

Performance Evaluation of Common bean (*Phaseolus vulgaris* L.) Genotypes at Areka, Southern Ethiopia

Research Article

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Abstract

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another for certain traits of interest under consideration that could be attributed to a number of factors. Understanding these variability, heritability and association between grain yield and other agronomic traits is necessary in plant breeding in order to select individual plant from population. In this context, a field experiment was conducted during 2019/20 cropping season at Areka Agricultural Research Center in southern Ethiopia with objective of evaluating common bean genotypes for their genetic variability and agronomic traits. Treatments used in this study were sixteen common bean genotypes (Awassa Dume, Nasir, Ibado, SER 119, SER 125, SER 26, Dme, Tatu, Remeda, Red Wolaita, DAB 277, Fot New Belge 58, Waju, DAB 96, Befort 15 and SER 12) and were laid out in a randomized complete block design (RCBD) with three replications. Common genotypes exhibited considerable variations for agronomic traits measured. Analysis of variance showed that genotypes Fort New Belge, Nasir, Remada, Red wolaita, and Waju took relatively longer days to flowering and physiological maturity whereas genotypes Awassa Dume, Ibado, SER119, SER26, Deme, Tatu, DAB 277 and DAB 96 exhibited shorter days to flowering and physiological maturity. Biomass yield was greatest for genotype SER 12 and lowest for Ibado whereas grain yield was highest for genotype SER 26 and the lowest grain yield was seen for genotype Ibado. Higher phenotypic variance was observed for plant height and leaf area while genetic variance was higher for plant height and TSW. Phenotypic coefficient of variation (PCV) was higher for stem diameter, internodes length, leaf area, LAI, biological yield, pods per plant and TSW. Days to flowering and pod length exhibited high H₂ estimates. In this context of plant breeding, traits that exhibited higher GCV, H₂ and GA would be useful as a base for selection of desirable traits under consideration. Therefore, selection for high mean values of biomass yield and harvest index could be considered as the simultaneous selection of genotypes for high gain yield.

Introduction

Common bean (*Phaseolus vulgaris* L.) belongs to the member of order *Rosales*, family *Leguminosae*, subfamily *Papilionoideae*, tribe *Phaseoleae* [6]. The crop is grouped as determinate or indeterminate based on the nature of growth habits which is strongly influenced by its growing environment [15]. Common bean is a highly polymorphic species showing considerable variations in growth nature, vegetative characters, color of flowers and seeds, size and shape of seeds and pods [19]. Its flowers perfect possess both male and female organs on the same flower where the crop is self-fertilized with pollination coinciding with the time of flower opening. Flowering in cultivars of determinate growth habit is occurring within 5-6 days whereas indeterminate types have an extended period of time usually 15-30 days [15].

Common bean is one of the most important food grain legumes in eastern and southern Africa, providing food for more than 100 million people [3]. It contains considerable amount of protein being high in lysine and a good source of energy making complement staple in the diet [22]. It is the second most important legume crop in Africa next to faba bean [5]. It is also the third most important source of calories for lower income African households after cassava and maize [5, 3]. In Ethiopia, common bean is the most important legume as an export commodity [9]. It is predominantly cultivated for cash in the central rift valley, but in other parts it is a major staple food supplementing the protein source for the poor farmers who cannot afford to buy expensive meat [11]. Common bean is produced in almost all regions of the country, particularly more concentrations in Oromiya and Southern regions which account for about 75% of total national pro-

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duction whereas the remaining 25% comes from Afar, Amhara, Tigray, Somali, Gambella and Benishangul-Gumuz regions [21]. Since common bean is grown in most parts of Ethiopia with a wide range of variation in altitude, rainfall, temperature, agricultural system and socio-economic factors, it is essential to assess the pattern of character variations among and between accessions to resolve the problems in different regions and adaptation zones. Hence, this study was initiated with objective of assessing the variability of common bean genotypes with respect to important quantitative and qualitative traits and their association of yield and related traits.

