

Evaluation of the yield and agronomic trait performance of BC2F2 common bean lines at Hawassa, Ethiopia

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Abstract. Ebrahim MS, Bisetegn KB, Tedla YR, Tufa MT. 2024. Evaluation of the yield and agronomic trait performance of BC2F2 common bean lines at Hawassa, Ethiopia. *Asian J Agric* 8: 50-56. The common bean is the most important legume in Ethiopia and is grown mainly for domestic consumption, export and as a source of protein. Farmers in the study area are still producing old varieties; therefore, the production decreases in the area, even though there are suitable environments for common bean production. Bean anthracnose is one of the major constraints that challenged the production of common bean in the study area. To address the above gap, to identify introgressed bean lines for anthracnose resistance with improved agronomic traits that were developed through backcross breeding program using pot experiments under screen house conditions. Twelve common bean genotypes, including eight developed BC2F2 lines, two parental lines, and two cultivars, were used to evaluate agronomic performance. Data on seven quantitative traits and three qualitative traits were collected from each tagged tested material. Analysis of variance revealed a highly significant difference ($p < 0.001$) in the agronomic traits of the BC2F2 line under screen house conditions. As a result, four BC2F2 lines (Plant-3, Plant-5, Plant-9, and Plant 15) exhibited significantly greater differences in the most important agronomic traits than the remaining studied plant materials. In the end, two lines identified to have better agronomic performance (Plant-3 and Plant-15) were selected and promoted for the future to be used for production after verifying in multiple locations for the study and similar agro-ecologies. The results will contribute to an increase in the production of this important crop under farmer conditions. They will significantly benefit and impact Ethiopia's regional and national common bean improvement programs.

Keywords: Better performance, developed lines, old variety, quantitative traits

INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is an autogamous ($2n=2x=22$) diploid legume most commonly grown in East and Central Africa (Gichangi et al. 2012). The common bean is the most important legume in Ethiopia and is grown mainly for domestic consumption and export and as a source of protein (Asfaw et al. 2009; Dejene et al. 2016). It is also used in crop rotation because it binds atmospheric nitrogen. According to FAOSTAT (2019), India, Myanmar, Brazil, the United States, China, Mexico, the United Republic of Tanzania, Uganda, Kenya, and Ethiopia are among the top 10 bean-growing countries globally, with India at the top. The area of the world was 329,824 hectares, with a production of 543,984 tons and a productivity of 1.64 tons/ha (FAOSTAT 2019). In Ethiopia, the acreage of common bean was 140,541.74 hectares, with a production of 242,773.54 tons. The national average was 1.75 tons/ha (CSA 2020). In the SNNPR, the area covered by common beans was 45,424.78 hectares, with a production of 7,095.28 tons and a productivity of 1.7 tons per hectare (CSA 2020).

Bean anthracnose is one of the major constraints on the production of common bean plants in Ethiopia. Developing more disease-resistant varieties is the most important goal of common bean breeding programs in Ethiopia. However,

disease resistance is not the only trait that needs improvement in a breeding program. Other factors, such as yield, plant architecture, and grain appearance, are critical to the success of common bean cultivars (Cunha et al. 2005; Menezes-Júnior et al. 2008; Mendes et al. 2009). Yield is the most important indicator of crop performance, but disease resistance is costly on the plant and thus has commercial significance because it may impede the most important goal of increasing yield (Brown 2002). Genetically diverse plants are critical for future improvements in meeting societal demands for food security under climate change scenarios (Bellucci et al. 2014). Previously, variability between developed common bean lines obtained by marker-assisted backcrossing breeding for different agronomic traits has been reported (Rahman et al. 2002; Tar'an et al. 2002; Rezene et al. 2018; and Okii et al. 2019). Moreover, marker-assisted backcrossing facilitated progeny selection by combining good agronomic traits with resistance loci and testing under screening house conditions.

