Studies on Genetic Variability of Common Bean (*Phaseolus vulgaris* L.) Varieties for Yield and Yield Related Traits in Western Ethiopia

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Abstract: The objectives of the study were to determine genetic variability, interrelationships among different traits, and to estimate genetic divergence among the nineteen common bean varieties. Nineteen common bean varieties were tested for yield and yield related traits in completely randomized block design in three replications at Uke Research and Technology Demonstration Site, in 2018 cropping season. The analysis of variance showed that the varieties were significantly different for all traits except for days to 50% flowering and number of seed per pod. Among all tested varieties Anger gave the maximum yield (4.03 t/ha) followed by Awash 1 (3.93 t/ha) and Awash-2 (3.49 t/ha). Genotypic and phenotypic coefficient of variation values greater than 30% were obtained for plant height, leaf area, pod length, and seed yield indicating high variations among the tested genotypes. Heritability values greater than 60% were obtained for plant height, leaf area, inter node length, pod length, number node per plant, number of pod per plant, 100-seed weight, seed yield, biological yield and harvest index; Genetic advance as a percent of mean values were greater than 30% for plant height, leaf area, inter node length, pod length, number of node per plant, number of pod per plant, seed yield, biological yield and harvest index indicating, the traits are governed by additive genes. Genotypic and phenotypic correlation coefficient showed that seed yield was significantly and positively correlated with biological yield and harvest index both at genotypic and phenotypic levels, indicating they are true indicator for higher seed yield. Whereas the correlation between seed yields and other traits not strong in magnitudes. The principal component analysis indicated that the first four principal components explained 84.78% of the total variation in the varieties, suggesting the characters considered were sufficient to explain the total variations. The genetic divergence (D^2) analysis indicated that the 19 varieties were grouped in to four clusters and distances between these clusters were significantly different between all the cluster combinations. This indicates that there is an opportunity to bring about improvement through hybridization of varieties from different clusters and subsequent selection from the segregating generations. Generally, the tested varieties had ample genetic variations and yield potential to use in the future breeding program in western Ethiopia.

Keywords: Common Bean, Genetic Advance, Genotype, Heritability, Phenotype

1. Introduction

Common bean (2n=2x=22) belongs to order Rosales, family Leguminosae, subfamily Papilionideae, tribe Phaseolea, subtribe Phaseolinae, genus Phaseolus [12]. It is an erect or twinning, annual, herbaceous plant with various growth habits, morphological traits, and seed and pod characteristics. The bean flower is perfect, possessing both male and female organs on the same flower, and is self-fertilized. Pollination coincides with the time when the flower opens [20].

Common bean is adapted to an altitude ranging from sea level to nearly 3000 m.a.s.l [12], but doesn't grow well below 600 m.a.s.l due to poor pod set caused by high temperature

[36]. It is an important food crop in eastern and southern Africa. Common bean is known as the second most important source of human dietary protein and the third most important source of calorie of all the agricultural commodities produced in eastern and southern Africa [32]. It is one of the most important pulse crops grown in many lowland areas of Ethiopia as a main crop and protein source. In additions to contributing to protein requirement, common beans, particularly the white colored ones are very important to fetch additional income for farmers [24, 21, 25]. At present different types of beans are grown in Ethiopia both as a sole crop and intercropped with cereals [25, 31]. These include, white pea beans as cash crop, different colored beans for local consumption, and climbing types to be used as green beans locally and other purposes.

Suitable production areas of bean in Ethiopia have been indicated as areas with an altitude between 1200 – 2200 m.a.s.l, mean maximum and mean minimum temperature of less than 30-32°C and greater than 10-12°C, respectively, and a rainfall of 350-500 mm well distributed over 70-100 days [20, 8]. Almost all types of soil with good drainage and reasonably high nutrient content are suitable for haricot bean production [36, 1].

According to [14] the area covered by common bean production in Ethiopia in 2017 was 113,249.95 ha and 244,049.94 ha for white and red common bean respectively with total area of 357,299.89 ha and total production of about 540,238.94 tons/ha. Generally, pulses covered 13.24% of the grain crop area; where common bean, faba bean and chickpea accounted for 2.86%, 3.56% and 2.07% respectively. Thus, common bean ranks second next to faba bean in terms of area coverage among pulse crops. The average white and red common bean productivity is 1.41 tons/ha and 1.56 tons/ha respectively.

