Advances in Crop Science and Technology: Open Access

Kayamo, Adv Crop Sci Tech 2023, 11:2

Research Article Open Access

Genetic Variability and Association of Traits in Yellow Gray Common Bean (*Phaseolus vulgaris* L.) Genotypes for Yield and Yield Related Traits in Sidama Region, Southern Ethiopia

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Abstract

The study of genetic variability in crop plants is important for improving the crops including common beans and enhancing production. This research was undertaken with the objectives to determine the magnitude of genetic variability and association of yield and yield related traits. Thirty six genotypes were evaluated using simple 6 × 6 lattice design at Hawassa. The analysis of variance revealed significant difference among genotypes for 13 traits studied except days to 50% emergence and number of primary branch. Highest GCV and PCV was found for plant height followed by number of pods per plant and number of seeds per plant; whereas, lowest GCV and PCV were observed for days to 50% flowering. Heritability in broad sense ranged from 96.7% for hundred seed weight to 14.7% for number of primary branches and genetic advance as percent of mean ranged from 63.8% for number of primary branches to 2.2% for days to 90% maturity. Highest broad sense heritability and high genetic advance as percent of mean were obtained for days to 50% emergence followed by plant height and number of pod per plant indicating the presence of additive gene action for the inheritance of these traits. Seed yield had significant and positive phenotypic and genotypic correlations with days to 90% maturity, stand count at harvest, number of seeds per plant, biological yield hundred seed weight and harvest index. Path analysis revealed that stand count at harvest, number of seeds per plant, biological yield, hundred seed weight and harvest index showed positive direct effect on seed yield. Whereas, number of pods per plant and protein content of seed had negative direct effect on seed yield at both phenotypic and genotypic level. The 36 common bean genotypes were grouped in to four clusters based on D^2 analysis. Maximum inter cluster distance was observed between cluster II and III (3734); whereas, minimum inter cluster distance was observed between cluster I and III (26.05). The genotype belonging to the distant clusters could be used for breeding program to obtain a wider range of variability. The first five principal components, whose Eigen values greater than one, accounted for 71% of the total variation among the genotypes. The variability of traits, which were exhibited among the genotypes, can serve in planning selection and crossing programs for the future common bean improvement. However, it requires multi location and over season trials to verify the stability of existing genotypic variability.

Keywords: Cluster analyses; Correlation; Variability; Heritability; Genetic advance

Introduction

The common bean (2n=2x=22) belongs to Leguminosae family, subfamily Papilionideae, tribe Phaseolea, sub tribe Phaseolinae, genus *Phaseolus*. 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 [1].

Common bean is originated in tropical America (Mexico, Guatemala and Peru), but there are also evidences for its multiple domestication within central America. Common bean is speculated to have been introduced to Ethiopia by the Portuguese in the 16th century [2].

Common bean is the most important grain legume in nearly all lowland and mid altitude areas of Ethiopia. The crop is adapted to an altitude ranging from sea level to nearly 3000 m.a.s.l, but doesn't grow well below 600 m.a.s.l due to poor pod set caused by high temperature [3]. Suitable production areas of bean in Ethiopia have been indicated as areas with an altitude between 1200 m.a.s.l-2200 m.a.s.l, mean maximum and mean minimum temperature of less than 30°C-32°C and greater than 10°C-12°C, respectively and a rainfall of 350 mm-500 mm well distributed over 70-100 days. Almost all types of soil with good drainage and reasonably high nutrient content are suitable for common bean production.

It is one of the major food and cash crops in Ethiopia and it has considerable national economic significance and also traditionally ensures food security in Ethiopia [4]. It ranks third as an export commodity in Ethiopia, contributing about 9.5% of total export value from agriculture. It is often grown as cash crop by small scale farmers. The majority of common bean producers in Ethiopia are small scale farmers and it is used as a major food legume in many parts of the

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Received: 09-August-2022, Manuscript No. ACST-22-71544; **Editor assigned:** 12-August-2022, PreQC No. ACST-22-71544 (PQ); **Reviewed:** 26-August-2022, QC No. ACST-22-71544; **Revised:** 10-February-2023, Manuscript No. ACST-22-71544 (R); **Published:** 17-February-2023, DOI: 10.4172/2329-8863.1000558

Citation: Kayamo EK (2023) Genetic Variability and Association of Traits in Yellow Gray Common Bean (Phaseolus vulgaris L.) Genotypes for Yield and Yield Related Traits in Sidama Region, Southern Ethiopia. Adv Crop Sci Tech 11: 558.

country where it is consumed in different types of traditional dishes [5].

Common bean seeds contain 20%-25% proteins, much of which is made up of the storage protein phaseolin [6]. Phaseolin is a major determinant of both quantity and nutritional quality of proteins in bean seeds. In addition to this, it is also important in providing fodder for feeding livestock and it contributes to soil fertility improvement through atmospheric nitrogen fixation during the cropping season [7]. Common bean adds not only diversity to production systems on resource poor farmers' fields but also it contributes to the stability of farming systems in Ethiopia.

The common bean production is greater than 28.9 million tons annually in the world with its production value of US million $5717. Since it is high in nutrient content and commercial potential, common bean holds great promise for fighting hunger, increasing income and improving soil fertility in sub Saharan Africa. The crop occupies more than 3.5 million hectares in sub Saharan, but production is concentrated in the densely populated areas of East Africa, the lakes region and the highlands of southern Africa. It is the second most important crop next to cow pea in eastern, central and southern Africa [8]. These regions are the primary bean growing regions in Africa, with a combined production of almost 1 million metric tons. The current annual national production of common bean using two seasons (Mehre and Belg season) in Ethiopia is estimated at 98,526.00 ha (white haricot bean) and 175,121.76 ha (red haricot bean) with a total production of 17.40 quintal and 18.00 quintals per hectare respectively. The total area under cultivation for common bean in Sidama was estimated to be 0.89% of total food grain production area of the zone (19,170.98) hectare of land and 384,494.46 tons of production with average productivity of 2.06 ton ha^{-1}.

Although the country is major common bean producer in Africa, the national average productivity of common bean is low (white and red common bean productivity is 1.74 tons/ha and 1.8 tons/ha respectively). This is primarily due to cultivation of few improved varieties for varied eco edaphic rain fed systems, poor adaptation, poor crop management, biotic (angular leaf spot, halo blight, antracnose, common bacterial blight and weed) and abiotic (drought, soil salinity and water logging) factors [9].

The demand for a variety with high yielding over a range of production environments is very high among growers. Hence, development of desirable verities with high yield potential, wider adaptability, biotic and a biotic stress tolerance is crucial. These depend upon the extent of genetic variability in the base population and availability of ample source of genetic variability is very important in a crop improvement program. Assessment of genetic variability, association of traits among themselves and with seed yield by a simple or complex paths and identification of ideal path for the improvement of yield potential is the breeder's responsibility. Therefore, many plant breeders measure the variability of chick pea with the help of genetic parameters, correlation coefficient and path analysis to determining the important traits influencing the dependent trait and it helps in the determination of selection criteria for simultaneous improvement of various traits along with economic yield for different location.

Despite common bean is the most economically important pulse crop grown in Ethiopia as a cash crop and its immense potential for improving the livelihood of thousands of smallholder farmers, its productivity has remained low. Several factors are accountable for this, in which infertility caused by soil erosion and continuous cultivation, moisture stress, lack of improved varieties and biotic factors (disease and pest) are put in the top list. Even if genetic variability studies have been conducted in Ethiopia by considerable number of researchers on common bean [10,11].

Even if ample of research works done around Sidama, limited source of genotypes, low yield potential, low adaptability, information on association of grain yield and yield related traits for common bean (yellow grey) of Sidama region agro ecology is not well addressed and noted that common bean variability and improvement studies were neglected in Sidama [12]. Thus, conducting research focusing on generating genetic information on variability and association of important traits of common bean (yellow gray) for further improvement through selection and/or hybridization to address farmers need by releasing high yielding and wider adaptable varieties because study area is dominated by red common bean production [13]. Therefore, this study was conducted with the following objectives:

- To assess variability and association of traits in common bean genotypes using quantitative, qualitative and quality traits.
- To evaluate the extent and pattern of genetic variability in common bean genotypes.
- To estimate the association among grain yield and yield related traits.
- To identify traits that accounts much for the total variation among the genotypes.
- To assess whether there is divergence among bean genotypes used in this study.

