

Research Article

Performance Evaluation of Common Bean (*Phaseolus vulgaris* L.) Genotypes for Yield and Related Traits at Areka, Southern Ethiopia

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Common bean is a source of dietary protein and the second most important legume crop in Africa next to faba bean. In Ethiopia common bean is the most important legume as the source of protein and export commodity. Hence, development of commercial varieties is one of the major tasks to meet increasing demand of the stake holders. To this effect, understanding the genetic variability, heritability and association between grain yield and other agronomic traits is necessary for effective plant breeding program. In this context, a field experiment was conducted during 2016/2017 cropping season at Areka Agricultural Research Center in southern Ethiopia with the objective of evaluating common bean genotypes for yield and related traits and also estimate the variability present among the genotypes. Treatments consisted of thirty three common bean genotypes were laid out in a randomized complete block design (RCBD) with three replications. Common bean genotypes exhibited considerable variations for agronomic traits and grain yield. Majority of the traits; plant height, number of nodes, internode length, leaf area, LAI, biological yield, pods per plant, HI and HSW had higher PCV. Genotypic coefficient of variance (GCV) varied from 1.88% to 37.72% with the highest GCV recorded for HSW. Heritability in broad sense (H^2) ranged from 0.52% to 95.33% with the highest value observed for HSW. The present study revealed significant variation among genotypes for traits considered except few insignificant traits. In addition, almost all the genotypes were well adapted to the study area and hence, the high yielding genotypes could be directly used as seed sources for production of common bean and some of the genotypes with best diseases resistance reaction, and with high heritability can possibly be used in common bean improvement program.

1. Introduction

Common bean is a source of dietary protein and the second most important legume crop in Africa next to faba bean [1]. It is the third most important source of calories for lower income African households after cassava and maize [1, 2]. In Ethiopia common bean is the most important legume as the source of protein and export commodity [3]. Common bean contains considerable amount of protein being high in lysine and a good source of energy making it a good complement staple in the diet [4, 5]. 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 [6].

Since common bean is cultivated in most parts of Ethiopia with a wide range of variation in altitude, rainfall, temperature, cropping 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. Assessing diversity in these germplasm introductions can possibly enable to identify elite genotypes with the greatest novelty and thus are most suitable for rescue or incorporation into crop improvement programs. In plant breeding, diversity can be assessed in different ways [7]. Plant breeding is essentially selection among the variables. Thus, an insight into the magnitude of variability present in a crop species is important as it allows effective selection [8]. Indeed, in selection for yield, more emphasis has to be given on the

attributes with low environmental variability. Classical methods of estimating diversity among groups of plants have relied chiefly upon morphological characters, which still play a central role in the analysis of genetic variability in crop species and their relatives [9]. Thus, this study was initiated with the objectives of estimating the genetic variability of Ethiopian common bean commercial cultivars and promising genotypes as well as to evaluate their performance for economically important quantitative and qualitative traits.

2. Materials and Methods

A field experiment was conducted during 2016/2017 cropping season at Areka Agricultural Research Center in southern Ethiopia. An approximate geographical coordinates of the site is 7°41' N latitude and 37°41' E longitude with an altitude of 1790 meters above sea level. Soil type of experimental site is classified as pyroclastic origin [10]. The mean annual rainfall is 1460 mm with a bimodal pattern which extends from March to September with the peak months from April to September. The mean minimum and maximum temperatures of the area are 15 and 26°C, respectively.

2.1. Treatments and Experimental Design. Treatments consisted in twenty two varieties and eleven advanced lines of common bean making a total of 33 genotypes (SEC 20, SMC 22, SMC 21, SEC 23, ALB 204, Waji, Brazil 1, SAB 735, Awash Melka, Awash 2, Melkadima, SER 125, Red Wolaita, Remeda, Nasir, SER 119, Duristu, Dimtu, Awassa Dume, Ibado, Goberasha, Roba, Brazil 2, Awash1, Deme, SAB 632, Tatu, ALB 179, ALB 209, ALB 61, ALB 25, NVA 682, NVA317) were used in the trial. The treatments were laid out in a randomized complete block design (RCBD) with three replications. The blocks were folded in order to reduce field variability. Each plot was 2.4 m wide and 2 m long with growth 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 in each plot. The 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 recommended NPS fertilizer was applied at planting time at a rate of 117 kg/ha. Urea was used as N source and applied at rate of 41 kg/ha at planting taking into consideration the N content in NPS fertilizer. All crop management practices such as cultivation, weeding etc., carried out as desired during crop growing period.

