# GENETIC VARIABILITY AND PATH COEFFICIENT ANALYSIS FOR YIELD AND YIELD RELATED TRAITS IN COMMON BEAN (*Phaseolus vulgaris* L.) ACCESSIONS AT HARAMAYA UNIVERSITY, EAST HARARGE, ETHIOPIA.

**MSc THESIS**

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**JUNE 2015**

**HARAMAYA UNIVERSITY, HARAMAYA**

# Genetic Variability and Path Coefficient Analysis for Yield and Yield Related Traits in Commons Bean (*Phaseolus vulgaris* L.) Accessions at Haramaya University, East Hararge, Ethiopia.

**A Thesis Submitted to the Department of Biology, College of Natural and Computational Sciences, School of Graduate Studies**

**HARAMAYA UNIVERSITY**

**In Partial Fulfillment of the Requirements for the Degree of Master of Science in Genetics**

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**JUNE 2015**
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**HARAMAYA UNIVERSITY**

**SCHOOL OF GRADUATE STUDIES**

As thesis advisors, we hereby certify that we have read and evaluated this Thesis entitled "**Genetic variability and Path Coefficient Analysis for Yield and Yield Related Traits in Common Bean (*Phaseolus vulgaris L.*) Accession at Haramaya University, East Hararge, Ethiopia"**

prepared under our guidance by Berecha Gutu. We recommend that it can be submitted as fulfilling of the thesis requirement

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As members of the Examining Board of the Final MSc. Open Defense examination, we certify that we have read and evaluated the thesis prepared by: Berecha Gutu and examine the candidate. We recommend that the thesis be accepted as it fulfills the requirement for the degree of Master of Science in Biology (Genetics).

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# DEDICATION

I dedicated this thesis manuscript to my father Gutu Regasa for his love, affection and unrestricted encouragement he offered me not only in accomplishing this research, but also for every success in my life.

## STATEMENT OF THE AUTHOR

By my signature below, I declare and affirm that this thesis is my own work I have followed all ethical and technical principle of schoolship in the preparation, data collection, data analysis and compilation of this thesis. Any scholarly matter that is included in the thesis has been given recognition through citation.

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# LIST OF ACRONYMS AND ABBREVIATIONS

| | |
|---|---|
| AMOVA | Analysis of molecular variance |
| ANOVA | Analysis of variance |
| CIAT | Centro International de Agricultural Tropical |
| CSA | Central Statistical Authority |
| GA | Genetic advance |
| GVC | Genotypic coefficient of variation |
| H | Heritability in Broad Sense |
| MARC | Melkasa Agricultural Research Center |
| MDS | Multi-Dimensional scale |
| PC | Principal Component |
| PCV | Phenotypic Coefficient of Variation |
| RAPD | Random amplified polymorphic DNA |
| UPGMA | Unweighted Pair Group Method with Arithmetic Mean |

# BIOGRAPHICAL SKETCH

The author was born in August, 1986 in Ambo town, Oromia Regional State. He attended his elementary and junior education at Goro Sole Elementary School, western Shewa, Ambo. Then he pursued secondary school education at Ambo Preparatory and comprehensive Senior Secondary School. After completing high school in year 2006, he joined Jimma University and graduated with B.ED degree in Biology in year 2008. Then the author was employed in Addis Ababa, Education Bureau in Akaki kality sub city at Fitawurari Abayneh metekia Secondary and preparatory School as Biology teacher and has worked for five years. He joined the School of Graduate Studies of Haramaya University in 2012 to pursue M.Sc. studies in Genetics as a self-sponsor.

# ACKNOWLEDGMENTS

I wish to acknowledge both of my advisors **Dr**. **Yohannes Petros** and **Dr. Meseret Chimdessa** for their helpful guidance, wisdom, experience, hard work and inspiration throughout my entire graduate studies and for providing me wonderful opportunity to study under their kind supervision and for their invaluable critical comments and patiently assisting me in various aspects of this thesis work from the very beginning of the proposal development. Their advice and suggestions greatly helped me in analyzing and interpreting the experimental data of my thesis, without their contributions this work would have been much less comprehensive.

I express my special thanks to Haramaya University, plant science department who provided me with plot of land, materials and other services acquisition during conduct the experiment.

I am obliged to extend my deepest gratitude to **Dr Habtamu Zelleke** who provided me with plot of land to conduct the experiment and helped me during plantation as my advisor.

I would like to express my appreciation and thanks to Melkasa Agricultural Research Center for providing me with germplasm to conduct the experiment.

Last, but not least, I want to express my deepest gratitude to my entire family members for their affection unreserved encouragement, inspiration and support throughout this research work

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## *ABSTRACT*

*Studying genetic variability in crop plants is important for improving the crops and enhancing production. Therefore, an experiment was conducted at Haramaya University's Research farm in main campus at Rare research site to assess the genetic variability and association among characters in twenty three common bean accessions and two varieties common bean and their contribution to yield. The experiment was laid out as simple lattice design with twenty five common bean genotypes planted in two replication. Data were collected on 13 quantitative characters including plant height, number of node on the main stem, internode length, number of pods per plant, pod length, number of seeds per pod, days to 50% flowering, days to 90% maturity, seed yield per plant, seed yield per plots, biological yield, harvest index and 100%seed weighted. High genotypic coefficients of variation (GCV) were observed for number of seeds per pod, number of nodes on the main stem and internode length. Heritability estimates ranged from 5.0% for number of pods per plant to 91.4% for harvest index. Genetic advance as percent of mean ranged from 1.26% for biological yield to 23.7% for number of seeds per pod. At phenotypic level, number of pods per plant exhibited positive and highly significant ($p \leq 0.01$) correlation with seed yield per plot. At the genotypic level, number of node on the main stem, seed yield per plot had positive and highly significant ($p \leq 0.01$) correlation with number of pods per plant. The maximum positive phenotypic direct effects on seed yield were observed in number of pods per plant and days to 50% flowering with the values 0.605 and 0.489 respectively. In conclusion, the result of this study demonstrated that there is sufficient genetic variability among the common bean genotypes and a number of characters were found to have high broad sense heritability, which could be used to improve the yield and other agronomic characters of the crops through selection or breeding. Inter-cluster distance ($D^2$) ranged from 34.09between cluster IV and I to 415.39 between clusters IV and II. Genotypes with maximum inter-cluster distances are genetically more divergent.*

***Key words**: Cluster, Correlation, GCV, Genetic advance, Heritability, PCV*

# 1. INTRODUCTION

All species of the genus of common beans (*Phaseolus vulgaris*) are diploid and most have 22 chromosomes (2n =22). A few species show an aneuploidy reduction to 20 chromosomes. The genome of common bean is one of the smallest in the legume family at 625 Mbp per haploid genome. The genus *Phaseolus* contains some 50 wild-growing species distributed only in the American. Asian *Phaseolus* have been reclassified as *Vigna* (McLean *et al*., 2008). These species represent a wide range of life histories (annual to perennial), growth habits (bush to climbing), reproductive systems, and adaptations (from cool to warm and dry to wet). The genus also contains five domesticated species. Common bean belongs to family Fabaceae. Common bean 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 particularly central Mexico is the leading common bean production in the world (Binam *et al.*, 2003).

The common bean is cultivated primarily for its dry seeds, green pods (as in snap beans), and green-shelled seed and in some tropical areas, bean leaves are cooked eaten like spinach and young leaves used in salads. Dried beans that do not meet human food quality standards are used as feed for livestock. Post-harvest plant remains are also used as feed for domesticated animals and Young tender leaves and flowers are also used as fresh vegetables in some Central and Eastern African, and in Latin America countries (Broughton *et al*., 2003).

Common bean is a major legume crop with significant nutritional importance. It is a major source of calories and protein source in many developing countries throughout the world (ADA, 2004). Common bean is a rich source of zinc and iron, two micronutrients depleted from individuals with AIDS (Buys *et al*., 2002). Diets containing foods rich in these micronutrients are suggested to benefit the health status of HIV infected patients (ADA. 2004; Kruzich *et al*., 2004).

Common bean also contains a protein that inhibits the HIV-1 reverse transcriptase, these proteins known as Lectin (Wong *et al*., 2006). Collectively, these features support the importance of common bean as one of the many factors that can address the AIDs problem through improved nutrition **(**Rabia *et al*., 2013).

According to Amare (1987) most of the area lies in sub humid highlands and semi-arid zone in the Rift Valley and eastern regions. Common beans intercrop with maize, banana, sorghum, cassava and sweet potato due to its short duration of maturity 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 (Wortmann *et al*., 2004).

According to Safari (1978) 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 assess 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. $D^2$ 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 (Broughton *et al*., 2003).

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 worldwide 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).

Common bean in Ethiopia is produced in almost all the regional states with varying intensity. Production is concentrated in two regions: Oromiya and the Southern National Nationality Peoples region (SNNPR), which account for about 75 percent of the total national production. The remaining 25 percent comes from Afar, Amhara, Tigray, Somali, Gambella and Benishangul-Gumuz (Legesse *et al*., 2006). Two use groups of common beans: white canning and coloured food type, are grown. The white beans dominate in the Oromiya region (North east rift valley), where more than 95 percent of farmers grow it and account for about 50 percent of total common bean production (Legesse *et al*., 2006)

According to Reed and Frankham (2001) characterization of genetic diversity of accessions can be achieved with phenotypic traits and molecular markers. Character 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. The situation can be attributed to a variety of reasons: the lack of tight linkage between molecular markers 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) (Delaney and Bliss, 1991a, 1991b; Van Trienderen *et al*., 2002) the authors 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 (Velasco *et al.*, 2007).

