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STUDIES ON GENETIC DIVERGENCE IN COMMON BEAN (*Phaseolus vulgaris* L.) INTRODUCTIONS OF ETHIOPIA

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Dedication

Dedicated to my beloved uncle Ato Seyoum Abebe who has sown an academic interest to my mind and passed without seeing my success.

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TABLE OF CONTENT Page

List of Tables **Page**

List of Figures Page

List of Appendices Page

Studies on Genetic Divergence in Common Bean (Phaseolus vulgaris L.) Introductions of Ethiopia

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Abstract: *One hundred and forty four common bean (Phaseolus vulgaris L.) germplasm introductions were evaluated for their diversity in 18 agronomic and morphological traits using D^2 statistics. High genotypic coefficient of variation (GCV) was observed for plant height, number of nodes on the main stem, 100-seed weight, number of pods per plant and internode length. For all the traits, estimates of phenotypic coefficients of variation (PCV) were higher than GCV, indicating presence of environmental influence. High heritability and genetic advance was observed for plant height, number of nodes on the main stem and 100-seed weight. Seed yield has significant and positive association with biological yield, number of pods per plant, number of seeds per pod, plant height, stem diameter, number of nodes on the main stem, days to flowering and days to maturity, whereas number of pods per plant, 100-seed weight and number of seeds per pod had the maximum direct effect on seed yield. The D^2 value data can be used in cluster analysis to identify groups of related cultivars. The genotypes were grouped in nine clusters on the basis of D^2 value. The clustering pattern was not influenced by the geographic diversity of the germplasms. Two major clusters, which corresponded to Mesoamerican and Andean origin, were observed. The intra- and inter-cluster D^2 values suggested that within cluster genetic diversity is narrow, but the genetic diversity among clusters is greater. Therefore, exploiting the diversity among clusters would broaden the genetic base of dry bean breeding populations.*

Keywords: *Genetic distance, genetic diversity, genetic variability, germplasms, correlation, path coefficient analysis, clustering*

I. Introduction

The common bean or haricot bean (*Phaseolus vulgaris* L.) plays a paramount role in human nutrition and market economies in the world. World common bean production can be conveniently grouped into twelve regions, the most important of which are Brazil, Mexico and Eastern African highlands. Beans are a major staple in these regions, which together contribute to half of the world's production. Latin America, the center of origin for the common bean (Gentry, 1969), is the leading bean producer in the world (Pachico, 1989). *Phaseolus vulgaris* became established as a food crop in Africa before the Colonial era (Allen *et al*., 1989).

Beans are grown on an area of greater than 14 million hectares annually in the world (Singh, 2001). It occupies 0.25 million-hectare areas with an average productivity of 8.61qt/ha in Ethiopia (CSA, 2005). According to Amare (1987), most of the area lies in sub humid highlands and semi-arid zone in the Rift Valley and eastern regions. It's grown aside as well as intercrop with maize, banana, sorghum, cassava and sweet potato due to its short duration and tolerance to shading (Westphal, 1974). Two crops per year are grown with saving time in January to May and June to September. Bean yields are only 20-35% of the genetic potential of improved varieties (Wartmann et al., 1998). Beans are grown for local consumption and for export as cash crops. It's consumed as seeds of dry beans or as pods of snap beans. These are significant source of protein dietary; fiber, calories, minerals and vitamins especially foliate.

Genetic improvement of the common bean in Ethiopia has been characterized by conservative breeding strategies designed to adhere to rigorous consumer preferences mainly market qualities and resistance to diseases that affect common bean production in the country (Amare and Haile, 1989). These factors have reduced the germplasm sources used in hybridization and have limited the genetic variability available for breeding programs. Over 1000 accessions of Phaseolus vulgaris germplasm introductions, representing world wide distribution mainly from countries Mexico, Brazil, USA, Guatemala, Honduras, El Salvador, Venezuela, Costa Rica, Colombia, Chile, Peru, Ecuador, Dominican Republic, Kenya, Burundi, Malawi, South Africa including local landraces of Ethiopia are currently available at Melkassa Agricultural Research Center

(MARC). For this study representative samples of the main introductions were evaluated to analyze the variation within the accessions.

Characterization of genetic diversity of accessions can be achieved with phenotypic traits and molecular markers. Phenotypic traits have the advantage that they may be directly related to the fitness of the populations and usefulness for plant breeding. Joint analyses of molecular and phenotypic diversity as well as attempts at predicting the breeding value for different phenotypic traits depending on the molecular marker diversity or genotype of the parents; generally show a poor correlation between the two types of data (Reed and Frankham, 2001). The situation can be attributed to a variety of reasons: the lack of tight linkage between molecular markers (mainly neutral) and genes coding for phenotypic traits that may be subjected to selection. Other possible reasons include the lack of correspondence in gene action between phenotypic traits (additive, dominance or epistatic action) and molecular markers (indirect measure of additive gene action), differences in heritability (low to high for phenotypic traits verses high for molecular markers), mutation rate and mutational input (high for polygenic phenotypic traits verses low for molecular markers). Various authors (Delaney and Bliss, 1991a, 1991b; van Trienderen et al. 2002) have therefore, proposed to assess and select for genetic diversity by analyzing genes directly involved in the traits of interest. Such studies include agronomic and morphological traits. If phenotypic observations are based on adequately large sample sizes and the physical traits measured show significant differences among populations, they can provide a reasonable representation of overall genetic performance (Humphreys, 1991).

Plant breeding is essentially selection of plants among the variables. Thus, an insight into the magnitude of variability present in a crop species is important as it allows effective selection. The total observable variation, phenotypic variation, is made up of genetic and environmental component of variations. Genotypic variation, which arises due to the genotypic difference and the base for selection is the main concern of plant breeders. Hence, in selection for yield, more emphasis has to be placed on those attributes with low environmental variability.

In common bean, architectural, phenological and yield components are collectively influencing seed yield. The relationships between yield and yield contributing traits in one hand and among

themselves on the other hand could be measured by correlation coefficient. The knowledge of this relationship helps to identify traits on which selection can be based for the implement of yield. Further more, selection via highly correlated characters become easy if the contribution of different characters to yield is quantified using path coefficient analysis. Path analysis splits the correlation coefficient into direct and indirect effects of a set of independent variables on the dependent variable yield.

With regard to morphological variation of Ethiopian common bean germplasm introductions, no study has been done in the past. Since common bean is grown in most parts of Ethiopia with a wide range of variation in altitude, rain fall, temperature, agricultural system and socio-economic factors, it is essential to asses the pattern of character variations among and between accessions to resolve the problems in different regions and adaptation zones. Assessing diversity in these germplasm introductions can help to identify elite genotypes with the greatest novelty and thus are most suitable for rescue or incorporation into crop improvement programs. In plant breeding, diversity can be assessed in different ways. But D^2 technique has been widely used in crops like maize, sorghum, pearl millet, wheat, linseed, cotton, tobacco, alfalfa, brassica, etc. (Murty and Arunachalan, 1966). D^2 statistics measure the forces of differentiation at intra and inter cluster levels and determine the relative contribution of each component trait to the total divergence. Its estimates are free from genetic assumptions and help to identify suitable germplasm for incorporation into plant breeding stocks.

II. Literature Review

Genetic diversity refers to the variation of genes within populations/species, making it possible to develop new breeds of crop plants and domestic animals and allowing species in the wild to adapt to the changing conditions. In crop plants, genetic diversity arises as consequences of interplay of evolutionary forces (mutation, selection and random genetic drift) and the influence of human through domestication and selection (Bhatt, 1970). Study of genetic diversity is the process by which variation among individuals or groups of individuals or populations is analyzed by a specific method or a combination of methods. The data often involve numerical measurements and in many cases, combinations of different types of variables. Diverse data sets have been used by researchers to analyze genetic diversity in crop plants; most important among such data sets are pedigree data, morphological data and biochemical data obtained by analysis of isozymes and storage proteins and, recently, DNA-based marker data.

Genetic relationships in crop species is an important component of crop improvement programs, as it serves to provide information about genetic diversity, and is a platform for stratified sampling of breeding populations. Accurate assessment of the levels and patterns of genetic diversity can be invaluable in crop breeding for diverse applications including (i) analysis of genetic variability in cultivars, (ii) identifying diverse parental combinations to create segregating progenies with maximum genetic variability for further selection, and (iii) introgressing desirable genes from diverse germplasm into the available genetic base. An understanding of genetic relationships among inbred lines or pure lines can be particularly useful in planning crosses, and in assigning lines to specific heterotic groups. Analysis of genetic diversity in germplasm collections can facilitate reliable classification of accessions and identification of subsets of core accessions with possible utility for specific breeding purposes. In this regard, literatures pertaining to the present work 'Studies on Genetic Diversity in Common Bean (*Phaseolus vulgaris* L.) Introductions of Ethiopia are reviewed under the following headings.

1. Genetic variability, heritability and genetic advance
2. Correlation and path coefficient analysis
3. Genetic divergence analysis through multivariate statistical techniques

2.1. Genetic Variability, Heritability and Genetic Advance

The value observed when a quantitative character is measured on an individual, is the phenotypic value. The phenotypic value is divided into genotypic and environmental components. An important objective is to assess the relative importance of the genotype ***versus*** environment. Hence, information about genetic parameters, such as heritability is relevant to decide which are the most suitable quantitative traits to be used in germplasm evaluation focused on pre-breeding and breeding. The heritability expresses the proportion of the total variance that is attributable to the average effects of genes, and this is what determines the degree of resemblance between relatives. The heritability has a predictive role expressing the reliability of the phenotypic value as a guide to the breeding value.

In the latest part of the 19^{th} century, Galton (1889) indicated that only a part of continuous variation was due to heredity. Johanssen's (1909) study in a self pollinated crop, French bean, highlighted the contribution of genetic and environmental components to the total variance and revealed that the genetic component was relatively constant over generations which were subsequently confirmed by East (1916). Fisher (1918) was the first person to separate genetic variance into sub-components: additive effect of genes, dominance deviation from the additive scheme and deviation from the additive scheme attributed to inter-allelic interactions

Lush (1949) defined heritability in "Broad-sense" as the ratio between the genotypic variance as a whole and that due to phenotype. Later, Hanssen *et al.,* (1956) suggested heritability in "Broad-sense" as the ratio of genotypic variance to the total variance. But, broad-sense heritability does not give a clear picture of transmissibility of variation from one generation to the next. Its utility in plant improvement program was limited since the genetic variation included is fixable additive effect and non-fixable dominance and epistatic effect. Thus, heritability in the "Narrow- sense" was defined as the ratio of additive genetic variance to the phenotypic variance (Lush, 1949).

Selection for traits having high heritability would be very effective as there would be a close correspondence between genotype and phenotype. But heritability estimates along with expected genetic gain are considered to be more useful in predicting the outcome of selecting the best individuals (Johanssen *et al.,* 1955). Improvement in the performance of selected over the original population can be termed as genetic advance. The ultimate goal of the plant breeder is to

have higher genetic advance for the material selected, since it is an indicator for the genetic improvement made in a population under selection. The genetic gain that can be expected for a particular character through selection is the product of heritability, phenotypic standard deviation and selection differential (Burton and Devane, 1953). It is clear that the heritability estimates either 'Broad Sense' or 'Narrow Sense' are useful only for the population or genotypes under consideration as these estimates vary with the sets of genotypes considered. Literatures with respect to genetic variability, heritability and genetic advance for yield and yield contributing characters in common bean have been reviewed.

Wallace and Munger (1966) reported harvest indices varying from 55 to 67% in 11 cultivars of common bean, and the cultivars with the highest harvest index had the lowest grain yield. However, harvest index has been suggested as a useful selection criterion for grain yield in many crops, including grain legumes (Debouck, 1991). In common bean, however, the value of harvest index, as a selection criterion for improvement of grain yield has not bean established.

Bean cultivars may display considerable variation for days to maturity, biological yield, seed yield and harvest index, especially at high latitudes (Debouck, 1991). Moreover, variation for these traits between gene pools seems to be greater than the difference within gene pools, especially for maturity and harvest index at lower latitudes in warm tropical environments closer to the equator. Zimmermann *et al*. (1984) studied heritability and correlations of yield, yield components and harvest index of four bean cultivars and their crosses in sole and intercropping systems. Values for yield, yield components and harvest index were always greater in sole crop than in intercrop. Broad sense heritability for harvest index was moderately high (60%) in sole crop and rather low (39%) in intercrop (Zimmermann *et al*., 1984). Zimmermann *et al*. (1984) also found broad sense heritability, H_{BS} (ratio of genetic to phenotypic variance) for seed yield and biomass yield. H_{BS} estimates for yield ranged from 0.5 to 0.94, while it ranged from 0.57 to 0.79 for biological yield.

Singh *et al.* (1994) reported the genetic variability in 7 French bean cultivars by analyzing five characters. The genotypes showed significant differences for all the five characters. Yield per plant and days to flowering showed the highest and lowest phenotypic and genotypic coefficients of variation, respectively. The narrow difference between phenotypic coefficients of variation

(PCV) and genotypic coefficients of variation (GCV) of the characters shows low environmental influence. The low PCV and GCV value for days to flowering indicated less scope to selection for this trait. Yield per plant had high GCV, genetic advance and heritability; pods per plant and pod length had moderately high GCV and genetic advance and high heritability.

Samal ***et al.*** (1995) examined performance, variability, correlation and co-heritability estimates in rajmash. They found significant differences for traits such as plant height, branches per plant, pod length, seeds per pod, yield per plant, 100-seeds weight, and days to 50% flowering. All the traits except branches per plant and pod length exhibited wide range of variability. The phenotypic and genotypic variances were maximum for yield per plant and minimum for branches per plant. The PCV had higher estimate than the corresponding GCV for all the traits. The small difference between PCV and GCV for days to flowering and pod length indicates that the variability was due to genotypic differences. The heritability estimates were higher for days to flowering, pod length and seeds per pod; and low for plant height, branches per plant, 100-seeds weight and yield per plant. Genetic advance and expected genetic advance (as percent of mean) was maximum for yield per plant (42.2) and seeds per pod (57.5) and minimum for pod length and plant height.

Raffi and Nath (2004) studied variability; heritability, genetic advance and relationship of yield and yield contributing characters in dry beans (***Phaseolus vulgaris*** L.). They found the highest genotypic and phenotypic variance by days to maturity (57.64 and 74.13) whereas pod length showed the lowest (1.84 and 2.30). In case of number of seeds per plant the variation between genotypic and phenotypic variance (29.17 and 48.66) and coefficient of variation (31.43 and 40.60) were found high indicating larger environmental effect. 100-seed weight showed the highest genotypic coefficient of variation and also had small difference in both genotypic and phenotypic variance (3.91 and 4.91) and coefficient of variation (42.19 and 42.29), indicating more or less equal genetic and environmental effect on the trait. Here, the environmental effect is negligible. In case of number of pods/plant, the difference between genotypic and phenotypic variation (1.08 and 1.97) and coefficient of variation (19.81 and 26.75) were found comparatively higher indicating less genotypic but more environmental effect on the trait. Raffi and Nath (2004), through path coefficient analysis, also identified a positive non-significant direct effect of

days to flowering on seed yield. Days to maturity and plant height had negative direct effects. The pod and seed characters had positive and significant direct effect on seed yield, indicating an increase in number of pods per plant, pod length, number of seeds per pod and 100-seed weight may be contributed directly to seed yield.

Singh (1985) identified the genotypic and phenotypic variability in 30 geographically diverse strains of pea from different countries. He found significant differences in the varieties for all the characters studied. Variability among varieties was low for days to 50% flowering, days to maturity and harvest index, however, grain yield, plant height; number of pods per plant number of primary branches per plant, main root length and nodules per plant showed a wide range of both genotypic and phenotypic variability. Heritability in broad sense (H_{BS}) was very high for days to flowering (98.3%), plant height (95.54%), nodules per plant (98.27%) and days to maturity (86.7%). Genetic gain was maximum for plant height, pods per plant, length of main root and primary branches per plant. However, genetic gain was of low magnitude for days to flowering, days to maturity and harvest index may be expected to be mainly due to non-additive gene action, whereas for those characters having high heritability and high genetic advance, was due to additive gene action.

Agrawal (1986) studied genetic variability in populations of chickpea crosses for days to flowering, days to maturity, primary and secondary branches per plant, plant height, pods per plant seeds per plant, seeds per pod, seed yield per plant and 100-seeds weight The seeds per plant and pods per plant showed high variability at both phenotypic and genotypic levels for some crosses. High GCV is an indication of the extent of fixable variation present in the population. The GCV and PCV were almost similar for days to flowering and days to maturity for all crosses; and 100-seed weight, seeds per plant and plant height for some crosses, indicating the major part of variation shared by genetic component. Wide differences between GCV and PCV indicated greater influence of environment on that trait. High genetic advance as percentage of mean coupled with high heritability estimates were found for days to flowering and days to maturity for all the crosses, indicating the major portion of genotypic variation attributable to additive gene action.

Atuahene-Amankwa and Michaels (1997), Davis and Evans (1977) and Escribano *et al.* (1994) estimated H_{BS} for seed yield per plant, number of pods per plant, number of seeds per pod and 100-seed weight in common bean. Heritability ranged from 0.05 to 0.94 for seed yield per plant, 0.16 to 0.95 for number of pods per plant, 0.30 to 0.94 for number of seeds per pod and 0.42 to 0.99 for 100-seed weight. According to them, heritabilities for seed yield and seed yield components varied from low to high.

Sarafi (1978) found high heritability estimates for number of pods per plant, number of seeds per pod and 100-seed weight in F_2 and F_3 generations in common bean. Genetic advance for number of pods per plant and number of seeds per pod was significantly different from mid-parent values, but genetic advance values for 100-seed weight were not significant.

Motto *et al.* (1978) studied the inheritance of seed size characteristics between a cross of the small-seeded wild bean NI 325676 and the large seeded cultivar Royal red. Additive gene effects largely controlled length, width, height and weight of seed, with heritability in narrow sense (H_{NS}) values ranging between 0.72 and 0.87. An average of at least 10 effective factors controlled the seed size difference between large-seeded cultivated and small seeded wild forms. Escribano *et al.* (1994) measured the length parallel to the hillum and height from the hillium to the opposite side of bean seed. They found H_{BS} ranged from 0.87 to 0.93 and 0.78 to 0.95 for seed length and height, respectively. They concluded heritability values for the seed size traits considered as high.

Tall plant height was dominant over short and was controlled by either a single gene or by a polygenic system in common bean. Davis and Evans (1977) observed H_{BS} values for stem height ranging between 0.34 and 0.88, whereas H_{BS} value for main-stem internode length was 0.88. Davis and Evans (1977) also found H_{BS} values for basal internodes diameter that is 0.48. They

observed H_{BS} values for nodes on the main stem and for the total numbers of nodes were 0.92 and 0.86, respectively.

Pod length is the exterior distance from the pod apex to the peduncle. H_{BS} ranged from 0.56 to 0.94 (Davis and Evans, 1977; Escribano *et al.*, 1994). Long pod was dominant over short pod and a single gene was responsible for its inheritance. Additive genetic variance was predominant in snap bean. H_{BS} values ranged from 0.58 to 0.91(Davis and Evans, 1977).

A study by CIAT (1979) to analyze germplasm variability by comparing 10,000 accessions of *Phaseolus vulgaris* showed days to flowering as a character having the lowest coefficient of variation among all growth habits. H_{BS} ranged from 0.57 to 0.98 for days to flowering (Davis and Evans, 1977; Escribano *et al.*, 1994).

Singh *et al.*, (1990) predicted heritability and actual gains from selection for seed yield, 100-seed weight and days to maturity. Seed yield had the lowest and 100-seed weight the highest heritability values; consequently predicted gain for 100-seed weight was high. Relatively low predicted and actual gains for days to maturity, in spite of its relatively high heritability, could likely be due to small variation for this trait among populations.

Scully *et al.,* (1991) found the heritability of phenological traits (days to flowering and days to maturity) greater than 0.93. The biomass, harvest index and yield had heritabilities of 0.90 to 0.93. The extremely high heritabilities for these traits were attributed to the large genetic diversity among the 112 genotypes. They also noted highly positive genetic, phenotypic and environmental correlations between yield and biomass yield. The genotypic correlations between yield and phenological traits (days to flowering and days to maturity) ranged from 0.30 to 0.42, with lower phenotypic correlations. Harvest index had the lowest correlation with seed yield at the phenotypic and genotypic level.

Percent protein in dry bean seeds ranges from 17% to 35% (Debouck, 1991). It comprises five principal fractions globulin-1 or phaseolin (36-46%), globulin-2 (5-12%), albumin (12-16%) prolamine (2-4%) and an alkali-soluble fraction (20-30). Thus, phaseolin is the major storage

protein of bean seeds and the one that has been investigated most thoroughly. Leleji *et al.* (1972) found broad-sense heritability, which varied from 30-64%. The broad-sense heritability estimates were two or three times larger than the narrow-sense estimates. The relatively low and variable broad-sense heritability estimates indicated the relatively strong effect of environmental variance. Kelly and Bliss (1975) also noted moderate heritability (0.69) for percentage protein in broad-sense. Leleji *et al.* (1972) also examined negative as well as positive associations between seed yield and percent protein, but only the negative values were statistically significant. Similar negative correlations occurred between pods per plant and percentage crude protein and also between number of seeds/plant and percentage crude protein. Negative correlation (0.30) between seed yield and percentage protein was also noted by Kelly and Bliss, (1975).

