Journal of Agricultural Science and Food Technology
Vol. 7 (5), pp. 82-90, October, 2021
ISSN: 2465-7522
Research Paper
https://doi.org/10.36630/jasft_21004
http://pearlresearchjournals.org/journals/jasft/index.html

Evaluation and genetic analysis of common bean genotypes (*Phaseolus vulgaris* L.) at Dibatie and Mandura, Northwestern Ethiopia

Gezahegn Tefera

Accepted 19 September 2021

Pawe Agricultural Research Center P.O. Box- 25, Ethiopia. Corresponding author E-mail: gezahegn.tefera@eiar.gov.et

ABSTRACT

Assessing and understanding the variations existing in crops due to genetic composition and environmental variability is very important in order to exploit the genetic constitution of crop plants. To this aim, variability measures such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are commonly used. Heritability and genetic advance are major concerns for common bean to identify important traits for common bean genetic improvement. The field experiment was conducted at Mandura and Dibatie research substations working with sixteen genotypes of the common bean during 2017/2018 in lattice design with three replications to evaluate the performance of common bean genotypes and estimate the genetic variability. Heritability and genetic advance were estimated in relation to yield and its component traits for future breeding programs. Combined analysis of variance across locations revealed highly significant variations among genotypes for all traits under study. The PCV ranged from 3.36% for days to flowering to 15.91% for a number of pods per plant while the GCV value ranged from 0.75% for days to flowering to 13.74% for the number of pods per plant. Broad sense heritability values ranged from 5.00% for days to flowering to 84.61% for a hundred seed weight. Generally, the result of the study showed that significant genetic variability among tested genotypes and a simple selection for effective improvement of these traits.

Keywords: common bean, genetic variability, genetic advance, heritability

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.), locally known as '*Boleqe'* in Ethiopia and commonly known as dry bean and haricot bean, is an important grain legume grown worldwide (Keba, 2018). In Ethiopia, common bean is the most important legume as a source of protein and export commodity (Yohannes et al., 2020). It grows in most of the agro-ecology zones from low land (300-1100 m.a.s.l.) to midland (1400-2000 m.a.s.l.) part of the country. Among the pulse crops cultivated in Ethiopia, common bean is the second largest in terms of production with a share of 16.22 %, next to faba beans (CSA, 2019). In the 2018/19 cropping season, common bean was produced on about 288637 ha of land from which 4883201 quintals of yield were obtained. The current national average yield of common bean is 1.69 t/ha, which is quite low compared with the yield potential of 3 to 4 t/ha observed in research fields (Blair et al., 2012; Beebe et al., 2013). The major production constraints that have been responsible for low productivity of the crop includes lack of improved varieties, insect pest and diseases, poor agronomic practices, drought stress, soil acidity and poor soil fertility (Keba, 2018; Assefa et al., 2019; Degu et al., 2020). Genetic improvement of common bean provides an opportunity to overcome some of these constraints through the exploitation of the genetic variability present in common bean germplasm. Assessing and understanding the variations existing in crops due to genetic composition and environmental variability is very important in order to exploit the genetic constitution of crop plants. Variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are grown (Allard, 1960). Estimation of variability existing among germplasma were measured using phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance are a major concern for common bean genetic improvement programs (Rahman et al., 2016; Tiwari et al., 2019). It is equally important to evaluate different common bean genetic backgrounds under different growing environment for adaptation and stability to improve production and productivity. Therefore, the objective of the present study was to

Table 1. Agro-climatic conditions of study locations.

Location	Soil type	Altitude (m.a.s.l)	Location		Rain fall (mm)	Temperature	
			latitude	longitude		min.	Max.
Dibatie	Nitosol	1572	10° 30'N	36° 10'E	1650-1700	15 °c	29 °c
Mandura	Nitosol	1455	11°04'N	36° 25'E	1100-1800	15°c	33 °c

Source: Pawe Agricultural Research Center (2016).

Table 2. List of common bean genotypes used in the study.