Plant breeding is essentially selection 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 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 (Raffi and Nath, 2004).

The knowledge of this relationship helps to identify traits on which selection can be based for the implement of yield. Furthermore, 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 (Buys *et al*., 2002).

The aim of this study to identify divergent genotypes that could be used as potential parents' in the future common bean breeding program.

**General Objectives**

- To assess the genetic variability and association among characters in common bean accession and their contribution to yield.

**Specific objectives**

- To determine the estimates of variability, Heritability and genetic advance in the common bean genotypes.
- To assess the extent of association of agronomic characters among themselves and with yield.
- To cluster common bean accession into genetically diverse groups.

# 2. LITERATURE REVIEW

## 2.1. Origin, Distribution and Genetic Diversity

Common bean originated in Latin America where its wild progenitor *(Phaseolus vulgaris*) has a wide distribution ranging from northern Mexico to northwestern Argentina. Large germplasm collections of domesticated and wild forms are located at CIAT, Cali, Colombia and USDA, Pullman, Washington, USA. The reference collection of Phaseolinae is located at the National Botanical Garden, Meise, Belgiumn. Common bean belong to native American traditionally grew bean with maize (corn) and squash (Gepts; 1998; NARO, 2000).

Genetic diversity refers to the variation of genes within populations/species, making it possible to develop new breeds of crop plants 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 humans through domestication and selection (CIAT, 2011).

CIAT (2011) study of genetic diversity is the process by which variation among 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 DNA-based marker data. As the closest crop relative to soybean, it is arguably the best diploid model for soybean. Extensive macrosynthentic relationships also exist between the species. These species also share a number of phenotypes that appear to be under the similar genetic control (Buys *et al*., 2002).

A careful reconstruction of the duplicated soybean genome relative to the common bean genome beyond the macro synthetic level could benefit both common bean and soybean by letting each take advantage of knowledge gained from the other species. Clearly a full genome sequence of common bean would accelerate the improvement of these two species. 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 (Broughton *et al.,* 2003).

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) introgression 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 (Mohammadi, and Prasanna, 2003).

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 determinate for climbing pole beans. However, no natural variability for them were 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 régimes. 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 landraces 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 Race Nueva Granda (N) represents the medium to large seeded accessions of bush growth habits, and includes the majority of the commercial large seeded cultivars in use today (Singh *et al.,* 1991a).

Race Nueva Granda (N) is the most widely cultivated Andean race, and is grown at both mid-attitudes of the Andeas and Africa, in warm lowland environment 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).

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 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 (McLean *et al.,* 1993).

McLean *et al.* (1993) Cluster analysis identified three major clusters, corresponding to the small (navy, small white and black), medium (pinto, 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 (Debouck, 1986).

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 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 (Singh *et al.,* 1991a)**.**

The integrity of red beans as distinct from black beans was conserved. These results suggest that selection for red seed color genes has resulted in the recovery of a sizeable portion of the red genome by different geographic origin using $D^2$ statistics. The analysis grouped the cultivars into 15 clusters, linkage drag (Singh *et al.,* 1997).

Singh *et al*. (1999) studied genetic divergence in 100 rice bean (*Vigna umbellate*) cultivars of the random distribution of cultivars into the different clusters indicated the weak relationship between genetic diversity and environmental variance mean high genetic diversity with low environmental variance.

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 (Johns, 1997).

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).

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, color 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, and 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 (Singh *et al*., 1999).

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 by (Beebe *et al*., 2000).

Beebe *et al.* (2000) DNA analysis 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 and resistance to diseases. Sub-race M1 composed mostly of small black beans, including almost all those of the popular type II growth habits (Singh *et al.*, 1991b).

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 (Hornakova et *al.*, 2003)

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 color, the third factor characterized the seed -size, length, width, height and the weight of thousand seeds (Vasic Mirjana, 2005).

The fourth factor characterized the secondary color and drawing of seed 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 sub groups could be identified in the dendrogram constructed by morphological data. Reported the divergence of dry bean breeding collections by using two qualitative and 13 quantitative traits. The first main component was named component of productivity since it determines the yield level. Pod numbers, 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 (Vasic Mirjana., 2005).

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 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 and100 seed weight (Beebe *et al.,* 2000).

## 2.2 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 (Scully *et al.,* 1991).

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 19th century, it was indicated that only a part of continuous variation was due to heredity (Singh *et al*., 1999).

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 (Lavin *et al.,* 2005).

Lush (1949), 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. He defined heritability in “Broad-sense” as the ratio between the genotypic variance as a whole and that due to phenotype 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 (Wortmann, 2004).

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. 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 (Colasanti *et al*., 2006).

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 dealing with to genetic variability, heritability and genetic advance for yield and yield contributing characters in common bean have been reviewed (Faure and Laurie, 2007).

Faure and Laurie (2007) 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. 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, and seed yield and harvest index, especially at high latitudes (Debouch, 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 (Raffi and Nath, 2004).

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) heritability or ratio of genetic for seed yield and biomass yield. Heritability 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.

Galindo *et al*. (2004) 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 identified a positive non-significant direct effect of days to flowering on seed yield through path coefficient analysis. 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. Identified the genotypic and phenotypic variability in 30 geographically diverse strains of pea from different countries.

Singh (1985) 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 was very high for days to flowering (98.3%), plant height (95.54%), nodules per plant (98.27%) and days to maturity (86.7%) (McLean *et al*., 2002).

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 (Singh, 1985).

In Singh (1985) studied the genotypic and phenotypic variability of pea, 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.

Amankwa and Michaels (1997) estimated heritability 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, heritability for seed yield and seed yield components varied from low to high (Safari, 1978). Found high heritability estimates for number of pods per plant, number of seeds per pod and 100-seed weight in F2 and F3 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. 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 heritability 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 (Motto *et al*., 1978).

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 heritability ranged from 0.87 to 0.93 and 0.78 to 0.95 for seed length and height, respectively. They concluded that 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 heritability broad sense values for stem height ranging between 0.34 and 0.88, whereas heritability value for main-stem internode length was 0.88 also found heritability broad sense values for basal internodes diameter that was 0.48. They observed heritability broad sense 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. Heritability broad sense 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. Heritability broad sense values ranged from 0.58 to 0.91 a study by (CIAT, 2011) 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. Heritability broad sense ranged from 0.57 to 0.98 for days to flowering (Escribano *et al*., 1994).

## 2.3 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).

Welsh *et al*. (1995) days to maturity are positively correlated with dry seed yield. However, observed 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 (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. 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 (Vasic *et al*., 1997).

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).

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)

# 3. MATERIALS AND METHODS

## 3.1. Description of the Experimental Site

The field experiment was conducted at Haramaya University Rare research Site during the summer season of 2014. Haramaya University is located at 515km East Addis Ababa Ethiopia at an altitude of 2011 meter above sea level with $9.0^0$N, latitude and$42.0^0$E longitude. The place has a mean maximum temperature of 28.5 $^0$c and mean minimum temperature of 12.26 $^0$c. It is situated in semi-arid tropical belt of eastern Ethiopia, characterized by sandy clay loam soil and with pH value 6.2- 6.8 sub humid type of climate with an average annual rain fall of about 550-790mm (HARC, 2014).

## 3.2. Experimental Materials.

Twenty-three accessations and two varieties of common bean obtained from Melkasa Agricultural Research Center were used for the study. The experiment was laid out on 5x5 simple lattice-designs with two replications. Each plot within a replication consisted of 25 genotypes. The position of each genotype within the plot was randomized. Each genotype within the plot was grown in a four row of 3m lengths. A spacing of 40cm between rows and 20cm between plants in a row was used. The crop was sown on 17$^{th}$ of July, 2014 and replant 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. The description of the common bean accessions used for this study is indicated in table 1.

Table 1. Common bean genotype used in the study

| S.no | Varieties | Types of materials |
|---|---|---|
| 1 | DAB 531 | Accession |
| 2 | DAB 515 | Accession |
| 3 | DAB 513 | Accession |
| 4 | DAB 529 | Accession |
| 5 | DAB 487 | Accession |
| 6 | DAB 511 | Accession |
| 7 | DAB 522 | Accession |
| 8 | DAB 538 | Accession |
| 9 | DAB 499 | Accession |
| 10 | DAB 497 | Accession |
| 11 | DAB 490 | Accession |
| 12 | DAB 481 | Accession |
| 13 | DAB 530 | Accession |
| 14 | DAB 489 | Accession |
| 15 | DAB 496 | Accession |
| 16 | DAB 483 | Accession |
| 17 | DAB 495 | Accession |
| 18 | DAB 535 | Accession |
| 19 | DAB 506 | Accession |
| 20 | DAB 523 | Accession |
| 21 | DAB 503 | Accession |
| 22 | Red Kidney bean | variety |
| 23 | DAB 505 | Accession |
| 24 | Milka dima bean | variety |
| 25 | DAB 357 | Accession |

DAB= Durango Andean Bean

## 3.3 Treatment and Experimental Design

Twenty-three common bean accessations and two varieties. Trial was laid out as simple lattice design with two replications at Rare research site. Each experimental unit had four rows, with row length of three meters. The spacing between plots, between rows and between plants was 1 m, 0.4 m, and 0.2m, respectively. The trial was planted on 17 July 2014 at Haramaya University, at Rare site. The experimental fields and experimental units were managed as per the recommended practices for common beans. Agronomic characters were determined on the averages of ten samples of plants that were randomly selected plants on plot basis. The ten representative plants per each plot were selected randomly and tagged for observations. In both cases data was collected from central two rows in each plot, excluding the border rows.

