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Path Coefficient, Genetic Divergent and Principal Component Analysis on Common Bean (Phaseolus Vulgaris L.) Genotypes in Sekota, North Western Ethiopia

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***Abstract*— Common bean (Phaseolus vulgaris L.) is a dual purpose, early matured low land pulse crop. Information on the genetic divergent, path coefficient and principal component analysis plays a vital role for further breeding activity in common bean. Therefore, this study was initiated with the objective of identifying superior lines for hybridization program, identify the traits that have direct and indirect effect on seed yield and to determine genetic similarity among genotypes using multivariate analysis on 64 genotypes using 8x8 simple lattice design at Aybra main research site during 2023 under rain fed conditions. Analysis of variance was performed using SAS software and the genetic divergent and principal component analysis were done using R software. The ANOVA revealed highly significant variations among genotypes for all the traits considered in the study and it suggest the possibility of estimating genetic divergent, path coefficient and principal component analysis. Branches per plant, above ground biomass and harvest index had significant positive direct effects on seed yield at the genotypic and phenotypic levels while days to maturity had a significant negative indirect effect with seed yield at the genotypic. The maximum inter cluster distance was found between clusters VII and VIII (D2 =351.39), followed by clusters V and VIII (D2 =331.23). The first five principal component axes accounted for 74.3% of the total variation, with eigenvalues greater than unity. The number of days to maturity, plant height, number of pods per plant, number seeds per pod, seed yield, and harvest index were the traits that contributed most of the variation in the first PCs. Therefore, selection based on direct and indirect effect of the traits and hybridization based on cluster distance could be possible for the improvement of common bean in the study area.**

Keywords*— *Common bean, Cluster analysis, traits, path coefficient, hybridization

I. INTRODUCTION

Common bean (Phaseolus vulgaris L.), popularly known as the dry bean, has massive, pinnately compound trifoliate leaves [23, 10]. It is the most important dual purpose crop in Ethiopia [6]. The common bean can grow anywhere from sea level to more than 3000 meters above sea level (m.a.s.l.), depending on the variety and it grows in warm areas with temperature fluctuations between 18 and 24 degrees Celsius, however it is difficult to form pods below 600 meters due to the high temperatures [16]. Path coefficient analysis is a standardized partial regression coefficient and a stoical tool developed by Wright [41]. It is considered useful for plant breeders because it splits the correlation coefficient into direct and indirect components.

Genetic divergence analysis is a useful method for selecting appropriate genotypes for a hybridization program [15 and 21].The D-square statistic (D2), also called generalized Euclidean distance, developed by [30] is used to classify objects/genotypes into different groups. Principal component analysis (PCA) is one of the most widely used multivariate statistical techniques and is applied in many scientific fields. According to [35] PCA can be used to identify the traits that have the greatest overall divergence along each differentiation axis. Characteristics with component lodging greater than ±0.3 are considered to have a large enough effect and are considered to be important characteristics, while characteristics with coefficient values less than 0.2 are considered to have no effect on overall variation [2].

Genetic diversity is essential to the ability of a species to persist because it allows changes in the genetic makeup to adapt to environmental changes and provides the necessary adaptability to the biotic and abiotic circumstances that exist in the environment. Plant breeders can benefit from path coefficient analysis, which separates the correlation coefficient into direct and indirect components [38; 37]. The grouping of genotypes using multivariate approaches can confer significant benefits to breeders of common beans. Information on the direct and indirect correlation of the traits also plays a significant role in the improvement of traits. However, there is currently a lack

of information regarding the genetic divergence and clustering of common bean in Wag-hemira. In order to improve common bean through crossing or direct selection, it is essential to first understand the genetic distance and the traits' association. Accordingly, the present study was devised to assess the 64 common bean fixed line genotypes with regard to quantitative traits, employing multivariate approaches to ascertain superior lines among them that could be utilized as parents in a prospective hybridization program, identify the traits responsible for a considerable proportion of the total variation among the genotypes through multivariate analysis (PCA), determine the genetic similarity among genotypes through multivariate analysis, and identify the traits exerting direct and indirect effects on seed yield of common bean in the study area.

II. Materials And Methods

A. Description of Experimental Location

The field experiment was conducted at the Sekota Dry Land Agricultural Research Centre, Aybra main research station, during the 2015/2016 EC (2023/24 GC) main cropping season. Aybra is located at 120 43′ 38″ N E longitude, 790 01′ 08 ″ E N latitude with an altitude of 1915 m.a.s.l. The site receives a mean minimum and maximum annual rainfall of 492 and 621 mm, with mean minimum and maximum temperatures of 15.4oC and 26.9oC, respectively (SDARC 2016/17). The study site is located in the Sekota district, Wag Hemira Zone of the Amhara National Regional State (ANRS) (Figure 1), which is 448 kilometers (km) away from Bahir dar (the regional capital of Amhara) and 738 kilometres (km) away from Addis Ababa (capital of Ethiopia). The dominant soil type is classified as vertisol. The general slope at the site varies between 0 and 8% but can normally be found in the 0-25% slope range [8] Sorghum (Sorghum bicolor), tef (Eragrostis tef (zucc.)) (Trotter), and barley (Hordeum vulgare L.) are the cereals, and common bean (Phaseolus vulgaris L.), mung bean (Vigna radiata), and filed pea (Pisum sativum L.) are some of the crops cultivated in the area (district) (personal observation and SWAO, 2023).