S.No	Genotypes	Status of the genotypes	Seed source	Year of release
1	DAB 220	Advanced lines	MARC	NR
2	DAB 241	Advanced lines	MARC	NR
3	DAB 245	Advanced lines	MARC	NR
4	DAB 259	Advanced lines	MARC	NR
5	DAB 251	Advanced lines	MARC	NR
6	DAB 320	Advanced lines	MARC	NR
7	DAB 288	Advanced lines	MARC	NR
8	DAB 292	Advanced lines	MARC	NR
9	DAB 278	Advanced lines	MARC	NR
10	DAB 298	Advanced lines	MARC	NR
11	DAB 237	Advanced lines	MARC	NR
12	DAB 283	Advanced lines	MARC	NR
13	DAB 396	Advanced lines	MARC	NR
14	DAB 265	Advanced lines	MARC	NR
15	DAB 247	Advanced lines	MARC	NR
16	GLP 2	Released variety (check)	MARC	2011

MARC= Melkassa Agricultural Research center, NR= not yet released.

evaluate the performance of common bean genotypes and estimate the genetic variability, heritability and genetic advance as a percent of mean in relation to yield and its component traits for future genetic improvement.

MATERIALS AND METHODS

Description of the experimental sites

The field experiment was conducted under rain-fed condition during 2017/2018 cropping season at Mandura and Dibatie research substations of Pawe Agricultural Research Center (PARC) which are located in Metekel zone, Benishangul-Gumuz region of Ethiopia. Mandura and Dibatie are located at 530 and 543 km respectively from Addis Ababa. The test locations where the present study was conducted are indicated in Table 1.

Plant materials

Sixteen common bean genotypes including one check are used for this experiment (Table 2). The aforementioned were obtained from Melkassa Agricultural Research Center.

Experimental design and trial management

Field experiment was laid out in 4x4 triple lattice design at each location. The plot size was 4 m long and 2.4 m wide (9.6m^2) with 6 rows. The space between rows and plants was 40 and 10 cm, respectively. Fertilizer rate of 100 kg/ha NPS (Diammonium Phosphate) was applied uniformly for all experimental plots during sowing. All additional field management practices were carried out according to agronomic recommendations.

Data collection

Data was collected on both plot on plant basis a random sampling technique with the use of descriptors for common bean (IBPGR, 1982).

Data collected on plot basis

Days to 50% flowering (DTF)

The number of days from emergence to 50% flowering of the plants per plot.

Hundred seed weight (HSW)

Was determined by taking a randomly sampled of 100 seeds from each experimental plot and adjusted them to 12.5% moisture content.

Grain yield (GY)

Grain yield in grams obtained from the two harvestable central rows of each plot and adjusted to 12.5% moisture content and then it was converted to tons per hectare.

Data collected on plant basis

Plant height

The height of five randomly taken plants was measured at maturity stage from the ground to the tip of the plant.

Number of pods per plant

Was determined by counting pods of the five randomly selected plants.

Number of seeds per pod

The seeds from pods of five randomly selected plants were counted and the average was taken

Statistical analysis

Homogeneity test

Before computing the combined analysis, homogeneity test for the error variance was performed using F-test according to (Fikreselas and Seboka, 2012) and the value was compared with the F table (Gomez and Gomez, 1984). The test indicated that the error means were homogeneous except for days to maturity and the data were combined for further analyses.

Analysis of variance (ANOVA test)

Comparisons of the relative efficiency of lattice design to Randomized Complete Block Design (RCBD) were checked. Lattice design was found to be more efficient than RCBD. The analysis of variance was carried out using GLM procedure of SAS version 9.3 (SAS, 2012), according to lattice design for both individuals and combined across locations. Mean comparisons among treatment means were conducted by the least significant difference (LSD) test at 5% levels of significance. The combined analysis of variance was calculated using the following model:

Pijkl = μ+ gi+ bk (j) (l) + rj(l) + Ll + (gl)il + eijkl

Where, Pijkl= phenotypic value of i^{th} genotype under j^{th} replication at l location and k^{th} incomplete block within replication j and location l, μ= grand mean, gi= the effect of i^{th} genotype, bk (j)(l)= the effect of incomplete blocks within replication j and location l, rj(l)= the effect of replication j within location l, Ll= the effect of location l, (gl)il = the interaction effects between genotype and location, and eijkl= the residual.

Estimation of Genetic Parameters

Estimates of variance components, phenotypic and genotypic coefficient of variation, broad-sense heritability, genetic advance and genetic advance as percent of the mean for the data combined over locations were computed according to Burton and DeVane (1953), Johnson et al. (1955), Singh and Chaudhary (1979) and Falconer and Mackay (1986).

