

**GENETIC VARIABILITY AND ASSOCIATION OF AGRONOMIC  
CHARACTERS IN COMMON BEAN (*Phaseolus vulgaris* L.), GROWN  
AT ZIWAY, EAST SHEWA, ETHIOPIA**

**MSc THESIS**

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**Genetic Variability and Association of Agronomic Characters in Common  
Bean (*Phaseolus vulgaris* L.), Grown at Ziway, East Shewa, Ethiopia**

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## **DEDICATION**

This manuscript is dedicated to my beloved family and my neighbors for helping me with affection and love and for their dedicated partnership in the success of my life.

## STATEMENT OF AUTHOR

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## **BIOGRAPHICAL SKETCH**

The author was born in Ethiopia Oromia regional state, East Shewa zone Adami Tullu Jido Kombolcha woreda on August 21, 1972 to his adored Father Gelgelu Hubeta and his Mother Warite Wataro.

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## ACRONYMS AND ABBREVIATIONS

|                |   |
|----------------|---|
| ADP            | Agricultural Development Project                  |
| ANOVA          | Analysis of Variance                              |
| CSA            | Central Statistics Authority                      |
| CV             | Coefficient of Variance                           |
| EARO           | Ethiopian Agricultural Research Organization      |
| FAO            | Food and Agriculture Organization                 |
| GA             | Genetic Advance                                   |
| GCV            | Genotypic Coefficient of Variation                |
| H <sup>2</sup> | Heritability in Broad Sense                       |
| IAR            | Institute of Agricultural Research                |
| PROTA          | Plant Resource of Tropical Africa                 |
| PCV            | Phenotypic Coefficient of Variation               |
| RCBD           | Randomized Complete Block Design                  |
| SAS            | Statistical Analysis System                       |
| USDA           | United States Department of Agriculture           |
| UBCDR          | University of Bonn Center of Development Research |

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**Genetic Variability and Association of Agronomic Characters in Common Bean  
(*Phaseolus vulgaris* L.), Grown at Ziway, East Shewa, Ethiopia**

**ABSTRACT**

*The purpose of this study was to estimate the extent of genetic variability of agronomic traits and their contribution to seed yield. Twelve quantitative characters including plant height, pods per plant, seeds per pod, days to flowering, seed yield per plots, harvest index and hundred seed weighted of twenty four genotypes of common bean (*Phaseolus vulgaris* L.) was studied. The experiment was conducted at Ziway farmer's field as randomized complete block design planted in three replications. Results showed that genotypes with more yields were identified as ARGANE for maximum seed yield per plot with values of (832g), GOFTA for pods per plant (24.3) and for above ground dry biomass (8636.66). The values of variation was wide for plant height, seed yield per plant, hundred seed weight and seed yield per plot while other characters showed low to fairly high range value. The mean square values showed significant variation among all 24 genotypes. Plant height hundred seed weight and harvest index showed high coefficients of variation in both genotypic and phenotypic. High heritability estimated from 60-97% were obtained for days to flowering, primary branches, Secondary branches, seeds per pod, Plant height, harvest index, seed yield per plot, hundred seed weight and above ground dry biomass. Above ground dry biomass seed yield per plot hundred seed weight and plant height showed high genetic advance. The magnitudes of genotypic correlation showed higher as compared to phenotypic correlations and in the same direction. Primary branches, above ground dry biomass, days to flowering, days to maturity, pods per plant, seeds per pod and hundred seed weight are traits of common bean which exerts positive direct and indirect influence on seed yield in both phenotypic and genotypic path coefficient analysis. 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.*

**Keywords:** Agronomic Character, Correlation, Genetic advance, Genetic variability Heritability

## 1. INTRODUCTION

Common bean (*Phaseolus vulagris* L), locally known as 'Boleqe' also known as dry bean, Haricot bean, kidney bean and field bean is a very important legume crop grown worldwide. It is an annual crop which belongs to the family Fabaceae. It grows best in warm climate at temperatures of 18 to 24°C (Teshale *et al.*, 2005).

Common bean (*Phaseolus vulgaris* L.) originated in Latin America where its wild progenitor has a wide distribution ranging from northern Mexico to northwestern Argentina. Common bean has two origins, a Mesoamerican and an Andean (Singh *et al.*, 1991). Several characters can be used to characterize genetic resources, particularly morphological and agronomic (Singh, 2001). Singh *et al.* (1991b) investigated genetic diversity in cultivated common beans by using marker based analysis of morphological and agronomic traits. 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. Fifth inter node 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).

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).

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 Andeans 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).

Wild beans grown in the wild are distributed at altitudes ranging from 500 to 2000 m and rain falls from 500 to 1800 mm. Two taxonomic sub-divisions have been described; *Phaseolus vulgaris* var *aborigineas* and *Phaseolus vulgaris* var *mexicanus*. They can be distinguished at both morphological and molecular levels, the levels of genetic diversity in the wild and cultivated forms and the genetic divergence between the wild and cultivated beans. The role of gene flow between wild and cultivated beans has gained prominence, on patterns of genetic diversity and pathogenesis of related organisms (Delgado, 1985).

Common bean is regarded as “Grain of hope” as it is an important component of subsistence agriculture and feeds about 300 million people in the tropics and 100 million people in Africa alone (FAO, 2010). It plays a paramount role in human nutrition and market economies in the world. The common bean is cultivated primarily for its dry seeds, green pods (as in snap beans), and green-shelled bean in some tropical areas. Bean leaves are cooked and 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. Young tender leaves and flowers are also used as fresh vegetables in some Central and Eastern African, and in Latin American countries (Broughton *et al.*, 2003).

Common Beans are a nearly "perfect" food. Nutritionally rich, they are also a good source of protein, folic acid, keeping malnutrition at bay. Any advances in scientific research that benefit bean yields, particularly in developing countries, help to feed the hungry and give hope for the future (FAO, 1997). Brazil is the world's largest producer of common bean, which is the main protein source in the average diet of the population (Costa *et al.*, 2011).

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, 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).

In common bean architectural, phenological and yield components are collectively influencing seed yield. The relationships between yield and yield contributing traits in one could be measured by correlation analysis (Raffi and Nath, 2004). The knowledge of these relationships helps to identify traits on which selection can be based for the improvement 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).

In Ethiopia, common beans are grown predominantly by smallholder producers as an important food crop and source of cash. It is one of the fast expanding legume crops that provide an essential part of the daily diet and foreign earnings for most Ethiopians (Girma, 2009). The major common bean producing areas of Ethiopia are central, eastern and southern parts of the country (CSA, 2011). The crop grows well between 1400 and 2000m above sea level (Fikru, 2007). 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 identify the pattern of character variations among and between varieties to resolve the problems in different regions and adaptation zones. Identification among varieties these can help to elite genotypes with the greatest novelty and

thus are most suitable for rescue or incorporation into crop improvement programs (Safari, 1978).

These days' farmers also prepare a local stew known as *shirowot* from some bean cultivars (Mekibib, 1997). Beans are generally characterized by their unstable yields resulting from biological, climate and edaphic factors that affect plant growth and productivity (Kristin *et al.*, 1997). The wide range of growth habits of haricot bean among varieties has enabled the crop to fit many growing situations. Among different growth habit of haricot bean prostrate bush types achieve rapid ground cover, compete with weeds and avoid competition with *teff* for labor. At the present time, the production and area coverage of haricot bean has been increasing from time to time because of the fact that the crop has immense potential for export In Ethiopia, common bean is one of the most important cash crops and source of protein for farmers. The country's export earnings are estimated to be over 85% of export earnings from pulses, (Negash, 2007). Overall, common bean ranks third as an export commodity in Ethiopia, contributing about 9.5% of total export value from agriculture. The production and area coverage of common bean has been increasing because of the fact that the crop has immense potential for export (Kristin *et al.*, 1997).

Nevertheless, despite its importance as a cash crop and its immense potential for improving the livelihood of thousands of small holder farmers, its productivity has remained low. This is due to the less attention given to the crop and limited research works undertaken for its improvements. Therefore, improving the agronomic characters of the crop based on the scientific research that contribute and enhance improvement of the seed yield becomes imperative.

### **Objective of the Study**

General Objective:

- To estimate the extent of genetic variability of agronomic traits and their contribution to seed yield.

### **Specific Objectives:**

- To estimate the magnitude of genetic variability of some agronomic characters in common bean.

- To estimate the phenotypic and genotypic coefficients of variation, heritability and genetic advance in the common bean genotypes.
- To assess the extent of association of agronomic characters among themselves and with seed yield of common bean.
- To estimate the relative contribution of the characters to the seed yield of common bean.

## 2. LITRATURE REVIEW

### 2.1. Origin and Distribution of Common Bean

A Mesoamerican origin of *Phaseolus vulgaris* is most likely located in Mexico, both from the analysis of the population structure and phylogeny and the confirmation of the occurrence of a bottleneck before domestication in the Andeans (Rossi *et al.*, 2009). The Mesoamerican origin is consistent with the known distribution of most of the close relatives of *Phaseolus vulgaris*, the much higher diversity of Mesoamerican wild bean compared with the diversity from South America, the occurrence of a severe bottleneck in the Andeans before domestication, and finally, the occurrence in Mesoamerica of wild beans that are closely related to those beans found in South America, both from the Andean and northern Peru–Ecuador gene pool (Rossi *et al.*, 2009).

Among the major dry bean producers, in decreasing order are Brazil, Mexico, the United state, Ethiopia, Uganda, Burundi, Tanzania, Turkey, Argentina, Rwanda, Angola and Colombia, (FAO,1997). Dry beans are grown in Latin America in region where the average mean temperature ranges between 17.5 and 25. Most of the production takes place in areas with mean temperature during the growing seasons of around 21. This corresponds to an average altitude of 1,250 m. in tropics (Laing *et al.*, 1984). During its evolution under domestication, common bean has experienced a widening of its ecological range, principally by adaptation to warmer temperature and long dry photo periods.

In Africa, common bean is grown mainly for subsistence, where the Great Lakes region has the highest per capita consumption in the world. It is a major source of dietary protein in Kenya, Tanzania, Malawi, Uganda, and Zambia. In Asia, dry beans are generally less important than other legumes, but exports are increasing from China. In Latin America, Africa, and Asia, the bean is primarily a small-scale crop grown with few purchased inputs, subjected to biological, edaphic, and climatic problems. Beans from these regions are notoriously low in yield, when compared to the average yields in the temperate regions of North America and Europe. Yet yields can be improved in all zones (FAO, 1997).

