

Research Article

# Genetic Variability and Character Association among Common Bean (*Phaseolus vulgaris* L.) Genotypes at Areka, Southern Ethiopia

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## Abstract

Evaluating genetic variability among genotypes is vital for identifying superior genotypes because selecting parents who create segregating populations is critical in breeding programs. The current study was done at Areka Agricultural Research Center during the 2020/21 major cropping season, with the goal of estimating genetic diversity and character connection among 25 common bean genotypes. The experiment consisted of two replications of a 5 x 5 simple lattice design. Data were obtained on 12 quantitative parameters, and the analysis of variance revealed extremely significant variations between genotypes for all characters. It demonstrated that genotypes vary significantly. GCV and PCV were highest in plant height, number of pods per plant, biological yield, number of seeds per plant, and seed yield, while lowest in days to flowering and days to maturity. Plant height, number of pods per plant, number of seeds per plant, biological yield, and seed yield all showed significant broad-sense heritability ( $H^2$ ) and high predicted genetic advance as a percentage of mean GAM. This suggested the presence of additive gene activity in the inheritance of these traits. The number of major branches per plant, biological yield, days of 50% flowering, hundred seed weight, and harvest index all show a highly substantial and positive link with seed yield at both genotypic and phenotypic levels. The biological yield and harvest index both have a strong positive direct effect on seed output. As indicated, these traits could be utilized for selection to increase seed output. Based on the D2 value, 25 common bean genotypes were divided into four clusters. Clusters I and IV had the greatest inter-cluster distance (766.78), whereas clusters I and II had the smallest (53.78). Breeding programs could use genotypes from distant clusters to increase variety. Thus, the enormous genetic variation among common bean genotypes must be evaluated for use in common bean breeding efforts.

## Keywords

Common Bean, Correlation, Genetic Advancement, Genetic Variability

## 1. Introduction

Crop plant genetic variability is the consequence of evolutionary processes (mutations, selections, migration, and random genetic drift), as well as human intervention through

selection and domestication [3]. The degree of genetic variety influences the amount of progress gained through selection and hybridization. The more distinct the two

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genotypes are, the higher the possibility of improvement through selection and hybridization [20].

Genetic modification of the common bean in Ethiopia has been designed to meet stringent consumer requirements, primarily market characteristics and resistance to illnesses that impact common bean production in the country [12]. Genetic variety serves as the foundation for crop development, and plant breeders employ it to direct and regulate the evolutionary process by creating new kinds. The level of genotypic and phenotypic variability in a species is critical for producing better varieties and starting a breeding program. Furthermore, the genotypic and phenotypic coefficients of variation are utilized to quantify the diversity in a specific population [9].

Heritability is significant to plant breeders because it measures the value of selection for certain characteristics in various types of progenies and serves as an indicator of transmissibility. It represents the heritable fraction of phenotypic variance and is an excellent indicator of character transmission from parents to children. According to [14]. Heritability in the broad sense estimates the ratio of total genetic variance, including additive, dominance, and epistatic variance, to phenotypic variance, whereas heritability in the narrow sense estimates only the additive portion of total phenotypic variance and expresses the extent to which phenotypes are determined by genes passed down from parents [26].

### 1.1. The Significance of the Review

Genetic association of breeding materials may aid in the preservation of genetic diversity among common bean genotypes as well as long-term selective gain. Furthermore, the correlation of features between yield, its components, and other economic factors is critical for selection in breeding programs [1].

Correlation study revealed that physical features accounted for the majority of genotypic correlation. Analysis of variance is used to determine whether there is a meaningful link between the characters evaluated. As a result, every breeding program aimed at boosting yield should analyze the relationship between yield and its features through genotypic and phenotypic correlation estimation, which greatly aids in the formulation of selection indices to aid in selection programs [25].

According to [7], the main production restrictions of common bean include the use of unimproved low-yielding cultivars, poor cultural practices, drought, low soil fertility, and illnesses (fungal, bacterial, and viral diseases; insect pests). Ethiopia's small-scale farms produce the majority of its beans using low-input agriculture. As a result, beans grown by these resource-poor farmers are more prone to disease and insect pest attacks, as well as abiotic stresses such as drought and low soil fertility.

The national average yield of common beans is 1.6 tons

per hectare, which is significantly lower than the output obtained at research locations (2.5 tons per hectare) utilizing improved cultivars [11]. The poor national yield is due to a lack of better varieties [4]. The [33] also found that disease and pests, drought, limited variety availability, the high cost of improved seed, and volatile product prices are important restrictions to common bean production. Lack of availability of sources and the extent of heterogeneity among genotypes in the area. However, it is critical to any crop development program in order to optimize selection gains. One strategy for increasing common bean yield is to select promising genotypes from various genetic backgrounds and then use them for hybridization [23]. To address the issues, it is critical to examine the pattern of character variation among and between genotypes. Genetic improvement to create genotypes with high yield potential and resistance to abiotic and biotic stressors is the most viable and environmentally benign way to boost common bean yield indefinitely.

Furthermore, one of the primary causes of the study area's low yield of common beans is a lack of improved high-yielding and disease-resistant varieties. There is a need to introduce improved common bean types into the targeted area. It is critical to increase productivity and production of common beans in the research area. As a result, it is critical to investigate genetic variability, heritability, genetic advance, and genotype clustering based on genetic differences and character associations, as this information can be used to improve common bean yield through breeding and to identify high-yielding genotypes to increase production and productivity.

### 1.2. Review Objective

The primary goal of this review is to determine the degree of genetic variation and character associations among common bean (*Phaseolus vulgaris* L.) genotypes. In addition, the review analyzes the extent of genetic variability, heritability, and genetic advance across common bean genotypes in terms of yield and yield-related features. Furthermore, it determines the relationship between main phenotypic characteristics.