$\sigma^2e = MSE$
$\sigma^2gl = (MSGXL - MSE)/R$
$\sigma^2g = (MSG - MSGXL/RL)$
$\sigma^2p = \sigma^2g + \sigma^2gl/L + \sigma^2e/LR = MSG/RL$

Where, σ^2e = environmental variance, σ^2gl = genotype by location variance, MSG = mean square of genotype, MSE = mean square, σ^2g = Genotypic variance, σ^2p = phenotypic variance, MSGxL = mean square of genotype by location interaction, R = number of replications and L = number of locations

$$\text{Phenotypic coefficients of variation}(PCV) = \frac{\sqrt{\sigma^2p}}{\bar{x}} x100$$

$$\text{Genotypic coefficients of variation }(GCV) = \frac{\sqrt{\sigma^2g}}{\bar{x}} x100$$

Where x̄ = grand mean of the traits under consideration.

$$\text{Heritability}(h^2b) = \frac{\sigma^2g}{\sigma^2p} \text{ x } 100$$

Where h^2b = heritability in broad sense

$$GA = k * \sigma p * h^2b$$

Where GA = expected genetic advance, K = constant (selection differential where K = 2.06 at 5% selection intensity), σp = phenotypic standard deviation on mean basis

$$GAM = \frac{GA}{\bar{x}} \text{ X } 100$$

Where GAM = genetic advance as percent of the mean, GA = genetic advance under selection, and x̄ = mean of the population in which selection is effective.

Cluster analysis

Clustering of genotypes was carried out using the average linkage method by PROC clustering strategy implemented in SAS version 9.3 and appropriate numbers of clusters were determined from the values of Pseudo F and Pseudo T^2 statistics (SAS, 2012)

Genetic divergence analysis

A measure of a group distance based on multiple traits was given by generalized Mahalanobis D^2 statistics (Mahalanobis, 1936) for quantitative characters. The distance between any two groups was estimated using SAS Version 9.3 (SAS, 2012)

Principal component analysis

Principal component analysis was computed using (R, 2020). Principal components (PCs) with Eigenvalue greater than 1.0 had been used as criteria to determine

Table 3. Mean square of combined analysis of variance for six traits of common bean genotypes evaluated at Mandura and Dibatie during the 2017/2018 cropping season.

	Mean square				
Traits	**Genotypes (df=15)**	**Location (df=1)**	**G x L (df=15)**	**Error (df=64)**	**CV(%)**
PHT	133.44**	1832.25**	27.07**	8.39	7.02
DTF	11.60**	928.15**	11.02**	1.32	2.80
PPP	7.49**	5.53*	1.90	1.34	16.51
SPP	0.48**	2.72**	0.19**	0.05	7.12
HSW	152.97**	47.32	23.54**	12.72	7.81
GY	282249.30**	89061.99	60272.88	50162.14	12.39

PHT=plant height (cm), **DTF**=days to flowering, **PPP**= pods per plant (number), **SPP**= seeds per pod (number), **HSW**=hundred seed weight (g), **GY**= grain yield (kg/ha), **DF**= degree of freedom, **CV** (%) = coefficient of variation, **G x L**= genotype by location interaction, * = significant at ($p \leq 0.05$), ** = highly significant at ($p \leq 0.01$)

Table 4. Range (minimum to maximum) and mean performance of different common bean genotypes for six traits evaluated across two testing locations.

Genotypes	PHT	DTF	PPP	SPP	HSW	GY
DAB 220	38.370	40.580	6.810	3.600	45.930	2031.900
DAB 241	42.370	41.040	6.080	3.260	44.270	1750.600
DAB 245	39.770	39.670	5.620	3.330	57.670	1983.800
DAB 259	37.730	41.330	6.640	3.380	41.600	1670.900
DAB 251	41.230	40.290	8.080	3.250	49.430	2101.300
DAB 320	52.400	43.040	6.880	3.080	39.330	1552.200
DAB 288	36.930	40.580	7.510	3.340	50.470	1970.500
DAB 292	39.170	39.170	5.590	2.850	43.830	1545.300
DAB 278	40.930	42.000	6.090	3.270	45.930	1667.800
DAB 298	37.170	40.420	5.290	3.670	45.200	1579.100
DAB 237	38.830	41.210	7.910	3.290	39.930	1971.900
DAB 283	39.470	41.750	8.480	2.670	42.900	1545.300
DAB 396	40.870	40.290	6.980	3.320	41.530	1737.600
DAB 265	40.530	40.130	7.830	2.900	43.070	1720.300
DAB 247	41.300	41.670	7.410	3.010	54.270	2221.600
GLP 2	52.900	44.920	9.190	2.790	44.930	1870.100
Min	36.930	39.170	5.290	2.670	39.330	1545.300
Max	52.900	44.920	9.190	3.670	57.670	2221.600
Mean	41.25	41.33	7.02	3.19	45.64	1807.5
LSD	3.34	1.33	1.34	0.26	4.11	258.32