Genetic variability is a prerequisite for an effective selection of any economically important plant species, and a critical survey of genetic variability is essentially aiming at developing high yielding varieties. The study of variability and heritability is of primary importance for an efficient breeding program as it provides a genetic basis for effective selections. The type of selection and progress from selection for a particular character depends, in part, on the magnitude of heritability estimates. This is because the expected response under selection is a function of heritability, variation and selection intensity [7]. Heritability serves as a guide to the reliability of phenotypic success [23].

There is wide genetic variation in common beans in growth habit (determinate vs. indeterminate), in days to maturity, in seed size, color and quality (cook ability and palatability), in vegetative and reproductive growth, pigmentation, and leaf size, shape and orientation and resistance to pests [33]. The choice of promising genotypes from diverse genetic base, and their subsequent utilization for hybridization is one of the strategies for improving the productivity of any crop including beans.

Therefore, this study was imitated with the following objective:

To determine the genetic variability, heritability and interrelationships of traits for common bean varieties in western Ethiopia.

2. Material and Methods

2.1. Descriptions of the Study Areas

The research was conducted in the main cropping season of 2018 at Uke which is the Research and Technology Demonstration sub site of Wollega University. Uke is located in Guto Gida district of East Wollega Zone of Oromia Regional State. The center is located about 365km far away from Addis Ababa and around 40 km far away from Nekemte in the northern direction on the main road to Bahirdar town. The site is about 1383 m.a.s.l. The site is located at 8°11'52'' and 10° 94'44'' north latitude and 36°97'51'' and 37°11'52'' east longitude. The area is characterized by mixed farming type dominantly by investors. The area receives rain once in a year which suitable to produce crops in once in a year. The temperature of the area is characterized by warm which suitable for different crops including vegetables and root crops. The pH of the soil is acidic with red color of Nitosol, a dominant soil type in the western Ethiopia.

2.2. Experimental Materials and Design

2.2.1. Treatments and Experimental Design

Nineteen varieties of common bean were used for the study. The varieties (genotypes) were grown in random complete block design in three replications with 4 rows (1.6 m) x 4 m length of total plot size of (6.4 m^2) of 40 cm between rows and 10 cm between plants. The two outer most rows at both ends of the plots were treated as borders leaving two middle rows of each of the genotypes for data collection. The experimental field was prepared by using farm tractor plough and it was ploughed three times, the first at the beginning of February 2018, the second at the beginning of April and the third for planting first of June 2018. The full dose of DAP (46% P$_2$O$_5$: 18% N) at the rate of (100 kg/ha) were drilled at planting time. Nitrogen fertilizer in the form of urea (46% N at a rate of 50 kg/ha were applied at time of sowing by mixing with DAP. The seeds were sown by hand in the rows as uniformly as possible and covered with soil manually. Moreover, all other necessary field management practices were carried out as per the recommendation.

2.2.2. Data Collection and Measurements

Data on phonological parameters, growth parameters, yield and yield components were collected.

Data to be collected on plot bases; Days to 50% flowering, Days to 95% maturity, Grain yield per ha, 100-Seed weight (g).

Data collected on individual plant basis and plot based were; Plant height (cm), Pod length (cm), Leaf area (cm^2), Number of nodes on the main axis, Internodes length (cm), Number of pods per plant, Number of seeds per pod, Grain yield per ha (ton/ha), Harvest Index, Biological yield (ton/ha).

2.2.3. Data Analyses

(i). Analysis of Variance

Data on phonological parameters, growth parameters, yield, and yield components were subjected to analysis of variance (ANOVA).

Student-Newman-Keuls Test (SNK) was used for mean separation at 5% probability level.

(ii). Correlation Analysis

Phenotypic and genotypic correlation coefficients were estimated using the standard.

(iii). Cluster Analysis

Clustering of genotypes into different groups were carried out by average linkage method and the appropriate number of clusters were determined from the values of Pseudo F and Pseudo T statistics using the SAS computer software facilities.

