

Identification of Cowpea (*Vigna unguiculata* L. Walp.) Genotypes Resistant against Ascochyta Blight in Western Himalaya

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ABSTRACT

Ascochyta blight holds a crucial significance in the context of cowpea cultivation, and its prevalence is a threat to this important food source and means of livelihood. During the three Kharif seasons from 2020-2022, ten (10) cowpea genotypes along with two susceptible check genotypes have been screened against Ascochyta blight under field conditions for the identification of promising genotypes. Screening has resulted in the identification of some promising cowpea genotypes. By combining the results from multiple years, consistent patterns, trends, and variations in disease score were identified for each genotype. Out of ten (10) genotypes, IITA-345 was resistant and, nine(09) genotypes, namely IITA-346, IITA-347, IITA-348, IITA-349, IITA-350, IITA-351, IITA-352, IITA-353, and IITA-354, were moderately resistant against the disease. Screening of cowpea genotypes leads to the identification of new sources of resistance against the disease that can serve as a potential donor in future cowpea improvement programs.

Key words: *Ascochyta blight, Cowpea, Screening, Vigna, Resistant, Susceptible.*

Introduction

The cowpea (*Vigna unguiculata* L. Walp.) has the potential to be an ideal crop for achieving food security in the face of climate change because of its many uses. Ascochyta blight is a serious and economically significant disease caused by *Ascochyta* spp. It can cause devastating losses in yield and quality of the cowpea crop if not properly managed. The primary symptoms of Ascochyta blight typically include the formation of small to medium-sized circular lesions on the leaves, which often exhibit a tan to brown coloration with a characteristic dark brown margin

(Batzer *et al.*, 2022). The lesions can enlarge, their shape may be more angular, their centers may dry out, and stem lesions can also develop, leading to sunken and discolored areas that may result in wilting or dieback (Liu *et al.*, 2016). The sunken, atypically shaped brown dots on the pods that are indicative of pod lesions may cause distortion and result in decreased quality. In severe cases, the disease can impact seeds, causing discolored or sunken lesions (Aysan and Horuz, 2015). To combat Ascochyta blight, integrated disease management practices are essential, and planting disease-resistant material is the best way to devise a sustainable, eco-friendly dis-

ease management program.

Materials and Methods

The current study was conducted during Kharif 2020, 2021, and 2022 in the experimental field of Division of Genetics and Plant Breeding, Faculty of Agriculture, SKUAST Kashmir, Wadura, Sopore, India (latitude 34° 10' N, longitude 74° 30' E). The germplasm was comprised of ten (10) cowpea genotypes obtained from the International Institute of Tropical Agriculture, Ibadan, Nigeria, besides two known susceptible check genotypes, *viz.*, C1 and C2. The genotypes were exposed to the *Ascochyta* blight under field conditions for three consecutive years. Disease scoring was done at the pod development stage, and five plants were randomly selected in each genotype for the purpose. Disease severity was recorded by using a 0 to 9 disease rating scale, where 0 = no visible disease symptoms, 1 = covering 10% leaf area, 2 = 11-20% leaf area, 3 = 21-30% of leaf area affected, 4 = 31-40% of leaf area affected, 5 = 41-50% of leaf area affected, 6 = 51-60% of leaf area affected, 7 = 61-70% of leaf area affected, 8 = 71-80% of leaf area affected, 9 = > 80% of the leaf area necrotic. Disease severity was calculated by using the formula $[\sum(n \times v) / N \times G] \times 100$, where n = the number of diseased leaves in each category, v = the numerical value of the category, N = total number of leaves examined, and G = highest grade value, *i.e.*, 9 in this case. Genotypes were categorized on the basis of disease severity: 0-10% = resistant (R), 10.1-30% = moderately resistant (MR), 30.1-60% = susceptible

(S), >60% = highly susceptible (HS).

Results

The data generated from the evaluation of cowpea germplasm against the *Ascochyta* blight over three consecutive years is presented in Table 1. Disease severity, providing a quantitative measure of the impact of *Ascochyta* blight, revealed that out of ten (10) genotypes during the year 2020, nine genotypes, *viz.*, IITA-345, IITA-346, IITA-348, IITA-349, IITA-350, IITA-351, IITA-352, IITA-353, and IITA-354, having a disease intensity of < 10% were resistant to the disease; IITA-347 was moderately resistant with a disease intensity of 27.3%. During 2021, three genotypes (IITA-345, IITA-346, and IITA-348) had disease intensity of <10% and seven (07) genotypes had disease intensity of 10% to 24.4%. while, during 2022, one genotype, IITA-345, was found to be resistant with a disease intensity of 0%, and the rest of the nine genotypes, *viz.*, IITA-346, IITA-347, IITA-348, IITA-349, IITA-350, IITA-351, IITA-352, IITA-353, and IITA-354, which possess a disease intensity of 10% to 27.1%, were moderately resistant. Resistant genotypes like IITA-345 showed low disease impact (< 0%), while susceptible genotypes like C1 and C2 exhibited higher disease severity (43.2 to 44.8%) during all three years.