2.2. Data Collection and Measurements. Plant parameters recorded were days to flowering, days to maturity, plant height, pod length, stem diameter, internode length, leaf area index (LAI), number of pods per plant, seeds per pod, grain yield, biomass yield, thousand seed weight (TSW) and harvest index (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. Plant height, stem diameter, internode length, number of pods per plant and seeds per pod were taken from five randomly selected

plants per plot. Leaf area per plant was measured by taking five plants from middle rows after initiation of flowering by using ruler/meter and calculated by using methods adopted in Areka research center and the resulting value was multiplied by correction factor 0.733 [11]. Leaf area index (LAI) was calculated as the ratio of total leaf area per ten plants (cm²) per area of land occupied by the plants. 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 straw weighed and total grain yield. Harvest index (HI) is the ratio of grain to the total biomass and estimated as:

$$HI = \frac{\text{grain yield}}{\text{biological yield}} \quad (1)$$

The estimation of genetic parameters were done to identify and ascertain the genetic variability among the genotypes and to determine the extents of environmental effect on various characters. Variance components due to phenotype (σ_p^2), genotype (σ_g^2), the environment (σ_e^2) were calculated by adopting the following formula suggested by Burton and DeVence [12]:

$$\text{Genotypic variance } (\delta^2 g) = \frac{MSg - Mse}{r} \quad (2)$$

$$\text{Phenotypic variance } (\delta^2 p) = \delta^2 g + \delta^2 e \quad (3)$$

$$\text{Environmental Variance } (\delta^2 e) = \text{error mean square} \quad (4)$$

where, MSg= mean square due to genotypes, MSe= mean square due to error, r= number of replication.

Phenotypic and genotypic coefficients of variances were calculated according to Singh [13] as:

$$PCV = \frac{\sqrt{\text{phenotypic variance}}}{\text{population mean for trait}} \text{ or } PCV = \frac{\sigma_p^2}{X} \times 100 \quad (5)$$

where PCV = phenotypic coefficient of variation

$$GCV = \frac{\sqrt{\text{genotypic variance}}}{\text{population mean for trait}} \text{ or } GCV = \frac{\sigma_g^2}{X} \times 100 \quad (6)$$

where GCV = genotypic coefficients of variation, X = the grand mean of a character.

Broad sense heritability (H^2) was calculated for each trait by using the formula [14]:

$$H^2 (\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100 \quad (7)$$

where, H = heritability in broad sense, σ_g^2 = genotypic variance, σ_p^2 = phenotypic variance.

Genetic advance (GA) under selection, assuming the selection intensity of 5% was calculated as proposed by Johnson et al. [15] as follows:

$$GA = K \cdot \sqrt{\frac{\sigma_g^2}{\sigma_p^2}} = K \cdot H \cdot \sqrt{\sigma_p^2} \quad (8)$$

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 [16]:

$$\text{GAM} = \frac{\text{GA}}{X} \times 100, \quad (9)$$

where, GAM = genetic advance as percent of mean, GA = genetic advance under selection, X = mean value of a trait.

Both genotypic and phenotypic correlation, which the inherent association between two variables were estimated by the formula suggested by Weber and Moorthy [17].

$$\text{rg}(xy) = \frac{\text{Gcov}(x,y)}{\sqrt{\sigma_g^2 x \cdot \sigma_g^2 y}}, \quad (10)$$

where: rg = genotype correlation coefficient, $\text{Gcov}(x,y)$ = genotype co-variance between, $\sigma_g^2 x$ = genotype variance for variable x , $\sigma_g^2 y$ = genotype variance for variable y .

$$\text{rp}(xy) = \frac{\text{Pcov}(x,y)}{\sqrt{\sigma_p^2 x \cdot \sigma_p^2 y}}, \quad (11)$$

where: rp = phenotype correlation coefficient, $\text{Pcov}(x,y)$ = phenotype co-variance between variable x and y , $\sigma_p^2 x$ = phenotype variance for variable x , $\sigma_p^2 y$ = phenotype variance for variable y .

Data of individual mean of ten randomly selected plants from each replication were subjected to statistical analysis. All Quantitative data were subjected to analysis of variance using SAS statistical analysis software version 8 [18]. Significant treatment means were separated using the least significant difference (LSD) test at 5% probability level.

3. Results and Discussion

3.1. Phenological Traits. Analysis of variance showed that genotypes were significantly differed for days to flowering and maturity Table 1. Generally days to flowering ranged from 43.0 to 56.3 and maturity from 75.0 to 92.0. Genotype SAB 632 flowered (43.0) and matured (75.0) early as compared to the other cultivars. On the other hand, genotype SEC 20 took the longest days to flowering (56.4) and maturity (92.2). Genotypes SEC 20, SMC 21, ALB 204, Awash 2, SER 125, Red Wolaita, SER 119, Dursitu, Dimtu, Awasa Dume, Ibado, Gobe Rashia, Roba, Awash 1, Deme, ALB 179, ALB 209, ALB 61, ALB 25 and NVA 517 took relatively longer days to flowering and physiological maturity. Conversely, genotypes SMC 22, Waji, Brazil 1, SAB 735, Awash Melka, Melka Dima, Ramada, Nasir, Awassa Dume, Brazil 2, SAB 632, Tatu and NVA 682 exhibited relatively shorter days to flowering and physiological maturity. The difference of 13.4 and 17.2 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 [7], Shahid and Kamaluddin [19] and Fahad et al. [20] that significant difference was observed for days to flowering and physiological maturity in common bean genotypes.