### 1.3. Review as Input for Many Stakeholders

This review can serve as useful feedback for numerous stakeholders in the agricultural sector: 1. Producers: Understanding genetic diversity across common bean genotypes is critical for common bean output and productivity. 2. Researchers: The review identifies knowledge gaps and areas that require additional research and development for the continuing advancement of climate-smart behaviors. 3. Extension service personnel: This review provides extension workers with the knowledge they need to successfully communicate the benefits and problems of common bean varieties in production to farmers, hence

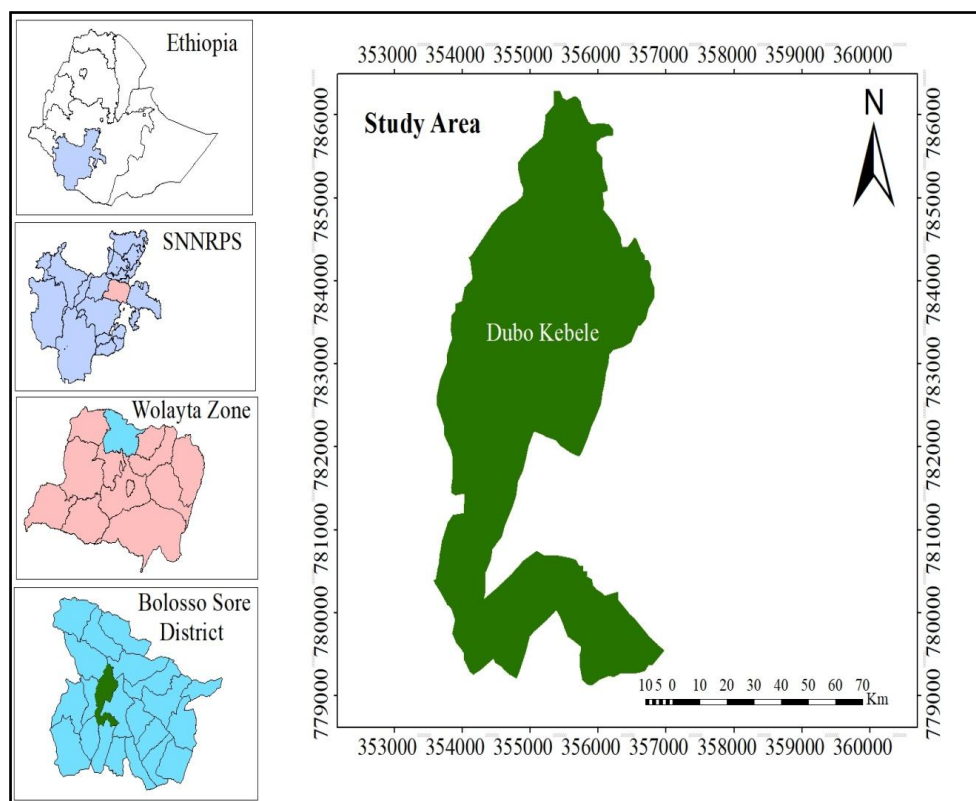
facilitating their adoption.

## 2. Review Methodology

### 2.1. Description of the Study Area

During the Meher season of 2020/21 (July-December), a field experiment was carried out at Bolosso Sore District's Areka Agricultural Research Center (AARC) in Southern

Nations Nationalities and Peoples Regional State (SNNPRS) under rain-fed circumstances. The average annual rainfall is 1460 millimeters. The mean minimum and maximum temperatures in the area were 15 and 26 degrees Celsius, respectively. The experimental site's approximate geographical coordinates are 7°41'N latitude and 37°41'E longitude, with an elevation of 1790 meters above sea level (Figure 1).



**Figure 1.** Location Map of Study Area.

### 2.2. Experimental Materials

Common bean MALB genotypes and one hawassa dume at check.

### 2.3. Experimental Treatments and Design

The Hawassa Agricultural Research Center provided the experimental genotypes, and the experiment included 25 treatments (24 inbred lines and one released variety). In this study, the Centro Internacional de Agricultura Tropical (CIAT), Cali, and Colombia were the first to introduce medium-sized bean varieties to Ethiopia. (Table 1). Treatments were distributed in a 5 x 5 basic lattice pattern with two replications. The plots were 2 m wide by 2 m long, with 5 rows of 20 seeds each. The distance between plots,

blocks, and replications was 50 cm, 1 m, and 1.5 m, respectively. Throughout the crop growth season, all crop management measures were implemented as desired.

### 2.4. Data Collected: Phonological and Growth Parameters

Days to 50% flowering—the data was recorded as the number of days from planting to 50% of the plants exhibiting flowering per plot.

Number of primary branches per plant: The number of shoots arising from the main stem was counted and recorded at physiological maturity.

Plant height (cm): The height was measured in centimeters from the ground level to the tip of the plant at maturity.

Days to physiological maturity (the data was recorded

when 90% of plants in the plot lose the green color of pod per plot. Yield and yield components.

Number of pods per plant: The mean number of pods was obtained from each plant at harvest after maturity.

Number of seeds per pod (the mean number of seeds was obtained from each pod at harvest after maturity)

Number of seeds per plant (Number of seeds was counted from ten randomly taken plants from the middle three rows and expressed as an average for each plot.

Biological yield/biomass yield/(kg/ha) (by an average from 10 plants was uprooted, cleaned, and weighted to get the biological yield per plant in grams.

Seed yield (kg/ha) (-dried grain yield was obtained from 10 plants within central rows of each plot that could be harvested, threshed separately, seeds weighted and recorded in kg, and adjusted to 12% moisture level and converted to kg ha<sup>-1</sup>.

Hundred seeds weight (g) (-It was determined by weighing 100 randomly sampled seeds and adjusting to 10% moisture level.

