	ASB 114
6	ASB 153
7	ASB 169
8	ASB 185
9	ASB 206
10	ASB 208
11	ASB 232
12	ASB 243
13	ASB 263
14	BASARA
15	AISB 50
16	KDS 753
17	JS 9305
18	RSB 179
19	RSB 181
20	RSB 539
21	RSB 541
22	RSB 543
23	RSB 544
24	RSB 545
25	RSB 546
26	RSB 550
27	RSB 551
28	RSB 552
29	RSB 553
30	RSB 554
31	RSB 556
32	RSB 556-2
33	RSB 1029
34	RSB 547
35	RSB 1059
36	RSB 1068
37	RSB 1070
38	RSB 1071
39	JS 335
40	BASARA

The genotypes were evaluated in a unreplicated trial with a row-to-row distance of 45 cm and plant-to-plant distance of 10 cm. The experiment was non replicated in three rows of 5 m length (each entry). All the recommended agronomical package and practices were followed throughout the experiment under unprotected conditions for diseases. Ten plants were randomly selected in each plot of each variety and tagged. The disease pressure was recorded from disease initiation upto harvesting (third week of September to last week of November). Weekly observations on disease severity were recorded on the basis of a 0 to 9 rating scale given by Mayee and Datar (1986) [9] and further converted into a percent disease index (PDI) using the following formula given by Wheeler (1969) [18]: = Percent Disease Index (PDI) Sum of individual disease rating Number of plants assessed × Maximum rating ×100.

Disease Severity (DS) was recorded on 0-9 standard disease rating scale (Mayee and Datar 1986) [9] and converted to percent disease index by using formula given by Wheeler (1969) [18]:

$$\text{Percent Disease Index (PDI)} = \frac{\text{Sum of individual disease rating}}{\text{Number of plant assessed} \times \text{Maximum rating}} \times 100$$

On the basis of the PDI on leaves and pods, soybean varieties were categorized into different categories according to the AICRP (2024) [2] as 0% = No infection/immune (I); 0-1% = Resistance response (R); 10.1-20% = Moderately resistant (MR); 20.1-30% = Moderately susceptible (MS); 30.1-50% = Susceptible (S) and > 50% = Highly susceptible (HS).

Results and discussion

The experimental results clearly demonstrated that the soybean genotypes exhibited differential reactions to anthracnose disease caused by *Colletotrichum truncatum* (Table 2). Disease pressure varied considerably among the forty soybean entries evaluated under field conditions, indicating a wide range of susceptibility levels. Notably, none of the tested genotypes exhibited complete resistance to anthracnose, highlighting the absence of highly resistant sources within the evaluated germplasm pool.

Disease Incidence and Severity

Percent disease incidence (PDI) among the genotypes ranged from 46.7 to 100.0 percent, reflecting substantial variation in disease expression. Several genotypes such as ASB 208, ASB 263, RSB 541, RSB 553, RSB 556, RSB 1059, RSB 1068 and JS 335 recorded 100 percent disease incidence indicating high susceptibility to anthracnose. Correspondingly, these genotypes also exhibited high disease severity values often exceeding 60 percent and were classified as highly susceptible with a disease rating of 9. High disease severity in these entries suggested favorable host-pathogen interactions that facilitated rapid pathogen colonization and symptom development.

In contrast, comparatively lower disease severity was recorded in a limited number of genotypes. The lowest disease severity values were observed in ASB 206 (11.11%), RSB 546 (14.81%) and RSB 544 (17.04%), despite moderate levels of disease incidence. This indicated that although infection occurred, disease progression and lesion development were relatively restricted in these genotypes.