Materials and Methods

Description of experimental sites

The experiment was conducted in Hawassa agricultural research center station in Sidama region, southern Ethiopia during main cropping season. It is found in the Ethiopian rift valley 7°3'11" to 7°08'4" latitude and 38°15'17" to 28°38'4" longitude. It is located 370 km away from Addis Abeba. The area is characterized by moist to sub humid, warm subtropical climate with an average temperature of 15°C-20°C annual precipitation ranges from 100 mm-1800 mm in bimodal distribution pattern, expected in March to April and June to August (Figure 1). The soil is loam characterized by slightly acidic pH and higher concentrations of micronutrients such as manganese, iron and zinc [14].

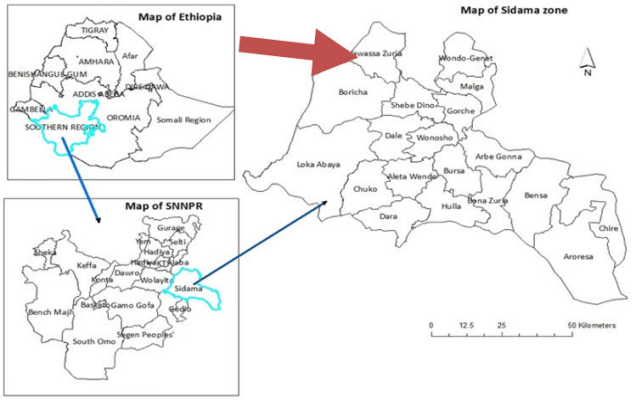

Figure 1: Schematic map of the study area.

Experimental material and design

The experimental materials used for this study were taken from the lowland pulse research program, of Hawassa Agricultural Research Center (HARC). A total of 36 advanced breeding yellow grey bean (08 Andean) genotypes which were recently introduced from ADP project including one released varieties (KAT-B1) as checks were incorporated for the study. These materials are listed below Table 1.

No	Genotypes	No	Genotypes
1	ADP0007	19	ADP0106
2	ADP0014	20	ADP0111
3	ADP0033	21	ADP0126
4	ADP0034	22	ADP0303
5	ADP0047	23	ADP0379
6	ADP0050	24	ADP0456
7	ADP0071	25	ADP0476
8	ADP0072	26	ADP0478
9	ADP0075	27	ADP0512
10	ADP0076	28	ADP0513
11	ADP0080	29	ADP0518
12	ADP0081	30	ADP0522
13	ADP0097	31	ADP0523
14	ADP0127	32	ADP0524
15	ADP0092	33	ADP0525
16	ADP0094	34	ADP0532
17	ADP0100	35	ADP0581
18	ADP0102	36	KAT-B1

Table 1: Description of common bean genotypes used in the experiment.

Experimental design, procedures and trial management

The field experiment was carried out using 6 × 6 simple lattice designs with two replications. The plot size was 4.8 m^2 *i.e.* 3 m length and 1.6 m width with spacing of 0.4 m and 0.1 m between rows and plants, respectively. Each plot had four rows and the spacing between incomplete blocks was 1 m and 0.4 m distance was kept between plots to separate two genotypes. Planting was done by hand drilling based on randomization used for the design. Fertilizer was applied at the rate of 100 kg ha^{-1} and 50 kg ha^{-1} NPS and urea respectively. All field activities (land preparation, planting, fertilizer application and weeding) were done as per recommended agronomic practices.

Data collection

The data were collected from the net plot area within two middle rows at randomly selected and tagged 5 individual plants by adopting. The data were collected both on plot and plant basis. The seed yield per plot was measured from the middle two rows and converted to hectare bases. All other parameters were recorded on plant basis by taking five plants randomly from each experimental plot according to Malik.

Data collected on plot basis

- **Emergence Date (DE):** Days from sowing to 50% seedling emergence.
- **Days to 50% Flowering (DF):** The numbers of days from planting to 50% of plants open flower was recorded.
- **Days to 95% Maturity (DM):** The numbers of days from sowing to 90% of plants in the plot reaching phenological maturity stage (as evidence of visualization of the plant stands when the color changed from green to brownish color of straw) was recorded.
- **Stand Count after Thinning (SCE):** Number of plants in a plot after thinning.
- **Stand Count at Harvest (SCH):** Number of plants in a plot at harvest.
- **Harvest Index (HI):** The value computed as the ratio of seed yield to total (seed plus straw) biomass multiplied by 100.
- **Hundred Seed Weight (HSW):** One hundred randomly counted seeds from the middle two harvested rows was weighed using sensitive balance.
- **Biomass yield (kg):** It is measured as the above ground weight by taking representative plants within the two central rows (1.2 m) harvested and measured in kilograms at maturity.
- **Seed yield (kg):** The seed yield were measured from the middle two harvested rows using sensitive balance and converted to hectare base.

Data collected on sample basis

- **Plant Height (PH):** Length of the central axis of the stem, measured from the soil surface up to the tip of the shoot.
- **Number of branches (count):** The number of primary branches of five randomly taken plants two middle rows excluding the main stem was counted at maturity and the average was taken per plot.
- **Number of Pods Per Plant (NPoPP):** Average number of mature pods, counted at harvest.
- **Number of Seeds Per Pod (NSPPo):** The total numbers of seeds in pods from five randomly taken plants.
- **Number of Seed Per Plant (NSPPL):** Number of seeds was counted from five randomly taken plants from the middle two rows and expressed as an average for each plot.

Data on quality traits (Protein analysis)

One hundred fifty grams of dried seed samples from each genotype was grinded using grinder at laboratory room. Then, two to three grams of seed flour were taken using small cups (internal diameter of 35 mm and depth of 8 mm) and were scanned by Near Infrared Spectroscopy (NIRS) mono chromator model FOSS 6500 (FOSS NIR Systems, Inc., Silver Spring, Denmark) to estimate the percentage of protein contents. Proximate compositions (list of the parameter) was predicted using plant based global calibration (infra soft international) from the collected spectra.

Disease score

Most common diseases on common bean like Common Bacterial Blight (CBB), Halo Blight (HB), Angular Leaf Spot (ALS), rust and anthracnose were scored after 21 days from planting by using the international board for plant genetic resources descriptor for common bean disease scale 1%-9%.

Data analysis

Analysis of variance: Analysis of Variance (ANOVA) was computed. The data that collected for each trait was subjected to analysis using Proc lattice and Proc GLM procedures of SAS version 9.2. Mean of traits were compared using Duncan Multiple Range Test (DMRT). In addition range, coefficients of phenotypic and genotypic variances and heritability were calculated from mean square values and grand mean for each trait (Table 2).

The mathematical model for simple lattice design was:

$Y_{ijr}=\mu+Ar+G_{ij}+B_{ir}+B_{jr}+e_{ijr}$

Where, Y_{ijr}=The value observed for the plot in the r^{th} replication containing the genotype G_{ij}, μ=grand mean, G_{ij}=genotype effect in the i^{th} row and j^{th} column, Ar=replication effect, $B_{ir}=i^{th}$ block effect, $B_{jr}=j^{th}$ block effect, e_{ijr}=the plot residual effect.

Source of variations	Degree of Freedom (DF)	Mean Square (MS)	Expected mean squares
Replication (r)	r-1	MSr	$\sigma^2e+g\sigma^2b+g\sigma^2r$
Block (b)	r (b-1)	MSb	$\sigma^2e+\sigma^2g$
Genotype (g)	g-1	MSt	$\sigma^2e+\sigma^2g+g\sigma^2b$
Error (e)	(b-1) (rb-b-1)	MSe	σ^2e
Total	rb^2-1	MST	
Note: b=blocks, g=number of genotypes, σ^2g=genotypic variance, r=number of replication, σ^2r =replication variance and σ^2e=environmental variance			

Table 2: ANOVA structure of simple lattice.

Estimation of genetic parameters

Different genetic parameters including genotypic variance (σ^2g), phenotypic variance (σ^2p), Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were estimated using the formula, adopted from Burton and De Vane and Johnson.