Farmers in the study area are still producing old varieties; however, the pathogen changes occasionally. As a result, the production decreases in the area, even though there are suitable environments for common bean production. Durable, resistant varieties of too many disease-causing pathogens are receiving increased priority

from farmers in Ethiopia. Again, in most cases, small-scale farmers in Ethiopia have not been using genetically resistant common bean cultivars, and they grow infected seeds. It would be very critical for farmers in the study area to have genetically resistant common bean cultivars. Therefore, identifying varieties that combine resistant loci to anthracnose and good agronomic traits is highly desirable. Even though developing bean varieties with higher disease resistance levels and good agronomic performance is the most important goal of common bean breeders in Ethiopia. However, the development of superior common bean varieties in the study area is few compared to the changing nature of the pathogen. Little, if any, information exists about these lineages that developed in Ethiopia. The results will contribute to an increase in the production of this important crop under farmer conditions. They will have a significant benefit and implication for Ethiopia's regional and national common bean improvement programs. To address the challenges of bean anthracnose in the study area, we have been done an experiment to introgress the Co-1⁴ resistance gene through marker assisted backcrossing experiments. The lines were developed through crossing the resistance lines with the susceptible lines and backcrossed up to two generations to fix the desired alleles. The resistance line selection is in such a way that the developed lines were tested for their marker presence and severity score using three anthracnose races. As a result we have been identified four lines were having the resistance reactions (two of them with marker presence and the remaining two is with marker absence) and developed backcross lines with resistance gene (Ebrahim et al. 2023). However, the agronomic performance thus lines were not studied; since disease resistance is not the only trait that could be improved in resistance breeding program. Even though, developing more disease-resistant varieties is the most important goal of common bean breeding programs in Ethiopia. Therefore, this study was conducted to identify introgressed bean lines for anthracnose resistance with improved agronomic traits.

MATERIALS AND METHODS

Description of study area

The study was conducted in the Molecular Biotech Lab and green house (with average temperature of 29°C and average relative humidity of 65%) at the Southern Agricultural Research Institute (SARI), located 7° 4' N latitude and 38° 31' E longitude and an altitude of 1700 m.a.s.l in Hawassa, Ethiopia during 2019/20 (Figure 1).

Experimental treatments, design and trial management

Eight BC2F2 lines, two parental lines, and two released varieties were grown under greenhouse conditions. A Completely Randomized Design (CRD) with four replications was employed, and the pots were grown in greenhouse conditions (Figure 3). The present study was conducted in the Molecular Biotech Lab and green house (with average temperature of 29°C and average relative humidity of 65%) at the Southern Agricultural Research Institute (SARI). Two seed of each indicated genotypes were planted in plastic pots filled with forest soil, sand and animal manure at ratio of 2:1:1. The trial was put in the screen house until all the desired parameters is collected i.e. up to three and half month starting from date of planting to harvesting.

Data collected

Quantitative traits

Days to emergence (DTE), days to flowering (DTF), days to maturity (DTM), pod per plant (PPP), seed per pod (SPP), seed yield per plant (SYPP) and hundred seed weight (HSW) were recorded on individual tagged plant.

Qualitative traits

The qualitative characteristics of common bean genotypes, such as seed size, seed color, and growth habit, were scored according to the descriptor (based on the IBPGR 1982). These morphological characters were scored through visual observations on an individual base using the descriptor list developed by International Board for Plant Genetic Resources (IBPGR).