PHT=plant height (cm), **DTF**=days to flowering, **PPP**= pods per plant (number), **SPP**= seeds per pod (number), **HSW**=hundred seed weight (g), **GY**= grain yield (kg/ha), **Min**=minimum and **Max**=maximum values of the trait evaluated, **LSD**= least significant difference

the number of PCs (Kaiser, 1960)

RESULTS AND DISCUSSION

The results from the combined analysis of variance across the two locations are presented in Table 3. The mean square due to genotypes showed highly significant differences for all of the studied traits, which could be exploited through selection, as variability within populations is a basic prerequisite for plant breeding program. Genotype by location interaction was highly significant for days to flowering, plant height and number of seeds per pod and hundred seed weight, indicating that the differential response of genotypes to different growing environments for the traits evaluated.

Mean Performance of the Genotypes

Based on the combined analysis, a wide range of variations was obtained for all traits studied. Plant height ranged from 36.93 to 52.90, followed by days to flowering, which ranged from 39.17 to 44.92, number of pods per plant ranged from 5.29 to 9.19, number of seeds per pod ranged from 2.67 to 3.17, hundred seed weight ranged from 39.33 to 57.65 and grain yield ranged from 1545.30 to 2221.60kg/ha (Table 4). This signifies the presence of a wide range of genetic

Table 5. Estimates of genetic parameters for 16 common bean genotypes grown at Mandura and Dibate using six yield contributing traits during 2017/18 cropping season.

Traits	σ^2g	σ^2p	GCV (%)	PCV (%)	h^2b (%)	GA at 5%	GAM (%)
PHT	17.73	22.24	10.21	11.43	79.71	7.74	18.77
DTF	0.10	1.93	0.75	3.36	5.00	0.14	0.35
PPP	0.93	1.25	13.74	15.91	74.63	1.72	24.46
SPP	0.05	0.08	6.90	8.88	60.42	0.35	11.05
HSW	21.57	25.50	10.18	11.06	84.61	8.80	19.28
GY	36996.07	47041.55	10.64	12.00	78.65	351.38	19.44

PHT=plant height (cm), **DTF**=days to flowering, **PPP**= pods per plant (number), **SPP**= seeds per pod (number), **HSW**=hundred seed weight (g), **GY**= grain yield (kg/ha).

variability among the evaluated characteristics and provides a better opportunity for further improvement through selection. The overall performance of the genotypes from the combined analysis were indicated in Table 4.

Estimate of variance components and coefficient of variation

The phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were computed to assess the existing variability in common bean genotypes. The PCV values were higher than the GCV values for all traits studied in the present study (Table 5), the magnitude of the difference was small for all traits. The GCV value ranged from 0.75 % for days to flowering to 13.74 % for number of pods per plant, whereas PCV value ranged from 3.36 % for days to flowering to 15.91 % for number of pods per plant. Subramanian and Madhavamenon (1973) and Deshmukh et al. (1986) classified values as low (<10%), moderate (10-20%) and high (>20%). Based on this, moderate PCV and GCV values were observed for plant height, number of pods per plant, hundred seed weight and grain yield, respectively, implying that selection based on these characters could be effective and genotypic potential could be predicted through their phenotypic expression. Low phenotypic and genotypic coefficients of variation were observed for days to flowering and number of seeds per pod, respectively, showing a narrow range of variability and high environmental influence on their expression with a low scope of selection. Similarly, Ejigu et al. (2018) reported medium GCV and PCV values for a number of pods per plant and grain yield, and low GCV and PCV values for days to flowering in common bean genotypes.