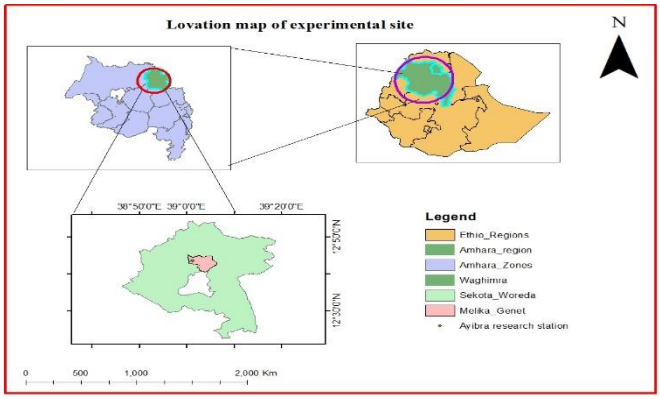

Figure1. Location of the study area in the Sekota District during the 2023 cropping season

B. Experimental Materials

The experiment included 64 small-seeded white-type common bean genotypes. Sixty-one of them are newly advanced (fixed line) genotypes that were developed by the Melkassa Agricultural Research Centre (MARC) for moisture deficit areas, and three common bean varieties namely Awash-2, Awash Melka and Awash Miten as standard checks. Both the newly developed genotypes and the checks were obtained from the National Low Land Pulse Research Coordinating Centre of the Melkassa Agricultural Research Centre (MARC).

C. Experimental Design and Management

The field experiment was conducted in a partially balanced simple lattice incomplete block design, with 8 x 8 arrangements. The individual plots size was contained rows of 2 meters (m) in length and width, each separated by 0.4 m in row spacing i.e. 2 m x2 m = 4 meter square (m2) in a grosses area and net area of 2 m x 1.2m (2.4m2) within a total field area of 20.2 m width x 40 m length (808 m2). The distances between plots, intra blocks, and replications were 0.5 m, 0.6 m, and 1 m, respectively. The treatments (genotypes) were allocated to plots at random within each intrablock and interblock (replication).

Fertilizer was applied to all plots uniformly in the form of NPSB fertilizers at a rate of 100 kilogram per hectare. NPSB fertilizer is an artificial soil fertilizer in which 100 kg of NPSB contains nitrogen (19 %, N), phosphorus (38 % P2O5), sulfur (7 % S), and boron (0.1 %) and all the NPSB fertilizer is applied by side dressing during planting. Each plot was evenly seeded by hand at its blanket recommendation of spacing between plants at 0.1 cm into the slighted hole at the recommended rate of 150 kg ha-1. To suppress flea beetles (Trirhabda flavolimbta), a two-times Karate chemical (1 L of the chemical dissolved in 200 L of water ha-1) was sprayed soon after the emergence of common beans when foliage beetles are seen on the leaves of the common beans. The second spray was made seven days after the first spray. All experimental plots were uniformly weeded manually at a frequency of two-time at the same time for all experimental plots.

D. Data Collection and Measurement

The pre and post-harvest data on grain yield and yield-related traits of common bean genotypes were collected on a plot and plant basis following the data scoring standards of the IBPGR for common beans [19]. Only three central rows were used for data collection. Five randomly selected plants from the three central rows of each plot (experimental unit) in each replicate were used for plant-based data collection after tagging. The averages of the five plants in each plot were used for statistical analysis of the traits recorded on a plant basis, while the data from all three central rows data were used for plot- based data.

1) Plot-based data

a) Days to 50% flowering (days)

The number of days was calculated by subtracting from sowing to a stage when 50% visual judgment of the plants in a plot produced flowers.

b) Days to 90% physiological maturity (days)

The number of days was calculated from sowing to 90% visual judgment of the plants that attained physiological maturity in each plot and when grains were difficult to divide by thumbnail.

c) Hundred Seed weight (g)

The grain weights of 100 seeds sampled at random from the total seeds harvested from the experimental plot were counted using an electronic seed counter weighted by using an electronic sensitive balance and recorded and adjusted to a eq (1)

$$10\%\ moisture\ content\ as = \frac{100-actual\ moisture\ content}{100-standard\ moisture\ content}\ X\ 100 \quad \text{.....(1)}$$

$$Yeild\ advantag = \left(\frac{Yeild\ of\ treatment\ A - Yeild\ of\ treatment\ B}{Yeild\ of\ treatment\ A}\right) * 100 \quad \text{.....(2)}$$

$$r_{ij} = p_{ij} + \sum\left(r_{jk}\ x\ p_{jk}\right) \quad \text{.....(3)}$$

$$Residual\ effect = \sqrt{1 - \sum\left(r_{ij} X\ p_{ij}\right)} \quad \text{.....(4)}$$

d) Seed yield (g/plot)