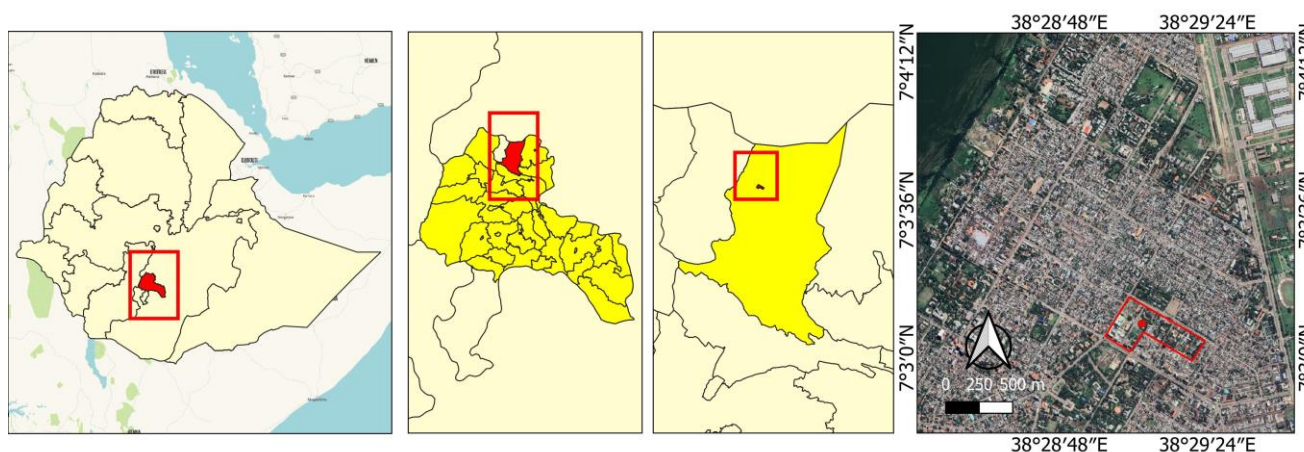


Figure 1. Study area location map in Southern Agricultural Research Institute (SARI), Hawassa, Ethiopia

Statistical analysis

Analysis of variance (ANOVA)

Analysis of Variance (ANOVA) was computed following the procedures for a Completely Randomized Design (CRD) using SAS 9.3. Mean comparisons among treatment means were conducted using the Least Significant Difference (LSD) test at 5% significance. The model used for CRD for evaluating agronomic traits is as follows:

$$X_{ij} = \mu + \alpha_i + \epsilon_{ij},$$

Where:

μ : Grand mean,
 α_i : Treatment effect
 ϵ_{ij} : Random error

RESULTS AND DISCUSSION

Performance of the BC2F2 lines yield and yield related traits

The BC2F2 lines showed significant differences ($p < 0.001$) in all quantitative traits analyzed (Table 1). Thus, the findings demonstrate the relative importance of selecting and promoting superior lines among segregants via future selection to increase the desired traits' yield. The presence of this variation in the backcrossed common bean lines tested might be due to the genetic heterogeneity between developed BC lines. It has been reported that extreme phenotypes between segregates are due to genetic recombination of alleles at multiple loci, epistasis, and reduced genotypic developmental stability (Schwarzbach et al. 2001; Hallauer et al. 2010). Pereira et al. (2013) found significant differences ($P < 0.05$) between developed common bean progenies for all assessed traits.

The average data of the eight selected BC2F2 lines revealed that Plant-12 was an early emergent line, while Plant-8 and Plant-15 were identified as late emergent lines (Table 2). Plant-12 had the lowest number of days to flower, while Plant-15 had the highest (Table 2). Among the BC2F2 lines, Plant-17 was observed to be an early maturing line compared to the recurrent parental line KT-IBM4 and the released varieties Ibbado and Tatu, while Plant-15 was observed to be a late maturing line based on its average performance for this trait (Table 2). Ferreira et al. (2012) reported significant variability among introgressed common bean lines regarding trait days to maturity. Plant-15 had the greatest number of seeds per pod, while Plant-12 had the lowest number of seeds per pod, according to Table 2.

Regarding to number of pods per plant, Plant-15 had the highest number of pods per plant, followed by Plant-5, Plant-17, Plant-2, and Plant-3, whereas Plant-12 had the lowest number of pods per plant (Table 2). It is important to note that plant 9 was identified as having a resistance reaction to the three tested races. Similarly, Mulanya et al. (2014) reported multiple resistance to anthracnose in snap beans. They reported four lines with multiple resistance to three diseases that had better pod yields than did existing

commercial varieties in Kenya, the findings of which support the present findings. Among the developed BC2F2 lines, Plant-15 had the highest seed yield per plant, followed by Plant-5 and Plant-9, while Plant-12 had the lowest seed yield per plant (Table 2). Eventhough, Plant-12 showed better performance in the trait seed yield per plant than the released variety (Ibbado), it does not performed best than the remaining developed lines based on this trait. Interestingly, these two specific lines, which presented higher seed yields per plant, were identified using a master marker as a linkage of *Co1*⁴ resistance loci. Thus, these results suggest that future improvements in selecting unique plants from evolved lines of common beans are crucial (Singh and Ocampo 1997). An equivalent result was reported by Moses (2017), who observed differences between developed lines in terms of anthracnose resistance and seed yield per plant, supporting this claim. Based on the average hundred-seed weight data, the highest hundred-seed weight was recorded for Plant-15, followed by Plant-9, while the lowest hundred-seed weight was recorded for Plant-2, as shown in Table 1. According to Singh and Schwartz (2010), common bean seed weight can range from 15-90 g per 100 seeds. Genotypes are divided into small-seed common beans with 100 seed weight <25 g, medium up to 40 g, and large-seed over 40 g (Singh and Schwartz 2010). Genotypes weighing greater than the seed weight are preferred for common beans because size is considered a quality parameter (Ejigu et al. 2017).