Materials and Methods

Experimental Site

Field experiment was conducted during 2019 cropping season at Areka Agricultural Research Center experimental field in southern Ethiopia. An approximate geographical coordinates of the site is 7°4'24' N latitude and 37°41'30' E longitude with an altitude of 1790 meters above sea level. The site is situated in the warm sub-humid lowlands (SH2) major agro ecology, which is tepid to cool-sub humid mid highlands. The average annual rainfall of the study area was 1520 mm, which occurs in two seasons in the year. The first short rain season is belg, which is from February to May and second main rainy season mehir which occurs from June to October. The average maximum and minimum temperature of Areka area are 25.4 and 13.4°C, respectively. Soil type of experimental site is classified as pyroclastic origin [1]. The major crops cultivated near the experimental site include common bean, maize, root and tuber crops.

Treatments and Experimental Design

Treatments used in this study were ten sesame varieties (Awassa Dume, Nasir, Ibadu, SER 119, SER 125, SER 26, Dme, Tatu, Remeda, Red Wolaita, DAB 277, Fot New Belge 58, Waju, DAB 96, Befort 15 and SER 12). The treatments were laid out in a randomized complete block design (RCBD) with three replications. Plot size was 2 m wide and 2.4 m long with gross area of 4.8 m². Seeds were hand planted by placing two seeds per hill and thinned after emergence in order to maintain the proposed plant density per plot. Inter and intra row spacing was 40 and 10 cm, respectively. Experimental field was ploughed, pulverized and leveled in order to get smooth seedbed. The recommend NPS fertilizer was applied at planting at rate of 117 kg/ha. Urea was used as N source and applied at rate 50 kg/ha at planting taking into consideration the N content in NPS fertilizer (14). All crop management practices such as cultivation, weeding etc., carried out as desired during crop growing period.

Data Collection and Measurements

Agronomic parameters recorded were days to flowering, days to physiological maturity, pod length, plant height, stem diameter, internode length, leaf area, leaf area index (LAI), number of pods per plant, seeds per pod, thousand seed weight (TSW), biomass, grain yield and harvest indexes (HI). Days to flowering was recorded as the number of days from planting to 50% of the plants exhibit flowering per plot. Days to physiological maturity was recorded when 50% of plants in the plot lose green color of

pod. Pod length, plant height, stem diameter, internode length, leaf area, LAI, number of pods per plant and seeds per pod were taken from five randomly selected plants per plot. Thousand seed weight (TSW) was measured by counting 250 representative samples from each plot and weighed with sensitive balance after adjusting moisture content at 10%. Grain yield was harvested from central rows by avoiding border effects and converted to kg/ha after adjusting moisture content at 10%. Biomass was determined as the sum of grain yield and straw weighed. Harvest index (HI) is the ratio of grain to the total biomass and estimated as:

$$HI = \text{Grain yield} / \text{Biomass yield}$$

Data were subjected to analysis of variance using the general linear model SAS version 9.1 (23). Treatments means were compared using the least significant difference (LSD) at 5% probability level. Genetic components were estimated in order to identify and ascertain the genetic variability among the genotypes and the extents of environmental effect on various characters. Variance components due to phenotype, genotype, the environment were calculated by adopting the following formula suggested by Burton and De vance (1953) [4]

$$\text{Genotypic variance } (\sigma^2g) = \frac{MSg - MSe}{r}$$

$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + \sigma^2e$$

$$\text{Environmental variance } (\sigma^2e) = \text{Error mean square}$$

Where,

$$MSg = \text{Mean squares due to genotypes}$$

$$MSe = \text{mean squares due to error}$$

$$r = \text{Number of replications}$$

According to Sigh, (2001) (29) the phenotypic and genotypic coefficients of variances were expressed as:

$$PCV = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Population mean for trait}} \text{ or } PCV = \frac{\sigma^2P}{X} \times 100$$

Where PCV = phenotypic coefficient of variation

$$GCV = \frac{\sqrt{\text{Genotypic variance}}}{\text{Population mean for trait}} \text{ or } GCV = \frac{\sigma^2g}{x} \times 100$$

Where GCV = Genotypic coefficient of variation

$$x = \text{the grand mean of a character.}$$

Heritability in broad sense was calculated for each trait by using the formula (2)

$$H2 (\%) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where:- H = Heritability in broad sense

σ^2g = Genotypic variance
 σ^2p = Phenotypic variance

Genetic advance (GA) under selection assuming the selection intensity of 5% was calculated as proposed by Johnson et al. (1988) (17) as follows.