The data spans three years to analyze the overall performance and trend of *Ascochyta* blight resistance in various cowpea genotypes. By combining the results from multiple years, we identified consistent patterns, trends, and variations in disease inten-

Table 1. Response of cowpea germplasm to *Ascochyta* blight under field conditions

S. No.	Genotypes	Disease intensity (%)			Disease scoring of 2022	Response on the basis of disease score of 2022
		2020	2021	2022		
1.	C1	43.2	44.2	47.8	5	S
2.	C2	44.8	48.2	43.5	5	S
3.	IITA-345	0	0	0	0	R
4.	IITA-346	2.7	2.8	13.8	2	MR
5.	IITA-347	27.3	23.5	26.7	3	MR
6.	IITA-348	2.7	6.8	27.1	3	MR
7.	IITA-349	4.2	12.5	22.8	3	MR
8.	IITA-350	4.6	18.9	12.1	2	MR
9.	IITA-351	3.8	24.4	14.2	2	MR
10.	IITA-352	2.8	14.3	16.4	2	MR
11.	IITA-353	3.8	16.2	12.1	2	MR
12.	IITA-354	4.6	14.2	16.2	2	MR

sity (D.I.) for each genotype. Out of all the genotypes across all three years, IITA-345 was resistant to the ascochyta blight; IITA-346, IITA-347, IITA-348, IITA-349, IITA-350, IITA-351, IITA-352, IITA-353, and IITA-354 were moderately resistant against the ascochyta blight. Some genotypes, such as IITA-346, IITA-348, IITA-349, and IITA-357, showed an increasing trend in resistance over the years, moving from resistant (R) to moderately resistant (MR). Other genotypes, like IITA-350 and IITA-351, displayed fluctuations in resistance levels, highlighting the dynamic nature of the interaction between cowpea genotypes and Ascochyta blight, while check genotypes like C1 and C2 maintained consistent susceptibility, staying in the Susceptible (S) category across all three years, indicating susceptibility to Ascochyta blight. The disease's intensity further supports its susceptibility category. Some genotypes consistently show very low disease intensity across all three years, indicating resistance to Ascochyta blight. The overall value of the data supports its classification as resistant.

Discussion

Ascochyta blight disease has emerged as a significant disease in cowpea, wherever cow peas are grown. In the current study of germplasm screening, Ascochyta blight severity was found to differ over the years. The data suggests that while some genotypes maintained consistent resistance or susceptibility to Ascochyta blight, others displayed variability over the three-year period. Differential expression of the disease is due to the expression of major genes of QTLs responsible for imparting resistance or susceptibility in particular genotypes. Similar phenomenon has been seen in the relative expression of cold tolerance in chickpea (Asma *et al.*, 2021). The transition of genotypes between resistance categories highlights the importance of continuous monitoring and evaluation for sustainable disease management strategies in cowpea cultivation.

Tadesse *et al.* (2017) discovered that the disease was more common during the flowering stage, with a documented disease incidence of chickpea blight ranging from 0 to 46.6%. The disease appears at every physiological stage, from seedling through maturity (Singh and Sharma, 1998). The management of crops and agricultural output are severely hampered by the presence of Ascochyta blight. Accord-

ing to Rubiales *et al.* (2018), Ascochyta blight resistance screening typically leaves a significant scope for varied disease manifestation under different circumstances. Since the fungus can persist for a long time on agricultural leftovers, seeds, and even soil, it is challenging to properly manage and treat the disease.

Conclusion

The findings of the present study recognize that Ascochyta blight severity varies with cultivar type and also with climatic factors which prevail at a particular place. However, the genotypes that were found resistant in all three years may have broader resistance spectrum, which are governed by multiple genes or quantitative trait loci. Nevertheless, these identified resistant genotypes are novel and will prove valuable genetic resources in future cowpea improvement program wherein breeding programmes can be initiated for incorporation of new resistant genes or major QTLs into commercial but susceptible varieties.

Conflicts of interest: The authors declare that there is no conflict of interest.

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