Estimates of broad-sense heritability (h^2b) and genetic advance (GA)

Heritability is the proportion of observed variability that is due to heredity, the remainder being due to environmental causes (Allard, 1960). It represents the effectiveness of the selection of genotypes that could be based on phenotypic performance. Heritability values are categorized as low (0-30%), medium (30-60 %) and high (>60%) as suggested by Johnson et al. (1955). The estimated heritability for the studied traits was presented (Table 5).

In the present study, all the measured traits expressed high heritability values except for days to flowering with heritability value of 5%. High heritability values were recorded for plant height (79.71%), followed by number of pods per plant (74.63%), hundred seed weight (84.61%) and grain yield (78.65%), which indicated that the variation observed was mainly under genetic control and less influenced by the environment and the possibility of progress from selection. Similar findings were also reported by Singh et al. (2018) and Kefelegn et al. (2020). The low heritability (5%) was recorded for days to flowering showing that the trait was highly influenced by environmental and genetic improvement, though selection for this trait could be difficult. Contrary to the present result, Singh et al. (2018) and Kefelegn et al. (2020) reported a high heritability value for days to flowering. The dissimilarity in this finding could be explained by the difference in genotype and test locations used.

High heritability does not always indicate high genetic advance, heritability in conjunction with genetic advance would give a more reliable index of selection for selecting superior varieties (Ali et al., 2002). Johnson et al. (1955), suggested genetic advance as a percent of mean can be classified as low (0-10%), moderate (10-20%) and high (20% and above). High heritability estimate along with high genetic advance as percent of mean was observed for number of pods per plant reflecting that this trait is controlled by additive genetic variance and selection may be effective in early generations for this trait (Table 5). Yohannes et al. (2020), reported similar result for number of pods per plant. Days to flowering showed low heritability accompanied with low genetic advance as

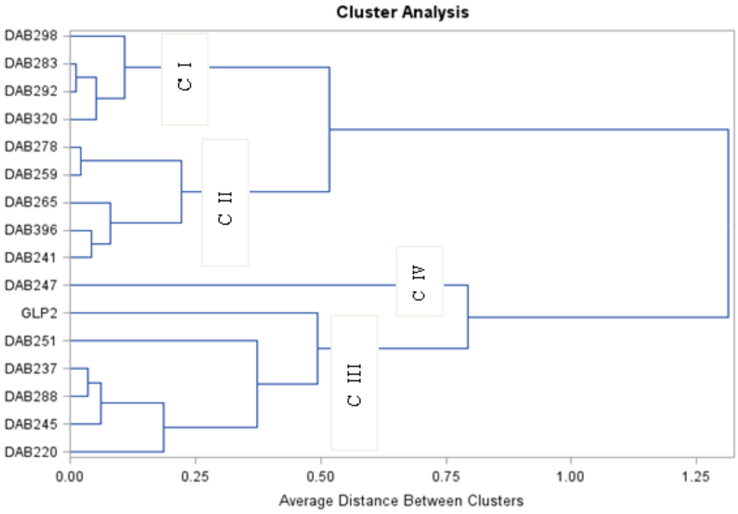

Figure 1. Dendrogram showing grouping of 16 common bean genotypes using yield and yield related traits.

Table 6. Cluster mean of 16 common bean genotypes evaluated in 2017/18 cropping season at Mandura and Dibatie

Traits	PHT	DTF	PPP	SPP	HSW	GY
C I	42.05	41.10	6.56	3.07	42.82	1555.48
C II	40.49	40.96	6.72	3.23	43.28	1709.44
C III	41.34	41.21	7.52	3.27	48.06	1988.25
C IV	41.30	41.67	7.41	3.01	54.27	2221.60

PHT=plant height(cm), **DTF**=days to flowering, **PPP**=number of pods per plant, **SPP**=number of seeds per pod, **HSW**=hundred seed weight(g), **GY**= grain yield(kg/ha).

percent of mean, this suggested that less scope for selection as they were more influenced environmentally. Similar results were also reported by Ejigu et al. (2018).