(iv). Principal Component Analysis

Principal component analysis was conducted based on correlation matrix to identify the traits contributing to a larger part of the total variation among the genotypes.

3. Results and Discussion

3.1. Analysis of Variance (ANOVA)

The mean square values from analysis of variance are presented in Table 1. The results showed that the varieties are significantly different (P<0.05) for all measured traits except for days to flowering and number of seeds per pod. The values for coefficient of variations are greater than 10 for, Grain filling period, Number of seeds per pod and Seed yield.

These also indicate that the varieties are different in many of the morphological traits that could be helpful in searching desirable traits for breeding program. [39] found significant variation for days to maturity, plant height, number of pods per plant, pod length and number of seeds per plant. [28] reported significant variation for plant height, number of pods per plant, 100-seed weight and seed yield per plant and [34] reported maximum variability for number of pods per plant.

3.2. Mean and Range Values for Different Agrnomic Traits of Common Bean

The results indicated that the values for mean, and ranges were higher for phonological traits such as grain filling period and days to 95% maturity; and similarly the values for vegetative parameters were higher for plant height, leaf area, and pod length. For yield and yield components the mean ranges were higher for number of pod per plant, 100-seed weight, biomass yield and grain yield indicating that there were variations among the tested varieties for the measured traits.

As can be observed from mean ranges, wide range of variability was observed for almost all the characters studied, except days to 50% emergency, days to 50% flowering and number of seed per pod The present study was in agreement with the findings of [42] who found significant differences for days to 50 per cent flowering, pod length and seed yield per plant; [4] reported highest variances for green pod yield per plant followed by number of pods per plant, 100-seed weight and plant height. [28] reported significant variation for plant height, number of pods per plant, 100-seed weight and seed yield per plant; and [34] reported maximum variability for number of pods per plant.

Table 1. Mean square for 14 traits for common bean varieties grown at Uke.

Traits	Replication (df=2)	Genotypes (df=18)	Error (df=36)	CV (%)
Days to flowering	15.23	22.65[ns]	15.41	8.60
Grain filling period	101.18	112.51**	37.19	15.95
Days to maturity	43.00	109.30**	21.39	5.51
Plant height (cm)	0.34	1221.45**	0.48	1.13
Leaf area (cm^2)	0.044	207.42**	0.044	0.95
Internodes length (cm)	0.60	10.63**	0.55	6.42
Number of nodes per plant	0.23	8.74**	0.19	4.86
Pod length (cm)	1.79	61.21**	0.43	4.45
Number of pods per plant	0.017	39.31**	0.017	0.93
Number of seeds per pod	0.54	1.86[ns]	1.69	22.74
Hundred seed weight (g)	5.52	28.74**	3.52	10.03
Seed yield (kg/ha)	0.015	2.284*	0.083	10.78
Biological yield (t/ha)	0.149	14.008.**	0.349	6.22
Harvest index	0.00011	0.0108*	0.00026	5.85

*, Indicate significance at the 0.05 probability levels. **, highly significant at 0.01 probability level. NS; indicates non significance at 0.05 probability level.

3.3. Estimation of Genetic Variances

The results for genotypic and phenotypic variances are presented in Table 2. The values for genotypic coefficient of variation were less than 10% for days to 50% flowering, days to 95% maturity and number of seed per pod. Genotypic

coefficient of variation values was ranged between 10% and 20% for days to 50% flowering, grain filing period, inter node length, number of node per plant, and 100-seed weight while it was greater than 20% for plant height, leaf area, pod length, number of pod per plant, seed yield, biological yield and harvest index. Similarly, phenotypic coefficient of variation values was less than 10% for days to 50% flowering and days

