Screening of common bean (*Phaseolus vulgaris* L.) germplasm against *Colletotrichum lindemuthianum* inciting bean anthracnose

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Abstract
Common bean is the most cultivated grain legume consumed globally. It is enriched in proteins, vitamins, minerals and fiber. Anthracnose disease incited by hemibiotrophic fungi Colletotrichum lindemuthianum is the most destructive disease of common beans. The present study was carried out to evaluate 87 common bean genotypes collected from different locations against C. lindemuthianum. Screening of genotypes for anthracnose resistance aids in the identification of 22 highly resistant genotypes namely PL 1, EC-400397, Hur 137, IC-199277, IC-258273, S 2, EC-400442, KB 4, Utkarsh, Hur 15, IC-260299, PDR 14, VL 125, Amber, Arun, EC-398591, EC-121013, S 6, BR 31, IC-328372, KB 12 and KB 6. These genotypes can act as potential donors of the resistant genes in marker-assisted selection (MAS) programmes for transferring the anthracnose resistance gene(s) into the susceptible genotypes.

Keywords: Screening, *Colletotrichum lindemuthianum*, Anthracnose disease, *Phaseolus vulgaris* L.

Introduction

Common bean (*Phaseolus vulgaris* L.) is an important grain legume consumed globally[6]. It belongs to family fabaceae with 11 pairs of chromosomes and a genome size of 473 Mb[21]. It is a self-pollinated crop. The annual production of common beans is 12 million tonnes worldwide with Brazil being the leading producer. Brazil along with the USA and Mexico are other leading countries producing 5.6 million tonnes of beans globally[8]. In India, area and production under common beans are 9.1 million ha and 3.63 million tonnes respectively[5].

Common beans are grown in Jammu and Kashmir, Himachal Pradesh, Uttar Pradesh, Maharashtra, Andhra Pradesh, Western and Eastern Ghats and North Eastern Plain zone[5]. These are rich in carbohydrates, proteins, vitamins (A, C, folate), fiber and minerals like iron, phosphorous, magnesium, manganese, zinc, copper and calcium and thus, provided valuable micronutrients to more than 300 million people in the tropics[3,4].

Anthracnose caused by *Colletotrichum lindemuthianum* is the most destructive disease of common beans[9]. It is typically spread by contaminated seeds. The disease is more prevalent in temperate and subtropical climates[18]. Moderate temperature with excessive humidity favoured disease development resulting in crop failure[27]. The symptoms of anthracnose appear on aerial parts of the plant such as leaves, stems and pods. The most prominent symptoms are black shrunken lesions with flesh-colored spores that emerge on pods. The lower surface of the leaf, together with the veins, develops brick-red to purple spots.

Lesions on veinlets on the upper surface of leaves may emerge later. The eye-shaped lesion is about 5-7 mm on older stems[28]. Pathogen development is also influenced by the susceptibility of the particular cultivar involved as well as favourable environmental conditions for fungal growth and spread[10]. The pathogen is highly variable with 45 races reported in North- Western Himalayas[2,25]. Crop rotation, seed and foliar fungicides application, clean seeds use and host resistance can all help to prevent the disease. The most cost-effective technique for reducing anthracnose in beans is host resistant[13,15]. The present study is carried out to evaluate common bean genotypes resistant to anthracnose disease under epiphytotic conditions.

Material and Methods

A total of 87 common bean genotypes were collected from various locations in Jammu and Kashmir. Released/ improved genotypes had also been collected from Central Pulse Research Institute, ICAR, Kanpur, National Bureau of Plant Genetic Resources (NBPGR, ICAR), Shimla and Vivekananda Parvatiya Krishi Anusandhan Sansthan (VPKAS-ICAR), Almora (Table 1).

The genotypes were screened for anthracnose resistance with *Colletotrichum lindemuthianum* isolate under epiphytotic conditions. The spore suspension was made by scraping the surface of freshly sporulating culture with a glass slide and adjusting the concentration with a haemocytometer to 1.2×10^6 spores/ ml. Common bean seeds of all the collected germplasm were sowed in potting compost in the greenhouse at 28 ± 3°C under a 16 h light: 8 h dark photoperiod with high humidity sufficient for bean germination.

Primary leaves of 10-day-old plants were inoculated by spraying the lower and upper surfaces of the leaves until run-off with the spore suspension (1.2×10^6 spores/ ml) and maintained in the greenhouse at 22°C under high humidity.

The disease reaction was scored using a 1-9 scale after 17 days[22] (Table 2). The cultivars were then classified into groups based on their PDI values as given in table 3[16] from which the percent disease severity was calculated[24].

Results

87 common bean genotypes were screened for anthracnose resistance under epiphytotic conditions during 2019. The disease severity was assessed using 1-9 scale after 17 days and the percent disease index was calculated. Disease severity varied among genotypes ranging from 1.48 percent to 66.66 percent. Based on percent disease index, the genotypes under study were divided into four reaction groups viz. highly resistant, moderately resistant, moderately susceptible and susceptible.