Environmental variance (σ^2e): σ^2_e=MSe

$$\text{Genotypic variance } (\sigma^2g):\sigma^2g=\frac{MSg-MSe}{r}$$

Where,

σ^2g=Genotypic variance

MSg=Mean Square due to genotypes

MSe=Environmental variance (error mean square)

r=Number of replication

Then, the phenotypic variance is estimated as the sum of the genotypic and environmental variances.

Phenotypic variance (σ^2p)=$\sigma^2g+\sigma^2e$

where,

σ^2p=Phenotypic variance

σ^2e=Environmental variance

Coefficients of variation at phenotypic and genotypic levels were estimated using the following formula:

$$GCV=\frac{\sqrt{\sigma 2g}}{\pi} * 100$$

$$PCV=\frac{\sqrt{\sigma 2p}}{\pi} * 100$$

Where,

GCV=Genotypic Coefficient of Variation

PCV=Phenotypic Coefficient of Variation

π=Grand mean of the characters under study

Deshmukh, et al. suggested that PCV and GCV values >20% are regarded as high, values 10% to 20% as medium, whereas values <10% are considered to be low. PCV and GCV were estimated based on this bench marks.

Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h^2) in the broad sense calculated according to the formula given by Allard.

Broad sense heritability (H^2)=[δ^2g/δ^2p] × 100

where,

H^2=Heritability in broad sense

σ^2g=Genotypic variance

σ^2p=Phenotypic variance (σ^2g)+(σ^2e)

σ^2e=Environmental variance

As suggested by Johnson, et al. (h^2) estimates will be categorized as:

Low=0%-30%

Medium=30%-60%

High=Above 60%

Genetic advance: Genetic Advance (GA) was calculated with the method suggested by Allard:

$$GA=k.\sigma^2_{p}.H^2$$

Where,

GA=Genetic Advance

K=constant=2.06 at 5% selection intensity

σ^2p= phenotypic standard deviation (square root of phenotypic variance)

H^2=Heritability in broad sense

Genetic advance as percent of mean

Genetic advance as percent of the mean were calculated to compare the extent of predicted advance of different traits under selection, using the following formula.

$$GAM=\frac{GA \times 100}{\pi}$$

Where,

GAM=Genetic Advance as percent of Mean

GA=Genetic Advance under selection

π=Grand mean of the trait

Correlation analysis

Phenotypic and genotypic correlations were estimated using the standard procedure suggested by Miller from the corresponding variance and covariance components.

$$r_g=\frac{gCOVX.Y}{\sqrt{\sigma 2gx\ .\ \sigma 2gy}}$$

$$r_p=\frac{PCOVX.y}{\sqrt{\sigma 2Px\ .\sigma 2Py}}$$

Where,

r_g=Genotypic correlation coefficient.

r_p=Phenotypic correlation coefficient.

Gcovxy=Genotypic covariance between variables x and y.

Pcovxy=Phenotypic covariance between variables x and y.

σ^2gx=Genotypic variance for variables x.

σ^2gy=Genotypic variance for variables y.

σ^2px=Phenotypic variance for variables x.

σ^2py=Phenotypic variance for variables y.

To test the significance of correlation coefficients, the following formulas were used [15]:

t=r/SE(r)

$SE(r)=1-r^2$

Where r is correlation coefficient. Then, the calculated t' values was compared with standard values at n-2 degrees of freedom and a levels of probability (where t is 0.05 and 0.01).

Path coefficient analysis

Path coefficient analysis was computed as suggested by Wright and worked out by Dewey and Lu using the phenotypic correlations to determine the direct and indirect effect of yield components on seed yield based on the following relationship.

$$rij=pij+\Sigma\, rik+pkj$$

Where,

rij=Mutual association between the dependent character;

i=(Yield related trait) and independent character;

j=(Seed yield) as measured by the correlation coefficients;

Pij= It is the components of direct effects of the independent character (i),

Σrik+pkj=Summation of components of indirect effect of a given independent character

i) On the given dependent character

j) *Via* all other independent characters (k)

Whereas the contribution of the remaining unknown characters is measured as the residual effect (R^2) which is calculated as:

$$\sqrt{1-R^2}$$

Where,

$R^2=\Sigma p_{ij}+r_{ij}$

Genetic divergence analysis

Genetic divergence analysis was computed based on multivariate an alysis using Mahalanobis's D^2 statistic by SAS Software program 9.4 [16].

Estimation of square cluster distance of genotypes

Genetic divergence refers to genetic distance among the genotypes under consideration. Genotypes are clustered based on similarity of characters. It is determined by using cluster analysis D-square statistics (D^2) is one of statistical technique developed by used to classify the different genotypes into different groups. The squared distances (D^2) for each pair of genotype combinations were computed using the following formula:

$D^2_{ij}=(X_i-X_j)\, S^{-1}\, (X_i-X_j)$

where, D^2_{ij}=The square distance between any two genotypes i and j;

X_i and X_j=The vectors for the values for genotype i^{th} and j^{th} genotypes, and

S^{-1}=The inverse of pooled variance covariance matrix

Clustering of genotypes

Based on the squared distances (D^2) values, clustering of genotypes was done using Tocher's method as described by Singh and Chaudhary.

Estimation of intra and inter-cluster squared distances

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

- Average intra and inter cluster D^2 values.
- Average intra cluster D^2, $D^2=\sum Di^2/n$, where, $\sum D^2i$ is sum of distances between all possible combinations (n) is the population included in a cluster.
- Average inter cluster D^2, $D^2=\Sigma D^2i/ni.nj$ Where, ni=number of population in cluster i, nj=number of population in cluster j.

Principal component analysis

Principal component analysis was performed using correlation matrix by employing past 1.93 to evaluate the contribution of each quantitative character in the total variation of genotypes. Number of factors retained were decided by looking at the eigen values (values>1.0). Those traits that had load coefficient values >0.40 (ignoring the sign) were considered as relevant scores for the PCAs. The general formula to compute scores on the first component extracted (created) in a principal component analysis is described as:

c1=b11(*x*1)+b12+···b1(*xp*)

Where,

c1=The subject's score on principal component 1 (the first component extracted).

b1p=The regression coefficient (or weight) for observed variable p, as used in creating principal component one.

xp=The subject's score on observed variable p.

Results and Discussion

Results obtained on variability assessment, associations among yield and yield related traits and genetic divergence are presented below. Implications of such studies in common bean improvement and breeding program for higher seed yield and other traits are also discussed.

Estimation of variability

Analysis of variance: The result of Analysis of Variance (ANOVA) for 15 traits at Hawassa is given in Table 3. There was highly significant different (P<0.01) among genotypes in days to flowering, stand count at emergence, plant height, number of pod per plant, number of seed per plant, harvest index, biomass yield, hundred seed weight, protein content and seed yield the existence of variability

among genotypes for these traits. And also there was highly significant difference among genotypes for common bacterial blight, angular leaf spot, halo blight and rust.

The present finding is consistent with the finding of who reported that significant difference for days to 50% flowering, days to maturity, plant height, number of pod per plant, number of seed per plant, harvest index, biomass yield and hundred seed weight of common bean [17-19].

Traits	Replication df=1	Genotypes df=35	Intra block error df=25	Block (rep) df=10	CV (%)
DE	0.004*	0.99ns	0.29	0.73ns	7.86
DF	1.2ns	12.9**	3.4	7.8ns	4.62
DM	18.62ns	22.8ns	15.5	13.21ns	5.01
SCE	73.25*	73.87**	10.47	13.25ns	2.94
SCH	1769.3**	536.4**	191.7	253.8ns	9.6
PH	353.1ns	672.5**	100.5	130.2ns	8.03
NPPPL	3.01ns	15.32**	2.5	6.47ns	14.36
NSPP	7.22**	0.59*	0.68	0.34ns	3.54
NSPPL	367.1ns	598.9**	83.5	133.5ns	13.5
NBPP	0.26ns	1.6ns	0.94	1.28ns	32
HI	9.54ns	280.04**	36.2	24.6ns	3.9
BY	2577.9ns	26155.2**	4169.4	3522.8ns	13.4
HSW	3.1ns	110.1**	2.7	1.7ns	4.41
PC	21.0ns	43.63**	1.76	12.23ns	6.27
SY	179.4ns	9887.9**	1338.75	1621.6ns	17.53
CBB	0.66ns	4.4**	0.4	2.59**	10.4
HB	01.78ns	3.3**	0.97	1.6ns	16.33
ALS	2.44*	2.88**	0.62	1.4*	12.66
RUST	1.14ns	2.8**	0.81	1.82ns	11.57

Note: Where, **=Highly significant at 0.01; *significant at 0.05; df=degrees of freedom; DEM: Days to 50% Emergence; DF: Days to 50% Flowering; DM: Days to 90% Maturity; SCE: Stand Count at Emergence; SCH: Stand Count at Harvest; PH: Plant Height; NBPP: Number of Primary Branch Per Plant; NPPPL: Number of Pod Per Plant; NSPP: Number of Seed Per Pod; NSPPL: Number of Seed Per Plant; HSW: Hundred Seed Weight; BM: Biological yield; P: Protein content; SY: Seed Yield; HI: Harvest Index and CV: Coefficient of Variation

Table 3: Mean square values of traits of 36 common bean genotypes tested at Hawassa during 2020 main cropping season.