to 95% maturity; and they were between 10 and 20% for inter nod length, number of nod per plant, and 100-seed weight while the values were greater than 20% for grain filling period, plant height, leaf area, pod length, number of pod per plant, number of seeds per pod, seed yield, biomass yield and harvest index. The close values for genotypic coefficient of variation and phenotypic coefficient of variation for most of the traits indicated that the less magnitude of environmental variances. According to [18] phenotypic coefficient of variation and Genotypic coefficient of variation 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 medium. Based on this delineation, Genotypic coefficient of variation and phenotypic coefficient of variation values were higher for, plant height, leaf area, pod length, number of pod per plant, seed yield, and HI. The high Genotypic coefficient of variation values of these characters suggested that the possibility of improving these traits through selection. Similar results were reported by [19] who found high Genotypic coefficient of variation values for pods per plant in common bean genotypes. The Genotypic coefficient of variation and phenotypic coefficient of variation values were medium for inter node length, number of node per plant, and 100-seed weight. On the other hand, low Genotypic coefficient of variation and phenotypic coefficient of variation values were obtained for days to 95% maturity and days to 50% flowering. Contrary to the present results the same author reported high Genotypic coefficient of variation for 100 seed weight. High phenotypic coefficient of variation values for number of pods per plant and seed yield were reported by different researchers [2, 30, 3] and the same sources indicated that pod per plant had high phenotypic coefficient of variation and high Genotypic coefficient of variation values. In the present study, the difference between phenotypic coefficient of variation and Genotypic coefficient of variation values were higher for number of seed per pod, days to 50% flowering and grain filling period indicating the high influence of environment on these characters. However, the difference was lower for all other traits suggesting minimal influence of environment on the expression of the characters.

The present results also agreed with those findings by; [16] who reported highest Genotypic coefficient of variation and phenotypic coefficient of variation for plant height and number of pod per plant; and with [44] who reported for number of branches per plant, number of pods per plant except for number of seeds per pod; [5] for number of pods per plant and plant height; [28] for plant height and number of pods per plant; [37] for number of pods per plant, plant height [35] for number of pods per plant and [10] for plant height, number of pods per plant.

The present study showed days to 50% flowering, days to 90% maturity and number of seed per pod had low Genotypic coefficient of variation estimates and the values were moderate for days to 50% emergency, grain filling period; inter node length, number of node per plant and 100-seed weight. Similar report was reported by [6] for days to maturity; and contradictory with the finding of [39] who

observed higher genotypic coefficient of variation value for days to 50% flowering. Higher phenotypic coefficient of variation than genotypic coefficient of variation indicated that most of the yield attributes were under the influence of environment [22].

3.4. Estimation of Heritability and Expected Genetic Advance

The results for heritability values and expected genetic advance are presented in Table 4. Estimates of heritability in broad sense ranged from 3.20% for number of seed per pod to 99.94% for leaf area. Estimates of heritability values are higher than 80% for plant height, leaf area, inter node length, pod length, number of node per plant, number of pod per plant, seed yield, biomass yield and harvest index and between 60 and 80% for 100-seed weight. The heritability values were between 40% and 60% for grain filling period and days to 95% maturity while the values were less than 40% for days to 50% flowering and number of seed per pod. The present results agree with the findings of [38, 27] who reported high heritability estimates for biomass yield/plant and pods/plant. According to [44] if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. But, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical due to the masking effect of the environment. High heritability value for 100 seed weight was reported by [30, 3]. Similarly, high heritability values for number of pods per plant (86.66%) and seed yield per plant (83.38%) were reported by [3]. The magnitudes of heritability values for the present study for most of the quantitative characters were moderate to high, which may be attributed due to uniform environmental conditions or one location. [15] explained that whenever values are stated for heritability of a character, it refers to a particular population under particular environmental conditions. The present result was disagreed with the findings of [30, 3] who reported that high heritability values for days to 50% flowering, number of seeds per pod and 100 seed weight.

The estimates for genetic Advance (GA) is highest for plant height (41.53 cm) followed by leaf area (17.12 cm^2), pod length (9.19 cm) and the values were lower for the others traits. This indicated that it could be realized that after one cycle of selection plant height can be improved by 41.53 cm in height using the same population. Similarly, the estimates of GAM were greater than 30% for plant height, leaf area, pod length, inter node length, number of node per plant, number of pod per plant seed yield, biomass yield and harvest index while it was less than 30% for the other traits. Genetic advance under selection (GA) refers the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity [44]. The character's plant height, leaf area and pod length were recorded high genetic advance coupled with high heritability estimates.