2.2. Correlation and Path Coefficient Analysis

Phenotypic and genotypic correlations have been computed by calculating the appropriate components of covariance and variance. Correlation coefficient provides a measure of the associations between characters.

Coyne (1968) examined high correlations between total seed yield and each seed yield component in spaced plant studies. Each component contributed about equally to total seed yield. Heritability of total seed yield and of each of the three yield components were evaluated and some yield components are found more heritable than total seed yield.

Days to flowering is positively correlated with days to maturity (Cerna and Beaver, 1990). Days to maturity are positively correlated with dry seed yield (Welsh *et al.*, 1995). However, Davis and Evans (1977) found negative phenotypic and genotypic correlations of 0.53 and 0.88, respectively, between yield and days to maturity.

Number of pods per plant is positively correlated with plant height (Arya *et al.*, 1999), but it is negatively correlated with crude protein (Leleji *et al.*, 1972) and pod length (Mehta *et al.*, 1997). Seed yield is positively correlated with number of pods per plant and number of seeds per pod (Atuahene-Amankwa and Michaels, 1997; Chand, 1999; Coimbra *et al.*, 1998; Samal *et al.*, 1995). Mebrahtu *et al.* (1991) noted positive correlation with plant height and seed size. Chand (1999) and Coimbra *et al.* (1998) found positive correlation of seed yield with 100-seed weight,

but it is negatively correlated with seed size (White and Gonzaleze, 1990), crude protein (Leleji *et al*., 1972).

According to Nienhuis and Singh (1986), seed yield was positively correlated with number of pods per plant, number of seeds per pod and all architectural traits except branches per plant. In contrast, seed weight was negatively correlated with seed yield, number of nodes per plant, number of nodes on the main stem; and positively correlated with main stem internode length.

Vasic *et al*. (1997) found correlations of plant height and productive height with yield, which were established, via the number of pods per plant and the number of seeds per plant. These results give a clear indication that the yield components are mutually very closely associated. Thus, they concluded that productivity was more dependent on the number of pods per plant than on the number of seeds per pod because the latter characteristic was quite stable in the climatic region. The authors exhibited a positive direct correlation between seed size and yield, which was masked by the negative correlation between seed size and the number of pods per plant.

100-seed weight is positively and strongly correlated with seed length and seed height (Zeven *et al*., 1999) but negatively correlated with number of pods per plant (Nienhuis and Singh, 1986). Seed length is positively correlated with pod length and seed height (Zeven *et al*., 1999). They also found positive correlations between pod length and number of seeds/pod, 100-seed weight, seed length and seed height.

A path coefficient analysis of some yield component interactions in common bean revealed that number of pods per plant exerts a preponderant direct effect upon yield (Duarte and Adams, 1972). In divergent parents with respect

to seed number per pod and seed weight, these components also assumed major roles in determining yield. Leaf number was highly associated with pod number per plant but leaf size was highly associated with seed size.

Singh *et al.* (1985) conducted path coefficient study in pea for ten quantitative traits. They concluded number of pods per plant, number of seeds per pod, 100-seed weight and harvest index are the main yield components affecting yield directly. High indirect effects were contributed by number of branches, plant height and flowering via number of pods per plant; by pod length via 100-seed weight and by maturity via both the component traits. Protein content had negligible effect on seed yield.

In parameters selection for yield improvement in French bean, Babar *et al.* (2002) identified positive and significant direct effect of days to flowering on seed yield while they found negative direct effects by days to maturity and plant height.

2.3. Genetic Diversity Study by Multivariate Methods

With increases in the sample sizes of germplasm accessions used in crop improvement programs, methods to classify and order genetic variability are assuming considerable significance. The use of established multivariate statistical methods is an important strategy for classifying germplasm, ordering variability for a large number of accessions, or analyzing genetic relationships among breeding materials. Multivariate statistical techniques, which simultaneously analyze multiple measurements on each individual under investigation, are widely used in analysis of genetic diversity irrespective of the data set (morphological, biochemical, or molecular marker data). (Mohammadi and Prasanna, 2003). A method utilizing multiple measurements, which are subject to multivariate analysis based on generalized distance as, indicated by D^2 statistic proved to be worth in quantifying the degree of divergence between genotypes or populations (Rao, 1952).

Different approaches to measurement of genetic distance have been proposed over the past few decades to suite various objectives (Mahalanobis, 1930, 1936) and (Rao, 1952, 1960). Mahalanobis D^2 statistic provided measure of the generalized distance in case of multiple measurements. D^2 statistics helped in the identification of genetically divergent genotypes that facilitated grouping and characterization using morphological and agronomic characteristics. The multivariate D^2 analysis has been favored as a tool in estimating genetic divergence for use in plant breeding, since it helps in the choice of parental combinations of the greatest promise.

In addition, "Cluster analysis" which refers to a group of multivariate techniques whose primary purpose is to group individuals or objects based on the characteristics they possess, so that individuals with similar descriptions are mathematically gathered into the same cluster (Hair *et al.*, 1995). The resulting clusters of individuals should then exhibit high internal (within cluster) homogeneity and high external (between clusters) heterogeneity. Thus, if the classification is successful, individuals within a cluster shall be closer when plotted geometrically and different clusters shall be farther apart (Hair *et al.*, 1995).

Cluster analysis based on algorithms such as UPGMA, UPGMC has drawbacks. For instance, these algorithms do not provide an objective definition of what constitutes an optimal tree or dendrogram, and systemic errors are likely to be introduced during cluster analysis reconstructions. However, Mahalanobis distance (D^2) between centroids (vectors of means) of the groups can be used to identify the best clustering algorithm (Franco *et al.*, 1997). The best clustering method produces the largest distance, D^2, among groups or clusters; this method may be particularly appropriate for quantitative data.

Determining the number of acceptable clusters involves in deciding the true or natural groups. An acceptable cluster is defined as a group of two or more genotypes with a within-cluster genetic distance less than the overall mean genetic distance and between cluster distances greater than their within cluster distance of the two clusters involved. One of the relatively simple ways of finding optimal number of clusters is the D^2. On the basis of D^2, the best point for cutting a

cluster is the one that shows the largest D^2 between centroids of the groups created at that point (Franco *et al*., 1997).

Literatures on multivariate statistical methods regarding the common bean and some other legume crops have bean reviewed below.

Diversity among *Phaseolus* species in relation to common bean is organized into primary, secondary, tertiary, and quaternary gene pools (Debouck, 1999). The primary gene pool of common bean comprises both cultivars and wild populations. The latter are the immediate ancestors of common bean cultivars (Gentry, 1969). Wild populations are distributed from northern Mexico to northwestern Argentina (Gepts *et al.*, 1986). Moreover, common bean is a non-centric crop, with multiple domestication sites throughout the distribution range in Middle and Andean South America (Gepts *et al.*, 1986). Hybrids between the wild and cultivated beans are fully fertile and have no major barriers (Motto *et al.*, 1978).

There are two major commercial classes of common bean, snap and dry beans. Snap bean cultivars possess a thick succulent mesocarp and reduced or no fiber in their green pod walls and sutures (Myers and Baggett, 1999). The green pods are harvested for fresh, frozen, and canning purposes. Among snap bean cultivars, there can be a large variation in growth habit and adaptation traits. Similarly, large variation in growth habit, phenological traits, seed size, shape, color, and canning and cooking qualities are found among dry bean cultivars (Singh, 1992). The largest production (>14 million hectares) and consumption of *P. vulgaris* in the world is of dry beans, followed by a much lower production of snap bean.

Genetic diversity in common bean is organized in large-seeded (>40g/100-seed weight) Andean and small (>25g/100-seed weight) and medium (25–40g/100-seed weight) seeded Middle American gene pools (Evans, 1973).

Malhotra *et al.* (1973) studied the relationship between geographic diversity and genetic divergence and the relative role of each character towards maximizing divergence in green gram. They used sixty strains of indigenous and exotic green gram and observed 7 quantitative

characters for each strain ANOVA revealed high significant differences among the strains for all studied characters. Pooled differences for the characters were also highly significant when tested by Wilk's criterion (X^2 = 1702.47 at 413 df). Based on the magnitude of the D^2 values, they found that days to flowering (45.14%) was the largest contributor to the divergence, followed by 100-seed weight (18.36%) and primary branches (15.93%). Pods per plant (2.43%) was found the least contributor. The 60 strains that are originated in different geographic areas were grouped into 14 clusters based on the values of D^2 with the consideration that strains within the clusters have smaller variation in D^2 values than strains between the clusters. The clustering pattern of the strains showed that genetic diversity was not directly related to geographic diversity because strains from one geographic area grouped into different or similar cluster. Thus it could be concluded that geographic diversity cannot be always used as an index of genetic diversity. Thus, days to flowering, 100-seeds grain weight and primary branches are in general responsible for genetic diversity in green-gram and can be used for selecting genetically divergent parents/lines.

Denis and Adams (1978) conducted factor analysis of 22 morphological traits related to yield in 24 diverse dry bean cultivars. They found about 93 % of the total variation is accounted for by the common elements, and the remaining 7.3% being attributable to trait-specific effects and errors. The first three factors accounted for 31, 31, and 15% of the variation from which to seek insight into the basic structural design of bean plants. Variables with the highest loadings on factor I were seed weight, pod fresh weight, pod thickness, pod breadth, pod length and basal internodes length. Factor II orthogonal to and equal in importance to factor I was characterized by high loadings on a group of related variables, such as total number of branches per plant, number of racemes on branches, number of nodes on branches, total number of pods per plant. Variables with high positive loading on the third axis included total number of nodes per plant, number of long internodes and average long internodes length.

An analysis of the descriptors, through principal component analysis of a set of about 1000 *Phaseolus vulgaris* accessions (CIAT, 1979), shows that only three factors or components are necessary to show 83% of total variability and included the following characters: factor 1 included for growth habit, plant height, nodes at flowing, racemes per plant, nodes at maturity, seeds per pod and 100 seed weight. Factor 2 accounted for 29% of total variability and included

leaflet length, leaflet width, stem thickness, dry matter yield and grain yield. Factor 3 involved characters such as length of hypocotyls; days to flowering, pods per plant, racemes with pods and duration of flowering.

Ghaderi *et al.* (1984) studied association between heterotic effects and parental distance for yield and morphological traits in dry edible bean and faba bean. Correlations between heterotic effects for yield at harvest and physiological maturity, and parental distance as estimated by Mahalanobis D^2, were positive and highly significant, 0.73 and 0.58, respectively for dry edible bean. The positive and significant correlation at physiological maturity confirms the associations of seed yield heterosis and parental distance; while its lower magnitude could be attributed to variability associated with the weight of the pods that were combined with the seed yield at this stage. Heterosis for pods per plant and seeds per pod were also significantly associated with D^2, though magnitudes of correlation coefficients were moderate, 0.57 and 0.54, respectively. However, heterosis for 100-seed weight, pod length, and immature seed and pod weight were not significantly associated with D^2. At the early seed filling stage, plants were at their peak of vegetative growth and the small green pods had primarily fleshy walls with seeds constituting a small percentage of the pod weight. The significant and positive correlation between leaf weight and D^2 (0.60) was all indication of positive correlation between plant vigor and distance, which could lead to higher seed yields.

After examining 18,300 accessions and working with samples of many of these in breeding programmes for several years, Singh (1989) found that: (1) in both Middle and South America, all four growth habits are represented in cultivated landraces, although in varying proportions; (2) in both regions there is a large variation in seed size, but South American forms, on the average, are larger; and (3) in both regions there seems to be a parallel between climate and growth habit. In both centers of domestication, for example, up right bush types are more common in relatively warmer lower altitudes, prostrate non-climbing and semi-climbing types are more common in semi-arid or drier areas at intermediate altitudes or at higher altitudes, and climbing beans are more common in cool and wet highlands. Marked differences in leaf size, branching pattern, internode length, inflorescence, flower, pod and seed characteristics are associated with groups of bean germplasm adapted to specific agro-ecological regions. Dry beans were classified into ten

gene pools based on these factors and other characteristics. The green or snap beans could be grouped in two additional gene pools, one for determinate bush and the other for the indeterminate non-climbing and climbing pole beans. However, no natural variability for them was found in the centers of domestication.

Singh *et al.* (1991a) proposed that within each gene pool three races could be distinguished on the basis of differences in plant and seed morphology and adaptation regimes. Within the Middle American gene pool, race Mesoamerica (M) is common to both Mexico and Central America and is characterized by relatively small seed and warm lowland adaptation. Most races of M land races have habits of type 2 or 3, although some have type 4 habits. Commercial classes within race M include small black, small Central American red and navy beans. Race Durango (D) is composed principally of growth habit type 3 genotypes with small leaves, medium seed size and adaptation to dry highlands of Mexico. Commercial race D classes include pinto, great northern and small red Mexican beans. Race Jalisco (J) is found in the more humid highland areas of Mexico and is composed of mostly climbing type 4 genotypes with medium seed size

The Andean gene pool was likewise subdivided into three races on the basis of morphological and ecological criteria (Singh *et al.*, 1991a). Race Nueva Granda (N) represent the medium to large seeded accessions of bush growth habits, and includes the majority of the commercial large seeded cultivars in use today. Race N is the most widely cultivated Andean race, and is grown at both mid-attitudes of the Andes and Africa, in warm lowland environments of Brazil, Mexico and the Caribbean, and in temperate climates of North America and Europe. Race Peru (P) consists of Andean climbing beans, most of which are adapted to highland environments. Race Chile (C) prostrate type III growth habit, medium sized, round to oval seed and usually red colors. This Race is often found at higher latitudes of Turkey, Iran, and China.

Singh *et al.* (1991b) investigated genetic diversity in cultivated common beans by using marker-based analysis of morphological and agronomic traits. In their study, principal component analysis showed that Mesoamerican and Andean cultigens (i.e. cultivated genotypes) had a distinct morphology and that the Mesoamerican group was morphologically more diverse than its Andean counterpart. Results from the multivariate analyses consistently identified fifth internode

length, number of nodes at first flower, leaflet size and seed weight as major traits separating cultigens of Andean and Mesoamerican origin. The Andean germplasm possessed a higher number of nodes to first flower and larger leaflets and seeds than Mesoamerican germplasm.

McClean *et al.,* (1993) grouped 143 North American commercial dry bean cultivars by using coefficient of parentage and cluster analysis. The analysis identified 16 clusters, with 13 entries unassigned, but listed with the most closely related clusters. Cluster analysis identified three major clusters, corresponding to the small (navy, small white and black), medium (pinto, GN, red Mexican and pink), and large (kidney) seed size groups.

Sarma and Roy (1994) classified 42 early maturing pigeon pea genotypes on the basis of D^2 analysis. The analysis of variance revealed significant differences among the 42 genotypes for all the characters under study, indicating considerable variation among the genotypes. The D^2 values ranged from 11.5 to 2658.6, reflecting wide diversity among the genotypes. Based on these values, they grouped the 42 genotypes into eight clusters. Cluster means for branches/plant pods/plant, harvest index and yield/plant were conspicuous and contributing more to the total genetic divergence, which was also reflected by their high coefficient of variation.

Jaylal (1994) carried out genetic divergence study in forty genotypes of soybean using Mahalanobis D^2 statistics. The Wilk's test revealed highly significant differences (χ^2 = 242.31) for all the characters, and he grouped the forty genotypes into 9 and 7 clusters respectively, based on physiological and yield attributes. The analysis for estimating the contribution of characters to the divergence indicated carotene content and total chlorophyll in the case of physiological and pods/cluster, branches/plant and seed yield/plant in the case of yield attributes contributed maximum to the total genetic divergence.

Beebe *et al.* (1995) verified distinct populations in black and red common bean breeding lines and cultivars when analyzed using RAPD markers. Small-seeded red and black beans pertain to the same Mesoamerican Race M (Singh *et al.*, 1991a) and are closely related. However, the separation of reds and blacks by RAPD suggested that grain color might reflect some consistent patterns of variation between their genomes. Several red-seeded lines had a greater percentage of

black parents in their pedigree than red parents. The integrity of red beans as distinct from black beans was conserved. These results suggest that selection for red seed colour genes has resulted in the recovery of a sizeable portion of the red genome by linkage drag.

Singh *et al*. (1997) studied genetic divergence in 100 rice bean (Vigna umbellata) cultivars of different geographic origin using D^2 statistics. The analysis grouped the cultivars into 15 clusters. The random distribution of cultivars into the different clusters indicated the weak relationship between genetic distance and geographic diversity. Cluster mean of characters indicated the importance of a character within the different clusters and its significance for improvement.

Johns *et al.* (1997) studied common bean landraces from Chile based on RAPD, and 20 morphological traits to classify into the two gene pools. Most of the Chilean landraces and commercial bean accessions can be classified into two major groups by RAPD markers, on the basis of their positions on the multi dimensional scale plot and the supporting cluster analysis and analysis of molecular variance. However, when the morphological distance matrix was plotted in two dimensions by MDS, only one large group was visible. Cluster analysis of the data showed that the accessions couldn't be reliably assigned to groups based solely on morphological traits, in contrast to the cluster analysis results with RAPD data. Seven of the 13 categorical traits showed a significant difference between the Andean and Mesoamerican groups, but no categorical trait score was able to accurately place the landraces into their proper gene pool, and there was overlap between the groups for all of the seven numerical traits scored.

Zeven *et al.* (1999) studied phenotypic variation in a core collection of common bean in the Netherlands using 14 quantitative and qualitative traits. Considerable variation among the accessions was recorded for each of the fourteen characters. Principal component (PC) analysis indicated that the first three PCs express 89% of the variation. The first PC separates the accessions mainly on seed (weight, height and length) and pod (height and length, colour intensity, beak curve and length) characteristics, whereas the second PC separates mainly on growth habit, pods/plant and seed length. The third PC separates mainly on flowering time, pods/plant, pod length, seeds/pod and seed width.

Duarte *et al.* (1999) examined genetic divergence among common bean cultivars from different races based on RAPD markers. Based on the matrix of genetic distances, three distinct procedures (AMOVA, clustering through UPGMA and projection of the distance into two dimensional space) were used to evaluate the efficiency of RAPD markers in grouping the cultivars according to the classification by domestication centers and races. The greatest variation determined by AMOVA (75.5%) occurred among domestication centers. The dendrogram clearly separates cultivars from the two domestication centers and confirms the AMOVA results. Within the Middle American domestication center, the greatest differentiation occurred between cultivars of the Durango/Jalisco races and cultivars of the Mesoamerican race. On the other hand, there was no marked grouping of cultivars in the races that composed the Andean South American domestication center, although the smaller genetic distance in this domestication center occurred among cultivars belonging to same race. In the two dimensional space, clear separation among cultivars from Middle American and Andean South American domestication centers observed, and within the Middle American domestication center, a certain differentiation among cultivars from the Mesoamerica race compared with cultivars from the Durango/Jalisco races.

DNA analysis by Beebe *et al*. (2000) with random amplified polymorphic DNA (RAPD) markers confirmed the existence of the three races, demonstrated the existence of sub-races, and indicated the existence of still another race among the climbing beans of Guatemala and neighboring countries. Race M is composed of two sub-races, M1 and M2. The division of race M is consistent with other phenotypic data that discriminate these groups, including plant habit, isozymes (Singh *et al.*, 1991b) and resistance to diseases. Sub-race M1 composed mostly of small black beans, including almost all those of the popular type II growth habits. The M2 group was much more diverse in seed colors than M1, including white, cream, brown, red, black, gray as well as mottled seed types. Most of the accessions were of growth habit type III although type 2 and 4 were also represented. Race D divided into two groups. These groups could be discriminated by growth habit, geographic distribution and seed type. A full range of colors and seed types were represented in-group D1. In contrast, group D2 represented a more limited range in seed types and a higher proportion of type IV habits that are typical of race Durango. One principal group was distinguished within race J.

Hornakova *et al* (2003) studied common bean landraces diversity collected in the western and Eastern Carpatien in Slovak Republic. They used morpho-agronomical traits to see the variability among the landraces. The variations, in 33 morphological and agronomical characteristics were reduced to ten by factor analysis, indicating about 76% of the total genetic variation. The first factor attributed with 14% the second and third with 10%, others below 10%. The first factor included the plant characteristics growth type, growth habit and plant height. The second factor characterized the pod - the presence of fiber, parchment coating and colour, the third factor characterized the seed -size, length, width, height and the weight of thousand seeds. The fourth factor characterized the secondary color and drawing of seed. The fifth one characterized the flower - the color of vexillum and wings, the sixth one pointing of the pod. Cluster analysis based on morphological traits grouped genotypes into two main branches according to the growth type (bush or climbing), seed size, and thousand-seed weight. Twelve subgroups could be identified in the dendrogram constructed by morphological data.