Range and mean performance of genotypes

Estimated range and mean of the traits are presented in above table 3. In this study the range of variation was wide for stand count at emergence, stand count at harvest, plant height, number of pods per plant, number of seeds per plant, hundred seed weight, biological yield, seed yield and harvest index while it was low to fairly high for the rest traits.

Stand count at emergence ranged from 90 for genotype ADP0034 to 120 for ADP0581. The longest maturity period was recorded for ADP0524 (87 days) whereas; the genotype ADP0522 (70 days) took shortest period to maturity. The wide range for traits among genotypes may be due to the wide genetic pool of common bean genotypes. Hence, there is an opportunity to find genotypes, which perform better in moisture stressed areas and suitable for high potential environment. Thus, the variability that has been exhibited by these genotypes can offer great flexibility for the development of suitable varieties for this study area. Here, genotypes showed shorter maturity period can be suitable for the areas where the terminal drought frequently occurs.

The minimum (20.5 cm) plant height was recorded by genotype ADP0524 whereas, the maximum was by genotype ADP0034 (103 cm). Number of seed per plant ranged from 20 for genotype KATB-1 to 119 for genotype ADP0050. Number of pods per plant ranged from 4 for genotype ADP0524 to 19 for genotype ADP0075. The genotype KATB-1 had the minimum number of seeds per plant whereas; genotype ADP0050 had the maximum number of seeds per plant.

Similarly finding was reported by reported similar minimum and maximum values with the above trait [20].

The minimum hundred seed weight was recorded by genotype ADP0524 (15.66 g) whereas the highest was by genotype ADP0303 (51.66 g). The genotype ADP0524 (1792.91 kg/ha) had the minimum biological yield while genotype ADP0127 (8226.7 kg/ha) had the maximum biological yield. Harvest index ranged from 17.1% for genotype KAT-B1 to 72.7% for genotype ADP0100. The present finding agrees with the findings of Singh and Berecha who reported the maximum and minimum mean value for hundred seed weight, biological yield and harvest index. The range for seed yield was also very wide from 335 kg/ha for genotype ADP0524 to 3130.1 kg/ha for genotype ADP0034. Similarly, Yonas found wide range variation for seed yield.

In general, the range and mean value in the present study suggest the existence of sufficient phenotypic variability among the tested genotypes for the majority of traits indicating high possibility for improvement of traits under consideration.

Estimates of genetic parameters

Estimates of phenotypic variances (σ^2p), genotypic variances (σ^2g), Phenotypic Coefficients of Variation (PCV), Genotypic Coefficients of Variation (GCV), broad sense heritability as well as genetic advance and genetic advance as percent of means were computed for the studied traits of common bean genotypes are presented in Table 4.

Traits	δ^2g	δ^2p	GCV	PCV	Range		Mean ± SE	H^2 (%)	GA	GAM (%)	R^2
					Min	Max					
DE	0.85	1.14	13.46	15.62	5	8	6.8355.59 ± 7.090.38	74.7	1.64	24	87.2
DF	4.5	8.32	0.02	6.85	38	47	42.11 ± 1.375	54.5	3.24	7.7	86.2
DM	3.65	19.15	2.4	5.6	70	87	78.51 ± 2.785	19.06	1.7	2.2	74.1
SCE	31.69	42.2	5.9	5.1	90	120	110.08 ± 2.3	75.2	10.47	9.5	92
SCH	184.1	375.8	19.2	27.4	25	110	70.78 ± 9.8	49	19.6	27.7	86.3
PH	320.48	420.99	32.2	36.9	20.5	103	55.59 ± 7.09	76.1	32.1	57.7	93.1
NPPP	5.23	7.94	20.1	24.6	4	19	11.45 ± 1.165	65.8	3.8	33.2	88.9
NSPPo	0.32	0.64	9.4	13.2	5	11	6.08 ± 0.585	50	0.82	13.5	79.5
NSPPI	272.8	356.34	24.4	27.9	20	119	67.69 ± 7.915	76.6	29.8	44	93.9
NBPPI	0.17	1.13	8.2	18	2	7	3.02 ± 0.7	14.7	32.1	63.8	71.7
HI	121.9	158.1	25.5	29.1	17.1	72.7	43.3 ± 4.233	77	19.9	46.1	93
BY	10992.9	15162.3	21.8	25.6	215.15	987.2	480.38 ± 45.65	72.5	183.9	38.3	91.6
HSW	54.14	55.96	19.8	20.1	15.66	51.66	37.2 ± 1.16	96.7	14.9	40	98.6
PC	3.4	4.24	8.7	9.71	17.2	27.2	21.21 ± 3.255	80.2	3.8	17.93	78.96
SY	4274.59	5613.3	31.3	35.9	335	3130.1	208.72 ± 25.85	76.2	117.3	56.2	92.5

Table 4: Estimates of genetic parameters for 15 traits of common bean genotypes.

Genotypic and phenotypic coefficient of variation: Estimate of different variance component (genotypic and phenotypic) and coefficient of variation (genotypic and phenotypic) are presented in table 4. According to Burton and Devane GCV and PCV values less than 10% between 10%-20% and above 20% were considered as low, medium and high, respectively. The present study showed that GCV value ranged from 2.4% for days to 95% maturity to 32.2% for plant height and PCV value ranged from 5.1% for stand count at emergence to 36.9% for plant height. High Genotypic Coefficient of Variation (GCV) and high Phenotypic Coefficient of Variation (PCV) were observed for plant height, number of pods per plant, number of seeds per plant, harvest index biological yield and seed yield. This indicates that availability of high genetic variation among the genotypes for these traits, indicating a wide scope for improving these traits through selection. Rafii and Nath, Lad, et al., Wondwosen Wondimu and AbebeBogale report similar result with the present study for number of seed per plant, plant height and number of pod per plant, seed yield, respectively. Likewise Simon, et al. reported as traits such as plant height, number of nodes, biological yield, pods per plant, harvest index and hundred seed weight had higher PCV. Conversely, traits like days to flowering stem diameter and seeds per pod exhibited moderate PCV whereas only days to maturity showed lower PCV with value below 10%.

Moderate GCV and PCV value were observed for days to 50% emergence and number of seeds per pod indicating that these traits are amenable for further improvement through selection. Berecha reported

similar result for number of seeds per pod. In addition, Wondwosen Wondimu and AbebeBogale also reported moderate GCV and PCV for hundred seed weight.

Low GCV and PCV observed for days to 50% flowering, days to 95% maturity, stand count at emergence and protein content. This would indicate the presence of considerable environmental influence on the phenotypic expression of these traits and they are also lowering responsive for selection in yellow grey common bean genotypes. Whereas low GCV and moderate PCV were observed for number of primary branch per plant and number of seed per pod. Indicating low genetic variation among the genotypes for these traits and practically difficult for their improvement through selection. WondwosenWondimu and AbebeBogale also observed low GCV and PCV for days to 50% flowering and days to 90% maturity.