## 3.4.Data Collection

According to Moussa *et al*. (2000) the pre and post harvesting observations were recorded from five randomly selected plants from each genotypes in each replication for all characters studied except days to flowering and day to maturity which were determined on plot basis; Altogether 13 agronomic characters of sampled plants were recorded.

### 3.4.1 Pre harvest data collection.

**1. Days to 50%flowering (DF):** Number of days from germination to when 50% of plants in a plot had opened flower.

**2. Days to 90% maturity (DM):-** Number of days from planting to when 90% of the plants in a plot changed the color of their pod from green to lemon yellow.

**3. Plant height (PH) (cm):** Length of the central axis of the stem, measured from the soil surface up to the tip of the stem.

**4. Internode Length (IL) (cm)**: Length of internodes on the main stem were measured in centimeters and divided by its number to get the average length of internodes.

**5. Number of pods per plant (PPL**): Average number of mature pods, counted at harvest on 10 randomly selected plants.

**6. Pod length (PL) (cm):** Average length of pods, measured at physiological maturity on 10 randomly selected plants and five randomly taken pods per plant.

**7. Number of Nodes on the main stem (NND):** Number of nodes from the cotyledonary node to the tip of the main stem was counted and recorded at physiological maturity as averages of the 10 sample plants randomly selected plants.

### 3.4.2 Post-harvest data collection.

**8. Biological Yield (BY):** The above ground parts of the plants were dried and averaged over the 10 sample plants to get the biological yield per plant in grams.

**9. Harvest Index (HI):** The harvest index was estimated by dividing total seed yield by biological yield.

$$\text{Harvest index} = \frac{\text{seed yield(gm)}}{\text{Biological yield (gm)}}$$ ( Debouck and Hidalgo, 1986)

**10. Seed yield per plant (SPL) (gm):** Average seed yield per plant, estimated as the means of 10 randomly selected plants.

**11. Number of seeds per pod (SPP):** Average number of seeds per pod, counted at harvest on 10 randomly selected plants, in five randomly taken pods per plant.

**12. Seed yield per plot (SYP**) **(gm**): seed yield in grams, harvested from plants in the two central rows.

**13. Hundred Seed Weight (HSW) (gm):** Weight of 100 seeds in grams was determined by weighting the mass of 100 seeds.

## 3.5. Statistical Data Analyses

### 3.5.1 Analyses of variance

Data were subjected to analysis of variance using the standard procedures analysis of variance of simple lattice design for all the character using General Linear Model (GLM) computer software's program (Table 2) and calculated by adopting the formulas suggested by different biometricians. Genetic parameter such as phenotypic and genotypic variance, heritability, phenotypic and genotypic coefficient of variations and genetic advance under selection were calculated by adopting the following formulas suggested by different biometricians:-

Table 2**.** Analysis of variance (ANOVA) of simple lattice design for 13 character of 23 accessions and 2 varieties.

| Source of variation | Df | SS | MS | F- value |
|---|---|---|---|---|
| Replication | r-1 | SSr | MSr | MSr/MSe |
| Genotype | $g^2$ -1 | SSg | MSg | MSg/ MSe |
| Block with in replication(b) | r(b-1) | SSb | MSb | MSb/ MSe |
| Intra- block error | (b-1)(rb-b-1) | SSe | MSe | |
| Total | (rb2-1) | SST | | |

Where,

r = Number of replication, g =Number of genotypes Df= degree of freedom, b= block, SSe= Sum square of error, MS = Mean squares, SS= Sum squares, SSg = Sum square of genotypes, SSr= Sum squares of replication, SSb= sum square of block, MSr = mean of square due to replication, MSg = mean of square due to genotypes, MSe = mean of square due to error SSe= Sum square of error, MSb= Sum square of block within replication, SST= Sum square of the total

### 3.5.2 Phenotypic and genotypic variation

Estimated of genetic parameter were done to identify and ascertain the genetic variability among the accession and to determine the extents of environmental effect on various character .component due to phenotypic variance($\sigma^2p$), genotypic($\sigma^2g$) variance and environmental variance($\sigma^2e$) were calculated by adopting the following formula suggest by Burton and De vence (1953):-

Environmental variance ($\sigma^2e$) =MSe (error mean square)

Genotypic variance ($\sigma^2g$) = $\frac{Msg-Mse}{r}$

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

Environmental variance ($\sigma^2e$) = Error mean square

Where,

MSg = Mean of squares due to genotypes

MSe = mean of square due to error

r = Number of replications

According to (Singh, 2001) the phenotypic and genotypic coefficients of variances were expressed by the following formula.

PCV = $\frac{\sqrt{\text{Phenotypic variance}}}{\text{population mean for trait}}$

Where PCV= phenotypic coefficient of variation

GCV= $\frac{\sqrt{\text{Genotypic varianceof genotype}}}{\text{population mean for the trait}}$

Where GCV= Genotypic coefficient of variation

### 3.5.3 Heritability in broad sense

Heritability in broad sense was calculated for each trait by using the formula (Allard, 1960)

$$H\ (\%) = \frac{\sigma^2 g}{\sigma^2 P} X\ 100$$

Where

H = Heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

### 3.5.4 Expected genetic advance

The expected genetics advance (GA) under selection, assuming the selection intensity of 5% be calculated as proposed by Johnson *et al.* (1955) as follows.

$$GA = K.\sqrt{\sigma^2 p} \ . \ \frac{\sigma^2 g}{\sigma^2 p} = K*H*\sqrt{\sigma^2 p} = K*H*$$

Where GA= expected genetic advance

K = the selection differential (K= 2.056 at 5% selection intensity)

Genetic advance as percent of mean was calculated to compare the extent of predicted advances of different traits under selection, using the formula

$$GAM = \frac{GA}{X} X\ 100 =$$ (Falconer and Mackey, 1996)

GAM = Genetic advance as percent of mean

GA = Genetic advance under selection

X = Mean value

### 3.5.5 Phenotypic and genotypic correlation

Both genotype and phenotypic correlation, which the inherent association between two Variables were estimated by the formula as suggested by (Weber and Moorthy, 1952).

$$rg\,(xy) = \frac{Gcov(x.y)}{\sqrt{\sigma^2 gx \,.\, \sigma^2 gy}}$$

Where rg =genotype correlation coefficient, Gcov (x.y) = genotype co-variance between Variable x and y, $\sigma^2$g x= genotype variance for variable x, $\sigma^2$g y= genotype variance for variable y.

$$rp(xy) = \frac{pcov(x.y)}{\sqrt{\sigma^2 px.\sigma^2 py}}$$

Where rp =phenotype correlation coefficient, pcov (x.y) = phenotype co-variance between variable x and y, $\sigma^2$px= phenotype variance for variable x, $\sigma^2$py= phenotype variance for variable y.

### 3.5.6 Path Coefficient Analysis

In path coefficient analysis, common bean yield per plot was taken as the resultant (dependent) variable while the rest of the characters considered as independent variables.

The direct and indirect effects of the independent characters on common bean yield per plants were estimated by the simultaneous solution of the following general formula suggested by (Dewy and Lu, 1959). $rij = pij + \sum rikPjk$ Where:

rij = mutual association between independent variable (i) and dependent variable (j) as measured by phenotypic and genotypic correlation coefficient.

pij = component of direct effect of independent variable (i) as measured by the phenotypic and genotypic path coefficient.

$\sum rikPjk$ = summation of components of indirect effect of a given independent variable (i) on a given dependent variable (j) via all other independent characters(K).

# 4. RESULTS AND DISCUSSION

## 4.1. Range and mean values.

The estimated range and mean of the studied 13 characters were shown in table 3. The ranges of different genotypes were recorded for plant height, number of node on the main stem, internode length, number of pods per plant, pod length, number of seed per pods, days to 50% flowering, days to 90% maturity, seed yield per plant, seed yield per plots, biological yield, harvest index and 100% seed weighted. Twenty three accession and two varieties had exhibited considerable variations for the 13 characters studied. Generally, the range of variation was wide for number of nodes on the main stem, biological yield, seed yield per plant, 100-seed weight and seed yield per plot while other characters showed low to fairly high range values. This result is supported with the findings of Singh *et al.(*1994) and Debouck(1991) who reported wide range of variation for seed yield per plant, biological yield, seed yield per plots plant height, 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 seed yield per plant, 100-seed weight, seeds per pod and days to flowering.

In the present study (Appendix table 1), the genotype DAB 511 that had took the shortest time to flower. The mean for days to flowering of DAB 511 was 45.92. The genotype that took longer time to 50% flowering stages were DAB 513(51.53), DAB 503(51.52), and Milka Dima (51.17).

The genotype that took the longest duration to 90% mature were Milka Dima (90.67) while the genotype DAB 538(75.67) took the earliest day to 90%mature.

The genotype DAB495 had the maximum number of node on the main stem at maturity with values of 88.71. This result is similar to finding of (Singh *et al*., 1994) who reported that the number of nodes on the main stem at maturity.

The genotype DAB513 had maximum heights of plants 37.19cm while the genotype DAB 506(27.86cm) had the minimum value for plant height. This result is supported with the findings of (Samal *et al*., 1995) who reported that the height of common bean varied from 27.6 cm to 39.09cm. The genotype DAB487 (6.46cm) had the maximum internode length while genotypeDAB357 (3.3cm) had minimum internode length.