The seed yield per plot after harvested, threshed, and cleaned was weight using a sensitive balance and then the moisture of the seed yield were adjusted to 10 % moisture level and converted to kg ha-1. Adjusted seed yield= (100-actual moisture content) / (100-standard moisture content) X obtained yield based on [17] formula. Yield advantage of the tested genotypes over the checks was calculated with eq (2)

Yield of treatment A refers to the yield obtained from the treatment being compared against (yield of the new genotype) and yield of treatment B refers to the yield obtained from the treatment to which treatment A is being compared (yield of the checks used during the study).

e) Biomass yield (g/plot)

The total biomass yield was recorded by weighing the total sun -dried above -ground biomass harvested from the three central rows and converted in to kg ha^{-1}.

f) Harvest index (%)

It was estimated by dividing the seed yield per plot by above ground biomass yield and multiplying by 100. i.e.seed yield(economic yield)/ above ground biomass x 100.

2) Plot-based data

a) Plant height (cm)

Plant height was measured in cm from ground level to the top of the plants at random from the three rows.

b) Number of primary branch/ plant (No.)

The total number of branches per plant from the five sampled plants from the central three rows of each plot excluding the main plant, were recorded by counting at maturity

c) Number pods per plant (No.)

In the central three rows, the total number of pods per plant at the time of harvest from five randomly selected plants is expressed as an average.

d) Number of seeds per pod (No.)

The number of seeds per pod was recorded by counting the number of seeds per pod on each pod and was expressed as an average of five plants on a plant.

E. Statistical Data Analysis

1) Analysis of Variance

The data collected for quantitative traits analysis were subjected to analysis of variance (ANOVA) for simple lattice design using the PROC LATTICE and PROC GLM procedures of SAS soft wear after testing ANOVA assumptions and relative efficiency (RE) of design (simple lattice) over RCBD. The normality of the data was checked using the Shapiro-Wilk test before analysis. The mean squares of the traits for which RE > 100% were taken from the lattice, while those for which RE< 100% were taken from the GLM results. The general linear model (GLM) is used to calculate the unadjusted block sum of squares, unadjusted treatment sum of squares, and intra block error and handles relating one or several continuous dependent variables to one or several independent variables. Estimates of genetic parameters and associations of traits (correlations) for the genotypes were continued based on the statistical significance of the mean squares of the genotypes.

F. Estimation of Genotypic and Phenotypic path Coefficients, clustering and principal component analysis

1) Estimation of Genotypic and Phenotypic path Coefficients

In this path coefficient analysis, seed yield and seed yield-related traits were denoted as dependent (response) and independent variables, respectively [35]. The direct and indirect effects of seed-related traits on seed yield were analyzed through path coefficient analysis. The analysis was computed as suggested by Dewey and Lu [11] using the following formula (3)

Where: rij= is the Mutual association between independent traits (i) and dependent traits (j) as measured by the correlation coefficient, Pij= Component of the direct effect of an independent trait (i) on a dependent variable (j).

$\sum$ rik *pkj = Summation of components of the indirect effect of a given independent traits via all other independent traits. The residual effect, which determines how best the causal factors account for the variability of the dependent factor grain yield, was calculated using the formula (4) [11].

Where: pij=Component of direct effects of the independent character (i) and dependent character (j) as it was measured by the path coefficient;

rij =Mutual association between the an independent character (i) and a dependent character (j) as it was measured by the correlation coefficient.

2) Cluster Analysis and Genetic Divergence

The appropriate number of clusters was determined based on Pseudo-F and Pseudo t2 values using the R software. The points where local peaks of the pseudo-F value join with a small value of the pseudo-t2 statistic followed by a larger pseudo-t2 value for the next cluster combination. The mean values of data were pre standardized to mean zero and variance of one to avoid bias due to the differences in measurement scales before computing because various traits were measured by different scales.

Based on the squared distance (D2) values, the 64 genotypes were grouped into different clusters on the basis of 10 traits by using R software. A dendrogram was build based on Ward's agglomerative hierarchical classification technique with Euclidian distance as a measure of dissimilarity by using R software.

Cluster means were calculated for individual traits on the basis of the mean performance of the genotypes included within the cluster. The generalized genetic distance (D2) between interclusters was calculated by the R core team procedure using the generalized Mahalanobis D2 statistics equation [30] as D2ij= (xi-xj) s-1(xi-xj). Where: D2ij=Generalize square distance between cluster i and j xi-xj= Difference between mean vector values for ith and jth cluster s-1= Inverse of pooled variance covariance matrix within groups. Average intra cluster D2 values were estimated using the formula: $\sum D2i/(ni)$ Where: $\sum D2i$ = Sum of distances between all possible combinations (n) of common bean genotypes included and n=is the number of genotypes within cluster i. The chi-squared test was used to determine the significance of the distance values. The D2 values obtained for all pairs of clusters are considered as the calculated values of Chi squared (X2) and were tested for significance at both the 1% and 5% probability levels against the tabulated value of X2 for the 'P-1' degree of freedom (DF), where P is the number of traits used for clustering genotypes [37].