Performance of the BC2F2 lines in terms of qualitative traits

There was a difference between the developed BC2F2 lines regarding seed size, seed color, and growth habit (Table 3). Based on the effect of the BC2F2 lines on seed size, five lines (Plant-3, Plant-5, Plant-8, Plant-9, and Plant-15) were categorized as large-seeded plants. However, two BC2F2 lines (Plant-2, and Plant-17) were categorized as medium-seeded plants (Table 3). Plant-12, was categorized as small seeded similar to the donor parent (Table 3). The variability may be due to the parental lines used, as crosses were made between the large-seeded and the small-seeded lines. Internaturely seeded beans weighing 25 g to 40 g per 100 seeds were used to characterize introgression between the gene pools through breeding programs (Gepts and Bliss 1988), confirming the current evidence. Consistent with the present findings, Musango et al. (2016) also noted that the observed difference between the tested common bean plants could be due to parental breeds between the two groups: Andean and Mesoamerican origin.

Five BC2F2 lines (Plant-3, Plant-5, Plant-8, Plant-9, and Plant-17) with red mottled seeds were identified, whereas three BC2F2 lines (Plant-2, Plant-12, and Plant-15) were identified by light red mottled seeds (Table 3 and Figure 2). The variability observed in these lines may be due to the difference in seed color between the parental lines used. Although bean seed size and color are of particular interest to consumers (Stoilova and Pereira 2013), these dominant properties of the seeds may reflect the preferences of farmers and consumers. Thus, this

discovery highlights the best lines for these specific traits that can be exploited for future common bean breeding in Ethiopia. Differences in seed color have been reported previously, confirming the results of previous studies (Beninger and Hasfied 1999; Musango et al. 2016). Looking at the growth habit of the BC2F2 lines, two lines (Plant-2 and Plant-8) were categorized as “type V”, while

six lines were categorized as “type I” (Table 3). Hence, this variation in growth habits among the developed BC common bean lines may be due to differences in the parental lines used. Similar results were observed when growth habit differences in the studied common bean genotypes were observed (Musango et al. 2016).

Table 1 Mean square values of twelve common bean genotypes evaluated for seven agronomic traits at Hawassa, Southern Ethiopia during 2020

SV	DF	DEM	DTF	DTM	PPP	SPP	SYPP	HSW
Genotypes	11	4.429	2.886	5.369	20.339	0.49	656.869	309.653
Error	36	0.354	0.763	1.645	1.354	0.069	8.062	2.558
P values	-	<0.001**	0.0012**	0.0035**	<0.001**	<0.001**	<0.001**	<0.001**

Note: * represents a highly significant difference, DEM: Days to emergence, DTF: Days to flower, DTM: Days to mature, SPP: Number of seeds per pod, PPP: Number of pods per plant, SYPP: Seed yield per plant in grams and HSW: Hundred-seed weight in grams

Table 2. Summary of twelve common bean genotypes evaluated for yield and agronomic traits at Hawassa, South Ethiopia during the year 2020