The genotype DAB 530(12.41cm) had the maximum length of pod while genotype DAB 497(9.537cm) had minimum length of pods. The genotype DAB513 (5.56) had the maximum number of seed per pods while DAB506 (1.99) genotype had minimum number of seed per pods. The genotypeDAB515 (51.87gm) had the maximum seed yield per plant while DAB499 (33.12gm) had minimum seed yield per plant. The genotype DAB499 had maximum seed yield per plot with values of (3215.98kg/ha) while DAB531 had the lowest seed yield per plot with values of (1735.72). This result relatively agrees with the findings of Raffi and Nath (2004) reported that the maximum and minimum seed yield in common bean genotypes.

The genotype DAB529 (52.16gm) had the maximum 100%seed weighted while genotype DAB506 (19.58gm) had minimum 100%seed weighted. This result agrees relatively with the finding of Samal *et al.* (1995) reported that range of variation for 100-seed weight in common bean genotypes.

The genotype Milka Dima had the maximum biological yield with value (537.16gm) while genotype DAB496 had minimum biological yield with value (199.95gm). This result agrees with the findings of (Singh, 2001) who reported the maximum and minimum mean value for biological yield, 100%seed weighted, seed yield of common beans. The genotype DAB496 had the maximum harvest index with value 0.194 while DAB499 genotype had minimum harvest index with value 0.062.

The range and mean values in this study suggest the existence of sufficient variability among the tested genotypes for the majority of the characters studied include number of node on the main stem, seed yield per plant, biological yield, harvest index, seed yield per plot, hundred seed weight and number of pod per plant and their considerable potential in improvement of common bean.

Table 3. Minimum and maximum and mean values for the 13 traits of the 23 accessions and 2 varieties of common bean.

| Trait | Minimum | | Maximum | | mean |
|---|---|---|---|---|---|
| | Values | Genotypes | Values | Genotypes | |
| DF | 39.76 | DAB 511 | 51.53 | DAB 503 | 45.92 |
| DM | 75.67 | DAB538 | 90.67 | Milk Dima | 84.92 |
| PH | 27.86 | DAB 506 | 37.19 | DAB 513 | 32.66 |
| PL | 9.53 | DAB 497 | 12.41 | DAB 530 | 11.14 |
| SPP | 1.99 | DAB 506 | 5.56 | DAB 513 | 3.79 |
| NND | 30.52 | DAB490 | 88.71 | DAB 495 | 51.46 |
| IL | 3.31 | DAB537 | 6.46 | DAB535 | 5.15 |
| SYL | 33.12 | DAB499 | 51.87 | DAB515 | 44.33 |
| BY | 199.95 | DAB 523 | 537.16 | Milka Dima | 353.59 |
| HI | 0.062 | DAB499 | 0.194 | DAB 496 | 0.135 |
| SYP | 1735.72 | DAB531 | 3215.98 | DAB522 | 2519.7 |
| HSW | 19.58 | DAB506 | 52.16 | DAB529 | 32.56 |
| PPL | 5.76 | DAB531 | 19.79 | DAB511 | 13.12 |

DF = Days to 50% flowering, DM = Days to 90% maturity, PH = Plant Height, NND = Number of node on the main stem, IL = Number of internode per plant, PL = Pod length, PPL = Number of pod per plant, SPP = Number of seed per pod, SYL =Seed yield per plant, HSW = Hundred seed weight, BY= Biological yield, HI = Harvest index, SYP= Seed yield per plot

## 4.2 Analysis of variance and variance components

### 4.2.1 Analysis of variance.

Analysis of variance (ANOVA) was carried out for seed yields and other the agronomic characters as outlined by (Gomez and Gomez, 1984). The results are presented in Table 4. The mean squares due to genotype were significant (P≤0.05) and highly significant (P ≤ 0.01) for all character studied. The highly significant differences indicate the existence of large variability among genotypes.

Table 4. Mean squares from analysis of variance for the 13quantitative character of common bean genotypes

| Trait | Replication | Genotype | Error | Block(rep) | CV% |
|---|---|---|---|---|---|
| Df | Df= 1 | Df= 24 | Df= 16 | | |
| DF | 2.9 | 10.96* | 3.79 | 7.19 | 4.2 |
| DM | 0.72 | 20.54* | 8.29 | 13.59 | 3.39 |
| PH | 27.68 | 5.01** | 2.08 | 10.08 | 4.41 |
| PL | 0.02 | 0.902** | 0.139 | 0.29 | 3.35 |
| SPP | 0.001 | 0.738** | 0.156 | 0.13 | 10.41 |
| NND | 910.79 | 184.79* | 79.33 | 149.4 | 17.31 |
| IL | 0.02 | 0.878** | 0.087 | 0.032 | 5.74 |
| SYL | 1.48 | 38.82** | 3.11 | 2.78 | 3.98 |
| BY | 642.11 | 4176.06* | 1358.34 | 5747.11 | 10.42 |
| HI | 0.0011 | 0.0067** | 0.0025 | 0.0005 | 3.13 |
| SYP | 5221554.65 | 152214.3* | 136148.03 | 249683.82 | 14.64 |
| HSW | 78.87 | 93.72ns | 57.21 | 109.06 | 23.23 |
| PPL | 320.04 | 9.22* | 8.35 | 7.94 | 22.02 |

*, **, ns, significant and highly significant at P≤0.05, P≤ 0.01 and non-significant respectively. DF = Days to 50% flowering, DM = Days to 90% maturity, PH = Plant Height, NND = Number of node on the main stem, IL = Number of internode per plant, PL = Pod length, PPL = Number of pod per plant, SPP = Number of seed per pod, SYL =Seed yield per plant, HSW = Hundred seed weight, BY= Biological yield, HI = Harvest index, SYP= Seed yield per plot Df= degree of freedom

### 4.2.2 Variance components

The genotypic ($\sigma^2g$) variance, phenotypic ($\sigma^2p$) variance and the genotypic coefficient of variations (GCV) and phenotypic coefficient of variations (PCV) are indicated in table 5. Higher genotypic ($\sigma^2g$) variance was observed for number of node on the main stem, biological yield and seed yield per plot. Moderate genotypic ($\sigma^2g$) variance were observed for seed yield per plant, hundred seed weight and low genotypic ($\sigma^2g$) variance were observed with pod length, number of seed per pod, internode length, harvest index, number of pod per plant, number of pod plant, plant height and days to 50% flowering. This result agrees with the findings of (Singh, 2001) reported that high genotypic variance for biological yield and seed yield in common bean genotypes.

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Higher phenotypic ($\sigma^2p$) variance from 30-60 were exhibited for number of nodes on the main stem (132.06), biological yield (2767.21), hundred seed weight (75), seed yield per plot(144181.16). Moderate phenotypic ($\sigma^2p$) variance from 20-30 were showed with seed yield per plant(20.96) and low phenotypic ($\sigma^2p$) variance below 20 were observed with pod length(0.52), number of seed per pod(0.44), days to maturity(14.41), internode length(0.47), harvest index, number of pod per plant(8.78), plant height(3.54), days to flowering(7.37). This result agrees with the findings of Raffi and Nath (2004) reported that high phenotypic variance for biological yield and hundred seed weight in common bean genotypes.

High genotypic coefficients of variations (GCV) were observed with number of seed per pod, internode length, number of nodes on the main stem, hundred seed weight. Moderate genotypic coefficients of variations (GCV) were observed with biological yield, seed yield per plant and low genotypic coefficients of variations (GCV) also were showed with number of pods per plant, plant height, days to flowering, days to maturity, seed yield per plot. This result agrees with the findings of (Singh, 2001) reported that high genotypic coefficients of variations for number of seed per pod and hundred seed weight in common beans genotypes.

Moderate phenotypic coefficients of variations (PCV) from 20-40% were observed with number of nodes on the main stem, hundred seed weight and number of pods per plant.

Low phenotypic coefficients of variations were observed with plant height, days to flowering, days to maturity, pod length number of seeds per pod, internode length, biological yield, seed yield per plot. This result agrees with the finding of Raffi and Nath (2004) also reported high PCV for internode length, number of node on the main stem and hundred seed weight in common bean genotypes.

### 4.2.3 Heritability and genetic advance

Estimates of heritability and genetic advance are indicated in table 5. High heritability estimates from 50-90% were obtained for pod length, number of seeds per pod, internode length, seed yield per plant, harvest index, seed yield per plot and biological yield. This indicates that the environment least influenced these characters. Results reported by Davis and Evans (1977) for number of seeds per pod, seed yield per plant, harvest index, and biological yield and by Motto *et al*. (1978) and Escribano *et al*. (1994) harvest index, biological yield are supportive to the present study. Moderate heritability from 20-40% was observed with days to flowering, plant height, number of nodes on the main stem, days to maturity and 100 seed weight and low heritability observed with number of pod per plant. This result agrees with at reported by Debouck, (1999) who has shown that in common bean, for days to flowering, plant height and number of nodes on the main stem are supportive to the present study.

Number of nodes on the main stem and seed yield per plant had relatively high genetic advance while for days to flowering, days to maturity and biological yield had relatively moderate genetic advance and all the rest traits had low genetic advance. This indicated the genotypes with high heritability had low environmental ($\sigma^2e$) influence.

Higher environmental ($\sigma^2e$) variance was showed for biological yield (1358.34), seed yield per plot(136148.03), number of nodes on the main stem(79.33), hundred seed weight(57.21) while low environmental ($\sigma^2e$) factor pod length, number of seed per pod, internode length, harvest index, number pod per plants. These indicated that genotypes with low heritability had high environmental influence. This result agrees with findings of Raffi and Nath (2004) reported high environmental influence for seed yield, hundred seed weight in common bean genotypes.