Table 1
Germplasm collection from different locations

Germplasm	Location
BR 1, BR 2, BR 3, BR 4, BR 5, BR 6, BR 7, BR 8, BR 9, BR 10, BR 15, BR 16, BR 18, BR 22, BR 30, BR 31, BR 36, BR 39	Bhadarwah, Doda, J&K
EC-13097, EC-121013, EC-398527, EC-398565, EC-398586, EC-398591, EC-400397, EC-400433, EC-400442, EC-405220, EC-500250, EC-500305, EC-500308, EC-500374, EC-500507, EC-530898, EC-531076, EC-755305, IC-043562, IC-199277, IC-202274, IC-243198, IC-258273, IC-258276, IC-260299, IC-260312, IC-260336, IC-262837, IC- 265932, IC-274530, IC-328372, IC-361884	NBPGR, Shimla
VL 63, VL 125	VPKAS, Almora
KB 1, KB 4, KB 5, KB 6, KB 7, KB 12, Jawala	Kupwara and Baramula, J&K
PL 1	Pulwama, J&K
S 1, S 2, S 3, S 4, S 5, S 6	Shopian, J&K
P 1, P 2, P 3, P 4, P 5, P 6, P 13, P 14, P 15, P 17, P 22, P 28, P 29, P 33	Poonch, J&K
Amber, PDR 14, Hur 137, Hur 15, Arun, Utkarsh	ICAR, Kanpur

BR= Bhaderwah; EC= Exotic collection; IC=Indigenous collection; VL=VPKAS, Almora; KB= Kupwara and Baramula; PL= Pulwama; S= Shopian; P= Poonch

Table 2
Disease severity scores with the respective symptoms

Score	Symptoms
1	Absence of symptoms
2	Up to 1% of the leaf veins affected, visible only on the lower leaf surface
3	Up to 3% of the leaf veins affected, visible only on the lower leaf surface
4	Up to 1% of the leaf veins affected, visible on both surfaces of the leaves
5	Up to 3% of the leaf veins affected, visible on both surfaces of the leaves
6	Leaf veins affected, visible on both leaf surfaces and the presence of some lesions on stems, branches and petioles
7	Necrotic spots on most of the leaf veins and in a large part of the adjacent mesophyll tissue, which ruptures, as well as the presence of abundant lesions on the stem, branches and petioles
8	Necrotic spots on almost all the leaf veins and very abundant on stem, branches and petioles, leading to ruptures, leaf shedding and reduction of plant growth
9	Most of the plants are dead

Table 3
Classification of cultivars into different categories based on percent disease index (PDI)

PDI (%)	Categories
0	Absolutely resistant (AR)
0.01	Highly resistant (HR)
12.22-33.33	Moderately resistant (MR)
34.44-55.55	Moderately susceptible (MS)
56.66-77.77	Susceptible (S)
78.88-100	Highly susceptible (HS)

Genotypes PL 1, EC-400397, Hur 137, IC-199277, IC-258273, S 2, EC-400442, KB 4, Utkarsh, Hur 15, IC-260299, PDR 14, VL 125, Amber, Arun, EC-398591, EC-121013, S 6, BR 31, IC-328372, KB 12 and KB 6 were highly resistant. Genotypes IC-243198, BR 8, IC-262837, BR 2, IC-361884, BR 5, EC-398565, EC-400433, EC-398586, EC-531076, BR 22, P 6, BR 9, EC-500250, IC-260312, BR 36, EC-530898, S 3, EC-500507, P 28, KB 5, BR 6, VL 63, IC-043562, KB 7, EC-500308, S 5, BR 10, BR 1, KB 9, P 1, IC-202274, EC-13097 and P 4 were moderately resistant.

Genotypes EC-398527, BR 4, P 17, KB 1, EC-500374, BR15, P 29, BR 18, P 15, P 2, EC-755305, P 14, P 33, EC-405220, IC-265932, S 4, EC-500305, S 1, BR 3, P 5, BR 16, IC-274530, BR 30, IC-258276, BR 39, IC-260336 and P 13 were moderately susceptible. Genotypes Jawala, BR 7, P 22 and P 3 were susceptible (Table 4).

Discussion

The use of anthracnose-resistant cultivars is the most successful, efficient and safe approach of managing anthracnose in common beans and it is simple for farmers to implement[12,17,26]. However, there is a breakdown of resistance as plants resistant to one race might be susceptible to other.

This is due to several pathogen races as well as diversity within the same pathogen race[1,7,11,20] and no single resistance gene effective against all races has been identified yet. As a result, the primary purpose of crop breeding programmes is to screen and identify bean genotypes with anthracnose resistance. This contributes in the development of cultivars with broad and durable anthracnose resistance. In this study, an isolate of *C. lindemuthiaum* was used to screen 87 common bean genotypes for anthracnose resistance under epiphytotic conditions.