$$GA = K \sqrt{\sigma^2p} \frac{\sigma^2g}{\sigma^2p} = K.H^* \sqrt{\sigma^2p}$$

Where: GA = Expected genetic advance
 K = The selection differential (K= 2.056 at 5% selection intensity)

Genetic advance as percent of mean was calculated to compare the extent of predicted advances of different traits under selection, using the formula given by Falconer and Mackey, (1996) [13]:

$GAM = GA/x \times 100$
 GAM = Genetic advance as percent of mean
 GA = Genetic advance under selection
 X = Mean value of a trait

Results and Discussion

Phenological Parameters

The data of phenological traits of genotypes is presented in Table 1. Analysis of variance showed that genotypes were significantly differed for days to flowering and physiological maturity. In general days to flowering and physiological maturity for common bean genotypes were ranged from 40.0 to 47.7 and 78.7 to 88.3, respectively. The longest days to flowering (47.7) and physiological maturity (88.3) were recorded for genotype Befort 15. The

shortest days to flowering (40.0) and physiological maturity was seen for genotype SER 125. As this investigation indicated that genotypes Fort New Belge, Nasir, Remada, Red Wolaita and Waju took relatively longer days to flowering and physiological maturity. Conversely, genotypes Awassa Dume, Ibado, SER119, SER26, Deme, Tatu, DAB 277 and DAB 96 exhibited relatively shorter days to flowering and physiological maturity. The difference of 7.70 and 10.00 days was observed between the longest and shortest days to flowering and maturity, respectively. This is an indication that there was a wide range of variability among genotypes for days to flowering and maturity. Similar findings were reported by Kassaye (2006) [18], Shahid and Kamaluddin (2013) [26] and Fahad et al.(2014) [12] that significant difference was observed for days to 50% flowering and physiological maturity in common bean genotypes.

Growth Parameters

The data of growth traits of genotypes is presented in Table 2. Analysis of variance indicated that genotypes were significantly differed for growth traits. Pod length ranged from 8.77 cm for Befort 15 to 12.10 cm for Deme whereas plant height ranged from shortest (51.00 cm) for Tatu and tallest height (104.00 cm) for Red Wolaita. Similarly, stem diameter ranged from 3.33 mm to 5.90 mm with greatest for genotype SER 12 and the least for SER125. In line with this, LA and LAI were varied from 35.00 to 71.00 cm² and 1.28 to 2.08, respectively. Both parameters were greatest for genotype Deme and smallest for genotype Waji. As this finding clearly indicated that common bean genotypes exhibited greater variations for growth parameters attributed to their inherent differences. Similar findings were reported by Scully et al. (1991) [24] and Kassaye (2006) [18] that significant difference was observed for plant height, pod length, stem diameter and leaf area in common bean genotypes. In contrast,

Table 1. Mean performance of genotypes for days to flowering and physiological maturity.

Genotype	Days to flowering	Days maturity
Awassa Dume	42.0cd	85.3a-c
Nasir	43.0bc	84.3a-d
Ibado	42.0cd	81.7b-d
SER 119	41.0cd	80.7cd
SER 125	40.0d	78.7d
SER 26	41.7cd	86.0a-c
Deme	41.3cd	83.3a-d
Tatu	41.0cd	83.0a-d
Remada	43.0bc	82.3a-d
Red Wolaita	42.7bc	81.0cd
DAB 277	41.7cd	80.3cd
Fort New Belge	44.3b	87.7ab
Waju	43.0bc	88.0a
DAB 96	42.0cd	85.0a-c
Befort 15	47.7a	88.3a
SER 12	47.0a	85.7a-c
LSD	2.1	6
CV (%)	2.9	4.4

Mean followed by different letters within columns are significantly different at 5% probability level

common bean genotypes did not show significant differences on internode length (Table 2).

Yield Components and Yield

Data of yield components and yield for genotypes are depicted in Table 3. Analysis of variance revealed that genotypes of common bean were significantly differed for number of pods per and TSW. The number of pods per plant was varied from 10.00 to 22.67.