Vasic Mirjana (2005) reported the divergence of dry bean breeding collections by using two qualitative and 13 quantitative traits. The principal component analysis showed decisive traits in genotype differentiation and the variability of the collections was interpreted based on the seven principal components. The first main component was named component of productivity since it determine the yield level. Pod number, grain mass, grain number/plant, productive plant height, plant height, grain color and grain oil content were the main contributors. These traits had the largest contribution in the divergence of the collections and carry the largest portion of its variability. Using this main component for genotype differentiation, one can distinguished between yielding genotypes with large number of pods and grain/plant, large productive height and high grain oil content. The second main component showed large variability for grain shape. The third main component comprises of direct grain-related yield components (grain number/pod, grain number/plant and 1000-grain mass). The fourth component would best describe genotype harvest ability since it comprises of the highest portion of first pod height with plant height influence. In the remaining three main components seed chemical composition content influence is dominant. Correlation of starch with the fifth main component is high, as well as correlation of cellulose with the sixth and protein with the seventh component.

Barelli ***et al.,*** (2005) used 35 landraces of common bean from Brazil to study the divergence among them. They evaluated traits like, number of days to emergence, number of days to flowering, height of the insertion of the first pod, longitudinal length of the pods, total number of pods/plant, number of total seeds/plant, number of seeds/pod and seed weight. The genetic distance measurements using generalized Mahalanobsis D^2 demonstrated greater dissimilarity between genotypes from Mesoamerica and Andean gene pools. Cluster analysis grouped the genotypes into nine clusters; with the most similar cultivars grouped in cluster I. cluster I to V contained landraces from Mesoamerican origin, whereas groups from VII to IX only possess Andean origin.

III. Objectives

3.1. General Objective

To assess genetic variability/diversity within and between common bean accessions and to classify genotypes based on the genetic distance.

3.2. Specific Objectives

- **Estimation of phenotypic and genotypic coefficient of variation, heritability and genetic advance of some agronomically important characters.**
- **To assess the extent of association between important agronomic characters among themselves and yield.**
- **To partition traits associations into direct and indirect effects using path coefficient analysis.**
- **To assess the magnitude of genetic diversity and classify under different groups based on the genetic distance**
- **To determine relative contribution of each component trait to the total divergence**
- **To identify divergent genotypes that could be used as potential parents' in the future common bean breeding program**

IV. Materials and Methods

This part portrays the details of materials and methods employed in the present investigation. It also depicts the statistical tools used in drawing inferences for the characters considered in the study.

4.1. Materials

The genotypes for the study were provided by the Lowland Pulse Project-Coordinating Center, Nazareth Agricultural Research Center (NARC), Nazareth. It consisted of 144 germplasm accessions including five check varieties of diverse nature originated from 18 countries viz.; Colombia, Ecuador, Chile, Peru, Venezuela, Dominican Republic, USA. Mexico, Brazil, Guatemala, Honduras, El Salvador, Costa Rica, Malawi, Burundi, Ethiopia, South Africa, Kenya (Appendix 1). The check varieties were among those released from Ethiopian Institute of Agricultural Research (EIAR).

The study was conducted in off-season, during February to June 2005 at the research farms of Nazareth research center of Ethiopian Institute of Agricultural Research (EIAR). Climatic conditions of the study site were as indicated in (Appendix 2).

3.2. Methods

The experiment was laid on 12x12 triple lattice-design with three replications. Each block within a replication consisted of 12 genotypes. The position of each genotype within the block was randomized. Each genotype within the block was grown in a single row of 5.5m lengths. A spacing of 60cm between rows and 15cm between plants in a row was used. The crop was sown on 11th of February 2005 and grown under a protective irrigation. Filling was done three days after germination to replace the ungerminated seed and to provide a uniform stand of plants. All agronomic practices recommended for the crop were followed during the crop-growing period.

3.2.1. Data Recording

The pre- and post-harvesting observations were recorded from randomly selected five plants from each genotype in each replication for all characters studied except days to flowering and days to maturity, which were determined from the whole plot. Altogether 18 agronomic and morphological traits of sampled plants and seeds (Appendix 3) were recorded according to *Phaseolus vulgaris* L. descriptor (Debouck and Hidalgo, 1986), at the correct growth stage of the plant for each character.

The data recording for each trait were carried out as follows.

1. **Seed yield and its components**

   1.1. Seed yield: dried plants were threshed separately and seeds obtained from them were weighted and averaged to get the seed yield per plant in grams.

   ***1.2. Biological yield*:** The five harvested plants from the above ground parts were dried and weighted to get the biological yield per plant in grams.

   1.3. Harvest Index: To estimate the harvest index, average seed yield was divided by the average biological yield.

$$\text{Harvest Index (HI)} = \frac{Seedyield(g)}{Biological yield(g)}$$

   1.4. Pods per plant: Fertile number of pods for sampled plants was counted and recorded.

   1.5. Seeds per pod: Determined from the average number of seeds per 30 pods per 5 sampled plants.

   ***1.6.* Hundred seed weight:** Determined from the average 100-seeds mass at (12-

14%) moisture content of the seed and expressed in grams.

2. Morphological traits

2.1. Pod length: Exterior distance of fully matured pod from the pod apex to the peduncle was measured in centimeters.

2.2. Plant height: The height of the plant from the ground surface to the tip of the main guide was recorded in centimeters.

2.3. Seed length and height: Average length and height in millimeter of 15 seeds from 5 plants was measured parallel to the hillium and from the hillium to the opposite side, respectively using vernier calliper.

2.4. Stem diameter: Diameter of the first internode on the main stem at about 3cm. from the ground level was measured using vernier calliper and recorded in millimeter.

2.5. Length and width of the central leaflet of the trifoliolate leaf: Length from the base to the tip and width across the leaf at its widest point of the central leaflet of the trifoliolate leaf originated at the forth node was measured and recorded in centimeters

2.6. Nodes at maturity: Number of nodes from the cotyledonary node to the tip of the main stem was counted and recorded at physiological maturity.

2.7. Internode length: Length of internodes on the main stem were measured and divided by its number to get the average length of the internodes.

3. Phenological traits

***3.1. Days to 50% flowering*:** Number of days taken by each genotype from the day of sowing to the day on which 50 per cent of the plants on a plot opened a flower.

***3.2. Days to 90% maturity*:** Number of days from sowing to the stage when 90% of the plants in a plot have changed the colour of their pods from green to lemon yellow.

4. Quality trait

4.1. Seed protein content: Protein content of the seeds was determined by the techniques developed in of International Livestock Research Institute. The laboratory analysis was carried out at Adami Tulla Agricultural Research Center Nutrition Laboratory. Seeds from the five plants per genotype were bulked and 25g of seeds per genotype were used for analysis. Dry seeds were ground in a Cyclotec 1090 grinding mill to a particle size that passes through a

0.5mm sieve. A 0.3g representative sample was taken from the flour before the chemical analysis. Total nitrogen was determined using the Kjeldahl method. Organic nitrogen from the flour sample was converted into ammonium ions by digestion with concentrated sulphuric acid in the presence of a catalyst such as a mixture of Potassium /Sodium sulphate (K_2SO_4 or Na_2SO_4) with Selenium or Copper sulphate ($CuSO_4$). Following Kjeldahl digestion, the digests were made alkaline and ammonium (NH_4^+) was determined by steam distillation of ammonia (NH_3), which involved trapping in boric acid and titration. The distillate was titrated against a standard acid (0.1N HCl). From this titration the amount of nitrogen were determined: it was multiplied by 6.25 to convert to crude protein. This conversion factor, found by determining the amino acid content, is an average value for conversion of nitrogen to protein in most plants. Calculation of total nitrogen and crude protein

$$\%N = \frac{14.01x(V-B)xN}{Wx10xDM\%} = \frac{1.401(V-B)N}{WxDM\%}$$

%Protein = %N x Factor specific for different products

Where, V = Volume of HCl consumed

B = Blank titration

N = Normality of HCl

W = Weight of sample taken

DM% = Dry matter of sample

3.3. Statistical Analyses

Data of individual mean of five randomly selected plants from each replication was subject to statistical analysis. Quantitative data, which were not normally distributed, could be subjected to data transformation before analysis. Data generated from this experiment were analyzed by using Alpha Lattice and SAS computer software at EIAR. The genetic parameters, genetic divergence (D^2) and canonical analysis for clustering were computed using SPAR I (Statistical Package for Agricultural Research Data Analysis I) software. The following statistical methods were employed for the analysis of data.

3.3.1. Analysis of Variance (ANOVA): The data of mean values for all characters were analyzed for their variance following triple lattice analysis (Cochran and Cox, 1957) on the out line presented below.

Sources of variation	Degrees of freedom	Sum of squares	Mean squares	Expected mean squares	" F " ratio
Replication	r-1	A	P		
Blocks (adj.)	r(k-1)	D	Q	$\sigma_e^2 + \frac{r-1}{r} k\sigma_b^2$	
Treatments (unadj.)	k^2-1	B	R	$r\sigma_g^2 + \sigma_e^2$	R/T
Treatments (adj.)	k^2-1	C	S	$r\sigma_g^2 + \sigma_e^2$	S/T
Intra-block error	(k-1)(rk-k-1)	E	T	σ_e^2	
Total	rk^2-1				

Least Significance Difference (LSD) = $t_{\alpha} aterrordfx\sqrt{AverageVariance}$

Where, r = number of replications

k^2 = total number of genotypes

k = number of genotypes in a row/column

A = replication sum of squares

B = treatment (unadjusted) sum of squares

C = treatment (adjusted) sum of squares (whenever S>T)

D = sum of square for blocks within replications (adjusted)

E = intra- block error sum of squares

P, Q, R, S and T = mean sum of squares replications, block (adjusted), treatment (unadjusted), treatment (adjusted) and intra- block error, respectively

$V_1 = V(\hat{t}_i - \hat{t}_i') = \frac{2\sigma^2}{r}(1 + \frac{1}{k}$, If the i^{th} and i'^{th} treatment occur together in a block

$V_2 = V(\hat{t}_i - \hat{t}_i') = \frac{2\sigma^2}{r}(1 + \frac{r}{k(r-1)}$, If the i^{th} and i'^{th} treatments do not occur together in any block

Average Variance = $\frac{n_1 v_1 + n_2 v_2}{n_1 + n_2}$, Where $n_1 = r(k-1)$ = the number of treatment each of which occur, say t_i in some block or other

$n_2 = (k-1)(k-+1-r)$ = number of treatments which do not occur t_i in any block

3.3.2. Estimation of genetic parameters: In order to identify and ascertain the genetic variability among genotypes, for the characters under study and to confirm the presence of environmental effect on various characters, different genetic parameters were estimated by adopting the following formula.

A. *Estimation of variance components:* Genotypic and phenotypic components of variance were estimated by the following formula of Burton and Devane (1953).

i. Genotypic variance, $\sigma_g^2 = \frac{\sigma_p^2 - \sigma_e^2}{r}$

Where, σ_p^2 = MSS treatment,

σ_e^2 = MSS error,

r = number of replication

ii. Phenotypic variance, $\sigma_p^2 = r\sigma_g^2 + \sigma_e^2$

iii. Genotypic coefficient of variability, $GCV = \frac{\sigma_g^{\ 2}}{\overline{X}} \times 100$

iv. Phenotypic coefficient of variability, $PCV = \frac{\sigma_p^{\ 2}}{\overline{X}} \times 100$

Where, $\overline{X}$ is the grand mean of a character.

B. *Heritability (H^2):* heritability in broad sense for all the characters was computed as suggested by Hansen *et al*., (1956).

$$H^2 = \frac{\sigma_g^{\ 2}}{\sigma_p^{\ 2}} \times 100$$

C. *Genetic Advance (GA):* Genetic advance for each character was worked out by adopting the formulae given by Johanssen *et al*. (1955) and genetic advance as percent of mean was calculated by dividing the genetic advance with the mean and multiplying it by 100.

$$GA = H^2 \sigma_p K$$

Where, K = Selection differential (2.06) at 5% intensity of selection

σ_p = The phenotypic standard deviation

3.3.3. Association of characters and Path coefficient analysis

A. ***Correlation coefficient (r):*** Genotypic and phenotypic coefficients of correlation between two characters were determined by using variance and covariance components as suggested by Weber and Moorthy (1952).

$$r_g(xy) = \frac{\mathrm{cov}_g(xy)}{\sigma_g^{1/2}(x) X \sigma_p^{1/2}(y)}$$

$$r_p(xy) = \frac{\mathrm{cov}_p(xy)}{\sigma_g^{1/2}(x) X \sigma_p^{1/2}(y)}$$

Where, $r_g(xy)$ and $r_p(xy)$ are genotypic and phenotypic correlation coefficients,

$Cov_g(xy)$ and $Cov_p(xy)$ are genotypic and phenotypic covariance of xy

$\sigma^{1/2}_g$ (x), $\sigma^{1/2}_p$ (x) and $\sigma^{1/2}_g$ (y), $\sigma^{1/2}_p$ (y) are genotypic and phenotypic standard deviations of x and y, respectively.

These coefficients of correlation were tested for their statistical significance by using t test as: $t = \frac{r\sqrt{(n-2)}}{\sqrt{(1-r^2)}}$, Where n = number of treatments.

The calculated value of "t" was compared with "t" table value at n-2 degrees of freedom at 1 and 5 percent level of significance.

B. ***Path coefficient analysis:*** Path coefficient analysis was carried out using the phenotypic correlation coefficient to further investigate the direct and indirect effects of selected contributing traits on seed yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1957). Standard path coefficient, which are the standard partial regression coefficients were obtained by solving the following set of "p" simultaneous equations through the use of Doolittle technique as described by Goulden (1959).

$$P_{O1} + P_{O2}r_{12} + - - - + P_{Op}r_{1p} = r_{O1}$$

$$P_{O1}r_{21} + P_{O2} + - - - + P_{Op}r_{2p} = r_{O2}$$

$$P_{O1}r_{p1} + P_{O2}r_{p2} + - - - + P_{Op} = r_{Op}$$

Where, - P_{01}, P_{02}, ….., P_{0p} are the direct path coefficient of variables 1, 2, 3, …, P on the dependent variable O.

- r_{12}, r_{13}, ….., r_{1p} are the possible correlation coefficients between independent variables.
- r_{01}, r_{02}, r_{03}, …., r_{0p} are the correlations between dependent and independent variable.

The indirect effect of the i[th] variable via the j[th] variable was obtained as $(P_{oj}Xr_{ij})$. The contribution of the remaining unknown factors is measured as the residual factor, which is calculated as:

$(P_{ox}^2) = 1 - \left[\sum P_{Oj}^2 + 2\sum P_{Oi}P_{Oj}r_{ij}\right]$, i # j or $(P_{ox}^2) = 1 - \left[P_{O1}r_{O1} + P_{O2}r_{O2} + - - - + P_{Op}r_{Op}\right]$

Residual factor = $\sqrt{P_{ox}^2}$

3.3.4. Test of significance of differences among genotypes/populations: This can be done in two ways:

a. By simple ANOVA as explained earlier. Significance of difference among treatments for all or majority of characters would justify further calculation of D^2.
b. A simultaneous test of significance of difference in the mean value of a number of correlated variables with regard to pooled effect was carried out using Wilk's lambda criterion (Λ) (Wilk's, 1932). For this purpose, sum of squares and sum of products of the experimental error were used and the significance of the genotypes was tested. The Wilk's lambda criterion was estimated using the following relationship.

$$\Lambda = \frac{|E|}{|T|}$$

Where, |E| = determinant of the error dispersion (error sum of squares and products) matrix, |T| = E + B (determinant of the error dispersion matrix plus

treatment dispersion which is population sum of squares and of sum of products) matrix.

The significance of Λ was tested by V-statistics (Bartlett, 1947) representing central χ^2 distributions at *pq* degree of freedom. V-stat = -mln = -mlogeΛ

Where, $m = t - \frac{(p+q+1)}{2}$

t = total degree of freedom (degree of freedoms for error plus genotypes).

p = number of characters

q = number of treatments or genotypes

If the significance of V-stat shows that the difference between the means in respect of the pooled effect of 'p' characters between different genotypes/populations is significant. Hence, further analysis can be made to estimate D^2 values.

3.4. Genetic divergence: Mahalanobis generalized distance (D^2) statistics was used for assessing the genotypic divergence between populations based on all morphological and agronomic characters of the common bean crop. The generalized distance between any two genotypes is defined as:

$$D^2 = \sum_i^p \sum_j^p \lambda_{ij} \delta_i \delta_j$$

Where, λ_{ij} = The reciprocal matrix to common dispersion matrix

δ_i = Difference between the mean values of the two populations for the i^{th} character $(\mu_{i1} - \mu_{i2})$

δ_j = Difference between the mean values of the two populations for the j^{th} character $(\mu_{j1} - \mu_{j2})$

μ = Vector of mean values

In a further simpler form:

$$D^2 = \sum_i^x d_i^2 = \sum_i^x (y_i^j - y_i^k)^2 \text{ , } (j \# k)$$

Where, y is the uncorrelated variable which varies from i = 1 to x, that is number of characters. The super scripts j and k represent a pair of any two genotypes, example 1-2, 1-3, 1-4,….., 1-n; 2-3, 2-4, …., 2-n; 3-4, 3-5, ….; (n-1)-n. Where n is the number of genotypes/populations. Thus, D^2 is the sum of squares of difference between any two genotypes for each of the uncorrelated variable (y_i) obtained by transforming correlated variables (x_i), through pivotal condensation method.

3.4.1. Significance of D^2 values: The D^2 value obtained for a pair of genotype/population is taken as the calculated value of χ^2 and is tested at 5% and 1% level against the tabulated value of χ^2 at 'p' degree of freedom. Calculated χ^2 > tabulated χ^2 indicated significance of the D^2 values.

***3.4.2. Contribution of individual characters for divergence*:** In all combinations $n(n-1)/2$ each character is ranked from 1 to p on the basis of $d_i = (y_i^j - y_i^k)$ values. Rank 1 refers to the highest mean difference while rank p (number of characters) to the lowest mean difference. Percent contribution of a character towards divergence is calculated by counting number of times a character appear first in ranking.

3.4.3. Clustering of genotypes/populations: All D^2 values are arranged in matrix form, based on the degree of divergence (D^2 values) between any two genotypes/populations. A logical grouping of genotypes was done following Tocher's method (Rao, 1952). This method starts with a pair of genotypes showing the smallest D^2 values to which the third genotype showing the smallest average D^2 value from the first two genotypes is added. Similarly the fourth genotype with the lowest difference from the first three and so on is added till the average D^2 jumps abruptly. Then the lastly added genotype is excluded from this cluster. Likewise, the second cluster is formed and the process is continued till all the genotypes are included into one or the other clusters.

3.4.4. Computation of Intra- and Inter-cluster Divergence: Intra-cluster is calculated by the formula $\sum D_i^2 / n$, where $\sum D_i^2$ is the sum of distances between all possible pairs of the genotypes/populations included in a cluster, n is the number of pairs in a cluster. Inter-cluster distance is calculated by averaging all possible D^2 values among genotypes/populations

belonging to different clusters concerned, divided by number of pairs involved. The formula is: $\sum D_{ij}^2 / n_i\, n_j$, where, $\sum D_{ij}^2$ is the sum of D^2 values of genotype pairs of clusters *i* and *j*; and n_i and n_j are the number of pairs of cluster *i* and j, respectively.

3.4.5. Cluster diagram: Diagrammatic representation of cluster divergence showing different genotypes/populations was obtained using $\sqrt{D^2}$ values between and within the clusters.

V. Results

The results of the experiment conducted to evaluate the variability of the different plant traits and to assess the genetic divergence in 144 genotypes are presented in this section under the following leadings.

1. Genetic variability: the components of variability considered were phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as percent of mean.
2. Character associations
3. Path coefficient analysis
4. Genetic divergence study through multivariate analysis.
   4.1. Group constellation
   4.2. Intra-and inter-relation of clusters
   4.3. Cluster mean analysis

5.1. Genetic variability

The mean sum of squares due to various sources of variation is presented in Table 1. An *F*-test showed that variation among genotypes was significant ($P<0.01$) for all quantitative characters studied. To understand the extent to which the observed variations were due to genetic factors, the range, mean, coefficient of variation (CV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance were computed for the 18 characters studied (Table 2) and represented graphically in Figs 1 and 2. It is evident from this table that large amount of variability was observed with respect to various characters studied.

The PCV ranged between 6.40 and 35.20 percent while GCV ranged between 5.93 and 28.51. Days to maturity showed the lowest PCV and GCV, while the highest PCV (35.20%) was recorded for internode length and highest GCV (29.09%) for plant height, respectively.