Harvest index (%) (- Is the ratio of grain to the total biomass and estimated as: X100

## 2.5. Data Analysis

### 2.5.1. Analysis of Variance (ANOVA)

The data was collected for each variable, and the means of ten randomly selected plants from Each plot was evaluated using the analysis of variance (ANOVA) approach with SAS syntax for basic lattice design using computer software version 9.2. Because of the flexibility of lattice design, comparisons of its relative efficiency to that of RCBD were made following data analysis [10]. The mean of the characters was compared using the Tukey test. Furthermore, ranges, phenotypic and genotypic variances, coefficients of phenotypic and genotypic variances, heritability, and genetic progress as percent of mean were determined from mean square values and grand mean for each character.

### 2.5.2. Estimation of Variance Components

Genetic parameters were estimated in order to discover and quantify genetic variability among genotypes, as well as to establish the amount to which environmental factors influence certain characteristics. Variance components related to phenotype ( $\sigma^2_p$ ), genotype ( $\sigma^2_g$ ), and the environment ( $\sigma^2_e$ ) were calculated by adopting the following formula suggested by [9].

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

$$\text{Phenotypic variance } (\delta^2_p) = \delta^2_g + \delta^2_e$$

$$\text{Environmental Variance } \delta^2_e = mse$$

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 [29] as:

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100 \quad GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

Where PCV=phenotypic coefficient variation, GCV=genotypic coefficients of variation,  $\bar{X}$ =the grand mean of a character.

### 2.5.3. Estimation of Heritability in Broad Sense

Broad sense heritability ( $H^2$ ) was calculated for each trait by using the formula [3],  $H^2(\%) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$

Where,  $H^2$ =heritability in broad sense,  $\sigma^2_g$ =genotypic variance,  $\sigma^2_p$ =phenotypic variance

### 2.5.4. Estimation of Genetic Advance

Genetic advance (GA) under selection, assuming the selection intensity of 5% was calculated as a formula of [16],  $GA = K.H.\sqrt{\sigma^2_p}$

Where: GA = expected genetic advance, K = the selection differential (K= 2.056 at 5% selection intensity).

Using the formula provided by [14], the magnitude of expected advancements of several qualities under selection was compared as a percentage of the mean.

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where, GAM = genetic advance as percent of mean, GA = genetic advance under selection,  $\bar{X}$  = mean value of a trait.

### 2.5.5. Clustering of Genotypes

SAS software version 9.2 was used to do cluster analysis on the 25 most prevalent bean genotypes. The generalized Mahalanobis  $D^2$  statistics.

*Estimation of intra and inter cluster squared distances*

Average intra and inter cluster  $D^2$  values estimated using the formula  $\frac{\sum D_i^2}{n}$  where,  $\sum D_i^2$  is the sum of distance between all possible combinations (n) of the genotypes included in a cluster. Significance of the squared distances for each cluster was tested against the tabulated  $\chi^2$  values at p-1 degree of freedom at 5% probability level. Where, p = number of traits used for clustering genotypes.

### 2.5.6. Association of Characters

*Estimation of correlation coefficients*

Both the genotypic and phenotypic correlation coefficient was calculated in which the inherent association between two variables was estimated by the formula suggested by [31].

$$rg(xy) = \frac{Gcov(xy)}{\sqrt{\sigma^2_{gx} \cdot \sigma^2_{gy}}}$$

Where: rg=genotype correlation coefficient, Gcov(xy)=genotype co-variance between  $\sigma^2_{gx}$ =genotype variance for variable x,  $\sigma^2_{gy}$ =genotype variance for variable y.

$$rp(xy) = \frac{Pcov(xy)}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$

Where: rp=phenotype correlation coefficient, Pcov(xy)=phenotype co-variance between variable x and y,  $\sigma^2_{px}$ =phenotype variance for variable x,  $\sigma^2_{py}$ =phenotype variance for variable y.

#### Estimation of path coefficient analysis

The path coefficient analysis used seed yield as the dependent variable and the remaining characters as the independent variables. The direct and indirect effects of the independent features on seed yield were calculated by simultaneous equation using the following formula as applied by [13]:

$$R_{ij} = P_{ij} + \sum R_{ik} P_{kj}$$

Where,  $R_{ij}$ =mutual association between the independent character (i) and dependent character, grain yield (j) as

measured by the correlation coefficients.  $P_{ij}$ =Components of direct effects of the independent character (i) was measured by the path coefficients and  $\sum R_{ik} P_{kj}$ =summation of components of indirect of a given independent character (i) on a given dependent character (j) via all other independent characters (k)

## 3. Results and Discussion

### 3.1. Analysis of Variance

Table 1 showed the mean squares for different characters. ANOVA found significant differences ( $p < 0.01$ ) among common bean genotypes in 12 quantitative characteristics. This suggested a high level of genetic diversity in the traits under study: DF50%, DM, PH, NPBP, SC, NPP, NSP, NSPP, HSW, BY, SY, and HI. Selection for these traits has a positive impact on genetic progress.

The current study's findings were consistent with those of [21], who discovered that all parameters, including 50% days of flowering, days of maturity, plant height, pods per plant, seed per pod, hundred seed weight, biological yield, harvest index, branch per plant, and grain yield, varied significantly between common beans.

**Table 1.** Showed the mean square for 12 quantitative characteristics of common bean genotypes.

Characters	Replication df=(1)	Genotypes df= (24)	Mse	Block/rep df=(8)	Intra block error df=(16)	CV%
DF	1.62	10.81**	2.6	2.65	3.01	4.2
DPM	0.72	10.76**	3.21	2.5	2.92	2.2
PH	0.72	301.46**	2.90	2.97	2.8	3.4
NPBP	0.18	1.54**	0.53	0.35	0.52	17.1
SC	28125	154791**	50563	19531	505626	3.5
NPP	1.62	42.90**	3.62	4.24	3.5	8.4
NSP	0.02	1.17**	0.36	0.34	0.37	10.7
NSPP	224.72	1882.80**	189.40	328.62	201.4	11
HSW	2.29	6.61**	1.76	1.32	1.54	5.2
B	133471	1758659**	270017	423965	307692	14.3
SY	250.25	453633**	66226	54186	63986	13.1
HI	5	84.87**	34.90	75.59	34.5	11.6

NB: \*\* and \* = significance at 0.01 and 0.05 probability levels, respectively.