Cluster Analysis

The D^2 values based on the pooled mean of genotypes resulted in classifying the sixteen common bean genotypes into four clusters as depicted in Figure 1. The mean value of the six quantitative traits in each cluster is presented in Table 6. Cluster I contained four genotypes (DAB292, DAB 283, DAB 320 and DAB 298), which were characterized by a low number of pods per plant, hundred seed weight and tall in height, while Cluster II comprised of five genotypes (DAB259, DAB 278, DAB 241, DAB 396 and DAB 265), which were characterized by short plant height and shorter period for flowering. Cluster III is comprised of six genotypes (DAB288, DAB 237, DAB 245, DAB 220, DAB 251 and GLP2) classified by a high number of pods per plant and seeds per pod. Cluster IV contained only one genotype (DAB247) characterized by a longer period for flowering, low number of seeds per pod, high grain yield and hundred seed weight. In conformity with this study, Negash (2006) classified 144 common bean germplasm into nine clusters. Kefelegn et al. (2020) also studied 15 released common bean varieties and grouped them into four clusters.

Genetic Distance (D^2) Analysis

The shortest squared distance was found between cluster-I and II (D^2 = 21.8), followed by cluster- II and III (D^2 = 77.07), indicating that such genotypes were not genetically diverse such genotypes were not recommended for creating variability through crossing within clusters (Table 7). These clusters have shown similar performance especially with mean number of pods per plant and seeds per pod, while they have the least similar performance with their plant height and grain yield. The maximum distance was found between cluster I and cluster IV (D^2 = 556.89), with a large difference among the traits in hundred seed weight and grain yield. The greater distance between clusters, indicating that the genotypes included in these clusters revealed a broad spectrum of genetic diversity and is very important for choosing parents for generating genetic variability through crossing and hybridization in

Table 7. Inter cluster distance (D^2) of four clusters constructed from 16 common bean genotypes.

Clusters	I	II	III	IV
I	0	21.8**	179.37**	556.89**
II		0	77.07**	362.23**
III			0	110.86**
IV				0

$X^2_{0.01}$=15.09, **=significant at 1% probability level.

Table 8. The eigenvalues and eigenvectors of the correlation matrix for 16 common bean genotypes tested using six yield contributing traits.

Components	PC1	PC2
Eigenvalue	2.64	1.65
% variance	44	27
Cumulative	44	71
Characters	**Eigenvector**	
Plant height	0.51	0.05
Days to flowering	0.52	0.11
Number of pods per plant	0.43	0.36
Number of seeds per pod	-0.43	-0.04
Hundred seed weight	-0.27	0.58
Grain yield	-0.13	0.72

common bean genetic improvement. Generally, crosses between distantly related clusters and individuals are expected to be more heterotic closely related genotypes (Kefelegn et al., 2020). In the present study, therefore, hybridization programme for common bean improvement between clusters I and IV would be more heterotic than those between clusters I and II. Hence, selecting parents from cluster III for number of pods per plant and seeds per pod, and parents from cluster IV for grain yield and hundred seed weight can be crossed and heterozygous offspring would be generated.

Principal Component Analysis

In this study, the eigenvalue for the first principal component accounted for 44% of total variation and the second principal component accounted for 27% and together, they accounted for about 71% of the total variation (Table 8). The first principal component is mostly influenced by plant height and days to flowering, while the second component is influenced by grain yield and hundred seed weight. A trait with a coefficient greater than 0.3, had a large enough effect and was considered as an important trait. Traits having less than 0.2 coefficient value were considered to be no effect on the overall variation (Adebisi et al., 2013). Thus, all studied traits except grain yield in PCA 1 and number of pods per plant, hundred seed weight and grain yield in PCA 2 have found large contribution to the total variation of the genotypes. The plot of PCA 1 and PCA 2 shows the relationship among the traits per genotype. DAB247 and GLP2 were the most unique genotypes among all tested genotypes (Figure 2). Their uniqueness is mostly described by characters like grain yield and hundred seed weight, and a number of pods per plant, days to flowering and plant height, respectively.

In a biplot analysis, the correlation coefficient between any of the two characters can be approximated by the cosine of the angle between the vectors (Yan and Kang, 2003). Two characters are positively correlated if the angle between vectors is <90, negatively correlated if the angle is >90, and independent if the angle is 90 (Yan and Rajcan, 2002). Based on these scholars, number of seeds per pods, number of pods per plant, days to flowering and plant height have a high positive correlation while they have a negative correlation with grain yield, hundred seed weight and number of seeds per plant. Hundred seed weight is highly and positively correlated with grain yield.