Table 1. Mean sum of square for 18 quantitative characters in common bean

Source fo Variation	df	Seed yield (gm/plant)	Biological yield (gm/plant)	Harvest index (HI)	Pods per plant	Seeds per pod	100 seed weight (gm)	Dry seed length (mm)	Dry seed height (mm)	Pod length (cm)
Replication	2	2218.767	4646.665	54.211	447.634	3.691	161.676	0.403	0.618	1.863
Genotype (Unadj.)	143	120.655**	289.985**	92.015**	109.565**	1.695**	279.054**	10.926**	1.702**	3.978**
Genotype (Adj.)	143	113.342**	274.125**	91.201**	102.116**	1.584**	253.848**	10.020**	1.701**	3.656**
Intra-block error	253	54.119	118.824	16.383	24.959	0.212	6.159	0.203	0.077	0.494
LSD (P>0.05)		11.65	17.35	6.70	8.08	0.72	4.07	0.71	0.46	1.14
LSD (P>0.01)		15.35	22.87	8.82	10.64	0.96	5.36	0.94	0.6	1.51
SE		4.394	6.511	0.024	2.963	0.275	1.477	0.259	0.170	0.408
CV (%)		24.00	23.10	6.10	21.20	11.00	7.40	3.80	4.20	7.10

** = Significant at 1% probability

Table 1. Continued…….

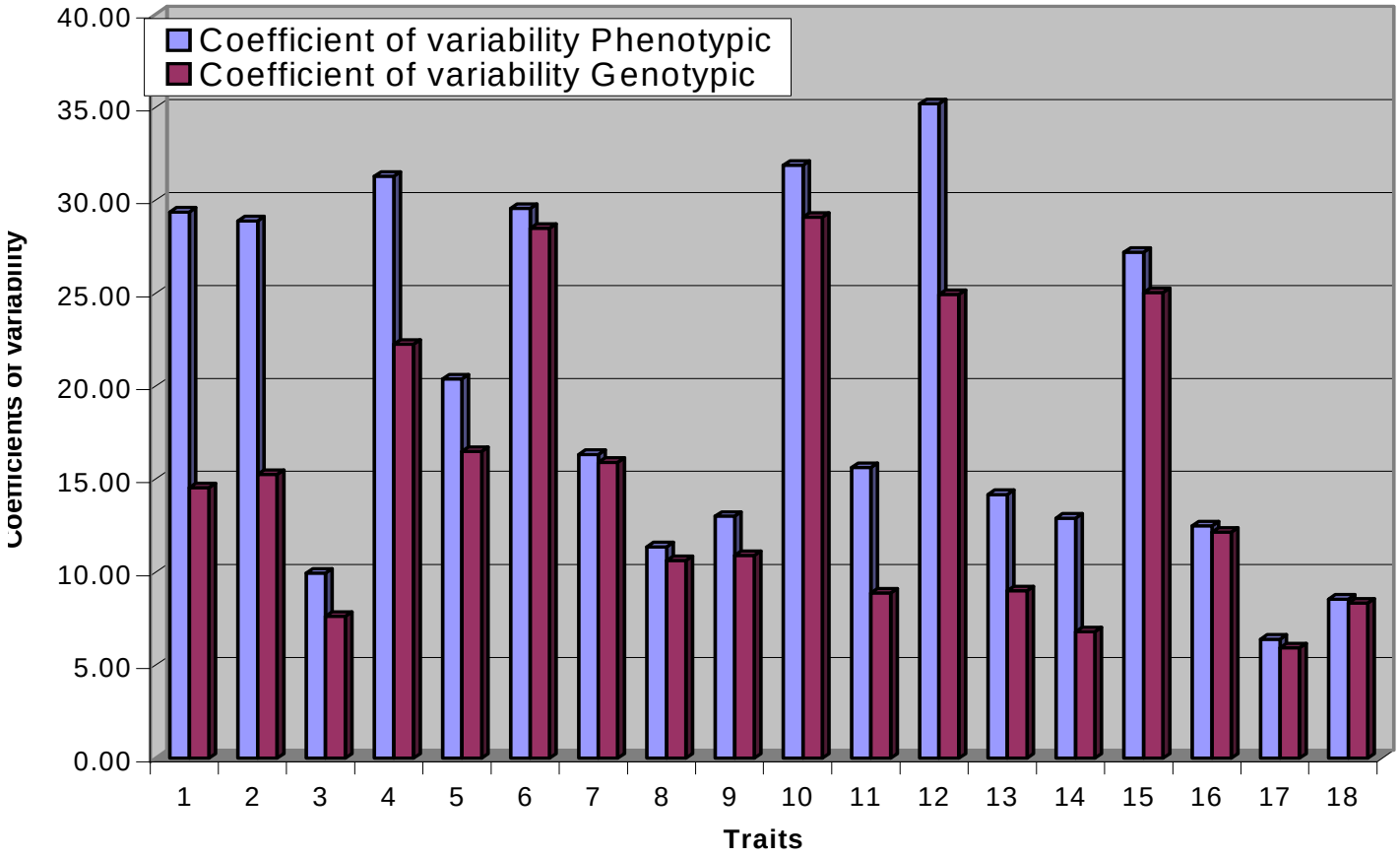
Source fo Variation	df	Plant height (cm)	Stem diameter (mm)	Internode length (cm)	C.trifoliolate leaf length (cm)	C.trifoliolate leaf width (cm)	No of nodes on the main stem	Days to 50% flowering	Days to 90% maturity	Protein content (%)
Replication	2	567.545	41.346	0.966	8.656	8.959	1.195	3.382	7.600	0.407
Genotype (Unadj.)	143	954.556**	2.150**	2.676**	4.572**	2.026**	29.820**	85.245**	71.508**	6.302**
Genotype (Adj.)	143	912.316**	1.965**	2.479**	4.129**	1.840**	28.567**	78.327**	68.047**	5.992**
Intra-block error	253	59.081	0.680	0.609	1.312	1.127	1.704	1.492	3.331	0.237
LSD (P>0.05)		12.45	1.34	1.29	1.92	1.34	2.09	2.00	3.02	0.78
LSD (P>0.01)		16.41	1.77	1.70	2.35	1.77	2.76	2.64	3.98	1.03
SE		4.487	0.497	0.458	0.673	0.622	0.770	0.723	1.089	0.3442
CV (%)		12.90	11.30	24.00	10.40	13.50	10.60	2.80	2.30	2.31

** = Significant at 1% probability

Table 2. Range, mean, phenotypic and genotypic coefficient of variability, heritability and genetic advance for 144 genotypes in common bean

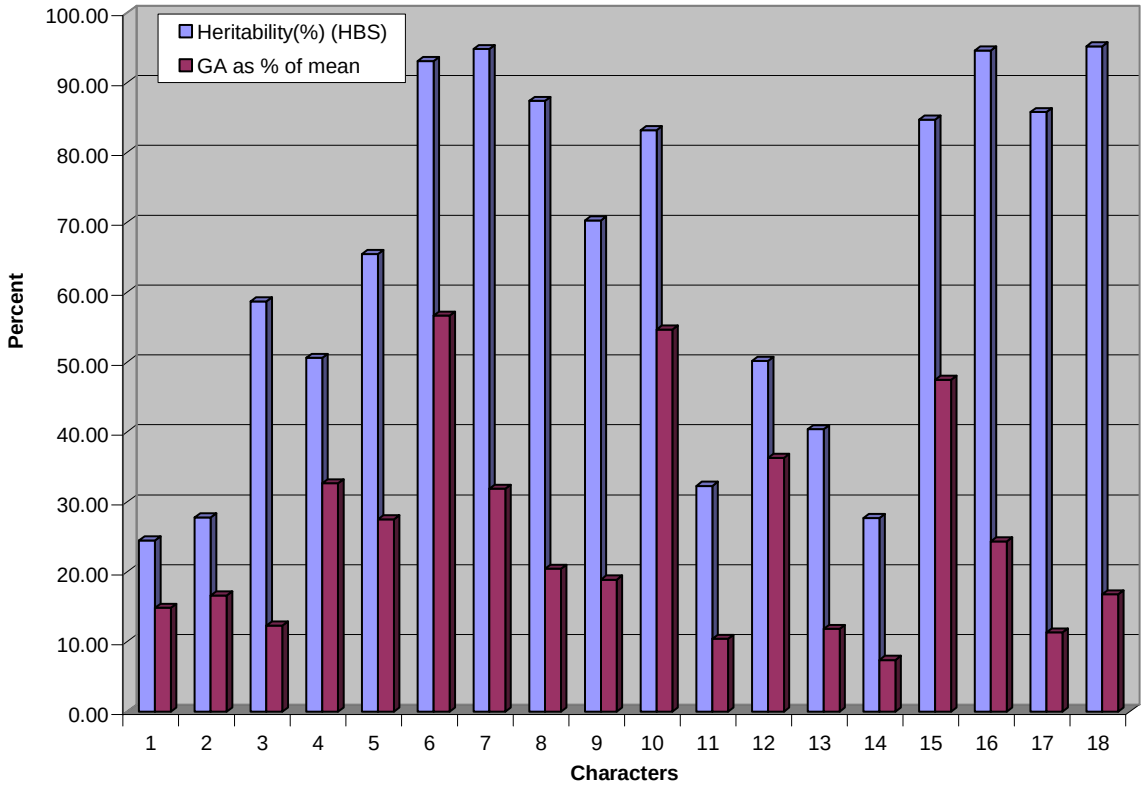
Characters	Ranege		Mean	CV (%)	Coefficient of variability		Heritability (%)	Genetic	GA as % of
	Minimum	Maximum			Phenotypic	Genotypic	(HBS)	advance	mean
Seed yield (gm/plant)	17.04	50.75	30.64	24.01	29.38	14.55	24.50	4.55	14.85
Biological yield (gm/plant)	25.06	78.70	47.20	23.09	28.91	15.25	27.80	7.83	16.63
Harvest Index	33.00	78.00	65.00	6.14	9.96	7.63	58.70	8.00	12.31
Pods per plant	11.05	38.04	23.57	21.20	31.30	22.27	50.60	7.70	32.67
Seeds per pod	1.80	6.28	4.18	11.01	20.40	16.51	65.50	1.15	27.51
100 seeds weight (gm)	13.76	55.33	33.41	7.43	29.56	28.51	93.10	18.93	56.66
Dry seed length (mm)	8.30	16.30	11.88	3.78	16.34	15.91	94.80	3.79	31.90
Dry seed width (mm)	5.25	8.96	6.95	4.17	11.37	10.63	87.40	1.42	20.43
Pod length (cm)	7.25	14.04	9.90	7.10	13.01	10.91	70.30	1.87	18.89
Plant height (cm)	29.01	158.84	59.37	12.95	31.89	29.09	83.20	32.45	54.66
Stem diameter (mm)	5.33	9.96	7.30	11.30	15.64	8.89	32.30	0.76	10.41
Internode length (cm)	1.84	6.81	3.25	24.00	35.20	24.94	50.20	1.18	36.31
Leaf length (cm)	7.37	15.74	11.00	10.41	14.19	9.02	40.40	1.30	11.82
Leaf width (cm)	5.56	12.17	7.85	13.53	12.92	6.80	27.70	0.58	7.39
Nodes at maturity	5.95	19.94	12.26	10.65	27.22	25.05	84.70	5.82	47.47
Days to flowering	33.25	52.02	43.43	2.81	12.50	12.16	94.60	10.58	24.36
Days to maturity	65.83	90.12	80.13	2.28	6.40	5.93	85.80	9.07	11.32
Protein content (%)	17.39	26.91	21.10	2.31	8.55	8.35	95.2	3.54	16.78

Fig 1. Phenotypic and genotypic coefficients of variability for 18 quantitative traits in common bean



T1 = Seed Yield/plant	T7 = Dry seed length	T13 = Leaf length
T2 = Biological Yield/plant	T8 = Dry seed height	T14 = Leaf width
T3 = Harvest index	T9 = Pod length	T15 = No of nodes on main stem
T4 = Pods/plant	T10 = Plant height	T16 = Days to 50% flowering
T5 = Seeds/pod	T11 = Stem diameter	T17 = Days to 90% maturity
T6 = 100-seed weight	T12 = Internode length	T18 = Protein content (%)

Eig 2 Heritability estimate and genetic advance as percent of mean for quantitative characters in common bean



T1 = Seed Yield/plant
T2 = Biological Yield/plant
T3 = Harvest index
T4 = Pods/plant
T5 = Seeds/pod
T6 = 100-seed weight
T7 = Dry seed length
T8 = Dry seed height
T9 = Pod length
T10 = Plant height
T11 = Stem diameter
T12 = Internode length
T13 = Leaf length
T14 = Leaf width
T15 = No of nodes on main stem
T16 = Days to 50% flowering
T17 = Days to 90% maturity
T18 = Protein content (%)

1. **Seed yield per plant:** The genotypes studied showed a wide range of variability for this character. Germplasms were yielding as low as 17.04g as high as 50.75g/plant for genotypes CIFEM 9111 and EAP-4. The mean seed yield was found to be 30.64g/plant. A relatively high PCV (29.38%) and moderate GCV (14.55%) values were recorded for this essential plant trait. The lowest heritability estimates (24.50%) were recorded with low genetic advance (14.85 %).
2. **Biological yield:** The range for biological yield varied between 25.06 for genotype FOT-52 to 78.70g/plant for EAP-4 among the 144 germplasms studied. A relatively high PCV (28.91%) and moderate GCV (15.25%) were recorded. A low value (27.80%) of heritability estimate was observed with low genetic advance (16.63 %).
3. **Harvest Index:** A wide range was observed here too; the minimum value being 33% and the highest 78% in respect of genotype CIFEM 91117 and NAZ, respectively. The mean harvest index was noted to be 65%. It is the other character having low PCV (9.96%) and GCV (7.63%). A heritability estimate of 58.7% was recorded with very low genetic advance of 12.31%.

Pods per plant: The pods per plant varied between 11.05 and 38.04 for genotypes FOT-52 and BlackDessie, respectively, with an average value of 23.57. High PCV (31.30%) and GCV (22.27%) were recorded for this trait. A moderate value of heritability (50.60%) was found accompanied with moderate genetic advance as percent of mean (32.67%).

5. **Seeds per pod:** Seeds per pod varied between 1.80 and 6.28 for genotypes CIFEM 91117 and EAP-10-88, respectively, with mean value of 4.18. A moderate value of PCV (20.40%) and GCV (16.51%) were recorded for this trait. Moderate (65.50%) heritability value and moderate genetic advance (27.51%) was observed.
6. **Hundred seed weight:** This trait showed a substantial variability. The value ranged from 13.76 to 55.33g for genotype Aurora and FOT-52, respectively, with a mean value of 33.41gm. A PCV (29.56 %) and GCV (28.51%) were recorded for it. The heritability estimates (93.10 %) of this trait were the highest among all traits with maximum genetic advance (56.66 %).
7. **Seed length:** This character showed range between 8.30mm and 16.30mm for genotypes Envoy and Horizon, respectively, with mean value of 11.88mm. Moderate values for PCV (16.34%) and GCV (15.91%) were observed. The second highest heritability estimate

(94.80%) with moderate genetic advance (31.90) as percent of mean were recorded by this trait.

8. **Seed width:** Range of values for this trait varied between 5.25mm to 8.96mm, with mean value of 6.95mm in respect of genotypes EAP-10-88 and Bayo zacatecas, respectively. The PCV and GCV values (11.37% and 10.63%), respectively, were small, but heritability estimate (87.40%) was high with moderate genetic advance (20.43%).
9. **Pod length:** The pod length in the genotypes studied varied between 7.25cm and 14.04cm for genotypes Envoy and Foxfire, respectively, with a mean length of 9.90cm. A relatively low value for PCV (13.01%) and GCV (10.91%) was recorded, but a moderate heritability estimate (70.30 %) with moderate genetic advance (18.89) was observed for this trait.
10. **Plant height:** A wide range was observed for this character. As short as 29.01 cm and as tall as 158.84 cm plants were observed in genotypes SK 93263 and Paragachi-Y, respectively, with mean plant height of 59.37 cm. The estimates of PCV and GCV were 31.89 % and 29.09 %, respectively. A high heritability estimate (83.20 %) with high genetic advance (54.66 %) was recorded for this character.
11. **Stem diameter:** As thin as 5.23 mm and as thick as 9.96 mm stem diameter for genotypes Pintovilla and Riotibagi, respectively, with a mean value of 7.30mm were recorded. The PCV observed was moderate (15.64 %), while GCV was low (8.89 %) in magnitude. A low heritability estimate (32.30 %) with very low genetic advance value (10.41%) was observed for this character.
12. **Internodes length:** The length of the internode ranged from 1.84 to 6.81cm, with a mean value of 3.25cm. Genotypes G21212 and Paragachi recorded the lowest and highest values, respectively. PCV and GCV were 35.20 % and 24.94 %, respectively. The PCV for this trait was the highest among all the traits studied. The estimates of heritability were average (50.20 %) with moderate genetic advance (36.31%).
13. **Length and width of the central trifoliolate leaf:** The length and width of the central trifoliate leaf ranged from 7.37 to 15.74 centimeters and 5.56 to 12.17 centimeters, with the overall mean of 11.00 and 7.85 centimeters, respectively. Genotypes Garbancilos-zarco and I-77 recorded the shortest and longest leaf while G 22005 and Carioca recorded the narrowest and widest leaf, respectively. PCV and GCV were 14.19 % and 9.02 % for

leaf length, while 12.92% and 6.80 % for leaf width, respectively. Heritability estimates of the traits that govern the two dimensions were low. It is 40.40 % for leaf length and 27.70 % for the leaf width. Genetic advance as percent of mean for each character, 11.82 and 7.39, respectively was also very low.

14. **Nodes at maturity:** The node number varied from 5.95 to 19.94 with a mean value of 12.26. Genotype I-77 recorded the lowest while Paragachi-Y showed the highest number of nodes on the main stem. PCV and GCV values were 27.22 and 25.05 %, respectively, relatively higher as compared to most of the other characters studied. Heritability estimate (84.70 %) was high with high genetic advance (47.47%).
15. **Days to 50% flowering:** The range observed for this character was 33 to 52 days; with an overall mean of 43.43 days. Genotypes BRB 205 and AFR-689 recorded the lowest and highest days to flower, respectively. Both PCV (12.50 %) and GCV (12.16 %) were low. However, it showed the third highest heritability estimate value (94.60 %) with moderate genetic advance (24.36%).
16. **Days to maturity:** Days required for 90 % physiological maturity, ranged from 66 to 90 days, the average being 80.13 days. SK 93263 and AND 1090 are the earliest and latest genotypes, respectively. Among all the traits studied, the lowest PCV (6.40 %) and GCV (5.93 %) were observed for this character. However, heritability estimate (85.80 %) was high accompanied with low genetic advance (11.32 %).
17. **Protein Content (%):** The protein content in genotypes varied from 17.39 to 26.91 % in respect of genotype and Envoy, respectively, with an average protein content of 21.10 %. PCV and GCV were 8.55% and 8.35 %, respectively. Heritability estimate was the highest (95.2 %) while the genetic advance was low (16.78 %).

5.2. Character Associations

In a practical breeding work, the improvement of a target trait can be achieved through indirect selection via other characters. This needs a good knowledge of the associations of the different characters with the target trait and among the different characters themselves.

In the present study, associations of traits for all the 18 quantitative characters were determined for the experimental materials considered (139 germplasm accessions and the 5 checks). Character correlations were made both at phenotypic (r_p) and genotypic (r_g) levels as shown in Tables 3 and 4.

From one hundred and fifty three [n (n-1)/2] correlations made for the 18 quantitative characters at each of the phenotypic and genotypic levels, 99 correlation coefficients at the phenotypic level and 123 correlation coefficients at the genotypic level were statistically significant irrespective of directions of association. At the genotypic level, 110 correlation coefficients were significant at 1 percent probability, while the remaining 13 showed significance at 5 percent probability. In the case of phenotypic correlations, 15 and 84 correlation coefficients were significant at 5 and 1 percent probability, respectively.

An examination into the correlation tables indicated that the magnitude of phenotypic correlation coefficients were greater than the genotypic coefficients for the main yield components (harvest index, number of pods per plant, number of seeds per pod and biological yield), but for other traits it was less than the genotypic coefficient.

1. Seed yield per plant: **Phenotypic and genotypic correlation coefficients showed seed yield to be strongly related with biomass yield (r_p = 0.94 and r_g = 0. 89). Similarly, high positive association was observed with number of pods per plant (r_p = 0.73 and r_g = 0.57). Positive and low to moderate correlation coefficients were observed with number of seeds per pod (r_p = 0.33 and r_g = 0.27), stem diameter (r_p = 0.23 and r_g = 0.36),**

number of nodes on the main stem (r_p = 0.35 and r_g = 0.69), days to flowering (r_p = 0.25 and r_g = 0.52) and days to maturity (r_p = 0.33 and r_g = 0.62), and harvest index (r_p = 0.21 and r_g = 0.16). Seed yield showed negative genotypic correlation with 100 seed weight, seed length, internode length, leaf dimensions and protein content. However, it had no significant association with seed height at both the genotypic and phenotypic level; and with pod length, 100 seed weight, seed length, internode length and leaf dimensions at the phenotypic level only.