DF = Days to flowering; DM = Days to physiological maturity; PH = Plant height (cm); NPBP = Number of primary branches per plant; SC = Stand count; NPP = Number of pods per plant; NSP=Number of seeds per pod; NSPP=Number of seed per plant; HSW= Hundred seed weight (g); BY= Biological yield; SY = Seed yield ( $\text{ha}^{-1}$ ) and HI= Harvest index.



## 3.2. Variance Components

### 3.2.1. Estimation of Genetic Parameters

The PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be moderate [9]. The estimation of genotypic variance ( $\sigma^2_g$ ), phenotypic variance ( $\sigma^2_p$ ), genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance at 5% selection intensity as percent of mean for 12 quantitative characters of common bean genotypes was presented in Table 2.

The study found that GCV and PCV values varied from 2.4% for days of physiological maturity to 24.63% for plant height, and 3.3% for days of physiological maturity to 26.1% for plant height, respectively. Characters with high GCV and PCV coefficients of variation were plant height (24.63 and 26.1), number of pods per plant (20 and 21.5), biological yield (22.23 and 25.95), number of seeds per plant (22.6 and 25), and seed yield (22.34 and 26.1).

The strong PCV and GCV estimations for these features suggested that yield increase through selection is conceivable due to the limited expression of environmental variation across common bean genotypes. This study was consistent with [6], which revealed high GCV and PCV values for plant height, pod number per plant, and seed production. Similarly, [32] observed significant GCV and PCV values for the parameters number of pods per plant and seed yield.

PCV values were generally higher than GCV values by a lesser margin for all characters. This was because the characters exhibited a masking effect from the environment, and overall PCV values were the consequence of GCV and environmental variations. This conclusion was consistent with the findings of [22], who found that the relative size of phenotypic coefficients of variation was greater than genotypic coefficients of variation for all traits, showing environmental effect on the traits.

### 3.2.2. Heritability and Genetic Advance

#### (i). Heritability

Estimated values of broad sense heritability ( $H^2$ ) for 12 characters ranged from (42.2%) for harvest index to (98.14%) for plant height in Table 5. [16] categorized heritability estimates as high (>60%), moderate (30–60%) and low (<30%). In the present study, six characters such as plant height (98.14%), days of flowering (61.3), numbers of pod per plant (84.43%), number of seed per plant (81), biological yield (73) and seed yield (74.5) exhibited high heritability ( $H^2$ ).

This finding indicated that the expression of the six characters was less influenced by environmental factors, implying that selection for these characters would be effective due to additive gene action and that the characters would be heritable enough to improve the yield of common bean genotypes. This study was consistent with the findings of [18], which found a high heritability value for days to 50% flowering, days to maturity, and plant height. [2, 15] obtained similar results for the same characters.

#### (ii). Genetic Advance

Table 2 showed the projected genetic progress as a percentage of the mean (GAM). The present study showed that high broad sense heritability ( $H^2$ ) coupled with high expected genetic advance as percent of mean (GAM %) for the characters plant height (98.14, and 50.2), numbers of pod per plant (84.43, and 37.4), number of seed per plant (81 and 53.7), biological yield (73.4, and 39.2), and seed yield (74.5, and 39.72). This revealed that direct selection of these traits was potential for genotype yield increase. Similar observations by [32] revealed a high GAM for number of seeds per plant, biological yield, and grain yield. According to [16], high heritability estimates combined with strong genetic progress are typically more useful in estimating the success of picking the best individuals.

**Table 2.** The Estimated values of variances, coefficients of variation, heritability, genetic advance and genetic advance as percent of mean for 12 characters.

characters	$\sigma^2_e$	$\sigma^2_g$	$\sigma^2_p$	GCV	PCV	$H^2(\%)$	GA	GAM (%)
DF50	2.6	4.11	6.71	4.96	6.34	61.3	3.3	8
DPM	3.21	3.78	6.99	2.4	3.3	54.1	2.93	3.62
PH	2.90	149.3	152.2	24.63	26.1	98.14	24.9	50.2
NPBP	0.53	0.5	1.04	16.9	24.2	50.1	1.05	24.88
SC	50563	52114	202677	11.16	15.66	50.75	330	16.2
NPP	3.62	19.64	23.25	20	21.5	84.43	8.35	37.4
NSP	0.36	0.41	0.77	11.23	15.4	53.3	0.97	16.9
NSPP	189.40	846.7	1036.1	22.6	25	81	54.2	53.7

characters	$\sigma^2_e$	$\sigma^2_g$	$\sigma^2_p$	GCV	PCV	$H^2(\%)$	GA	GAM (%)
HSW	1.76	2.43	4.19	6.35	8.6	58	2.45	10.24
BY	270017	744321	1014338	22.23	25.95	73.4	1522.4	39.2
SY	66226	193703.5	259929.5	22.34	24.87	74.5	782.4	39.72
HI	34.90	25.1	59.6	10.1	15.3	42.2	6.65	13.18

$\sigma^2_g$  = genotypic variance,  $\sigma^2_p$  = phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation,  $H^2$  = Broad sense heritability, GA = Genetic advance and GAM=Genetic advance as percentage of mean

This conclusion supported the findings of [5], who showed that genetic advance as a percentage of the mean was high for grain yield, biomass yield, and number of pods per plant, but low for days to maturity, days to blooming, and number of seeds per pod.