While evaluating 19 genotypes of common bean in the present study, high heritability with high genetic advance for plant height, indicating that this trait could be predominantly governed by additive gene action and selection of this could be more effective for desired genetic improvement. [26] reported high heritability (broad sense) with high expected genetic advance for plant height.

In the present investigation, high heritability for leaf area, number of pod per plant, number of node per plant, pod length, inter node length, harvest index, seed yield and biomass yield were also associated with high expected genetic advance as a percent of mean, indicating that these characters are controlled by additive gene action hence, there could be further improvement through selection for these characters. Similar, finding was reported by [16] for pod length and plant height. [39] reported high heritability and genetic advance as a percent of mean values for days to flowering, days to maturity and plant height and Asati and [44] reported high heritability and genetic advance as a percent of mean for plant height. [28] reported high heritability (broad sense) with high genetic advance for leaf area and plant height and [37] for plant height and 50 per cent flowering. Higher values for heritability and genetic advance indicate increase in the efficiency of the selection in breeding programme by assessing the influence of environmental factors and additive gene action.

Expected genetic advance as a percent of mean (GA%) was high for plant height (67.8%), leaf area (76.92%), inter node length (30.25%), pod length (62.51%), number of node per pod (38.9%), number of pod per plant (52.54%), seed yields (62.63%), biomass yield (44.54%), harvest index (42.31%) and 100-seed weight (26.8%), similar result was reported for pod length, biomass yield, inter node length and number of pod plant by [17]. Moderate genetic advance as percent of mean was recorded for characters' days to emergency (15.28%), grain filling period (17.13%) and days to maturity (10.11%) and low GA% for days to flowering (2.58%) and number of seed per pod (1.53%) which was similar for days to flowering with the findings of [44]. Plant height, leaf area, inter node length, pod length, number of node per plant, number of pod plant, seed yield, biomass yield and harvest index showed high heritability with high genetic advance as a percent of mean as a result of genetic variability. This indicated the prevalence of additive gene action governing these traits so that improvement through appropriate selection method is possible. The present result was similar with the findings of [17] reported high heritability and genetic advance as percent of mean for number of pod per plant and seed yield.

Table 2. Genetic components of variance, heritability and genetic advance of common bean varieties evaluated at Uke, 2018.

Traits	Range	Mean ± SE	σ^2g	σ^2p	σ^2e	GCV (%)	PCV (%)	H (%)	GA	GAM (%)
DF	41.00-50.33	45.65±0.62	2.41	17.82	15.41	3.40	9.25	13.53	1.18	2.58
GFP	28.00-49.00	38.25±1.42	25.11	62.30	37.19	13.10	20.64	40.30	6.55	17.13
DM	75.00-95.00	83.89±1.40	29.30	50.69	21.39	6.45	8.49	57.81	8.48	10.11
PH (cm)	30.30-120.00	61.26±1.19	406.99	407.47	0.48	32.93	32.95	99.88	41.53	67.80
LA (cm^2)	5.70-40.00	22.26±1.74	69.13	69.17	0.04	37.35	37.36	99.94	17.12	76.92
INL (cm)	8.00-14.43	11.57±0.43	3.36	3.91	0.55	15.84	17.09	85.91	3.50	30.25
POL (cm)	5.63-22.57	14.68±1.04	20.26	20.69	0.43	30.66	30.98	97.94	9.18	62.51
NNP	3.60-12.33	9.00±0.4	2.91	2.93	0.02	18.94	19.01	99.35	3.50	38.90
NPP	900.-21.00	14.18±0.83	13.10	13.12	0.02	25.52	25.54	99.86	7.45	52.54
NSP	4.33-7.00	5.72±0.18	0.06	1.75	1.69	4.14	23.11	3.20	0.09	1.53
HSW (g)	12.00-22.97	18.71±0.7	8.41	11.93	3.52	15.50	18.46	70.49	5.01	26.80
SY (t/ha)	1.33-4.03	2.67±0.22	0.734	0.817	0.0830	32.081	33.850	89.822	1.672	62.633
BY (t/ha)	6.54-13.62	9.51±0.45	4.55	4.90	0.35	22.44	23.28	92.88	4.24	44.54
HI	0.19-0.3900	0.28±0.0200	0.0040	0.0040	0.0003	21.3030	22.0920	92.9890	0.1180	42.3180