3.2. Growth Traits. Analysis of variance indicated that genotypes were significantly differed for growth traits Table 1. Plant height for genotypes ranged from the shortest (25.7 cm) for NVA 682 and the tallest plant (56.3 cm) for Nasir Table 1. Similarly, stem diameter ranged from 3.00 cm to 5.7 cm with greatest for genotype SEC 20 and the least for Tatu. Number of nodes per stems is one of the growth traits varied from 5.33 to 9.00 cm with the greatest number of nodes per stem exhibited for ALB 61 and the lowest for Melka Dima. Internode length ranged from 4.00 cm which was the least for genotype ALB 209 to the greatest for genotype Nasir with mean internode length of 7.33 cm. In line with this, leaf area and LAI were varied from 13.33 cm² and 4.18, respectively. Both parameters were greatest for genotype Deme and smallest for genotype Waji Table 1. This result showed that the growth traits measured were significantly differed due to the existence of inherent genetic variations among the genotypes.

3.3. Yield Components and Yield. Analysis of variance revealed that genotypes of common bean were significantly differed for yield components and yield Table 2. The number of pods per plant and seeds per pod were varied from 5.33 to 22.67 and 3.00 to 5.72. The highest number of pods per plant (22.67) and seeds per pod were recorded for genotype SEC 20. The lowest number of pods per plant (5.33) and seeds per pod (3.00) were observed for genotype Tatu. Genotypes had variable HSW which ranged from 13.67 to 48.67 g where the highest HSW (48.67 g) was achieved from genotype Deme and the lowest HSW (13.67 g) was obtained from Awash Melka. Biological yield as affected by genotypes ranged from 4333 to 17670 kg/ha. The greatest biological yield (17670 kg/ha) was recorded for genotype SEC 20 and the lowest (4333 kg/ha) was for Tatu. Indeed, the biological yield difference of 13337 kg/ha achieved between the highest and the lowest genotypes. Grain yield for genotypes varied from 1147 to 4462 kg/ha. The highest grain yield (4462 kg/ha) was obtained from genotype SEC 20 and the lowest (1147 kg/ha) from genotype Awash Melka. Harvest index (HI), which is the physiological efficiency and ability of a crop for converting the total dry matter into economic yield [21]. Hence, HI reflects the proportion of assimilate distribution between economic and total biomass yield. It ranged from 0.10 to 0.17 with the highest HI (0.17) for genotype ALB 204 and the lowest HI (0.10) for Ramada.

3.4. Variance Components

3.4.1. Phenotypic and Genotypic Variations. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population under consideration. Phenotypic variance varied from 0.05 for HI to 1282.70 for biological yield Table 3. Higher phenotypic variance ($\geq 100\%$) was observed for plant height, biological yield and HSW. In line with this, higher magnitude of difference between genotypic and environmental variance was observed for the

TABLE 1: Mean performance of genotypes of common bean for phenological and growth traits.