3) Principal Component Analysis

A data matrix of 10 (number of traits studied) x 64 (number of genotypes used in the study) was prepared for principal component analysis. Principal component analysis was performed using R Software to determine the contribution of each quantitative trait to the total variation in the genotypes. Therefore, the principal components (PCs), with eigenvalues greater than 1 explained by the total variation among genotypes for all traits were retained. Principal components (PCs) with eigenvalues greater than unity, and component lodgings greater than ± 0.3 were considered to be meaningful and valuable [2].

III. Results And Discussion

A. Analysis of Variance and Experimental Design Selection

The results of the analysis of variance (ANOVA) for 10 traits are presented in (Table I). There were highly significant ($P<0.01$) differences among the tested common bean genotypes for all traits in this study. This justified the need to estimate subsequent statistical analyses such as clustering, divergence, and path coefficients for the genotypes. The findings of highly significant differences among the genotypes for traits under study suggest the existence of sufficient genetic variability in the materials used for this study.

TABLE I. MSE

	Mean square s(MS)						
Trait	Replication DF=(1)	Block(adjusted) DF(=14)	Genotype adjusted DF(=63	Error DF(=49	CV (%)	RE to RCBD	R^2
DF	2.531	3.978	36.008**	7.77	5.1	89.15	0.85
DM	13.1328	10.8025	26.0634**	7.86	3.4	102.14	0.77
PH	5.2669	11.571	88.610**	9.72	7.3	101.65	0.92
BPP	0.1158	0.23089	1.1199**	0.19	10.1	106.81	0.87
PPP	0.057	2.98	36.609**	1.36	6.9	112.81	0.96
Spp	0.5	0.26268	0.37289**	0.14	8.1	111.81	0.76
HsW	2.712	2.549	35.331**	3.46	6.5	94.12	0.92
AGB	2900	681892	1806001**	744551	12.8	98.13	0.74
Sy	86808	98965	483292**	184041	14.92	102.05	0.80
HI	29.035	24.627	89.068**	34.239	14.69	104.75	0.77

Where: ** highly significant ($P \leq 0.01$, significant; DSF=Days to 50% Flowering; DSM=Days to Maturity; Ph=Plant height; Bpp=Branch per plant; PPP=Pod per plant; HsW=100 seed weight; AGB= Aboveground biomass; Sy= Seed yield; HI=Harvest index; RE=Relative efficiency and RCBD= Randomized complete block design, R2=coefficient of determination.

B. Path coefficient analysis

1) Phenotypic path analysis

The harvest index (0.940) and biological yield (0.748) had high significant positive direct effects on seed yield (Table II). High direct effects indicate a real relationship between these traits and seed yield. Therefore, selection for these traits would have a reasonable effect and improve seed yield in common bean. These traits should be considered as important selection criteria in common bean breeding programme, as an increase in these traits will lead to an increase in seed yield. Similarly [4, 3, 20, 22, 26 and 27] reported biological yield and harvest index had positive direct effect on seed yield. The phenotypic residual effects (R=0.027) were low, indicating that 97.3% of the seed yield of common bean was determined by the traits studied in this experiment. Other independent variables or seed yield related traits that are not included in this experiment are expected to have a small effect of only 2.7% on seed yield. This result suggests that the traits included in this study are adequate, although additional traits may be needed to fully explain seed yield. This finding is consistent with [32] who reported that 92.9% of the variation in seed yield in common bean genotypes at the phenotypic level was due to causal factors, while only 7.1% was due to other factors that were not included in their study. Similarly, [5] found that 91.8% of the variation in seed yield was due to causal factors and only 8.2% was due to other

factors not included in their study at the phenotypic level in common bean genotypes.

TABLE II. ESTIMATES OF DIRECT (BOLD) AND INDIRECT EFFECTS (OFF THE DIAGONAL) OF DIFFERENT TRAITS ON SEED YIELD AT THE PHENOTYPIC LEVEL IN 64 SMALL-SEEDED COMMON BEAN GENOTYPES

Traits	Df	Dm	PH	Bpp	PPP	Spp	Hsw	AGB	HI	Rp
Df	**-0.017**	-0.003	-0.004	0.0011	0.0009	0.0047	-0.007	-0.090	-0.752	0.090
Dm	-0.002	**-0.026**	-0.006	0.0008	-0.008	0.0021	-0.008	-0.052	-0.315	0.047
PH	0.002	0.0006	**0.034**	-00007	-0.009	-0.026	0.022	0.016	0.1324	0.170
Bpp	0.005	0.0005	0.006	**-0.004**	-0.017	-0.083	0.036	0.1442	0.0520	0.190
PPP	0.002	-0.003	0.004	-0.009	**-0.074**	-0.017	0.035	-0.114	0.0909	0.070
Spp	0.003	0.0002	0.003	-0.011	-0.004	**-0.030**	0.004	-0.417	0.1394	0.070
Hsw	0.001	0.0002	0.006	-0.012	-0.021	-0.009	**0.012**	0.0789	-0.153	0.060
AGB	0.002	0.0000	0.001	-0.008	0.0001	0.0017	0.013	**0.7461**	-0.315	0.440
HI	0.002	0.0001	0.048	-0.002	-0.007	-0.044	-0.020	-0.250	**0.9411**	0.670

Residual effect = 0.027. Note: BPP = branch per plant, AGB = aboveground biological yield per hectare, HI= harvest index, and SyrP = phenotypic correlation coefficient with seed yield.