Table 5. Estimates of Phenotypic (σ2p) and Genotypic (σ2g) variance, Phenotypic(PCV) and Genotypic(GCV) Coefficient of variability, Broad sense Heritability(H), Expected Genetic Advances (GA) and Genetic Advances as percent of the mean(GAM%)for13characters.

| Trait | ($\sigma^2$p) | ($\sigma^2$g) | $\sigma^2$e | PCV% | GCV% | H% | GA | GAM% |
|---|---|---|---|---|---|---|---|---|
| DF | 7.37 | 3.59 | 3.78 | 4.12 | 4.48 | 48.71 | 2.71 | 5.902 |
| DM | 14.41 | 6.13 | 8.28 | 4.47 | 2.92 | 42.53 | 3.32 | 3.91 |
| PH | 3.54 | 1.47 | 2.07 | 5.76 | 3.71 | 41.52 | 1.61 | 4.92 |
| PL | 0.52 | 0.39 | 0.13 | 6.46 | 5.57 | 75 | 1.11 | 9.98 |
| SPP | 0.44 | 0.29 | 0.15 | 17.41 | 14.25 | 65.91 | 0.89 | 23.71 |
| NND | 132.06 | 52.73 | 79.33 | 22.33 | 14.11 | 39.92 | 9.43 | 18.32 |
| IL | 0.47 | 0.39 | 0.087 | 13.39 | 12.04 | 82.29 | 1.16 | 22.52 |
| SYL | 20.96 | 17.85 | 3.11 | 10.33 | 9.52 | 85.16 | 8.02 | 18.09 |
| BY | 2767.21 | 1408.87 | 1358.34 | 14.88 | 10.61 | 50.91 | 4.47 | 1.26 |
| HI | 0.0035 | 0.0032 | 0.0003 | 11.66 | 11.26 | 91.42 | 0.11 | 21.74 |
| SYP | 144181.16 | 8033.13 | 136148.03 | 15.06 | 3.56 | 55.51 | 433.28 | 17.19 |
| HSW | 75.46 | 18.25 | 57.21 | 26.69 | 13.11 | 24.18 | 4.32 | 13.27 |
| PPL | 8.78 | 0.44 | 8.34 | 22.58 | 5.0 | 5.01 | 0.31 | 2.36 |

DF = Days to 50% flowering, DM = Days to 90% maturity, PH = Plant Height, NND = Number of node on the main stem, IL = Number of internode per plant, PL = Pod length, PPL = Number of pod per plant, SPP = Number of seed per pod, SYL =Seed yield per plant, HSW = Hundred seed weight, BY= Biological yield, HI = Harvest index, SYP= Seed yield per plot.

## 4.3. Association of characters.

In the present study, associations of traits for all the 13 quantitative characters were determined for the experimental materials considered 23 accession and two varieties.

### 4.3.1. Correlation of analysis.

#### 4.3.1.1 Phenotypic and genotypic correlation seed yield with yield related characters.

The estimation of genotypic and phenotypic correlation coefficient among 13 characters are shown in table 6.

The correlation coefficient analysis showed that seed yield per plants had positive significant association ($p \leq 0.05$) of the character with number of seed per pod, harvest index and plant height at the phenotypic level, irrespective of directions of association. This indicating genotypes with high number of seed per pod, harvest index and plant height producing high seed yield. The correlation coefficient analysis exhibited that seed yield per plant showed negative significant ($p \leq 0.05$) association with days to flowering, pod length of the traits at the phenotypic level. This indicating genotype with a late day to flowering and short pod length producing low seed yield per plants. This result agrees with (Coimbra *et al.*, 1998) who reported that both pods length and day to50%flowering have been negative significant associated with seed yield per plants.

Seed yield per plants also exhibited positive significant association ($p \leq 0.05$) of the trait with number of seed per pod and number of pod per plants at genotypic level. The correlation coefficient analysis exhibited that seed yield per plot highly significant ($p \leq 0.01$) and positively association with number of pod per plants both at phenotypic and genotypic level. These indicating genotypes with high number of pods per plant producing high seed yield per plot. The correlation coefficient analysis showed that seed yield per plot had positively and significant ($P \leq 0.05$) association with number of node on the main stem, harvest index at phenotypic level while day to 90% maturity, plant height, number of node on the main stem and harvest index at genotypic level. These indicate that the genotype with late mature, high harvest index, long plant height, high nodes on the main stem producing high seed yield.

#### 4.3.1.2 Correlation among yield related trait

Estimation of correlation coefficient among yield related traits are shown in table 6. The correlation coefficient analysis exhibited that biological yield showed positive significant ($p \leq 0.05$) correlated with number of pod per plant, pod length at phenotypic level while with pod length at the genotypic level. These indicate genotype with high number of pod per plants, long pod length producing high biological yield. This result agrees with (Scully *et al*., 1991) who reported that positively significant association between pod length, number of pods per plant and biological yield. The biological yield had exhibited negatively significant correlated with plant height and internode length at phenotypic level. This indicating genotype with short plant height and internode length, producing low biological yield. The correlation coefficient analysis exhibited that harvest index showed a significant positive association with seed yield per plant at phenotypic level. These show that genotype with high seed yield per plot producing high harvest index. The correlation analysis showed that plant height had exhibited positively significant ($P \leq 0.05$) association with number of nodes on the main stem (rp=0.274*), seed yield per plant (rp=0.269*) at phenotypic level while with seed yield per plot (rg=0.047*) at genotypic level. These indicate genotype with long plant height producing high seed yield and high number of node on the main stem. Plant height exhibited negatively significant correlated ($p \leq 0.05$) with pod length, biological yield at phenotypic level. This showing that genotypes with low pod length and short plant height producing low biological yield.

The correlation coefficient analysis of pod length showed positive significant ($p \leq 0.05$) association with number of seeds per pod and biological yield at the phenotypic level while with biological yield at the genotypic level. This indicating genotype with long pod length producing high number of seeds per pod and high biological yield. It showed negative association with plant height, seed yield per plant at the phenotypic level. These indicating the genotype with short pod length produced low seed yield per plant.

Both phenotypic and genotypic level number of nodes on the main stem had showed positive and highly significant ($p \leq 0.01$) associations were observed with number of pod per plant (rp=0.681** and rg =0.671**). In addition to this trait showed positive significant association ($p \leq 0.05$) with plant height, seed yield per plot at the phenotypic level and seed yield per plot at the genotypic level. These indicated the genotype with

high number of node on the main stem producing high number of pod per plant and producing high seed yield.

The correlation of days to 50% flowering exhibited positive and highly significant associations ($p \leq 0.01$) were observed with day to 90% maturity (rp=0.817** and rg = O.799**). This exhibited the genotypes with short day to 50% flowering producing early90% maturity. Day to 50% flowering also exhibited negative and significant correlation with seed yield per plant at phenotypic level and number of node on the main stem at genotypic level.

Both phenotype and genotypic the correlation analysis revealed that days to 90% maturity showed positive and highly significant ($p \leq 0.01$) correlated with days to flowering (rp=0.817** and rg = O.799**). At phenotypic level**,** internodes length exhibited negative significant correlation with biological yield. These indicating genotypes with high internode producing high biological yield. It also revealed significantly negative associations with days to Flowering and days to maturity, number of seed per pods at the phenotypic level whereas days to Flowering, number of seed per pods. This result agrees with (Vasic *et al*., 1997) who reported that biological yield exhibited negatively significant correlation with internode length.

The correlation coefficient analysis exhibited that number of pods per plant had positive and highly significant ($p \leq 0.01$) correlated with number of nodes on the main stem (rp=0.68** and rg =0.67**), seed yield per plot (rp=0.58** and rg =0.47**) and positively significant ($p \leq 0.05$) correlated with biological yield at the phenotypic level while seed yield per plant at the genotypic level. These indicating genotypes with high number of pods per plant produced from high number of nodes on the main stem and with high number of pods producing high number of seed yield per plant and per plot.

Table 6. Correlation coefficient at genotypic (above diagonal) and phenotypic (below diagonal) levels of various characters.

| TRAIT | DF | DM | PH | PL | SPP | NND | IL | SYL(g) | BY(g) | HI | SYP(kg/ha) | HSW | PPL |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | | O.799** | 0.184 | -0.009 | 0.095 | -0.232* | 0.013 | -0.042 | -0.214 | 0.039 | 0.214 | 0.211 | -0.056 |
| DM | 0.817** | | -0.062 | 0.093 | -0.057 | -0.298 | 0.193 | 0.072 | -0.049 | -0.347 | 0.080* | 0.023 | 0.055 |
| PH | -0.028 | -0.145 | | -0.102 | 0.203 | 0.266 | -0.104 | -0.175 | -0.317 | 0.018 | 0.047* | 0.069 | 0.067 |
| PL | -0.061 | 0.077 | -0.299* | | 0.278 | -0.223 | -0.120 | -0.131 | 0.342* | 0.072 | -0.039 | -0.030 | 0.246 |
| SPP | 0.068 | -0.092 | 0.148 | 0.239* | | -0.053 | -0.161 | 0.155* | 0.045 | 0.044 | 0.091 | 0.101 | -0.073 |
| NND | -0.196 | -0.283* | 0.274* | 0.128 | -0.030 | | 0.084 | 0.045 | 0.134 | 0.151 | 0.440* | 0.037 | 0.671** |
| IL | -0.031 | 0.103 | -0.145 | -0.108 | -0.127 | 0.100 | | 0.078 | -0.289 | 0.154 | -0.054 | 0.140 | 0.173 |
| SYL(g) | -0.004* | 0,099 | 0.269* | -0.112* | 0.127* | 0.013 | 0.055 | | -0.005 | 0.236 | -0.066 | 0.911 | 0.012* |
| BY(g) | -0.092 | -0.077 | -0.269* | 0.237* | 0.023 | -0.014 | -0.215* | 0.042 | | 0.092 | 0.263 | -0.265 | 0.271 |
| HI | -0.191 | -0.310 | -0.024 | 0.088 | 0.069 | 0.110 | 0.124 | 0.239* | 0.043 | | 0.325* | -0.054 | 0.016 |
| SYP(kg/ha) | 0.048 | -0.038 | 0.071 | -0.025 | 0.057 | 0.445* | 0.008 | 0.041 | 0.270 | 0.252* | | -0.042 | 0.475** |
| HSW | 0.048 | 0.113 | 0.004 | -0.063 | 0.044 | -0.015 | 0.078 | 0.861 | -0.001 | -0.080 | 0.123 | | -0.013 |
| PPL | -0.004 | -0.016 | 0.163 | 0.192 | -0.009 | 0.681** | 0.146 | 0.034 | 0.261* | 0.054 | 0.583** | 0.076 | |

DF = Days to 50% flowering, DM = Days to 90% maturity, PH = Plant Height, PL = Pod length, SPP = Number of seed per pod, NND = Number of node on the main stem, IL = internode length, SYL =Seed yield per plant, BY= Biological yield, HI = Harvest index, SYP= Seed yield per plot, HSW = Hundred seed weight, PPL = Number of pod per plant.