Table 2: Evaluation of soybean genotypes for resistance to soybean anthracnose

S. No	Germplasm	Percent disease Incidence (PDI)	Disease severity	Rating
1	ASB 15	73.3	40.00	7
2	ASB 101	83.3	32.96	7
3	ASB 104	93.3	48.89	7
4	ASB 107	63.3	40.37	7
5	ASB 114	80.0	38.52	7
6	ASB 153	60.0	27.41	5
7	ASB 169	76.7	44.81	7
8	ASB 185	63.3	38.15	7
9	ASB 206	53.3	11.11	3
10	ASB 208	100.0	65.93	9
11	ASB 232	53.3	30.37	5
12	ASB 243	50.0	43.33	7
13	ASB 263	100.0	74.07	9
14	BASARA	66.7	45.93	7
15	AISB 50	50.0	21.11	5
16	KDS 753	73.3	39.26	7
17	JS 9305	83.3	49.26	7
18	RSB 179	80.0	34.81	7
19	RSB 181	70.0	32.59	7
20	RSB 539	46.7	18.52	5
21	RSB 541	100.0	28.89	7
22	RSB 543	No germination		
23	RSB 544	60.0	17.04	5
24	RSB 545	86.7	51.11	9
25	RSB 546	56.7	14.81	5
26	RSB 550	70.0	34.81	7
27	RSB 551	86.7	26.67	7
28	RSB 552	56.7	24.81	5
29	RSB 553	100.0	55.56	9
30	RSB 554	60.0	34.07	7
31	RSB 556	100.0	70.37	9
32	RSB 556-2	73.3	46.67	7
33	RSB 1029	70.0	43.33	7
34	RSB 547	83.3	50.37	7
35	RSB 1059	100.0	68.15	9
36	RSB 1068	100.0	62.59	9
37	RSB 1070	66.7	27.04	3
38	RSB 1071	90.0	52.22	9
39	JS 335	96.7	60.37	9
40	BASARA	100.0	57.78	9
	CD ($p = 0.05\%$)	2.51	-	-
	SE. m (±)	0.83	-	-
	CV (%)	4.34	-	-

Reaction of Genotypes to Anthracnose

Based on disease severity ratings, three genotypes Basara, ASB 206 and RSB 1070 were categorized as moderately resistant. These genotypes recorded disease ratings of 3 reflecting their ability to limit symptom expression and pathogen spread under natural epiphytotic conditions. Such moderate resistance is often governed by partial or quantitative resistance mechanisms which although insufficient to prevent infection entirely can significantly reduce disease impact and yield loss.

Seven genotypes namely ASB 1532, ASB 232, AISB 50, RSB 539, RSB 544, RSB 546 and RSB 552 were classified as moderately susceptible with disease ratings of 5. These entries showed intermediate disease severity 14.81 to 30.37 percent suggesting partial tolerance to anthracnose and were not ideal sources of resistance they may still be useful in breeding programs aimed at accumulating minor resistance genes. The majority of the genotypes fell under the susceptible to highly susceptible categories, exhibiting disease ratings of 7 and 9. These genotypes showed extensive lesion development, stem blight, pod infection and premature defoliation which are characteristic symptoms of soybean anthracnose. The high susceptibility observed in widely cultivated varieties such as JS 335 raises concerns regarding the vulnerability of existing cultivars to anthracnose epidemics.

Implications for Breeding and Disease Management

The absence of resistant genotypes emphasizes the need for intensified screening of larger and more diverse germplasm collections to identify novel sources of anthracnose resistance. The moderately resistant genotypes identified in the present study Basara, ASB 206 and RSB 1070 represent valuable genetic resources that can be exploited in soybean improvement programs. These genotypes may serve as donor parents for incorporating partial resistance traits into high-yielding but susceptible cultivars. The observed variability in disease response also highlights the complex nature of host-pathogen interactions in soybean anthracnose. Environmental conditions, pathogen virulence and host genetic background collectively influenced disease development. Similar patterns of differential genotype response to *C. truncatum* have been reported by earlier researchers who emphasized the scarcity of complete resistance and the predominance of partial resistance in soybean germplasm.

Discussion

The findings of the present investigation are in agreement with previous reports indicating that high levels of resistance to soybean anthracnose are rare and most genotypes exhibit moderate to high susceptibility under conducive conditions. Earlier studies have also reported that partial resistance characterized by reduced lesion size and delayed symptom expression, plays a crucial role in disease management. Such resistance is considered more durable and stable across environments compared to single-gene resistance.