2) Genotypic path analysis

(Table III) presents the genotypic direct and indirect effects of various traits on seed yield. At the genotypic level, path coefficient analysis revealed that the harvest index (0.85) and above ground biological yield (0.67) had positive direct effects on seed yield, indicating that these yield components positively influenced seed yield and a true relationship of the traits. Indirect selection based on the harvest index and biological yield can effectively improve seed yield in small-seeded common bean. Studies by [22 and 26] have shown that these traits have a strong positive direct effect on seed yield at the genotypic level. However, [9] report that the harvest index has an indirect effect on seed yield.

TABLE III. ESTIMATES OF DIRECT (BOLD) AND INDIRECT EFFECTS (OFF THE DIAGONAL) OF DIFFERENT TRAITS ON SEED YIELD AT THE GENOTYPIC LEVEL IN 64 SMALL-SEEDED COMMON BEAN GENOTYPES

Traits	Df	Dm	PH	Bpp	PPP	Spp	Hsw	AGB	HI	Rg
Df	**-0.0405**	-0.0036	-0.0041	-0.0035	0.00081	0.0110	0.0038	0.0168	0.0003	0.03
Dm	-0.0073	**-0.0199**	-0.02	-0.0039	-0.0008	0.0192	-0.0017	-0.0138	-0.2525	0.3
PH	0.0406	0.0098	**0.0403**	0.0154	-0.0009	-0.0054	0.0273	-0.0745	0.0845	0.06
Bpp	0.0123	0.0066	0.0053	**0.0155**	-0.0023	-0.0187	0.0421	0.1803	-0.0114	0.19
PPP	0.0040	-0.002	0.0046	0.0033	**-0.008**	-0.0034	0.0391	-0.0355	0.1105	0.07
Spp	0.0062	0.0053	0.0030	0.003	-0.0004	**-0.0719**	-0.0009	-0.0717	0.1041	0.02
Hsw	0.0012	0.0025	0.0086	0.0038	-0.0025	0.0049	**0.1278**	0.0838	-0.2709	0.16
AGB	-0.0007	0.0004	-0.045	0.0031	0.0004	0.0077	0.0161	**0.6651**	-0.1645	0.5
HI	0.0000	0.0057	0.0039	-0.002	-0.001	-0.086	-0.004	-0.126	**0.8665**	0.74

Residual effect = 0.0204. Note: BPP = branch per plant, AGB = aboveground biological yield per hectare, HI= harvest index, and SyrG = genotypic correlation coefficient with seed yield.

In addition, days to maturity (-0.038) had a negative direct effect on seed yield at the genotypic level (Table III). These negative effects may lead to a decrease in seed yield. The data shows that early maturing accessions had a higher seed yield per hectare than late-maturing accessions. Therefore, selecting against this trait could increase the seed yield per hectare. This result is consistent with the findings of [12, 26 and 36], who reported a negative direct effect of days to maturity on the seed yield of common bean genotypes. However, [40 and 32] reported a positive correlation between days to maturity and seed yield. This may be because under optimal environmental conditions, a longer time to maturity increases the seed yield, likely because more photosynthesis is diverted to the seed. Therefore biomass yield and the harvest index can be used as indirect selection criteria for improving common bean seed yield in the area.

The genotypic residual effect (R=0.02) showed that 98% of the seed yield of common bean was contributed by the studied traits in this path analysis. The experiment expected that other independent variables not included would only have a 2% influence on seed yield. This result shows that the traits included in this path analysis study are adequate, even though other traits may also be necessary. Similarly, [5] reported that 97.39% and 95.99% of the total variation in seed yield was explained by the study variables at the genotypic level for common bean genotypes in Goro and Ginnir, Southeast Ethiopia. In line with this result, [9] reported that 94% of the variability in seed yield was explained by the study variables at genotypic levels on soybean genotypes at Pawe.

C. Cluster Analysis and Genetic Divergence

1) Cluster analysis

The genotypes were grouped into eight distinct clusters, forming different hierarchical subgroups (Figure 2, figure 3 and (Table IV). These suggest that the tested genotypes are genetically diverse and have different backgrounds. Similar reported done by [5] grouped 64 small-seeded common bean genotypes into eight genetically distinct clusters in the Bale and East Bale Zones. Similarly, [14] grouped 100 common bean

genotypes into eight clusters. [29], also grouped 100 common bean genotypes into eight groups in Brazil. Cluster I had the highest number of genotypes, with 27, while cluster VIII had the lowest, with only three genotypes.