The highest number of pods per plant (22.67) was recorded for genotype Nasir and the lowest mean number of pods per plant (10.00) was seen for genotype Deme. Thousand seed weight was ranged from 198 to 475 g where the highest TSW (475 g) was achieved from genotype Deme and the lowest TSW (198 g) was obtained from Red Wolaita. Conversely, number of seeds per pod for genotypes was not significant (Table 3). In line with this, significant differences were detected on biomass and grain yield in response to common bean genotypes (Table 3). Biomass as

Table 2. Mean performance of genotypes of common bean for growth traits.

Genotype	Pod length (cm)	Plant height (cm)	Stem diameter (mm)	Internode length (cm)	Leaf area (cm ²)	LAI
Awassa Dume	9.22gh	74.67c-e	3.67c	3.67	48.33b-d	1.61bc
Nasir	10.33ef	66.33de	3.80c	4.67	53.67bc	1.77a-c
Ibado	11.80bc	69.67de	5.33ab	4.67	53.67bc	1.58b-d
SER 119	9.57f-h	78.00b-d	3.47c	4	52.33bc	1.49b-d
SER 125	9.00gh	79.33b-d	3.33c	4.33	52.33bc	1.42b-d
SER 26	9.57f-h	99.67ab	3.37c	3.33	41.67cd	1.34cd
Deme	12.10a	95.00a-c	4.00bc	5	71.00a	2.08a
Tatu	10.23ef	51.00e	3.57c	3.67	63.00ab	1.85ab
Remada	11.33cd	99.33ab	4.33bc	4	51.00b-d	1.49b-d
Red Wolaita	9.90e-g	104.00a	3.80c	4.67	49.67b-d	1.54b-d
DAB 277	11.43cd	83.67a-d	3.77c	5.33	60.33ab	1.76a-c
Fort New Belge	12.57ab	72.67c-e	3.57c	4.67	53.67bc	1.46b-d
Waju	9.77fg	94.33a-c	3.57c	4.33	35.00d	1.45d
DAB 96	10.70de	100.67ab	4.67a-c	4	47.00b-d	1.28b-d
Befort 15	8.77h	84.67a-d	3.87c	2.67	48.33b-d	1.42b-d
SER 12	9.53f-h	102.00ab	5.90a	5	53.67bc	1.42cd
LSD	0.92	24.36	1.33	NS	16.34	0.45
CV (%)	5.2	17.3	19.9	22.2	17.8	17.7

Mean followed by different letters within columns are significantly different at 5% probability level, NS= not significant

Table 3. Mean performance of genotypes of common bean for yield components and yield.

Genotype	Pods per plant	Seeds	TSW	Biomass	Grain yield	HI
		per pod	(g)	(kg/ha)	(kg/ha)	
Awassa Dume	21.67a	5	220jk	6365c-e	3524b-d	0.55a-e
Nasir	22.67a	5.33	199k	6362c-e	3264cd	0.49b-f
Ibado	12.33bc	5.33	439b	5370e	3078d	0.58a-c
SER 119	12.33bc	5.33	257h	8124bc	3662bc	0.49c-f
SER 125	10.67bc	5	232ij	6654b-e	3460b-d	0.52b-e
SER 26	16.00a-c	5.43	251hi	7546b-d	4308a	0.61ab
Deme	10.00c	5.33	475a	7094b-e	3125cd	0.45d-f
Tatu	12.67bc	4.33	299ef	5741de	3232cd	0.55a-e
Remada	18.00ab	4.67	375c	6296c-e	3194cd	0.51b-f
Red Wolaita	11.33bc	5.33	198k	8472b	3466b-d	0.39f
DAB 277	11.00bc	4.67	319de	5671de	3009d	0.52b-e
Fort New Belge	11.67bc	5.33	282fg	6367c-e	3229cd	0.52b-e
Waju	18.33ab	4.67	281fg	5926de	3200cd	0.56a-d
DAB 96	12.67bc	4.33	341d	5463de	3492b-d	0.66a
Befort 15	20.67a	5	265gh	6342c-e	3472b-d	0.54a-e
SER 12	17.47a-c	5.33	249hi	10718a	3997ab	0.44ef
LSD	7.99	NS	22	2095	556	0.11
CV (%)	31.9	15.6	4.71	18.52	9.76	14.15