Heritability: Estimates of heritability are presented in table 4. In the present study, heritability varied from 96.7% hundred seed weight to 14.7% for number of primary branches. High heritability values indicated the genotypic variance constitute a major portion of the total phenotypic variations. But, low heritability value indicated relatively high contribution of the environment to the phenotype. According to Robinson heritability value <30 categories as low, between 30-60 medium, above 60 high. Based on this delineation days to 50% emergence (74.7), stand count at emergence (75.2), plant height (76.1), number of pod per plant (65.8), number of seed per plant (76.6), harvest index (77), biological yield (72.5), hundred seed weight (96.7), protein content (89.6) and seed yield (76.2) exhibited high heritability value. Hence, success of crop improvement through selection could be possible. Similarly, Lad, et al. and Langat, et al. reported high heritability value for, number of seed per plant and plant height. BerechaGutu also reported high heritability value for harvest index.

Moderate heritability values were recorded for stand count at harvest (49), days to 50% flowering (54.5) and number of seed per pod (50). Ejigu, et al. reported moderate heritability value for number of pod per plant. Rafii and Nath, Ahmed and Kamaluddin, Berecha and Terefu also reported moderate heritability value for number of seed per pod and days to 50% flowering. However, selecting superior individuals based on heritability estimates alone may not be evidence for genetic improvement hence, heritability estimates along with genetic advance would be more useful in predicting the effectiveness of selecting the best individuals.

Genetic advance: The value of expected Genetic Advance (GA) and Genetic Advance as percent of Mean (GAM) is presented in table 4. High values of GAM are indicative of additive gene action, whereas low values are indicative of non-additive gene action. In the present study, the expected genetic advance as percent of mean ranged from 63.8% for number of branch per plant to 2.2% for days to 90%maturity. According to Johnson, GAM values less than 10 regarded as low, between 10-20 moderate; whereas above 20 are considered as high. Based on this delineation high GAM at 5% selection intensity was obtained for days to 50% emergence (24), stand count at harvest (27.7), plant height (57.7%), number of pod per plant (33.2%), number of seed per plant (44%), biological yield (38.3%), hundred seed weight (40%), seed yield (56.2%) and harvest index (46.1%). Similarly, the present study agrees with the findings of Awol, et al. who reported that Genetic Advance as percentage of the Mean (GAM) was high for grain yield, biomass yield, number of pods per plant hundred seed weight while low GAM was obtained for days to maturity, days to flowering and number of seeds per pod.

Lad, et al. reported high GAM for plant height, number of pod per pant and harvest index. WondwosenWondimu and AbebeBogale also reported high GAM for number of seed per plant, biological yield and grain yield.

Moderate GAM at 5% selection intensity was obtained for number of seed per pod (13.5%). According to Johnson high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. In this study days to 50% emergence, plant height, number of pod per plant, number of seed per plant, biological yield, 100 seed weight, seed yield and harvest index had high heritability with high GAM and stand count at harvest had moderate heritability with high GAM. This would probably indicate the presence of additive gene action for the inheritance of these traits and simple selection would be effective for improving these traits.

Lad, et al. reported high GAM with high heritability for plant height and harvest index. Terefu also reported moderate heritability with high GAM for grain yield. Moderate heritability coupled with moderate genetic advance as percent of mean was recorded for number of seed per pod. This suggests that these traits are primarily under genetic control and selection based on the phenotype performance of genotypes for these traits might improve the performance of the progenies Ejiguet observed moderate heritability with moderate GAM for number of seed per pod.

In the present study plant height, number of seed per plant, biological yield and seed yield had high heritability, GCV and GAM value indicating the major portion of genetic variation attributable to additive gene action. Therefore, this trait can be effectively improved through selection. Lad, et al. also reported high heritability, GCV and GAM value for plant height. Similarily Besufikad, Ghodrati, Badkul, Hakim, et al., Mesfin, Santosh, et al. high heritability coupled with high genetic advance as percent of mean has been reported for plant height, grain yield, number of seeds and number of pods.

Association of traits

The association pattern among yield components help to select the superior genotypes from divergent population based on more than one interrelated characters. The degree of association between pairs of traits at genotypic and phenotypic level was estimated and results are presented in table 4.

Genotypic and phenotypic correlation of seed yield with other related traits: Genotypic and phenotypic correlation analysis indicated that seed yield showed positive and highly significant (<0.01) association with days to 90% maturity (r_p=0.43, r_g=0.5), stand count at harvest (r_p=0.38, r_g=0.55), number of seeds per plant (r_p=0.57, r_g=0.59), biological yield (r_p=0.6, r_g=0.65),hundred seed weight (r_p=0.44, r_g=0.44) and harvest index (r_p=0.74, r_g=0.75). This would indicate that these traits could be used as indirect selection criteria for maximizing seed yield. In addition, the occurrence of positive significant association of seed yield with most of its yields component revealed less complex inter relationship between yield and yield components. Such situation is favorable from breeding point of view because phenotypic selection for one trait may bring correlated response for improvement of other traits which are positively associated with it. Similarly Ejigu, et al. reported positive and highly significant genotypic and phenotypic association of seed yield with number of primary branches, number of seed per pod and number of seed per plant. Berecha also reported positive and highly significant

genotypic and phenotypic association of seed yield with number of pods per plant and a significant and positive genotypic and phenotypic association of seed yield with harvest index.

Seed yield had positive and significant genotypic correlation and highly significant phenotypic correlation with number of pod per plant (r_p=0.34, r_g=0.366). This indicates that these traits can be improved simultaneously. Aziza also reported positive and highly significant phenotypic correlation of seed yield with number of pod. It had also positive and non-significant genotypic and phenotypic correlation with days to 50% emergence (r_p=0.15, r_g=0.22), days to 50% flowering (r_p=0.1, r_g=0.08), stand count at emergence (r_p=0.1, r_g=0.08), and number of seed per pod (r_p=0.17, r_g=0.2). This indicates that selection for these traits may not improve seed yield. The present results also in agreement with the findings of earlier studies.

Phenotypic and genotypic correlation coefficient among other traits: Days to 90% maturity had positive and highly significant genotypic and phenotypic correlation with biological yield (r_p=0.4, r_g=0.48). This indicates genotypes taking longer to mature also have higher biological yield. This result agrees with the findings of Ejigu, Aziza and Berecha.

The result further indicated that number of seeds per plant had positive and highly significant correlation with number of pods per plant (r_p=0.64, r_g=0.69) and number of seeds per pod (r_p=0.6, r_g=0.7) both at genotypic and phenotypic level. This indicates that genotypes with high number of seeds per plant had high number of pods per plant and seed per pod. Similar result also observed by Ejigu, et al. It had also positive and highly significant genotypic and phenotypic correlation with stand count at harvest (r_p=0.32, r_g=0.39) and harvest index (r_p=0.45, r_g=0.4).

Plant height showed positive correlation with biological yield (0.05, 0.04) both at genotypic and phenotypic level. This would suggest that genotypes with taller plant height had high biological yield. It had also positive and highly significant genotypic and phenotypic association with number of primary branch (0.34, 0.4). Similarly Kassa reported positive and highly significant association of biological yield with number of pod per plant and days to maturity at both phenotypic and genotypic level.

A positive and highly significant correlation exist between biological yield and days to maturity (0.31, 0.48) and number of seed per plant (0.4, 0.5) both at genotypic and phenotypic level but it had negative and non-significant correlation with number of primary branch (-0.08, 0.12) both at genotypic and phenotypic level. Similarly Legesse reported positive and highly significant association of biological yield with number of pod per plant and days to maturity at both phenotypic and genotypic level.

Hundred seed weight exhibited positive and highly significant phenotypic and genotypic correlation with days to 50% emergence (0.33, 0.35) and harvest index (0.42, 0.4). This indicated that early emerged leads to better seed weight regarding to early maturity and increase in harvest index would also lead to a significant increase in hundred seed weight.

Harvest index showed positive and significant genotypic and highly significant phenotypic correlation with stand count at harvest (0.31, 0.4), number of pod per plant (0.33, 0.35), number of seed per plant (0.45, 0.5). Aditya and Mahbub reported significant and positive association among yield related traits and that would indicate an increase in the value of one of these traits would increase the value of another trait. Generally, positive and significant associations of pairs of characters at phenotypic and genotypic levels justify the possibility of simultaneous response to selection. But, negative correlations make difficult the simultaneous improvement of those traits (Table 5).