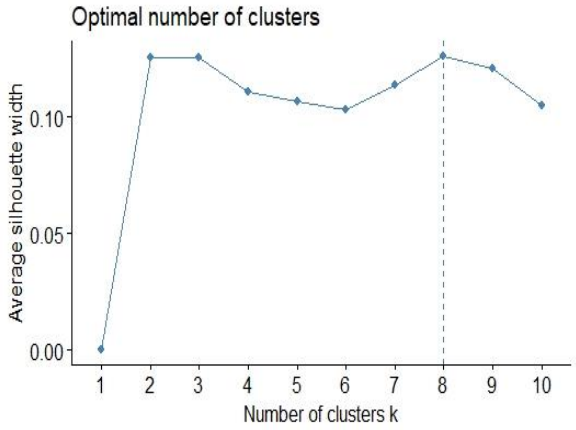

Figure 2. The possible number clustered of the 64 common bean genotypes using silhouette width methods

TABLE IV. DISTRIBUTION AND GROUPING OF 64 SMALL-SEEDED COMMON BEAN GENOTYPES INTO EIGHT DIFFERENT CLUSTERS BASED ON THE MAHALANOBIS (D^2) DISTANCE FOR 10 TRAITS

Cluster	No genotype	proportion in %	List of Genotypes
I	27	42.18	6, 18, 8, 22, 34, 62, 5, 33, 13, 56, 37, 2, 51, 28, 16, 26, 15, 44, 50, 60, 3, 36, 7, 32, 46, 1, 52
II	6	9.37	4, 29, 54, 39, 23,31
III	4	6.25	9, 24, 19, 43
IV	5	7.83	10, 17, 38, 11, 61
V	8	12.5	12, 59, 40, 63, 55, 58, 45, 49
VI	4	6.25	14, 53, 21, 57
VII	7	10.94	20, 47, 26, 35, 64, 41, 42
VIII	3	4.68	27, 30, 48

A total of 26 new genotypes and one standard check variety constituted for 42.18%, were grouped into cluster I, whereas cluster VIII contained only 3 genotypes, accounting for 12.5%. Cluster V comprised 8 genotypes (10.93%), including seven new genotypes and one standard check. Cluster VII contained 7 genotypes (10.93%), including 6 new genotypes and one standard check variety. Cluster II include six new genotypes (9.37%), while cluster IV included 5 new genotypes (7.8%). Both cluster III and cluster VI contained 4 (6.25%) new genotypes each (Table IV). The standard check variety (genotypes 62, 63, and 64) was grouped in clusters I, V, and VII, indicating a close relationship with these clusters compared to other genotype clusters.

2) Cluster means analysis

The mean values of clusters for 10 traits of 64 common bean genotypes are presented in (Table V). The cluster I genotypes were characterized by longer flowering times, shorter plant heights, greater numbers of branches per plant, greater aboveground biomass, lower seed yields, and lower harvest index (Table V). Cluster II genotype had a medium seed yield, tallest plant height, greater number of branches per plant, greater number of seeds per pod, medium hundred seed weight, and medium biomass values, higher seed yield and higher harvest index. The cluster III genotypes had longer days to flowering and maturity, shorter plant heights, lower numbers of branches, medium numbers of pods per plant, high to medium aboveground biomass, lower hundred seed weights, greater seed yields, and higher harvest indices.

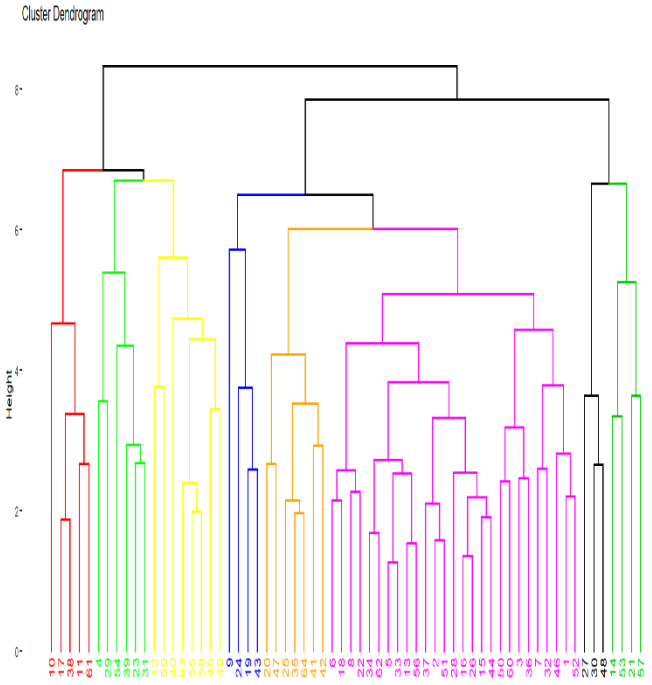

Figure 3. Dendrogram constructed using 10 traits of 64 common bean genotypes used for the study
NB. Key: **Cluster IV**, **Cluster II**, **Cluster V**, **Cluster III**, **Cluster VII**, **Cluster I**, **cluster VIII** and **cluster VI**

Cluster IV genotype is characterized by a longer time to flowering and maturity, shorter plant height, medium to high number of branches per plant, and low to high number of pods per plant. It also has the maximum number of seeds per pod, medium to high hundred seeds weight, higher aboveground biomass, low seed yield, and low harvest index compared to those of the other clusters. The cluster V genotype exhibited shorter days to flowering and maturity, taller plant heights, fewer pods per plant, greater aboveground biomass, greater seed yield, and greater harvest index.