Common bean (*phaseolus vulgaris* L.; $2n= 2x=22$ ) is grown on all continents except Antarctica. The principal products are dry beans (seed harvested at complete maturity). Shell beans (seed harvested at physiological maturity, i.e. before the desiccation associated

with complete maturity sets in). And green or snap beans pod harvested before the seed development phase (FAO, 1997). The common dry bean is the most important food legume for direct consumption in the world. Among major food crops, it has one of the highest levels of variation in growth habit, seed characteristics (size, shape, and colour), maturity, and adaptation. It also has a tremendous variability (> 40,000 varieties). Germplasm collection in beans compares well with other important commodities on a worldwide basis.(Costa *et al.*, 2011).

Common bean is one of the major food and cash crops in Ethiopia and it has considerable national economic significance. It is often grown as cash crop by small scale farmers and used as a major food legume in many parts of the country where it is consumed in different types of traditional dishes (Kedir *et al.*, 2014).

## **2.2. Nutritional Value of Common Beans**

Legumes are the plant foods that contain highest levels of protein and can supply an average of 16-20% of the total protein intake. Common bean is a good source of protein and has been used as a substitute for other sources of plant (soy), and animal (milk) proteins. It is used in the industrial preparation of commonly consumed foods such as Ice cream, or regionally consumed foods such as miso in Japan, and kishk in Eastern Europe. Bean protein has also been used in combination with rice in nutritious weaning food (FAO/WHO, 1991).In Ethiopia; dry beans are major source of proteins in the lowlands where they are consumed as Nifro, Wasa, Shirowat, soup and samosa. They are important export crop especially navy beans from the Central Rift Valle region and some parts of east and west highlands.( Katungi *et al.*, 2011).

Common Beans are nutrient-rich foods; they contain a variety of vitamins, minerals and other nutrients while providing moderate amount of calories. Beans provide protein, fiber, foliate, iron, potassium and magnesium while containing little or no total fat, trans-fat, sodium and cholesterol (USDA, 2012).There are nutritional and anti-nutritional factors and fibers in common bean seed. The nutritional quality of protein from common bean cultivars obtains from the amino acid composition of the proteins such as cystein and methionine that are found in common bean as cystein and methionine sulphate respectively (More, 1963).

The consumption of dry common beans (*Phaseolus vulgaris*) has been associated with a decrease risk for a wide variety of chronic and degenerative diseases such as cancer, obesity, diabetes and cardiovascular diseases. Beans are considered as a good source of high protein content, complex carbohydrates, dietary fiber and some vitamins and minerals. In addition to these nutritional components, common beans are rich in a variety of several phytochemicals with potential health benefits such as polyphenolic compounds, fiber, lectins and trypsin inhibitor (Reynoso *et al.*, 2006).

## **2.3. Genetic Variability, Heritability and Genetic Advance**

### **2.3.1. Genetic variability**

Variability is defined as the occurrence of differences among individuals due to differences in their genetic composition or environment in which they are raised (Allard, 1960). Genotypic variability is the component of variation, which is due to the genotypic differences among individuals within the population, and is the main concern of plant breeders. The amount of variation present in any population is measured and expressed in terms of variance. All the variability present in biological systems can be attributed to genotype and /or environment (Falconer and Mackay, 1996).

Genetic variability is of the prime interest to the plant improvement because proper management of this diversity can produce permanent gain in the performance of the plant and the environment is the sum total of all things to which an organisms is exposed. Thus environmental deviations such differences on fertility level of experimental units, moisture contents of the soil, and seasonal fluctuations contribute to the component of variation (Falconer and Mackay, 1996). Estimates genotypic coefficients of variations are used to study the variability that exists in a given population. Genetic variability for economically important traits and extent to which the desirable characters are heritable is an essential prerequisite for successful breeding crops (Dudley and Moll, 1969).

The study of the morphological, yield, yield component and quantitative traits revealed that significant genetic variability existed in these genotypes. Analysis of the quantitative characters revealed presence of significant genetic variation for all the characters (Rafi and Nath (2004) and Dursun (2007).

### 2.3.2. Heritability

Allard (1960) used the term heritability to specify the heritable portion of the total genetic variability. Falconer and Mackay (1996) define heritability as the measure of the correspondence between breeding values and phenotypic values. In general, the degree to which the variability of a character is transmitted to the progeny is referred to as its heritability. Heritability estimates provide an indication of the expected response to selection in a segregating population and they are useful tools in designing an effective breeding program (Burton and de Vane, 1953).

Information on the nature and magnitude of variability and heritability in population is one of the prerequisites for successful breeding program in selecting genotypes with desirable characters hence, it is essential to divide the observed variability into its heritable and non-heritable components. Easily measured traits with high heritability might be used for rapid screening of large volumes of early generation materials for specific traits (Dudley and Moll, 1969).

Heritability estimates can be used to predict genetic advance under selection so that breeders can anticipate improvement from types and intensities of selection. Heritability estimates and genetic advance should always be considered simultaneously, because high heritability will not be always associated with high genetic advance which is mainly due to additive gene effect. But if the heritability is due to dominance and epistasis, the genetic advance would be low (Panes, 1957).

From breeding point of view usefulness of a character is related to its onward transmission from the parent to the progeny. A quantitative measure that provides information about the correspondence between genotypic and phenotypic variance is heritability (Amin *et al.*, 1992). Heritability in a broad sense estimates the ratio of total genetic variance including additive, dominance, and epistatic variance, to the phenotypic variance whereas heritability in the narrow sense estimates only the additive portion of the total phenotypic variance, and it expresses the extent to which phenotypes are determined by the genes transmitted from parents. For selection, estimate of high heritability and high genetic gain should be considered together (Panes, 1957).

The Broad " heritability gives an idea about portion of observed variability attributable to genetic difference. In other words, heritability indicates the accuracy with which a genotype

can be identified by its phenotypic performance. Indeed, heritability in broad sense contains both additive and non-additive effects (Hanssen *et al.*, 1956).

### **2.3.3. Genetic advance**

Genetic advance is the measure of improvement that can be achieved by practicing selection in population. Which means; it measures the expected genetic progress that would result from selecting the best performing genotypes for a character being evaluated. Genetic advance under selection indicates measure of the difference between the mean genotypic value  $s$  of the original population for a given character (Allard, 1960). It is affected by factors like intensity of selection, heritability and phenotypic variance. High genetic advance coupled with high heritability is an indication of more additive gene action. Reports on high genetic advance would available for all the characters studied except days to 50 percent flowering and fruit colour which was moderate to low (Panese, 1957).

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 can be expected for a particular character through 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 (Miraza *et al.*, 2011).

High genetic advance and high heritability is the outcome of additive gene action and vice versa indicates presence of more non-additive gene action. Traits like days to maturity, pods per plant, hundred seed weight and seed yield plant, had high heritability and expected genetic gain. These traits are expected to be governed more by additive gene effects and improvement could be made through selection in the existing material. For other traits like pod length and protein content hybridization followed by selection is expected to yield some good recombinant (Panese, 1957).

## 2.4. Association of Characters

### 2.4.1. Correlation analysis

Correlation, indicated by a correlation coefficient, is the measure of a linear association between traits. Correlation measures the degree of association, genetic or non-genetic, between two or more traits. If genetic association exists, selection for one trait will cause changes on other traits (Hallauer and Miranda., 1988). Correlation, therefore, is helpful in determining whether the component characters of a complex trait like yield characters of crop plants are generally correlated. There are three types of correlations; phenotypic, genotypic, and environmental correlations. Phenotypic correlation measures the extent to which two observed characters are linearly related. Environmental correlation arises entirely due to environmental effects. Genetic correlation is the measure of the extent to which the same gene or closely linked genes cause simultaneous variation in two different traits. The two possible causes of genetic correlation are attributed to pleiotropism and /or linkage (Allard, 1960).

Estimation of phenotypic and genotypic correlation between various agronomic characters may provide information necessary to show the relationship between characters. Understanding the interrelationships among various characters under different conditions, directly or indirectly affecting yield is essential in formulating selection criteria. Thus, the estimates of degree of phenotypic and genotypic correlation of yield with yield related traits are very important to utilize the available variability through selection. Correlation among characters may arise from linkage or from developmental genetic interaction, with or without purely phenotypic components (Jalata *et al.*, 2011).

Correlation measured by a correlation coefficient is important in plant breeding because it measures the degree of association (genetic and non-genetic) between two or more traits. The concept of correlation has been first given by Galton (1889) and since then it is believed that knowledge of the nature and magnitude of genetic association among components of economic worth can help in improving the efficiency of selection by making possible use of suitable combination of characters.

The phenotypic correlations among traits reflect observed relationship between traits arising from the combined effects of genotype and environment, whereas genetic correlations

estimate the association between traits, resulting either from linkage or pleiotropic effects between the traits. In crop improvement, breeding value correlations are more useful, especially for indirect selection and this type of selection can be advantageous over direct selection, only when the selected trait has very high heritability, and breeding value correlation between two traits is very high. Compensation between yield components may lead to variation in correlation pattern, and therefore, stresses is importance for genotype-environment interaction and their contribution to “genetic slippage” in the selection of complex characters (Johnson *et al.*, 1955).

Thus, studies under different environments might give a clear and reliable picture of association which can be effectively utilized during selection of breeding programmers. The correlated changes in yield and yield components may at times lead to physiological efficient genotypes for expression of yield. In presence of substantial breeding value correlation between two traits, selection in one trait will cause a change in its mean through additive gene effects of selected individuals and simultaneously cause an indirect change in the mean of the other trait.

Knowledge of correlations among common bean traits is important for several reasons; it is possible to fully perceive the diversity of breeding material, to identify traits needed by a common bean genotype, to grow successfully under certain ecological conditions, to identify and avoid characters that have little or no importance and use of some traits in the selection programs, to define breeding target and cultivates model, and to recognize impediments and benefits of a breeding progress well in advance.

#### **2.4.2. Path coefficient analysis**

Path coefficient analysis is a very important statistical tool that indicates which variables exert influence on other variables (effects). A path coefficient is simply a standardized partial regression coefficient and measures the direct influence of one variable upon another and permits the separation of the correlation into components of direct and indirect effects. Path coefficient analysis specifies the cause and measures the relative importance of characters, while correlation measures only mutual association without considering causation (Dewey and Lu, 1959).

In any breeding program of complex characters such as yield of which direct selection is not effective, it become essential to measure the contribution of each of the component

variables to the observed correlation and to partition the correlation into components of direct and indirect effect (Giriraji and Vijayakumar, 1974). Path analysis has proven useful providing additional information that describes cause and effect relationships, such as between yield and yield components (Gravios and Helm, 1992). It is therefore, essential to identify degree of association of various quantitative characters in order to initiate an effective selection program aimed at genetic improvement of crop yield.