CONCLUSION

Assessment of genetic variability exists at phenotypic level and genetic level such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability and genetic advance are a major concern for common bean genetic improvement to identify the most important traits in common bean breeding program. The estimated GCV and PCV values ranged from low to medium for all traits studied. The PCV values were higher than the GCV values for all traits observed in the present study. However, the magnitude of the difference was small for all traits and measured traits showed high heritability values except days to flowering with heritability value of 5%.

High heritability estimate coupled with high genetic advance as percent of mean was observed for a number of pods per plant. Days to flowering showed low heritability accompanied with low genetic advance as percent of the mean. Generally, the result of the present study showed significant genetic variability among

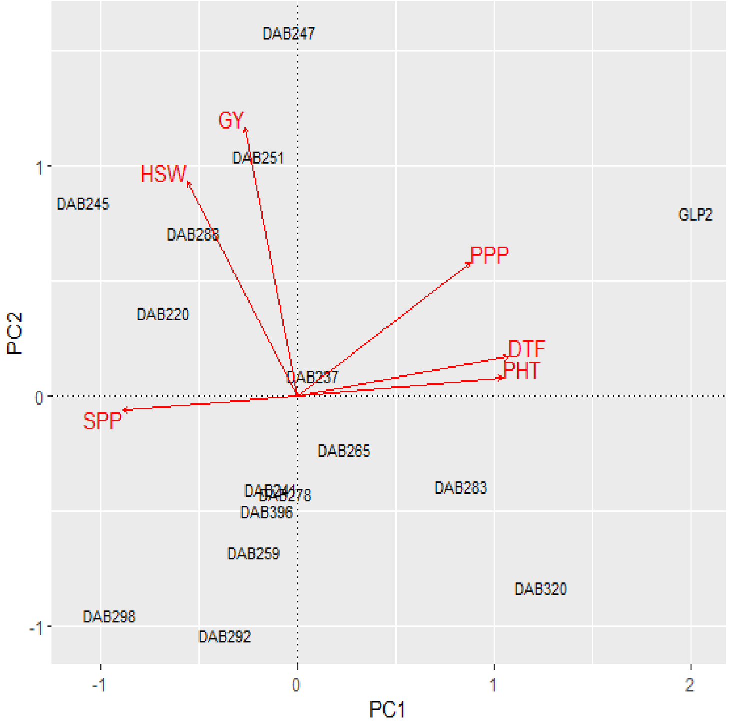

Figure 2. Correlation of traits and arrangement of 16 common bean genotypes of biplot.

tested genotypes and simple selection for effective improvement of these traits.

ACKNOWLEDGEMENTS

The author would like to thank Ethiopian Institutes of Agricultural Research (EIAR) and Melkessa Agricultural Research center (MARC) for giving the study materials funding for this study.

REFERENCES

Adebisi MA, Okelola FS, Ajala MO, Kehinde TO, Daniel IO, and Ajani OO (2013). Evaluation of Variations in Seed Vigour Characters of West African Rice Genotypes Using Multivariate Technique. American Journal of Plant Sciences, 04(02):356-363.

Ali Z, Khan AS and Asad MA (2002). Salt Tolerance in Bread Wheat: Genetic Variation and Heritability for Growth and Ion Relation. Asian Journal of Plant Sciences, 1(4):420-422.

Allard RW (1960). Principle of Plant Breeding. Jhon Wiley and Sons. Inc.

Assefa T, Assibi Mahama A, Brown AV, Cannon EKS, Rubyogo JC, Rao IM, Blair MW and Cannon SB (2019). A review of breeding objectives, genomic resources, and marker-assisted methods in common bean (*Phaseolus vulgaris* L.). Molecular Breeding, 39(2):20.

Beebe SE, Rao IM, Blair MW and Acosta-Gallegos JA (2013). Phenotyping common beans for adaptation to drought. Frontiers in Physiology, 4:1-20.

Blair MW, Galeano CH, Tovar E, Muñoz Torres MC, Castrillón AV, Beebe SE and Rao IM (2012). Development of a Mesoamerican intra-genepool genetic map for quantitative trait loci detection in a drought tolerant × susceptible common bean (*Phaseolus vulgaris* L.) cross. Molecular Breeding, 29(1):71-88.