Traits	DE	DF	DM	SCE	SCH	PH	NPoPPL	NSPPo	NSPPL	NBPP	HI	BY	HSW	PC	SY
DE		-0.2^{ns}	0.096^{ns}	0.21^{ns}	0.058^{ns}	0.044^{ns}	0.058^{ns}	0.29^{ns}	0.19^{ns}	0.11^{ns}	0.21^{ns}	0.03^{ns}	0.47**	-0.2^{ns}	0.22^{ns}
DF	-0.17^{ns}		0.25^{ns}	0.02^{ns}	0.25^{ns}	0.2^{ns}	0.49**	0.1^{ns}	0.3*	0.03^{ns}	-0.06^{ns}	0.26^{ns}	-0.27^{ns}	-0.1^{ns}	0.08^{ns}
DM	0.15^{ns}	0.19^{ns}		0.09^{ns}	0.27^{ns}	0.20^{ns}	0.32*	0.06^{ns}	0.25^{ns}	0.17^{ns}	0.3^{ns}	0.48**	0.24^{ns}	-0.12^{ns}	0.5**
SCE	0.2^{ns}	0.01^{ns}	0.06^{ns}		0.07^{ns}	0.11^{ns}	-0.11^{ns}	-0.08^{ns}	-0.1^{ns}	0.1^{ns}	0.006^{ns}	0.03^{ns}	0.23^{ns}	0.02^{ns}	0.08^{ns}
SCH	0.01^{ns}	0.17^{ns}	0.14^{ns}	-0.01^{ns}		0.13^{ns}	0.37*	0.25^{ns}	0.39**	-0.06^{ns}	0.4**	0.3^{ns}	0.2^{ns}	-0.56**	0.55**
PH	0.01^{ns}	0.13^{ns}	0.18^{ns}	0.08^{ns}	0.14^{ns}		0.14^{ns}	0.03^{ns}	-0.1*	0.4**	-0.1^{ns}	0.04^{ns}	0.08^{ns}	0.13^{ns}	0.09^{ns}
NPoPPL	0.01^{ns}	0.43**	0.24*	-0.1^{ns}	0.27*	0.13^{ns}		0.2^{ns}	0.69**	-0.3^{ns}	0.35*	0.3^{ns}	0.2^{ns}	-0.46**	0.3*
NSPPo	0.13^{ns}	0.04^{ns}	0.05^{ns}	-0.15^{ns}	0.29**	-0.05^{ns}	0.11^{ns}		0.7**	0.02^{ns}	0.07^{ns}	0.24^{ns}	0.1^{ns}	-0.2^{ns}	0.2^{ns}
NSPPL	0.14^{ns}	0.27*	0.25*	-0.1^{ns}	0.32**	-0.07^{ns}	0.64***	0.6**		-0.2^{ns}	0.4**	0.5**	0.2^{ns}	-0.6**	0.59**
NBPP	-0.02^{ns}	0.04^{ns}	0.12^{ns}	0.08^{ns}	-0.007^{ns}	0.34**	-0.07^{ns}	-0.08^{ns}	-0.18^{ns}		-0.13^{ns}	-0.12^{ns}	0.07^{ns}	0.2^{ns}	-0.13^{ns}
HI	0.14^{ns}	-0.02^{ns}	0.31**	0.01^{ns}	0.31**	-0.1^{ns}	0.33***	0.08^{ns}	0.45***	-0.03^{ns}		0.05^{ns}	0.4**	-0.75**	0.75**
BY	0.06^{ns}	0.21^{ns}	0.31**	0.02^{ns}	0.25*	0.05^{ns}	0.29*	0.17^{ns}	0.4**	-0.08^{ns}	0.15^{ns}		0.15^{ns}	-0.42**	0.65**
HSW	0.39**	-0.21^{ns}	0.23*	0.22^{ns}	0.15^{ns}	0.1^{ns}	0.2^{ns}	0.11^{ns}	0.2^{ns}	-0.08^{ns}	0.42***	0.15^{ns}		-0.33*	0.44**
PC	-0.14^{ns}	-0.14^{ns}	-0.2^{ns}	0.003^{ns}	-0.38*	0.07^{ns}	-0.4**	-0.14^{ns}	-0.57	0.07^{ns}	-0.74**	-0.34*	-0.33*		-0.79**
SY	0.15^{ns}	0.1^{ns}	0.43**	0.1^{ns}	0.38**	-0.04^{ns}	0.37**	0.17^{ns}	0.57**	-0.009^{ns}	0.74**	0.6**	0.44**	-0.82**	

Note:**=Highly significant*=Significant Ns: Non-significant, EM: days to 50% emergence, DF: Days to 50% Flowering, DM: Days to 90% Maturity, PH: Plant Height, NPBPPI: Number of Primary Branch Per Plant, NPoPP: Number of Pod Per Plant, NSPPO: Number of Seed Per Pod, NSPPI: Number of Seed Per Plant, HSW: Hundred Seed Weight, BY: Biological Yield, SY=Seed Yield, PC: Protein Content and HI: Harvest Index

Table 5: Correlation coefficient at genotypic (above diagonal) and phenotypic (below diagonal) levels for 15 traits.

Path coefficient analysis

The genotypic and phenotypic correlation was partitioned into direct and indirect effects to know the relative importance of the components to enhance seed yield.

Genotypic path coefficient analysis: The genotypic direct and indirect effects of different traits on seed yield are indicated on Table 6. Path analysis revealed that harvest index, biological yield, stand count at harvest and hundred seed weight showed strong positive direct effect on seed yield with the value of 0.72, 0.62, 0.12 and 0.069 respectively. Hence, these four characters could be considered in the improvement of common bean seed yield.

In other words, favorable direct effects of biological yield, harvest index, hundred seed weight and stand count at harvest on grain yield indicate that the true relationship and direct selection for these traits may also increase and give better response for improvement of seed yield per hectare. Highest negative direct effect on yield showed by protein content (-0.085) and followed by days to 90% maturity (-0.04) and number of pod per plant (-0.12). These negative direct effects on seed yield indicate direct selection of these traits is not effective for common bean seed yield improvement. These findings were supported by the findings of many authors.

Number of pod per plant and days to 90% maturity had positive correlation on seed yield but it exerts negative direct effect on seed yield. The negative direct effect of this trait might counter balance by positive indirect effect through stand count at harvest, number of seed per plant, biological yield, hundred seed weight and harvest index on seed yield so this indicating that indirect selection of number of pod per plant through stand count at harvest, number of seed per plant, biological yield, hundred seed weight and harvest index might be helpful in yield improvement but since the direct effect was negative and strong so direct selection for these traits to improve yield will not be desirable.

Terefu, and Aziza, reported that positive indirect effect of number of pod per plant on seed yield through days to maturity, plant height and number of seed per pod. Aziza, also reported positive indirect effect of number of pod per plant on seed yield through number of seed per plant and number of primary branches.

Days to 90% maturity exerted high positive indirect effect on seed yield through stand count at harvest, number of seed per plant, biological yield, hundred seed weight and harvest index counterbalances the very low direct effect of this trait on seed yield. Lad et al. also reported similar result with the present study.

Stand count at harvest, number of pod per plant and hundred seed weight exerted maximum positive indirect effect on seed yield *via* harvest index. Number of seed per plant exerted maximum positive indirect effect on seed *via* biological yield. Ejiguet, et al. also reported positive indirect effect of number of seeds per pod and number of pod per plant on seed yield through number of seeds per plant. In present study, improving these traits may increase seed yield as well as performance of some traits. The negative indirect effect of harvest index on grain yield through biological yield may be due to their negative association at genotypic level.

From genotypic path coefficient analysis the residual effect was R=0.241, this indicates that traits, which are included in the genotypic path analysis, explained 76% of the total variation in seed yield in which the traits, considered for the study were appropriate for yield improvement in common bean.