Mean followed by different letters within columns are significantly different at 5% probability level, NS= not significant

affected by genotypes ranged from 5370 kg/ha to 10718 kg/ha. The greatest biomass (10718 kg/ha) was recorded for genotype SER 12 recorded and the lowest (5370 kg/ha) was for Ibado. Indeed, the biomass difference of 5348 kg/ha achieved between the highest and the lowest genotypes. On the other hand, grain yield for genotypes varied from 3078 kg/ha to 4308 kg/ha. The highest grain yield (4308 kg/ha) was obtained from genotype SER 26 and the lowest (3078 kg/ha) from genotype Ibado. Harvest index (HI) is the physiological efficiency and ability of a crop for converting the total dry matter into economic yield [27]. It ranged from 0.39 to 0.66 with the highest HI (0.66) for genotype DAB96 and the lowest HI (0.39) for Red Wolaita. This finding clearly indicated that common bean genotypes exhibited greater variations for yield and yield component parameters attributed to their genotypic variability. Similar findings were reported by Scully et al. (1991) [24] and Legesse et al. (2006) [21] that significant difference was observed for biomass, grain yield and TSW in common bean genotypes. Moreover, Emishaw (2007) [10] and Daniel et al. (2014) [8] reported the existence of genotypic variation in grain yield and yield components of common bean genotypes.

Variance Components

Phenotypic and Genotypic Variations: The data for phenotypic (σ_p) and genotypic (σ_g) coefficient of variability for genotypes are depicted in (Table 4). Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population under consideration (4 and 32). The phenotypic variance of common bean genotypes varied from (0.008) for HI to (125.11) for leaf area. Higher phenotypic variance (≥ 100) was observed for plant height and leaf area. In line with this, higher magnitude of difference between genotypic and environmental variance was observed for the characters of plant height and leaf area. This implies greater influence of environmental factors for the phenotypic expression of these characters [4; 8]. Relatively medium phenotypic variance (50-100) was seen for TSW. Lower phenotypic variance was recorded for days to flowering, days to maturity, pod length, stem diameter, inter node length, LAI, pod per plant, seeds per pod, biological mass, grain yield and HI. On

the other hand, genotypic variance ranged from 0.003 to 167.75 with the higher genotypic variance for plant height only. Lower genotypic variance (σ_g) was observed for days to flowering, days to maturity, pod length, stem diameter, internodes length, leaf area, LAI, pod per plant, seeds per pod, biomass, grain yield, TSW and HI. Similar finding was reported by Singh et al. (1994) [28] that genotypic variance (σ_g) was different with respect to different agronomic traits for different common bean genotypes. This probably indicated that higher magnitude of difference between genotypic and environmental variance was observed for the characters plant height, leaf area, pod per plant and days to maturity. Thus, it was an indication that greater influence of genetic rather than environmental factors for the phenotypic expression of those characters like days to flowering, pod length and TSW.

In general phenotypic coefficient of variation (PCV) varied from (4.99) for days to maturity to (38.24) for pod per plant (Table 4). According to Sivasubramanian and Madhavamenon (1973) [31] PCV grouped as high if PCV > 20%, moderate if PCV is 10-20% and low if PCV is below 10%. Based on this grouping, traits plant height, stem diameter, internodes length, leaf area, LAI, biological yield, pods per plant, and TSW had higher PCV. Conversely, pod length seeds per pod, grain yield and HI exhibited moderate PCV whereas days to flowering and days to maturity showed lower PCV with PCV value below 10%. This reflected the pronounced influence of environmental factors for the expression of the characters. This finding is in agreement with the result of Kasaye (2006) that reported higher PCV for plant height, number of nodes on main stem, pods per plant, internode length and TSW. Moreover, Kumar et al. (2009) (20) was also reported moderate PCV for grain yield, HI and tillers per plant for wheat cultivars. In line with this, genotypic coefficient variance (GCV) varied from 1.67 to 27.38% (Table 4). The highest GCV (27.38) was recorded for TSW while the lowest GCV (1.67) for seed per pod. As this investigation indicated that higher GCV (> 20%) was observed for pod per plant and TSW. whereas moderate GCV (10-20%) was recorded for plant height, pod length, stem diameter, leaf area, biomass and HI. On the other hand, lower GCV (< 10%) was seen for days to flowering, days to maturity; inter node length,

Table 4. Phenotypic and genotypic coefficient of variability, heritability and genetic advance for genotypes.