SN	Genotypes	Days to flowering	Days to maturity	Plant height (cm)	Stem diameter (mm)	Nodes per stem	Inter node length (cm)	Leaf area (cm ²)	LAI
1	SEC 20	56.4 ^a	92.1 ^a	31.3 ^{bc}	5.70 ^a	6.00 ^{b-d}	5.33 ^{a-c}	18.33 ^{c-g}	3.39 ^{a-e}
2	SMC 22	46.3 ^{e-h}	75.0 ^e	29.0 ^{bc}	4.00 ^{d-f}	5.67 ^{cd}	5.00 ^{bc}	15.33 ^{c-g}	1.49 ^{g-j}
3	SMC 21	53.0 ^{a-e}	89.0 ^{a-c}	34.0 ^{bc}	4.33 ^{c-e}	6.67 ^{a-d}	5.00 ^{bc}	21.33 ^{a-g}	2.29 ^{b-j}
4	SEC 23	53.0 ^{a-e}	90.0 ^{a-c}	29.7 ^{bc}	5.33 ^{ab}	5.67 ^{cd}	5.33 ^{a-c}	15.00 ^{fg}	2.40 ^{b-j}
5	ALB 204	52.3 ^{a-e}	92.0 ^a	28.0 ^c	4.33 ^{c-e}	6.33 ^{b-d}	4.67 ^c	21.33 ^{a-g}	2.93 ^{a-g}
6	Waji	45.3 ^{f-h}	75.0 ^e	45.3 ^{a-c}	4.33 ^{c-e}	6.33 ^{b-d}	7.00 ^{ab}	13.33 ^g	1.12 ^j
7	Brazil 1	43.7 ^{g-h}	75.0 ^e	33.7 ^{bc}	3.67 ^{e-g}	6.00 ^{b-d}	5.33 ^{a-c}	22.00 ^{a-g}	1.57 ^{f-j}
8	SAB -735	44.3 ^{g-h}	75.0 ^e	34.3 ^{bc}	3.33 ^{fg}	6.00 ^{b-d}	5.33 ^{a-c}	20.7 ^{a-g}	1.35 ^{h-j}
9	Awash Melka	44.0 ^{g-h}	75.0 ^e	27.7 ^c	3.67 ^{e-g}	5.67 ^{cd}	5.33 ^{a-c}	13.34 ^g	1.22 ^{ij}
10	Awash 2	55.0 ^{a-b}	91.3 ^{a-b}	41.3 ^{a-c}	4.33 ^{c-e}	7.33 ^{a-d}	6.00 ^{a-c}	20.00 ^{b-g}	2.05 ^{c-j}
11	Melka Dima	47.7 ^{c-h}	87.7 ^{b-c}	31.3 ^{bc}	4.67 ^{b-d}	5.33 ^d	5.33 ^{a-c}	25.00 ^{a-e}	2.24 ^{c-j}
12	SER 125	56.3 ^a	92.0 ^a	36.0 ^{bc}	5.67 ^a	6.33 ^{b-d}	5.67 ^{a-c}	19.00 ^{b-g}	3.10 ^{a-f}
13	Red Wolaita	50.3 ^{a-g}	86.7 ^c	44.0 ^{a-c}	3.67 ^{e-g}	7.67 ^{a-d}	6.00 ^{a-c}	21.33 ^{a-g}	2.14 ^{c-j}
14	Ramada	46.7 ^{d-h}	78.3 ^{d-e}	38.3 ^{a-c}	4.00 ^{d-f}	6.67 ^{a-d}	6.00 ^{a-c}	16.70 ^{d-g}	2.01 ^{d-j}
15	Nasir	48.7 ^{b-h}	88.7 ^{a-c}	56.3 ^a	4.67 ^{b-d}	7.33 ^{a-d}	7.33 ^a	16.33 ^{e-g}	1.92 ^{e-j}
16	SER 119	53.0 ^{a-e}	90.7 ^{a-c}	33.0 ^{bc}	5.67 ^a	7.33 ^{a-d}	4.33 ^c	23.33 ^{a-f}	2.74 ^{a-i}
17	Dursitu	54.3 ^{a-c}	90.7 ^{a-c}	36.3 ^{a-c}	4.33 ^{c-e}	7.33 ^{a-d}	5.00 ^{bc}	20.33 ^{b-g}	2.03 ^{d-j}
18	Dimtu	50.3 ^{a-g}	90.0 ^{a-c}	32.7 ^{bc}	5.00 ^{a-c}	7.67 ^{a-d}	4.67 ^c	15.67 ^{e-g}	1.68 ^{f-j}
19	Awassa Dume	46.7 ^{d-h}	75.0 ^e	37.0 ^{a-c}	3.67 ^{e-g}	7.00 ^{a-d}	6.00 ^{a-c}	15.00 ^{fg}	1.19 ^j
20	Ibado	52.7 ^{a-e}	88.7 ^{a-c}	32.7 ^{bc}	4.67 ^{b-d}	8.33 ^{ab}	4.67 ^c	24.33 ^{a-f}	2.57 ^{b-j}
21	Gobe RASHIA	54.3 ^{a-c}	90.0 ^{a-c}	29.3 ^{bc}	5.00 ^{a-c}	6.33 ^{b-d}	4.67 ^c	27.67 ^{a-c}	2.79 ^{a-h}
22	Roba	51.7 ^{a-f}	91.3 ^{ab}	34.3 ^{bc}	4.00 ^{d-f}	7.00 ^{a-d}	5.33 ^{a-c}	20.33 ^{b-g}	3.06 ^{a-f}
23	Brazil 2	45.3 ^{f-h}	75.2 ^e	44.0 ^{ac}	3.67 ^{e-g}	7.00 ^{a-d}	6.00 ^{a-c}	28.00 ^{a-c}	2.14 ^{c-j}
24	Awash 1	51.7 ^{a-f}	81.7 ^d	39.7 ^{a-c}	4.00 ^{d-f}	7.33 ^{a-d}	5.33 ^{a-c}	16.00 ^{e-g}	1.95 ^{e-j}
25	Deme	54.7 ^{ab}	92.0 ^a	49.0 ^{ab}	5.33 ^{ab}	8.33 ^{ab}	6.00 ^{a-c}	30.33 ^a	4.18 ^a
26	SAB 632	43.0 ^h	75.0 ^e	28.3 ^c	3.33 ^{fg}	6.33 ^{b-d}	4.33 ^c	25.00 ^{a-e}	1.80 ^{f-j}
27	Tatu	44.3 ^{g-h}	76.7 ^e	37.0 ^{a-c}	3.00 ^g	6.00 ^{b-d}	6.00 ^{a-c}	18.33 ^{c-g}	1.32 ^{h-j}
28	ALB 179	51.3 ^{a-f}	89.3 ^{a-c}	32.3 ^{bc}	4.33 ^{c-e}	6.00 ^{b-d}	6.00 ^{a-c}	26.33 ^{a-d}	3.58 ^{a-c}
29	ALB 209	51.3 ^{a-f}	88.3 ^{a-c}	29.0 ^{bc}	4.00 ^{d-f}	8.00 ^{a-c}	4.11 ^c	20.33 ^{b-g}	2.29 ^{b-j}
30	ALB 61	51.3 ^{a-f}	88.3 ^{a-c}	29.7 ^{bc}	4.33 ^{c-e}	9.00 ^a	4.00 ^c	15.00 ^{fg}	1.86 ^{e-j}
31	ALB 25	53.3 ^{a-d}	89.7 ^{a-c}	32.3 ^{bc}	4.33 ^{c-e}	7.33 ^{a-d}	4.33 ^c	21.67 ^{a-g}	2.74 ^{a-i}
32	NVA 682	43.7 ^{g-h}	76.7 ^e	25.7 ^c	4.00 ^{d-f}	6.00 ^{b-d}	4.33 ^c	26.67 ^{a-c}	3.54 ^{a-d}
33	NVA 517	53.7 ^{a-c}	88.3 ^{a-c}	44.7 ^{a-c}	4.67 ^{b-d}	8.00 ^{a-c}	5.67 ^{a-c}	28.67 ^{ab}	3.81 ^{ab}
	LSD	6.7	4.3	20.10	0.87	2.33	2.26	9.98	1.50
	CV	8.33	3.12	34.8	12.4	20.9	26.1	29.6	40.6