## 4.4. Path Coefficient Analysis

In the present study, seed yield per plot was considered as effect dependent on eleven independent variables, which were considered as causes. The independent characters were: harvest index, 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 biological yield.

### 4.4.1 Phenotypic direct and indirect effect of various characters on seed yield per plot.

Phenotypic direct and indirect effect characters on seed yield per plot are indicated in table 7.The path coefficient analysis at the phenotypic level based on seed yield per plot as dependent variable revealed that the independent variables were: 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 biological yield, harvest index. Considering the direct effect of each character on seed yield per plot, number of pod per plant and days to 50% flowering showed the highest phenotypic direct effect with value of 0.6049 and 0.4887 respectively. These results agree with that of (Babar *et al*., 2002) who reported path analyses of seed yield and its component and demonstrated that biological yield and number of seed per pod had the highest correlation with seed yield. In addition to having the maximum phenotypic direct effect, number of pod per plant, days to 50% flowering and 100 seed weight exhibited a positive direct effect on seed yield per plot. The number pods per plants exhibited the highest positive direct effect on seed yield. It also showed the second highest negative indirect effect on seed yield plot via plant height (0.712). However, the positive indirect effects were also recorded for this trait via biological yield (0.496).

The character that exerted the highest negative phenotypic direct effect on seed yield were recorded for plant height(1.005) and pod length(0.51), followed by day to90% maturity(0.36), number of node on the main stem(0.23), internode length(0.0268). The plant height had the highest negative direct effect on seed yield that exhibited the highest negative indirect effects on seed yield through biological yield (0.73), number pods per plant (0.712) and hundred seed weight (0.684) and it recorded a positive high

and moderate indirect effect on seed yield through number pods of per plant (0.429) and hundred seed weight (0.245). Days to 90% maturity was also observed to have positively high and moderate indirect effect on seed yield through day to flowering (0.407) and plant height (0.279), respectively, but it recorded a negative moderate indirect effect on seed yield through number pods per plant. Harvest index had low positive direct effect on seed yield and it also recorded lowest negative indirect effect on seed yield through number of seed per pod and internode length.

Therefore it is evident from the result of this study that high consideration should be given for number of pod per plant, days to 50% flowering, 100-seed weight, biological yield and number of seed per pod. This result agrees with that of Raffi and Nath, (2004) who reported that number of seeds per pod to have direct effects on seed yield, indicating its importance in selection for improving the yield of crop.

Table 7. Phenotypic direct effect path (bold face) and indirect effect (off diagonal) of various characters on seed yield per plot.

| Traits | DF | DM | PH | PL | SPP | NND | IL | BY | HI | HSW | PPL |
|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | **0.4887** | -0.2966 | 0.0222 | 0.1045 | 0.0215 | 0.0163 | 0.0027 | 0.0287 | -0.0022 | -0.0554 | -0.1126 |
| DM | 0.4065 | **-0.3566** | 0.2793 | 0.0300 | -0.0055 | 0.0016 | -0.0025 | 0.0630 | -0.0054 | -0.1092 | -0.1857 |
| PH | -0.0108 | 0.0992 | **-1.0048** | 0.2061 | 0.0701 | 0.0901 | 0.0056 | -0.1370 | 0.0006 | 0.2449 | 0.4285 |
| PL | -0.1003 | 0.0210 | 0.4065 | **-0.5095** | 0.0124 | 0.0414 | 0.0014 | 0.0034 | 0.0006 | -0.0737 | 0.0030 |
| SPP | 0.0619 | 0.0117 | -0.4153 | -0.0372 | **0.1695** | 0.1090 | 0.0089 | -0.0788 | -0.0004 | 0.0931 | 0.1860 |
| NND | -0.0351 | 0.0025 | 0.3987 | 0.0929 | -0.0813 | **-0.2271** | -0.0108 | 0.1023 | -0.0011 | 0.0126 | -0.1625 |
| IL | -0.0499 | -0.0332 | 0.2107 | 0.0262 | -0.0564 | -0.0916 | **-0.0268** | 0.0700 | -0.0008 | -0.0173 | -0.0624 |
| BY | -0.0742 | 0.1191 | -0.7292 | 0.0093 | 0.0708 | 0.1230 | 0.0099 | **0.1888** | 0.0025 | 0.1420 | 0.4958 |
| HI | -0.1481 | 0.1331 | -0.0402 | -0.0198 | -0.0050 | 0.0170 | 0.0016 | -0.0324 | **0.0144** | 0.0192 | 0.0411 |
| HSW | -0.0752 | 0.1082 | -0.6839 | 0.1044 | 0.0438 | -0.0079 | 0.0013 | -0.0745 | 0.0008 | **0.3598** | 0.3240 |
| PPL | -0.0910 | 0.1095 | -0.7118 | -0.0025 | 0.0521 | 0.0610 | 0.0028 | -0.1547 | 0.0010 | 0.1927 | **0.6049** |

**Residual= 1.3937**

DF = Days to flowering, DM = Days to maturity, PH = Plant Height, PL = Pod length, SPP = Number of seed per pod, NND = Number of node on main stem, IL = Number of internode per plant, BY= Biological yield, HI = Harvest index HSW = Hundred seed weight, PPL=Number of pod per plant

## 4.5. $D^2$ Analysis

The $D^2$ (General Mahalanobis Distance ) statistics has found favor as a tool for estimating genetic variability, which is the basis in choosing parents for hybridization in a successful crop improvement and breeding programs. 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. Based on the $D^2$ values between the 23 accession and two varieties were grouped into 4 clusters (table 8). Among these, cluster II was the largest and consists of 9 genotypes, followed by cluster IV with 7 genotypes. Clusters III and I contained 6 and 3genotypes, respectively.

Cluster analysis 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).

Table 8. Cluster number with their respective genotype.

| Cluster | No of Genotypes | Germplasm |
|---|---|---|
| I | 3 | DAB 531 accession |
| | | DAB 490 accession |
| | | DAB 523 accession |
| II | 9 | Milka Dima variety |
| | | DAB 496 accession |
| | | DAB 535 accession |
| | | DAB 503 accession |
| | | DAB505 accession |
| | | DAB 483 accession |
| | | DAB 506 accession |
| | | DAB 495 accession |
| | | Red kidney variety |
| III | 6 | DAB 522 accession |
| | | DAB 499 accession |
| | | DAB 357 accession |
| | | DAB 538 accession |
| | | DAB 513 accession |
| | | DAB 487 accession |
| IV | 7 | DAB 497 accession |
| | | DAB 530 accession |
| | | DAB 481 accession |
| | | DAB 515 accession |
| | | DAB 511 accession |
| | | DAB 529 accession |
| | | DAB 489 accession |

DAB= Durango Andean Bean

### 4.5.1 Cluster means Analysis

As indicated in Table 8, germplasm accessions in clusters III were the earliest in days to flowering, where as those genotypes in clusters I, II and VI were of late type. The genotypes in cluster I had late maturity while the genotypes in cluster II were the earliest to 90% maturity. The highest mean for plant height was recorded by genotypes in cluster II while the lowest mean for plant height was recorded by genotypes in cluster I. The lowest mean value for number of seeds per pod was recorded by the genotype in Cluster IV while the highest mean value for number of seeds per pod was recorded by the genotype in Cluster III. The mean of pod length ranged from 11.01cm to 11.55cm for genotypes in clusters II and IV, respectively.

Average value of nodes on the main stem varied from 61.89 in cluster I to 42.29 in cluster IV. The mean of internode length ranged from 5.43cm to 4.71cm for genotypes in clusters I and III, respectively. The highest mean cluster value for seed yield per plant was recorded by genotypes in cluster III while the lowest mean cluster value for seed yield per plant was recorded by genotypes in cluster IV. The highest mean cluster value for biological yield was recorded by cluster II, while the lowest by cluster IV.