Genotype	DTE	DTF	DTM	SPP	PPP	SYPP	HSW	DTE
KTIBMV4	6.5 ^e	38.25 ^{abc}	78.75 ^{cde}	4.0 ^b	9.75 ^{de}	43.75 ^{cd}	41.15 ^c	6.5 ^e
KTRWA77	6 ^e	37.5 ^{bcd}	78.5 ^{de}	4.0 ^b	10.55 ^d	33.00 ^e	20.5 ^g	6 ^e
Plant-2	7.5 ^{dc}	37.50 ^{bcd}	78.25 ^{de}	4.0 ^b	13.00 ^b	45.50 ^c	28.32 ^e	7.5 ^{dc}
Plant-3	8 ^{abc}	37.50 ^{bcd}	78.5 ^{de}	4.0 ^b	12.75 ^b	41.50 ^{cd}	42.12 ^c	8 ^{abc}
Plant-5	8 ^{abc}	37 ^{cd}	80.5 ^{abc}	4.0 ^b	13.75 ^b	59.50 ^b	43.12 ^c	8 ^{abc}
Plant-8	8.75 ^a	38.25 ^{abc}	79.75 ^{abcd}	4.0 ^b	11.00 ^{cd}	39.75 ^d	43.05 ^c	8.75 ^a
Plant-9	6.75 ^{ed}	38.25 ^{abc}	79.75 ^{abcd}	4.0 ^b	12.50 ^{bc}	57.25 ^b	45.47 ^b	6.75 ^{ed}
Plant-12	6 ^e	36.25 ^d	79.75 ^{abcd}	3.5 ^c	8.5 ^e	32.25 ^e	26.02 ^f	6 ^e
Plant-15	8.75 ^a	39.5 ^a	81.25 ^a	4.75 ^a	16.50 ^a	67.00 ^a	51.02 ^a	8.75 ^a
Plant-17	7.75 ^{bc}	37.5 ^{bcd}	77.5 ^e	4.0 ^b	13.25 ^b	43.75 ^{cd}	34.05 ^d	7.75 ^{bc}
Ibbado	8.75 ^a	38.75 ^{ab}	78.75 ^{cde}	3.25 ^c	10.25 ^d	29.75 ^{ef}	42.77 ^c	8.75 ^a
Tatu	8.5 ^{ab}	38.25 ^{abc}	81 ^{ab}	4.0 ^b	9.50 ^{de}	32.25 ^e	35.05 ^d	8.5 ^{ab}
CV (%)	7.82	2.30	1.61	6.65	9.88	6.69	4.0	7.82
LSD (5%)	0.85	1.25	1.83	0.37	1.66	4.07	2.29	0.85

Note: DTE: Days to emergence (No.), DTF: Days to flower (No.), DTM: Days to mature (No.), SPP: Seed per pod (No.), PPP: Pod per plant (No.), SYPP: Seed yield per plant (gram) and HSW: Hundred seed weight (gram)

Table 3. Summary of twelve common bean genotypes evaluated for three qualitative traits at Hawassa, Southern, Ethiopia during the year 2020

Genotype	SC	SZ	GH
KTIBMV4	LRM	LS	I
KTRWA77	R	SS	V
Plant-2	LRM	MS	V
Plant-3	RM	LS	I
Plant-5	RM	LS	I
Plant-8	RM	LS	V
Plant-9	RM	LS	I
Plant-12	LRM	SS	I
Plant-15	LRM	LS	I
Plant-17	RM	MS	I
Ibbado	RM	LS	I
Tatu	DRM	MS	I

Note: SC: Seed colour, SZ: Seed size, GH: Growth habit, LRM: Light red mottled, R: Red only, RM: Red mottled, DRM: Dull red mottled, LS: Large seeded, MS: Medium seeded and SS: Small sized

Correlation of grain yield with other traits

The analysis of the relationship among characters and their association with yield is essential to establish selection criteria (Singh et al. 1990). Therefore, understanding of interrelationships of seed yield and of the magnitudes of phenotypic correlations of seed yield and its components among yield related traits are highly crucial to utilize the existing variability through selection. Phenotypic correlation estimates between the various characters are indicated in Table 4. Seed yield had positive and significant correlation with number of seed per pod, and number of pod per plant (Table 4). These results are in accordance with the findings of Salehi et al. (2010). The finding of Daniel et al. (2015) showed that common bean grain yield was positively and significantly correlated with pod per plant and seeds per pod. Akhshi et al. (2015) also reported a strong positive correlation of seed yield with seed number per plant. However, Daniel et al. (2015) reported a negative and significant correlation of days to harvest maturity with seed yield across locations and over stress regimes.



Figure 2. Sample photo of BC2F2 common bean lines showing seed color variability



Figure 3. Common beans genotypes plants grown in the screen house

Grain yield showed significant and negative correlation with days to flowering and days to maturity (Table 4). Negative correlation was indicated inverse relationship between earliness characters and grain yield that is desirable if stresses such as terminal heat and drought are expected. This negative correlation between grain yield and days to flowering is in harmony with the finding of Daniel et al. (2015).