characters plant height and biological yield. This implies greater influence of environmental factors for the phenotypic expression of these characters. Relatively medium phenotypic variance (50–100%) observed for days to maturity whereas, relatively lower phenotypic variance was recorded for days to flowering, number of nodes, stem diameter, inter node length, leaf area, LAI, pods per plant, seeds per pod and HI. On the other hand, genotypic variance ranged from 0.01 to 763.32 with higher genotypic variance for biological yield and HSW. Moderate genotypic (σ_g^2) variance were observed for days to maturity and grain yield. Lower genotypic variance (σ_g^2) was observed for plant height, stem diameter, number of node on the main stem, internode length, LAI, biological yield, seeds per pod. Singh [13] reported that genotypic variance was (σ_g^2)

variable for different agronomic traits of different common bean genotypes.

In general phenotypic coefficient of variation (PCV) varied from 8.55 for days to maturity to 48.02 for LAI Table 3. According to Sivasubramanian and Madhavamenon [22] 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 such as plant height, number of nodes, internode length, leaf area, LAI, biological yield, pods per plant, HI and HSW had higher PCV. Conversely, traits like days to flowering stem diameter and seeds per pod exhibited moderate PCV where as only days to maturity showed lower PCV with PCV value below 10%. This reflected the pronounced influence of environmental factors for the expression of these characters. This

TABLE 2: Mean performance of genotypes of common bean for yield and yield components.