DF-days to 50% flowering, PH-plant height, LA- leaf area, INL- inter node length, NNP; number node per plant, NPP- number of pods per plant, DM- days to 95% maturity, GFP-grain filling period, NSP-number of seeds per pod, HSW-hundred seed weight, GY (t/ha)-grain yield in ton per hectare, By (t/ha)-biomass yield in ton per hectare, HI-harvest index. σ^2g-genotypic variance, σ^2p-phenotypic variance, σ^2e-environmental variances, GCV (%)-genotypic coefficient of variation; PCV (%)-phenotypic coefficient of variation, H (%)-broad sense heritability, GA-genetic advance, GAM (%)-genetic advance as percentage of the mean.

3.5. Estimates of Correlation Coefficients at Phenotypic and Genotypic Levels

The results of genotypic and phenotypic correlation coefficients are presented in Table 5. Seed yield was significantly and positively correlated with biomass yield and harvest index at genotypic and phenotypic levels. Whereas the correlation coefficients of grain yield with grain filling period and days to 95% maturity at phenotypic level was positive but non-significant. [41] reported that a day to maturity was significantly and positively correlated with grain filling period and seed yield. The characters including days to 50% flowering, plant height and hundred seed weight had negative and significant correlations with seed yield both at genotypic and phenotypic levels except for plant height which was non-significant at genotypic level. This indicates that the varieties taking longer days to flower, higher in plant height and higher in hundred seed weight had lower seed yield. The correlation coefficients of seed yield with other traits had non-significant or lower in magnitude at both genotypic and phenotypic levels. Similarly, other researcher reported that significant and positive correlation of seed yield with harvest index [41]; seed yield and number of pods per plant and biomass yield [29]. Contrary to the present finding,

[34, 11] reported that significant and positive correlation coefficients of seed yield with number of pods per plant, pod length; and hundred seed weight [11].

Table 3. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients of yield and yield related traits of 19 common bean varieties.

Traits	DF	PH	LA	INL	POL	NNP	GFP	DM	NPP	NSP	HSW	SY	BY	HI
DF		0.012	0.052	-0.12	0.14	-0.01	-0.46**	0.07	0.12	0.01	-0.14	-0.28*	-0.29*	-0.22
PH	0.02		0.08	0.18	0.62**	0.5**	-0.4**	-0.44**	0.02	-0.26*	0.22	-0.26*	-0.19	-0.33**
LA	0.08	0.08		-0.35**	0.34**	0.31*	-0.29*	-0.29*	-0.28*	0.07	0.17	-0.04	0.16	-0.21
INL	-0.27	0.19	-0.36		-0.12	-0.17	-0.05	-0.13	-0.28*	0.14	0.07	-0.21	-0.32**	-0.11
POL	0.23	0.63**	0.35	-0.11		0.48**	-0.14	-0.07	0.01	0.03*	0.13	-0.23	-0.19	-0.3*
NNP	-0.01	0.51*	0.31	0.15	0.48*		-0.37**	-0.42**	0.34**	0.14	0.17	-0.04	0.02	-0.15
GFP	-0.26	-0.53**	-0.39	-0.11	-0.19	-0.50*		0.85**	-0.01	-0.29*	-0.16	0.19	0.1	0.23
DM	0.19	-0.53**	-0.35	0.23	0.10	0.51*	0.89**		0.06	-0.32**	-0.26*	0.04	-0.07	0.13
NPP	0.17	0.02	-0.28	0.31	0.01	0.35	0.02	0.06		0.08	-0.01	-0.1	-0.05	-0.08
NSP	-0.02	0.45*	0.13	0.21	0.05*	0.31	0.67**	-0.69**	0.13		0.25*	-0.19	-0.13	-0.25*
HSW	-0.16	0.24	0.19	0.08	0.14	0.16	0.31	-0.39	-0.01	0.56*		-0.35*	-0.07	-0.51**
SY	-0.46*	-0.26	-0.03	0.22	0.25	0.05	0.25	0.04	-0.10	0.29*	-0.37*		0.83**	0.94**
BY	-0.47*	-0.2	0.17	0.34	0.21	0.02	0.11	-0.1	-0.05	-0.16	-0.04	0.83**		-0.63**
HI	-0.35	-0.3	-0.21	0.11	0.3	0.16	0.29	0.14	-0.08	-0.39	-0.56**	0.93**	-0.62**	