Traits	DM	SCH	NPPPL	NSPPL	HI	BY	HSW	PC	rg
DM	-0.04	0.17	-0.04	0.02	0.21	0.18	0.016	-0.01	0.49
SCH	-0.01	0.12	-0.045	0.028	0.25	0.18	0.014	-0.005	0.54
NPPPL	-0.013	0.044	-0.12	0.05	0.29	0.13	0.014	-0.04	0.37
NSPPL	-0.01	0.05	-0.08	0.073	0.3	0.25	0.013	-0.005	0.61
HI	-0.012	0.06	-0.042	0.032	0.72	0.034	0.03	-0.064	0.75
BY	-0.019	0.036	-0.035	0.033	0.04	0.62	0.01	-0.046	0.65
HSW	-0.009	0.024	-0.024	0.038	0.29	0.09	0.069	-0.028	0.44
PC	0.005	-0.085	0.055	-0.054	-0.44	-0.16	-0.043	-0.085	-0.79
Residual=0.24									

Note: DM: Days to 90% Maturity, SCH: Stand Count at Harvest, NPoPPL: Number of Pod Per Plant, NSPPL: Number of Seed Per Plant, HI: Harvest Index, BY: Biological Yield, HSW: Hundred Seed Weight, and PC: Protein Content.

Table 6: Estimates of direct (bold diagonal) and indirect (above and below diagonal) effects at genotypic level of 14 traits on seed yield.

Phenotypic path coefficient analysis: The phenotypic direct and indirect effects of different trait on seed yield are provided in Table 7. Highest positive phenotypic direct effect on seed yield was showed by harvest index (0.49) and biological yield (0.48) and followed by hundred seed weight (0.08), number of seed per plant (0.03), days to 905 maturity (0.003) and stand count at harvest (0.0009). These positive direct effect of the character on seed yield showed that indirect selection based on these characters will be rewarding for common bean seed yield improvement and important consideration should be given for these traits while practicing selection aimed at the improvement of seed yield. Hence indirect selection based on these traits could be effective to improve common bean seed yield. Legesse also reported maximum positive phenotypic direct effect of biological yield and harvest index on seed yield. These findings were supported by the findings of many authors.

Number of pods per plant (-0.11) had negative direct effect on seed yield followed by protein content (-0.29) but its effect is negligible compare to the residual effect. The negative direct effect of the above

character on seed yield indicates direct selection of this character is not effective for crop improvement. Legesse observed similar result with the present study. Terefu and Ejigu, et al. also observed similar result for number of pod per plant and pod length, respectively.

In the present finding number of seed per plant exerted positive indirect effect *via* all traits except number of pod per plant. Since number of pod per plant had highly significant positive phenotypic association and low negative direct effect on seed yield indirect selection of this trait *via* stand count at harvest, number of seed per plant, harvest index, biological yield and hundred seed weight may improve seed yield. Aziza observed similar result with the present study.

Protein content also exerted negative indirect effect on seed yield through days to 90% maturity, stand count at harvest, number of seed per plant, harvest index and biological yield. Berecha also reported negative indirect effect of number of seed per pod on seed yield through plant height and number of pod per plan and negative indirect effect of harvest index on seed yield through plant height and biological yield.

From the phenotypes path analysis the residual effect was R=0.252 which implies that the traits included in the phenotypic path analysis, explained 74.8% of total variation in seed yield of common bean genotypes and 25.2% were contribution of other factors.

Traits	MD	SCH	NPPPL	NSPPL	HI	BY	HSW	PC	rp
MD	0.03	0.0013	-0.058	0.008	0.15	0.2	0.02	0.05	0.4
SCH	0.004	0.0009	-0.03	0.0096	0.156	0.12	0.013	0.11	0.38
NPPPL	0.007	0.0003	-0.11	0.019	0.16	0.14	0.016	0.12	0.34
NSPPL	0.008	0.000009	-0.07	0.03	0.22	0.2	0.016	0.17	0.57
HI	0.009	0.0003	-0.04	0.03	0.49	0.024	0.03	0.21	0.75
BY	0.01	0.00022	-0.03	0.01	0.024	0.48	0.012	0.09	0.61
HSW	0.08	0.024	-0.21	0.07	0.23	0.07	0.08	0.09	0.44
PC	-0.006	0.0007	0.04	-0.02	-0.36	-0.16	-0.03	-0.29	-0.82
Residual=0.25									

Table 7: Estimates of direct (bold diagonal) and indirect (above and below diagonal) effects at phenotypic level of 14 traits on grain yield.

Genetic divergence analysis

Based on D^2 value, 36 common bean genotypes were grouped into 4 clusters presented in Table 8. The number of genotypes varies from one in cluster II to sixteen in cluster III (Figure 2). Distribution of genotypes into four clusters implied the prevalence of genetic variation among genotypes for most of the traits under consideration. Cluster III was the largest cluster which comprises sixteen genotypes followed by cluster I with thirteen genotypes. Cluster II was the smallest and consisted of only one genotype. Panchbhaiya, et al. grouped into six cluster of common bean.

Cluster	Count	Genotypes	Proportion
	13	ADP0007, ADP0518, ADP0076, ADP0081, ADP0476, ADP0512, ADP0581, ADP0126, ADP0522, ADP0512,ADP0524, KAT-1, ADP0525	36.11
2	1	ADP0034	2.8
	16	ADP0014, ADP0111, ADP0033, ADP0072, ADP0097, ADP0456, ADP0050, ADP0071, ADP0094, ADP0100, ADP0106, ADP0478, ADP0092, ADP0303,ADP0532, ADP0127	44.44
4	6	ADP0047, ADP0379, ADP0075, ADP0080, ADP0523, ADP0102	16.66

Table 8: The distribution of 36 common bean genotypes in to four clusters based on D^2 analysis.

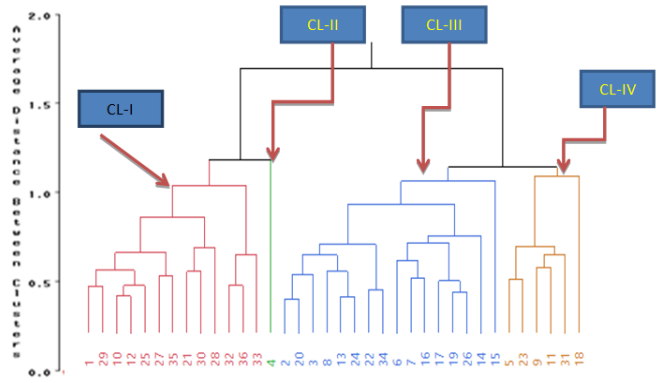

Figure 2: Dendrogram showing 36 common bean genotypes grouped based 15 traits by using ward method.

Cluster distances analysis: The cluster formation and finding out intra and inter cluster divergence provides a basis for selecting genetically divergent parents and it may be useful to produce crosses between genotypes belonging to the clusters separated by large estimated distances.

The average intra and inter distance D^2 value are indicated in Table 9. Inter cluster distance ranged from 26.05 to 3734. The maximum inter cluster distance was observed between cluster II and III (3734) followed by cluster II and IV (3652), I and II (3530). Genotypes belonging to the clusters with maximum inter cluster distances are genetically more divergent and hybridization between genotypes of divergent clusters is likely to produce wide variability with desirable segregants. The minimum inter cluster distance was observed between cluster I and II (26.05). Thus, crossing of genotypes from these two clusters may not produce high heterotic values in the F1''s and broad spectrum of variability in segregating (F2) populations. Parents for hybridization could be selected on the bases of large inter cluster distance for isolating useful recombinants in the segregating generation.

The maximum distance in cluster III (57.46) followed by cluster I (33.77) and cluster II (20.04). The minimum intra cluster distance was observed from cluster II (0.0). Showing that the genotypes in this group were genetically closer than any other groups but genotypes in the same cluster are not exactly the same hence, better to consider individual parent characterization while selecting for crossing report maximum intra and inter-cluster distance in common bean genotypes.

Cluster	1	2	3	4
1	33.77	3530	26.0464	35.5766
2		0	3734	3652
3			57.46	30.4984
4				20.05

Table 9: Intra (bold diagonal) and inter Mahalanobis distance among genotypes among 36 common bean genotypes.

χ^2=22.36 at 1% probability level and X^2=27.69 at 5% probability level at n-1 degree of freedom where n is the number of traits considered.

Cluster mean analysis: Mean value of the traits for each cluster is given in Table 10. Based on mean value of 15 traits cluster I is characterize by medium value of plant height, protein content and harvest index and also had high seed yield next to cluster IV. It also characterized by lowest value of days to 50% flowering, days to maturity, number of seed per pod, number of seed per plant and biological yield. Haralayya and Vidyakar revealed first level priority as far producers put productivity, resistance, adaptation traits and to be followed by market and taste. In line with these from cluster mean values, genotypes in cluster I deserve consideration for their direct use as parents in hybridization programs to develop high yielding and early maturing varieties.