Table 3. Phenotypic correlation coefficients of the 18 quantitative characters

	T1	T2	T3	T4	T5	T6	T7	T8	T9	T10	T11	T12	T13	T14	T15	T16	T17	T18
T1	**1.00**	0.94**	0.21**	0.72**	0.33*	-0.06	-0.12	0.00	0.07	0.39**	0.23**	0.01	0.02	0.04	0.35**	0.25**	0.33**	-0.06
T2		**1.00**	-0.11	0.75**	0.32**	-0.1	0.15*	-0.08	0.05	0.43**	0.35**	0.01	0.06	0.08	0.41**	0.37**	0.45**	-0.01
T3			**1.00**	-0.03	0.09	0.12	0.09	0.25**	0.09	-0.11	-0.34**	-0.02	-0.13	-0.13	-0.20**	-0.35**	-0.33**	-0.17*
T4				**1.00**	0.34**	-0.55**	-0.55**	-0.42**	-0.32**	0.31**	0.31**	-0.23**	-0.11	-0.05	0.47**	0.46**	0.40**	0.05
T5					**1.00**	-0.67**	-0.61**	-0.55**	-0.11	0.10	0.25**	-0.19*	-0.21**	-0.06	0.37**	0.43**	0.30**	-0.08
T6						**1.00**	0.90**	0.80**	0.49**	-0.06	-0.25**	0.39**	0.29**	0.14*	-0.45**	-0.56**	-0.30**	-0.09
T7							**1.00**	0.69**	0.62**	-0.19*	-0.23**	0.35**	0.35**	0.20**	-0.50**	-0.56**	-0.34**	-0.12
T8								**1.00**	0.23**	0.02	-0.34**	0.30**	0.08	0.01	-0.30**	-0.54**	-0.35**	0.03
T9									**1.00**	-0.12	0.01	0.26**	0.36**	0.29**	-0.29**	-0.23**	-0.15*	-0.11
T10										**1.00**	0.12	0.17*	-0.16*	-0.18*	0.70**	0.38**	0.41**	0.18*
T11											**1.00**	-0.05	0.14*	0.24**	0.32**	0.38**	0.36**	0.01
T12												**1.00**	0.24**	0.12	-0.10	-0.21**	-0.14*	-0.01
T13													**1.00**	0.79**	-0.33**	-0.14*	-0.06	-0.14*
T14														**1.00**	-0.27**	-0.11	-0.10	-0.09
T15															**1.00**	0.65**	0.50**	0.16*
T16																**1.00**	0.76**	0.11
T17																	**1.00**	-0.05
T18																		**1.00**

*, ** = Significant at 5% and 1%, respectively.

T1 = Seed Yield/plant
T2 = Biological Yield/plant
T3 = Harvest index
T4 = Pods/plant
T5 = Seeds/pod
T6 = 100-seed weight
T7 = Dry seed length
T8 = Dry seed height
T9 = Pod length
T10 = Plant height
T11 = Stem diameter
T12 = Internode length
T13 = Leaf length
T14 = Leaf width
T15 = No of nodes on main stem
T16 = Days to 50% flowering
T17 = Days to 90% maturity
T18 = Protein content (%)

Table 4. Genotypic correlation coefficients of the 18 quantitative characters

	T1	T2	T3	T4	T5	T6	T7	T8	T9	T10	T11	T12	T13	T14	T15	T16	T17	T18
T1	**1.00**	0.89**	0.16*	0.57**	0.27**	-0.16*	-0.25**	-0.09	-0.14*	0.62**	0.36**	-0.25**	-0.22**	-0.38**	0.69**	0.52**	0.62**	-0.23**
T2		**1.00**	-0.32**	0.61**	0.27**	-0.23**	-0.29**	-0.25**	-0.19*	0.65**	0.67**	-0.24**	-0.18*	-0.32**	0.78**	0.72**	0.83**	-0.07
T3			**1.00**	-0.13	0.00	0.14*	0.11	0.33**	0.12	-0.17*	-0.64**	-0.02	-0.10	-0.07	-0.26**	-0.47**	-0.51**	-0.23**
T4				**1.00**	0.51**	-0.78**	-0.80**	-0.67**	-0.68**	0.34**	0.50**	-0.58**	-0.46**	-0.51**	0.67**	0.67**	0.57**	0.05
T5					**1.00**	-0.82**	-0.72**	-0.67**	-0.24**	0.08	0.45**	-0.42**	-0.40**	-0.19*	0.50**	0.54**	0.39**	-0.10
T6						**1.00**	0.93**	0.83**	0.61**	-0.06	-0.43**	0.57**	0.51**	0.35**	-0.51**	-0.60**	-0.36**	-0.10
T7							**1.00**	0.70**	0.76**	-0.20**	-0.39**	0.49**	0.56**	0.41**	-0.56**	-0.59**	-0.40**	-0.13
T8								**1.00**	0.29**	0.02	-0.59**	0.45**	0.15*	0.09	-0.36**	-0.59**	-0.43**	0.02
T9									**1.00**	-0.21**	-0.14*	0.39**	0.55**	0.43**	-0.38**	-0.29**	-0.22**	-0.13
T10										**1.00**	0.10	0.18*	-0.34**	-0.52**	0.76**	0.43**	0.50**	0.20**
T11											**1.00**	-0.34**	0.05	0.12	0.51**	0.75**	0.73**	-0.01
T12												**1.00**	0.45**	0.19*	-0.20**	-0.31**	-0.20**	-0.01
T13													**1.00**	0.75**	-0.57**	-0.22**	-0.07	-0.26**
T14														**1.00**	-0.59**	-0.18*	-0.13	-0.26**
T15															**1.00**	0.72**	0.60**	0.18*
T16																**1.00**	0.83**	0.11
T17																	**1.00**	-0.06
T18																		**1.00**

*, ** = Significant at 5% and 1%, respectively.

T1 = Seed Yield/plant
T2 = Biological Yield/plant
T3 = Harvest index
T4 = Pods/plant
T5 = Seeds/pod
T6 = 100-seed weight
T7 = Dry seed length
T8 = Dry seed height
T9 = Pod length
T10 = Plant height
T11 = Stem diameter
T12 = Internode length
T13 = Leaf length
T14 = Leaf width
T15 = No of nodes on main stem
T16 = Days to 50% flowering
T17 = Days to 90% maturity
T18 = Protein content (%)

2. Biological yield: **This character showed strong relationship with seed yield. It observed moderate and high phenotypic and genotypic correlations, respectively, with plant height, stem diameter, number of nodes on the main stem, days to flowering and days to maturity. Moderately high genotypic and high phenotypic coefficients were recorded with number of pods per plant. Even though there were no significant associations of biomass yield with harvest index, 100 seed weight, seed length, seed height, pod length, internode length and leaf dimensions at the phenotypic level, it is negatively correlated with these characters at the genotypic level with low values of association coefficient.**
3. Harvest index: **Harvest index exhibited a significant negative association with stem diameter, number of nodes on the main stem, days to flowering and days to maturity at both phenotypic and genotypic level, while it showed similar association with biological yield and plant height only at the genotypic level. On the other hand, it is positively correlated with seed yield and seed height for both correlation coefficient types. But in all cases, the magnitude of the association value ranged from low to moderate (Tables 3 and Table 4).**
4. Pods per plant: **The analysis showed that this trait had a significant positive association with seed yield, biomass yield, seeds/pod, plant height, stem diameter, number of nodes on the main stem, days to flowering and days to maturity. It also revealed significantly negative associations with 100-seed weight, seed length, seed height, pod length and internode length at both genotypic and phenotypic level. In addition, it was genotypically associated with leaf dimensions in the negative direction. The strong positive correlations that were recorded**

with seed yield and biomass yield were phenotypic, whereas the strong negative ones observed with 100-seed weight and seed length were genotypic. The magnitude of the correlation coefficient varied from low to high, irrespective of direction of association for both genotypic and phenotypic values.

5. Seeds per pod: **This trait showed low to medium significant positive correlation with seed yield, biomass yield, pods per plant, and stem thickness, nodes on the main stem, days to flowering and days to maturity. On the contrary, significantly and negatively low to high association values were observed with 100-seed weight, seed length, seed height and internode length. Seeds per pod also revealed low negative association with pod length and leaf dimensions at genotypic level. Strong negative correlations were recorded genotypically, with characters 100-seed weight (r_g = 0.82) and seed length (r_g = 0.72).**
6. Hundred seed weight: **Significantly positive associations were detected with seed length, seed height, pod length, internode length and leaf dimensions. Its association with number of pods per plant, number of seeds per pod, stem diameter, number of nodes on the main stem, days to flowering and days to maturity were significant but negative at both phenotypic and genotypic levels. It also showed significantly negative associations with seed and biomass yield at the genotypic level. This trait observed strongly positive correlations with seed length (r_p = 0.80 and r_g = 0.83), however, it recorded strongly negative correlations with number of seeds per pod (r_g = 0.82) and number of pods per plant (r_g = 0.78) only at the genotypic level.**
7. Seed length: **The association of seed length with 100-seed weight, seed height, pod length, internode length and leaf dimensions were positive**

and significant at both phenotypic and genotypic levels. However, it is negatively correlated with number of pods/plant, number of seeds/pod, plant height, stem diameter, number of nodes on the main stem and with phenological traits. In addition, negatively low associations were detected between this trait and seed yield and biomass yield at the genotypic level.

8. Seed height: **This character intimately associated with 100-seed weight (r_p = 0.80 and r_g = 0.83) in the positive direction. Significantly positive associations were also observed with harvest index, 100-seed weight, seed length, pod length and internode length, while negative correlations found with number of pods/plant, number of seeds/pod, number of nodes on the main stem and phenological traits at both phenotypic and genotypic levels.**
9. Pod length**: This trait showed a relatively strong significant positive correlation with seed length (r_g = 0. 76) only at the genotypic level. The remaining correlation values ranged from low to medium irrespective of the directions of correlation both at phenotypic and genotypic level.**
10. Plant height: **At both phenotypic and genotypic level of measurements, plant height exhibited significant positive and negative association with 12 of the characters. Values of significant correlations varied between 0.16 and 0.70 at phenotypic level and between 0.17 and 0.76 at genotypic level for its association with harvest index and number of nodes on the main stem, respectively.**
11. Stem diameter: **This character showed positively high correlation value with phenological traits at genotypic level, while it showed small to medium negative associations with seed traits and 100-seed weight. The association it exhibited with seed yield, biomass yield, pods per plant**

and seeds per pod were also positive and significant but its correlation with harvest index was moderately high and significantly negative at the genotypic level.

12. Internodes length: **Internodes length exhibited significant association with all the characters except harvest index and days to maturity at the genotypic level, however significant correlations were found with number of pods/plant, number of seeds/pod, 100-seed weight, dry seed length, dry seed height, pod length and plant height at phenotypic level irrespective of directions of association.**
13. Leaf dimensions: **Strong positive associations were observed among themselves (leaf length and width). The other significant positive or negative correlation values, both at the phenotypic and genotypic level ranged from low to medium.**
14. Number of nodes on the main stem: **Strong positive and significant associations were observed with biomass yield, plant height and days to flowering all at the genotypic level. In addition, this character exhibited significant association (positive / negative) with all characters again at genotypic level and with 16 characters except internode length at the phenotypic level.**
15. Days to 50% flowering: **The correlation analysis revealed that this trait showed strong positive association with days to maturity, number of nodes on the main stem, stem diameter and biomass yield at the genotypic level, while with days to maturity only at phenotypic level. The analysis also showed significant association of the character with 16 of the traits at the genotypic level and 15 of the traits at the phenotypic level, irrespective of directions of association. It showed a non-significant association with protein content at the genotypic and with**

leaf width and protein content at the phenotypic levels. Traits positively associated with days to flowering were seed yield, biomass yield, number of pods per plant, number of seeds per pod, plant height, stem diameter, number of nodes on the main stem and days to maturity with moderate to high correlation coefficients. The other traits: harvest index, seed weight, seed length, seed height, pod length, internodes length and leaf dimensions were negatively associated with days to flowering at low to medium range values.

16. Days to 90% maturity: **Significantly positive and negative associations of this trait were observed with fourteen characters both at phenotypic and genotypic level except leaf dimensions and protein content. Days to maturity exhibited significant positive correlation with days to flowering, stem diameter and biomass yield at genotypic level, but only with that of days to flowering at the phenotypic level. The correlation trends with other traits were similar as that of days to 50% flowering.**
17. Protein content: **With the exception of harvest index (r_p = 0.17 and r_g = 0.23), plant height (r_p = 0.18 and r_g = 0.26), leaf length (r_p = 0.14 and r_g = 0.26) and number of nodes on the main stem (r_p = 0.16 and r_g = 0.18) all other correlation coefficients were non-significant at genotypic and phenotypic level. However, it was negatively correlated with seed yield and leaf width at genotypic level.**

5.3. Path Coefficient Analysis

Seed yield is a polygenic trait; hence direct selection for this character may often be misleading. The components that determine the yield are the best indices for selection. Therefore, knowledge of the association between important yield attributes and seed yield may help the breeder to identify

suitable donors for any successful breeding. Path analysis can provide an effective means of partitioning the correlation coefficient into direct and indirect effects.

In the present study, seed yield was considered as effect dependent on eleven independent variables, which were considered as causes. The independent characters were: harvest index, number of pods per plant, number of seeds per pod, 100-seed weight, pod length, plant height, internode length, number of nodes on the main stem, days to 50% flowering, days to 90% maturity and protein content. The direct and indirect effects were presented on Table 5

Table 5. Direct and indirect effects of yield components and some yield contributing characters with seed yield

	HI	Pdpp	Sdpp	Sdwt	PdL	PltHt	IntdL	Node	DTF	DTM	PC	CorCo
HI	**0.13**	-0.08	0.01	0.14	0.00	-0.01	0.00	-0.01	-0.01	-0.01	0.00	**0.16**
Pdpp	-0.01	**0.96**	0.20	-0.48	-0.02	0.03	0.00	0.02	0.02	0.01	0.00	**0.72**
Sdpp	0.00	0.36	**0.54**	-0.56	-0.01	0.01	0.00	0.02	0.02	0.01	0.00	**0.38**
Sdwt	0.02	-0.56	-0.36	**0.83**	0.02	-0.01	0.00	-0.02	-0.02	-0.01	0.00	**-0.11**
PdL	0.01	-0.28	-0.06	0.39	**0.05**	-0.01	0.00	-0.01	-0.01	0.00	0.00	**0.09**
PltHt	-0.01	0.32	0.08	-0.08	-0.01	**0.08**	0.00	0.03	0.01	0.01	0.00	**0.43**
IntdL	0.00	-0.20	-0.11	0.31	0.01	0.01	**-0.01**	0.00	-0.01	0.00	0.00	**0.00**
Node	-0.03	0.47	0.22	-0.39	-0.01	0.06	0.00	**0.04**	0.02	0.01	0.00	**0.39**
DTF	-0.05	0.46	0.25	-0.48	-0.01	0.03	0.00	0.03	**0.03**	0.02	0.00	**0.28**
DTM	-0.05	0.37	0.19	-0.26	-0.01	0.03	0.00	0.02	0.03	**0.02**	0.00	**0.35**
PC	-0.02	0.04	-0.04	-0.08	-0.01	0.01	0.00	0.01	0.00	0.00	**0.02**	**-0.06**

Residual = 0.10

The main diagonal (bold) is direct effects

1. HI = Harvest index
2. Pdpp = Pods/plant
3. Sdpp = Seeds/pod
4. Sdwt =100-seed weight
5. PdL = Pod length
6. PltHt = Plant height
7. IntdL = Internode length
8. Node = Nodes on main stem
9. DTF = Days to 50% flowering
10. DTM = Days to 90% maturity
11. PC = Protein content (%)

Considering the direct effect of each character on seed yield, number of pods/plant had the highest positive direct effect (0.96), followed by 100-seed weight and number of seeds/pod. Internode length had low and negative direct effect on seed yield. Pod length, plant height, number of nodes on the main stem, days to 50% flowering, days to 90% maturity and protein content recorded low positive direct effect, while harvest index exhibited a moderate direct effect. The indirect effect of harvest index via 100-seed weight (0.14) was positive and comparable to the direct effect. The residual factor was calculated to be 0.1030.

The character that exerted the highest positive direct effect, also showed a high indirect negative effects (0.48) on seed yield through 100 seed weight. On the contrary, it recorded positive and moderate indirect effect on seed yield via number of seeds/pod (0.20). The direct effect of number of seeds pert pod (0.54) was high. It also showed the second highest negative indirect effect (0.56) on seed yield through 100 seed weight. However, positive indirect effects were also recorded for this trait through number of pods/plant (0.36). 100-seed weight showed the highest (0.56) negative indirect effect on seed yield through number of pods per plant and number of seeds per pod (0.36).

Positive indirect contribution of pod length (0.39) to seed yield was recorded through 100 seed weight. Relatively comparable negative indirect

contributions of this character on seed yield were through number of pods per plant. Internode length also contributed its indirect contribution through 100-seed weight (0.31), but an equivalent negative indirect contribution was observed via number of pods per plant (0.20) and number of seeds per pod (0.11) on seed yield.

Even though it recorded low direct effect, plant height had a high positive indirect effect towards seed yield through number of pods per plant (0.32). Number of nodes on the main stem showed a positively high and moderate indirect effects on seed yield via number of pods per plant (0.47) and number of seeds per pod (0.22), respectively, but it recorded a negative indirect effect on seed yield through 100-seed weight.

The direct effect of days to flowering was negative and negligible; however it exerted a high positive indirect effect towards seed yield via number of pods per plant (0.46) and number of seeds per pod (0.25). In addition to this, days to flowering exerted high and negative indirect contributions on seed yield via 100 seed weight (0.48). Days to maturity also observed positive indirect effects on seed yield via number of pods per plant (0.37) and number of seeds per pod (0.19). Its indirect effect through 100-seed weight (0.26) was negative. On the other hand, protein content, which showed a non-significant association with seed yield at phenotypic level, also recorded very low direct and indirect effects on seed yield both in the positive and negative directions.

5.4. D^2 Analysis

Genetic divergence in a population, especially with respect to the characters in which improvement is sought, is an indispensable prerequisite for successful crop improvement program. The D^2 statistics has found favor as a tool for estimating genetic divergence, which is

the basis in choosing parents for hybridization in a breeding program. Progenies derived from diverse crosses are expected to show a broad spectrum of genetic variability providing greater scope for isolating high yielding segregants in the succeeding generations. In the present study, the D^2 was analyzed using 139 common bean germplasm accessions and the 5 checks.

Test of significance: The analysis of variance for each individual character showed highly significant differences among the genotypes for all the 18 characters studied (Table 1). However, yield and yield components (seed yield, biological yield, harvest index, pods per plant, seeds per pod and 100-seeds weight), some morphological characters (pod length, internode length, number of nodes on the main stem and plant height), phenological traits (days to 50% flowering and days to 90% maturity) and protein content (%) were analyzed by the D^2 technique. The square of the distance (D^2 value) between any two genotypes calculated as sum of squares of difference between the mean values of all the 13 transformed variables were obtained for further analysis. Each genotype produced 143 combinations and totally, 10296 D^2 values were obtained for all the genotypes considered. The D^2 values were tested for their significance using Hotelling's T^2 statistics. The pooled divergence for all the characters within the genotypes, tested by the Wilk's lambda criterion, was significant (χ^2 = 4967.09 for 1859 DF). Hence the analysis of genetic divergence among genotypes used in the study was considered relevant.

Contribution of different characters towards divergence: The analysis of the contribution of each character towards the expression of genetic divergence (Table 6) indicated that protein content contributed maximum (18.95%) followed by days to 50% flowering (16.60%) to the total genetic divergence in the genotypes studied. These two traits followed by 100-seed weight (10.50%), number of seeds per pods (10.45%), days to 90% maturity (10.15%), plant height (8.15%), number of nodes on the main stem (6.95%), pod length (5.39%) and number of pods per plant (4.82%) totally accounted for more than 90% of total genetic divergence in the materials. Harvest index (1.51%), seed yield (1.83%), internode length (1.99%) and biomass yield were the least contributor to the divergence.

Table 6. Contribution of each character to the total divergence

Characters	T1	T2	T3	T4	T5	T6	T7	T8	T9	T10	T11	T12	T13	Total
No of times appearing first in ranking	188	280	155	496	1076	1081	555	839	205	716	1709	1045	1951	10296
Percent contribution	1.83	2.72	1.51	4.82	10.45	10.50	5.39	8.15	1.99	6.95	16.60	10.15	18.95	100.00

T1 = Seed yield/plant
T2 = Biological yield/plant
T3 = Harvest index
T4 = Pods/plant
T5 = Seeds/pod
T6 = 100-seed weight
T7 = Pod length
T8 = Plant height
T9 = Internode length
T10 = Number of nodes on main stem
T11 = Days to 50% flowering
T12 = Days to 90% maturity
T13 = Protein content (%)

The closest and distant relatives: Arranging the D^2 values in ascending/descending order, enabled to detect the closest and distant relatives. The smallest D^2 value (4.13) was obtained by combining genotype UTT 28-175 from Guatemala with genotype CAP-4 from Brazil. The D^2 value of the most distantly related combination was 818.82, between genotype FOT-65 and EAP-4 from Colombia and Chile followed by ENVOY combined with FOT-65 with D^2 value of 794.73.