DF-days to flowering, PH-plant height, LA- leaf area, INL- inter node length, POL-pod length, NNP; number node per plant, NPP- number of pod per plant, DM- days to maturity, GFP-grain filling period, NSP-number of seed per pod, HSW-hundred seed weight, SY-seed yield, BY-biomass yield, HI-harvest index. *; significant difference at 0.05 probability level, **; significant at 0.01 probability level.

Table 4. Eigenvectors and eigen values of the first four principal components (PCs) for 14 characters of 19 common bean varieties.

Characters	Eigenvectors			
	Princ1	Princ2	Princ3	Princ4
Days to 50% flowering	0.131	0.117	0.178	0.620
Days to grain filling period	0.352	0.118	-0.080	-0.049
Days to 95% maturity	0.361	0.088	-0.021	-0.019
Plant height (cm)	-0.093	0.409	0.163	0.397
Leaf area (cm)	0.341	0.149	0.066	0.090
Inter-node length (cm)	-0.022	-0.003	0.500	0.496
Pod length (cm)	-0.216	0.299	0.352	0.078
Number of nodes per plant	0.312	0.170	-0.073	-0.071
Number of pods per plant	0.350	0.157	0.051	-0.036
Number of seeds per pod	0.350	0.154	-0.006	-0.091
Hundred seed weight (g)	0.346	0.133	-0.095	-0.068
Seed yield (t/ha)	0.199	-0.409	0.357	0.188
Biomass yield (t/ha)	0.178	-0.257	0.493	0.071
Harvest index	0.150	-0.475	0.099	0.199
Eigen value	7.325	2.550	1.653	1.188
Percent of total variance explained	48.83	17.00	11.02	7.92
% of cumulative total variance explained	48.83	65.83	76.85	84.78

3.6. Principal Component Analysis

The results of principal component analysis are presented in Table 4. The results showed that four principal components (PC1 to PC4) with eigenvalues of 7.33, 2.55, 1.65 and 1.18 respectively, accounted for 84.77% of the total variation in the present population. This indicated that the characters studied had enough to show the variations in the populations. The first two principal components PC1 and PC2 with values of 48.83% and 17% respectively contributed more to the total variation. According to [13] characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in the present study, differentiation of the varieties into different clusters was more due to the characters including Grain filling period, days to 95% maturity, leaf area, pod length, number of node per plant, number of pod per plant, number of seed per pod, and 100-seed weight.

The characters including plant height, pod length and number of node per plant contributed more than the others in the second principal component (PC2); similarly, characters including inter node length, biomass yield, days to 50% emergency and grain yield contributed more than the others for total variations in the third principal component (PC3) and characters including days to 50% flowering, inter node length and plant height had more contribution than the another for the total variation in the fourth principal component (PC4). The Eigen root of first principal component was accounted approximately 48.83% of total variation followed by second to four components which accounted 17%, 11.02%, and 7.92% of total variation presented among the varieties, respectively. Similar studies were reported by [9], who reported the first four principal components were the most contributors in

variation in case of pinto bean.

3.7. Cluster Analysis

The mean values of the 14 characters in each cluster are presented in Table 5. The results showed that cluster I consisted of 5 varieties including Anger, Awasadume, Argane, Awash-1 and Awash-2. Similarly, cluster II had consisted of 1 variety, TR-13. Cluster III had eight varieties including Ramada, Tabor, Red-Wolyta, Roba-1, Omo-95, Dimtu, Dursitu and Nasir. Cluster IV had five varieties including Mexican-142, Awash-Melka, Chore, Melka-Dima and Nazreth-2.