SN	Genotype	Pods per plant	Seeds per pod	HSW (g)	Biological yield (kg/ha)	Grain yield (kg/ha)	HI
1	SEC 20	22.67 ^a	5.72 ^a	16.33 ^{n-q}	17670 ^a	4462 ^a	0.12 ^{fj}
2	SMC 22	8.33 ⁱ⁻ⁿ	4.33 ^{c-e}	19.67 ^{l-n}	7667 ^{j-m}	1938 ^{pq}	0.12 ^{fj}
3	SMC 21	8.33 ⁱ⁻ⁿ	4.70 ^{b-d}	19.33 ^{mn}	9000 ^{g-k}	2355 ^{m-o}	0.12 ^{d-h}
4	SEC 23	18.00 ^b	5.33 ^{ab}	15.33 ^{pq}	15000 ^{a-d}	3718 ^c	0.11 ^{g-j}
5	ALB 204	15.33 ^{b-d}	4.70 ^{b-d}	23.00 ^{j-l}	11670 ^{d-i}	3545 ^{c-e}	0.17 ^a
6	Waji	11.00 ^{e-j}	4.33 ^{c-e}	28.00 ^{hi}	12000 ^{c-h}	3430 ^{d-f}	0.13 ^{c-f}
7	Brazil 1	9.33 ^{g-n}	3.70 ^{e-g}	34.67 ^{ef}	9333 ^{g-k}	2587 ^{lm}	0.13 ^{c-e}
8	SAB-735	7.67 ^{j-n}	3.01 ^g	31.00 ^{gh}	6667 ^{k-m}	1775 ^q	0.12 ^{d-h}
9	Awash Melka	7.33 ^{j-n}	4.33 ^{c-e}	13.67 ^q	5000 ^{lm}	1147 ^s	0.11 ^{ij}
10	Awash 2	10.67 ^{f-k}	4.70 ^{b-d}	15.00 ^{pq}	8000 ^{i-m}	1833 ^q	0.11 ^{h-j}
11	Melka Dima	9.00 ^{h-n}	4.00 ^{d-f}	39.00 ^d	12330 ^{c-j}	3642 ^{cd}	0.14 ^{b-d}
12	SER 125	14.67 ^{b-f}	5.00 ^{a-c}	23.67 ^{jk}	16670 ^{ab}	4235 ^{ab}	0.12 ^{fj}
13	Red Wolaita	10.67 ^{f-k}	4.70 ^{b-d}	19.33 ^{mn}	9333 ^{g-k}	2310 ^{no}	0.12 ^{fj}
14	Ramada	9.00 ^{h-n}	4.00 ^{d-f}	37.67 ^{de}	13330 ^{b-f}	3017 ^{h-j}	0.10 ^j
15	Nasir	13.33 ^{c-g}	5.33 ^{ab}	19.33 ^{mn}	11670 ^{d-i}	3343 ^{e-g}	0.13 ^{c-f}
16	SER 119	14.67 ^{b-f}	5.00 ^{a-c}	26.00 ^{ij}	15670 ^{a-c}	4238 ^{ab}	0.12 ^{d-h}
17	Dursitu	11.33 ^{d-j}	4.70 ^{b-d}	19.00 ^{m-o}	11330 ^{d-f}	4113 ^b	0.12 ^{d-h}
18	Dimtu	12.00 ^{c-i}	5.00 ^{a-c}	18.33 ^{m-p}	11330 ^{d-f}	2832 ^{i-k}	0.12 ^{e-i}
19	Awassa Dume	13.00 ^{c-h}	5.00 ^{a-c}	19.67 ^{l-m}	10000 ^{f-k}	3058 ^{hi}	0.14 ^{bc}
20	Ibado	6.33 ^{l-n}	3.33 ^{fg}	45.67 ^{ab}	11000 ^{e-j}	3235 ^{f-h}	0.13 ^{c-e}
21	Gobe Rashia	7.33 ^{j-n}	4.33 ^{c-e}	43.00 ^{bc}	12000 ^{c-h}	3370 ^{e-g}	0.13 ^{c-e}
22	Roba	10.00 ^{g-m}	5.70 ^a	15.67 ^{o-q}	7667 ^{j-m}	2145 ^{op}	0.13 ^{c-e}
23	Brazil 2	10.33 ^{g-l}	4.00 ^{d-f}	33.00 ^{fg}	10670 ^{f-j}	2828 ^{i-k}	0.12 ^{d-h}
24	Awash 1	13.33 ^{c-g}	4.00 ^{d-f}	16.67 ^{n-q}	9333 ^{g-k}	2813 ^{j-l}	0.12 ^{e-i}
25	Deme	6.00 ^{mn}	4.00 ^{d-f}	48.67 ^a	14670 ^{a-e}	3715 ^c	0.12 ^{fj}
26	SAB 632	6.67 ^{k-n}	3.70 ^{e-g}	38.00 ^{de}	8333 ^{h-l}	2220 ^{no}	0.13 ^{c-g}
27	Tatu	5.33 ⁿ	3.00 ^g	30.00 ^{gh}	4333 ^m	1475 ^f	0.15 ^b
28	ALB 179	14.67 ^{b-f}	4.70 ^{b-d}	23.67 ^{jk}	12000 ^{c-h}	3312 ^{e-g}	0.13 ^{c-f}
29	ALB 209	15.00 ^{b-e}	4.70 ^{b-d}	23.00 ^{j-l}	12330 ^{c-g}	3413 ^{d-f}	0.13 ^{c-f}
30	ALB 61	15.00 ^{b-e}	4.00 ^{d-f}	20.33 ^{k-m}	11330 ^{d-j}	2710 ^{kl}	0.13 ^{c-g}
31	ALB 25	15.67 ^{bc}	3.70 ^{e-f}	21.00 ^{k-m}	12330 ^{f-k}	3172 ^{gh}	0.13 ^{c-g}
32	NVA 682	6.33 ^{l-m}	3.33 ^{fg}	40.67 ^{cd}	10330 ^{b-f}	2453 ^{mn}	0.11 ^{g-j}
33	NVA 517	9.67 ^{g-m}	3.70 ^{e-f}	39.00 ^d	13330 ^{b-f}	4325 ^{ab}	0.14 ^{bc}
	LSD	4.0	0.97	3.61	3717	239	0.01
	CV	22.41	13.8	8.3	20.7	15.49	13.04

finding is in agreement with the result of Kassaye [7] that reported higher PCV for plant height, number of nodes on main stem, pods per plant, internode length and HSW. Generally in common bean, a wide range of GCV and PCV values were reported by [23–25]. Moreover, Berhanu [26], Kumar et al. [27], and Baranwal et al. [28] were also reported moderate PCV for grain yield, TSW and tillers per plant for wheat cultivars. In line with this, genotypic coefficient variance (GCV) varied from 1.88% to 37.72% (Table 3). The lowest GCV (1.88%) was recorded for inter node length while the highest GCV (37.72%) for HSW. As this investigation indicated that higher GCV (>20%) was observed for LAI, biological yield, pods per plant, HSW and grain yield whereas moderate GCV (10–20%) was recorded for stem diameter, leaf area and seeds per pod. This finding disagrees with the result of Ejigu et al. [29] who reported low GCV for number of pods per plant and HSW. On the other hand, lower GCV (<10%)

was seen for days to flowering, days to maturity, plant height, number of nodes on main stem, internode length and HI. This finding is in agreement with the result of Ejigu et al. [29] that reported low GCV for days to flowering and days to maturity. Singh [13] reported that there was wider genotypic variability with respect to agronomic traits in different common bean genotypes.

3.4.2. Heritability and Genetic Advance. In general heritability in broad sense (H^2) ranged from 0.52% for internode length which was the lowest to 95.33% for HSW which was the highest value (Table 3). Johnson et al. [30] classified heritability estimates as low (<30%), moderate (30–60%) and high (>60%). Based on this classification, days to maturity, pods per plant, HSW and grain yield exhibited high H^2 estimates indicating that environment has low influence for the expression of the characters which suggests direct

TABLE 3: Phenotypic and genotypic coefficient of variability, heritability and genetic advance for genotypes.