5.4.1 Group Constellation

Group constellation was carried out following Tocher's method (Rao, 1952), which utilizes the D^2 value. When D^2 values were arranged in ascending order (data not shown) for each genotype, the D^2 value of close relatives varied from 4.13 to 818.82. Hence the maximum level of cluster formation was fixed as 818.82. Starting with two nearest entries, new entries were added in the cluster until the average D^2 values of added genotype remain below the maximum level fixed for cluster formation otherwise, eliminated and used in other cluster formation. The above criterion holds true for the remaining cluster constellation too.

Based on the D^2 values between the 144 genotypes, all the materials can be grouped into 9 clusters (Table 7). Among these, cluster I was the largest and consists of 40 genotypes, followed by cluster II with 26 genotypes. Clusters III, IV and VII contained 20, 17 and 11 genotypes, respectively. Clusters V and VI each had 13 genotypes, whereas cluster VIII had 3 genotypes. Cluster IX was unique since it had only one genotype. One of the five check cultivars, Roba-1 and the other two, Awashmelka and Dimtu were grouped in the biggest and the next biggest

Table 7. Cluster number with their respective germplasm accessions and their source

Clusters	No of Genotypes	Germplasm name	Country of Origin	Clusters	No of Genotypes	Germplasm name	Country of Origin
I	40	EAP-233	Mexico	II	26	AURORA	USA
		PAC-29	Mexico			GRYPHON	USA
		DRESDEN	USA			AWASH MELKA	USA
		UTT 28-175	Guatemala			BRB 222	Brazil
		STT 165-92	Guatemala			H-92	Burundi
		ACC No 1207	Honduras			AN-9021455	Brazil
		STARLIGHT	USA			CARIOCA	Brazil
		ALPINE	USA			DOR 526	Guatemala
		LE-93-7	Mexico			XAN-310	Mexico
		ABRITUS	USA			DICTA 100	Honduras
		G 92317	Mexico			DOR 799	Guatemala
		SEQ-44	Guatemala			DIMTU	Guatemala
		AFR-689	Mexico			9356-26	Costa Rica
		VAX-1	Mexico			VAX-3	Mexico
		VAX-2	Mexico			EAP-10-88	Honduras
		BAYO 400	Chile			UCR-3	USA
		A-804	Brazil			LM-93203224	Brazil
		Carioca Pitico	Brazil			COPINHA	Brazil
		EAP-506	Mexico			FM-M-38-1	Mexico
		FEB-208	Mexico			CIFAC 91140	Mexico
		PEROLA	USA			RIO TIBAGI	Brazil
		RH-31-04	Mexico			BLACG HAWK	Brazil
		ROBA-1	Brazil			ICB-67	Guatemala
		LM-93204487	Brazil			ICTA JU 95-113	Guatemala
		CAP-4	Brazil			TLP-20	Costa Rica
		RAB 585	Mexico			BLACK DESSIE	Ethiopia
		RAZ 54	Brazil	III	20	WU3 94-9	Mexico
		UCR-5	USA			Galbande-mold	Guatemala
		DOR 716	Guatemala			PINTO VILLA	Mexico
		EAP-12-88	Honduras			HATTON	USA
		MD-30-18	Honduras			G 22005	Mexico
		LR-93201343	Brazil			M/LKK 26	Malawi
		ICTA JU-95-4	Guatemala			91: 360P	Brazil
		FM 94043	Mexico			BELDAKMI RR-5	Colombia
		I-66	Venezuela			CO-57914	Colombia
		51-1-1-1	Costa Rica			EARLY RAY	USA
		AN-9021337	Brazil			MAVERIC	USA
		CB-9021806	Brazil			PINTO 89	Chile
		G 21212	Mexico			CHASE	USA
		ICTA OSTUA	Guatemala			Bayo zacatecas	Chile

Table 7. Continued ……

Clusters	No of Genotypes	Germplasm name	Country of Origin	Clusters	No of Genotypes	Germplasm name	Country of Origin
III	20	Garbancillos	Mexico	V	13	559 FIN-11	Chile
		Bayo madero	Chile			547SEQ 1019	Chile
		RAB 484	Colombia			FOT-62	Chile
		NAZ	Peru			FOXFIRE	USA
		55012	Costa Rica	VI	13	TY-3396-1	Chile
		L 94C 356 LE	Costa Rica			MX-8385-14T	Mexico
IV	17	HAL-5	Chile			MX 8729-5-A	Mexico
		AFR-733	Colombia			BAYO MOCHICA	Chile
		PI 415965	Peru			AZTEC	USA
		SK 93263	Colombia			ATNDABA	Brazil
		A-197	Colombia			511CIFAC 91135	Peru
		L-306003	Brazil			531MX9065-9T	Mexico
		FOT-52	Colombia			PARAGACHI-Y	Peru
		FOI-15	Colombia			519CIFAC 91148	Chile
		CIFAC 87110	Peru			CIFAC 91147	Chile
		ANT-22	Colombia			EAP-4	Chile
		DRK-140	USA			FM 94010	Peru
		ROSADO	Colombia	VII	11	OMAR V	Ethiopia
		URIBE	Ecuador			SEQ-1037	Chile
		I-77	Venezuela			SEQ-1019	Chile
		764FOI-20	Colombia			AFR-630	Chile
		630ESLEC	Colombia			SEQ-1031	Chile
		BRB 232	Peru			PARAGACHI	Mexico
V	13	TAYLOR	USA			POMPADUR-G	Dominican Rep.
		HORIZON	USA			FOT-65	Colombia
		CALIMA	Colombia			FIN-10	Peru
		CHOCHO	Dominican R.			848AFR-726	Chile
		CAL-182	Colombia			850AFR-737	Chile
		BRB 205	Peru	VIII	3	CIFEM 91117	Peru
		ARS-R-93001	Colombia			OBO-A-074	Mexico
		GOBERASHA	Colombia			AND 1090	Colombia
		DRK-142	USA	IX	1	ENVOY	USA

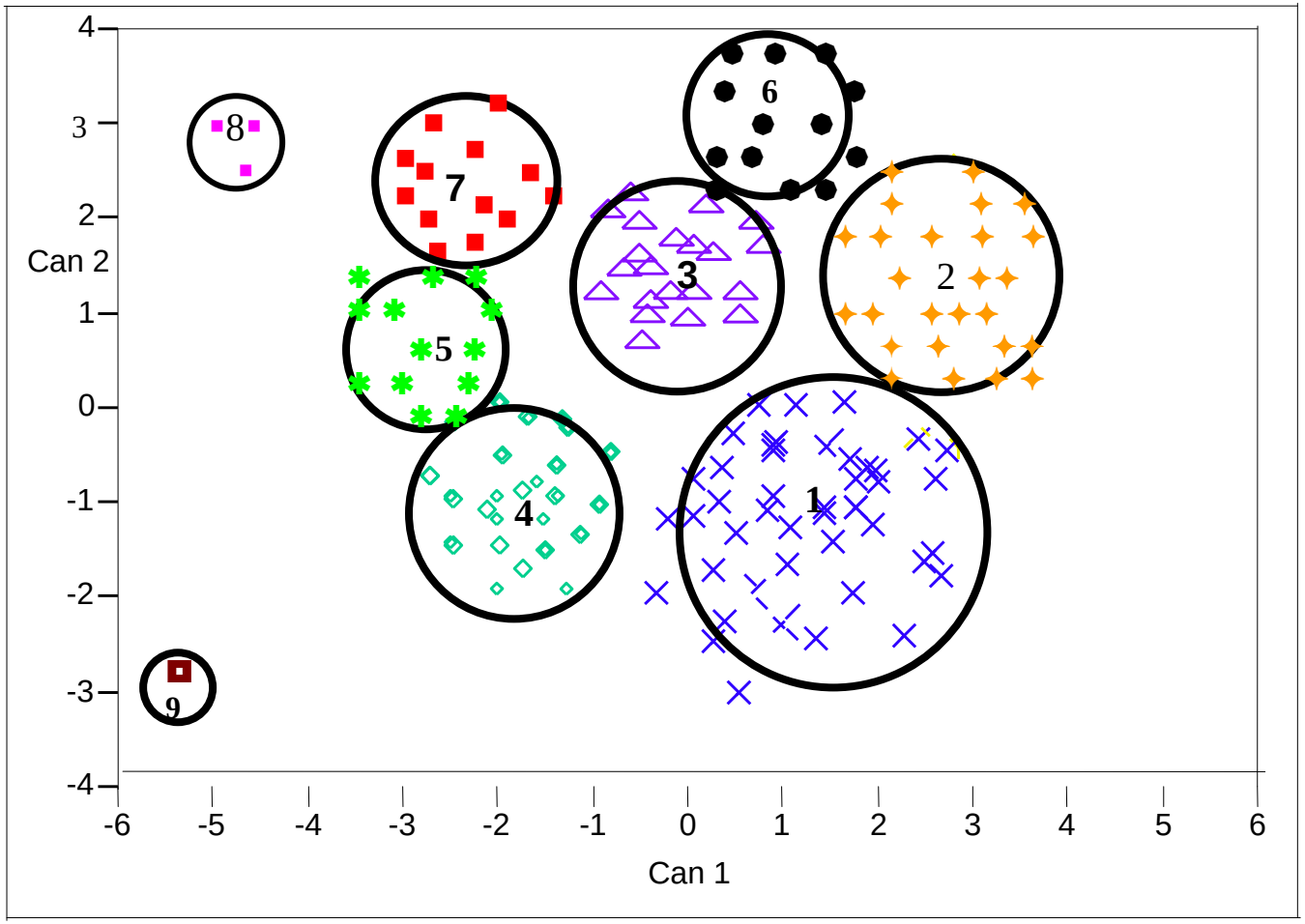


Fig 3. Scatterplot of the nine cluster groupings in relation to the two representative axes of the first two canonical variates (Can 1 and Can 2) in 13 characters evaluated.

clusters, respectively. The rest two, GOBARASHA and ATNDABA were grouped in clusters V and VI, respectively. The clustering pattern revealed that each cluster consisting of more than one strain from different country of origin.

According to Figure 3, the results demonstrated a scatterplot related to the first two canonical variate, in a bi-dimensional space. The first two canonical variate explained 64.02% of the among accession variance. Each canonical variate is the linear combination of the independently measured variables that has the greatest possible variance. The first canonical variate, which dominated by large loadings from days to flowering, 100-seed weight, number of seeds per pod, days to maturity, number of nodes on the main stem, plant height, pod length and number of pods per plant, while the second dominated by a large loading from percentage protein content. This indicated that the genetic composition of the accessions differ mostly in their percentage protein content, days to flowering, 100-seed weight, number of seeds per pod, days to maturity, number of nodes on the main stem, plant height, pod length and number of pods per plant. This graphic representation also confirmed the Tocher's method of grouping the accessions into clusters.

5.4.2. Intra-and inter-cluster distances

The average intra-and inter-cluster D^2 values and their square root (D value) are depicted in (Table 8). The intra-cluster distances ranged from 0 (in monogenotypic cluster) to 8.93 in cluster VIII. Clusters I, II, IV and V; III, VI, and VII, respectively, had more or less similar intra-cluster distances (Table 8). The minimum inter-cluster distance was 5.52 between clusters IV and V. Both these clusters together accounted for 30 genotypes of all the genotypes of diverse origin. The maximum distance (68.15) was recorded between clusters VIII and IX, which together covered only 4 genotypes of all the materials. All other inter-cluster D^2 values were lying between these two values. Cluster IX exhibited a distant relationship to most of the clusters.

5.4.3. The nearest and distant clusters

As indicated in Table 9, cluster I showed a close relationship with cluster II followed by clusters III and VI. Cluster II was nearest to cluster VI, but farthest to cluster IX. Cluster IV and V followed by cluster VII exhibited an

intimate relationship with cluster III. A very close proximity was observed between clusters IV and V followed by clusters I and II. A distant relationship was observed between cluster IX and Clusters II, V, VI, VII and VIII.

Table 8. Intra- (main diagonal) and inter-cluster D^2 values along with their D value in parenthesis

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**4.29**	5.91	11.85	20.04	19.4	10.98	16.59	19.4	33.18
	(2.07)	(2.43)	(3.44)	(4.48)	(4.40)	(3.31)	(4.07)	(4.40)	(5.76)
II		**3.68**	21.26	39.05	31.71	8.16	28.92	29.59	57.32
		(1.92)	(4.61)	(6.25)	(5.63)	(2.86)	(5.38)	(5.44)	(7.57)
III			**6.08**	9.88	8.17	18.74	12.13	36.45	33.95
			(2.47)	(3.14)	(2.86)	(4.33)	(3.48)	(6.04)	(5.83)
IV				**4.68**	5.52	39.98	15.89	35.31	30.57
				(2.16)	(2.35)	(6.32)	(3.99)	(5.94)	(5.53)
V					**4.13**	28.88	11.59	30.22	49.83
					(2.03)	(5.37)	(3.41)	(5.50)	(7.06)
VI						**6.8**	19.51	20.1	64.22
						(2.61)	(4.42)	(4.48)	(8.01)
VII							**5.57**	15.21	52.53
							(2.36)	(3.90)	(7.25)
VIII								**8.93**	68.15
								(2.99)	(8.26)
IX									**0.00**
									(0.00)

Table 9. The nearest and distant clusters from each cluster based on D value

Clusters	No of genotypes grouped	Nearest clusters	Farthest clusters
I	40	II, III, VI	IX
II	26	I, VI	IV, V, IX
III	20	IV, V, VII	VIII, IX
IV	17	III, V	II, VI, VIII, IX
V	13	III, VII	II, VI, VIII, IX
VI	13	I, II	IV, IX
VII	11	III, V	II, IX
VIII	3	VII	III, IV, IX

IX	1		From all clusters

5.4.4. Cluster mean analysis

As indicated in Table 10, germplasm accessions in clusters III, IV, V and IX were the earliest in days to flowering, whereas those in clusters II and VIII were of late type. Cluster IV means for pods per plant was the lowest, while those in cluster II showed the highest pods per plant and seeds per pod, and the genotypes were late in maturity. The highest mean seed yield, biological yield and plant height were recorded by genotypes in cluster VI. The highest mean cluster value for harvest index was recorded by cluster III, while the lowest by cluster VIII. Genotypes in cluster III also exhibited earliness in flowering and maturity. With respect to 100-seed weight, genotypes grouped in clusters IV, V, VII and VIII recorded large mean values, while those grouped in cluster VIII recorded the highest mean value. Average value of nodes on the main stem varied from 6.83 for cluster IV to 15.16 for cluster VIII. The mean of pod length ranged from 7.32cm to 11.99cm for genotypes of clusters IX and V, respectively. Cluster mean for days

Table 10. Mean value of 13 quantitative characters for nine clusters formed

Clusters	Yld	Byld	HI	Pdpp	Sdpp	SdWt	PdL	PltHt	IntdL	Node	DTF	DTM	PC
I	30.73	48.56	63.28	25.86	4.66	26.12	9.53	60.07	2.89	13.66	46.99	81.85	21.76
II	39.56	61.88	64.18	32.65	5.23	23.94	9.49	62.97	2.66	14.50	48.10	84.12	20.06
III	33.58	46.14	72.91	22.06	4.05	38.26	9.76	59.88	3.17	11.56	37.60	74.75	21.05
IV	23.77	36.53	65.46	16.86	3.42	42.77	9.99	36.99	3.08	6.83	37.59	76.18	20.81
V	31.25	46.71	67.20	18.32	3.69	46.63	11.99	45.62	3.15	7.93	38.00	77.92	20.46
VI	42.82	64.65	66.18	30.37	3.95	36.18	9.94	92.19	3.27	15.08	47.15	84.04	21.74
VII	30.68	47.70	64.31	18.65	3.68	45.73	10.70	68.96	5.61	12.69	41.18	79.32	21.04
VIII	28.75	56.85	50.04	18.40	3.49	47.60	10.48	79.98	4.25	15.16	48.83	86.17	21.85
IX	17.98	28.84	62.59	28.50	3.68	17.50	7.32	34.50	2.51	11.34	37.00	68.00	26.50

Yld = Seed yield/plant
Byld = Biological yield/plant
HI = Harvest index
Pdpp = Pods/plant
Sdpp = seeds/pod
SdWt = 100-seed weight
PdL = Pod length
PltHt = Plant height
IntdL = Internode length
Node = Number of nodes on the main stem
DTF = Days to 50% flowering
DTM = Days to 90% maturity
PC = Protein content (%)

to 90% maturity varied from 68.00 days for genotype in cluster IX to 86.17 days for genotypes in cluster VIII. Cluster IX, with a single genotype exhibited the lowest mean for seed and biological yield, 100-seed weight, plant height and internode length, while it showed the highest mean cluster value for protein content. The longest internode length was recorded by genotypes of cluster VII.

VI. Discussion

Crop breeders ascribe genetic improvement in any crop plant to the amount of variability present in the germplasm. This is judged based on the knowledge of the extent of variability and the genetic diversity available in the breeding material at hand. In this study, 144 genotypes including the 5 checks were evaluated to study the genetic potential they possess with respect to 18 quantitative characters. The results obtained on some genetic parameters and genetic divergence study through multivariate technique was discussed as follows.

6.1. Genetic variability studies

The pooled analysis of variance for 144 genotypes indicated that the genotypes varied among themselves with respect to the 18 characters studied. Furthermore, all the sum of squares due to genotypes was adjusted except harvest index, which indicate the advantage of using lattice design over randomized complete block design.

Genotypes with the lowest and highest values with respect to the characters studied are presented in Appendix 4. The genotypes exhibited considerable variation for the 18 characters studied. Generally, the range of variation was wide for plant height, number of nodes on the main stem, biological yield, seed yield, 100-seed weight and harvest index, while other characters showed low to fairly high range values. Wallace and Munger (1966) reported large variation (55-67%) for harvest index. Considerable variation for days to maturity, biological yield, seed yield and harvest index were also reported by (Debouck, 1991). Singh *et al.* (1994) reported high range of variation for yield per plant

followed by pods per plant and days to flowering, while it was lowest for pod length. Moreover, Samal *et al.* (1995) observed high range of variation for yield per plant, 100-seed weight, seeds per pod and days to flowering; though they obtained narrow range for plant height and pod length. From the result it is observed that those characters with the higher range of values were also had higher mean values and vice versa. This could indicate that there is sufficient room to improve characters with wider range of variability.

The range in mean values reflects the extent of phenotypic variance present in the materials being studied. Thus, it would be erroneous to infer on the magnitude of variability based on range of a parameter since it is composed of genetic and non-genetic variance components. Hence partitioning of the total variability into genetic and non-genetic variance is required. Johansson (1909) and East (1916) were pioneers in this regard. Since then, it had come to be an accepted biometrical norm in plant breeding studies to ascertain the true breeding value of genotypes. The phenotypic variance indicates the amount of variance, which is due to differences in phenotypic values, whereas the genotypic variance indicates the magnitude of variance arising from the difference in genotypic values. But, the phenotypic and genotypic variance values cannot be used for comparing the degree of variability for different characters as the mean of the characters to be measured could also be different. Hence, the coefficient of variation, which is calculated by considering the respective means have been used for the comparisons. Higher estimates of these coefficients indicate wider diversity and vise versa. On the other hand, narrow differences between the phenotypic and genotypic coefficient of variations implies low sensitivity of a character to environmental effects.

The values of PCV and GCV were high for plant height, number of nodes on the main stem, number of pods per plant, internode length and 100-seed weight. Seed yield per plant and biological yield per plant showed high value for PCV and a relatively moderate one for GCV. In the case of yield per plant and pods per plant, the present result agrees with the results of Samal *et al.* (1995), Singh *et al.* (1994) and Raffi and Nath (2004). All the authors observed high variability for these traits. Moreover, Raffi and Nath, reported high values for 100-seed weight

and moderate values for plant height; whereas Samal *et al.* observed low values for these traits. Singh (1985) observed high values for seed yield, plant height and pods per plant.

Low values for PCV and GCV were observed for days to flowering, days to maturity, leaf dimensions, stem diameter, pod length, harvest index, protein content and for dry seed height. The result obtained was in accordance with the works of Raffi and Nath (2004), Samal *et al.* (1996), Singh *et al.* (1994), Singh (1985) and Agrawal (1986). Samal *et al.* and Singh *et al.*, observed high and low value for pod length, while Raffi and Nath reported a moderate PCV and GCV values for pod length. Singh (1985) reported similar result for harvest index in chickpea.

The difference between PCV and GCV were low for days to flowering, days to maturity, 100-seeds weight, dry seed length, plant height, number of nodes on the main stem, dry seed height and protein content, indicating a lesser influence of environment on these characters. However, the gap between the two components in seed yield per plant, biological yield per plant, leaf dimensions, stem diameter, internode length, number of pods per plant, number of seeds per pod and harvest index was wide, recognizing the importance of environmental effect on these traits. Hence the variability between PCV and GCV indicating the major portion of variation shared by genetic or phenetic component. This also implies that phenotypic variability can be used as reliable measure of genotypic variability.