Trait	σ_p	σ_g	σ_e	PCV	GCV	H ² (%)	GA(%)
Days to flowering	5.32	3.7	1.16	5.4	4.5	69.55	7.72
Days to maturity	17.53	4.15	13.38	4.99	2.43	23.67	14.14
Plant height	381	167.75	213.36	23.05	15.2	44.02	20.9
Pod length	1.86	1.55	0.31	13.07	11.94	83.33	22.45
Stem diameter	0.98	0.31	0.64	24.31	13.88	32.63	16.34
Inter node length	1.07	0.18	0.89	24.33	9.98	16.82	9.66
Leaf area	125.11	39.09	86.02	21.43	11.98	16.82	13.78
LAI	0.1	0.02	0.08	20.4	9.12	20	26.58
Pod per plant	33.51	10.55	22.98	38.24	21.68	31.48	25.65
Seed per pod	0.63	0.01	0.62	15.62	1.67	1.59	0.51
Biological mass	0.25	0.11	0.13	25.13	16.67	44	45.32
Grain yield	0.03	0.01	0.02	17.49	10	33.33	11.89
TSW	62.07	36.58	25.26	27.89	21.48	59.3	20.15
Harvest index	0.008	0.003	0.005	17.2	10.53	37.5	6.91

LAI, seed per pod and grain yield. Similar findings were reported by Sivasubramanian and Madhavamenon (1973) [31] and Singh et al. (1999) [30].

Heritability and Genetic Advance: Heritability in broad sense and genetic advance estimate for characters under study are shown in Table 4. In general heritability in broad sense (H^2) ranged from 1.59% for seed per pod which was the lowest to 83.33% for pod length which was the highest value. Johnson et al. (1955) (16) classified heritability estimates as low (< 30%), moderate (30-60%) and high (> 60%). Based on this classification, days to flowering and pod length exhibited high H^2 estimates. This result revealed that environment has low influence for the expression of the characters which suggests direct selection using these characters as major contributors of yield components to improve yield of the study area [25]. Thus, selection could be effective in genotypes for these traits and the possibility of improving common bean grain yield through direct selection for grain yield related traits. Relatively moderate H^2 was recorded for traits plant height, stem diameter, pod per plant, biomass, grain yield, TSW and HI which may be occurred due to influence of the environment on the polygenic nature of these traits. It was observed that heritability (H^2) was low for traits days to maturity, inter nod length, leaf area, LAI and, seed per pod. Low heritability that occurred for these traits limits the possibility of including the traits in order to select desirable genotypes. This may be due to the higher influence of environment for the expression of phenotypic variation than genotypic variation. Singh (2001) [29] and Degewione et al. (2013) [7] were also reported high level of heritability for days to flowering and grain yield in wheat. In line with this, genetic advance as a percent mean was ranged from 0.51% for seed per pod to 45.32% for biomass (Table 4). As suggested by (31), genetic advance as percent of mean was classified as low (<10%), moderate (10-20%) and high (>20%). Based on this classification, traits like plant height, pod length, LAI, biomass yield, pods per plant and TSW exhibited high genetic advance. Traits days to maturity, stem diameter, leaf area and grain yield attained moderate genetic advance. In contrast, days to flowering, internodes length, seed per pod and HI had low genetic advance. Pod length exhibited high heritability coupled high genetic advance. Moreover, traits like plant height, pod per plant, biological mass and TSW showed moderate heritability coupled high genetic advance. Hence, these traits should be given top priority during selection breeding in common bean because they are the major portion of genetic variation attributable to additive gene action and selection may be effective in early generations for these traits. On the other hand, stem diameter and grain yield associated with moderate heritability with moderate genetic advance. Moderate heritability accompanied with moderate genetic advance as percent of mean was recorded by stem diameter and grain yield. Additive and non-additive gene actions are involved in the expression of these traits [31].

Conclusion

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another for certain characters of interest under consideration which could arise due to a number of factors. Understanding these variability, heritability and association between grain yield and other agronomic traits is necessary in plant breeding, especially for

the individual plant selection. Analysis of variance revealed that genotypes of common bean significantly differed for yield components and yield. Thus, testing of common bean genotypes is among the best technologies to improve productivity and for specific area recommendation. Results of this experiment showed that genotype SER 126 gave the highest grain yield. However, the experiment should be repeated across locations and years for a wide range of recommendation.

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