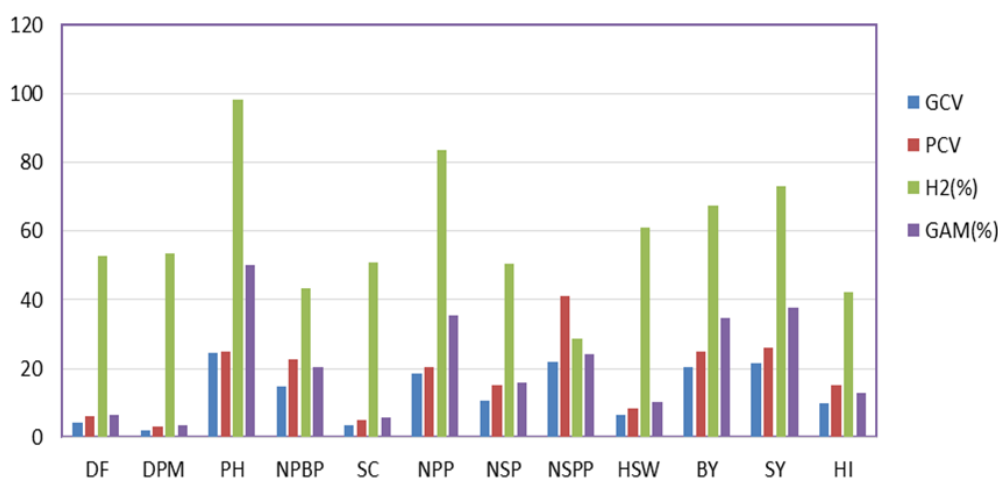


Figure 2. Graph for GCV, PCV, heritability and genetic advance as percent of mean of 12 characters.

GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation. H2 Broad sense heritability and GAM = Genetic progress as a proportion of the mean, DF = Days to 50% flowering; DM = Days to 90% maturity. PH=Plant height. NPBP = Number of primary branches per plant; NPP = Number of pods per plant; NSP = Number of seeds per pod; NSPP = Number of seeds per plant; SC = Stand count; HSW = Hundred seed weight; BY = Biological yield; SY = Seed yield; and HI = Harvest index.

### 3.3. Cluster Analysis

#### 3.3.1. Clustering of Genotypes

Based on the D2 value, 25 common bean genotypes were grouped into 4 clusters in Table 3. The genotypes within similar clusters were more closely related than genotypes in different clusters. Cluster II was the largest, which consisted of 10 genotypes, followed by cluster III with 7 genotypes. Cluster I consisted 5 genotypes where by cluster IV was smallest and consisted 3 genotypes. The presence of

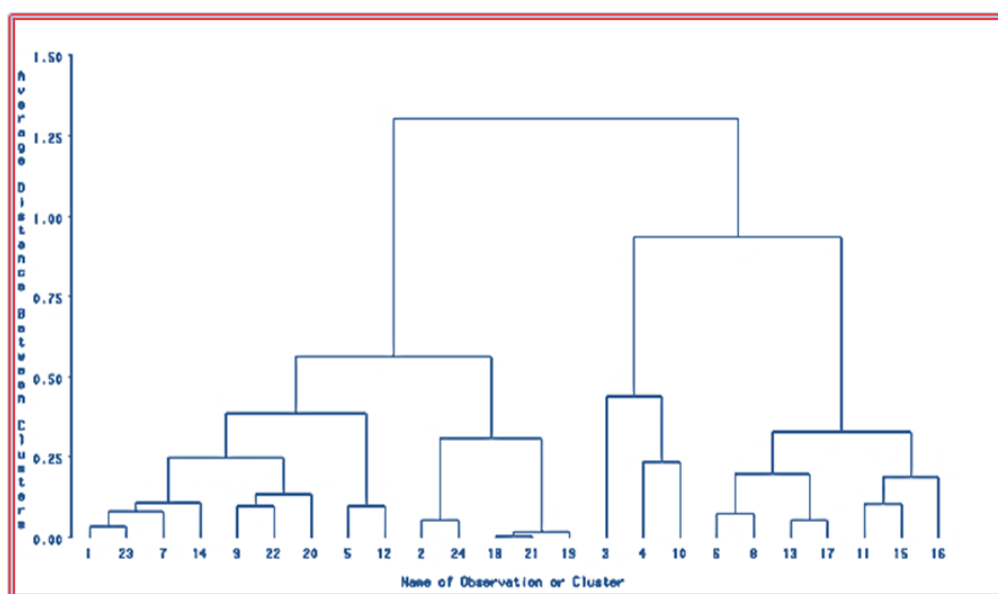
considerable genetic diversity among clustered genotypes made a great opportunity for yield improvement through selection and hybridization of common bean genotypes. Each cluster had its own characteristic feature for its cluster formation. The genotypes grouped into cluster I have the shortest plant height; early mature and low yielders, while genotypes falling into cluster II were medium in the mentioned characters. The genotypes found in cluster III were high yielding, and direct selection would be an effect. Also, cluster IV had a medium seed yield and matured early.

**Table 3.** The distribution of 25 common bean genotypes in to 4 clusters based on  $D^2$  analysis.

No of cluster	No of genotypes	Genotypes clustered
I	5	MALB-89, MALB-135, MALB-173, MALB-131, MALB-106,
II	10	MALB-172, MALB-176, MALB-125, Hawassa dume, MALB-175, MALB-53, MALB-105, MALB-113, MALB-155, MALB-167
III	7	MALB-168, MALB-122, MALB-82, MALB-44, MALB-17, MALB-157, MALB-132,
IV	3	MALB-104, MALB-90, MALB-115,

The results were consistent with the findings of [17], which categorized 20 common bean accessions into 5 clusters, with the II cluster having the most genotypes, followed by clusters III and IV. This result was also consistent with the findings of [24], in which 41 mung bean

genotypes were grouped into five clusters using hierarchical cluster analysis, with cluster II containing the most genotypes (23) followed by cluster III (6) and cluster IV (6), and cluster I and cluster V containing the fewest genotypes (3).