Disease resistance is not the only trait that must be improved in a breeding program. Other factors, such as yield, plant architecture, and grain appearance, are critical to the success of bean varieties (Cunha et al. 2005; Menezes-Júnior et al. 2008; Mendes et al. 2009). Yield is the single most important indicator of crop performance. However, disease resistance is reportedly costly for the plant and has commercial significance because it may hinder the most important objective of increasing yield (Brown 2002). Liebenberg et al. (2005) reported the successful gene pyramiding of three rust resistance genes, Ur-3+, Ur-5, Ur-11, and other uncharacterized genes in advanced common bean lines. Field testing for agronomic performance of the lines showed that resistance was considerably improved without yield loss.

Previously, variability between developed common bean lines obtained by marker-assisted backcrossing breeding has been reported in terms of traits, flowering

days, maturity, seeds per pod, pods per plant, seed weight (Tar'an et al. 2002) and hundred-seed weight (Rezene et al. 2018), confirming the present study. Additionally, Reddy and Singh (1990) and Rahman et al. (2002) reported the occurrence of intergenerational variation in the trait of backcrossing to pods per plant in common bean lines, suggesting that the current results are confirmed. Several agronomic traits evaluated significantly differed between the developed common bean lines (Okii et al. 2019). Hybrids between the Mesoamerican and Andean gene pools are highly important for plant breeding, where there is often a need to recombine Mesoamerican and Andean traits (Johnson and Gepts 2002). According to Blair et al. (2010), hybridization can result in the emergence of novel genotypes and phenotypes (e.g., resistance to pathogens, nutritional quality, and seed size) that are absent in either parental taxa. Alternatively, hybrid traits predominating over parental phenotypes (transgressive segregation) can lead to evolutionary novelty (Allendorf and Luikart 2007). The selection must consider the growers' and consumers' demands (Ramalho et al. 1998). Therefore, this study considered the three most important qualitative traits (seed size, seed colour and growth type). Therefore, the selected BC2F2 lines can improve agronomic performance because of their red-mottled seed color, large-seeded nature, and type I growth habits.

Table 4. Correlation analysis of grain yield with other traits at Hawassa, Southern Ethiopia in the year 2022

	DTE	DTF	DTM	SPP	PPP	SYPP	HSW
DTE	1	-0.108	-0.180	0.077	0.321*	0.266	0.344*
DTF	-0.108	1	0.329*	-0.325*	-0.474**	-0.647**	-0.121
DTM	-0.180	0.329*	1	-0.251	-0.520**	-0.386**	-0.224
SPP	0.077	-0.325*	-0.251	1	0.545**	0.505**	0.156
PPP	0.321*	-0.474**	-0.520**	0.545**	1	0.758**	0.262
SYPP	0.266	-0.647**	-0.386**	0.505**	0.758**	1	0.154
HSW	0.344*	-0.121	-0.224	0.156	0.262	0.154	1

Note: DTE: Days to emergence (No.), DTF: Days to flower (No.), DTM: Days to mature (No.), SPP: Seed per pod (No.), PPP: Pod per plant (No.), SYPP: Seed yield per plant (gram) and HSW: Hundred seed weight

Generally, a highly significant difference was observed for days to emergence, days to flowering, days to maturity, pod per plant, seed per pod, 100-seed weight, and yield per plant. Regarding the present experiment, genotypic variation in grain yield and yield components (Emishaw 2007) has been reported for common beans. Data for the number of pods per plant, seeds per pod, seed yield, and hundred seed weight showed highly significant ($P < 0.01$) differences among varieties. The current variations in yield components among varieties consent with previous reports (Daniel et al. 2014). In line with the findings (Shahid 2013; Fahad et al. 2014), it was reported that significant variability was observed in days to flowering, days to maturity, pods per plant, seed yield per pod, hundred seed weight, and yield. This study followed the works of Zelalem (2014) regarding qualitative traits of the tested genotypes showing differences in seed size, color, and growth habit.

In conclusion, the analysis of variance results revealed highly significant differences ($p < 0.001$) among the BC2F2 lines for all the quantitative traits considered. Finally, four BC2F2 lines (Plant-3, Plant-5, Plant-9 and Plant-15) were identified as better for most of the agronomic traits studied than were their parental lines and the two released common bean varieties based on the trait days to emergence, flowering, maturity, number of seed per pod, number of pod per plant, seed yield per plant and hundred seed weight. Therefore, based on these results, the two lines that exhibited better agronomic performance and having Co-1⁴ anthracnose R-gene background (Plant-3 and Plant-15) should be improved and promoted as potential parental lines for the next crossing.

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