### 3. MATERIALS AND METHODS

#### 3.1. Description of the Study Area

Ziway is found in the Great East African Rift Valley area of Ethiopia. It is found in Eastern shewa zone of Oromiya region, which is 163km to the south east of Addis Ababa. The climate is warm with mean annual precipitation and temperature of 837mm and 19.3°C, respectively (Koppen, 2011). Soil types around Ziway mostly are silt and silty sand, which have clay content (Alemayehu, 2015).

#### 3.2. Preparation of Experimental Materials

Twenty four varieties of common bean (*Phaseolus vulgaris* L.), were obtained from Melkassa, Agricultural Research Center (Table 1).

**Table 1. The common bean (*Phaseolus vulgaris* L.), genotypes obtained from Melkassa Agricultural Research Center**

| No | Genotypes   | No | Genotypes |
|----|-------------|----|-----------|
| 1  | KAT-B9      | 13 | DEME      |
| 2  | KAT-B1      | 14 | SAB-736   |
| 3  | NASIR       | 15 | LEHODE    |
| 4  | ARGANE      | 16 | MELKEDIMA |
| 5  | AWASH MELKA | 17 | CHERCHER  |
| 6  | MELKE       | 18 | SAB-632   |
| 7  | ROBA        | 19 | DRK       |
| 8  | BATU        | 20 | SER-119   |
| 9  | AWASH-1     | 21 | ECAB-0056 |
| 10 | AWASH-2     | 22 | SER-125   |
| 11 | GOFTA       | 23 | GLP-2     |
| 12 | BRAZIL-1    | 24 | ECAB-0081 |

Source; Melkassa Agricultural Research Center

#### 3.3. Experimental Design

The experiment was done in a Randomized Complete Block design with three replications. Each plot with 1.6m wide and 2m long and consisting of four rows.

### 3.4. Data collection

Data on individual plant basis was collected per plot of plants from each rows of plot. Each genotype was planted in the plots with a distance of 40cm between the rows and plant to plant distance of 10cm in a row. A total of 12 variables were considered for the study as indicated below. All agronomic practices properly done as per the recommendation for common bean (Zelalem, 2013). Data was subjected to Analysis of variance (ANOVA) Using SAS 9.2 the experimental fields were well prepared and standard recommended package of practices were followed to raise a good crop. Data of all individual plant traits evaluated based on their means.

**Days to flowering (DF):**The number of days from the date of sowing to the date at which about 50% of the plants in a plot showed blooming on about 50% of their flower buds.

**Days to maturity (DM):** The number of days from the date of sowing to a stage when 90% of plants have reached their physiological maturity.

**Primary branches per plant (PB):** The average number of primary branches based on the individual plants per plot.

**Secondary branches per plant (SB):** The average number of secondary branches formed on primary branches recorded for all plants in each plot.

**Plant height (PH):** The height of the plants in each plot was measured from the ground surface to the top of the main stem at maturity in centimeters and the average recorded.

**Pods per plant (PPP):** The total number of pods was from each plants of the plot were taken and the average recorded.

**Seeds per pod (SPP):** The average number of seeds per pod was obtained from each plant of the plots.

**Seed yield per plant (YPP):** The average seed yield in grams was obtained for the plants for each plot and their means recorded.

**Seed yield per plot (SYPP):** was measured in grams from each plot after drying in sun moisture was adjusted by moisture taster.

**100 seed weight (HSW):** two samples of 100 seeds were randomly taken from each plot and the means recorded in gram.

**Above ground dry biomass (AGDB):** The total above ground biological yield per plot was weighed and recorded.

**Harvest index (HI):** To estimate the harvest index, average seed yield was divided by the average biological yield.

$$\text{Harvest index} = \frac{\text{seedyeild}(kg)}{\text{biological yeild}(kg)} \text{ (Debouck and hidalgo, 1986).}$$

### 3.5. Statistical Analysis

#### Analysis of variance (ANOVA)

Data was subjected to statistical analysis according to the procedure of randomized complete block design as shown below (Gomez and Gomez, 1984). SAS computer software version 9.2 (SAS, 2008) was used for data statistical analysis.

**Table 2. RCBD Analysis of Variance (ANOVA) and expected mean square**

|             |             |           |                            |
|-------------|-------------|-----------|----------------------------|
| Replication | r-1         | MSr (M1)  | $\sigma^2_e + r\sigma^2_g$ |
| Genotype    | g-1         | MSg ((M2) | $\sigma^2_e + \sigma^2_g$  |
| Error       | (r-1) (g-1) | MSe (M3)  | $\sigma^2_e$               |

Where, r=number of replication; g=number of genotypes; MSr=mean of squares due to replication's=mean of square due to genotypes; MSe= mean of square due to error, a  $\sigma^2_e$ =error variance and  $\sigma^2_g$ =genotypic variance respectively. Where, r-1, g-1 & (r-1) (r-g) are degree of freedom.

#### 3.5.1. Estimation of genetic parameters

The phenotypic and the genotypic coefficients of variation were estimated according to the method suggested by Mirza et al (2011) as follows;

Environmental variance ( $\delta^2_e$ ) =MSE (square).

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

Phenotypic variance ( $\delta^2_p$ ) = $\delta^2_g + \delta^2_e$

Environmental variance ( $\delta^2_e$ )=mean square

Where,  $M_s_g$ = mean square due to genotype

$M_s_e$ =Environmental variance

$r$ =the number of replication

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

$$\text{Phenotypic coefficient of variation (PCV)} \quad PCV = \frac{\sqrt{\delta^2_p}}{X} \times 100$$

Where; PCV=Phenotypic coefficient of variation

$X$ =Mean value of the trait.

$$\text{Genotypic coefficient of variation (GCV)} \quad GCV = \frac{\sqrt{\delta^2_g}}{X} \times 100$$

Where; GCV=Genotypic coefficient of variation & Estimation of Heritability and genetic Advance.

Broad sense heritability ( $H^2_b$ ) shall be expressed as the percentage of the ratio of the genotypic variance ( $\delta^2_g$ ) to the phenotypic variance ( $\delta^2_p$ ) and was estimated on genotype mean basis as described by Allared (1960) as:

$$H^2_b = \frac{\delta^2_g}{\delta^2_p} \times 100$$

Where;  $H^2_b$ = heritability in broad sense

( $\delta^2_p$ )=phenotypic variance

$\delta^2_g$ = genotypic variance

Then the genetic advance for selection intensity ( $k$ ) at 5% (2.06) was estimated by the formula of (Johnson *et al.*, 1955b).

$$\text{Genetic advance (GA)} = H^2_b * K * \delta p$$

Where: GA=expected genetic advance;

$\delta p$ =phenotypic standard deviation;

$H^2_b$ =heritability in a broad sense and  $k$ =selection intensity.

The genetic advance as percent of population mean was also estimated by following the procedure of Johnson *et al.* (1955b).

$$\text{Genetic advance per population mean} = (GA / \text{ground mean}) * 100$$

GAM = Genetic advance as percent of mean

GA = Genetic advance under selection

X = Mean value

### 3.5.2. Association of characters

#### 3.5.2.1. Correlation coefficient (r)

Phenotypic correlation is the relationship between two variables, which includes both genotypic and environmental effects and genotypic correlation the inherit association between two variables, phenotypic and genotypic correlation coefficient was estimated using the standard procedure suggested by Dewey and Lu, (1959) from corresponding variance and co-variance components as ;

$$\text{Phenotypic correlation} = r_{p(xy)} = \frac{COV_p(xy)}{\sqrt{V_p(x)}\sqrt{V_p(y)}}$$

$$\text{Genotypic correlation} = r_{g(xy)} = \frac{COV_g(xy)}{\sqrt{V_g(x)}\sqrt{V_g(y)}}$$

Where;  $COV_p(xy)$  and  $COV_g(xy)$  are phenotypic and genotypic covariance between x and y characters.

$V_p(x)$  and  $V_g(x)$  represent variances of x character and  $V_p(y)$  and  $V_g(y)$  denote variance of y character at phenotypic and genotypic level, respectively.

#### 3.5.2.2. 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).  $r_{ij} = p_{ij} + \sum r_{ik}p_{jk}$  Where:

$r_{ij}$  = mutual association between independent variable (i) and dependent variable (j) as measured by phenotypic and genotypic correlation coefficient.

$p_{ij}$  = component of direct effect of independent variable (i) as measured by the phenotypic and genotypic path coefficient.

$\sum r_{ik}p_{jk}$  = 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

The present study deals with a field experiment carried out with 24 varieties common bean to evaluate variability in morphological characters, extent of genetic variability, and association of agronomic characters between yield and yield components and path analysis of the genotypes on the bases of yield and yield components. The results obtained in the present investigation and the discussions are given below.

### 4.1. Genetic Variability and Agronomic Characters of some Common Bean Varieties

The minimum, maximum, and mean values for 12 characters were shown in table 3. The values of different traits of the genotypes were recorded for days to flowering, days to maturity, Primary branches per plant, Secondary branches per plant, plant height, pods per plant, seeds per pod, seed yield per plant, seed yield per plots, hundred seed weighted, above ground dry biomass, and harvest index. Twenty four genotypes have exhibited considerable variations for the 12 characters studied. Generally, the values of variation was wide for plant height, seed yield per plant, hundred 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 ( Berecha, 2015) who observed high range of variation for seed yield per plant, hundred seed weight, seeds per pod and days to flowering.

In the present study, the genotype of BATU (42) took the shortest days to flowering while AWASH MELKA (60.33) took the longest days to flowering. The mean for days to flowering was 47.22. The genotype DEME had maximum heights of plants 97.6cm while the genotype KAT-B<sub>9</sub> (32cm) had the minimum value for plant height. The genotype ROBA (6.02) had the maximum seeds per pod while BATU (3.7) had minimum seeds per pod. MELKE had maximum seed yield per plant (37.575g), while DRK minimum seed yield per plant (14.273g) genotype. The genotype ARGANE had maximum seed yield per plot with values of (832g) while BRAZIL-1 had the lowest seed yield per plot for values of (291.41g). This result relatively agrees with the findings of Raffi and Nath (2004) who reported the maximum and minimum seed yield in common bean genotypes. The genotype (SAB-632) had the maximum hundred seed weighted (47.87g) while ROBA had minimum hundred seed weighted (15.61g). This result agrees fairly with the findings of (Berecha,

2015) who reported the value of variation for hundred seed weight in common bean genotypes.

The genotype BRAZIL-1 had the maximum harvest index with value (0.313) while BATU genotype had minimum harvest index with value 0.04. 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 including primary branches per plant, above ground dry biomass, pods per plant and their considerable potential for improvement of common bean.