**Figure 3.** A dendrogram demonstrated the genetic diversity of 25 common bean genotypes using 12 quantitative characters.

### 3.3.2. Intra and Inter Cluster Distance Analysis

The average intra and inter cluster distances,  $D^2$  values were indicated in Table 4. The inter cluster distance analysis showed highly significant ( $P < 0.01$ ) difference among all clusters. This result was in line with the finding of [34] who reported that the pair-wise generalized square distance ( $D^2$ ) between the six clusters was highly significant difference between all cluster pairs. The maximum average intra cluster  $D^2$  was obtained in cluster IV ( $D^2 = 4.24$ ) followed by cluster I ( $D^2 = 3.21$ ) and cluster III ( $D^2 = 2.54$ ). The lowest  $D^2$  was recorded in cluster II ( $D^2 = 1.83$ ). Indicated that, the genotypes in each cluster (or each group) were genetically closer than those in other cluster (other groups).

Clusters I and IV had the greatest inter-cluster distance (766.78), followed by clusters II and IV (430.95) and I and III (262.11), indicating that the genotypes with the greatest inter-cluster distance were genetically more divergent and would produce greater genetic diversity through hybridization. According to [35], higher inter-cluster distance increases the likelihood of obtaining transgressive segregates and maximizing heterosis by crossing accessions from different clusters, as unrelated genotypes are more likely to contribute unique desirable alleles at different loci. Cluster III and IV (142.63) and Cluster II and III (84.87) had moderate inter-cluster distances across genotypes in the two clusters.



**Table 4.** Showed the average intra (bold diagonal) and inter cluster distance (upper diagonal) for 25 common bean genotypes based on 12 quantitative characters.

Cluster	I	II	III	IV
I	3.21	53.78**	262.11**	766.78**
II		1.83	84.87**	430.95**
III			2.54	142.63**
IV				4.24

$\chi^2 = 19.67$ , and 24.72 at 5% and 1% probability level respectively

### 3.3.3. Cluster Mean Analysis

Table 5 displays the mean values of four clusters for 12 characteristics of common bean genotypes. Cluster I included five genotypes and was differentiated by a more earlier flowering (39.83) and maturity date (80.5) than cluster IV. This suggested that genotypes in this cluster could be chosen for their early flowering and ripening traits in future crop development. These findings were consistent with the findings of [30], which showed that a cluster I had the shortest time to flowering and maturity for common bean genotypes, so they might be used to explore the potential of selecting early mature cultivars for arid areas to avoid yield loss due to water constraint. Cluster I also had the lowest plant height in cm (37.2), the number of primary branches per plant (3.6), the number of stand counts per hectare (194000), the number of pods per plant (16.9), the number of seeds per pod (5), the number of seeds per plant (83.8), the hundred seed weight in grams (21.6), the biological yield per hectare in kg (3675), the seed yield per hectare in kg (1659.17), and the harvest index (45.19).

**Table 5.** Showed the mean values of four clusters for characteristics of common bean genotypes.

Characters	I	II	III	IV
DF	39.83	41.55	40.71	40.3
DM	80.5	82	79.3	80.5
PH	37.2	51.2	54.92	52.5
NPBP	3.6	4.25	4.57	4.3
SC	194000	200500	210357	222083
NPP	16.9	18.25	21	19.83
NSPP	83.8	90.4	93	97
NSP	5	5.2	5.4	6
HSW	21.67	24.015	25	24.3
BY	3675	3837.5	4038.7	4007

Characters	I	II	III	IV
SY	1659.17	1977.08	2032.8	1997
HI	45.19	51.52	50.3	49.84

## 3.4. Association Between Characters

### 3.4.1. Estimates of Correlation Coefficients at Phenotypic and Genotypic Levels

Table 6 showed the predicted correlation coefficients between all analyzed common bean genotype features at both the phenotypic and genotypic levels. Characteristics such as number of primary branches per plant, biological yield, days of 50% flowering, hundred seed weight, and harvest index were highly significant ( $P < 0.01$ ) and were correlated with seed yield at genotypic and phenotypic levels.

### 3.4.2. Genotypic and Phenotypic Correlation of seed Yield with Other Characters

Table 6 revealed a substantial ( $P < 0.01$ ) genotypic relationship between seed yield, flowering days, primary branch count, seed weight, biological yield, and harvest index. This conclusion is consistent with the findings of [27], who discovered significant relationships between seed yield, days to bloom, and hundred seed weight. [1] and [8] found a positive and significant association between days to blooming and grain production in common beans. There was a significant correlation ( $P < 0.05$ ) between seed yield and days of physiological maturity ( $r_g = 0.413$ ), plant height ( $r_g = 0.448$ ), and number of seeds per plant ( $r_g = 0.492$ ). As a result, any improvements in these features would lead to a large rise in grain yield.

### 3.4.3. Genotypic and Phenotypic Correlation Coefficient Among Other Characters

There were strong genotypic and phenotypic relationships ( $P < 0.01$ ) between days of 50% flowering and days to maturity ( $r_g = 0.772$ ,  $r_p = 0.758$ ). Table 6. This suggested that early blooming genotypes could mature earlier, and that selecting genotypes for excellent performance of these features reduced seed output. This observation is consistent with [6], which revealed that genotypes with early flowering tend to mature early. Days of 50% flowering were positively and significantly associated with plant height at the genotypic level. The findings revealed that genotypes that take longer to blossom also had higher plant height.

In general, phenotypic correlation coefficients were smaller than genotypic correlation coefficients. This is owing to the natural relationship between pairs of features in common bean genotypes. Most of the analyzed traits demonstrated Positive and significant associations at both the genotypic and phenotypic levels indicated the possibility of

correlated response to selection, but negative correlations at the phenotypic and genotypic levels preclude simultaneous

improvement of the traits under discussion.