Cluster II is characterized by characterize by high value of number of seed per pod, number of seed per plant and protein content. Hence, genotypes included in this cluster could be used for developing varieties with maximum number of pod per plant and number of seed per plant and it had the second best value for number of seed per pod and seed per plant next to cluster I. It was also characterized by seed yield. Similarly, Altaye reported high value for number of seed per pod and number of seed per plant.

Cluster III is characterized by high value for number of number of pod per plant, biomass yield and harvest index but lowest value for number of stand count at 50% emergence and number of pod per plant. Genotypes included in this cluster characterize by late maturity next to cluster IV. This result agrees with the report of Very, et al.

Cluster IV characterized by having lowest number of primary branch, protein content and medium value of harvest index and it also cauterized by high value of hundred seed weight, biomass yield and seed yield. It was also consisted late flowering and maturing genotypes hence, they could be used for selection of late maturity cultivars and high seed yield. Therefore, genotype included in these cluster could be select for the above traits for further crop improvement.

The current finding exerted the average cluster mean of 15 traits revealed that none of the clusters contained genotype with all the desirable characters and so recombinant breeding between genotypes of different clusters are needed. In addition, to create genetic variability in diverse desirable traits, multiple crosses are performing using these divergent parental lines may give good results. Similarly, Haralayya, et al., Vidyakar, et al., Altaye, et al. and Very, et al. stated that selection of parents should also consider the superior advantage of each cluster and each genotype within a cluster depending on specific objective of hybridization.

	I	II	III	IV
DE	6.615	7	6.969	6.9
DF	41.846	45.5	42.344	41.5
DM	75.731	76.5	79.781	81.3
SCE	109.038	111	110.563	94.25
SCH	59.3462	72	78.3125	75.16
PH	52.6423	99	43.5375	86.6
NPoPP	10.4231	9.9	12.1875	11.6
NSPPo	5.6923	7.5	6.9063	6
NSPPl	53.538	91.5	79.469	63
NBPPl	3.077	3	2.688	3.8
HI	33.465	25.25	51.894	44.73
BY	334.597	528.03	535.743	512.0
HSW	30.814	29.725	39.841	41.96
PC	22.685	23.15	19.953	21.1
SY	347.7	144.21	228.42	355.7

Table 10: Mean value of six clusters for 15 traits.

Principal component analysis

Principal Component Analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis for differentiation. PCA was used to find out the traits, which accounted more for the total variation.

The first five PCAs were found important and explained 71% of the total variation and provided in Table 11. PC1 explained 33%, PC2 showed 12%, PC3 explained 10%, PC4 had 9% and PCA5 7%. Traits such as number of pod per plant, number of seed per plant, biological yield, harvest index and seed yield explain highest variation of the PCA1 through positive loading and high negative effect of protein content. Similarly, the high contribution of hundred seed weight and number of seed per plant in the first principal component were reported by Arora, et al.

Days to 90% maturity, days to 50% emergence, stand count at emergence and hundred seed weight explain the highest variation on PCA2 through positive loading and number of pods per plant, number of seeds per pod, number of seeds per plant and biomass yield and plant height through negative loading.

The trait that contribute most to PCA3 were days to flowering, days to maturity, stand count at emergence and plant height through positive loading while, number of seed per pod, number of seed per plant, harvest index and seed yield through negative loading. Similar studies were reported by Madakbas, et al. and Stoilova, et al.

Days to 50% emergence, plant height, biomass yield, number of seed per pod and number of seed per plant weight explain the highest variation on PCA4 through positive loading and number of pods per plant, days to 50% flowering, days to 90 maturity, number of primary branch and harvest index through negative loading.

The fifth principal component affected by days to 50% emergence, days to 50% flowering, days to 90% maturity, number of seeds per pod, number of seed per plant, number of seed per plant, number of primary branch, harvest index and hundred seed weight through positive loading and stand count at emergence and harvest, plant height and seed yield through negative loading to the genetic variation. The character contributing the maximum loading for variation should be given greater emphasis. Similar findings was reported by Panchbhaiya, et al., Ankit, et al., Madakbas, et al., Stoilova, et al. and Yonas who reported that principal component analysis in genetic variability study of common bean and reported similar result which agreed with current study.

Traits	PCA1	PCA2	PCA3	PCA4	PCA5
DE	0.13	0.37	0.05	0.47	0.18
DF	0.11	-0.46	0.25	-0.22	0.23
DM	0.23	0.05	0.3	-0.09	0.13
SCE	0.006	0.35	0.23	-0.12	-0.3

SCH	0.23	-0.1	0.06	0.03	-0.26
PH	0.03	-0.05	0.61	0.12	-0.18
NPPP	0.29	-0.27	0.08	-0.06	-0.003
NSPP	0.18	-0.19	-0.09	0.51	0.4
NSPPL	0.37	-0.23	-0.14	0.18	0.26
NBPP	-0.03	0.13	0.05	-0.12	0.52
HI	0.33	0.24	-0.27	-0.26	0.08
BY	0.27	-0.13	0.12	0.03	-0.4
HSW	0.22	0.45	0.07	0.09	0.01
PC	-0.37	-0.08	0.16	0.22	0.1
SY	0.4	0.15	-0.06	-0.06	-0.17
Eigen value	5.01	1.73	1.49	1.36	1.08
Proportion (%)	0.33	0.12	0.1	0.09	0.07
Cumulative (%)	0.33	0.45	0.55	0.64	0.71

Table 11: Eigenvalues, total variance, cumulative variance and eigenvectors for 15 traits of common bean genotypes.

Conclusion

Knowledge on the extent of genetic variability and the degree of relationship among yield and the other agronomic character are important in plant breeding program as they provide the basis for selection. The analysis of variance showed highly significant difference for days to 50% flowering, stand count at emergence and harvest, plant height, number of pod per plant, number of seed per plant, harvest index, biomass yield, hundred seed weight, protein content and seed yield traits studied. It also shows significant difference for number of seed per pod and non-significant difference for days to 50% emergence and days to 90% maturity. The highly significant difference indicates the existence of large variability among genotypes.

The highest seed yield was recorded for genotype ADP0034 (3130.1 kg/ha) followed by ADP0127 (2958.5 kg/ha) and ADP0111 (2933.3 kg/ha), while the lowest seed yield was gained for ADP0524 (1335 kg/ha). In this study days to 50% emergence, plant height, number of pod per plant, number of seed per plant, harvest index, biomass yield and seed yield had high heritability with high Genetic Advance as percent of Mean (GAM). This indicates the selection would be easier and effective for improving these traits.

Recommendation

Correlation and path coefficient analysis showed days to 50% emergence, days to 50% flowering, stand count at emergence, stand count at harvest, plant height, number of primary branches per plant, number of seed per plant, biological yield, hundred seed weight and harvest index had positive correlation and direct effect on seed yield. Hence, these traits could be considered in the improvement of common bean seed yield.

The cluster analysis based on D^2 analysis classifies 36 genotypes into 4 clusters. The intra cluster distance ranged from 0 to 57.46 and inter cluster distance ranged from 26.05 to 3734. The maximum intra cluster distance was observed in cluster III and the maximum inter cluster distance was obtained between cluster II and III. This result indicates the presence of variability within and among genotypes studied and also genotypes from distant inter cluster (from cluster II and III (3734)) could be used as a parental material for crossing. Maximum genetic recombination and variation in the subsequent generation is expected from these crosses that involve parents from the clusters characterized by maximum distances, crosses between genotypes of cluster III with cluster IV and cluster III might be the best scenario to develop moderately better genetic recombination and generate desirable segregants.

The principal component analysis based on correlation matrix yielded 5 principal components account 71% of the total variation. The first principal component was accounted 33% followed second to fifth components which accounted 12%, 10%, 9% and 7% of the total variation presented among genotypes, respectively. However, one season experiment would not realize genotypes variability in response of environment, because quantitative traits are polygenic and profoundly influenced by the environment. Thus, further experiment on these genotypes in changed over seasons is required. It should be advisable to study more available germplasm over years and locations to detect more accessions as well as to confirm the difference of the traits identified as predictors of economic yield.

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