**Table 3. Genetic Variability and Agronomic Characters of some Common Bean Varieties**

| Traits | Genotypes   | Minimum score | Genotypes   | Maximum Score | Mean   | SD     |
|--------|-------------|---------------|-------------|---------------|--------|--------|
| DF     | BATU        | 42            | AWASH MELKA | 60.33         | 47.222 | 5.168  |
| DM     | KAT-B1      | 65.67         | AWASH MELKA | 87            | 75.847 | 4.924  |
| PB     | BATU        | 4             | LEHODE      | 12.67         | 9.574  | 2.306  |
| SB     | SAB-632     | 11.58         | LAHODE      | 34.8          | 16.503 | 4.786  |
| PH     | KAT-B9      | 32            | DEME        | 97.6          | 48.935 | 19.959 |
| PPP    | DRK         | 11.4          | GOFTA       | 24.3          | 19.714 | 3.397  |
| SPP    | BATU        | 3.7           | ROBA        | 6.02          | 4.613  | 0.665  |
| YPP    | DRK         | 14.273        | MELKE       | 37.575        | 26.33  | 6.177  |
| SYPP   | BRAZIL1     | 291.41        | ARGANE      | 832           | 574.67 | 121.58 |
| HSW    | ROBA        | 15.61         | SAB-632     | 47.87         | 30.888 | 9.813  |
| AGDB   | AWASH MELKA | 3999.33       | GOFTA       | 8636.66       | 6131   | 1535   |
| HI     | BATU        | 0.04          | BRAZIL1     | 0.313         | 0.1025 | 0.036  |

SD=standard deviation, DF=Days to flowering, DM=Days to maturity, PB=Primary branches per plant, SB=Secondary branches per plant, PH=Plant height, PPP=Number of pods per plant, SPP=Seeds per pod, YPP= Seed yield per plant, SYPP=Seed yield per plot, HSW=hundred Seed weight, AGDB= above ground dry biomass, HI=Harvest index.

## 4.2. Analysis of Variance

The result of analysis of variance of 12 characters for 24 common bean genotypes tested at Ziway is presented in the Table 4. The highest mean square had observed by above ground dry biomass (7070772.1) followed by Seed yield per plot (44348.43), plant height (1195.10), hundred seed weight (288.87), seed yield per plant (123), days to 50%

flowering (80.12 ), days to 90% maturity ( 72.75), secondary branches (68.69), and the least square value had observed by pods per plant (34.630), primary branches (15.96), seeds per pods (1.325) the harvest index ( 0.00378). Endeshaw (1996) reported mean values are useful to determine variations within and between populations. This is highly significant variation among all the 24 genotypes for all the traits investigated except DM and PPP. This indicates that the mean square due to genotype was significant variation among all the 24 genotypes for DF, PB, SB, PH, SPP, YPP, SYPP, HSW, AGDB, and HI indicates that the existence of high genetic variability and this shows high probability of improvement of traits through selection (Berecha, 2015).

**Table 4. Analysis of Variance**

| Source of variation | Df  | DF      | DM    | PB      | SB      | PH        | PPP    | SPP     | YPP    | SYPP       | HSW      | AGDB        | HI        |
|---------------------|-----|---------|-------|---------|---------|-----------|--------|---------|--------|------------|----------|-------------|-----------|
| Replication         | 2   | 0.680   | 35.68 | 0.770   | 7.482   | 39.492    | 4.344  | 0.473   | 6.0244 | 8688.257   | 3.638    | 1351910.2   | 0.00036   |
| Genotype            | 23  | 80.12** | 72.75 | 15.96** | 68.69** | 1195.10** | 34.630 | 1.325** | 123**  | 44348.43** | 288.87** | 7070772.1** | 0.00378** |
| Error               | 0.5 | 13.61   | 33.88 | 0.689   | 5.393   | 70.12     | 10.904 | 0.154   | 39.563 | 329.108    | 5.723    | 1246858.0   | 0.00059   |
| CV%                 |     | 7.81    | 7.67  | 8.67    | 14.072  | 17.112    | 16.750 | 8.520   | 23.885 | 21.36      | 7.745    | 18.211      | 23.851    |

\*,\*\* indicate significance at the 5% and 1% probability levels, respectively

df =Degree of freedom, DF=Days to flowering, DM=days to maturity, PB=Primary branches per plant, SB=Secondary branches per plant, PH=Plant height, PPP=Number of pods per plant, SPP=Seed per pod, YPP= seed yield per plant, SYPP=Seed yield per plot, HSW=hundred Seed weight, AGDB=above ground dry biomass and HI=Harvest index, CV=Coefficient of variations

### 4.3. Genetic Variability of some Agronomic Characters of some Common Bean

#### 4.3.1. Genotypic and phenotypic variations, heritability and genetic advance

Estimation of genotypic variance ( $\sigma^2_g$ ), phenotypic variance ( $\sigma^2_p$ ) and environmental variance ( $\sigma^2_e$ ) of different traits for twenty four common bean genotypes are given in the Table 5. The progress of breeding for such economic traits is determined by magnitude and nature of their genotypic and phenotypic variability.

High genotypic coefficients of variations (GCV) were observed for plant height (39.57), harvest index (31.82), hundred seed weight (31.45), secondary branches (27.83), primary branches (23.57), above ground dry biomass (22.73), seed yield per plot (20.35), while Moderate genotypic coefficients of variations (GCV) were observed for seed yield per plant (14.80), pods per plant (14.28), seeds per pod (13.55), While low genotypic coefficients of variations (GCV) were observed for days to flowering (9.97), and days to maturity (4.75). This result agrees with the findings ((Singh, 2001; cited in Berecha, 2015) reported that high genotypic variance for seed yield per plot and seed yield in common bean genotypes.

High phenotypic coefficients of variations (PCV) were observed for, plant height (43.1), while Moderate phenotypic coefficients of variations (PCV) were observed for, primary branches (25.1), pods per plant (22.0), and seed yield per plot (20.6). harvest index (39.77), hundred seed weight (32.3), secondary branches per plant (31.1), above ground dry biomass (29.1), seed yield per plant (28.1) Low phenotypic coefficients of variations were observed for harvest index, and seeds per plant (15.9), and days to flowering (12.6), and days to maturity (9.02). This result agrees with the findings of (Berecha, 2015) reported that high phenotypic variance for biological yield and hundred seed weight in common bean genotypes.

Table 5. Estimation of genetic ( $\delta^2 g$ ) phenotypic ( $\delta^2 p$ ) and environmental ( $\delta^2 e$ ) components of variances broad sense heritability ( $H^2 b$ ), phenotypic (PCV), genotypic (GCV) coefficients of variability, and expected genetic advances (GA), and as percent of the mean

| Traits | Mean     | $\delta^2 g$ | $\delta^2 p$ | $\delta^2 e$ | $H^2 b$ | PCV    | GCV    | GA       | GMA%     |
|--------|----------|--------------|--------------|--------------|---------|--------|--------|----------|----------|
| DF     | 47.220   | 22.160       | 35.770       | 13.610       | 61.950  | 12.600 | 9.970  | 7.632    | 16.164   |
| DM     | 75.840   | 12.960       | 46.820       | 33.890       | 26.910  | 9.020  | 4.750  | 3.793    | 5.001    |
| PB     | 9.573    | 5.090        | 5.780        | 0.689        | 88.060  | 25.100 | 23.570 | 4.360    | 45.570   |
| SB     | 16.500   | 21.090       | 26.490       | 5.393        | 79.650  | 31.100 | 27.830 | 8.440    | 51.170   |
| PH     | 48.930   | 374.900      | 445.110      | 70.120       | 84.240  | 43.100 | 39.570 | 36.543   | 74.676   |
| PPP    | 19.710   | 7.910        | 18.812       | 10.904       | 42.050  | 22.000 | 14.280 | 3.760    | 19.070   |
| SPP    | 4.612    | 0.390        | 0.544        | 0.154        | 72.220  | 15.900 | 13.550 | 1.093    | 23.770   |
| YPP    | 26.330   | 15.190       | 54.759       | 39.563       | 27.750  | 28.100 | 14.800 | 3.060    | 11.415   |
| SYPP   | 574.600  | 13685.700    | 14014.800    | 329.100      | 97.651  | 20.600 | 20.357 | 237.680  | 41.359   |
| HSW    | 30.880   | 94.380       | 100.110      | 5.723        | 94.400  | 32.300 | 31.450 | 19.450   | 62.940   |
| AGDB   | 6131.000 | 1941304.700  | 3188162.700  | 1246858.000  | 60.890  | 29.120 | 22.730 | 2239.670 | 36.530   |
| HI     | 0.103    | 0.001        | 0.002        | 0.001        | 63.990  | 39,77  | 31.820 | 5.370    | 5239.243 |

DF=Days to flowering, DM=Days to maturity, PB=Primary branches per plant, SB=Secondary branches per plant, PH=Plant height, PPP= pods per plant, SPP=Seeds per pod, YPP= Seed yield per plant, SYPP=Seed yield per plot, HSW=hundred Seed weight, AGDP= above ground dry biomass, HI=Harvest index. GAM%=Genetic advances as percent of the mean.

Note: GCV based on Knight (1979) 0-10% = low, 10-20%=medium, >20% =high. Heritability based on Stanfield (1983)  $0 \leq x \leq 0.2$  = low,  $0.2 \leq x \leq 0.5$  = medium,  $x > 0.50$  = high. GA based on Hadiati et al. (2003), 0-7% = low, 7-14% = medium and >14,1 = high. Based on Berecha (2015).  $\delta^2 p=30-60$ , high, 20-30 medium, below 20 low. PCV= $\geq 40$  high, 20-40 medium, < 20 low, are criteria used for category

#### 4.3.2. Estimate of heritability and genetic Advance

Estimates of heritability and genetic advance are indicated in table 5. High heritability estimates from 60-97% were obtained for days to flowering, primary branches, Secondary branches, seeds per pod, Plant height, harvest index, seed yield per plot, hundred seed weight and above ground dry biomass. This result agrees with at reported by Berecha (2015) who has reported similar results that seeds per pod, seed yield per plot, harvest index, and above ground dry biomass had high heritability estimate in common bean genotype. Moderate heritability from 20-50% was observed for pods per plant, seed yield per plant, and days to maturity. Above ground dry biomass (2239.6) and seed yield per plot (237.68) plant height (36.543), hundred Seed weight (19.45),) had relatively high genetic advance while days to flowering (7.632), secondary branches per plant (8.440) had relatively moderate genetic advance and all the other traits had low genetic advance. This indicated that genotypes with high heritability had low environmental ( $\sigma^2_e$ ) influence. Higher environmental ( $\sigma^2_e$ ) variance was observed for above ground dry biomass (1246885), seed yield per plot (329.10) and plant height (70.12), Moderate environmental ( $\sigma^2_e$ ) variance was recorded for days to maturity (33.89), and seed yield per plant (39.56) while low environmental ( $\sigma^2_e$ ) variance was recorded for seed per pod (0.154), harvest index (0.0005), and Primary branches (0.689). These indicated that genotypes with low heritability had high environmental influence. This result agrees with findings of Berecha, (2015) who reported high environmental influence for seed yield per plot, and hundred seed weight in common bean genotypes.