**Table 6.** Shows the genotype (above diagonal) and phenotype (below diagonal) correlation coefficients for 12 characters among 25 common bean genotypes.

	DF50	DPM	PH	NPBP	SC	NPP	NSP	NSPP	HSW	BY	SY	HI
DF50	1	0.758**	0.346NS	0.494*	-0.14NS	0.355*	0.080NS	0.401*	0.356*	0.443*	0.57**	0.369*
DPM	0.724**	1	0.360NS	0.428*	-0.12NS	0.25N	0.088NS	0.383*	0.29NS	0.33NS	0.413*	0.387*
PH	0.319*	0.328*	1	0.478*	0.330NS	0.83**	-0.19NS	0.649**	0.870**	0.403*	0.448*	0.19NS
NPBP	0.419**	0.426**	0.447**	1	0.240NS	0.59**	-0.16NS	0.481**	0.603**	0.702**	0.89**	0.649**
SC	-0.06NS	-0.03NS	0.299*	0.260*	1	0.503*	0.374*	0.596**	0.568**	0.23NS	0.14NS	0.376*
NPP	0.257*	0.202NS	0.803**	0.574**	0.394**	1	-0.23NS	0.732**	0.905**	0.442*	0.492*	0.27NS
NSP	0.035NS	0.005NS	-0.17NS	-0.11NS	0.297*	-0.2NS	1	0.445*	-0.2NS	-0.28NS	-0.2NS	0.33NS
NSPP	0.313*	0.254*	0.625**	0.440**	0.502**	0.74**	0.465**	1	0.708**	0.24NS	0.397*	0.504*
HSW	0.233NS	0.259*	0.798**	0.608**	0.392**	0.85**	-0.08NS	0.649**	1	0.426*	0.53**	0.35NS
BY	0.364**	0.257*	0.369**	0.622**	0.043NS	0.423*	-0.18NS	0.24NS	0.410**	1	0.87**	0.10NS
SY	0.457**	0.369**	0.432**	0.851**	0.179NS	0.49**	-0.02NS	0.379**	0.511**	0.825**	1	0.566**
HI	0.255*	0.279*	0.197NS	0.551**	0.346**	0.259*	0.223NS	0.378**	0.325*	-0.05NS	0.51**	1

Where, \*\* = highly significant, \* = significant, NS = Non-significant.

### 3.5. Path Coefficient Analysis

#### 3.5.1. The Direct and Indirect Effects of Different Genotypes on Grain Yield

The present study found that biological yield (0.774) and harvest index (0.423) had a considerable positive direct effect on seed yield. This demonstrated the genuine link between these traits, and direct selection was beneficial for increasing seed yield in common bean. These characteristics likewise showed a positive and very significant connection with grain yield (Table 7).

Biological yield showed a high positive indirect connection with days of 50% flowering (0.3428), days of maturity (0.2615), plant height (0.3118), number of major branches (0.543), number of seeds per plant (0.1833),

number of pods per plant (0.342), and hundred seed weight (0.329). Harvest index exhibited a positive strong indirect effect on days of 50% flowering (0.1561), days of maturity (0.1637), numbers of primary branches (0.2745), number of seeds per plant (0.1590), and number of pods per plant (0.104).

The residual effect determined unaccounted variability in the dependent variable (seed yield). Its value of 0.09 suggested that the characters included in the path analysis accounted for 91% of the variation in seed yield. Other independent variables not included in this experiment were estimated to have only a 9% influence on grain output (Table 7). According to [28], the residual effect of other features, environmental conditions, and sample errors or combinations on seed yield.

**Table 7.** Shows the estimated direct (bold diagonal) and indirect (off diagonal) effects of nine characteristics on grain yield at the genotypic level in common bean genotypes.

	DF50	DPM	PH	NPBP	NSPP	NPP	HSW	BY	HI	gr
DF50	0.0127	0.0299	-0.036	0.0377	0.0008	0.0016	-0.014	0.3428	0.156	0.57**
DPM	0.0106	0.0358	-0.013	0.0332	-0.009	0.0011	-0.002	0.2615	0.163	0.413*
PH	0.0051	0.0127	-0.038	0.0327	0.0096	0.0039	-0.008	0.3118	0.079	0.448*

	DF50	DPM	PH	NPBP	NSPP	NPP	HSW	BY	HI	gr
NPBP	0.0069	0.0173	-0.018	0.0686	0.0094	0.0028	-0.006	0.5432	0.274	0.89**
NSPP	0.0004	-0.002	-0.015	0.0276	0.0234	0.0024	-0.006	0.1833	0.159	0.39*
NPP	0.0045	0.0090	-0.030	0.0402	0.0117	0.0047	-0.01	0.3420	0.104	0.49*
HSW	0.0044	0.0104	-0.032	0.0413	0.0132	0.0043	-0.01	0.329	0.148	0.53**
BY	0.005	0.0120	0.0151	0.048157	0.0055	0.0021	-0.042	0.7738	0.0439	0.87**
HI	0.004687	0.013847	-0.007	0.044521	0.008792	0.001174	-0.00345	0.080477	0.4230	0.566**

Residual = 0.09

Note: DF50=Days of 50% flowering; DPM= Days of physiological maturity; PH = Plant height (cm); NPP = Number of pod per plant; NSPP= Number of seed per plant; NPBP = Number of primary branch per plant; HSW = hundred seed weight (g); BY = biological yield (ha-1) and HI= harvest index

### 3.5.2. Phenotypic Direct and Indirect Effects of Different Features on Grain Yield

Table 8 shows the estimated phenotypic direct and indirect effects of nine distinct features on seed yield. Biological yield (0.8146) had the strongest positive direct effect on seed yield, followed by harvest index (0.5326). This finding was consistent with [6], which found that biological yield (0.81) and harvest index (0.57) had the strongest positive phenotypic direct effect on seed yield. [19] also found the strongest positive phenotypic direct influence of biological yield and harvest index on seed yield.