Table 4
Screening of genotypes for anthracnose resistance

Genotype	Percent disease index	Disease reaction
IC-243198	30.58%	MR
EC-398527	37.03%	MS
BR 8	33.33%	MR
PL 1	10.84%	HR
EC-121013	1.48%	HR
IC-262837	27.77%	MR
BR 2	33.17%	MR
IC-361884	17.45%	MR
BR 5	31.74%	MR
EC-400397	11.11%	HR
Hur 137	7.40%	HR
IC-199277	10.84%	HR
EC-398565	27.77%	MR
IC-258273	8.33%	HR
BR 4	41.66%	MS
EC-400433	13.88%	MR
EC-398586	31.70%	MR
S 2	7.40%	HR
EC-531076	33.33%	MR
EC-400442	8.33%	HR
KB 4	11.11%	HR
P 17	55.55%	MS
KB 1	41.66%	MS
BR 22	21.36%	MR
EC-500374	55.55%	MS
Utkarsh	1.48%	HR
BR 15	38.79%	MS
P 6	32.40%	MR
P 29	41.97%	MS
BR 9	32.71%	MR
BR 18	43.64%	MS
EC-500250	32.40%	MR
P 15	37.03%	MS
P 2	55.55%	MS

IC-260312	22.22%	MR
BR 36	31.74%	MR
EC-755305	37.05%	MS
Hur 15	1.48%	HR
P 14	36.10%	MS
P 33	43.20%	MS
EC-405220	56.23%	MS
IC-265932	39.15%	MS
EC-530898	27.77%	MR
S 3	12.34%	MR
S 4	37.03%	MS
BR 31	10.84%	HR
EC-500305	55.55%	MS
IC-260299	11.11%	HR
EC-500507	30.94%	MR
PDR 14	6.66%	HR
P 22	66.66%	S
BR 7	58.32%	S
P 28	20.05%	MR
Jawala	66.66%	S
VL 125	6.66%	HR
KB 5	20.83%	MR
Amber	1.48%	HR
S 1	37.03%	MS
Arun	5.12%	HR
BR 6	31.74%	MR
EC-398591	11.11%	HR
VL 63	13.07%	MR
IC-043562	24.69%	MR
KB 7	17.35%	MR
EC-500308	16.20%	MR
BR 3	39.68%	MS
IC-328372	9.47%	HR
S 5	26.61%	MR
P 5	39.50%	MS
BR 10	26.61%	MR
BR 16	36.50%	MS
BR 1	25.30%	MR
IC-274530	40.48%	MS
KB 9	26.84%	MR
BR 30	36.55%	MS
IC-258276	55.55%	MS
P 1	33.33%	MR
BR 39	47.00%	MS
IC-260336	39.68%	MS
IC-202274	31.74%	MR
P 13	41.66%	MS
KB 12	6.47%	HR
EC-13097	20.07%	MR
KB 6	1.48%	HR
S 6	6.66%	HR
P 3	66.66%	S
P 4	32.40%	MR

AR: absolutely resistant; HR: highly resistant; MS: moderately resistant, MS: moderately susceptible, HS: highly susceptible and S: susceptible

Twenty-two genotypes were found to be highly resistant including PL 1, EC-400397, Hur 137, IC-199277, IC-258273, S 2, EC-400442, KB 4, Utkarsh, Hur 15, IC-260299, PDR 14, VL 125, Amber, Arun, EC-398591, EC-121013, S 6, BR 31, IC-328372, KB 12 and KB 6. Thirty-four genotypes were moderately resistant including IC-243198, BR 8, IC-262837, BR 2, IC-361884, BR 5, EC-398565, EC-400433, EC-398586, EC-531076, BR 22, P 6, BR 9, EC-500250, IC-260312, BR 36, EC-530898, S 3, EC-500507, P 28, KB 5, BR 6, VL 63, IC-043562, KB 7, EC-500308, S 5, BR 10, BR 1, KB 9, P 1, IC-202274, EC-13097 and P 4. Twenty-seven genotypes were moderately susceptible including EC-398527, BR 4, P 17, KB 1, EC-500374, BR 15, P 29, BR 18, P 15, P 2, EC-755305, P 14, P 33, EC-405220, IC-265932, S 4, EC-500305, S 1, BR 3, P 5, BR 16, IC-274530, BR 30, IC-258276, BR 39, IC-260336 and P 13 and four genotypes namely Jawala, BR 7, P 22 and P 3 were susceptible.

In Ethiopia, 19.4 percent genotypes were found to be resistant to the pathogen's virulent races whereas 16.2 percent were found to be highly susceptible[26]. Three genotypes were found to be moderately resistant, ten genotypes to be moderately susceptible and seven genotypes to be susceptible in another study[16]. Resistance to different races of pathogen in indigenous and exotic accessions was also reported in Himachal Pradesh[19]. G 2333, Widusa, Cornell 49292, TO, Perry Marrow, PI 207262, Mexique 222 and Kaboon, KRC- 5 are some of these. In another study, 10 lines (IC-328537, IC-328538, IC-448888, IC-313294, IC-278723, IC-339645, IC-341862, EC-169813, EC-398530 and EC-500226) were identified[23]. The identified resistant genotypes can act as a potential donor of resistant genes in breeding programmes to develop cultivars with broad and durable resistance to anthracnose.

Conclusion

In the present study, 22 common bean genotypes were found to be highly resistant to anthracnose disease. The benefit of screening resistant varieties enhances the possibility to select for a broad range of anthracnose resistance. It also helps to understand the variability of the common bean anthracnose disease.

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