The estimates of phenotypic variance were higher than the corresponding estimates of genotypic variance for all the traits. This results agree with (Syed *et al.*, 2012 who. reported similar results.

### 4.4. Association of Phenotypic and Genotypic Correlation

#### 4.4.1. Association of phenotypic correlation

In correlation analysis, correlation studies permit the feasibility of indirect selection, when direct selection becomes inapplicable due to various causes. Pearson correlation coefficients for both genotypic and phenotypic associations among the characters are given in Table 6.

The data regarding phenotypic correlation estimates (Table 6) depicted that magnitude of phenotypic correlation coefficient for days to flowering at ( $p \leq 0.01$ ) showed positive and highly significant correlation with Primary branches, seeds per pod and negative and highly significant at ( $p \leq 0.01$ ) correlation with hundred seed weight, and showed positive and significant with days to maturity and harvest index. Primary branches showed positive and highly significant at ( $p \leq 0.01$ ) correlation with pods per plant. Secondary branches showed positive and highly significant ( $p \leq 0.01$ ) correlation with plant height, seed yields per plant, above ground dry biomass and negative highly significant ( $p \leq 0.01$ ) correlation with harvest index. Plant height at ( $p \leq 0.01$ ) showed positive and highly significant correlation with above ground dry biomass and negative highly significant at ( $p \leq 0.01$ ) correlation with harvest index and positive and significant for seed yield per plant and hundred seed weight. Pods per plant correlation showed positive and highly significant correlation with seed yield per plant. Seeds per pod showed negative and highly significant correlation with hundred seed weight, above ground dry biomass and showed negative and significant correlation with seed yield per plant. Seed yield per plant showed positive and highly significant correlation with hundred seed weight, and with above ground dry biomass. Seed yield per plot showed positive and highly significant correlation with harvest index and showed negative and significant correlation with hundred seed weight. Hundred seed weight showed positive and highly significant correlation with above ground dry biomass. Above ground dry biomass showed negative and highly significant correlation with harvest index.

These results at phenotypic level shows that Seed yield per plot had positive highly significant correlation with harvest index. It indicates genotype with high seed yield per plot producing high harvest index Seed yield per plant had positive and highly significant correlation with primary branches, pods per plant, seeds per pod, These indicating genotypes with high seed yield produced from high pods per plant, primary branches, and from seeds per pod and Seed yield per plant had negative and highly significant correlation with hundred seed weight, indicating that genotypes with high pods per plant and seeds per plant less hundred seed weight (Berecha, 2015) reported similar result.

**Table 6. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among 12 characters of common bean**

| Variable | DF           | DM           | PB           | SB           | PH           | PPP          | SPP          | YPP          | SYPP         | HSW          | AGDB         | HI           |
|----------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| DF       | <b>1.000</b> | 0.519**      | 0.495*       | 0.139        | 0.125        | 0.172        | 0.500*       | 0.290        | 0.943        | -0.452       | -0.354       | 0.005        |
| DM       | 0.215*       | <b>1.000</b> | 0.139        | 0.356        | 0.191        | 0.256        | 0.606        | 0.264        | -0.023       | 0.235        | -0.098       | 0.214        |
| PB       | 0.366**      | 0.069        | <b>1.000</b> | 0.210        | 0.236        | 0.580*       | 0.424*       | -0.143       | 0.412        | -0.592*      | -0.104       | -0.048       |
| SB       | 0.098        | 0.167        | 0.176        | <b>1.000</b> | 0.617**      | 0.443        | -0.175       | 0.706*       | -0.135       | 0.086        | 0.627 *      | -0.428       |
| PH       | 0.090        | 0.092        | 0.203        | 0.505**      | <b>1.000</b> | 0.087        | -0.179       | 0.596        | -0.182       | 0.222        | 0.064*       | -0.561*      |
| PPP      | 0.088        | 0.087        | 0.353**      | 0.256**      | 0.052        | <b>1.000</b> | 0.014        | 0.615**      | 0.260        | -0.475       | 0.538        | -0.219       |
| SPP      | 0.333**      | 0.269        | 0.336        | -0.132       | -0.139       | 0.149        | <b>1.000</b> | -0.780*      | 0.107        | -0.645**     | -0.697**     | 0.704*       |
| YPP      | 0.120        | 0.073        | -0.071       | 0.332**      | 0.288*       | 0.278**      | -0.347*      | <b>1.000</b> | -0.167       | 0.968**      | 0.113**      | -0.020       |
| SYPP     | 0.149        | -0.121       | 0.382        | -0.119       | -0.165       | 0.167        | 0.089        | -0.087       | <b>1.000</b> | -0.292       | -0.129*      | 0.83**       |
| HSW      | -0.345**     | -0.120       | -0.539       | 0.075        | 0.198*       | -0.299       | -0.578**     | 0.495**      | 0.280*       | <b>1.000</b> | 0.421        | -0.069**     |
| AGDB     | -0.218       | -0.040       | -0.076       | 0.436**      | 0.460**      | 0.272*       | -0.463**     | 0.515**      | 0.099*       | 0.319**      | <b>1.000</b> | -0.86*       |
| HI       | 0.020*       | 0.089        | -0.039       | -0.304**     | -0.409**     | -0.132       | 0.473        | -0.009       | 0.065**      | -0.053       | -0.534**     | <b>1.000</b> |

\*,\*\* indicate significance at the 5% and 1% probability levels, relatively

#### 4.4.2. Association of genotypic correlation

The Genotypic correlation coefficient analysis showed that days to flowering at ( $p \leq 0.01$ ) showed positive and highly significant correlation with days to maturity, and at ( $p \leq 0.05$ ) showed positive and significant correlation with primary branches and seeds per pod. Primary branches at ( $p \leq 0.05$ ) showed positive and significant correlation with seeds per pod, pod per plant and negative and significant correlation with hundred seed weight. Secondary branch at ( $p \leq 0.01$ ) showed positive and highly significant correlation with plant height and showed positive and significant correlation with seed yield per plant and above ground dry biomass. Plant height at ( $p \leq 0.05$ ) showed positive and significant correlation with above ground dry biomass, and showed negative and significant correlation with harvest index. Pod per plant at ( $p \leq 0.05$ ) showed positive and significant correlation with seeds seed yield per plant. Seeds per pod at ( $p \leq 0.01$ ) showed negative and highly significant correlation with hundred seed weight and above ground dry biomass and at ( $p \leq 0.05$ ) showed positive and significant correlation with hundred harvest index and negative and significant correlation seed yield per plant. Seed yield per plant at ( $p \leq 0.01$ ) showed positive and highly significant correlation with hundred seed weight. Seed yield per plot at ( $P \leq 0.01$ ) showed negative and highly significant correlation with harvest index and at ( $p \leq 0.05$ ) showed negative and significant correlation with above ground dry biomass. Hundred seed weight at ( $p \leq 0.01$ ) showed negative and highly significant correlation with harvest index. Above ground dry biomass at ( $p \leq 0.05$ ) probability level showed negative and significant correlation with harvest index. These results agree with (Berecha, 2015) that shows pods per plant positive and significant correlation with seed yield per plant and plant height positive and significant with above ground dry biomass.

Generally in both genotypic and phenotypic Correlation analysis, the magnitudes of genotypic correlation were higher as compared to their corresponding phenotypic correlations indicating the inherent relationship among the characters studied (Table 6). Correlation studies showed that for most character pairs, genotypic and phenotypic associations were in same direction and the genotypic estimates were higher than the phenotypic ones, indicating an inherited association between the characters (Syed *et al.*, 2012).

### 4.4. 3. Path coefficient analysis

Association among important yields attributes and seed yield may help the breeder to identify specific traits for any successful breeding. A selection criterion was contributed to selection based on direct and indirect effects. Path coefficient analyses also have been used to evaluate selection criteria in several crops. This technique is useful in determining the direct influence of one variable on another and separates the correlation coefficient in to its components of direct and indirect effects (Rodriguez *et al.*, 2001; cited in Mokonnen *et al.*, 2014). In path coefficient analysis, seed yield per plot is considered as dependent variable and the other traits such as primary branches, secondary branches, seeds per pod, pods per plant, seed yield per plant, hundred seed weight, plant height, days to flowering, days to maturity, above ground dry biomass, and harvest index considered as independent variables.

#### 4.4.3.1. Phenotypic path coefficient

Phenotypic direct and indirect effects of characters on seed yield per plot are indicated in (table 7). Considering the direct effect of each character on seed yield per plot primary branches (0.226), pods per plant (0.221), seeds per plant (0.133), hundred seed weight (0.300), and above ground dry biomass (0.456) showed phenotypic positive direct effect on the seed yield per plot and days to flowering (-0.326), days to maturity (-0.144), secondary branches (-0.384), plant height (-0.420), seeds per pods (-0.354), and harvest index (-0.158) showed phenotypic negative direct effect on the seed yield per plot.

Above ground dry biomass (0.456) exhibited the highest phenotypic positive direct effect on seed yield and the second and third highest positive direct effect on seed yield were exhibited by hundred seed weight (.300) and primary branches (0.226) respectively. However, plant height (-0.420), secondary branches (-0.384), and seed per pod (-0.354), showed first, second and third phenotypic negative direct effect on the seed yield per plot 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 pods per pod had the highest correlation with seed yield.. Days to flowering showed phenotypic positive indirect effect on seed yield through seeds per plant, hundred seed weight, and above ground dry biomass. Days to maturity, exhibits positive phenotypic indirect effect on seed yield through hundred seed weight and above ground dry biomass but exhibits

negative phenotypic indirect effect on seed yield through all other remains. Primary branches, showed phenotypic positive indirect effect on seed yield through Days to maturity, secondary branches, plant height, pods per plant and seeds per pod, but it also showed negative indirect effect on seed yield through seed yield per plant, hundred seed weight, above ground dry biomass and harvest index. Plant height showed positive indirect effect on seed yield through seed yield per plant and harvest index. Pods per plant showed phenotypic positive indirect effect on seed yield through days to maturity, days to 50% flowering, seed yield per plant, hundred seed weight above ground dry biomass, harvest index. These results agree with that of Babar *et al.*, (2002) that 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.