The largest mean cluster value for harvest index was recorded by cluster II, while relatively lowest by cluster I. Cluster IV means seed yield per plot was the lowest, while the genotype in cluster II showed the highest seed yield per plot. Cluster I mean 100 seed weight was the lowest, while the genotype in cluster II showed the highest 100-seed weight. The highest mean for number of pod per plant was recorded by genotypes in cluster II while the lowest by cluster IV. The genotypes in cluster I exhibited highest mean values for days to flowering, days to maturity, number of node on main stem, number of internode per plant while the lowest mean value for hundred seed weight, harvest index, plant height. The genotypes in cluster II showed that the largest mean values were for hundred seed weight, biological yield, harvest index, number of pod per plant, seed yield per plot while the lowest mean values were for Pod length. The genotypes in cluster III showed that the largest mean values for seed yield per plant while the lowest for day to 90% maturity.

Table 8. Mean values of four clusters for 13 traits of 23 accessions and 2 varieties common beans.

| Trait | Cluster I (3) | Cluster II (9) | Cluster III (6) | Cluster IV (7) |
|---|---|---|---|---|
| DF | 47.23 | 45.50 | 44.73 | 45.62 |
| DM | 87.23 | 83.49 | 83.02 | 85.23 |
| PH | 30.29 | 35.73 | 33.53 | 31.40 |
| PL | 11.13 | 11.00 | 11.07 | 11.55 |
| SPP | 3.48 | 4.03 | 4.17 | 3.39 |
| NND | 61.89 | 45.34 | 47.26 | 42.29 |
| IL | 5.43 | 5.13 | 4.71 | 5.36 |
| SYL(g) | 46.16 | 41.11 | 46.61 | 39.96 |
| BY(g) | 280.34 | 467.93 | 398.31 | 240.29 |
| HI | 0.146 | 0.134 | 0.161 | 0.099 |
| SYP(kg/ha) | 2200.14 | 3134.61 | 2703.40 | 1823.26 |
| HSW | 29.06 | 38.25 | 33.64 | 29.13 |
| PPL | 10.80 | 17.02 | 14.45 | 9.16 |

DF=day to 50%, DM = Days to 90% maturity, PH = Plant Height, NND = Number of node on the main stem, IL = Number of internode per plant, PL = Pod length, PPL = Number of pod per plant, SPP = Number of seed per pod, SYL =Seed yield per plant, HSW = Hundred seed weight, BY= Biological yield, HI = Harvest index, SYP= Seed yield per plot

### 4.5.2 Intra-and inter-cluster distances

It is important to consider the practical significance of grouping the genotypes into different clusters and estimating the genetic distance among 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)

The average intra-and inter-cluster $D^2$ values and their square root (D value) are depicted in table 10. The intra-cluster distances ranged from 2.043 in cluster I to 4.24 in cluster IV. Clusters II and III respectively, had more or less similar intra-cluster distances (Table 10). The maximum inter cluster distance (415.39) was recorded between cluster II and IV while the minimum inter-cluster distance (34.09) was recorded between clusters I and IV. 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).

Table 9. Intra- (main diagonal) and inter-cluster D2 values along with their D value in parenthesis

| Cluster | I | II | III | IV |
|---|---|---|---|---|
| I | **2.0433** | 284.41** | 106.39** | 34.09 |
| II | | **2.85** | 50.65** | 415.39** |
| III | | | **2.55** | 199.86** |
| IV | | | | **4.24** |

**Chi-square($x^2$) =42.98**

# 4. SUMMARY AND CONCLUSION

Knowledge of relationship among yield and the other agronomic characters is important in plant breeding, especially for the individual plant selection. If the aim of a planned breeding programme is to increase seed yield to determine associations between certain agronomical characters and seed yield provides direction correctly of plant breeding programs. The field experiments were conducted at Haramaya University in main campus at Rare research site, 25 common bean genotypes were evaluated in 2014 main crop season ( July to December) to estimate the magnitude of variability and association among yield and yield related traits.

The genotypes exhibited considerable variation for the 13 characters studied. Generally, wide range of variations were recorded for number of node on the main stem, seed yield per plant, biological yield, hundred seed weight, seed yield per plot. The genotypeDAB515 (51.87gm) had the maximum seed yield per plant while DAB499 (31.12gm) had minimum seed yield per plant. The genotype DAB499had maximum seed yield per plot with values of (3215.98kg/ha) while DAB531had the lowest seed yield per plot with values of (1735.72). The genotypeDAB529 (52.16gm) had the maximum 100%seed weighted while genotype DAB506 (19.58gm) had minimum 100%seed weighted.

The genotype Milka Dima had the maximum biological yield with value (537.16gm) while genotype DAB496 had minimum biological yield with value (199.95gm). Higher phenotypic variance was observed with number of nodes on the main stem, biological yield, hundred seed weight, seed yield per plot. Moderate phenotypic variance were observed with days to maturity, seed yield per plant and low phenotypic variance were observed with pod length, number of seed per pod, internode length, harvest index, number of pod plant, plant height, days to flowering. High genotypic coefficients of variations (GCV) were observed with number of seed per pod, internode length, number of nodes on the main stem and hundred seed weight while Moderate genotypic coefficients of variations (GCV) were observed with biological yield, seed yield per plant. High phenotypic coefficients of variations (PCV) were observed with number of

nodes on the main stem, number of seed per pod, internode length, biological yield, hundred seed weight, seed yield per plot, number of pod plant while Moderate phenotypic coefficients of variations (PCV) were observed with harvest index, pod length, seed yield per plant and low phenotypic coefficients of variations were observed with plant height, days to flowering and days to maturity.

High heritability estimates were obtained for pod length, number of seed per pod, internode length, seed yield per plant, harvest index, seed yield per plot, biological yield while low heritability also observed with 100 seed weight, pod per plant. Number of nodes on the main stem and seed yield per plant had relatively high genetic advance while for days to flowering, days to maturity and biological yield had relatively moderate genetic advance and all the rest traits had low genetic advance.

The correlation analysis showed that plant height exhibited positively significant ($P \leq 0.05$) with number of nodes on the main stem ($rp=0.274^*$), seed yield per plant ($rp=0.239^*$) association at phenotypic level while with seed yield per plot ($rg=0.047^*$) at genotypic level. These indicate genotype with long plant height producing high seed yield and high number of node on the main stem. Plant height exhibited negatively significant ($p \leq 0.05$) correlated with pod length, biological yield at phenotypic level. This showing that genotypes with low pod length and plant height producing low biological yield.

The correlation coefficient analysis of pod length showed positive significant ($p \leq 0.05$) association with number of seeds per pod and biological yield at the phenotypic level while with biological yield at the genotypic level. This indicating genotype with long pod length producing high number of seeds per pod and high biological yield. It showed negative association with plant height, seed yield per plant at the phenotypic level. These indicating the genotype with short pod length produced low seed yield per plant. At both phenotypic and genotypic level number of nodes on the main stem exhibited positive and highly significant associations ($p \leq 0.01$) were observed with number of pod per plant ($rp=0.681^{**}$ and $rg =0.671^{**}$). In addition to this trait showed positive significant ($p \leq 0.05$) association with plant height, seed yield per plot at the phenotypic level and seed yield per plot at the genotypic level. These indicated the genotype with high number of

node on the main stem producing high number of pod per plant and producing high seed yield.

The correlation of days to 50% flowering exhibited positive and highly significant ($p \leq 0.01$) associations were observed with day to 90% maturity (rp=0.817** and rg = O.799**). This exhibited the genotypes with short day to 50% flowering producing early90% maturity. Day to 50% flowering also exhibited negative and significant ($p \leq 0.05$) correlation with seed yield per plant at phenotypic level and number of node on the main stem at genotypic level.

Both at phenotype and genotypic the correlation analysis revealed that days to 90% maturity showed positive and highly significant ($p \leq 0.01$) correlation with days to flowering (rp=0.817** and rg = O.799**). At phenotypic level, internodes length exhibited negative significant correlation with biological yield. These indicating genotypes with high internode producing high biological yield. It also revealed significantly negative associations with days to Flowering and days to maturity, number of seeds per pod at the phenotypic level whereas days to Flowering, number of seed per pods.

The correlation coefficient analysis exhibited that number of pods per plant had positive and highly significant ($p \leq 0.01$) association with number of nodes on the main stem (rp=0.68** and rg =0.67**), seed yield per plot (rp=0.58** and rg =0.47**) and significant ($p \leq 0.05$) positively correlation with biological yield at the phenotypic level while seed yield per plant at the genotypic level. These indicating genotypes with high number of pods per plant produced from high number of nodes on the main stem and with high number of pods producing high number of seed yield.

Number of pod per plant and days to 50% flowering exhibited the highest phenotypic direct effect on seed yield per plot. The plant height had the highest negative direct effect exhibited the highest indirect negative effects on seed yield through biological yield, number pods per plant and hundred seed weight and it recorded a positive high and moderate indirect effect on seed yield through number pods per plant and hundred seed weight. Days to 90% maturity also observed positively high and moderate indirect effect on seed yield via day to flowering and plant height, but it recorded a negative moderate indirect effect on seed yield through number pods per plant. Harvest index had low

positive direct effect on seed yield and it also recorded lowest negative indirect effect on seed yield through number of seed per pod and internode length. Significant diversity was observed among the 23 accessions and two varieties of common bean 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. Intra-cluster distance ($D^2$) ranged from 2.043 between clusters I to 4.24 between clusters IV. Inter-cluster distance ($D^2$) ranged from 34.09between cluster IV and I to 415.39 between clusters IV and II. The clusters mean analyses enabled to classify the cluster, into early and late flowering, early and late maturing, low and high yielding.