Burton GW and DeVane EH (1953). Estimating Heritability in tall fescue (*Festuca Arundinacea*) from Replicated Clonal Material 1. Agronomy Journal, 45(10):478-481.

CSA (2019). Report on area and production of major crops: Vol. I.

Degu T, Yaregal W and Gudisa T (2020). Status of Common Bean (*Phaseolus vulgaris* L.) Diseases in Metekel Zone, North West Ethiopia. Journal of Plant Pathology and Microbiology, 11(5):1-8.

Deshmukh S, Basu M and Reddy P (1986). Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. Indian J. Agric. Sci., 56:816-821.

Ejigu E, Wassu M and Berhanu A (2018). Genetic variability, heritability and expected genetic advance of yield and yield related traits in common bean genotypes (*Phaseolus vulgaris* L.) at Abaya and Yabello, Southern Ethiopia. African Journal of Biotechnology, 17(31):973-980.

Falconer D and Mackay F (1986). An Introduction to Quantitative Genetics (4th edn). Longman.

Fikreselas M and Seboka H (2012). Genetic Variability on Seed Yield and Related Traits of Elite Faba Bean (*Vicia faba* L.) Genotypes. Pakistan Journal of Biological Sciences, 15(8): 380-385.

Gomez KA and Gomez AA (1984). Statistical procedures for agricultural research. John Wiley and Sons.

IBPGR (1982). International Board for Plant Genetic Resources Descriptors for Phaseolus vulgaris. IBPGR Secretariat.

Johnson HW, Robinson HF and Comstock RE (1955). Estimates of Genetic and Environmental Variability in Soybeans 1. Agronomy Journal, 47(7):314-318.

Kaiser HF (1960). The Application of Electronic Computers to Factor Analysis. Educational and Psychological Measurement, 20(1):141-151.

Keba HA (2018). Adaptability evaluation of common bean (*Phaseolus vulgaris* L.) genotypes at Western Ethiopia. Journal of Agricultural Biotechnology and Sustainable Development, 10(7):140-146.

Kefelegn N, Mekibib F and Dessalegn Y (2020). Genetic Advancement and Variability of Released Common Bean (*Phaseolus vulgaris* L.) Varieties from 1974–2009 GC in Ethiopia. Advances in Agriculture, 2020:1-7.

Mahalanobis PC (1936). On the generalized distance in statistics. National Institute of Science of India.

Negash K (2006). Studies on genetic divergence in common bean (*Phaseolus vulgaris* L.) introductions of Ethiopia. Unpublished MSc thesis, School of Graduate Studies of Addis Ababa University in Applied Genetics (Biology). Addis Ababa, Ethiopia.

R (2020). R: A language and environment for statistical computing. R

Foundation for Statistical Computing, Vienna, Austria. https://www.r-project.org/.

Rahman MA, Kabir ML, Hasanuzzaman M, Rahman MA, Rumi RH and Afrose MT (2016). Study of variability in bread wheat (*Triticum aestivum* L.). Inter. J. Agro. Agri. Res, 8(5): 66-76.

SAS (2012). Statistical analysis System. Version 9.3. SAS Institute Inc. Cary, NC., USA.

Singh DK, Singh DP and Singh SS (2018). Studies of Genetic variability, heritability and genetic advance for yield and related traits in French bean (*Phaseolus vulgaris* L.). Journal of Pharmacognosy and Phytochemistry, 7(2):236-240.

Singh R and Chaudhary B (1979). Biometrical methods in quantitative genetic analysis. Kalyani Publishers.

Subramanian S and Madhavamenon P (1973). Combining ability in rice. Madras Agricultural Journal, 60:419-421.

Tiwari DN, Tripathi SR, Tripathi MP, Khatri N and Bastola BR (2019). Genetic Variability and Correlation Coefficients of Major Traits in Early Maturing Rice under Rainfed Lowland Environments of Nepal. Advances in Agriculture, 2019:1-9.

Yan W and Kang MS (2003). GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists. CRC PRESS.

Yan W and Rajcan I (2002). Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Science, 42(1):11-20.

Yohannes S, Loha G and Gessese MK (2020). Performance Evaluation of Common Bean (*Phaseolus vulgaris* L.) Genotypes for Yield and Related Traits at Areka, Southern Ethiopia. Advances in Agriculture, 2020: 1-8.