Therefore it is evident from the result of this study that, high attention should be, given to primary branches, pods per plant, seed yield per plant, hundred seed weight and above ground dry biomass to improve seed yield per plot. This result agrees with that of (Berecha, 2015) who reported that pods per plant, hundred seed weight and above ground dry biomass those have direct effects on seed yield, indicating its importance in selection for improving the yield of this crop.

**Table 7. Estimation of direct (bold diagonal) and indirect effects (off diagonal) of eleven traits on seed yield at phenotypic level in common bean genotypes.**

| Variable | DF            | DM            | PB           | SB            | PH            | PPP          | SPP           | YPP          | HSW          | AGDB         | HI            | Rp       |
|----------|---------------|---------------|--------------|---------------|---------------|--------------|---------------|--------------|--------------|--------------|---------------|----------|
| DF       | <b>-0.326</b> | -0.070        | -0.119       | -0.032        | -0.029        | -0.029       | -0.108        | 0.039        | 0.112        | 0.071        | -0.007        | -0.498   |
| DM       | -0.031        | <b>-0.144</b> | -0.010       | -0.024        | -0.013        | -0.013       | -0.039        | -0.010       | 0.017        | 0.006        | -0.013        | -0.274   |
| PB       | 0.083         | 0.016         | <b>0.226</b> | 0.040         | 0.046         | 0.080        | 0.076         | -0.016       | -0.122       | -0.017       | -0.009        | 0.403**  |
| SB       | -0.029        | -0.049        | -0.068       | <b>-0.384</b> | -0.194        | -0.098       | 0.051         | -0.128       | -0.029       | -0.168       | 0.117         | -0.979   |
| PH       | -0.038        | -0.039        | -0.085       | -0.212        | <b>-0.420</b> | -0.022       | 0.058         | -0.121       | -0.083       | -0.193       | 0.172         | -0.983   |
| PPP      | 0.019         | 0.019         | 0.078        | 0.057         | 0.011         | <b>0.221</b> | 0.033         | 0.061        | -0.066       | 0.060        | -0.029        | 0.464    |
| SPP      | -0.118        | -0.095        | -0.119       | 0.047         | 0.049         | -0.053       | <b>-0.354</b> | 0.123        | 0.205        | 0.164        | -0.167        | -0.318** |
| YPP      | -0.016        | 0.010         | -0.009       | 0.044         | 0.038         | 0.037        | -0.046        | <b>0.133</b> | 0.066        | 0.069        | -0.001        | 0.325**  |
| HSW      | -0.104        | -0.036        | -0.162       | 0.023         | 0.059         | -0.090       | -0.173        | 0.149        | <b>0.300</b> | 0.096        | -0.016        | 0.046*   |
| AGDB     | -0.099        | -0.018        | -0.035       | 0.199         | 0.210         | 0.124        | -0.211        | 0.235        | 0.146        | <b>0.456</b> | -0.244        | 0.762    |
| HI       | -0.003        | -0.014        | 0.006        | 0.048         | 0.065         | 0.021        | -0.075        | 0.001        | 0.008        | 0.085        | <b>-0.158</b> | -0.016*  |

DF=Days to 50% flowering, DM=Days to 90% maturity, PB=Primary branches per plant, SB=Secondary branches per plant, PH=Plant height, PPP= pods per plant, SPP=Seeds per pods, YPP=seed yield per plant, SYPP=Seed yield per plot, HSW=100 Seed weight, AGDB= above ground dry biomass, HI=Harvest index.  $v_p$ =phenotypic correlation coefficient,  $r_p$ =residual effect at phenotypic level.

#### 4.4.3.2. Genotypic path coefficient

The genotypic direct and indirect effect of different traits on seed yield is presented in Table 8. Primary branches showed positive and higher phenotypic direct effect on seed yield per plot showed also highest positive genotypic direct effect on seed yield per plot. It had positive indirect effect on seed yield per plot through days to flowering, days to maturity, secondary branches, plant height, pod per plant, seeds per pod. However it showed negative indirect effect on seed yield per plot through, seed yield per plant, hundred seed weight, above ground dry biomass and harvest index. Pods per plant showed positive indirect effect on seed yield through harvest index and hundred seed weight, while with others showed negative indirect effect on seed yield per plot. Seeds per pod showed positive indirect effect on seed yield through primary secondary branches, plant height, hundred seed weight and harvest index, showed negative indirect effect on seed yield through days to flowering, days to maturity, and plant height. Seed yield per plant showed positive indirect effect on seed yield through days to flowering, primary branches, seeds per pod and harvest index. Hundred seed weight showed positive indirect effect on seed yield through secondary branches, plant height, and seed yield per plant and above ground dry biomass. Above ground dry biomass showed positive indirect effect on seed yield through secondary branches, plant height, pod per plant, and number of seed per plant, and hundred seed weight and above ground dry biomass. Harvest index showed positive indirect effect on seed yield through primary branches, secondary branches, plant height, pods per plant, seed yield per plant, hundred seed weight, and above ground dry biomass (Singh, 2001) who reported .Similar results.

Generally it was observed that various traits of common bean such, primary branches, above ground dry biomass, days to flowering, days to maturity, and others which exerts positive direct and indirect influence on seed yield are important to improve seed yield of common bean for the future breeding programs.

**Table 8. Estimation of direct (bold diagonal) and indirect effects (off diagonal) of eleven traits on seed yield at genotypic level in common bean genotypes.**

| Variabl | DF           | DM           | PB           | SB            | PH            | PPP           | SPP           | YPP           | HSW          | AGDB         | HI            | Rg       |
|---------|--------------|--------------|--------------|---------------|---------------|---------------|---------------|---------------|--------------|--------------|---------------|----------|
| e       |              |              |              |               |               |               |               |               |              |              |               |          |
| DF      | <b>0.129</b> | 0.028        | 0.047        | 0.013         | 0.012         | 0.011         | 0.043         | -0.016        | -0.045       | -0.028       | 0.003         | 0.197**  |
| DM      | 0.012        | <b>0.055</b> | 0.004        | 0.009         | 0.005         | 0.005         | 0.015         | 0.004         | -0.007       | -0.002       | 0.005         | 0.105    |
| PB      | 0.199        | 0.038        | <b>0.545</b> | 0.096         | 0.111         | 0.192         | 0.183         | -0.039        | -0.294       | -0.041       | -0.021        | 0.969    |
| SB      | -0.017       | -0.029       | -0.030       | <b>-0.171</b> | -0.086        | -0.044        | 0.023         | -0.057        | -0.013       | -0.074       | 0.052         | -0.446   |
| PH      | -0.037       | -0.038       | -0.084       | -0.208        | <b>-0.412</b> | -0.021        | 0.057         | -0.119        | -0.082       | -0.189       | 0.168         | -0.965   |
| PPP     | -0.007       | -0.007       | -0.029       | -0.021        | -0.004        | <b>-0.083</b> | -0.012        | -0.023        | 0.025        | -0.023       | 0.011         | -0.173** |
| SPP     | -0.025       | -0.020       | -0.025       | 0.010         | 0.010         | -0.011        | <b>-0.075</b> | 0.026         | 0.044        | 0.035        | -0.036        | -0.067** |
| YPP     | 0.002        | -0.001       | 0.001        | -0.004        | -0.004        | -0.004        | 0.005         | <b>-0.013</b> | -0.007       | -0.007       | 0.000         | -0.032*  |
| HSW     | -0.015       | -0.005       | -0.024       | 0.003         | 0.009         | -0.013        | -0.026        | 0.022         | <b>0.045</b> | 0.014        | -0.002        | 0.008**  |
| AGDB    | -0.058       | -0.011       | -0.020       | 0.116         | 0.123         | 0.072         | -0.123        | 0.137         | 0.085        | <b>0.266</b> | -0.142        | 0.445    |
| HI      | -0.002       | -0.010       | 0.004        | 0.034         | 0.046         | 0.015         | -0.053        | 0.001         | 0.006        | 0.059        | <b>-0.111</b> | -0.011   |

\*,\*\* indicate significance at the 5% and 1% probability levels, relatively

DF=Days to flowering, DM=Days to maturity, PB=Primary branches per plant, SB=Secondary branches per plant, PH=Plant height, PPP=pods per plant, SPP=Seeds per pod, YPP=Seed yield per plant, SYPP=Seed yield per plot, HSW=hundred Seed weight, AGDB= above ground dry biomass, HI=Harvest index,  $r_g$ =genotypic correlation coefficient,  $r_g$ =residual effect at genotypic level

## 5. SUMMARY, CONCLUSION AND RECOMMENDATIONS

### 5.1. Summary and Conclusion

Field experiments were conducted at Ziway farmers field, 24 common bean genotypes were evaluated in 2016 main crop season ( June to October) to estimate the magnitude of variability and association among yield and yield related traits.

In this study area more attention should be given to plants like, genotype ROBA (6.02) for maximum seeds per pod. MELKE for maximum seed yield per plant (37.575g), genotype ARGANE for maximum seed yield per plot with values of (832g), GOFTA for pods per plant (24.3) and for above ground dry biomass (8636.66), genotype BRAZIL-1 for harvest index (0.313) and the genotype BATU for the shortest days to flower (42).

The highest mean square had observed for above ground dry biomass (7070772.1) followed by Seed yield per plot (44348.43), plant height, hundred seed weight (288.87), seed yield per plant (123), days to flowering (80.12), days to maturity (72.75), secondary branches (68.69), and the least square value had observed by pods per plant (34.630), primary branches (15.96), seeds per pods (1.325), and the harvest index (0.00378). Mean square showed that highly significant variation among all the 24 genotypes for all the traits investigated except DM and PPP.

High genotypic coefficients of variations (GCV) were observed for plant height (39.57),harvest index (31.82), hundred seed weight (31.45)., hundred seed weight (31.45), secondary branches (27.83) while Moderate genotypic coefficients of variations (GCV) were observed for primary branches (23.57), above ground dry biomass (22.73), seed yield per plot (20.35), seed yield per plant (14.80) , pods per plant (14.28), seeds per pod (13.55), While low genotypic coefficients of variations (GCV) were observed for days to flowering (9.97), and days to maturity.

High phenotypic coefficients of variations (PCV) were observed for seed yield per plot, plant height (43.1), harvest index (39.77), hundred seed weight (32.3), secondary branches per plant (31.1), above ground dry biomass (29.1), seed yield per plant (28.1) while Moderate phenotypic coefficients of variations (PCV) were observed for, primary branches (25.1), and pods per plant (22.0), Low phenotypic coefficients of variations were

observed with harvest index, and seeds per plant (15.9), and days to flowering (12.6), and days to maturity (9.02).