The coefficient of variation (PCV or GCV) reveals the extent of variability present for different characters but not the heritable portion of variability. To have the knowledge of heritable portion of variability, it is necessary to estimate the heritability of each character. The 'Broad Sense' heritability gives an idea about portion of observed variability attributable to genetic difference. In other words, heritability indicates the accuracy with which a genotype can be identified by its phenotypic performance. In deed, heritability in broad sense contains both additive and non-additive gene effects (Hanson *et al.*, 1956).

High heritability estimates were obtained for days to flowering, plant height, number of nodes on the main stem, days to maturity, 100 seed weight, dry seed length and height and protein content. This indicates that the environment least influenced these characters. Results reported by Davis

and Evans (1977) for days to flowering, plant height and number of nodes on the main stem, and by Motto *et al.* (1978) and Escribano *et al.* (1994) for 100 seed weight, seed length and height are supportive to the present study, but the former observed moderate heritability value for days to maturity. Scully *et al.* (1991) observed high heritability value for days to flowering and days to maturity, while Singh (1990) reported high value for days to maturity and 100-seed weight. Sarafi (1978) also reported high heritability value for 100-seed weight. Raffi and Nath (2004) reported high heritability for days to flowering, plant height, 100-seed weight and days to maturity. Singh (1985) and Agrawal (1986) also observed a very high heritability value for days to flowering and days to maturity, but Agrawal observed moderate value for plant height in chickpea. The high heritability of days to flowering was also in line with the variability study made by Singh *et al.* (1994) and Samal *et al.* (1995); however, Samal *et al.* reported low heritability estimate for plant height and a relatively moderate one for 100-seed weight. In the case of protein content, Leleji *et al.* (1972) and Kelly and Bliss (1975) reported moderate heritability value that is contrary to the present result in common bean.

Internode length, pods per plant, pod length, seeds per pod and harvest index showed moderate heritability. The result is in accordance with Davis and Evans (1977) for internode length, number of pods per plant and pod length, and with that of Zimmermann *et al.* (1984) for harvest index, but Scully *et al.* (1991) reported high heritability for harvest index. Raffi and Nath (2004) and Singh *et al.* (1994) also reported moderate value for number of pods per plant. In the case of pod length and number of seeds per pod, Samal *et al.* (1995) reported high values of heritability estimate and Singh *et al.* (1994) observed similar result for pod length as Samal *et al.* However, Escribano *et al.* (1994) and Raffi and Nath (2004) reported moderate heritability estimate for pod length that is similar to the present result.

Seed yield per plant, biological yield per plant, leaf dimensions and stem diameter showed low heritability. The low heritability for these characters indicates high effect of environment on the traits. Zimmermann *et al.* (1984) observed moderate values for biological yield and low to high heritability values for seed yield. Contrary to the present result, Scully *et al.* (1991) reported high heritability values for seed yield, biological yield and harvest index. Samal *et al.* (1995) also observed the low value for yield per plant, but Raffi and Nath (2004) and Singh *et al.* (1994)

reported moderately high estimate of heritability for seed yield per plant. Moderate heritability for seed yield per plant was also reported by Agrawal (1986) in pea variability study. In the case of stem diameter, Davis and Evans (1977) observed similar result to the present study.

Heritability value alone provides no indication of the amount of genetic progress that would result from selecting the best individuals. Earlier workers discussed the limitation of estimating heritability in 'Broad Sense' as it includes both additive and non-additive gene action. High heritability estimate in broad sense would be a reliable tool of selection if accompanied by high genetic advance.

High heritability estimate coupled with high genetic advance as percent of mean was observed for 100-seed weight, plant height and number of nodes on the main stem. On the other hand, dry seed length and days to 50% flowering observed high heritability with moderate genetic advance as percent of mean, indicating the major portion of genetic variation attributable to additive gene action. Raffi and Nath (2004) reported similar result for plant height and 100-seed weight, but Samal *et al.* (1995) observed low heritability with low genetic advance as percent of mean. Sarafi (1978) noted high genetic advance as percent of mean for pods per plant and seeds per pod and low genetic advance as percent of mean for 100-seed weight. Singh *et al.* (1990) also reported high heritability with high genetic advance for 100-seed weight while they observed high heritability with low genetic advance for days to maturity.

High heritability with low genetic advance as percent of mean was recorded for days to maturity, dry seed height and protein content. Although environmental influence is less in these traits, simple selection will not be effective as decreased genetic advance is indication of prevalence of non-additive gene action (Samal *et al.*, 1995; Singh, 1985; Singh *et al,* 1994).

Moderate heritability accompanied with moderate genetic advance as percent of mean was recorded by internode length, number of pods per plant and seeds per pod. Additive and non-additive gene actions are involved in the expression of these traits. Harvest index and pod length showed moderate heritability with low genetic advance as percent of mean. This suggests that the non-genetic component of the total variability is high. For conditions of medium heritability with low genetic advance, there is low proportion of genotypic component in the total variability and these characters are conditioned by non-additive gene action. Therefore, they are not reliable for selection. Leaf dimensions, stem diameter, seed yield per plant and biological yield per plant showed low heritability accompanied with low genetic advance as percent of mean. These conditions suggested that less scope for selection, as they were more influenced by environment and accounted for non-additive gene effects. Samal *et al.* (1995) reported high hertitability coupled with high genetic advance as percent of mean for pod length, high heritability combined with low genetic advance as percent of mean for days to flowering and low heritability with high genetic advance as percent of mean for seed yield per plant. Raffi and Nath (2004) observed high heritability coupled with high genetic advance as percent of mean for days to flowering, days to maturity and pod length, but moderate heritability with high genetic advance for number of pods per plant, seeds per pod and seed yield per plant.

As indicated in Table 4, 100-seed weight, plant height and number of nodes on the main stem exhibited high PCV and GCV, and high heritability coupled with high genetic advance; indicating the availability of sufficient variation that can be made in use of for selection. On the other hand, characters like

days to maturity and protein content showed high heritability, but PCV and GCV were low. Here, there is a need to create variation; once variability is created they are ready to selection.

6.2 Correlation and Path Analysis

6.2.1. Correlation among Traits

The magnitude and direction of association among characters would be measured by correlation coefficient. Knowledge of correlations among bean traits is important for several reasons: it is possible to fully perceive the diversity of breeding material, to identify traits needed by a bean genotype to grow successfully under certain ecological conditions, to identify and avoid characters that have little or no importance and use of some traits in the selection program, to define breeding target and cultivars model and to recognize impediments and benefits of a breeding process well in advance. With characters that exhibited positive correlations, simultaneous improvement in two or more characters is possible. The negative correlation of some important characteristics may lead to some undesirable selection based on these characters. The negative correlations of these character pairs were to impose problem in combining important yield components in one genotype. To improve the yield components with negative association, suitable recombination may be obtained through biparental mating, mutation breeding or diallel selective mating for breaking undesirable linkages.

In the present work, genetic correlation coefficients recorded higher magnitude than the phenotypic correlation coefficients except the associations made among seed yield, biological yield, harvest index, number of pods per plant and seeds per pod. This indicates that, even though there are inherent associations between the characters studied, the relationships between traits were under the influence of environment and genotype-environment interaction.

The phenotypic correlation (r_p) among traits reflects observed relationship between traits arising from the combined effects of genotype and environment, whereas genetic correlations (r_g) estimate the association between traits resulting either from linkage or pleiotropy (Falconer and Macky, 1996). The phenotypic correlation coefficients for most of the traits were low. Those

characters that showed genotypic correlation with seed yield would be of limited use in direct selection for seed yield, since selection is usually based on phenotypic expression of the trait. Environmental correlation (r_e) reflects a similarity or dissimilarity in the response of two traits to a common environment. The environmental correlations do not carry forward to future generations, unless certain permanent environmental effects, such as soil type affect the expression of these traits.

Genetic, phenotypic and environmental correlations between yield and biological yield were the highest and positive followed by between number of pods per plant and biological yield as well as between number of pods per plant and seed yield. These correlations suggested that the genes conditioning seed yield, biological yield and number of pods per plant were closely linked in coupling phase and the traits respond similarly to the environment (Scully ***et al.*** 1991).

Seed yield was positively associated with biomass yield, harvest index, number of seeds per pod, number of pods per plant, plant height, stem diameter, number of nodes on the main stem, days to flowering and days to maturity at the genotypic level, however it was negatively correlated with 100 seed weight, seed length and height, pod length, internode length and leaf dimensions. All the characters except seed height showed significant associations with seed yield irrespective of direction of correlations. The magnitude of associations ranged from low (0.14) with pod length to high (0.89) with biomass yield. In several correlation studies conducted, both number of pods per plant and number of seeds per pod have bean positively associated with bean yield (Atuahene-Amankwa and Michaels, 1997; Chand, 1999; Coimbra *et al.*, 1998; Coyne, 1968; Duarte and Adams, 1972; Nienhuis and Singh, 1986; Samal *et al.*, 1995), but seed weight is often negatively correlated with seed yield as well as with pods per plant and number of seeds per pod (Nienhuis and Singh, 1986; White and Gonzales, 1990; Vasic *et al.* 1997). However, Chand (1999) and Coimbra *et al.* (1998) reported a positive correlation of seed yield with 100

seed weight. Arya *et al.* (1999) reported a positive correlation of pods per plant with plant height and Leleji *et al.* (1972) observed a negative correlation of crude protein with pod per plant. Chand (1999), Nienhuis and Singh (1986) and Vasic *et al.* (1997) also reported positive correlation of seed yield with architectural traits (plant height, number of nodes on the main stem, etc.). Scully *et al.* (1991) reported strong positive association between seed yield and biomass yield, while positive association with harvest index and phenological traits were observed which is in agreement with the present result. This correlation suggested that the genes conditioning biomass and seed yield were closely linked in coupling phase and these traits respond similarly to the environment. The authors also noted low positive correlation of seed yield with harvest index and moderately positive with that of phenological traits, while Welsh *et al.* (1995) observed a positive correlation of seed yield with days to maturity. However, Zimmerman *et al.* (1984) reported a positively high and significant correlation between seed yield and harvest index in intercrop. Adams (1982) reported a positive association between seed yield and number of nodes on the main stem, but they observed negative correlation between this character and 100-seed weight. Seed yield is also negatively correlated with crude protein (Leleji *et al.*, 1972; Kelly and Bliss, 1975). Since branch growth seems more affected by environmental conditions, the number of main stem nodes might be a more reliable selection criterion.

Correlations of 100-seed weight with seed yield components and other plant traits are important for breeding work. 100-seed weight had low to very high negative correlations with plant height, number of nodes on the main stem, stem diameter, phenological traits and yield components. However, it had moderate to very high positive correlations with leaf dimensions, internode

length, pod length and seed traits. The present result is in agreement with the results obtained by Vasic *et al.* (1997). Zeven *et al.* (1999) also reported a similar result for the correlations observed between 100-seed weight and seed traits. Leaf size and internode length were the other traits, which are positively associated with 100-seed weight. The result obtained by Duarte and Adams (1972) and Denis and Adams (1978) confirmed the present result for leaf size. However, Adams (1982) reported internode length as an important trait, which is positively associated both with seed yield and 100-seed weight. The other character that exhibited a very weak and negative association with seed yield, but highly and positively correlated with 100-seed weight was pod length. Similar result to this was reported by Zeven *et al.* (1999) and Samal *et al.* (1995). However; pod length is one of the main yield components in French bean.

6.2.2. Path Coefficient Analysis

Simple correlation does not consider the complex relationships between the various traits related the dependent variable (Mebrahtu *et al.*, 1991). Correlation coefficients show relationships among independent variables and the linear relationship between these variables. But it is not sufficient to describe these relationships when the causal relationship among variables is needed. It has been suggested that yield components have either a direct or an indirect effect on seed yield, or both. Therefore, it was essential to determine the effects of yield components on seed yield. Consequently, path coefficient analysis is the most common statistical method used for this purpose. Thus, it is possible to calculate both direct and indirect effects of yield components on seed yield through the other components.

Days to flowering had a moderately positive correlation with seed yield but had very low positive direct effect. The positive correlations were due to the moderate positive indirect effects via number of pods per plant and number of seeds per pod. Similarly, days to maturity had positive association with seed yield, but its direct effect was also positive and very low. The positive

association was entirely due to the positive indirect effects through number of pods per plant and number of seeds per pod. Both of these phenological traits contributed negative indirect effects through 100-seed weight. Raffi and Nath (2004) reported a positive non-significant direct effect by days to flowering while Babar *et al.* (2002) observed a positive and significant direct effect for days to flowering. Both of the authors reported a negative direct effect of days to maturity on seed yield.

Plant height and number of nodes on the main stem had moderately positive correlations with seed yield but produce positively low direct effects to seed yield. These developmental traits had a high positive indirect effect through number of pods per plant, for both the traits and through number of seeds per pod for number of nodes on the main stem, too. Number of nodes on the main stem also had negative indirect effect through 100-seed weight. Babar *et al.* (2002) and Raffi and Nath (2004) reported similar result for plant height. The negative indirect effects through seed size may take place because plant height and number of nodes on the main stem indirectly facilitates pod formation, thereby increasing the total number of seeds per plant of smaller size, as the number of seeds is negatively associated with seed size. The total food material synthesized and transported to the seeds in a plant, distributed in case of more pods per plant resulting in smaller seed size (Singh *et al.*, 1985). Vasic *et al.* (1997) also noted the correlation of plant height with seed yield via the number of pods per plant and number of seeds per pod. These results put a clear indication that the yield components are mutually and very closely associated.

Pod length had low negative association with seed yield through its low positive direct effect on seed yield. The high positive indirect effect via 100-seed weight was nullified by the negative indirect effects through number of pods per plant and number of seeds per pod. Singh *et al.* (1985) reported similar result to the present study in pea.

The number of seeds per pod, which had moderate association with seed yield, also exhibited high and positive direct effect on seed yield. The moderate association was due to high negative indirect effect through 100-seed weight (0.56) and moderately positive indirect effect via number of pods per plant (0.36). Thus, number of seeds per pod affected seed yield both directly and

indirectly. Raffi and Nath (2004) reported similar result to the present study; on the contrary Duarte and Adams (1972) observed a high positive direct effect of this trait on seed yield.

Harvest index directly affected seed yield with low positive correlation of 0.13. Considering indirect effects via yield contributing traits, it had low and comparable effect with direct effect via 100-seed weight. The present result is in agreement with the results reported by Singh ***et al.*** (1985) in pea crop. Protein content had very low direct and indirect effects on seed yield, in addition to its non-significant association with seed yield.

The main yield components in common bean are number of pods per plant, number of seeds per pod and 100-seed weight (Duarte and Adams, 1972; Raffi and Nath, 2004; Sarafi, 1978). In the present set of materials, number of pods per plant had high positive correlation and the highest direct effect to seed yield while low negative correlation with high direct effect was found for 100-seed weight. In addition to this, developmental and phenological traits; namely, pod length, internode length, plant height, number of nodes on the main stem, days to flowering and days to maturity ultimately contributed through number of pods per plant, 100-seed weight and in the number of seeds per pod. From these results, number of pods per plant, 100-seed weight and number of seeds per pod might serve as the main contributing traits of yield in common bean. Similar conclusion was reached to the present result by Singh ***et al.*** (1985) in pea crop. Raffi and Nath (2004) and Duarte and Adams (1972) also reported similar results for yield component traits (number of pods per plant, 100-seed weight and number of seeds per pod) in common bean.

Most yield contributing characters acted through number of pods per plant and some through 100-seed weight or number of seeds per pod or through all these component traits. More emphasis should be given to these traits during selection. While selecting high yielding genotypes, a compromise must be worked out so that another does not nullify the advance in a component trait. Protein content is inversely related to seed yield at low correlation coefficient values. The direct and indirect effects of protein content on seed yield were also negligible. Although a negative correlation generally existed between yield and crude protein percentage in dry beans, enough variation occurred to select plants that combined relatively high yields with relatively high percent protein. Thus both yield and protein content might be increased

simultaneously. However to achieve high total protein, increased yield appears to have greater potential for success.

6.3. Genetic Divergence analysis through Multivariate Techniques

The development of new varieties is mainly governed by the magnitude of genetic variability in the base material and extent of variability for the desired characters. Genetically diverse parents are likely to produce high heterotic effects and desirable segregants. Several measures of genetic distance have been proposed so far of which Mahalanobis generalized distance is a powerful tool to measure genetic divergence within a set of genotypes. Mahalanobis D^2 considers the variation produced by any character and the consequent effect that it bears on the other character. This statistical tool has been employed widely to resolve genetic divergence at inter-varietal and sub-species level in classifying crop plants (Rao, 1960). This is possible by clustering the genotypes based on D^2 values, as it represents the index of genetic diversity among genotypes and clusters.

The genetic dissimilarity measurement using generalized Mahalanobis distance (D^2) indicated that the genotypes with greater dissimilarity were FOT-65 and EAP-4, because they showed the maximum combination value that is 818.82. FOT-65 belongs to the Andean, while EAP-4 is belongs to the Mesoamerican origin. Genotypes UTT-28-175 and CAP-4 were the most similar.

6.3.1. Clustering genotypes

Based on the D^2 value, the 144-germplasm accessions of common bean were grouped into 9 clusters. As indicated in (Table 7), it is essential to note that out of 144 germplasm accessions introduced from 14 different countries, 40

germplasm accessions representing 8 countries were grouped in the same cluster, cluster I. The trend was repeated in almost all the clusters except the monogenotypic cluster, IX. Genotypes introduced from the same country have been grouped in different clusters. For instance, genotypes introduced from USA were grouped in 6 of the 9 clusters formed. This is an indication for the absence of relationship between genetic diversity and geographic diversity. Earlier workers have discussed genetic drift; selection pressure and environment could cause greater diversity than geographic distance (Bhatt, 1970; Murthy and Arunchalm, 1966). The results reported in this paper are also in agreement to these findings. Similarly, Malhotra *et al.* (1973) and Singh *et al.* (1997) observed no relationship between geographic diversity and genetic distance.

The results presented by Tochers method demonstrated that the most divergent, FOT-65 and EAP-4 were placed in clusters V and VI, respectively, and the most similar UTT-28-175 and CAP-4 in the same cluster I. Clusters I, II and VI contained genotypes from Mesoamerican origin, whereas clusters IV, V, VII and VIII only possessed genotypes of Andean origin. However, those grouped in cluster III are intermediary. The present result is in agreement with the results obtained by Barelli *et al.* (2005), Johns *et al.* (1997) and Duarte *et al.* (1999). McClean et al. (1993) also reported three major groups from 16 identified clusters in North American commercial dry bean cultivars.

The clustering process also formed a monogenotypic cluster. This may be associated with intensive natural and human selection for diverse adaptive gene complexes. The impact of human selection in genetic divergence can

further be substantiated by the formation of cluster III. Genotypes grouped in this cluster combined useful traits and selected for their medium plant height, medium seed size, upright growth habit and high harvest index, which made them distinct from other germplasm accessions. The general description of each of the clusters in this classification is as follows.

Genotypes of cluster I is characterized by indeterminate erect growth habit II with relatively short internode length and node numbers ranging from 13 to 17. Plant height varies between 50 and 70cm with small terminal guide. Leaf size is small to intermediate and the pod length is less than 10cm. Beebe *et al.* (1995) and Beebe *et al.* (2000) grouped these types of Central American landraces as sub-race M_1 in a Race Mesoamerican (M).

Genotypes of cluster II are characterized by small-seeded cultivars of diverse seed colors (white, pink, cream, red, black, gray as well as mottled seed types). Most of the accessions are of growth habit II, though some type III are included. Their plant height varies between 60 and 70cm and the node number on the main stem ranged from 13 to 20. The internodes are small to medium in length and pod set is concentrated in the basal nodes. Pod length and seed number per pod are similar with that of genotypes in cluster I. Genotypes included in this cluster have high number of pods per plant and they are high yielder as compared to genotypes in cluster I. Beebe *et al.* (2000) classified these types of landraces as sub-race M_2 in Race Mesoamerican (M), while Singh (1989) grouped them in the Middle American center as *gene pool 3*.

Genotypes included in cluster III are of diverse types. It comprises genotypes of growth habit I, II and III. They have medium plant height and upright growth with medium leaf and seed size. They have high harvest index compared to the genotypes in the other clusters. However, genotypes included in cluster IV and V are characterized by determinate growth habit I of medium and large seeds mostly kidney, cylindrical and somewhat rectangular shapes. The number of internodes varies from 6 to 8 and leaves are often very large. Their stem contains 2-3 long internodes and pods are long with 4 to 5 seeds. The observed difference between the

genotypes in the two clusters lay on their number of pods, yielding ability and flowering days. Singh (1989) and Singh *et al.* (1991a) grouped these types of germplasms as gene pool 7 and Race Nueva Granada (N), respectively, in the South American Center.