Trait	σ_p^2	σ_p^2	σ_e^2	PCV	GCV	H (%)	GA (%)
Days to flowering	28.92	11.58	17.34	10.76	6.80	40.00	10.37
Days to maturity	52.66	45.66	7.00	8.55	7.96	86.70	16.15
Plant height	149.55	-2.24	147.31	34.57	-4.24	-1.50	-2.23
Number of nodes	2.20	0.15	2.05	21.72	5.71	6.90	2.69
Stem diameter	0.67	0.38	0.29	18.93	14.30	56.90	26.54
Inter node length	1.91	0.01	1.90	26.00	-1.88	-0.52	-2.85
Leaf area	47.43	9.98	37.45	33.30	15.30	21.00	15.53
LAI	1.23	0.35	0.88	48.02	25.56	28.33	27.62
Biological yield	1282.70	763.32	519.38	32.53	25.10	59.50	40.04
Pods per plant	19.76	13.51	6.25	39.86	32.96	68.40	53.20
Seeds per pod	0.74	0.38	0.36	19.85	14.25	51.55	12.59
Harvest index	0.05	0.01	0.04	38.63	7.73	20.00	26.37
HSW	105.25	100.34	4.91	38.63	37.72	95.33	74.52
Grain yield	87.29	65.79	21.50	31.20	27.10	75.40	46.95

selection using these characters as major contributors of yield components to improve yield of common bean genotypes. This high heritability may be due to additive gene effects hence these traits are likely to respond to direct selection in order to improve common bean grain yield through direct selection for grain yield related traits. Relatively moderate H^2 was recorded for traits days to flowering, stem diameter, biological yield and seeds per pod which may be occurred due to influence of the environment on the polygenic nature of these traits. On the other hand, H^2 was low for traits plant height, number of nodes on main stem, internode length, leaf area, LAI and HI that 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.

Genetic advance as a percent mean was ranged from 2.23% for plant height to 74.52% for HSW Table 3. This result indicated that selecting the top 5% of the genotypes could result in an advance of 2.23–74.52% over the respective population mean. As suggested by Sivasubramanian and Madhavamenon [22], genetic advance as percent of mean was classified as low (<10%), moderate (10–20%) and high (>20%). Based on this classification, traits like stem diameter, LAI, biological yield, pods per plant, HI, HSW and grain yield exhibited high genetic advance. Traits days to flowering, days to maturity, leaf area and seeds per pod attained moderate genetic advance. In contrast, plant height, number of nodes on main stem and internode length had low genetic advance. Trait like number of pods per plant, HSW and grain yield exhibited high heritability coupled with high genetic advance while stem diameter and biological yield showed moderate heritability coupled with high genetic advance. Hence, these traits should be given top priority during selection in common bean breeding 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. In line with this, days to flowering and seeds per pod associated with moderate heritability with moderate genetic advance. Moderate heritability accompanied with moderate genetic advance as percent of

mean was recorded by days to flowering and seeds per pod. Both additive and nonadditive gene actions are involved in the expression of these traits. This result agreed with the findings of Alemayehu [23] that reported moderate estimates of H^2 coupled with moderate genetic advance for number of seeds per pod in common bean.

3.4.3. Phenotypic and Genotypic Correlations. The data for phenotypic and genotypic correlation of genotypes are depicted in Table 4. Genotypic correlation coefficient values ranged from -0.74 to 0.99. Stem diameter ($r_g=0.84$), LAI ($r_g=0.74$), biological yield ($r_g=0.96$), pods per plant ($r_g=0.56$), seeds per pod ($r_g=0.34$), days to flowering ($r_g=0.73$) and days to maturity ($r_g=0.59$) exhibited significant and positive genotypic association with grain yield where the highest genotypic correlation coefficient was recorded for biological yield. This indicates that the genotypes with high leaf area index, vegetative yield, pods per plant and seeds per pod were producing higher grain yield. In addition to this the late flowering and maturing type of genotypes were also producing higher yield rather than early flowering and maturity type. This result was similar with the findings of Kifle et al. [31], Kumar et al. [32], and Ebrahimnejad and Rameeh [33] who reported the positive and significant association of grain yield with biological yield. Sadeghi et al. [34] reported highly significant correlations of seed yield with seed number per plant, seed number per pod, pod number per plant, days to flowering and HSW. In line with this, stem diameter ($r_g=0.93$), LAI ($r_g=0.80$), pods per plant ($r_g=0.61$), seeds per pod ($r_g=0.38$), days to flowering ($r_g=0.78$) and days to maturity ($r_g=0.61$) showed significant positive genotypic correlation with biological yield Table 4. Similarly, stem diameter with LAI ($r_g=0.84$), pods per plant ($r_g=0.59$), seeds per pod ($r_g=0.55$), days to flowering ($r_g=0.99$) and days to maturity ($r_g=0.79$) had significant positive association.

In general phenotypic correlation coefficients for agronomic traits ranged from -0.62 to 0.93 Table 4. Stem diameter ($r_p=0.74$), LAI ($r_p=0.52$), days to flowering ($r_p=0.58$), days to maturity ($r_p=0.55$), biological yield ($r_p=0.93$) and pods per plant

TABLE 4: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for agronomic traits of common bean genotypes.