Days to flowering, primary branches, Secondary branches, seeds per pod, Plant height, harvest index, seed yield per plot, hundred seed weight and above ground dry biomass. showed high heritability estimates pods per plant, showed moderate heritability estimate while seed yield per plant, and days to maturity showed low heritability estimates.

Seed yield per plot had positive highly significant correlation with harvest index. Seed yield per plant had positive and highly significant correlation with primary branches, pods per plant, seeds per pod, and had negative and highly significant correlation with hundred seed weight showed, estimation of correlation coefficient at phenotypic level.

The magnitudes of genotypic correlation were higher as compared to their corresponding phenotypic correlations. Genotypic and phenotypic associations were in same direction and the genotypic estimates were higher than the phenotypic ones, indicating an inherited association between the characters.

. Above ground dry biomass (0.456) exhibited the highest phenotypic positive direct effect on seed yield and the second and third highest positive direct effect on seed yield were exhibited by hundred seed weight (.300) and primary branches (0.226) respectively.

It was observed that various traits of common bean such, primary branches,, above ground dry biomass, days to flowering, days to maturity, and others which exerts positive direct and indirect influence on seed yield are important to improve seed yield of common bean for the future breeding programs.

## 5.2. Recommendation

- It is recommended that the experiment have to be repeated for several consecutive years and in more different agro-climatic zones in order to get concrete and full information about the plant.
- Further studies on common bean genotypes with large sample size to get consolidated information that is essential in breeding programs.

## 6. REFERENCES

- ADA (American Dietetic Association). 2004. Position of the American Dietetic Association and dietitians of Canada: nutrition intervention in care of persons with human immunodeficiency virus infection. *JADA* 104: 1425-1441
- Alemayehu, Teferra, 2015. Investigation into some dynamic properties of soils around Ziway, January, 2015.
- Allard , R.W. 1960. Some parameters of population variability and their implication in plant breeding. In Norman A.G. *Advances in Agronomy*, Academic Press, New. Pp: 281-325.
- Amin, M.R.,Barma, N.C. and Razzaque. 1992. Variability, Heritability, Genetic Advance and correlation Study in some quantitative characters in Duramwheat, *Rachis*, News Letter.11: 30-32
- Babar, M.A.,M.A. Newaz and M.A.H.S. Jahan. 2002.Identification of selection parameters for yield improvement in French bean. *Bangladesh Journal of Agriculture Sciences*. 29: 85-89.
- Berecha Gutu 2015 Genetic Variability and Path Coefficient Analysis for Yield and Yield related Traits in Commons Bean (*Phaseolus vulgaris* L.) Accessions at Haramaya University, Haramaya..
- Broughton WJ, Hernandez G, Blair M, Beebe S, Gepts P, Vanderleyden J. 2003. Beans (*Phaseolus spp.*) –model food legumes. *Plant and Soil* 252:55-128.
- Burton, G.W.and Devane C.H. 1953. Estimating heritability in tall fescue (*Festucaarundinacea*) from replicated clonal material. *Agron. J.*, 45 : 478-481.
- Buys H, Hendricks M, Eley B, Hussey G .2002.The role of nutrition and micronutrientsin pediatric HIV infrection.*SADJ*57:454-456
- Central Statistics Authority (CSA). 2011. Agricultural Sample Survey 2010/11. Report on Area and Production of Crops (Privat3 Peasant Holdings, “Meher” Season), Vol. IV *Statistical Bulletin* 446, Addis Ababa: May, 2011. 1-82.
- Costa, J.G.C., Melo LC, Pereira ES, Del Peloso. MJ, Faria LC, DíazJLC, Wendland A and RavaCA .,2011.BRSE splendor Common bean cultivar with black grain, upright growth and disease resistance. *Crop Breeding and AppliedBiotechnology*11: 276-27..
- Debouck,D.G.and Hidago. R. 1986. Morphology of the common bean Plant study guide.CIAT.coli, Colombia. 16-25.
- Delgado salimas, A. 1985.Systematic of the genus *Phaseolus* (leguminose), In North and Central America; PhD Thesis. Univ. of Texas, Austin (UMI. No 8527553).
- Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass production. *Agronomy Journal* 51.515-518.

- Dudley, J.W. and Moll, R.H. 1969. Interpretation and use of estimates of heritability and genetic variance in plant breeding. *Crop sci.*, 9: 257-267.
- Dursun, A. 2007. Variability, heritability and correlation studies in bean (*Phaseolus vulgaris* L.) genotypes. *World J. Agrl. Sci.*, 3(1) : 12-16.
- Endashew, B. 1996. Morphological analysis of *Eragrostis tef*: detection for regional patterns of variation. *SINET: Ethiop., J. Sci.* 19:117\_140.
- Falconer, D.S. and Mackey, F.C. 1996. Introduction to Quantitative Genetics. Longman. New York. Pp:464..
- FAO. 1997. Databases. <http://www.fao.org/WAICENT/Agricul.htm>.
- FAO. 2010. *STAT, 2010* Food and Agriculture Organization of the United Nations. Web. <http://faostat.fao.org/default.aspx>. citation key.fao.2010.Data sheets.
- FAO/WHO. 1991. Protein quality evaluation, Food and Agricultural Organization of the United Nations, ROME. *Journal of Agri food chem* 29, 1068\_1074 (1981).
- Fikru, Mekonnen. 2007. Haricot bean (*Phaseolus Vulgaris* L.) variety development in the lowland areas of Wollo. Proceedings of the 2nd Annual Regional Conference on Completed Crops Research Activities 18 - 21 September 2007, Bahir Dar, Ethiopia, pp 86-93.
- Galton, F. 1889. Natural Inheritance, London. *The correlations between relatives on the supposition of Mendelian inheritance*. *Trans. r. Soc. Edinb*, 52:399-433.
- Girma Abebe. 2009. Effect of NP Fertilizer and Moisture Conservation on the Yield and Yield Components of Haricot Bean (*Phaseolus Vulgaris* L.) In the Semi-Arid Zones of the Central Rift Valley in Ethiopia. *Advances in Environmental Biology*, 3: 302-307.
- Gomez, K.A. and Gomez, A.A. Statistical procedures for agricultural research. Second edition. International Rice Research Institute. John Wiley and Sons Inc. 1984: 304 - 308.
- Gravios, K.H. and Helm, R.S. 1992. Path analysis of rice yield and yield components as affected by seed rate. *Agro. journal*. 84: 1-4.
- Griraji, K. And Vijayakumar, S. 1974. Path coefficient analysis of yield attributes in mung bean. *Ind. journal. genet.* 34:27-30.
- Hadiati, S., H.K. Murdaningsih, and Neni Rostini, 2003, 'Parameter of the component character of fruit on some accession of pineapple', *Zuriat*, 14(2) : 53-58
- Hallauer, A.R. and Miranda, 1988. Quantitative Genetics in Maize Breeding. Second edition. Iowa State University Press. Ames, pp:468.
- Hanssen, C..H., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies of yield in segregating populations of Korean lespedeza. *Agron. J.*, 48 : 268-272.

- Jalata, Zerihun., Ayana, Amsalu. and Zeleke, Habtamu. 2011 Variability, Heritability and Genetic Advance for some yield and yield related traits in Ethiopia berley (*Hordeum vulgare L.*). Landraces and crosses. *Int. journal Plant Breeding and Genetic*. 5: 44-52.
- Johnson, H.W., Robinson, H.F. and Comstock, R.G. 1955b. Genotypic and Phenotypic correlation in soybean and their implication in selection. *Argon. Journal*. 47:477-483.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soy beans. *Agronomy Jour*. 47: 314-318.
- Katungi Enid and Setegn Gebeyehu (2011) Enhanced seed accessibility and adoption of improved common bean varieties in Ethiopia: monitoring early adoption of improved varieties –Survey report (in press.)
- Kedir Oshone, Setegn Gebeyehu, Kindie Ttesfaye., 2014 Assessment of Common bean (*Phaseolus vulgaris L.*) Seed quality produced under different cropping systems by small holder farmers in eastern Ethiopia. volume 14 No-1 March 2014.
- Knight, R., 1979, Quantitative genetics, statistics, and plant breeding. In : Halloran, G.M., R.. Knight, K.S. Mc Whirter, and D.H.B. Sparrow. A Course Manual of Plant Breeding Australian Vice-Chancellors Climittee.
- Koppen W., Gelger R. 2011. Climate Ziway-Ethiopia- World climate data. [www climate data eu/climate.php?10c=etzz0030](http://www.climate-data.eu/climate.php?10c=etzz0030) and lang.en.
- Kristin, A., Schneider, R., Rosales, S., Francisco, I., Benito, C., Jorge, A., Acosta-Gallegos, Porfirio., R, Nasrat, W. & James, D.K. 1997. Improving Common Bean Performance under Drought Stress. *Crop Sci.*, 37: 43-50.
- Kruzich LA, Marquis GS, Carriguiry AL, Wilson CM, Stephensen CB., 2004. US youths in the early stages of HIV disease has low intakes of some micronutrients important for optimal immune function. *J Am Diet Assoc* 104: 1095-1101
- Laing, D. R., Jones, P. G. and Davis, H. C. 1984. Common Bean (*Phaseolus vulgaris L.*). *The physiology of tropical field crops*. pp. 305-353. Goldsworthy, P. R. and Fisher, N.M., eds. New York, USA. John Wiley.
- Machado. C.M., Ferruzzi, M.G., Nielsen, S.S. 2008. Impact of the hard-to-cook phenomenon on phenolic antioxidants in dry beans (*Phaseolus vulgaris*). *Journal of Agricultural and Food Chemistry* 56: 3102-3110.
- McClellan, P.E., Myers, J.R. and Hammond, J.J. 1993. Coefficient of parentage and cluster analysis of North American dry bean cultivars. *Crop Sci*. 33:190–197
- Mekibib, F. 1997. Farmer participation in common bean genotype evaluation, the case of Eastern Ethiopia experimental Agriculture, 33: 399- 408.
- Mekonnen., T., W., W., Adugn and G. Tsige, 2014. Correlation and path coefficient analysis Among yield component traits of Ethiopian Masterd (*Brassica carinata a brun*) at Adet, north western, Ethiopia. *Journal of plant sciences*, 2(2): 89-96.