The plants of the cluster VI genotype, on the other hand, had fewer pods per plant and fewer seeds per pod, medium aboveground biomass, lower seed yield, and a lower harvest index. Cluster VII genotypes were distinguished by longer days to maturity, tallest plant height, maximum number of pods per plant, medium number of branches per plant, higher hundred seed weight, medium aboveground biomass, lower seed yield and harvest index. Cluster VIII genotypes were characterized by late flowering and maturity, lower aboveground biomass, greater hundred-seed weight, lower seed yield, and medium harvest index. In this study, clusters III, IV, and V were identified as high yielders, while clusters VII and VIII were identified as low yielders. By crossing clusters with wider inter cluster distances that have superior mean performance for desirable traits, reasonable changes can be achieved. Cluster V was found to be early maturing. Cluster IV was identified as a high yielder, and cluster V was identified as both early maturing and high yielding. In contrast, clusters VII and VIII were identified as late maturing clusters with low seed yield traits. Therefore, crossing clusters IV and VII will result in a new high-yielding genotype. Similarly, crossing clusters V and VIII will produce new genotypes that are both early maturing and high yielding, making them suitable for moisture deficit environments such as the study areas due to their wider genetic distance.

TABLE V. MEAN VALUES OF CLUSTERS FOR 10 TRAITS OF 64 COMMON BEAN GENOTYPES

Clusters	DsF	Dsm	Ph	Bpp	PPP	Spp	HsW	AGB	SY	HI
C1	54.9	84.1	35.62	4.48	15.92	4.61	29.05	7504.02	2277.76	30.97
C2	53.47	82.18	44.51	4.79	17.58	4.64	27.95	6610.68	2699.54	41.19
C3	56.07	84.29	37.11	3.09	15.41	4.24	23.17	6562.36	2912.17	45.24
C4	53.4	83.1	42.76	5.2	22.2	3.78	32.74	7654.8	3060.94	40.29
C5	53.19	76.25	48.54	4.53	14.11	4.53	30.24	7011.29	2873.31	40.23
C6	56.29	83.93	41.74	3.84	13.8	3.65	25.56	6292.2	2103	34.12
C7	54.33	83.33	49.83	4.27	27.5	4.33	33.9	6656.83	2321.13	34.98
C8	54.86	81.71	46.1	3.79	16.11	4.37	31.47	5574.32	1956.2	35.11

Where:- c1-c8 are number of clusters, Dsf days to flowering, DsM, days to maturity, Ph= plant height, Bpp= number of braches per plant, Ppp= number of pods per plant, Spp= number of seeds per pod, Hsw= 100 seed weight, AGB= aboveground biomass, Sy= seed yield and HI= harvest index

3) Genetic divergence analysis

The genotypes were categorized into eight distinct clusters based on a cluster analysis of 10 quantitative traits. The chi-square test showed statistically significant differences between most of the clusters. (Table VI) Presents the average intra cluster (differences among genotypes within the same cluster) and inter cluster (differences among genotypes between different clusters) distance (D2) values. The inter-cluster distances ranged from 10.21 to 351.39, while the intra-cluster distances ranged from 2.96 to 4.22 (Table VI). The results show that the distances between clusters were greater than those within clusters, indicating variability among the tested genotypes of different groups and both heterogeneous and homogeneous nature within and between clusters.

TABLE VI. AVERAGE INTRA (BOLD FACE) AND INTER PAIRWISE GENERALIZED SQUARE DISTANCE (D2) VALUES OF EIGHT CLUSTERS OF 64 COMMON BEAN GENOTYPES

Clusters	C1	C2	C3	C4	C5	C6	C7	C8
C1	**4.22**	10.21^{ns}	43.79^{**}	96.56^{**}	20.23*	60.43^{**}	35.94^{**}	201.22^{**}
C2		**3.29**	13.97^{ns}	48.86^{**}	52.03^{**}	29.35^{**}	76.05^{**}	128.12^{**}
C3			**2.96**	19.45*	111.78^{**}	18.38^{*}	131.45^{**}	70.25^{**}
C4				**3.62**	196.79^{**}	57.06^{**}	204.54^{**}	38.79^{**}
C5					**3.04**	117.03^{**}	33.34^{**}	331.13^{**}
C6						**3.2**	149.99^{**}	92.78^{**}
C7							**3.99**	351.39^{**}
C8								**3.38**

Where ns= non-significant and *, ** significance at the 5% and significance at the 1% probability level, and X^2= 21.67 at 5% and 16.92 at 1%.