	SD	LA	LAI	BY	PPP	SPP	HSW	HI	GY	DF	DM
SD		0.09 ^{NS}	0.84*	0.93*	0.49*	0.55*	0.01 ^{NS}	-0.24 ^{NS}	0.84*	0.99*	0.79*
LA	0.15 ^{NS}		0.69*	0.18 ^{NS}	-0.58*	-0.82*	0.99*	0.36*	0.27 ^{NS}	0.11 ^{NS}	0.25 ^{NS}
LAI	0.54*	0.72*		0.80*	0.21 ^{NS}	0.09 ^{NS}	0.38*	0.08 ^{NS}	0.74*	0.94*	0.81*
BY	0.82*	0.24 ^{NS}	0.56*		0.61*	0.38*	0.14 ^{NS}	-0.08 ^{NS}	0.96*	0.78*	0.61*
PPP	0.39*	-0.33*	0.08 ^{NS}	0.53*		0.74*	-0.66*	0.08 ^{NS}	0.56*	0.67*	0.51*
SPP	0.45*	-0.33*	0.07 ^{NS}	0.32*	0.59*		-0.74*	-0.13 ^{NS}	0.34*	0.63*	0.58*
HSW	0.07 ^{NS}	0.70*	0.37*	0.23 ^{NS}	-0.59*	-0.62*		0.21 ^{NS}	0.16 ^{NS}	-0.27 ^{NS}	-0.21 ^{NS}
HI	-0.13 ^{NS}	0.18 ^{NS}	0.07 ^{NS}	-0.06 ^{NS}	0.10 ^{NS}	-0.08 ^{NS}	0.13 ^{NS}		0.23 ^{NS}	0.07 ^{NS}	0.09 ^{NS}
GY	0.74*	0.29 ^{NS}	0.52*	0.93*	0.49*	0.28 ^{NS}	0.23 ^{NS}	0.19 ^{NS}		0.73*	0.59*
DF	0.72*	0.19 ^{NS}	0.58*	0.57*	0.44*	0.44*	-0.16 ^{NS}	0.02 ^{NS}	0.58*		0.99*
DM	0.71*	0.21 ^{NS}	0.59*	0.54*	0.47*	0.49*	-0.17 ^{NS}	0.09 ^{NS}	0.55*	0.92*	

* indicates significant differences at 5% level and 'ns' indicates non-significance.

($r_p=0.49$) had significant positive correlation with grain yield where the highest phenotypic correlation coefficient was recorded between grain yield and biological yield. The significant and positive correlation of these traits with grain yield was probably due to more photosynthetic product partitioned to grain that increased their weight [35]. Biological yield showed significant positive associations with stem diameter ($r_p=0.82$), LAI ($r_p=0.56$), pods per plant ($r_p=0.53$), seeds per pod ($r_p=0.32$), days to flowering ($r_p=0.57$) and days to maturity ($r_p=0.54$). Moreover, significant positive association were observed between LAI with stem diameter ($r_p=0.54$), HSW ($r_p=0.37$), leaf area ($r_p=0.72$), days to flowering ($r_p=0.58$) and days to maturity ($r_p=0.59$). Similarly significant positive association were observed between pods per plant with stem diameter ($r_p=0.39$), seeds per pod ($r_p=0.59$), days to flowering ($r_p=0.44$) and days to maturity ($r_p=0.47$). Stem diameter was revealed significant positive association with seeds per pod ($r_p=0.45$), days to flowering ($r_p=0.72$) and days to maturity ($r_p=0.71$). In addition seeds per pod with days to flowering ($r_p=0.44$) and days to maturity ($r_p=0.49$), leaf area with HSW ($r_p=0.70$) and days to flowering with days to maturity ($r_p=0.92$) were revealed significant positive association.

4. Concussion

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 SEC 20 gave the highest grain yield. With respect to diseases reactions, genotypes SEC 20, SMC 22, ALB 204, Waji, Awash Melka,

Awash 2, SER 125, Ramada, SER 119, Dimtu, Awassa Dume, Roba, ALB 179 and ALB 61 found to be resistant to angular leaf spot. In line with this, genotypes Waji, Awash Melka, Awash 2, Melka Dima, SER 125, Red Wolaita, Nasir and Gobe Rashia were not totally attacked by bean rust exhibiting best resistant reaction. Phenotypic coefficient of variation (PCV) varied from 8.55 for days to maturity to 48.02 for LAI where traits plant height, number of nodes, internode length, leaf area, LAI, biological yield, pods per plant, HI and HSW had higher PCV. Genotypic coefficient variance (GCV) varied from 1.88% to 37.72% with the highest GCV recorded for HSW. Heritability in broad sense (H^2) ranged from 0.52% to 95.33% with the greatest observed for HSW. Genetic advance as a percent mean was ranged from 2.23% for plant height to 74.52% for HSW. The present study revealed significant variation among genotypes for traits considered except few insignificant traits. In addition, almost all the genotypes were well adapted to the study area and hence, the high yielding genotypes could be directly used as seed sources for production of common bean and genotype with best diseases reaction with high heritability can possibility used in common bean improvement program in breeding.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Conflict of Interest

The authors declare that there is no conflict of interest regarding publication of this manuscript.

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