# 6. RECOMMANDATION

It is importance 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 starts and hybridization carried out between clusters rather than within clusters. The present study 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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# 8. APPENDIX

Table Appendix 1. Mean performance of 13 quantitative characters of 23accessions and 2 varieties of common bean.

| NO | Entry | DF | DM | PH | PL | SPP | NND |
|---|---|---|---|---|---|---|---|
| 1 | Milka dima | 51.17 | 90.66 | 35.74 | 11.21 | 4.41 | 33.37 |
| 2 | DAB 357 | 45.09 | 81.09 | 35.72 | 10.72 | 4.26 | 32.88 |
| 3 | DAB515 | 46.67 | 80.17 | 36.69 | 10.11 | 4.11 | 44.42 |
| 4 | DAB513 | 51.17 | 89.16 | 37.19 | 11.06 | 5.56 | 42.57 |
| 5 | DAB 529 | 46.66 | 85.16 | 36.94 | 11.21 | 4.16 | 33.67 |
| 6 | DAB 487 | 43.17 | 85.66 | 33.64 | 11.41 | 3.81 | 41.57 |
| 7 | DAB 511 | 39.75 | 78.24 | 34.03 | 10.81 | 3.51 | 71.67 |
| 8 | DAB 522 | 44.17 | 83.16 | 34.29 | 11.46 | 3.16 | 49.27 |
| 9 | DAB 538 | 40.17 | 75.66 | 36.79 | 11.46 | 3.81 | 54.07 |
| 10 | DAB 499 | 49.24 | 86.23 | 36.76 | 9.91 | 3.57 | 51.65 |
| 11 | DAB 497 | 46.59 | 86.13 | 34.09 | 9.53 | 3.95 | 65.80 |
| 12 | DAB 490 | 41.67 | 80.66 | 33.04 | 10.91 | 3.91 | 30.52 |
| 13 | DAB 481 | 42.17 | 81.66 | 28.89 | 11.81 | 4.61 | 38.02 |
| 14 | DAB 530 | 45.67 | 83.66 | 31.49 | 12.41 | 4.96 | 38.22 |
| 15 | DAB 489 | 45.59 | 86.09 | 32.56 | 11.62 | 3.91 | 39.01 |
| 16 | DAB 496 | 47.47 | 88.11 | 31.54 | 10.05 | 2.61 | 68.11 |
| 17 | DAB 483 | 44.83 | 88.33 | 31.81 | 10.78 | 3.89 | 65.35 |
| 18 | DAB 495 | 45.47 | 83.61 | 29.94 | 11.80 | 3.76 | 88.71 |
| 19 | DAB 535 | 42.98 | 81.11 | 29.29 | 11.65 | 3.16 | 74.11 |
| 20 | DAB 506 | 48.83 | 88.83 | 27.86 | 10.78 | 1.99 | 68.82 |
| 21 | DAB 523 | 48.66 | 88.16 | 28.99 | 12.41 | 2.71 | 49.92 |
| 22 | DAB 503 | 51.52 | 90.88 | 29.01 | 10.99 | 4.64 | 56.02 |
| 23 | Red kidney | 44.74 | 87.19 | 28.89 | 11.99 | 3.26 | 46.43 |
| 24 | DAB 505 | 48.02 | 86.38 | 28.56 | 10.94 | 3.64 | 56.12 |
| 25 | DAB 531 | 46.52 | 86.88 | 32.17 | 11.34 | 3.54 | 46.42 |
| 26 | Grand means(ẋ) | 45.92 | 84.92 | 32.66 | 11.14 | 3.79 | 51.46 |
| 27 | CV% | 4.23 | 3.38 | 4.41 | 3.35 | 10.41 | 17.3 |

DF = Days to 50% flowering, DM = Days to 90% maturity, PH = Plant Height, PL = Pod length, SPP = Number of seed per pod, NND = Number of node on the main stem, IL = internode length, SYL =Seed yield per plant, BY= Biological yield, HI = Harvest index, SYP= Seed yield per plot, HSW = Hundred seed weight, PPL = Number of pod per plant

Table Appendix ( Continued )

| NO | Entry | IL | SYL | BY | HI | SYP | HSW | PPL |
|---|---|---|---|---|---|---|---|---|
| 1 | Milka dima | 4.90 | 48.82 | 537.16 | 0.083 | 2178.88 | 29.26 | 18.11 |
| 2 | DAB 357 | 3.31 | 40.21 | 499.88 | 0.074 | 3065.81 | 33.14 | 12.65 |
| 3 | DAB515 | 5.55 | 51.87 | 428.54 | 0.108 | 2788.38 | 40.86 | 14.06 |
| 4 | DAB513 | 5.40 | 48.07 | 445.19 | 0.097 | 3100.03 | 49.66 | 19.11 |
| 5 | DAB 529 | 3.70 | 51.17 | 464.44 | 0.099 | 2605.53 | 52.16 | 17.26 |
| 6 | DAB 487 | 6.70 | 42.12 | 414.21 | 0.09 | 3140.48 | 35.76 | 17.26 |
| 7 | DAB 511 | 5.10 | 44.43 | 396.02 | 0.101 | 2847.94 | 42.66 | 19.79 |
| 8 | DAB 522 | 4.80 | 42.92 | 499.28 | 0.079 | 3215.98 | 33.41 | 18.46 |
| 9 | DAB 538 | 5.25 | 42.22 | 479.22 | 0.081 | 3066.78 | 42.31 | 17.76 |
| 10 | DAB 499 | 5.29 | 31.12 | 469.79 | 0.062 | 3218.55 | 35.19 | 16.86 |
| 11 | DAB 497 | 4.82 | 50.37 | 267.35 | 0.158 | 2587.19 | 27.24 | 12.20 |
| 12 | DAB 490 | 5.40 | 42.87 | 311.96 | 0.121 | 1877.98 | 33.81 | 11.76 |
| 13 | DAB 481 | 4.60 | 42.47 | 436.62 | 0.089 | 2910.83 | 25.76 | 10.16 |
| 14 | DAB 530 | 4.50 | 40.97 | 299.94 | 0.120 | 2468.43 | 22.96 | 11.56 |
| 15 | DAB 489 | 4.70 | 45.00 | 495.24 | 0.083 | 2715.52 | 23.86 | 16.12 |
| 16 | DAB 496 | 5.96 | 47.32 | 196.22 | 0.194 | 2086.47 | 37.13 | 7.95 |
| 17 | DAB 483 | 5.43 | 37.73 | 242.13 | 0.135 | 2327.51 | 36.88 | 8.31 |
| 18 | DAB 495 | 5.36 | 46.13 | 280.37 | 0.141 | 2274.72 | 44.68 | 11.25 |
| 19 | DAB 535 | 6.46 | 44.83 | 254.27 | 0.149 | 2072.87 | 25.73 | 12.65 |
| 20 | DAB 506 | 5.58 | 48.87 | 230.51 | 0.175 | 2356.11 | 19.58 | 7.86 |
| 21 | DAB 523 | 4.80 | 37.47 | 199.95 | 0.158 | 1856.08 | 28.41 | 9.96 |
| 22 | DAB 503 | 5.12 | 48.55 | 223.61 | 0.178 | 2114.22 | 22.66 | 9.36 |
| 23 | Red kidney | 5.58 | 45.86 | 312.25 | 0.128 | 2288.27 | 23.28 | 13.51 |
| 24 | DAB 505 | 4.52 | 47.30 | 246.54 | 0.160 | 2102.17 | 22.31 | 8.16 |
| 25 | DAB 531 | 5.87 | 39.55 | 208.96 | 0.159 | 1735.72 | 25.16 | 5.76 |
| 26 | Grand means(ẋ) | 5.15 | 44.33 | 353.59 | 0.123 | 2519.7 | 32.56 | 13.12 |
| 27 | CV% | 5.73 | 3.97 | 10.42 | 3.13 | 14.64 | 23.23 | 22.02 |

DF = Days to 50% flowering, DM = Days to 90% maturity, PH = Plant Height, PL = Pod length, SPP = Number of seed per pod, NND = Number of node on the main stem, IL = internode length, SYL =Seed yield per plant, BY= Biological yield, HI = Harvest index, SYP= Seed yield per plot, HSW = Hundred seed weight, PPL = Number of pod per plant.

Table of Appendix 2. Mean square of 13 characters of 23accessions and 2 varieties of common bean.

| | | | Mean square | | |
|---|---|---|---|---|---|
| Traits | replication | Block(rep) | Genotypes | Error | CV% |
| DF | 2.9 | 7.19 | 10.96 | 3.79 | 4.2 |
| DM | 0.72 | 13.59 | 20.54 | 8.29 | 3.39 |
| PH | 27.68 | 10.08 | 5.01 | 2.08 | 4.41 |
| PL | 0.02 | 0.29 | 902 | .139 | 3.35 |
| SPP | 0.00 | 0.13 | 738 | .156 | 10.41 |
| NND | 910.79 | 149.4 | 184.79 | 79.33 | 17.31 |
| IL | 0.02 | 0.032 | 0.878 | 0.087 | 5.74 |
| SYL | 1.48 | 2.78 | 38.82 | 3.11 | 3.98 |
| BY | 642.11 | 5747.11 | 4176.06 | 1358.34 | 10.42 |
| HI | 0.0011 | 0.0005 | 0.0067 | 0.0025 | 3.13 |
| SYP | 5221554.65 | 249683.82 | 152214.3 | 136148.03 | 14.64 |
| HSW | 78.87 | 109.06 | 93.72 | 57.21 | 23.23 |
| PPL | 320.04 | 7.94 | 9.22 | 8.35 | 22.02 |

PH = Plant Height, NND = Number of node on main stem, IL = Number of internode per plant, PL = Pod length, SPP = Number of seed per pod, HSW = Hundred seed weight, BY= Biological yield, HI = Harvest index PPL=Number of pod per plant

**Appendix figure 1**