The identification of genotypes with lower disease severity despite moderate disease incidence suggests the presence of tolerance mechanisms which could contribute to yield stability under disease pressure. Integrating these genotypes with appropriate agronomic practices and fungicidal management strategies could significantly reduce anthracnose-related yield losses. Comparable stability in moderately resistant (MR) categories has been documented by Bhatt *et al.* (2022) [3] who reported that soybean varieties expressing moderate resistance under natural epiphytotic conditions consistently maintained lower pod blight and anthracnose intensities across multiple locations. Similarly, Amrate *et al.* (2023) [1] demonstrated that moderately resistant germplasm experienced significantly reduced yield losses under natural disease pressure, underscoring the value of MR lines as reliable donors in resistance breeding programs. In addition, studies by Kumawat *et al.* (2020) [7] and Singh *et al.* (2021) [15] revealed that soybean genotypes exhibiting partial resistance to *Colletotrichum truncatum* showed stable performance across seasons, characterized by restricted lesion development and delayed disease progression.

Further evidence was provided by Patil *et al.* (2019) [10] who observed that moderately resistant soybean lines maintained lower anthracnose severity under varying agro-climatic conditions, suggesting the involvement of quantitative resistance mechanisms. Likewise, Das *et al.* (2022) [4] reported that MR genotypes demonstrated reduced pod infection and improved yield stability compared to susceptible checks even under high disease pressure. Collectively, these studies corroborate the present findings reinforcing that moderately resistant soybean lines can sustain consistent field-level resistance despite environmental fluctuations and therefore represent dependable genetic resources for anthracnose resistance breeding.

References

1. Amrate PK, Singh SK, Rajput LS, Patel S. Stability of moderate resistance to anthracnose in soybean under natural epiphytotic conditions. Legume Research. 2023;46(4):521-527.
2. AICRP. Annual Progress Report (Soybean). Indore: All India Coordinated Research Project on Soybean, ICAR-Indian Institute of Soybean Research; 2024.
3. Bhatt PS, Mishra N, Yadav RK. Multi-location evaluation of soybean genotypes for resistance to pod blight and anthracnose. J Mycol Plant Pathol. 2022;52(1):45-52.
4. Das A, Paul S, Mukherjee A. Field performance of soybean genotypes against anthracnose under high disease pressure. Plant Pathol J. 2022;38(2):134-141.
5. Gupta SK, Paul YS. Diseases of soybean and their management. Plant Dis Res. 2002;17(1):1-16.
6. Khare MN, Chacko KC. Anthracnose of soybean in India. Indian Phytopathol. 1983;36(1):113-116.
7. Kumawat G, Gupta S, Singh SK. Partial resistance to anthracnose in soybean and its implication in breeding programs. Soybean Res. 2020;18(2):67-73.
8. Mathpal S, Choudhary S, Sharma P. Fungicide resistance and environmental concerns in soybean disease management. Int J Chem Stud. 2020;8(3):2780-2785.
9. Mayee CD, Datar VV. Phytopathometry. Parbhani: Marathwada Agricultural University; 1986.
10. Patil VM, Deshmukh AJ, Pawar SV. Reaction of soybean genotypes to anthracnose under different agro-climatic conditions. Int J Curr Microbiol Appl Sci. 2019;8(9):1450-1457.
11. Rajput LS, Amrate PK, Singh SK. Status of anthracnose resistance in Indian soybean germplasm. Indian J Agric Sci. 2021;91(5):735-739.
12. Reimann S, Deising HB. Fungicide resistance in plant pathogenic fungi. J Phytopathol. 2000;148(1):1-9.
13. Sharma OP, Giri P, Sharma P. Nutritional and medicinal importance of soybean. J Food Legumes. 2011;24(3):175-181.
14. Sharma P, Singh SK, Amrate PK. Epidemiology and management of soybean anthracnose in India. Indian Phytopathol. 2021;74(2):345-354.
15. Singh SK, Amrate PK, Rajput LS. Host-pathogen interaction in soybean anthracnose caused by Colletotrichum truncatum. J Plant Dis Prot. 2021;128(4):901-909.
16. SOPA. Soybean Processors Association of India: Annual Report 2024-25. Indore: SOPA; 2025.
17. Unnikrishnan R, Nath BS. Hazardous effects of pesticide residues on human health. Environ Toxicol. 2000;15(3):241-246.
18. Wheeler BEJ. An introduction to plant diseases. London: John Wiley and Sons Ltd.; 1969.
19. Zhu Y, Wang Y, Li H. Advances in breeding for anthracnose resistance in soybean. Front Plant Sci. 2022;13:864215.