Based on phenotypic path coefficient analysis, the residual

effect was  $R=0.11$ , indicating that the characters included in the phenotypic path analysis explained 89% of the total variation in seed yield and were considered suitable for yield improvement in common bean genotypes.

Overall, the residual effect was 0.09 and 0.11 at the genotypic and phenotypic levels, respectively. This revealed that the nine traits accounted for 91% of grain yield variability at the genotypic and 89% at the phenotypic levels. These findings revealed that the features considered in this study did not explain for all of the diversity in seed yield observed. As a result, selection and hybridization provide numerous chances for increasing the yield of common bean genotypes.

**Table 8.** Shows the estimated direct (bold diagonal) and indirect (off diagonal) effects of nine characteristics on grain yield at the phenotypic level in common bean genotypes.

	DF50	DPM	PH	NPBP	NSPP	NPP	HSW	BY	HI	pr
DF50	0.046765	-0.03139	-0.00269	0.021602	-0.00016	-0.00345	-0.00253	0.263934	0.177912	0.457**
DPM	0.036103	-0.04066	-0.00231	0.020927	0.00015	-0.00226	-0.00258	0.235423	0.1875	0.369**
PH	0.017209	-0.01285	-0.00731	0.020117	-0.00068	-0.00876	-0.00695	0.300592	0.091619	0.432**
NPBP	0.022447	-0.01891	0.00327	0.045004	-0.00089	-0.00626	0.00529	0.506689	0.309481	0.851**
NSPP	0.003554	0.00281	0.0023	0.018767	-0.00214	0.00502	0.00456	0.204468	0.180043	0.379**
NPP	0.014778	-0.00842	-0.00587	0.025832	0.00099	-0.0109	-0.00745	0.344581	0.129439	0.49**
HSW	0.013562	-0.01204	0.00583	0.027363	-0.00112	0.00933	-0.00871	0.333991	0.173118	0.511**
BY	0.015152	0.01175	-0.0027	0.027993	0.00054	-0.00461	0.00357	0.814612	-0.00959	0.825**
HI	0.015619	-0.01431	-0.00126	0.026147	-0.00072	-0.00265	-0.00283	-0.01466	0.53267	0.51**

Residual = 0.11

## 4. Summary, Conclusions and Recommendations

### 4.1. Summary

The current review included 25 common bean genotypes assessed at the Areka Agricultural Research Center in  $5 \times 5$  basic lattice designs. Variance analysis revealed significantly significant differences between common bean genotypes for the traits investigated. The highly significant difference revealed a substantial degree of heterogeneity among genotypes.

The GCV and PCV values varied from 2.4% for days of physiological maturity to 24.87% for plant height and 3.3% for days of physiological maturity to 26.1% for seed yield, respectively. The highest range of GCV and PCV for these parameters revealed the low expression of environmental variation among common bean genotypes and the possibility of yield improvement through selection.

Estimated values of broad sense heritability ( $H^2\%$ ) for 12 characters ranged from (42.2%) for harvest index to (98.14%) for plant height). The characters such as plant height, days of flowering and number of pod per plant, number of seed per plant, biological yield and seed yield exhibited high heritability ( $H^2\%$ ). This result indicated that genetic effects had a strong influence on the expression of these characters, that selection for these characters would be effective due to their additive gene action, and that the characters would be sufficiently heritable to boost the yield of common bean genotypes.

High broad sense heritability ( $H^2$ ) coupled with high expected genetic advance as percent of mean (GAM %) for the characters plant height, numbers of pod per plant, number of seed per plant, biological and seed yield. This indicated direct selection of these characters would be possible for yield increment of the genotypes.

There were positive and highly significant genotypic and phenotypic relationships between characters' days of 50% flowering and days to maturity. This suggested that early flowering genotypes could mature earlier. The magnitude of phenotypic correlation coefficients was less than genotypic correlation coefficients. This study demonstrated the presence of an inherent relationship between diverse features, which supports the potential of correlated response to selection. The characteristics' biological yield and harvest index showed a strong positive and direct effect on seed production. This demonstrated the genuine link between these traits, and direct selection was beneficial for increasing seed yield in common bean.

Based on  $D^2$  value, 25 common bean genotypes were grouped into 4 clusters. Genotypes within similar clusters were more closely connected than genotypes from other groupings. The largest inter-cluster distance was reported between cluster I and IV (766.78), followed by cluster II and IV (430.95), and I and III (262.11), indicating that the

genotypes with maximum inter-cluster distance were genetically more divergent and produced broader variety through hybridization.

### 4.2. Conclusions and Recommendations

The results of the current investigation suggested that the tested genotypes exhibited high genetic variability. Characters with a high GCV, heritability, genetic advance, positive correlation coefficient, and direct effect on seed yield should be carefully considered. Thus, there is a significant chance for yield increase through indirect selection and hybridization, which entails crossing common bean genotypes from various divergent clusters. Furthermore, genotypes in cluster III should be prioritized because they produced the highest average seed yield (kg ha<sup>-1</sup>). Selection and hybridization of the tested genotypes would result in a significant increase in the target area's common bean yield. Because this discovery is based on one year and one location, it is suggested that the experiment be repeated over several years in different climatic zones to gain trustworthy information regarding common bean genotypes. To reach meaningful conclusions and suggestions, more research on a large number of genotypes and quality criteria is required.

## Abbreviations

AARC	Areka Agricultural Research Center
ATA	Agricultural Transformation Agency
CIAT	Centro Internacional de Agricultura Tropical
CSA	Central Statistic's Agency
ETB	Ethiopian Birr
GDP	Gross Domestic Production
SARI	Southern Agricultural Research Institute
SNNPR	Southern Nation, Nationalities and Peoples Region

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## Conflicts of Interest

The author declares no conflicts of interest.

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