The largest inter-cluster distance was observed between clusters VII and VIII (D2 = 351.39), followed by clusters V and VIII (D2 = 331.23), IV and VIII (D2 = 204.54), IV and V (D2 = 196.79), and VI and VII (D2 = 149.99), indicating greater genetic divergence between these clusters. The genotype members of distant clusters (clusters VII and VIII, V and VIII, IV and VII, IV and V, and clusters VI and VII) can be used in breeding programmes to achieve a high level of heterotic expression in the F1 generation. This can be achieved by combining desirable traits with greater heterotic potential and a wider range of variability in the recombinant and segregating F2 generation. The selection of better parents from these clusters for hybridization programmes can help to achieve ideal segregates and/or recombinants. The minimum distance between clusters was recorded between clusters I and II (D2 = 10.21), followed by clusters II and 3 (D2 = 13.97), clusters III and VI (D2 = 18.38), and clusters III and IV (D2 = 19.45). The close genetic relationship between genotype members in these

clusters suggests that crossing genotypes from these clusters may not result in greater heterotic value in F1 and a wide range of variability in the segregating F2 population. Cluster 1 had the greatest average intra cluster distance (D2 = 4.22), indicating greater genetic divergence among its members than among the other clusters. Cluster III had the lowest intra cluster distance (D2 = 2.96), followed by cluster 5 (D2 = 3.04). Similarly, on the different prats of Ethiopia, the presences of genetic divergence on common bean was reported in common bean genotypes based on clustering analysis by [5, 14, 26, 34 and 36].

TABLE VII. EIGENVECTORS, EIGENVALUES, PERCENTAGES AND CUMULATIVE VARIANCES OF THE FIRST FIVE PRINCIPAL COMPONENTS (PCS) FOR 10 TRAITS OF 64 COMMON BEAN GENOTYPES

Trait	PC1	PC2	PC3	PC4	PC5
Days to 50% flowering	0.298	0.104	0.181	0.096	-0.415
Days to 90% maturity	-0.202	0.080	-0.106	0.692	0.257
Plant height	0.331	-0.064	0.142	-0.213	-0.529
Branch per plant	0.454	-0.300	0.010	-0.045	0.226
Pod per plant	0.266	-0.210	0.162	0.614	-0.150
Seed per pod	0.272	-0.019	0.304	-0.104	0.534
100- seed weight	0.209	-0.506	0.041	0.209	-0.301
Above ground biomass	0.158	-0.220	-0.777	-0.070	0.128
Harvest index	0.354	0.610	0.171	0.150	-0.117
Seed yield	0.464	0.410	-0.428	0.082	-0.045
Eigen value	2.130	1.69	1.37	1.17	1.04
Proportion variance in each PC (%)	21.4	16.9	13.8	11.7	10.5
Cumulative variance (%)	21.4	38.3	52.1	63.8	74. 3

D. Principal Component Analysis

The genotypic residual effect (R=0.02) showed that 98% of the seed yield of common bean was contributed by the studied traits in this path analysis. The experiment expected that other independent variables not included would only have a 2% influence on seed yield. This result shows that the traits included in this path analysis study are adequate, even though other traits may also be necessary. Similarly, [5] reported that 97.39% and 95.99% of the total variation in seed yield was explained by the study variables at the genotypic level for common bean genotypes in Goro and Ginnir, Southeast Ethiopia. In line with this result, [9] reported that 94% of the variability in seed yield was explained by the study variables at genotypic levels on soybean genotypes at Pawe.

IV. CONCLUSIONS

The analysis of variance revealed highly significant (P<0.01) differences among the genotypes for most traits considered in this study. Path coefficient analysis revealed that the number of branches per plant, above-ground biomass, and harvest index had direct effects on seed yield at genotypic and phenotypic level. Days to maturity had a negative direct effect on seed yield at the genotypic level. The cluster analysis grouped the 64 genotypes into eight distinct clusters and this suggest that the tested genotypes are genetically diverse and have different backgrounds. The greatest inter cluster distance was found between cluster VII and VIII, followed by cluster V and cluster VIII, as well as between cluster IV and cluster VII, indicating greater genetic divergence between these clusters. The minimum distance between clusters was recorded between clusters I and II (D2 = 10.21), followed by clusters II and 3 (D2 = 13.97), clusters III and VI (D2 = 18.38), and clusters III and IV (D2 = 19.45) indicates genetic relationship between genotype members and crossing genotypes from these clusters may not result in greater heterotic value in F1. The first five PCs with eigenvalues greater than unity explained 74.3% of the total variation in which days to maturity, plant height, pods per plant, seed per pod, seed yield, and harvest index were the traits that contributed most to the variation in PC1-PC5. Therefore, selection based on direct and indirect effect of the traits and hybridization based on the cluster distance could be possible for common bean improvement.

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