- Mirza, M.Y., kham, M.A., Akmal, M., Mohammed, A.S., Nawaz M.S., Nawaz N. Ullah. 2010. Estimation of Genetic parameters to formulate selection strategy for increased yield in Linseed. *Pak.journal .Agri. Res*, 24:19-24.
- Moore, S. 1963. On the determination of systemic .*Journal Biol .,chem.*. 238; 235—237.of morpho-agronomical and RAPD data.*Scientia Agricola* 64: 256-262.
- Negash R 2007. Determinants of adoption of improved haricot bean production package in Alaba special woreda, southern Ethiopia. MSc Thesis, Haramaya University.
- Panse.V.G. 1957.Genetic of quantitative characters in relation to plant breeding.*Indian J. Genet.*,17 : 318-328.
- Rabia Hamid, Akbar Masood, Ishfak H. Wani, and ShaistaRafiq. 2013. Lectins: Proteinswith Diverse Applications. *J App Pharm Sci.* ;3 (4 Suppl 1): S93-S103
- Raffi, S.A. and Nath, U.K. 2004.Variability, heritability, genetic advance and relationships of yield and yield contributing characters in dry bean (*P. vulgaris* L.).*J. Biol. Sci.*, 4: 157-159.
- Reynoso-Camacho, R, Ramos-Gomez, M and Loarca-Pina, G. Bioactive components in common beans (*Phaseolus vulgaris* L.) Advances in Agricultural and Food Biotechnology, 2006: 217- 236 ISBN: 81-7736-269-0os-
- Rodrigues, LS, Antunes, I.F., Teixeira, M.G. and Silva, J.B. 2002.Divergênciagenética entre cultivars locais e cultivares melhoradasdfeijão.PesquisaAgropecuáriaBrasileira
- Rossi, S.,Hallett, M., Rossini, P.M.,Pascualleon, A. 2009. *Linkage disequilibrium and population structure in wild and domesticated populations of Phaseolus vulgaris L. EvolAppl* 2:504–522.
- Safari, A. 1978.A yield component selection experiment involving American and Iranian cultivars of common bean. *Crop Sci.* 18: 5-7.
- SAS, 2008 . Description how to configure L.SI , SAS2 based controllers by using L. SI software tools.
- Singh SP, Gepts P and Debouck DG (1991) Races of common bean (*Phaseolus vulgaris*, Fabaceae). *Economic Botany*45: 379-396.
- Singh, S. P. 1991. Breeding for seed yield. Common beans.Research for crop improvement.pp.383-429.van Schoonhoven, A.and Voysest, O., eds.CAB International inassociation with Centro Internacional de Agricultura Tropical (CIAT), Cali, Colombia.
- Singh, S.P. 2001. Broadening the genetic base of common bean cultivars: a review.*Crop Science* 41: 1659-1675.
- Singh, S.P., Gepts, P. and Debouck, D.G. 1991a. Races of common bean (*Phaseolus vulgaris*, Fabaceae). *Economic Botany* 45: 379–396.

- Singh, S.P., Gutiérrez, J.A., Molina, A., Urrea, C. and Gepts, P. 1991b. Genetic diversity in cultivated common bean. II. Marker-based analysis of morphological and agronomic traits. *Crop Sci.* 31:23-31
- Singh, S.P., P. Gepts, and D.G. Debouck. 1991. Races of common bean (*Phaseolus vulgaris*, Fabaceae). *Econ. Bot.* 45:379–396
- Syed.Mudasir1,\*PA.Sofi1,MNKhan2,NRSofi3andZADar(2012),Geneticdiversityvariability and character association in local common Bean (*Phaseolus vulgaris*L.) germplasm of Kashmir. *Electronic Journal of Plant Breeding*, 3(3):883-891 ISSN 0975-928X <http://sites.google.com/site/ejplantbreeding>.
- Teshale, Assefa, Girma, Abebe, Chemed, Fininsa, Bulti, Tessema & Abdel-Rahman M. Al-Tawaha. 2005. Participatory Bean Breeding with Women and Small Holder Farmers in Eastern Ethiopia. *World Journal of Agricultural Sciences*, 1: 28-35.
- United States Department of Agriculture, Agricultural Research Service. 2012. USDA National Nutrient Database for Standard Reference, Release 25. Nutrient Data Laboratory Home Page. Available from: [www.ars.usda.gov/ba/bhnrc/nd](http://www.ars.usda.gov/ba/bhnrc/nd) University of Bonn, Center of Development Research.
- Wong JH, Zhang XQ, Wang HX, Ng TB., 2006. A mitogenic defense from white cloud bean (*Phaseolus vulgaris*). *Peptides* 27, 2075-2081.
- Zelalem.Zewdu.2013.Evaluation of agronomic traits of different haricot bean (*Phaseolus Vulgaris* L.) Pawa Agricultural Research Center P.Box-25, Ethiopia. E-mail: [zelalemzewdu19@gmail.com](mailto:zelalemzewdu19@gmail.com). Accepted 11 December.

## 7. APPENDIX

Appendix Table 1. Mean, CV and LSD % of 12 characters of 24 common bean genotypes used in the study

| Genotypes          | DF    | DM    | PB    | SB    | PH    | PPP   | SPP  | YPP    | SYPP   | HSW   | AGDB    | HI    |
|--------------------|-------|-------|-------|-------|-------|-------|------|--------|--------|-------|---------|-------|
| KAT-B <sub>9</sub> | 44.66 | 65.66 | 10.26 | 12.8  | 32    | 20.65 | 3.83 | 27.605 | 757.33 | 35.96 | 7678.33 | 0.1   |
| KAT-B1             | 48.33 | 65.66 | 11.26 | 15.16 | 46.93 | 20.6  | 3.84 | 30.087 | 501.86 | 32.98 | 6112    | 0.08  |
| NASIR              | 47.33 | 75.33 | 8     | 14.7  | 59.63 | 18.18 | 5.22 | 18.325 | 490.66 | 19.33 | 6271.33 | 0.08  |
| ARGANE             | 49.66 | 75.66 | 10.93 | 14.06 | 35.8  | 21.33 | 5.36 | 23.455 | 832    | 20.33 | 4033.66 | 0.206 |
| AWASH MELCA        | 60.33 | 87    | 11.73 | 17.66 | 35.86 | 21.5  | 5.69 | 26.275 | 480    | 22.66 | 3999.33 | 0.123 |
| MELKE              | 43.66 | 79.33 | 6.53  | 16.8  | 55.53 | 21.6  | 4.61 | 37.575 | 608    | 39.66 | 7805.66 | 0.1   |
| ROBA               | 54.33 | 78.33 | 11.33 | 17.86 | 37.86 | 21.2  | 6.02 | 19.712 | 597.33 | 15.61 | 4846.66 | 0.126 |
| BATU               | 42    | 73    | 4     | 22.06 | 32.4  | 19.7  | 3.7  | 28.408 | 384    | 34.82 | 8566.66 | 0.04  |
| AWASH-1            | 47    | 77    | 10.63 | 13.23 | 32.93 | 18.73 | 5.45 | 17.354 | 608    | 15.94 | 4176.66 | 0.143 |
| AWSH-2             | 45.33 | 72.33 | 11.33 | 13.86 | 37.2  | 18.47 | 5.41 | 18.501 | 608    | 18.78 | 4339    | 0.14  |
| GOFTA              | 43.33 | 74.66 | 12    | 18.53 | 84.46 | 24.27 | 4.52 | 27.53  | 448    | 24    | 8636.66 | 0.063 |
| BRAZIL-1           | 42.66 | 76    | 6.8   | 16.8  | 44.53 | 18.8  | 4.78 | 36.293 | 291.41 | 47.78 | 6458.66 | 0.313 |
| DEME               | 54    | 75    | 8.53  | 18.6  | 97.6  | 15.46 | 4.34 | 29.62  | 480    | 43.37 | 7551.33 | 0.06  |
| SAB-736            | 42.66 | 74.33 | 10    | 12.6  | 35    | 23.33 | 4.29 | 32.089 | 533.33 | 32    | 5966    | 0.09  |
| LEHODE             | 44.33 | 79.33 | 12.66 | 34.8  | 94.53 | 22.26 | 4.27 | 33.88  | 595.2  | 35.72 | 8613.33 | 0.07  |
| MELKEDIMA          | 45.33 | 79.66 | 6.26  | 12.93 | 38.86 | 16.4  | 4.1  | 23.975 | 593.49 | 36.21 | 5338    | 0.11  |
| CHERCHER           | 55    | 73.66 | 10.6  | 19.73 | 35.06 | 23.6  | 4.48 | 21.763 | 682.66 | 21    | 5767.66 | 0.116 |
| SAB-632            | 42    | 73.66 | 8     | 11.57 | 33.13 | 12.47 | 4.9  | 23.122 | 608    | 47.87 | 4748.33 | 0.13  |
| DRK                | 42.33 | 69.33 | 6     | 12.4  | 40.6  | 11.4  | 3.99 | 14.273 | 416    | 42.66 | 3665.66 | 0.113 |
| SER-119            | 43.66 | 77    | 11.6  | 12.93 | 39.6  | 21.73 | 4.7  | 23.593 | 640    | 23    | 7278.66 | 0.09  |
| ECAB-0056          | 44    | 77    | 6.93  | 16.8  | 46.46 | 20.4  | 3.71 | 33.031 | 661.33 | 43    | 8054.66 | 0.083 |
| SER-125            | 46.66 | 75    | 8.66  | 13.33 | 39.37 | 17.2  | 4.94 | 22.185 | 650.66 | 25.66 | 5040    | 0.126 |

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|           |       |       |       |       |       |       |      |        |        |       |         |       |
|-----------|-------|-------|-------|-------|-------|-------|------|--------|--------|-------|---------|-------|
| GLP-2     | 47    | 75    | 10    | 18.86 | 57.73 | 22.53 | 3.95 | 36.252 | 674.13 | 41.01 | 7272    | 0.103 |
| ECAB-0081 | 55.66 | 78    | 11.86 | 17.6  | 72.86 | 17.66 | 4.7  | 26.786 | 650.66 | 32.21 | 6733.33 | 0.106 |
| MEAN      | 42.22 | 75.84 | 9.57  | 16.50 | 48.93 | 19.71 | 4.61 | 26.333 | 574.67 | 30.88 | 6131.40 | .102  |
| CV        | 7.811 | 7.674 | 8.67  | 14.07 | 17.11 | 16.75 | 8.52 | 23.886 | 9.98   | 7.74  | 18.211  | 23.85 |
| LSD%      | 6.06  | 9.56  | 1.36  | 3.81  | 13.76 | 5.42  | 0.64 | 3.425  | 94.29  | 3.93  | 1835.2  | .0402 |

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Appendix Table 2. : Image of flowering and matured plan



1. The plant when starting to flower



2. The plant at 90% maturity