Genotypes clustered in cluster VI are characterized by indeterminate growth habit III with small elongated leaves, short internodes, medium sized pods and round to oval seeds (3-5 per pod). Fruiting is sparse and along the length of stems and branches and they are prostrate. Singh (1989) and Singh *et al.* (1991a) classified these types as *gene pool 9* and Race Chile (C), respectively, in the South American Center. Whereas genotypes included in cluster VII and VIII are characterized by type II and III growth habits of medium and large seeds of mostly elongated kidney and cylindrical shapes. The number of nodes on the main stem varies from 12 to 15 and has long internodes. Leaves are large and pods are long. The difference in the two clusters is in yielding ability, in harvest index, biological yield, etc. Singh (1989) classified these types as *gene pool 8* in the South American Center.

Cluster IX with a solitary genotype, can be characterized by small seeds, indeterminate growth habit II, short plant height (less than 50cm), short pod length and 4 to 6 seeds per pod. Leaf size and internode lengths are small with node number varying 9 to11. Singh (1989) grouped such type in the Middle American center as *gene pool 1*.

Character-wise ranks have shown that no single character had a lion share to total divergence. However, protein content contributed (18.95%), the largest share to the divergence, followed by days to 50% flowering (16.60%), 100 seeds weight (10.50%), number of seeds/pod (10.45%), days to maturity (10.15%), plant height (8.15%), number of nodes on the main stem (6.95%) and pod length (5.39%). This could imply that the genotypes included in the study were divergent for most of the traits studied. This is clearly visible on (Table 6). It is clear that these characters are the basic attributes of plant architecture, which need greater attention, as they accounted for more than 85% of total divergence in the materials. In common bean, the present result is in accordance with the study conducted by (CIAT, 1979) in which plant height, 100-seed weight, nodes at maturity, seeds per pod, pods per plant and days to flowering were among the traits

contributing maximum to the total variability. Singh et al. (1991b) reported number of nodes on the main stem and 100-seed weight were among the major traits separating cultigens of Andean and Mesoamerican origin, whereas, Denis and Adams (1978) considered characters 100 seed weight, pod length, number of pods per plant and number of nodes on the main stem as a potent factor of divergence in dry beans. Hornakova ***et al.*** (2003) also observed plant height, 1000 seed weight, and days to flowering as a major contributing trait in the diversity assessment of Western and Eastern Carpathian common bean landraces. Malhotra ***et al.*** (1973) reported days to flowering and 100 seeds weight contribute more towards diversity in the green-gram divergence study. Arunchalam (1966) suggested that the most potent factors for divergence are also important for fitness under natural condition. Jaylal (1994) also reported carotene content, total chlorophyll, pods per cluster, branches per plant and seed yield per plant as the main contributing characters to the total divergence in soybean. Zeven ***et al.*** (1999) noted seed characteristics (weight, height and length), pod characteristics (height, length and colour), pods per plant, seeds per pod and flowering time as the main contributing trait for divergence.

6.3.2. Intra- and Inter- Cluster D^2

The inter-cluster distances were greater than intra-cluster distances, revealing considerable amount of genetic diversity among the genotypes studied (Table 8). Inter-cluster distance is the main criterion for selection of genotypes using D^2 analysis. 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 segregant (Sarma and Roy, 1994).

The maximum inter-cluster distance (68.15) was recorded between cluster VIII and cluster IX followed by the one between clusters VI and cluster IX (64.22) suggesting wide diversity among these groups. On the other hand, the minimum distance between clusters IV and V (5.52) and clusters I and II (5.91) indicated their close relationship.. Theoretically, crossing of genotypes belonging to the same cluster is not expected to generate superior hybrid or segregant, because genotypes grouped in the same cluster diverge little from one another. However, it is a general notion that the larger is the divergence between the genotypes, the higher will be the heterosis. In

this context, it is important to consider the practical significance of grouping the genotypes into different clusters and estimating the genetic distance between them, which represents an index of genetic diversity among clusters (Bhatt, 1970). It may be useful to produce crosses between genotypes belonging to the clusters separated by large estimated distances (Bhatt, 1970). Success might therefore be expected through making crosses between the genotypes from cluster VIII and cluster IX, followed by the one between clusters VI and cluster IX. Genotypes from these clusters can be selected for hybridization program that can evolve highly heterotic crosses, which might prove potential in isolating superior segregants. However in selecting parental material, important characteristics such as pest and disease resistance, quality of produce, stability of performance and cross compatibility should also be considered (Bhatt, 1970). Ghaderi et al. (1984) observed correlations between heterotic effects for yield; number of pods per plant, and number of seeds per pod and parental distance, which were positive and highly significant in dry edible bean. They also reported heterosis for plant height, number of pods/plant; nodes with more than one pod/plant and pod bearing stems were positively associated with D^2 in faba bean.

Arunchalam (1981) and Ghaderi et al. (1984) indicated that too high a divergence might not produce the highest frequency of heterotic crosses. Parents chosen to be genetically divergent through D^2 analysis can fail at times, to show higher gene frequency difference. According to Falconer and Mckay (1996) heterosis is a direct function of the square of gene frequency difference between parent population and their dominance effect. Internal cancellation of dominance effect due to its direction or its modification by additive X additive gene interaction, hence, can reduce the heterosis to be realized in the presence of sufficient genetic divergence.

6.2.3. Cluster Mean Analysis

Cluster means revealed appreciable variation for various characters (Table 10). The differences were more conspicuous for seed yield and biological yield per plant, harvest index, number of pods per plant, 100-seed weight and plant height. A close look into the cluster means revealed that clusters differ in respect of different characters. Cluster VI containing the thirteen genotypes recorded the highest seed yield, biological yield, plant height and they are late in maturity. Cluster II observed the second highest seed and biological yield per plant, while it recorded the highest pods per plant and seeds per pod. Genotypes in this cluster also observed the lowest mean

protein content. Cluster III recorded the highest harvest index, while cluster VIII showed the lowest value. Cluster IX yielded the minimum seed yield and gave the lowest 100-seed weight. This cluster also showed the shortest internode length, pod length and plant height. Genotypes in clusters II and VI are late in maturity and high yielding, whereas genotypes grouped in clusters III and V are good yielding and early in flowering and maturity. Cluster III recorded relatively average (optimum) values for all of the traits considered except harvest index that was the maximum value among the clusters. In general, the present study revealed that considerable genetic diversity is present among the entries for yield and its attributes. Six clusters were superior: clusters II and VI for seed yield and biological yield, cluster III for harvest index and most of the traits, cluster II for number of pods per plant and number of seeds per pod, clusters V and VIII for 100-seeds weight and pod length and cluster IX for protein content and earliness. Singh *et al.* (1997) reported the importance of cluster mean of a character within the different clusters and its significance for improvement, which is in agreement with the present result. Intercrossing between genotypes of these diverse clusters would generate a broad spectrum of variability for effective selection in the segregating generations for the development of high yielding cultivars.

Here, it is important to note that in calculating cluster mean, the superiority of a particular genotype with respect to a given character can be diluted by other genotypes that are related and grouped in the same cluster which are inferior or intermediary for that character in question. Hence, apart selection of a line from the cluster, which has high inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence with respect to a character of interest. In other words, if a breeders intention were to improve the number of pods per plant, he would select parents that are highly divergent with respect to this character.

VII. Conclusion

One hundred and forty four genotypes of common bean (*Phaseolus vulgaris L*) were evaluated in a triple lattice design for 18 quantitative traits to elucidate information on the nature and magnitude of genetic variability and the degree of genetic divergence. The experiment was carried out during the off-season, February to June 2005, at the research farms of Nazareth Agricultural Research Center (NARC) of Ethiopian Institute of Agricultural Research (EIRO).

The pooled analysis of variance for all the 144 genotypes revealed significant difference among genotypes for all the 18 quantitative characters studied. The value of PCV was greater than GCV with respect to all characters. PCV and GCV values were observed to be higher for plant height, nodes on the main stem, number of pods per plant, 100-seed weight and internode length, but the value of PCV and GCV were higher and intermediate for biological and seed yield, respectively. Number of seeds per pod and dry seed length recorded moderate PCV and GCV values. The observed values for harvest index stem diameter, leaf dimensions, dry seed length, protein content, days to flowering and days to maturity were low.

Broad sense heritability ranged from 24.50% (for seed yield per plant) to 95.2% (for protein content). Low estimates of heritability were observed for seed yield, biological yield, stem diameter and leaf dimensions, whereas 100-seeds weight, dry seed length, dry seed height, plant height, nodes on the main stem, protein content, days to 50% flowering and Days to 90% maturity showed higher heritability estimate. The remaining traits showed moderate values.

Plant height, number of nodes on the main stem and 100-seed weight showed higher heritability estimates coupled with high genetic advance. This indicates that the traits are mainly governed by additive gene action, and hence are responsive to phenotypic selection. High heritability and moderate genetic advance was observed for dry seed length, dry seed height and days to flowering indicating both additive and non-additive gene actions are responsible for their expression. Number of pods per plant, seeds per pod, pod length and internode length had moderate heritability and moderate genetic advance suggesting the prevalence of non-additive gene action in the expression of the traits.

Except for biological yield, harvest index, number of pods per plant and number of seeds per pod genotypic correlation coefficients were higher than phenotypic correlation coefficients. Seed yield had significant positive correlations with biological yield, harvest index, number of pods per plant, number of seeds per pod, plant height, stem diameter, number of nodes on the main stem, days to flowering and days to maturity both at phenotypic and genotypic level. Correlations between seed yield and 100-seed weight, dry seed length, pod length, internode length, leaf dimensions and protein content were negative but significant at genotypic level. Seed yield showed no correlation with dry seed height. Phenotypic path analysis for seed yield indicated that number of pods per plant; 100-seed weight and number of seeds per pod have high positive direct effect on seed yield, accordingly. These three traits were also the main characters through which other contributing traits influence seed yield.

Significant diversity was observed among the common bean accessions studied. The D^2 analysis is useful in computing the combined measure of variation and identifying the most influential

traits associated with variation among genotypes. The most influential traits in this study are percentage protein content, DTF, 100-seed weight, DTM, seeds per pod, plant height, number of nodes, pods per plant and pod length. Additionally, the use of cluster analysis is successful in differentiating the accessions into similar groups on the basis of morphological and agronomic traits. The characterization of the variation of these traits among the accessions that will permit plant breeders to focus on particular traits that are linked to accession variation and to discern traits that are not close indicators of accession variability.

The D^2 value ranged from 4.13 to 818.82 in a 10296 combinations of the 144 genotypes. Genotypes UTT 28-175 and CAP-4 showed the smallest, while genotypes FOT-65 and EAP-4 showed the highest genetic distance. Grouping the genotypes into cluster using Tocher's method resulted in the formation of 9 clusters. Cluster I had the maximum genotypes among the clusters, while cluster IX contained a single genotype. Inter-cluster distance (D^2) ranged from 5.52 between cluster IV and V to 68.15 between clusters VIII and IX. The clusters mean analyses enabled to classify the cluster, into early and late flowering, early and late maturing, low and high yielding, and etc. types. Cluster VI followed by cluster II were the highest yielding and pod bearing clusters found in the grouping process.

VIII. Recommendation

It is essential to determine how the influential traits lead to an improved common bean cultivar. The future breeding program utilizing the studied accession should be based on the genetic analysis of various tarts and hybridization carried out between clusters rather than within clusters

The present investigation showed significant variation between genotypes for the traits considered. Improvement in seed yield could be achieved by direct or indirect selection for high yielding genotypes or for yield components positively associated to yield. The inter-crossing of genotypes showing greater genetic divergence should result in superior heterotic crosses and also, generate valuable segregant in later generations. It is expected that better

performing varieties could be generated to increase productivity in common bean substantially.

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X. Appendices

Appendix 1. List of germplasm accessions and their country of origin

No	Germplasm	Country of Origin	No	Germplasm	Country of Origin
1	WU3 94-9	Mexico	37	BRB 222	Brazil
2	HAL-5	Chile	38	A-804	Brazil
3	EAP-233	Colombia	39	CARIOCA PITICO	Brazil
4	PAC-29	Mexico	40	EAP-506	Colombia
5	DRESDEN	USA	41	FEB-208	Colombia
6	UTT 28-175	Guatemala	42	H-92	Burundi
7	STT 165-92	Guatemala	43	PEROLA	USA
8	ACC No 1207	Honduras	44	RH-31-04	Chile
9	STARLIGHT	USA	45	ROBA-1	Brazil
10	ALPINE	USA	46	BAYO MOCHICA	Chile
11	OMAR V	Ethiopia	47	AN-9021455	Chile
12	AURORA	USA	48	L-306003	Brazil
13	LE-93-7	Mexico	49	LM-93204487	Brazil
14	ABRITUS	USA	50	91: 360P	Brazil
15	G 92317	Mexico	51	AZTEC	USA
16	AFR-733	Colombia	52	BELDAKMI RR-5	Colombia
17	PI 415965	Peru	53	CO-57914	Colombia
18	CIFEM 91117	Peru	54	EARLY RAY	USA
19	ENVOY	USA	55	MAVERIC	USA
20	SEQ-44	Guatemala	56	PINTO 89	Chile
21	GALBANDE-MOLD	Guatemala	57	CARIOCA	Brazil
22	GRYPHON	USA	58	TAYLOR	USA
23	SK 93263	Colombia	59	CHASE	USA
24	AWASH MELKA	USA	60	BAYO ZACATECAS	Chile
25	TY-3396-1	Chile	61	GARBANCILLOS ZARCO	Mexico
26	AFR-689	Chile	62	BAYO MADERO	Chile
27	VAX-1	Mexico	63	CAP-4	Brazil
28	VAX-2	Mexico	64	SEQ-1037	Chile
29	PINTO VILLA	Mexico	65	FOT-52	Colombia
30	MX-8385-14T	Mexico	66	FOI-15	Colombia
31	HATTON	USA	67	ATNDABA	Brazil
32	G 22005	Mexico	68	RAB 585	Colombia
33	A-197	Colombia	69	DOR 526	Guatemala
34	M/LKK 26	Malawi	70	CIFAC 87110	Peru
35	BAYO 400	Chile	71	RAZ 54	Brazil
36	MX 8729-5-A	Mexico	72	RAB 484	Colombia

Appendix 1. Continued …….

No	Germplasm	Country of Origin	No	Germplasm	Country of Origin
73	ANT-22	Colombia	109	GOBERASHA	Colombia
74	SEQ-1019	Chile	110	DRK-142	USA
75	AFR-630	Chile	111	BRB 232	Peru
76	SEQ-1031	Chile	112	511CIFAC 91135	Peru
77	UCR-5	USA	113	531MX9065-9T	Mexico
78	DRK-140	USA	114	PARAGACHI-Y	Peru
79	XAN-310	Colombia	115	519CIFAC 91148	Peru
80	DOR 716	Guatemala	116	CIFAC 91147	Peru
81	HORIZON	USA	117	EAP-4	Peru
82	ROSADO	Colombia	118	559 FIN-11	Peru
83	URIBE	Ecuador	119	LM-93203224	Brazil
84	DICTA 100	Honduras	120	547SEQ 1019	Chile
85	DOR 799	Guatemala	121	FOT-62	Chile
86	DIMTU	Guatemala	122	COPINHA	Brazil
87	PARAGACHI	Peru	123	55012	Costa Rica
88	9356-26	Costa Rica	124	L 94C 356 LE	Costa Rica
89	VAX-3	Mexico	125	FOXFIRE	USA
90	CALIMA	Colombia	126	FIN-10	Peru
91	POMPADUR-G	Dominican Rep.	127	FM-M-38-1	Peru
92	CHOCHO	Dominican Rep.	128	FM 94043	Peru
93	FOT-65	Colombia	129	848AFR-726	Chile
94	OBO-A-074	Peru	130	CIFAC 91140	Peru
95	NAZ	Peru	131	850AFR-737	Peru
96	I-77	Venezuela	132	FM 94010	Peru
97	EAP-10-88	Honduras	133	I-66	Venezuela
98	CAL-182	Colombia	134	RIO TIBAGI	Brazil
99	UCR-3	USA	135	BLACG HAWK	Brazil
100	EAP-12-88	Honduras	136	51-1-1-1	Costa Rica
101	MD-30-18	Honduras	137	AN-9021337	Brazil
102	BRB 205	Peru	138	CB-9021806	Brazil
103	LR-93201343	Brazil	139	G 21212	Mexico
104	764 FOI-20	Colombia	140	ICTA OSTUA	Guatemala
105	630ESLEC	Colombia	141	ICB-67	Guatemala
106	AND 1090	Colombia	142	ICTA JU 95-113	Guatemala
107	ICTA JU-95-4	Guatemala	143	TLP-20	Costa Rica
108	ARS-R-93001	Colombia	144	BLACK DESSIE	Ethiopia

Appendix 2. Climatic Conditions of the study area in 2005 crop season.

Month	Rainfall (mm)	Maximum T^0 (^{0}C)	Minimum T^0 (^{0}C)	Relative Humidity (%)	Soil T^0 at 20cm (^{0}C)	Latitude	Longitude	Altitude	Soil Type
January	18.2	28.1	11.8	49	25.6	8o24'	39o21'	1550m	Sandy Loam
February	2.4	31.0	13.1	40	27.0				
March	84.5	30.7	15.6	49	28.1				
April	99.3	31.9	15.0	46	28.7				
May	90.6	-	15.8	62	26.9				
June	74.3	-	16.9	53	27.9				
July	112.4	-	16.5	64	24.9				
August	229.5	27.2	16.1	65	25.6				
September	126.1	27.9	15.5	68	25.7				
October	3.8	29.5	11.9	43	26.9				
November	9.4	28.7	11.3	39	26.9				
December	0	27.9	8.1	38	24.0				

Appendix 3. Agronomic and morphological traits used for bean germplasm characterization

	Traits (variables)	How measured	Character unit
1	Seed yield	Average seed yield of five plants	Grams per plant
2	Biological yield	Average biomass yield of five plants	Grams per plant
3	Harvest index	Ratio of seed yield to biological Yield	
4	Plant height	Length of the main stem	Centimeter
5	Days to 50% flowering	No of days 50% plants had at least one flower	Number
6	Days to 90% maturity	No of days 90% plants in a plot reach maturity	Number
7	Nodes at maturity	No of nodes on the main stem	Number
8	Internode length	Average length of internodes on the main stem	Centimeter
9	Length and width of the central trifoliolate leaf	Average length and width of the central trifoliolate leaf from five plants	Centimeter
10	Stem diameter	Diameter between the cotyledonary and primary leaf	Millimeter
12	Pods per plant	Total number of pods on the main-stem and the branches	Number
13	Pod length	Average length of 15 pods per five plants	Number
14	Seeds per pod	Average No of seeds/30pods/5plants	Number
15	100 seed weight	Average weight of 100 seeds erom five plants	Grams/100seeds
16	Seed length and height	Average length and height of 15 seeds per 5 plants	Millimeter
17	Protein content		Percentage

Appendix 3. Genotypes that showed the lowest and highest values for each of the 18 characters

Characters	Genotype name/Accession number	
	With the lowest value	With the highest value
Seed yield/plant	CIFEM91117, FOT-52, BRB232	EAP-4, 531MX 9065-9T, Paragachi-Y
Biological yield/plant	FOT-52, FOI-15, BRB232, SK93263	EAP-4, 511CIFAC91135, Paragachi-Y
Harvest index	CIFEM91117, OBO-A-074, AND1090	55012, L94C356LE, G22005, 91:360P
Pods per plant	FOT-52, FOI-15, DRK-140, 630ESLEC	Blackdessie, AURORA, RioTibagi
Seeds/pod	CIFEM91117, 848AFR-726, FOT-65	EAP-10-88, Blackhawk, RAZ-54, AURORA
100 seed weight	AURORA, GRYPHON, DRESDEN	764 FOI-20, SEQ-1031, FOT-52
Seed length	ENVOY, GRYPHON, AURORA	630ESLEC, FOT-52, HORIZON
Seed height	EAP-10-88, AURORA, I-77	630ESLEC, Bayozacatecas, Bayomadero
Pod length	ENVOY, GRYPHON, URIBE	FOXFIRE, FIN-10, 547SEQ1019, HORIZON
Plant height	SK93263, Hal-5, BRB232	CIFEM91117, MX-8385-14T, Paragachi-Y
Stem diameter	Pintovilla, Bayozacatecas, NAZ	RioTibagi, I-66, DIMTU.
Interned length	G21212, ICTAOSTUA, Blackdessie	Paragachi, Pompadure-G, FOT-65
Nodes	Hal-5, I-77, 764FOI-20	CIFEM91117, Paragachi, I-66
Leaf length	Garbancilloszarco, HATTON, G22005	AFR-733, I-77, FOXFIRE
Leaf width	G22005, Garbancillozarco, CB-9021806	AFR-733, I-77, FOXFIRE
Days to flowering	BRB205, Garbancilloszarco, 764FOI-20	AFR-689, EAP-4, VAX-2
Days to maturity	ENVOY, SK93263, L94C356LE	AND1090, LM93203224, Paragachi-Y
Protein content	XAN-310, VAX-3, I-77	EAP-4, 559 FIN-11, ENVOY