***Table 5.** Mean values of traits in each cluster for the 19 common bean varieties.*

Traits	CI	CII	CIII	CIV
Days to 50% flowering	46.7	45.6	44.0	44.5
Days to grain filling period	44.6	33.7	35.0	38.6
Days to 95% maturity	90.8	79.0	81.0	84.0
Plant height (cm)	62.2	65.1	120.0	37.6
Leaf area (cm^2)	31.8	17.9	18.0	19.9
Inter-node length (cm)	10.9	11.6	14.4	11.7
Pod length (cm)	12.3	16.9	22.5	11.7
Number of nodes per plant	10.5	7.9	8.6	9.1
Number of pods per plant	18.6	11.5	12.0	13.5
Number of seeds per pod	6.6	5.1	5.0	5.6
Hundred seed weight (g)	21.9	16.3	17.5	19.0
Seed yield (t/ha)	3.1	2.1	2.2	3.3
Biomass yield (t/ha)	10.2	8.3	8.4	9.5
Harvest index	0.30	0.24	0.26	0.35
Number of varieties in each cluster	5	1	8	5
Name of varieties	Anger, Awasadume, Argane, Awash-1 and Awash-2	TR-13	Ramada, Tabor, Red-Wolyta, Roba-1, Omo-95, Dimtu, Dursitu and Nasir	Mexican-142, Awash-Melka, Chore, Melka-Dima and Nazreth-2

CI-Cluster 1; CII-Cluster 2; CIII- Cluster 3; CIV- Cluster 4.

3.8. Estimation of Intra and Inter Cluster Square Distances (D$^{2)}$

The results of average intra and inter cluster D^2 values are presented in Table 6. Maximum average intra cluster D^2 was obtained in cluster III (D^2=33.3) followed by cluster I and cluster IV (D^2=14.9) while the lowest D^2 was recorded in clusters II (D^2=0.0), which indicates the presence of less variability within these clusters. The χ^2- test for the four clusters indicated that there was statistically significant difference among all the clusters. The highest average inter cluster D^2 was recorded between cluster III and cluster IV (D^2=1628.8) followed by cluster I and cluster III (D^2=1339.6) and cluster II and cluster III (D^2=1339.6) which revealed that these clusters were genetically more divergent from each other.

Crosses involving parents belonging to most divergent clusters would be expected to manifest maximum heterosis and wide variability in genetic architecture [43]. In the present study, Cluster III followed by Clusters II and I were the most divergent clusters from Cluster IV. However, the chance of getting segregants with a high yield level is quite limited when one of the clusters has a very low yield level [40]. Cluster II had the lowest mean performance in seed yield and other characters' important characters. This indicates that the chance of getting segregants with high yield is limited between crosses of cluster II with the other clusters. The selection of parents should also consider the special advantages of each cluster and each genotype within a cluster depending on specific objectives of hybridization [43, 13]. Thus, in the present result crosses involving Cluster III with Cluster IV, and Cluster III with cluster I are suggested to exhibit high heterosis and could result in segregates with higher seed yield. The present study revealed the presence of significant genetic variability among the tested genotypes. Thus, there is an opportunity to improve yield through hybridization of genotypes from different clusters and subsequent selection from segregating advanced generations.

***Table 6.** Average intra (diagonal and bold) and inter cluster D^2 values among four clusters in 19 common bean varieties.*

Cluster	CI	CII	CIII	CIV
CI	14.9	585.6	1339.6	711.5
CII		0.0	1339.6	711.5
CIII			33.3	1628.8
CIV				14.9

χ^2=22.307 and 24.996 at 5% and 1% probability level respectively.

4. Conclusion

The research was conducted on 19 common bean varieties collected from Bako Agricultural Research Center with three replications under Randomized Complete Block Design. This study generally indicated that there was significant genetic variability or divergence among the varieties for most of the traits considered. Thus, there is enormous opportunity in the improvement program of the common bean through direct

selection rather than a lengthy crossing program and hybridization involves crossing of the genotypes from different clusters would produce viable and a potential segregate population.

5. Recommendation

Common bean is the most important crop for our people as a cash and food crops, the research on evaluation must be conducted. The present study was conducted only for a single season on a single location in west Ethiopia, so the future researcher must conduct on different locations for many seasons to evaluate the best varieties of common bean.

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